

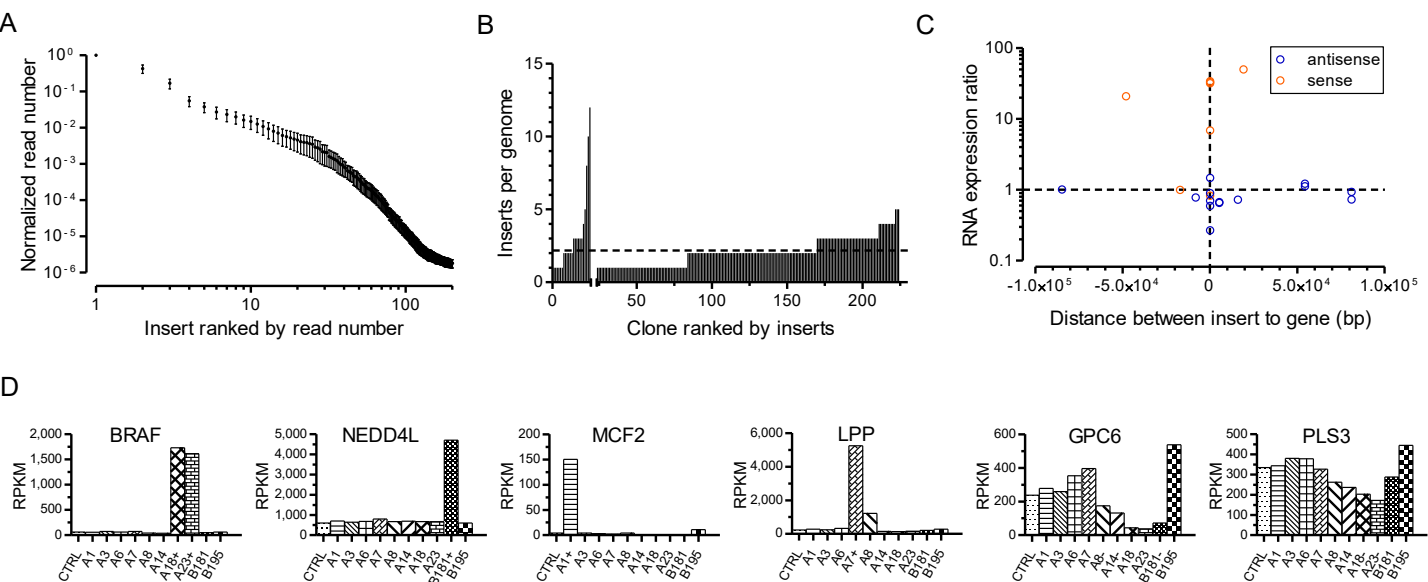


Figure S1. Characterization of transposon inserts.

(A) Distribution of sequencing read signal associated with top 100 insertion sites across ten resistant pools. x-axis, inserts ranked in each pool by read number; y-axis, read number normalized to the most abundant reads of each pool. Error bars denote standard error of mean.

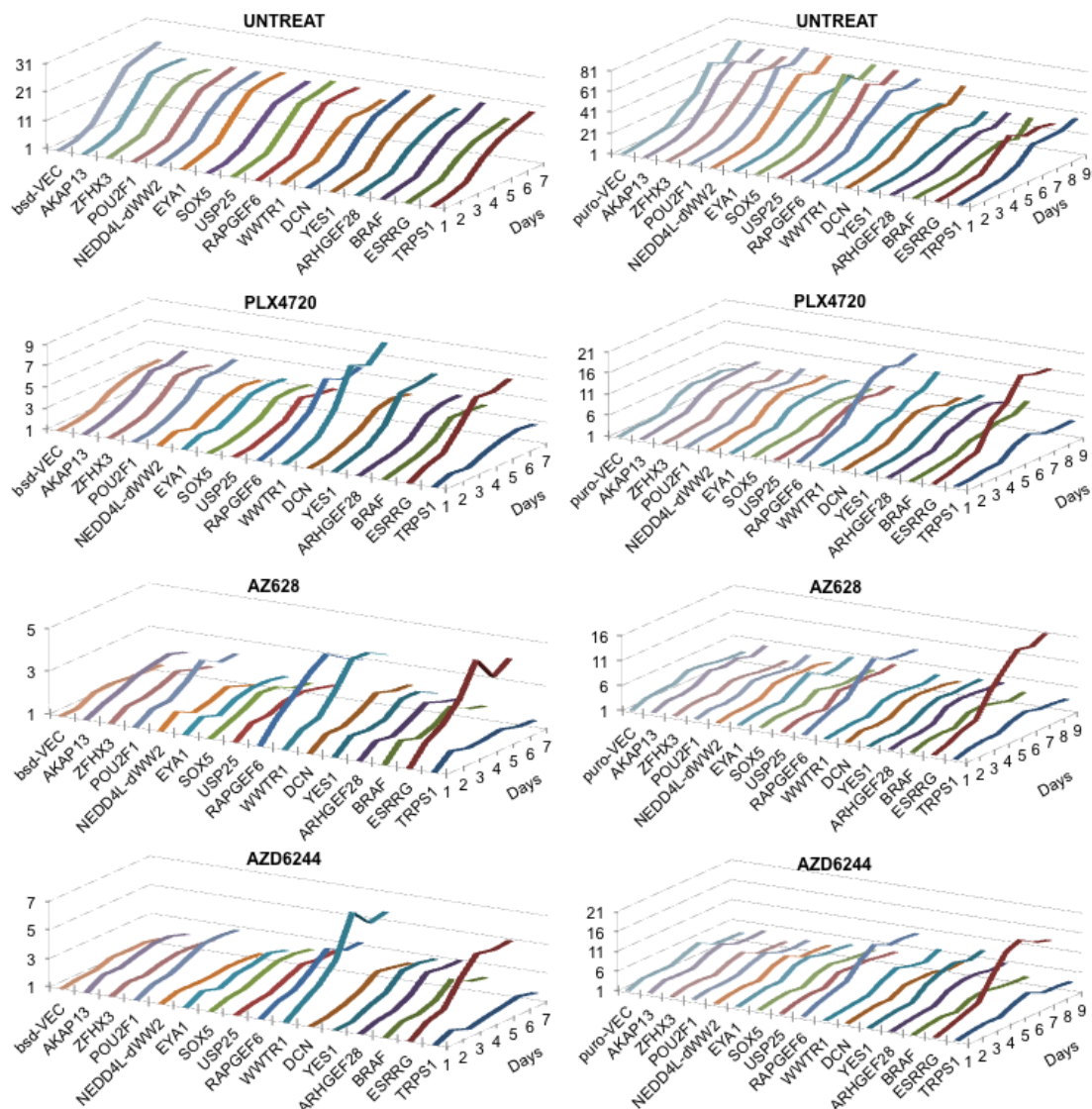
(B) Number of inserts per clone. The dash line indicates the mean. Primary and limiting-dilution clones are separated by a gap in the x-axis.

(C) Gene expression relative to insertion position. Expression is affected by distance (x axis) and direction (sense or antisense) of PB inserts to the gene body. Negative distance values indicate inserts are upstream of the gene while positive values for downstream, and zero for intragenic inserts.

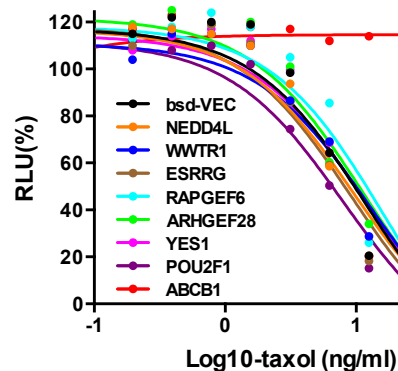
(D) Gene expression detected by RNA-seq in ten clones and a control sample (CTRL). Clones with the corresponding gene perturbed by transposon are labeled with a "+" for activation or "-" for disruption. RPKM, reads per kilobase million.

A

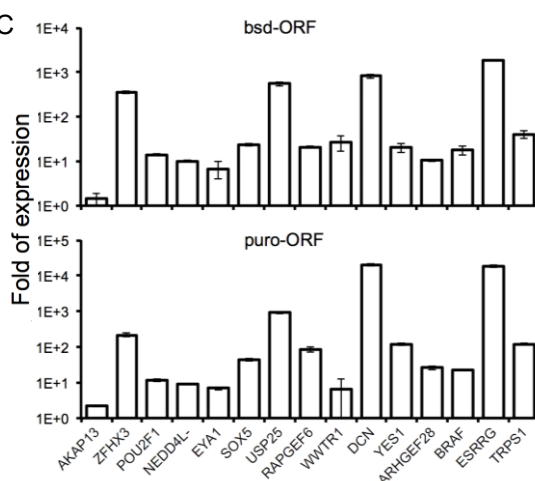
Fold from Day-0



B



C



D

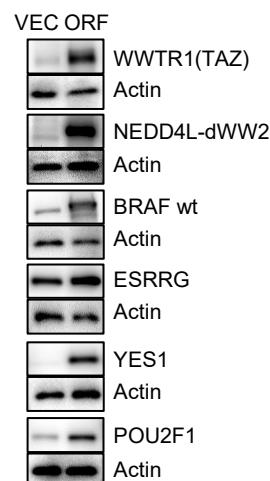


Figure S2, Effect of candidate resistance genes on proliferation evaluated by cDNA overexpression.

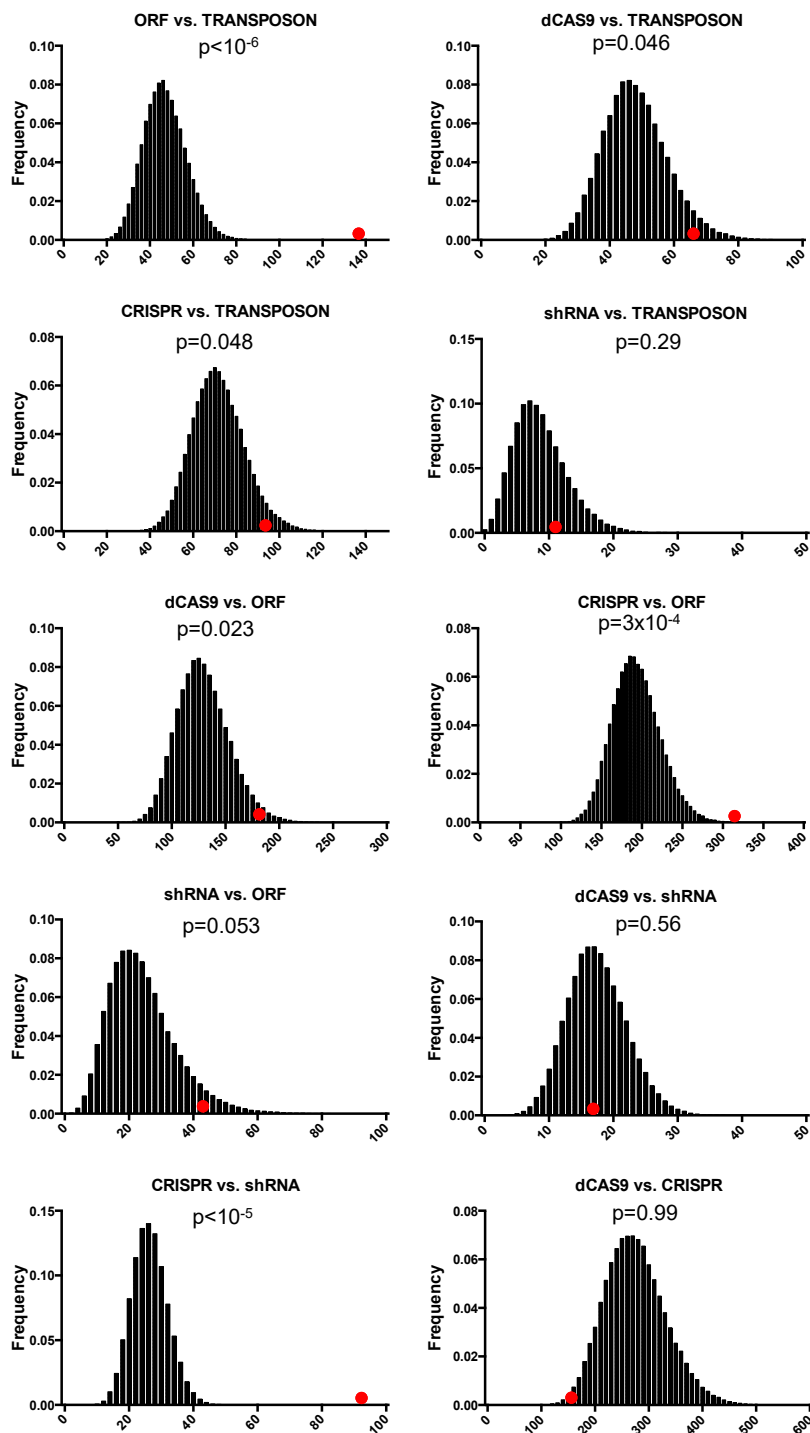
(A) Proliferation of A375 cells infected with lentiviral cDNA constructs across 7 or 9 days. Cells were either untreated, or treated with PLX4720, AZ628, or AZD6244 and normalized to Day-0. Each cDNA construct was subcloned into two lentivirus vectors (bsd-ORF and puro-ORF) for independent experiments.

(B) Dose responses of cells to paclitaxel (taxol). The taxol resistance gene ABCB1 was used as a control.

(C) Quantitative PCR for the indicated genes normalized to vector control cells. Error bars denote SEM, n=3. NEDD4L-dWW2 or NEDD4L- represents a WW2-domain-deletion isoform.

(D) Western blots of blasticidin vector (VEC) or ORF overexpression (ORF) proteins.

A



B

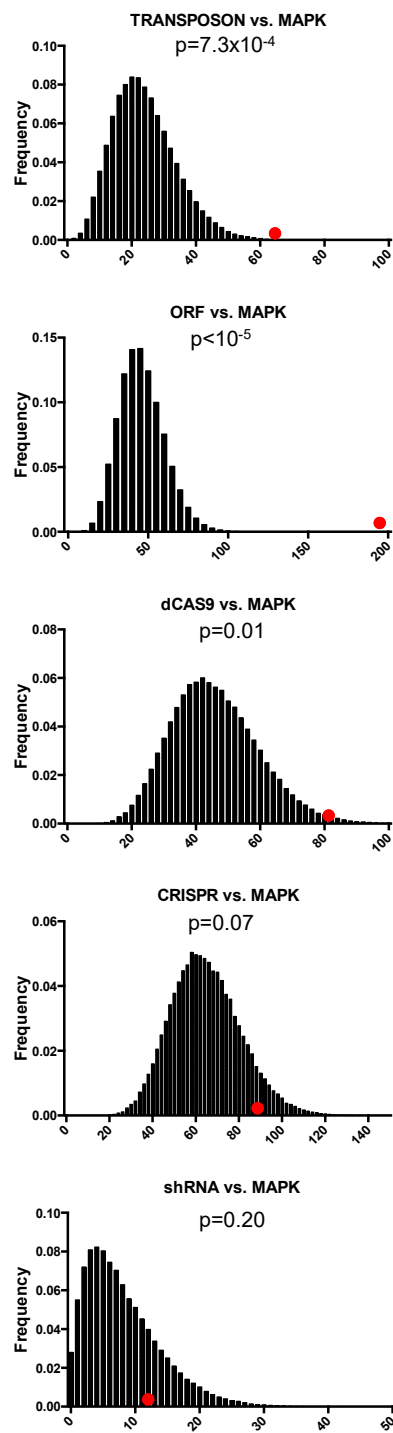
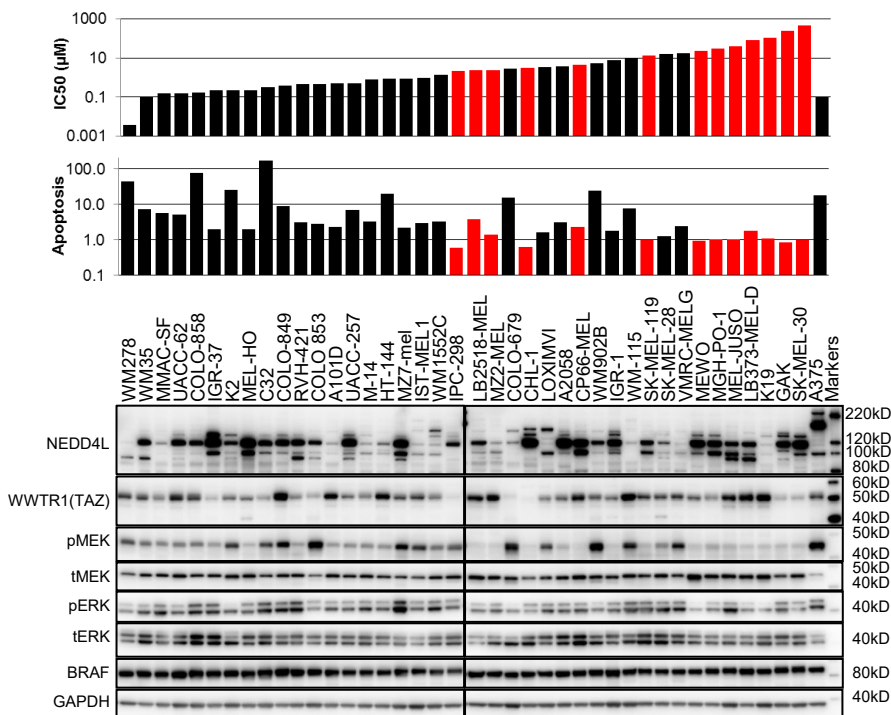


Figure Statistical test for gene list connectivity based on STRING across multiple screens.

(A) Distributions of STRING connections between genetic screens using genes across 10^6 (for ORF vs. TRANSPOSON) or 10^5 (for others) random picks from corresponding backgrounds. Red dots indicate the observed number of connections between two genesets.

(B) Distributions of STRING connections between transposon and MAPK components.

A



B

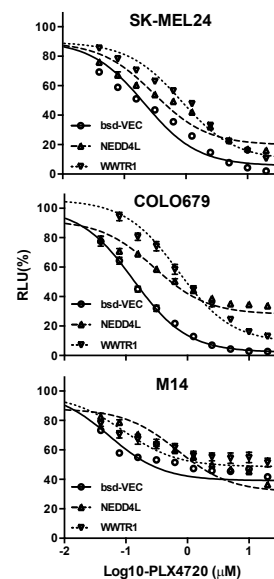


Figure S4. TAZ and NEDD4L protein expression versus sensitivity in melanoma cell lines.

(A) NEDD4L and TAZ (WWTR1) expression and MAPK signaling across melanoma cell lines. Expression of the indicated proteins by western blot performed across lysates of melanoma cells lines. Lysates were loaded from left to right according to sensitivity to PLX4720 in two gels processed in the same experiment. The corresponding IC₅₀s measured by CellTiter-Glo and apoptosis induction determined using Caspase-Glo normalized to total cell number are shown in the top and middle histograms. BRAF V600E or V600D mutants are denoted as black columns while BRAF wildtypes are in red.

(B) PLX4720 dose response of different melanoma cell lines with NEDD4L or WWTR1 lentiviral overexpression. Error bars denote SEM, n=4.

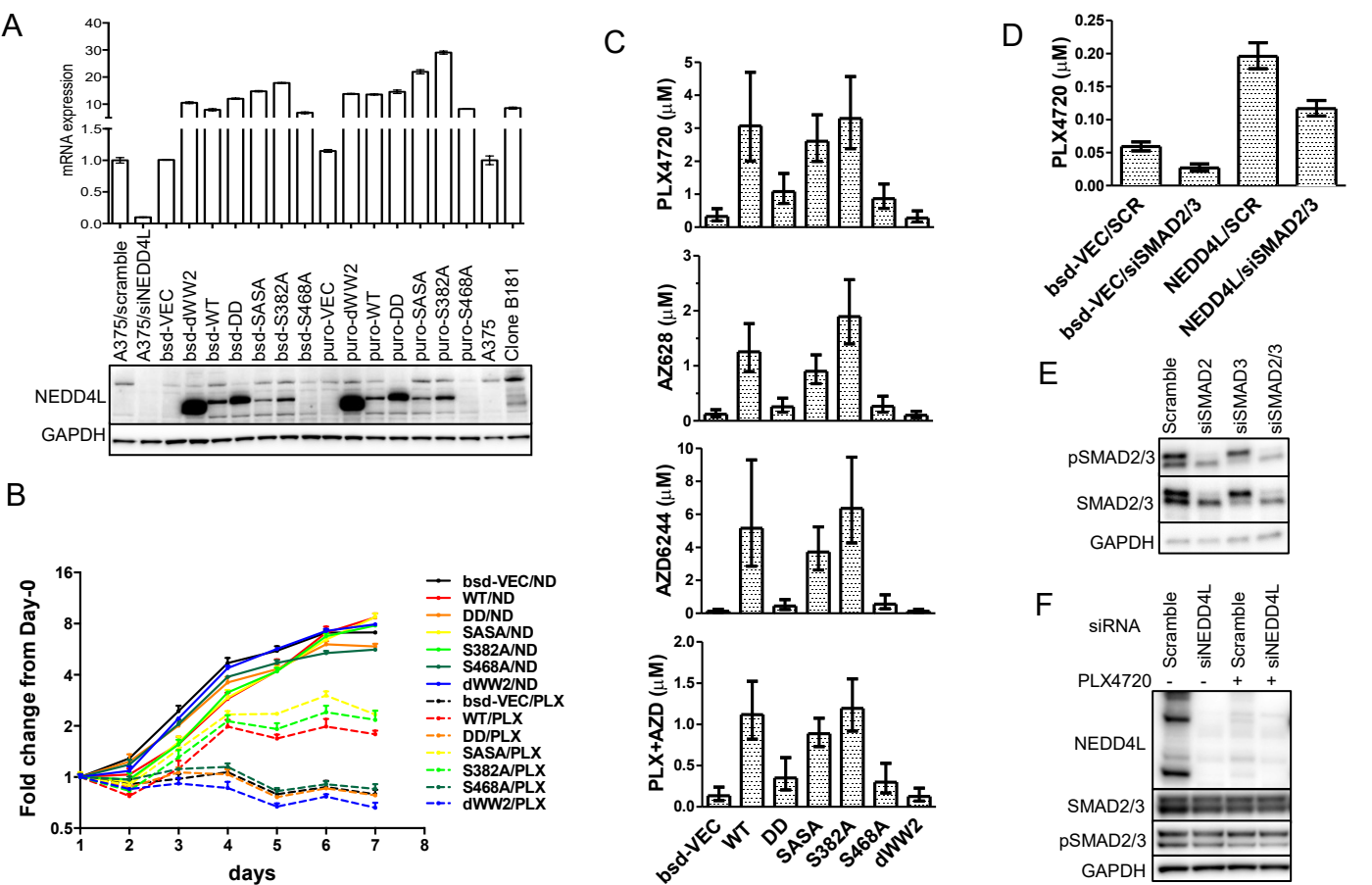


Figure S5. NEDD4L mutation activities.

(A) NEDD4L mutants expressed in two sets of vectors (bsd- and puro-). mRNA levels are shown as column graph on the top (mean $\pm$ SEM, $n=2$), and proteins are shown at the bottom. A transposon clone (B181) with insert in *NEDD4L* gene is also included in the assay.

(B) Proliferation of mutants either in the absence of drug (ND, solid lines) or presence of 0.5 μ M PLX4720 (PLX, dash lines). Error bars denote SEM, $n=3$.

(C) IC₅₀ of NEDD4L-mutant-expressing A375 cell lines treated with PLX4720, AZ628, AZD6244, and combination of PLX4720 and AZD6244. In the combinatorial treatment, PLX4720 and AZD6244 concentrations were fixed at 5:1 and the y-axis indicated PLX4720 concentrations. Error bars denote 95% CI.

(D) IC₅₀ of PLX4720 of vector control and *NEDD4L*-overexpressing cells with *SMAD2/3* knockdown. Values are shown as mean $\pm$ 95% CI, $n=3$.

(E) *SMAD2/3* knockdown reduces both phospho- and total *SMAD2/3*.

(F) *NEDD4L* knockdown does not increase total or phospho-*SMAD2/3*.

A

Patient	#7	#12	#25	#2	#6	#13	#24	#19	#34	#9	#22	#16	#15	#10
RECIST (shrink%)	100	89	64	61	60	58	53	49	49	45	42	20	17	13
PFS (month)	17	12	3	9	21	9	2	17	15	7	3	11	6	3

B

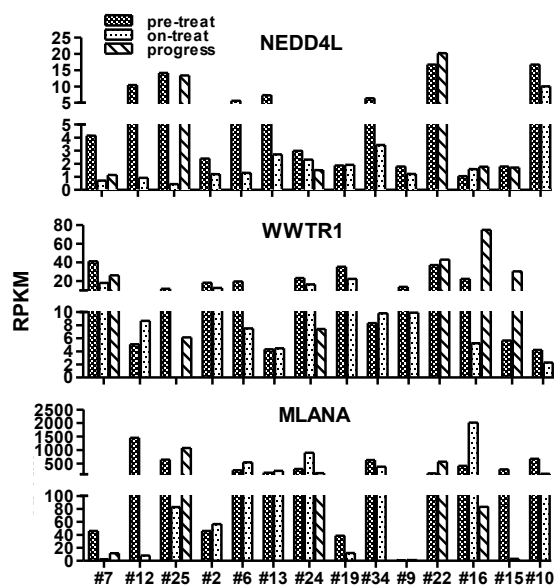


Figure S6. *WWTR1* and *NEDD4L* expression versus treatment outcome.

(A) Response Evaluation Criteria In Solid Tumor (RECIST) and Progression Free Survival (PFS) are indicated for each patient. (B) *NEDD4L*, *WWTR1*, and a melanoma biomarker *MLANA* mRNA expression in patient samples sorted by RECIST scores. Y-values indicated reads per kilobase million (RPKM) of RNA-Seq.

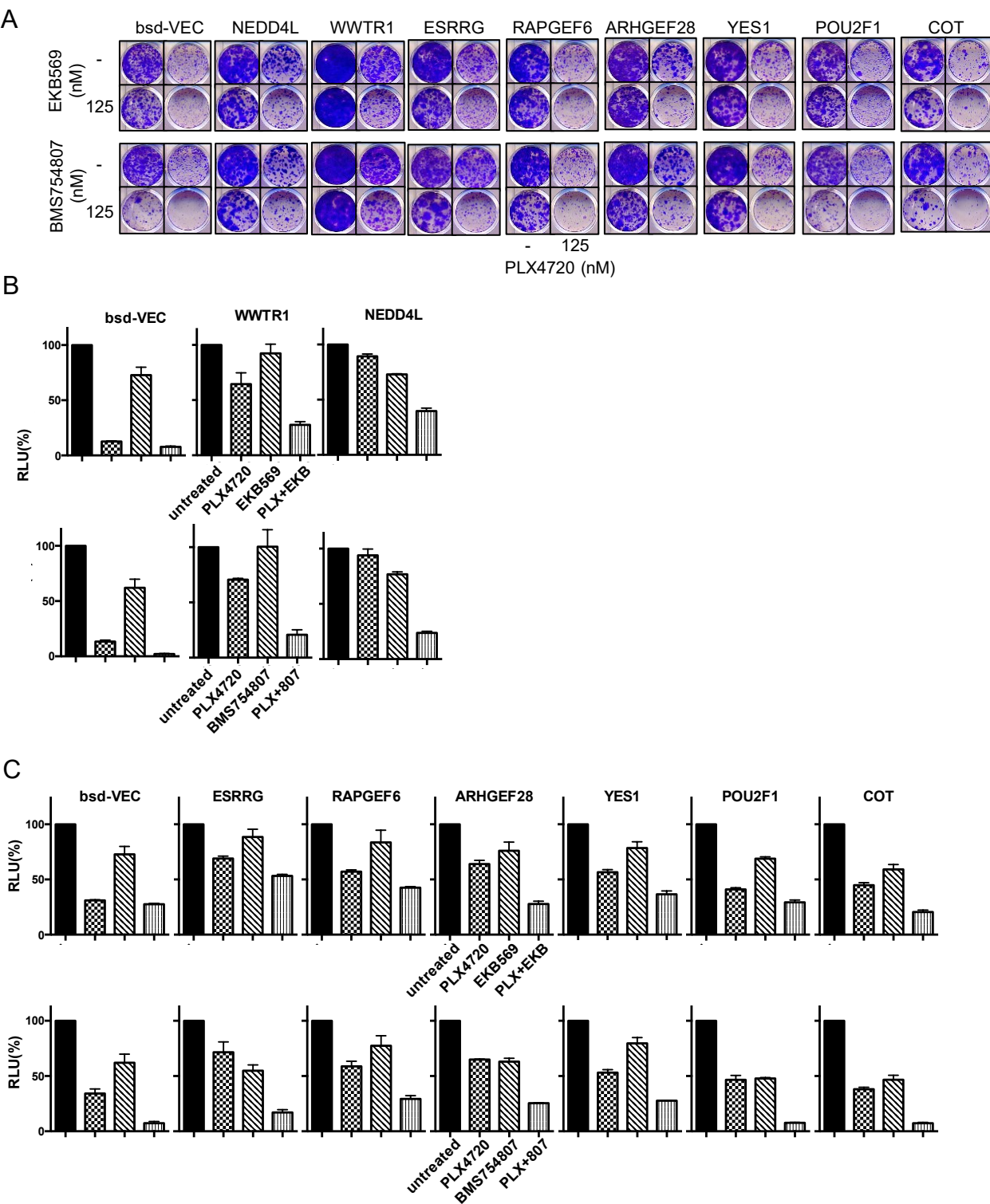


Figure S7. EGFR and IGF1R inhibitions broadly resensitize resistant cells.

(A) Resensitization measured by clonogenic assays after 12-day drug treatments.

(B) And (C) Responsiveness of resistance-gene-overexpressing A375 cells to 150nM PLX4720, 250nM EKB569, 250nM BMS754807, or combinations, in 5-day viability assays measured by CellTiter-Glo. Bars denote mean $\pm$ SEM, n=3. Note the two panels were prepared from different experiments and the baselines should only be compared within each panel.

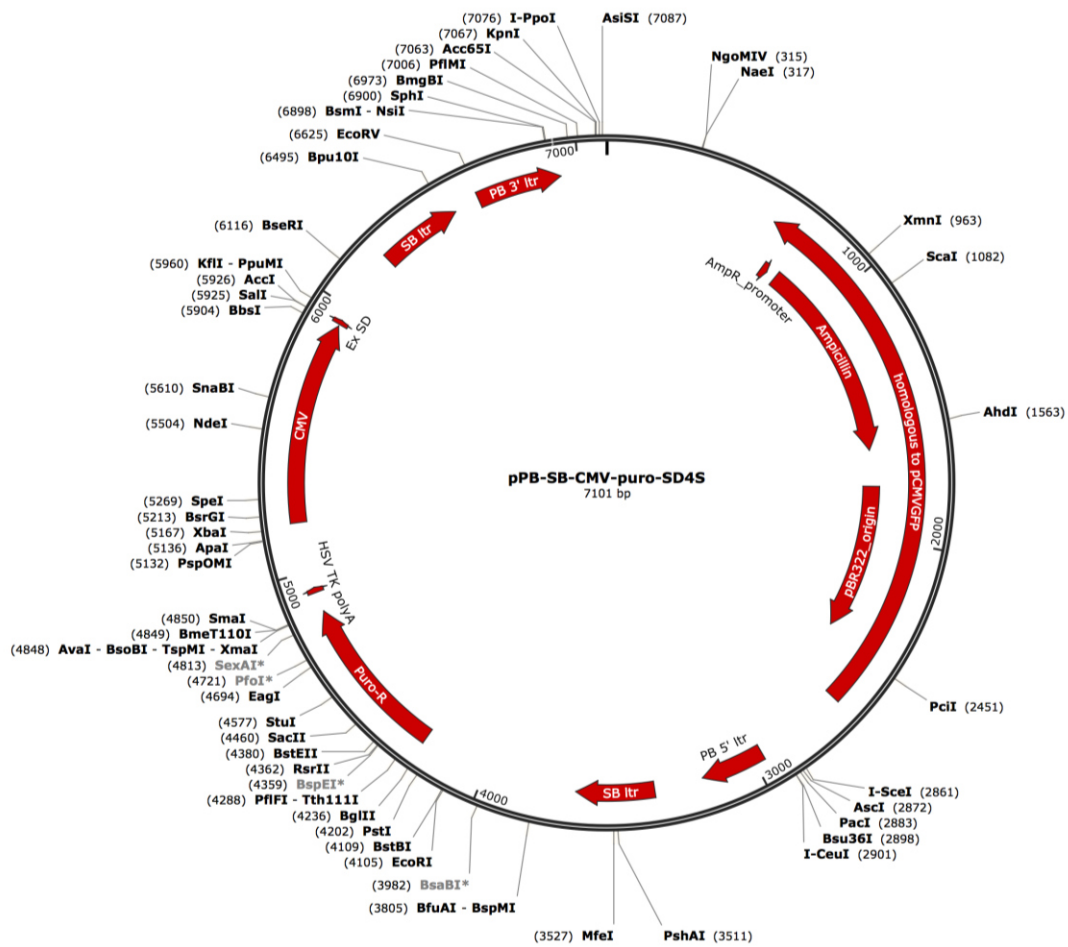


Figure S8. Plasmid map of a PB-SB dual-LTR plasmid.
Full sequence can be found in the Supplementary Text. Plasmid map is drawn using SnapGene.

Table S1. Gene annotation of top 100 inserts in each resistant pools.

Genes identified by the transposon screens were listed with gene name, location of the strongest insert, read number normalized to total reads, number of insert sites, number of insert events, and predicted effect on gene expression. Insert events refer to either hits in more than one resistant pool or multiple sites within a pool. High confidence hits are shaded. Activated genes predicted from insert orientation and proximity were marked with a "+".

Gene	position	normalized read number	insert sites	insert events	effect prediction
NEDD4L	chr18:55950431	0.124757854	20	32	+
EYA1	chr8:72248874	0.089242154	5	11	+
POU2F1	chr1:167276097	0.001102743	9	9	+
BRAF	chr7:140483217	0.068029828	3	8	+
ZFHX3	chr16:73044366	0.01682473	4	7	+
TRPS1	chr8:116654858	0.010065441	4	7	+
ZFHX4	chr8:77680504	0.004624953	6	7	+
RAPGEF2	chr4:160201207	0.001658968	5	7	+
ARHGEF28	chr5:73387835	0.061110225	4	6	+
VAV1	chr19:6781988	0.050608724	3	6	+
PLS3	chrX:115045927	0.053414439	2	5	
GPC6	chr13:94958370	0.041735035	4	5	
WWTR1	chr3:149386508	0.002125591	3	5	+
RAPGEF6	chr5:130954965	0.000865833	4	5	+
AKAP13	chr15:86140331	0.00015078	5	5	+
CREM	chr10:35416711	0.083409724	1	4	
LOC339622	chr21:26523838	0.029561512	1	4	
PABPC4L	chr4:136144718	0.028789137	1	4	
ESRRG	chr1:217205344	0.000410911	4	4	+
FOXP2	chr7:114311067	0.000300021	4	4	
HGSNAT	chr8:43068098	4.27768E-06	1	4	
CHST9	chr18:24786338	0.072273833	1	3	+
YES1	chr18:764184	0.003844651	1	3	+
ITSN2	chr2:24431266	0.002247845	1	3	
UHMK1	chr1:162458565	0.002008196	2	3	+
KCNT2	chr1:196390818	0.001911316	2	3	+
TMTC2	chr12:84130047	0.001428221	1	3	
LINC00433	chr13:89236670	0.001016377	2	3	
CHRM3	chr1:239740372	0.000693113	3	3	+
RUNX1	chr21:36556891	0.000603355	2	3	+
PCDH7	chr4:31968961	0.000294649	2	3	
CDH6	chr5:31075168	0.000270435	3	3	+
ATP10A	chr15:26112320	0.000231617	2	3	+
MECOM	chr3:169274502	0.000136276	3	3	+
HNF4G	chr8:76554297	0.000110049	3	3	+
PLSCR5	chr3:146661822	9.40574E-05	3	3	+
DCN	chr12:91640705	0.08953968	2	2	+
GCKR	chr2:27754219	0.007159953	1	2	
PRRX1	chr1:170751740	0.006859031	1	2	
HACE1	chr6:105198339	0.006766768	1	2	
IRF2	chr4:185347059	0.004900672	1	2	
PDE8A	chr15:85566976	0.003901193	1	2	
GPR68	chr14:91702157	0.003284196	1	2	
ANTXR2	chr4:81035247	0.002618165	2	2	+
ZFPM2	chr8:106720552	0.001970573	1	2	
KCNIP4	chr4:21761680	0.001840868	1	2	
DOCK10	chr2:225931999	0.001770084	1	2	+
WIPF1	chr2:175433818	0.001569414	1	2	
ADAD1	chr4:123354498	0.001347241	1	2	

IFLTD1	chr12:25892844	0.001336861	2	2	+
SNX6	chr14:35077412	0.001305134	1	2	
MAGI1	chr3:65546848	0.001198649	1	2	
LGR5	chr12:71972099	0.00117545	1	2	
NINJ2	chr12:741286	0.001099148	1	2	
UGGT2	chr13:96499087	0.000948455	1	2	
TBX22	chrX:79209729	0.000837512	1	2	+
CCDC85A	chr2:57425826	0.000786263	1	2	
MLIP	chr6:53988277	0.000763219	1	2	
LINC00410	chr13:91258712	0.000759805	1	2	
CDH18	chr5:19363294	0.000688564	1	2	
LRIG2	chr1:113570807	0.000663611	1	2	+
SLC38A2	chr12:46756165	0.000639206	1	2	
KLF12	chr13:74173242	0.000625679	1	2	
IRF6	chr1:209975965	0.000590138	1	2	
CDC73	chr1:193734204	0.000556566	2	2	
ADHFE1	chr8:67357341	0.000534965	1	2	
CCDC146	chr7:76848650	0.000507018	1	2	
PRR20A	chr13:57324142	0.000493846	1	2	+
ZNF507	chr19:32855050	0.000477758	1	2	
SLC33A1	chr3:155564810	0.000449301	1	2	
SLC35F3	chr1:234111768	0.000429366	2	2	
NELL2	chr12:45065753	0.000409009	2	2	
MMP2	chr16:55481440	0.000372005	1	2	+
CHM	chrX:85333141	0.000371544	1	2	+
SEMA6A	chr5:115803054	0.000362896	1	2	
ETV3	chr1:157192476	0.000351274	1	2	
SFRP1	chr8:41071553	0.000345057	2	2	
GRM8	chr7:125487419	0.000322023	1	2	
SUMO1P1	chr20:52461649	0.000304771	2	2	
EPHA7	chr6:93926717	0.000246283	1	2	
SKAP2	chr7:26795532	0.000245428	1	2	
TENM2	chr5:167216727	0.000243735	2	2	
GPR113	chr2:26568090	0.000236747	1	2	
SYT11	chr1:155838789	0.000227882	1	2	
PPP1R32	chr11:61246147	0.000207267	1	2	+
PDZRN4	chr12:41919728	0.000207106	2	2	
FAM160A1	chr4:152311074	0.000200392	1	2	
DLGAP1	chr18:4229157	0.000196429	2	2	+
DYNLRB2	chr16:80297982	0.000190899	1	2	+
PTPRQ	chr12:81083502	0.000169875	2	2	
PTPRZ1	chr7:121634925	0.000144196	2	2	
LECT1	chr13:53334923	0.000141454	2	2	+
LOC440970	chr3:84856401	0.00012964	2	2	
RAF1	chr3:12676395	0.000126965	2	2	+
KCNIP1	chr5:169960664	0.000125178	2	2	+
PDZRN3	chr3:73722713	0.00010972	2	2	+
UBE3C	chr7:156946062	0.000103337	1	2	
MCTP2	chr15:95406428	0.000100099	2	2	+
SCAF8	chr6:155124040	9.42242E-05	2	2	+
PDE4DIP	chr1:145079838	8.90799E-05	2	2	+
BCAS3	chr17:59299832	8.334E-05	2	2	
LRRRC4C	chr11:41574598	6.53463E-05	2	2	
PDHA2	chr4:96999245	6.47557E-05	2	2	+
SOX5	chr12:24034694	6.14684E-05	2	2	+
C15orf54	chr15:39449477	4.77028E-05	2	2	+

ARID1A	chr1:27030884	4.65088E-05	2	2	+
PIK3C2G	chr12:18640893	4.49689E-05	2	2	
SEMA3D	chr7:84961632	4.01151E-05	2	2	
PCDH10	chr4:134339579	3.68791E-05	2	2	
GALNTL6	chr4:173827520	3.42353E-05	2	2	
USP25	chr21:17125119	3.39345E-05	2	2	+
ISL1	chr5:51204000	3.29618E-05	2	2	
NRXN1	chr2:52337792	3.06241E-05	2	2	
DNAJC11	chr1:6749931	2.81239E-05	1	2	
TRIT1	chr1:40353511	2.77346E-05	2	2	+
MIER1	chr1:67455740	2.76698E-05	2	2	
DIRAS2	chr9:93465100	2.45587E-05	2	2	
MTIF2	chr2:55481487	2.20394E-05	1	2	
LSAMP	chr3:115708792	2.09054E-05	2	2	
GLIS3	chr9:4236392	2.0867E-05	2	2	
KIAA1217	chr10:24607748	1.81614E-05	2	2	
AGBL1	chr15:87833699	9.21117E-06	2	2	
FAM5C	chr1:190399982	8.23231E-06	2	2	
OR7E156P	chr13:65216283	5.42119E-06	2	2	
RAPGEF4	chr2:173736632	4.14936E-06	2	2	+
MIR3134	chr9:115061321	2.95895E-06	2	2	+
LOC91948	chr15:98411062	2.69692E-06	2	2	
ELK3	chr12:96527329	1.41589E-06	2	2	
NEDD9	chr6:11399655	0.024332366	1	1	
KTN1	chr14:56156632	0.006445131	1	1	
SNX14	chr6:86254232	0.003121453	1	1	
PPARG	chr3:12393983	0.002801048	1	1	
ADAM9	chr8:38909781	0.002794283	1	1	
PTEN	chr10:89665859	0.002759531	1	1	
ALKBH3	chr11:43900878	0.002112448	1	1	
PTPLB	chr3:123224149	0.00202505	1	1	
C11orf74	chr11:36912050	0.002022545	1	1	
POU2F2	chr19:42623258	0.001859275	1	1	
COL4A5	chrX:107817324	0.001830524	1	1	
LOC401164	chr4:189360387	0.001553745	1	1	
UTS2D	chr3:191032332	0.001398728	1	1	
HHEX	chr10:94492359	0.001333613	1	1	
PABPC5	chrX:90362114	0.001107525	1	1	
LOC284379	chr19:54117726	0.0011036	1	1	
LAP3	chr4:17587613	0.001096961	1	1	
LOC100507377	chr12:74799042	0.00090126	1	1	
RAPGEF1	chr9:134558995	0.000668089	1	1	
WAPAL	chr10:88167724	0.000632046	1	1	
CEP85L	chr6:118976173	0.000612548	1	1	
FST	chr5:52636515	0.000584702	1	1	
PRICKLE2	chr3:64278730	0.000568649	1	1	
FAM178A	chr10:102700865	0.000562971	1	1	
MAST4	chr5:66026949	0.000464309	1	1	
PSMD7	chr16:73965121	0.000457342	1	1	
LOC100506422	chr9:26192125	0.000437125	1	1	
TECRL	chr4:64478136	0.000436194	1	1	
MPZL1	chr1:167740772	0.000404302	1	1	
LRP6	chr12:12355944	0.000371183	1	1	
VCPIP1	chr8:67540411	0.000342114	1	1	
RAB9BP1	chr5:104221937	0.000328634	1	1	
RNU6-19	chr14:76775154	0.000319185	1	1	

SH3RF3	chr2:109801346	0.000300477	1	1
GDAP2	chr1:118457277	0.00029428	1	1
DPRX	chr19:54139229	0.000289511	1	1
CCDC178	chr18:30713405	0.000286508	1	1
LOC100505776	chr18:69180152	0.000283114	1	1
GATA6	chr18:19771280	0.000272498	1	1
C14orf37	chr14:58642680	0.000262099	1	1
COG6	chr13:40225285	0.000237566	1	1
SCAMP1	chr5:77670237	0.000234822	1	1
SGMS1	chr10:52360891	0.000234641	1	1
FRMD4B	chr3:69422307	0.000231077	1	1
IL1RAPL1	chrX:28570271	0.000207124	1	1
RASGRF1	chr15:79255277	0.000204199	1	1
DUSP10	chr1:222146289	0.000201623	1	1
CDH8	chr16:61304485	0.000201089	1	1
FASLG	chr1:172707625	0.000197864	1	1
C9orf84	chr9:114583916	0.00019553	1	1
GTF2E1	chr3:120474691	0.000194862	1	1
NBAS	chr2:15249735	0.000190784	1	1
SLC6A15	chr12:84560099	0.000187427	1	1
BTG1	chr12:92658834	0.000185961	1	1
SMIM13	chr6:11136824	0.000184718	1	1
DRAM2	chr1:111642324	0.000182365	1	1
NENF	chr1:212609814	0.000181167	1	1
ATXN1	chr6:16879247	0.000181109	1	1
LINC00550	chr13:69856519	0.00017871	1	1
TMPRSS15	chr21:19717179	0.000174528	1	1
BARX2	chr11:129484977	0.000174512	1	1
AGBL3	chr7:134820438	0.000171148	1	1
MBD5	chr2:149292679	0.000169467	1	1
SRSF4	chr1:29491984	0.000164962	1	1
CLCN3	chr4:170556703	0.000162908	1	1
MIR4436A	chr2:89155362	0.000162436	1	1
OTUD1	chr10:23793288	0.000161517	1	1
PKIG	chr20:43246434	0.000161192	1	1
LCORL	chr4:17979366	0.000158304	1	1
P4HA3	chr11:73974432	0.000157544	1	1
HAO1	chr20:7458615	0.000157133	1	1
PIAS1	chr15:68420179	0.000145008	1	1
HMBBOX1	chr8:28774123	0.000142904	1	1
HMHB1	chr5:143268331	0.000137041	1	1
ZNF618	chr9:116695185	0.000134435	1	1
BBS12	chr4:123680569	0.000131275	1	1
NAV3	chr12:78560659	0.000130615	1	1
DUSP3	chr17:41841141	0.000127732	1	1
PROM1	chr4:16016722	0.000126191	1	1
VPS13B	chr8:100702251	0.000125194	1	1
ZFAND5	chr9:74951759	0.000120305	1	1
PDZD2	chr5:32008137	0.000118319	1	1
LHX8	chr1:75417683	0.000117168	1	1
TCF7L2	chr10:114647939	0.000116324	1	1
HSF2	chr6:122738804	0.000112035	1	1
MCTP1	chr5:94170273	0.000110972	1	1
TCP11	chr6:35124410	0.000110721	1	1
ASTN2	chr9:119655075	0.000110574	1	1
SFTA1P	chr10:10833674	0.000102609	1	1

DYRK2	chr12:68031055	0.000101977	1	1
CD38	chr4:15883016	0.000101349	1	1
MIR4302	chr12:25920639	0.000100749	1	1
ZCRB1	chr12:42696421	9.90296E-05	1	1
MNAT1	chr14:61198115	9.72652E-05	1	1
CCSER1	chr4:91493890	9.72563E-05	1	1
P4HA1	chr10:74826558	9.58511E-05	1	1
CBX5	chr12:54628029	9.54831E-05	1	1
C7orf66	chr7:108979702	9.39268E-05	1	1
UBE2D2	chr5:138912792	9.04708E-05	1	1
TPH2	chr12:72457080	8.99904E-05	1	1
PUS7L	chr12:44097394	8.96976E-05	1	1
SAMD4A	chr14:55055626	8.82273E-05	1	1
LOC100216546	chr7:104640474	8.78984E-05	1	1
ROCK1	chr18:18656553	8.75247E-05	1	1
ELMO1	chr7:37331862	8.60423E-05	1	1
DYM	chr18:46661964	8.41502E-05	1	1
ZNF608	chr5:124588940	8.28506E-05	1	1
MYSM1	chr1:59127758	8.05237E-05	1	1
ARID1B	chr6:157315777	7.90638E-05	1	1
PGAP1	chr2:197779319	7.64605E-05	1	1
LOC100129034	chr9:127120324	7.5283E-05	1	1
TRERF1	chr6:42357215	7.30489E-05	1	1
CAMK2G	chr10:75632940	7.20827E-05	1	1
ACIN1	chr14:23546344	7.10684E-05	1	1
FAT2	chr5:150990641	6.92838E-05	1	1
MTRNR2L6	chr7:142395525	6.90509E-05	1	1
KIAA1731	chr11:93408275	6.85355E-05	1	1
TMEM229A	chr7:123768606	6.808E-05	1	1
AKIRIN2	chr6:88441345	6.7729E-05	1	1
GPR110	chr6:47018714	6.76516E-05	1	1
RP1-177G6.2	chrX:139737858	6.4339E-05	1	1
ABTB2	chr11:34343365	6.42998E-05	1	1
RNF8	chr6:37319198	6.39392E-05	1	1
ZNF804A	chr2:185198546	6.3305E-05	1	1
PAPLN	chr14:73722879	6.22693E-05	1	1
GOT2	chr16:58824041	6.08224E-05	1	1
PAIP2B	chr2:71438858	6.02185E-05	1	1
LOC401497	chr9:30899633	5.74567E-05	1	1
ANXA2P3	chr10:66953016	5.67769E-05	1	1
MBOAT1	chr6:20174163	5.66822E-05	1	1
CSGALNACT1	chr8:19416805	5.62751E-05	1	1
GPR156	chr3:119865469	5.61131E-05	1	1
LMO7	chr13:76425598	5.61024E-05	1	1
DTNA	chr18:32437976	5.59681E-05	1	1
RAI1	chr17:17646823	5.59563E-05	1	1
ACTL7B	chr9:111523123	5.55069E-05	1	1
PURG	chr8:30840266	5.44583E-05	1	1
TFAP2D	chr6:50554229	5.40382E-05	1	1
ANKRD28	chr3:15833763	5.39339E-05	1	1
PCDH17	chr13:59109348	5.39287E-05	1	1
ZNF438	chr10:31248923	5.35428E-05	1	1
RBMXL2	chr11:7160212	5.33194E-05	1	1
ERCC6L2	chr9:98679479	5.28701E-05	1	1
ADPGK-AS1	chr15:73097963	5.05462E-05	1	1
MIR4437	chr2:182103309	4.96166E-05	1	1

KLHL12	chr1:202883375	4.92609E-05	1	1
AMOTL1	chr11:94497780	4.92558E-05	1	1
COL24A1	chr1:86208901	4.88246E-05	1	1
DOK6	chr18:67322462	4.81471E-05	1	1
KRT18	chr12:53362164	4.80859E-05	1	1
KRIT1	chr7:91848849	4.8085E-05	1	1
LCP1	chr13:46705895	4.79561E-05	1	1
CSK	chr15:75075243	4.77474E-05	1	1
HSPB1	chr7:75933515	4.73874E-05	1	1
RBM19	chr12:114250490	4.70785E-05	1	1
MAP4K5	chr14:50888767	4.67941E-05	1	1
UBE2E2	chr3:23508763	4.63397E-05	1	1
GUSBP1	chr5:21664122	4.52283E-05	1	1
QPCT	chr2:37620005	4.51275E-05	1	1
RREB1	chr6:7112902	4.49773E-05	1	1
LRP1B	chr2:141219428	4.44781E-05	1	1
TAF2	chr8:120720152	4.34559E-05	1	1
ARL6	chr3:97506979	4.33274E-05	1	1
PRRC2C	chr1:171537561	4.2849E-05	1	1
TMC1	chr9:75168048	4.25035E-05	1	1
TMTC3	chr12:88734320	4.23497E-05	1	1
FGFR1	chr8:38331127	4.22151E-05	1	1
OXR1	chr8:107082285	4.20639E-05	1	1
ZBTB20	chr3:114766652	4.20507E-05	1	1
SMG9	chr19:44251969	4.08946E-05	1	1
SP4	chr7:21447248	4.0294E-05	1	1
FOXB2	chr9:79709245	3.95902E-05	1	1
OLFML2A	chr9:127587348	3.93015E-05	1	1
BCKDHB	chr6:81225741	3.91515E-05	1	1
CDKAL1	chr6:21185855	3.86048E-05	1	1
HSD52	chr1:59582933	3.85298E-05	1	1
GPRIN3	chr4:90172371	3.84548E-05	1	1
BHLHE40	chr3:5095217	3.81163E-05	1	1
PPAP2B	chr1:56747830	3.74747E-05	1	1
ACTBL2	chr5:56965484	3.71515E-05	1	1
MED1	chr17:37572098	3.70397E-05	1	1
CDK8	chr13:26934427	3.67716E-05	1	1
GAREM	chr18:29969017	3.67529E-05	1	1
NR2C1	chr12:95441336	3.65705E-05	1	1
FAM27A	chr9:45685367	3.6455E-05	1	1
FRAT1	chr10:99068319	3.61826E-05	1	1
IQCH	chr15:67789776	3.57535E-05	1	1
SLC25A33	chr1:9560677	3.53823E-05	1	1
EPHX1	chr1:226004628	3.38355E-05	1	1
LPAR1	chr9:113721504	3.36818E-05	1	1
NLN	chr5:65140753	3.36318E-05	1	1
DPY19L2P4	chr7:89599212	3.34043E-05	1	1
GLG1	chr16:74519476	3.22136E-05	1	1
RGS5	chr1:163187061	3.18098E-05	1	1
PHLDB2	chr3:111568188	3.16765E-05	1	1
CYLC2	chr9:105193929	3.13556E-05	1	1
LINC00351	chr13:85586013	2.98888E-05	1	1
TXNDC16	chr14:52899792	2.90843E-05	1	1
MIRLET7BHG	chr22:46526092	2.90711E-05	1	1
CDH9	chr5:27106151	2.85165E-05	1	1
KLF5	chr13:73863701	2.77442E-05	1	1

CCDC102B	chr18:66475694	2.75966E-05	1	1
TMEM196	chr7:19932078	2.72821E-05	1	1
ALX1	chr12:85661232	2.7272E-05	1	1
AHCYL1	chr1:110553387	2.72334E-05	1	1
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ABLIM1	chr10:116427520	2.553E-05	1	1
YPEL5	chr2:30322575	2.51971E-05	1	1
KRT34	chr17:39534696	2.50731E-05	1	1
LINC00536	chr8:116825989	2.41457E-05	1	1
LSP1P3	chr5:28475743	2.40603E-05	1	1
BAI3	chr6:69382550	2.40007E-05	1	1
ZFAND3	chr6:37730334	2.36736E-05	1	1
IGJ	chr4:71542320	2.35573E-05	1	1
TMEM38B	chr9:108962020	2.35535E-05	1	1
ZCCHC24	chr10:81188241	2.33524E-05	1	1
SYBU	chr8:110625565	2.2636E-05	1	1
C2orf71	chr2:29314365	2.25601E-05	1	1
RBM46	chr4:155771549	2.2559E-05	1	1
RAB11FIP5	chr2:73356872	2.24173E-05	1	1
MTHFS	chr15:80135763	2.24103E-05	1	1
TPST1	chr7:65721676	2.18264E-05	1	1
RORB	chr9:77131382	2.16462E-05	1	1
PITX2	chr4:111544487	2.15468E-05	1	1
MIR221	chrX:45504047	2.1006E-05	1	1
DSC3	chr18:28537934	2.05992E-05	1	1
KCNK2	chr1:215165498	2.04163E-05	1	1
KALRN	chr3:123942617	1.96282E-05	1	1
LINC00837	chr10:29314876	1.96205E-05	1	1
GPNMB	chr7:23288228	1.95489E-05	1	1
PYDC2	chr3:191295304	1.91287E-05	1	1
NAA50	chr3:113453595	1.89053E-05	1	1
FBXO15	chr18:71437358	1.89048E-05	1	1
C1orf105	chr1:172437100	1.86372E-05	1	1
AHCY	chr20:32925180	1.85906E-05	1	1
EPHA8	chr1:22924427	1.85744E-05	1	1
TSN	chr2:123480299	1.84814E-05	1	1
ELF3	chr1:202011572	1.83907E-05	1	1
VDAC3	chr8:42250115	1.82722E-05	1	1
HDX	chrX:83743207	1.80766E-05	1	1
TOX3	chr16:52506371	1.7627E-05	1	1
CGGBP1	chr3:88134242	1.75769E-05	1	1
PKHD1	chr6:51733532	1.72541E-05	1	1
MIPEPP3	chr13:21943685	1.68925E-05	1	1
FAM3C	chr7:121220335	1.68088E-05	1	1
RYR2	chr1:237907819	1.6718E-05	1	1
DLG1	chr3:196836288	1.60673E-05	1	1
SEMA3C	chr7:80719031	1.60649E-05	1	1
SLC24A2	chr9:19818017	1.6045E-05	1	1
SERPINB3	chr18:61326903	1.60115E-05	1	1
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ERP27	chr12:15062621	1.57488E-05	1	1
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ZNF695	chr1:247165170	1.5531E-05	1	1
SPATA6	chr1:48963284	1.54333E-05	1	1
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SND1	chr7:127603737	1.52989E-05	1	1
FAM208A	chr3:56676019	1.49966E-05	1	1
ADAMTSL3	chr15:84337574	1.46647E-05	1	1
MIR100HG	chr11:121957408	1.46204E-05	1	1
ARPP21	chr3:35949810	1.43927E-05	1	1
IGDCC4	chr15:65704486	1.43505E-05	1	1
MARCH6	chr5:10331938	1.42572E-05	1	1
MURC	chr9:103408070	1.41928E-05	1	1
ROBO1	chr3:80578500	1.40215E-05	1	1
ADAMTSL1	chr9:18692850	1.3813E-05	1	1
LINC00704	chr10:4272123	1.35474E-05	1	1
AR	chrX:66873356	1.33857E-05	1	1
CACNA1E	chr1:181361535	1.30433E-05	1	1
DOCK6	chr19:11318495	1.29611E-05	1	1
ERCC3	chr2:128044274	1.28936E-05	1	1
RPS7P5	chr1:240122402	1.27968E-05	1	1
VENTXP1	chrX:26777915	1.27647E-05	1	1
NAT2	chr8:18291899	1.25717E-05	1	1
MIR3977	chr5:82050552	1.22125E-05	1	1
GALNT10	chr5:153641583	1.21645E-05	1	1
FAM96A	chr15:64379065	1.2143E-05	1	1
AHR	chr7:17312579	1.20511E-05	1	1
EIF4G2	chr11:10815129	1.20188E-05	1	1
NHSL1	chr6:138915744	1.1963E-05	1	1
MIR4493	chr11:123177064	1.1598E-05	1	1
DNAJC3	chr13:96401602	1.15404E-05	1	1
ARL8B	chr3:5211672	1.13968E-05	1	1
KCNH8	chr3:19088235	1.13943E-05	1	1
ENC1	chr5:73919237	1.11677E-05	1	1
LINC00333	chr13:85212244	1.08231E-05	1	1
NEGR1	chr1:73047190	1.05722E-05	1	1
TCF7L1	chr2:85333922	1.05412E-05	1	1
UGP2	chr2:64093710	1.04818E-05	1	1
SPIRE1	chr18:12605124	1.01675E-05	1	1
PMS1	chr2:190650215	9.67181E-06	1	1
SBF2	chr11:9908279	9.62697E-06	1	1
ANXA10	chr4:168631705	9.57082E-06	1	1
RLF	chr1:40599751	9.48093E-06	1	1
ALG9	chr11:111658727	9.47436E-06	1	1
SEL1L	chr14:82524065	9.46385E-06	1	1
MTX2	chr2:177272555	9.46364E-06	1	1
ABI3BP	chr3:100731128	9.24807E-06	1	1
MCPH1	chr8:6494210	9.19051E-06	1	1
YTHDC2	chr5:112905776	8.72641E-06	1	1
GABRA5	chr15:27135387	8.6035E-06	1	1
PCGEM1	chr2:193408806	8.29414E-06	1	1
RAP1GDS1	chr4:99342850	8.19189E-06	1	1
TPRKB	chr2:73946755	8.11187E-06	1	1
ZNF708	chr19:21442024	7.95246E-06	1	1
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RSBN1L	chr7:77414403	7.69393E-06	1	1
ALG10	chr12:33971946	7.58899E-06	1	1
SOX6	chr11:16541400	7.54519E-06	1	1
ABI1	chr10:27103979	7.54203E-06	1	1
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TAF1B	chr2:10067917	7.45338E-06	1	1
VAPB	chr20:56963565	7.36405E-06	1	1
NAV2	chr11:19709216	7.29101E-06	1	1
ZNF217	chr20:52299695	7.16043E-06	1	1
CTDSPL	chr3:37973819	7.10822E-06	1	1
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CCDC14	chr3:123671688	6.6342E-06	1	1
SCLT1	chr4:129941085	6.60646E-06	1	1
DEFB121	chr20:29990873	6.56519E-06	1	1
PLK1S1	chr20:21138992	6.50559E-06	1	1
LSM14A	chr19:34493625	6.3831E-06	1	1
NPAS2	chr2:101517561	6.19736E-06	1	1
MEFV	chr16:3296165	6.1585E-06	1	1
IPO5	chr13:98648879	6.10066E-06	1	1
C16orf52	chr16:22058083	6.04386E-06	1	1
ETS1	chr11:127840164	6.01073E-06	1	1
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PTGER3	chr1:71429731	5.85181E-06	1	1
HABP2	chr10:115300211	5.78751E-06	1	1
AMY1A	chr1:104294376	5.76607E-06	1	1
LINC00210	chr1:218159405	5.73996E-06	1	1
PKD2L1	chr10:102048658	5.68285E-06	1	1
SLC6A7	chr5:149583133	5.66556E-06	1	1
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ANK3	chr10:62067747	5.60295E-06	1	1
GRIN2A	chr16:9808539	5.48295E-06	1	1
PDLIM1	chr10:97000006	5.4357E-06	1	1
LPHN2	chr1:82373115	5.42215E-06	1	1
SOBP	chr6:107963851	5.38869E-06	1	1
GSG1	chr12:13302527	5.34016E-06	1	1
RGMB	chr5:97418590	5.15093E-06	1	1
CT64	chr3:163079044	5.08367E-06	1	1
PIP4K2A	chr10:22880689	5.08315E-06	1	1
DENND4C	chr9:19355541	5.07271E-06	1	1
EN1	chr2:119493025	4.98199E-06	1	1
ARHGAP32	chr11:129093644	4.9756E-06	1	1
PSMD12	chr17:65331548	4.94981E-06	1	1
PLA2G4A	chr1:188035074	4.94037E-06	1	1
PRPF38A	chr1:52880637	4.85031E-06	1	1
RAPGEF5	chr7:22296797	4.84925E-06	1	1
GLI3	chr7:42189731	4.62596E-06	1	1
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INTS9	chr8:28714621	4.5172E-06	1	1
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FAM129A	chr1:184901547	4.29028E-06	1	1
S100A2	chr1:153541101	4.28355E-06	1	1
PAQR3	chr4:79845878	4.2833E-06	1	1
TMED7-TICAM2	chr5:115001591	4.24123E-06	1	1
PIK3R5	chr17:8818652	4.21553E-06	1	1
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EIF3IP1	chr7:109097341	4.14079E-06	1	1
ATXN8OS	chr13:70945183	4.09594E-06	1	1
LYZL4	chr3:42414473	4.06605E-06	1	1
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TTC14	chr3:180228211	4.02654E-06	1	1

AADAC	chr3:151557990	4.0011E-06	1	1
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GABRA2	chr4:4622211	3.88376E-06	1	1
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DOCK7	chr1:62982053	3.84182E-06	1	1
SLC36A4	chr11:92905307	3.79954E-06	1	1
ZNF107	chr7:64164544	3.72733E-06	1	1
LRRIQ1	chr12:85651067	3.69757E-06	1	1
BCLAF1	chr6:136625087	3.59895E-06	1	1
TMEM248	chr7:66350776	3.45107E-06	1	1
PIWIL2	chr8:22149931	3.39336E-06	1	1
MAP7D2	chrX:20132880	3.36296E-06	1	1
TEX26	chr13:31561229	3.35201E-06	1	1
OSBPL8	chr12:76791392	3.34389E-06	1	1
IL1RAPL2	chrX:104966813	3.34084E-06	1	1
SSBP2	chr5:80897421	3.28429E-06	1	1
NUPR1L	chr7:56329635	3.28429E-06	1	1
SLC37A2	chr11:124927958	3.2826E-06	1	1
CASK	chrX:41853829	3.25721E-06	1	1
TENM3	chr4:183388116	3.22892E-06	1	1
AOX1	chr2:201459144	3.19559E-06	1	1
PDS5A	chr4:40009189	3.19005E-06	1	1
PCDH15	chr10:55372252	3.09438E-06	1	1
KIAA1109	chr4:123192860	3.0556E-06	1	1
PRB2	chr12:11586586	3.02115E-06	1	1
BCAT1	chr12:24859438	3.00663E-06	1	1
PAPSS2	chr10:89488360	2.94489E-06	1	1
MIR31HG	chr9:21509765	2.90447E-06	1	1
KSR2	chr12:118325199	2.89096E-06	1	1
MIR548AS	chr13:104673300	2.87156E-06	1	1
DCTN4	chr5:150144552	2.83804E-06	1	1
MIR4465	chr6:141622859	2.83201E-06	1	1
KRAS	chr12:25406576	2.81569E-06	1	1
EBF2	chr8:25916384	2.8123E-06	1	1
ALPL	chr1:21841118	2.80178E-06	1	1
ZMYM4	chr1:35753055	2.71513E-06	1	1
ANK1	chr8:41769846	2.63097E-06	1	1
MIR4500HG	chr13:87296318	2.59366E-06	1	1
GPR98	chr5:90554750	2.58105E-06	1	1
DISP1	chr1:223147051	2.53697E-06	1	1
PTPRU	chr1:29835532	2.49429E-06	1	1
MCF2	chrX:138677077	2.44016E-06	1	1
TLE4	chr9:82006428	2.40228E-06	1	1
CPSF2	chr14:92628564	2.3403E-06	1	1
NOX4	chr11:89076178	2.31312E-06	1	1
ZFP37	chr9:115794661	2.29786E-06	1	1
RAB28	chr4:13377256	2.2722E-06	1	1
LOC340094	chr5:4546809	2.26141E-06	1	1
KCND2	chr7:119880465	2.25601E-06	1	1
ZIC1	chr3:147518581	2.22745E-06	1	1
STAT4	chr2:191889978	2.19889E-06	1	1
FRK	chr6:116313575	2.19889E-06	1	1
EPB41L2	chr6:131242649	2.19711E-06	1	1
SPCS3	chr4:177306013	2.17567E-06	1	1
PP12613	chr4:122686566	2.16684E-06	1	1

RHOT1	chr17:30492942	2.13766E-06	1	1
CDH10	chr5:24709731	2.13661E-06	1	1
COQ7	chr16:19081549	2.11322E-06	1	1
FSTL5	chr4:163161694	2.10431E-06	1	1
SUCNR1	chr3:151719573	2.10065E-06	1	1
MYO16	chr13:109977212	2.08193E-06	1	1
C11orf44	chr11:130469123	2.0559E-06	1	1
CXCR4	chr2:137203502	2.04531E-06	1	1
LOC147093	chr17:39715456	2.04473E-06	1	1
SKP1P2	chr12:17263656	2.03583E-06	1	1
DGKB	chr7:14378648	2.00703E-06	1	1
GRM5	chr11:88265428	1.95828E-06	1	1
OR5H2	chr3:98021510	1.90764E-06	1	1
NCAM2	chr21:22452081	1.8883E-06	1	1
ZCCHC12	chrX:118006903	1.88822E-06	1	1
LOC100129027	chr21:47180697	1.87369E-06	1	1
COPZ2	chr17:46100055	1.84687E-06	1	1
LINC00645	chr14:27861781	1.84434E-06	1	1
SERGEF	chr11:17870754	1.80879E-06	1	1
ZRANB2-AS2	chr1:71779924	1.77202E-06	1	1
FIGN	chr2:164781973	1.75615E-06	1	1
SMC2	chr9:106603930	1.75031E-06	1	1
ANGPT1	chr8:108317194	1.72553E-06	1	1
PHF21A	chr11:46014946	1.67301E-06	1	1
MBNL1-AS1	chr3:151815287	1.67164E-06	1	1
LOC100302640	chr3:106929962	1.64436E-06	1	1
OR4L1	chr14:20521150	1.62908E-06	1	1
FRMD4A	chr10:14004157	1.56214E-06	1	1
SSFA2	chr2:182798148	1.53962E-06	1	1
TFPI	chr2:188607567	1.51958E-06	1	1
TFAP2C	chr20:55470608	1.51958E-06	1	1
CNTN3	chr3:74163157	1.51576E-06	1	1
CLLU1OS	chr12:92733157	1.51576E-06	1	1
C3orf38	chr3:88676426	1.51118E-06	1	1
GTF2F2	chr13:45807700	1.51108E-06	1	1
ALG13	chrX:110987084	1.49159E-06	1	1
SRL	chr16:4267917	1.47144E-06	1	1
GRIA4	chr11:105516929	1.45002E-06	1	1
TNFRSF11A	chr18:60065108	1.42164E-06	1	1
NXT1	chr20:23332388	1.42013E-06	1	1
PAM	chr5:102270293	1.4089E-06	1	1
BMP8A	chr1:39962912	1.39438E-06	1	1
MIR890	chrX:145023693	1.39081E-06	1	1
SMO	chr7:128851007	1.36058E-06	1	1
TSPAN11	chr12:31136286	1.36033E-06	1	1
FBXW7	chr4:153140767	1.33732E-06	1	1
RLTPR	chr16:67677128	1.33043E-06	1	1
LRRC8D	chr1:90378914	1.31765E-06	1	1
SATB2	chr2:199710014	1.30471E-06	1	1
CNIH3	chr1:224744698	1.28552E-06	1	1
LOC100130264	chr20:19249747	1.26468E-06	1	1
TES	chr7:115871721	1.25439E-06	1	1
CRIM1	chr2:36674895	1.22181E-06	1	1
MAPRE2	chr18:32562730	1.1959E-06	1	1
DCBLD2	chr3:98606532	1.16909E-06	1	1
CYTH1	chr17:76708215	1.1187E-06	1	1

PKIA	chr8:78880836	1.10391E-06	1	1	
ZNF680	chr7:63991801	1.08936E-06	1	1	
ARAP2	chr4:34645314	1.08714E-06	1	1	
SETD4	chr21:37279613	1.08714E-06	1	1	
DUT	chr15:48615763	1.08165E-06	1	1	
ALG14	chr1:95477920	1.07631E-06	1	1	
APPBP2	chr17:58611625	1.0683E-06	1	1	
CECR2	chr22:17888531	1.06199E-06	1	1	
STAC3	chr12:57638553	1.06136E-06	1	1	
WWP2	chr16:69900466	1.06136E-06	1	1	
YTHDF3	chr8:64137266	1.06104E-06	1	1	
BBS9	chr7:33341249	1.04815E-06	1	1	
SCAF11	chr12:46307948	1.04641E-06	1	1	
DNAJC13	chr3:132126926	1.03807E-06	1	1	
HIST1H2BD	chr6:26174906	1.01817E-06	1	1	
STEAP1	chr7:89792015	9.87678E-07	1	1	
PRKCQ-AS1	chr10:6706518	9.77599E-07	1	1	
SPATA17	chr1:218046444	9.64584E-07	1	1	
MIR147A	chr9:123042716	9.58634E-07	1	1	
APOB	chr2:21239485	9.32432E-07	1	1	
ASB17	chr1:76460048	9.27208E-07	1	1	
PRKAA1	chr5:40784085	9.20969E-07	1	1	
CDH13	chr16:83466830	9.19887E-07	1	1	
DCAF12	chr9:34099112	9.00279E-07	1	1	
ELP2	chr18:33740884	8.84988E-07	1	1	
EDIL3	chr5:83710671	8.76816E-07	1	1	
ROR2	chr9:94486709	8.76816E-07	1	1	
TXNDC8	chr9:113113451	8.76816E-07	1	1	
WIPF3	chr7:29873355	8.46691E-07	1	1	
GALNT2	chr1:230002108	8.45656E-07	1	1	
MLLT10	chr10:21937422	7.86661E-07	1	1	
LOC646329	chr7:130584382	7.35719E-07	1	1	
MLLT3	chr9:20387541	7.26238E-07	1	1	
TNFSF18	chr1:172957318	7.15562E-07	1	1	
PIEZO2	chr18:11372112	7.07991E-07	1	1	
PLXNA4	chr7:132272386	7.0517E-07	1	1	
MYO5A	chr15:52753989	6.96644E-07	1	1	
TRIO	chr5:14314892	6.85927E-07	1	1	
EMP1	chr12:13356334	6.64491E-07	1	1	
CD59	chr11:33736302	6.43056E-07	1	1	
TRIM29	chr11:120032251	6.21621E-07	1	1	
CNTNAP2	chr7:146399353	6.1398E-07	1	1	
BRIP1	chr17:59916516	6.09659E-07	1	1	
ZBTB8B	chr1:32895413	5.89992E-07	1	1	
C3orf79	chr3:153246449	5.89992E-07	1	1	
SERTAD2	chr2:64966153	5.89468E-07	1	1	
NOVA1	chr14:26421751	5.84544E-07	1	1	
OR2K2	chr9:113952519	5.64387E-07	1	1	
FLJ26245	chr16:35002116	5.54309E-07	1	1	
ULK4	chr3:41481089	5.44231E-07	1	1	
MRPS30	chr5:44892518	5.44231E-07	1	1	
RBL2	chr16:53507564	5.44231E-07	1	1	
ATF6	chr1:161887231	5.34152E-07	1	1	
SMARCA2	chr9:2028681	5.34152E-07	1	1	
GCFC2	chr2:75927564	5.22891E-07	1	1	
BCHE	chr3:165510119	5.14445E-07	1	1	

NFXL1	chr4:47893050	5.14445E-07	1	1
SLC35F4	chr14:58083207	5.14445E-07	1	1
ZNF692	chr1:249166593	5.11327E-07	1	1
MAML3	chr4:140680831	5.11327E-07	1	1
MGST2	chr4:140621611	5.03693E-07	1	1
GLUD2	chrX:121043501	4.93842E-07	1	1
BRAT1	chr7:2578045	4.93839E-07	1	1
BNC2	chr9:16707692	4.70113E-07	1	1
GPC5	chr13:92790761	4.63604E-07	1	1
ALDH3A2	chr17:19561329	4.53525E-07	1	1
NGFRAP1	chrX:102631363	4.53525E-07	1	1
GPR176	chr15:40197033	4.43447E-07	1	1
ADAMTS9-AS2	chr3:64966071	4.36534E-07	1	1
CACNG7	chr19:54442107	4.36534E-07	1	1
TCHH	chr1:152091980	4.21218E-07	1	1
ZNF660	chr3:44649045	4.1813E-07	1	1
RNF217	chr6:125400510	3.93055E-07	1	1
BANK1	chr4:102720093	3.92169E-07	1	1
DAPK1	chr9:90295717	3.82977E-07	1	1
ANP32E	chr1:150181372	3.69375E-07	1	1
LOC644838	chr2:67526759	3.53995E-07	1	1
HEY2	chr6:126072688	3.53995E-07	1	1
DIS3L	chr15:66594669	3.53995E-07	1	1
RBFOX1	chr16:6601479	3.53995E-07	1	1
CHST6	chr16:75515368	3.53995E-07	1	1
GNG7	chr19:2551003	3.53995E-07	1	1
PACSLN2	chr22:43353530	3.48594E-07	1	1
NBEA	chr13:35993950	3.42664E-07	1	1
ATP11B	chr3:182620326	3.34504E-07	1	1
DCUN1D1	chr3:182674600	3.34504E-07	1	1
KCNN2	chr5:113490124	3.34504E-07	1	1
CSNK1G3	chr5:123149816	3.34504E-07	1	1
REV1	chr2:100066619	3.34329E-07	1	1
APTX	chr9:33012126	3.34329E-07	1	1
ABI3	chr17:47294176	3.32585E-07	1	1
PRPF18	chr10:13654435	3.12429E-07	1	1
FBXL7	chr5:15951751	3.02216E-07	1	1
DPP6	chr7:154600699	2.94996E-07	1	1
IRAK1BP1	chr6:79337562	2.82194E-07	1	1
ZBTB38	chr3:141106744	2.7533E-07	1	1
EYA4	chr6:133542316	2.61446E-07	1	1
PGA5	chr11:61015430	2.55663E-07	1	1
NR2C2	chr3:15079339	2.50878E-07	1	1
TRAM1L1	chr4:118112967	2.50878E-07	1	1
KCNA7	chr19:49577959	2.50878E-07	1	1
GPR85	chr7:112700922	2.46921E-07	1	1
ZEB1	chr10:31893698	2.35997E-07	1	1
NLRC4	chr2:32493523	2.32396E-07	1	1
LOC728342	chr5:117265406	2.32396E-07	1	1
UNC5D	chr8:34923228	2.32396E-07	1	1
GCNT2	chr6:10600131	2.31802E-07	1	1
LACE1	chr6:108854877	2.17871E-07	1	1
PAK6	chr15:40527399	2.17871E-07	1	1
HPVC1	chr7:54386578	2.16331E-07	1	1
TMPRSS6	chr22:37480133	2.16331E-07	1	1
C22orf34	chr22:49759550	2.16331E-07	1	1

UFM1	chr13:38991048	2.03347E-07	1	1
NEGR1-IT1	chr1:72300981	2.01567E-07	1	1
FMO2	chr1:171163824	1.96664E-07	1	1
C1orf100	chr1:244555854	1.96664E-07	1	1
MYADML	chr2:34294094	1.91489E-07	1	1
ROBO2	chr3:76731822	1.88822E-07	1	1
VGLL3	chr3:86955670	1.8141E-07	1	1
LDLRAD3	chr11:36142205	1.74297E-07	1	1
ADAMTS18	chr16:77431230	1.74297E-07	1	1
TNIK	chr3:170829874	1.71332E-07	1	1
MPHOSPH8	chr13:20173814	1.71332E-07	1	1
ACTL8	chr1:18244791	1.67252E-07	1	1
CD1C	chr1:158279409	1.67252E-07	1	1
IGSF8	chr1:160076992	1.67252E-07	1	1
ARIH2	chr3:48965176	1.67252E-07	1	1
MIR548I1	chr3:125492167	1.67252E-07	1	1
PRR23A	chr3:138726573	1.67252E-07	1	1
GSX2	chr4:54994283	1.67252E-07	1	1
LOC100144602	chr4:66577791	1.67252E-07	1	1
LOC100505875	chr4:80160771	1.67252E-07	1	1
IPO11	chr5:61859972	1.67252E-07	1	1
MYOT	chr5:137195006	1.67252E-07	1	1
PPP1R2P3	chr5:156240329	1.67252E-07	1	1
QKI	chr6:164844173	1.67252E-07	1	1
HGF	chr7:81318751	1.67252E-07	1	1
SEMA3E	chr7:83155731	1.67252E-07	1	1
GRM3	chr7:85877827	1.67252E-07	1	1
DPYSL2	chr8:26458936	1.67252E-07	1	1
FAM84B	chr8:127632268	1.67252E-07	1	1
ACER3	chr11:76547704	1.67252E-07	1	1
PLBD1	chr12:14739932	1.67252E-07	1	1
CRY1	chr12:107552424	1.67252E-07	1	1
SLITRK6	chr13:86529470	1.67252E-07	1	1
PRKCH	chr14:61774886	1.67252E-07	1	1
LOC283585	chr14:87306396	1.67252E-07	1	1
MNS1	chr15:56808385	1.67252E-07	1	1
MEF2A	chr15:100237202	1.67252E-07	1	1
AIPL1	chr17:6189126	1.67252E-07	1	1
KCNG1	chr20:49664120	1.67252E-07	1	1
ADARB1	chr21:46664466	1.67252E-07	1	1
CXorf57	chrX:105815497	1.67252E-07	1	1
ASCC3	chr6:101360583	1.61254E-07	1	1
UCP2	chr11:73692233	1.61254E-07	1	1
MIR548A3	chr3:103225119	1.45248E-07	1	1
SNX2	chr5:122120746	1.45248E-07	1	1
ITFG3	chr16:283517	1.45248E-07	1	1

Table S2. List of resistant clones.

Clones A1-A23 were isolated from screened plate and B1-B201 were from limiting dilution of resistant pools. Each insert was annotated orientation. A negative distance value indicates insert upstream of gene, positive value for downstream, and 0 for intragenic. CMV antisense of the host gene body.

clone	insert	insert	insert
A1	chrX:138684373 MCF2 0/+	chr17:39095514 KRT23 -1679/+	chr18:25449894 CDH2 81035/-
A2	chr4:186742830 SORBS2 0/-	chr14:55490722 WDHD1 0/+	chr12:69246594 CPM 0/+
A3	chr2:203664266 ICA1L 0/-	chr11:16146421 SOX6 0/-	chr11:113652668 CLDN25 1462/+
A4	chr5:109326726 LOC100289673 10552	chr2:190016957 COL5A2 0/+	chr10:63732986 ARID5B 0/+
A5	chr18:24786338 CHST9 -21037/+	chr13:82153549 SPRY2 -1238464/+	
A6	chr2:220825933 MIR4268 -54648/-	chr5:122026084 SNX2 -84665/-	chr9:99951467 LOC100499484 -49240/
A7	chr2:83256616 LOC1720 171724/-	chr1:51138260 FAF1 0/-	chr3:187823607 LPP-AS2 45386/-
A8	chr13:94939649 GPC6 0/-	chr2:39231446 SOS1 0/+	
A9	chr13:94939649 GPC6 0/-		
A10	chr13:94939649 GPC6 0/-		
A11	chr13:94939649 GPC6 0/-		
A12	chr13:94939649 GPC6 0/-		
A13	chr13:94939649 GPC6 0/-		
A14	chr13:94939649 GPC6 0/-		
A15	chr13:94939649 GPC6 0/-	chr9:108030042 SLC44A1 0/-	
A16	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	
A17	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	
A18	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	chr14:56156632 KTN1 5331/-
A19	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	
A20	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	chr8:68050488 CSPP1 0/-
A21	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	chr7:114567455 MDFIC 0/-
A22	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	chr14:56156632 KTN1 5331/-
A23	chrX:115045927 PLS3 160749/-	chr7:140460815 BRAF 0/+	chr14:56156632 KTN1 5331/-
B1	chr10:35416711 CREM 0/-		
B2	chr13:94939649 GPC6 0/-		
B3	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B4	chr7:140483217 BRAF 0/+		
B5	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B6	chr13:94939649 GPC6 0/-		
B7	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B8	chr13:94939649 GPC6 0/-		
B9	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B10	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B11	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B12	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B13	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B14	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B15	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B16	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B17	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B18	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B19	chr13:94939649 GPC6 0/-		
B20	chr13:94939649 GPC6 0/-		
B21	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B22	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B23	chr7:140483217 BRAF 0/+		
B24	chr13:94939649 GPC6 0/-		
B25	chr13:94939649 GPC6 0/-		

B26	chr7:140483217 BRAF 0/+		
B27	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B28	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B29	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B30	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B31	chr7:140483217 BRAF 0/+		
B32	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B33	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B34	chr13:94939649 GPC6 0/-		
B35	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B36	chr13:94939649 GPC6 0/-		
B37	chr13:94939649 GPC6 0/-		
B38	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B39	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B40	chr13:94939649 GPC6 0/-		
B41	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B42	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B43	chrX:115044473 PLS3 159295/-		
B44	chr13:94939649 GPC6 0/-		
B45	chr13:94939649 GPC6 0/-		
B46	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B47	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B48	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B49	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B50	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B51	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B52	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B53	chr13:94939649 GPC6 0/-		
B54	chr7:140483217 BRAF 0/+		
B55	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B56	chr13:94939649 GPC6 0/-		
B57	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B58	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B59	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B60	chr13:94939649 GPC6 0/-		
B61	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B62	chr7:140483217 BRAF 0/+		
B63	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B64	chr7:140483217 BRAF 0/+		
B65	chr13:94939649 GPC6 0/-		
B66	chr7:140483217 BRAF 0/+	chr13:94939649 GPC6 0/-	
B67	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B68	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B69	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B70	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B71	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B72	chr13:94939649 GPC6 0/-		
B73	chr7:140483217 BRAF 0/+	chr13:94939649 GPC6 0/-	
B74	chr13:94939649 GPC6 0/-		
B75	chr7:140460815 BRAF 0/+	chrX:115044473 PLS3 159295/-	
B76	chr7:140483217 BRAF 0/+		
B77	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B78	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	

B79	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B80	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B81	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B82	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B83	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B84	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B85	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B86	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B87	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B88	chr2:68244025 C1D 25306/+		
B89	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B90	chr7:140483217 BRAF 0/+		
B91	chr13:94939649 GPC6 0/-		
B92	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B93	chr7:140483217 BRAF 0/+		
B94	chr13:94939649 GPC6 0/-		
B95	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B96	chr7:140483217 BRAF 0/+		
B97	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B98	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B99	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B100	chr13:94939649 GPC6 0/-		
B101	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr13:94939649 GPC6 0/-
B102	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B103	chr13:94939649 GPC6 0/-		
B104	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B105	chr13:94939649 GPC6 0/-		
B106	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B107	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B108	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B109	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B110	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr7:140483217 BRAF 0/+
B111	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr7:140483217 BRAF 0/+
B112	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B113	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B114	chr7:140483217 BRAF 0/+		
B115	chr13:94939649 GPC6 0/-		
B116	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B117	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B118	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B119	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B120	chr21:38722375 DYRK1A -17483/-	chr19:16137669 LINC00661 0/+	chr8:114360638 CSMD3 0/-
B121	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B122	chr7:140483217 BRAF 0/+	chr13:94939649 GPC6 0/-	
B123	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B124	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr7:140483217 BRAF 0/+
B125	chr7:140460815 BRAF 0/+		
B126	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr12:56345588 DGKA 0/-
B127	chr7:140460815 BRAF 0/+		
B128	chr3:178840783 PIK3CA -25527/+	chr1:214688471 PTPN14 0/+	chr3:178500378 KCNMB2 0/+
B129	chr13:94939649 GPC6 0/-		
B130	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr7:140483217 BRAF 0/+
B131	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-

B132	chr21:38722375 DYRK1A -17483/-	chr19:16137669 LINC00661 0/+	chr8:114360638 CSMD3 0/-
B133	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr2:15098373 NBAS 208658/-
B134	chr7:140483217 BRAF 0/+		
B135	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr13:94939649 GPC6 0/-
B136	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B137	chr10:35416711 CREM 0/-		
B138	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	
B139	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B140	chr13:94939649 GPC6 0/-		
B141	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	chr3:12621903 MKRN2 0/-
B142	chr12:91548330 DCN 0/-	chr12:78560659 NAV3 0/+	
B143	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B144	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-	
B145	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B146	chr13:94939649 GPC6 0/-		
B147	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B148	chr12:33996081 ALG10 -179134/-	chr4:99319442 RAP1GDS1 0/-	
B149	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B150	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr2:68244025 C1D 25306/+
B151	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr13:94939649 GPC6 0/-
B152	chr7:140483217 BRAF 0/+	chr13:94939649 GPC6 0/-	chr12:91548330 DCN 0/-
B153	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B154	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B155	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-	chr7:140483217 BRAF 0/+
B156	chr13:94939649 GPC6 0/-		
B157	chr12:91548330 DCN 0/-		
B158	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr13:94939649 GPC6 0/-
B159	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B160	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B161	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B162	chr7:140483217 BRAF 0/+		
B163	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B164	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B165	chrX:115045927 PLS3 160749/-	chr7:140483217 BRAF 0/+	
B166	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-	
B167	chr7:140483217 BRAF 0/+	chr13:94939649 GPC6 0/-	
B168	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B169	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B170	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B171	chr13:94939649 GPC6 0/-		
B172	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B173	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B174	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B175	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B176	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B177	chr13:94939649 GPC6 0/-		
B178	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-
B179	chr7:140483217 BRAF 0/+		
B180	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr13:94939649 GPC6 0/-
B181	chr13:94939649 GPC6 0/-	chr18:55917356 NEDD4L 0/+	
B182	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr13:94939649 GPC6 0/-
B183	chrX:115045927 PLS3 160749/-	chr7:140483217 BRAF 0/+	
B184	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chr14:56156632 KTN1 5331/-

B185	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B186	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B187	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B188	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B189	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B190	chr7:140483217 BRAF 0/+		
B191	chrX:115044473 PLS3 159295/-		
B192	chr12:91548330 DCN 0/-		
B193	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B194	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B195	chr6:11399655 NEDD9 -17075/+		
B196	chrX:115045927 PLS3 160749/-		
B197	chr7:140460815 BRAF 0/+		
B198	chr13:94939649 GPC6 0/-	chr1:170751740 PRRX1 43200/+	chr3:12621903 MKRN2 0/-
B199	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	chrX:115044473 PLS3 159295/-
B200	chr7:140460815 BRAF 0/+	chrX:115045927 PLS3 160749/-	
B201	chrX:115045927 PLS3 160749/-		

stated for genomic position, proximal gene, and relative distance and / promoter orientations are denoted as "+" for sense strand and "-" for

[illegible]

[illegible]

[illegible]

chr5:116549795 LOC728342 -201412/+	chr5:37169570 C5orf42 0/-	
chr1:170751740 PRRX1 43200/+		
chr13:94939649 GPC6 0/-		
chr3:12676395 RAF1 0/+		
chr13:94939649 GPC6 0/-		
chr8:78880836 PKIA -547499/+		
chr11:34343365 ABTB2 0/-		
chr7:140483217 BRAF 0/+	chr3:12676395 RAF1 0/+	

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Table S3. Gene expression proximal to transposon inserts in 10 clones.

Listed are clone ID, insert position, gene name, distance between insert and gene body (negative value for upstream, 0 for intragenic, and positive for downstream), RPKM, RNA ratio, p- and q-values (Pval, Qval) for the three nearest genes. Ratio is capped at 50 and marked with an n.d. if not determined.

clone	position	first gene							name	distance
		name	distance	strand	RPKM	RNA ratio	Pval	Qval		
B181	chr18:55917356	NEDD4L	0	+	4702	6.89	0.0E+00	0.0E+00	MIR122	-200949
	chr13:94939649	GPC6	0	-	72	0.27	9.9E-27	4.5E-25	DCT	152191
B195	chr6:11399655	NEDD9	-17075	+	111	1.00	1.0E+00	1.0E+00	TMEM170B	-138804
A1	chr17:39095514	KRT23	-1679	+	n.d.				KRT39	19154
	chr18:25449894	CDH2	81035	-	621	0.73	5.7E-09	3.0E-07	CHST9	-684593
	chrX:138684373	MCF2	0	+	150	32.70	4.0E-35	1.5E-32	F9	38757
A3	chr11:16146421	SOX6	0	-	41	1.09	7.3E-01	1.0E+00	C11orf58	-613726
	chr11:113652668	CLDN25	1462	+	n.d.				ZW10	-8184
	chr2:203664266	ICA1L	0	-	31	1.38	3.3E-01	9.7E-01	FAM117B	29787
A6	chr2:220825933	MIR4268	-54648	-	n.d.				SLC4A3	319232
	chr5:122026084	SNX2	-84665	-	336	1.01	9.7E-01	1.0E+00	SNX24	-155075
	chr5:139358867	NRG2	0	-	52	1.47	7.8E-02	3.3E-01	PSD2	134820
	chr9:99951467	LOC100499484	-49240	+	n.d.				LOC100499484-C90	-49240
A7	chr1:51138260	FAF1	0	-	315	0.90	1.9E-01	5.5E-01	DMRTA2	-249142
	chr2:83256616	LOC1720	171724	-	n.d.				FUNDC2P2	-1E+06
	chr3:187823607	LPP-AS2 (LPP)	45386	-	n.d.				LPP	-48055
A8	chr2:39231446	SOS1	0	+	271	0.82	2.1E-02	8.9E-02	ARHGEF33	28857
	chr13:94939649	GPC6	0	-	174	0.70	4.5E-04	3.3E-03	DCT	152191
A14	chr13:94939649	GPC6	0	-	132	0.59	1.1E-06	9.8E-06	DCT	152191
A18	chr7:140460815	BRAF	0	+	1731	31.97	0.0E+00	0.0E+00	NDUFB2	54370
	chr14:56156632	KTN1	5331	-	584	0.67	7.0E-15	2.2E-13	RPL13AP3	-76330
	chrX:115045927	PLS3	160749	-	203	0.68	1.5E-05	1.2E-04	AGTR2	-256030
A23	chr7:140460815	BRAF	0	+	1612	34.14	0.0E+00	0.0E+00	NDUFB2	54370
	chr14:56156632	KTN1	5331	-	498	0.66	6.0E-15	1.1E-13	RPL13AP3	-76330
	chrX:115045927	PLS3	160749	-	172	0.66	1.0E-05	6.9E-05	AGTR2	-256030

positive value for downstream), strand orientation ("+" and "-"), RNA-Seq read signal (RPKM, read per kilobase million), ratio to sterisk if control expression is undetectable.

second gene					third gene						
strand	RPKM	RNA ratio	Pval	Qval	name	distance	strand	RPKM	RNA ratio	Pval	Qval
+	n.d.				MIR3591	201028	-	n.d.			
+	n.d.				TGDS	286658	+	136	1.04	8.0E-01	1.0E+00
-	40	1.34	2.3E-01	5.7E-01	SMIM13	260687	-	n.d.			
+	386	50*	3.5E-105	6.4E-102	KRT40	38453	+	n.d.			
-	n.d.				AQP4-AS1	933985	+	n.d.			
-	n.d.				ATP11C	124131	+	137	0.92	5.4E-01	1.0E+00
+	438	0.84	9.4E-03	1.0E-01	PLEKHA7	662785	-	32	1.36	3.4E-01	9.8E-01
-	203	0.78	1.1E-02	1.1E-01	USP28	15928	-	188	0.72	8.8E-04	1.6E-02
+	47	0.83	3.2E-01	9.5E-01	WDR12	81056	-	220	0.93	4.5E-01	1.0E+00
+	118	1.28	1.0E-01	4.0E-01	STK11IP	344761	+	127	0.76	2.2E-02	1.3E-01
-	130	0.79	5.3E-02	2.5E-01	MGC32805	-211303	+	n.d.			
+	n.d.				PURA	-134840	+	331	1.11	2.2E-01	6.6E-01
+	n.d.				LOC340508	-107241	-	n.d.			
-	n.d.				CDKN2C	-296106	+	391	1.49	8.2E-07	1.5E-05
-	n.d.				SUCLG1	1394030	+	301	0.95	5.4E-01	1.0E+00
+	5249	20.83	0.0E+00	0.0E+00	FLJ42393	-72723	+	n.d.			
-	n.d.				LOC375196	-43962	+	n.d.			
+	n.d.				TGDS	286658	+	121	1.01	1.0E+00	1.0E+00
+	n.d.				TGDS	286658	+	98	0.91	4.9E-01	9.6E-01
-	257	1.12	2.2E-01	5.3E-01	NDUFB2-AS1	-63939	+	n.d.			
-	n.d.				LINC00520	91220	+	n.d.			
-	n.d.				LUZP4	503807	-	n.d.			
-	243	1.22	3.2E-02	9.8E-02	NDUFB2-AS1	-63939	+	n.d.			
-	n.d.				LINC00520	91220	+	n.d.			
-	n.d.				LUZP4	503807	-	n.d.			

Table S4. STRING connections between screens.

Lists of genes from each screen and their STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) connections to other genes

PB	ORF	dCAS9	CRISPR	shRNA	CRISPR	PB	ORF	dCAS9	shRNA	dCAS9	PB	ORF	CRISPR
NEDD4L	8	3	11	1	RPS19	0	2	1	2	MARCH13	0	0	0
EYA1	10	4	7	0	TCOF1	2	3	0	0	AARSD1	0	0	0
POU2F1	7	5	9	1	NIP7	1	5	4	3	ABLIM2	7	13	2
BRAF	11	4	3	0	ARL17A	0	0	0	0	ACP6	0	0	0
ZFHX3	6	0	6	1	RPS18	0	1	3	1	ACVR2A	0	3	0
TRPS1	4	1	2	0	RPS11	1	0	1	1	ADORA1	1	11	1
ZFHX4	1	0	0	0	RPL32	0	1	1	1	AKR1B1	0	1	0
RAPGEF2	8	5	3	0	DENR	2	3	2	3	ANKRD29	0	1	0
ARHGEF28	16	6	6	0	RPL6	1	8	4	9	AP4B1	0	1	1
VAV1	26	11	14	3	ACTL6A	4	7	2	5	APBB1	3	17	60
PLS3	0	1	7	0	PPAN	8	3	2	2	ARHGAP6	0	0	0
GPC6	0	1	0	0	ENO1	11	15	11	4	ARHGEF1	8	17	9
WWTR1	16	2	4	0	ASH2L	3	9	1	1	ARHGEF2	10	25	35
RAPGEF6	5	2	2	0	SNRPF	1	5	2	4	ARHGEF5	0	0	0
AKAP13	11	5	3	0	GABPA	6	5	0	0	ATL1	0	0	0
CREM	16	2	8	1	VOPP1	0	0	1	0	ATP10A	5	4	6
LOC339622	1	0	0	1	RSL1D1	0	3	2	0	B4GALNT2	0	0	0
PABPC4L	0	0	0	0	URB1	0	2	1	0	BCAP29	0	0	3
ESRRG	24	1	3	0	MRP63	3	2	1	0	BCAR1	4	12	3
FOXP2	34	4	10	1	NAA30	1	2	0	0	BCAR3	3	2	3
HGSNAT	1	1	2	0	KPNB1	5	6	1	2	BCAS3	14	28	24
CHST9	0	0	0	0	LSM2	0	0	0	1	BCL7C	1	2	18
YES1	19	6	8	1	MASP2	1	2	0	1	BRI3	0	4	8
ITSN2	2	1	3	0	DEFB131	0	0	0	0	BRINP1	0	0	0
UHMK1	2	0	1	1	NHP2L1	1	2	3	2	C11orf21	0	0	0
KCNT2	0	1	2	0	RPS15A	3	4	2	1	C14orf39	0	0	0
TMTC2	0	1	0	0	EEF1A1	2	8	5	1	C19orf18	0	0	0
LINC00433	1	0	0	1	RBX1	4	11	5	2	C19orf68	0	0	0
CHRM3	8	2	2	0	RPL8	1	5	1	1	C3orf27	0	0	0
RUNX1	31	5	18	4	POLR2I	2	3	2	3	C9orf50	0	0	0
PCDH7	0	3	0	0	NUTF2	1	3	1	1	CA12	0	4	5
CDH6	1	1	0	0	TPT1	5	5	5	3	CA3	0	0	0
ATP10A	4	4	6	0	ATP6V0C	0	2	0	0	CCER1	0	0	0
MECOM	22	5	8	2	RPL7A	1	2	1	1	CCND2	13	23	17
HNF4G	5	0	0	0	EEF2	1	9	5	2	CDR2	1	0	0
PLSCR5	0	0	0	0	COPB1	5	10	4	1	CEP63	1	1	3
DCN	10	3	9	2	RBMX2	1	6	0	2	CGB8	0	0	0
GCKR	4	1	1	0	POLR3H	5	2	1	1	CGNL1	3	2	3
PRRX1	7	1	7	0	RPL10	1	8	1	2	CHID1	2	4	6
HACE1	3	0	4	0	TUBG1	2	6	3	2	CHN2	8	17	4
IRF2	9	2	6	0	KCNJ16	4	0	1	0	CHST15	0	0	0
PDE8A	1	0	0	2	ZNF207	1	2	1	1	CNR1	1	1	3
GPR68	7	1	0	0	CAPZB	0	0	0	0	COA3	0	1	8
ANTXR2	8	4	13	1	HNRNPU	0	10	2	3	COL25A1	1	6	1
ZFPM2	10	1	4	2	RPL37	1	2	1	1	CPEB1	0	0	0
KCNIP4	0	0	0	0	CAPZA1	1	4	0	0	CPLX2	2	1	3
DOCK10	0	0	0	1	SS18L2	0	2	0	0	CRB2	0	3	4
WIPF1	5	0	1	2	PRPF38B	3	1	0	2	CST5	0	1	0
ADAD1	0	1	5	1	MAPK1	21	51	19	7	DAG1	7	8	2
IFLTD1	0	0	0	0	MOCS3	1	2	2	0	DCAF7	0	0	0

SNX6	1	2	2	1
MAGI1	1	1	1	0
LGR5	9	2	3	0
NINJ2	0	0	0	0
UGGT2	0	0	1	1
TBX22	9	1	3	0
CCDC85A	1	0	3	0
MLIP	0	1	0	0
LINC00410	1	0	0	1
CDH18	1	0	0	0
LRIG2	3	1	0	0
SLC38A2	3	2	8	2
KLF12	2	1	0	0
IRF6	13	3	10	1
CDC73	2	1	21	0
ADHFE1	9	4	9	1
CCDC146	1	0	1	0
PRR20A	0	0	0	0
ZNF507	1	0	0	0
SLC33A1	1	0	7	1
SLC35F3	0	0	1	0
NELL2	2	1	0	0
MMP2	19	9	7	1
CHM	2	1	12	2
SEMA6A	7	2	9	0
ETV3	2	1	2	0
SFRP1	5	6	5	0
GRM8	5	4	2	1
SUMO1P1	1	0	0	1
EPHA7	7	4	1	0
SKAP2	3	0	1	1
TENM2	0	0	0	0
GPR113	0	0	0	0
SYT11	5	2	5	0
PPP1R32	3	0	0	0
PDZRN4	2	0	3	0
FAM160A1	0	0	0	0
DLGAP1	2	0	1	0
DYNLRB2	2	0	6	2
PTPRQ	0	0	0	0
PTPRZ1	4	4	0	0
LECT1	1	1	1	0
LOC440970	1	0	0	1
RAF1	23	5	11	2
KCNIP1	3	3	0	0
PDZRN3	4	0	2	0
UBE3C	1	0	5	0
MCTP2	0	0	1	0
SCAF8	2	2	15	2
PDE4DIP	2	0	0	0
BCAS3	1	1	4	1
LRRC4C	2	0	1	1
PDHA2	0	1	3	1

POP7	0	2	0	2
UTP18	1	7	2	1
PSMC2	3	7	7	2
PIGW	0	0	0	0
RPL30	2	5	1	1
DCPS	0	1	1	3
RPS21	0	0	0	0
BEX1	1	2	1	1
SNRNP70	1	6	5	2
H3F3B	18	40	13	9
RPL38	1	1	1	1
TSR1	1	6	2	2
SNRNP200	0	3	1	1
ZNRD1	0	2	0	0
TFAM	3	8	2	1
PDAP1	0	2	0	0
OCM	2	3	1	0
PCF11	2	1	0	2
C6orf226	0	0	0	0
PPP2CA	3	14	2	2
RAE1	4	6	0	1
CIRH1A	0	4	0	1
DDX42	0	2	0	1
RPS5	2	6	2	2
SART3	0	2	2	0
CTU2	0	3	0	0
SBDS	0	5	1	0
HSD17B10	0	7	3	2
OR5K3	0	0	0	0
PMF1	0	1	0	0
ZNF259	1	0	2	0
MTA3	1	1	0	1
ANKRD49	0	0	0	0
PCBP1	1	4	3	3
FCF1	1	1	1	0
CTNBL1	0	1	0	1
TUBGCP3	3	0	3	1
KDSR	0	1	1	0
HSPA8	4	19	5	3
ZFH3	4	6	0	1
DYNLL1	7	7	3	2
C17orf81	0	0	0	0
POLR3K	1	4	1	1
SAE1	1	9	1	4
TBCA	1	4	1	2
RPS27A	31	75	24	8
ARMC7	0	0	0	0
POLR1B	3	3	1	1
FAM96B	1	3	3	2
RPL13	1	2	3	1
CUL1	4	21	7	3
SUPT6H	2	2	2	0
YY1	15	23	7	5

DDX11	7	16	9
DNASE1L2	10	16	11
DTX3	0	2	1
DYRK3	0	0	0
EFNA1	6	12	1
EGFR	29	54	35
EIF4EBP2	0	0	0
EPAS1	0	0	0
FGD1	7	17	8
FGF17	2	8	5
FGF8	10	16	11
FICD	1	3	4
FOXJ1	0	0	0
FOXO4	0	0	0
FSD1	0	0	0
GAB2	0	0	0
GABRQ	0	0	0
GBE1	0	4	8
GCK	3	9	5
GCNT1	4	4	6
GLIS3	2	5	1
GPR35	0	6	0
GSR	2	6	7
HDX	0	0	0
HMGXB3	0	0	0
HOXB4	0	0	0
IER3IP1	0	2	1
IFNGR1	2	9	1
IGF1R	9	20	14
INHBA	0	1	15
IQGAP3	4	2	7
ISLR2	0	0	0
ITGA9	2	5	1
ITGB3	0	0	0
ITGB5	1	6	1
JUN	0	0	0
KCND1	2	0	0
KCTD20	1	2	1
KIAA0040	0	0	0
KIAA1804	1	3	5
KRAS	0	6	0
LAMP5	0	2	0
LOC1027248	0	0	0
LOC730183	0	1	0
LPAR1	5	11	0
LPAR5	0	1	0
LRRC10B	0	0	0
LYPD2	1	1	5
MAGEB6	0	0	0
MAP3K11	1	11	3
MDK	3	1	1
MECOM	6	18	2
MEIS2	2	21	0

SOX5	11	2	5	1
C15orf54	0	0	0	0
ARID1A	4	1	8	2
PIK3C2G	4	0	3	1
SEMA3D	1	0	0	0
PCDH10	2	0	1	0
GALNTL6	0	0	0	0
USP25	1	0	5	1
ISL1	22	6	9	1
NRXN1	1	3	4	0
DNAJC11	0	0	1	0
TRIT1	1	2	16	3
MIER1	5	1	9	1
DIRAS2	1	2	1	0
MTIF2	3	3	49	2
LSAMP	1	0	0	1
GLIS3	4	1	0	0
KIAA1217	4	3	3	0
AGBL1	0	0	1	0
FAM5C	1	0	0	1
OR7E156P	1	0	0	1
RAPGEF4	16	2	4	1
MIR3134	1	0	0	1
LOC91948	1	0	0	1
ELK3	2	0	4	0
NEDD9	7	4	3	1
KTN1	0	0	0	0
SNX14	4	1	2	0
PPARG	35	9	28	3

RANBP1	0	9	2	3
RPL13A	1	3	1	1
BUD31	1	3	0	1
CDC45	0	11	3	3
NOC4L	0	4	0	0
EXOSC8	3	3	1	2
DGCR8	2	10	1	2
EXOSC5	1	5	2	3
USP1	4	4	3	5
ANAPC7	1	4	1	1
CCDC73	0	0	0	0
RBBP5	2	5	1	0
ARL2	1	3	0	0
RFC5	3	6	2	3
HDAC3	6	23	3	7
PSMB3	1	5	3	2
RAB1B	8	18	8	1
EIF3H	2	4	2	2
C15orf63	0	0	0	0
GTPBP4	0	5	1	3
PSMA6	2	4	3	1
COX6B1	1	6	3	2
ZBTB80S	1	1	0	0
EIF6	0	10	3	4
CDAN1	5	3	2	1
RSL24D1	2	4	2	2
PES1	1	5	1	1
SKP1	8	21	8	6
EIF1	1	3	1	2
HSPD1	7	18	5	3
PFDN6	0	0	1	0
MED21	2	9	3	2
WDR55	0	1	0	0
CWC25	1	1	0	0
RPA3	0	4	3	0
UTP14A	0	7	1	1
CHORDC1	3	3	0	1
RBM48	2	0	0	0
DDX41	0	7	1	2
PSME3	0	6	3	0
AURKA	2	13	5	3
NCL	3	16	2	3
RPS9	1	2	2	1
POLR3B	5	2	2	1
MPLKIP	1	3	4	0
UFD1L	1	5	0	1
ZMYND8	1	1	0	0
CCNA2	1	14	7	4
ALG2	2	3	1	1
RPAIN	0	1	0	0
EIF2S2	2	6	5	1
SNAPC4	2	0	0	1
FCGR1A	3	11	4	1

MGAT3	0	0	0
MLLT6	0	0	0
MMRN2	1	4	10
MRFAP1	1	3	9
MRPS35	2	3	42
MSRB3	2	0	1
NBL1	0	3	4
NEFM	0	0	0
NEIL3	1	2	18
NEK5	1	2	1
NFS1	3	14	8
OSBPL1A	3	0	2
P2RY1	0	0	0
P2RY8	1	3	2
PABPC5	2	1	3
PAK7	0	0	0
PBX1	2	9	1
PBX2	0	1	0
PCDH7	3	0	0
PDCD4	0	9	11
PHB	2	9	25
PHC2	0	3	5
PLEKHG5	1	13	2
PLXDC2	3	3	0
PPDPF	0	0	0
PRKCE	0	0	0
PROM1	7	16	7
PSMF1	0	1	15
PYGO1	0	3	0
RAB42	0	0	0
RAPGEF1	7	13	2
RASGRF1	3	15	8
RASSF5	3	17	5
RHOG	0	0	0
RNF223	0	0	0
RNF41	0	1	4
RNF6	1	4	4
RPS16	1	4	42
RRAS2	9	17	11
SEBOX	0	0	0
SHB	1	7	1
SIGIRR	1	3	1
SLC19A2	1	3	1
SLC25A20	2	3	5
SLC2A3	0	0	0
SLC32A1	5	3	2
SNED1	0	1	0
SNX13	3	1	1
SOCS6	0	0	0
SPHK1	1	4	10
SSC5D	0	0	0
STAT4	3	15	8
STAU2	4	1	5

PFDN4	2	4	0	1
C5orf62	0	0	0	0
C7orf23	0	0	0	0
PGP	0	2	0	0
ACTR6	5	6	4	2
CNPY2	0	1	4	1
CCDC58	0	0	1	0
MCM3AP	1	0	0	0
SERAC1	0	0	0	0
RFC3	3	3	1	5
POLR1A	3	2	1	1
TRMT6	0	3	0	0
YPEL1	0	0	0	0
TRIAP1	0	0	0	0
TOR1B	0	0	0	0
OR5AR1	0	0	0	0
MAX	6	16	4	3
STX18	1	3	0	0
SNRPG	2	2	1	2
RBMX	3	6	1	1
POLRMT	0	0	0	0
GCSH	3	2	3	2
PDRG1	0	1	0	0
NRF1	2	6	0	0
EIF5	2	3	1	2
ELAC2	2	7	1	0
RAN	12	13	9	5
BCAS2	2	3	3	3
CTU1	0	0	0	0
CNIH4	0	0	0	1
EXOSC1	1	2	1	0
GINS2	0	2	3	0
TAF1C	1	4	0	1
TARS	4	3	4	2
RPL36	2	2	1	3
MRPS18C	0	0	1	0
MRPL36	0	0	1	0
MFAP1	0	1	2	1
FAM185A	0	0	0	0
VN1R2	0	0	0	0
VPS13D	1	0	0	0
ANAPC1	2	3	2	0
CEBPZ	7	7	1	2
FARSA	2	5	1	1
NBR1	2	3	1	4
XPO1	0	0	0	0
KRTCAP2	1	0	1	1
C19orf69	0	0	0	0
RRP1B	0	4	0	0
SPTLC1	1	2	1	0
CFHR4	1	0	0	0
SRCAP	3	3	2	1
HAUS1	2	1	2	1

TAPBP	1	1	5
TAS2R19	0	1	0
TCEA2	1	2	11
TCF7L1	0	0	3
TEAD4	1	4	4
TFAP2C	1	5	4
TFEB	3	28	5
TMEM129	0	0	0
TMEM133	0	1	0
TMEM199	0	0	0
TMEM26	0	0	1
TNFRSF1B	7	17	8
TNNC1	1	3	2
TNRC18	3	0	0
TOR3A	0	0	0
TRIB1	1	9	5
TRIM65	0	3	5
TRIM7	0	0	0
TYW1	1	1	3
UBE2E3	0	0	0
VKORC1	1	5	7
VSX1	4	2	2
WNT7A	6	6	0
ZASP	0	0	0
ZCCHC11	12	17	11
ZFHx4	7	9	9
ZNF582	0	1	1
ZNF704	4	12	3
ZNF747	0	0	0
ZNF83	0	3	4

ATR	4	6	5	1
AHSA2	3	1	1	0
SPHAR	2	0	1	0
NUPL1	1	2	0	0
SMG1	0	4	0	1
KIAA0586	0	1	1	0
RPP21	0	0	0	4
LSM11	0	0	0	0
NDNL2	2	0	1	0
ACTL6B	2	4	1	3
MMS22L	1	2	1	0
UBA52	29	73	24	8
PPP2R3C	1	1	1	1
PRPF6	2	2	0	1
ATP5I	0	0	0	0
HCFC1	5	15	1	2
PABPN1	0	11	0	1
SFSWAP	1	1	0	0
GINS1	1	2	2	1
ATP5B	4	10	5	4
PPP4C	1	8	3	3
ZNF513	0	2	1	0
C15orf42	0	0	0	0
CHKA	1	11	4	1
RBM39	0	1	2	1
HAUS5	0	0	0	0
FANCM	1	2	0	0
DNAJC17	0	1	0	0
C21orf59	0	0	0	0
TDO2	0	0	0	0
BRAT1	0	1	0	0
TOMM22	0	1	1	1
OVGP1	1	1	1	0
SMC5	0	0	1	1
C19orf52	0	0	0	0
U2AF1	1	3	0	2
HORMAD2	1	1	0	0
GLRA1	6	4	3	0
FAM98B	0	0	0	0
MYC	29	53	16	6
PDCD7	0	1	0	0
PSIP1	4	7	0	2
HELZ	1	2	0	1
ANKLE2	0	0	0	1
RPS6	5	13	8	3
PADI4	1	4	1	1
PRPF38A	0	0	0	0
GTF3C1	1	4	0	1
ASNS	1	4	0	0
PPYR1	0	0	0	0
SUZ12	3	15	2	3
SAFB	2	6	0	0
SPC24	0	2	2	0

FAM63B	0	0	0	0
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enesets. PB, transposon.

shRNA	ORF	PB	dCAS9	CRISPR	shRNA
0	NR4A1	5	3	5	2
0	TFEB	3	17	5	1
0	POU5F1	4	2	10	2
0	YAP1	6	5	9	1
0	MITF	7	4	15	3
0	GCM2	5	1	1	0
0	ETV1	5	2	6	1
1	HNF4A	14	9	17	3
0	MYOD1	16	12	22	4
3	TFAP2A	12	1	8	1
0	FOXP3	10	8	9	4
0	ASCL2	2	3	7	1
4	MEOX2	1	0	0	0
0	HOXD9	6	8	15	2
0	FOXA3	3	0	1	2
0	TLE1	3	2	11	1
0	ASCL4	0	0	2	0
0	ETS2	5	3	5	2
1	TGIF1	1	0	1	0
0	SOX14	4	1	1	0
2	PASD1	0	0	3	0
0	HOXC11	5	0	4	0
0	EBF1	9	4	8	2
0	JUNB	8	5	11	2
0	KLF6	4	2	8	3
0	SATB1	1	1	6	1
0	SHOX2	5	1	1	0
0	GPR101	0	2	5	1
0	GPR35	0	5	0	0
0	LPAR1	5	9	0	0
2	GPR132	2	1	7	0
0	GPR52	0	1	0	0
0	GPR161	1	0	0	0
2	GPR119	2	1	1	0
0	GNA15	3	7	15	3
0	P2RY8	1	2	2	0
0	NGEF	5	3	3	0
0	PLEKHG5	1	11	2	0
2	ARHGEF9	3	2	9	2
0	PLEKHG3	0	0	0	0
0	PLEKHG6	1	1	1	0
0	RASGRP4	0	1	2	1
1	ARHGEF19	1	0	0	0
0	ARHGEF3	3	3	0	0
0	RAF1	10	5	11	2
0	PAK3	3	2	8	0
0	PAK1	6	11	15	3
0	MOS	1	1	3	0
0	FBXO5	1	1	40	3
0	TNFAIP1	0	0	2	0

shRNA	PB	ORF	dCAS9	CRISPR
NF1	15	25	5	16
HOXD8	2	3	1	4
COL8A1	1	0	1	0
VCX3A	0	0	0	1
POFUT1	1	4	1	7
NCF1	2	12	1	1
MAP1S	0	2	1	9
MRS2	10	4	3	20
MORF4	1	1	0	0
EMP2	1	0	2	1
TNKS1BP1	1	0	1	1
POTEB	0	0	0	0
TFDP1	0	6	2	22
ZNF606	2	0	0	0
HSPC105	1	1	0	0
ATP1A1	2	6	1	9
LOC402434	1	1	0	0
WDR57	0	4	0	36
RPL6	1	8	4	54
RPP21	0	0	0	15
MED12	1	15	1	18
SFPQ	2	5	0	27
CSRNP1	0	8	1	0
SPOCK3	3	0	1	0
FYB	4	15	1	5
HDAC2	13	29	7	58
GSK3A	4	11	4	10
PRKACB	1	4	4	5
THNSL2	0	0	0	0
C2Oorf85	0	0	0	0
CHMP2A	1	6	1	16

1	KLHL10	0	0	4	2
1	ARIH1	0	0	10	0
0	FRS3	0	2	1	0
0	SQSTM1	7	1	16	4
0	GAB1	3	2	1	0
7	RAPSN	2	1	0	0
0	CARD9	1	4	6	2
0	WDR5	3	2	32	2
2	LCK	15	9	13	3
1	HCK	6	6	8	2
1	AHDC1	2	0	1	0
0	BEND5	1	0	0	0
0	PVRL1	4	2	2	0
0	UNC45B	1	1	2	0
0	FGR	9	9	11	2
0	AXL	0	1	2	0
0	FGF6	0	5	3	1
0	PI16	0	0	1	0
1	RIT1	1	0	2	1
0	RIT2	1	0	0	0
0	SAMD4B	0	1	7	0
0	PSMC5	4	3	42	2
0	ICAM3	2	3	1	2
0	ADAP2	1	1	1	3
0	KCTD17	0	0	1	0
0	SLC35A4	0	0	3	0
0	VPS28	1	2	16	1
0	MPPED1	1	0	1	0
3	MECP2	8	5	15	4
0	BRMS1L	2	1	8	1
1	FBP1	3	3	10	0
0	MLYCD	2	1	4	0
0	DNAJC5B	0	0	5	1
0	BCL2L1	5	3	16	2
0	IGHA2	1	0	3	0
0	FOS	26	22	42	4
0	XBP1	2	1	9	0
0	MAFB	3	3	4	0
0	WWTR1	16	2	4	0
0	SATB2	6	2	4	1
0	ESRRG	22	1	3	0
0	NR4A2	5	1	2	2
0	SP6	1	0	5	0
0	MEIS2	2	17	0	1
0	HAND2	5	1	10	0
0	HEY1	5	3	9	2
0	NFE2L1	1	1	4	0
0	FOXP2	24	4	10	1
1	HEY2	4	0	5	1
3	ISX	0	0	0	0
0	OLIG3	3	1	2	0
0	TP53	28	21	74	9
1	ZNF423	3	0	1	0

0	FOXJ1	4	3	3	0
0	MYF6	3	5	8	0
1	PURG	2	1	3	0
0	ZNF503	1	0	0	0
2	SIM2	9	2	9	2
0	CRX	2	3	6	0
0	SP8	7	2	2	0
0	USF1	7	1	17	2
0	NANOG	11	7	20	3
0	LPAR4	0	0	0	0
4	MAS1	8	4	5	3
0	GPR4	3	1	0	0
0	ADCY9	3	4	8	2
0	HTR2C	4	3	3	0
0	ADORA2A	0	2	4	0
0	GPBAR1	0	0	0	0
0	GPR3	1	0	0	0
0	VAV1	14	11	14	3
0	MCF2L	3	2	2	0
0	TBC1D3G	0	1	1	0
1	ARHGEF2	1	3	3	1
1	RASGRP3	2	2	1	0
0	SPATA13	1	3	5	1
0	IQSEC1	0	3	0	0
0	RAPGEF4	11	2	4	1
0	RASGRP2	4	4	0	1
1	PRKACA	8	6	10	3
0	NF2	3	4	9	2
0	PRKCE	8	3	5	1
0	MAP3K14	1	0	0	1
0	KLHL3	0	0	3	0
1	TRIM62	0	0	1	0
1	KLHL2	2	2	7	0
0	TRIM50	0	0	2	1
0	CRKL	6	15	11	1
0	CRK	12	13	12	2
1	TRAF3IP2	1	0	1	0
1	TEX11	3	0	1	0
1	CIQA	1	0	0	1
0	SRC	33	25	34	6
0	BTK	4	4	10	2
0	LYN	0	0	0	0
0	KLHL34	0	1	1	1
1	WDR18	1	2	31	1
0	PCDHGB1	0	0	0	0
0	TEKT5	0	1	0	0
0	TYRO3	6	5	8	0
0	FGFR2	16	12	12	3
0	CHGA	5	5	5	2
1	IFNA10	0	1	0	0
0	RHOBTB2	3	2	1	0
1	SAMD4A	1	0	9	0
0	FXR2	2	1	7	1

0	ATAD1	5	2	13	0
0	F3	10	4	11	1
0	RGS11	2	1	1	0
0	KCTD1	0	2	1	0
1	SLC4A2	1	1	0	0
0	MAGEA9	0	0	0	0
1	PPP1CA	6	12	85	9
0	EIF4H	0	3	35	3
0	TPI1	1	6	32	0
0	NASP	0	0	0	0
0	TNFRSF13B	1	0	2	0
2	CYP2E1	1	1	2	0
1	CCDC150	0	1	1	0
0					
0					
1					
1					
0					
0					
0					
0					
1					
2					
0					
2					
2					
0					
1					
0					
0					

Table S5. Core geneset highly connected to all screens.

List of genes from RefSeq database with at least 10 STRING connections to each screen geneset, excluding the small geneset of shRNA screen.

Gene	ENSP_ID	PB	ORF	dCAS9	CRISPR	shRNA
CD4	ENSP00000011653	18	46	19	45	8
ESR1	ENSP000000206249	25	54	23	70	4
VCL	ENSP000000211998	11	24	10	10	1
MAPK1	ENSP000000215832	21	51	19	28	7
RNASEH2A	ENSP000000221486	10	20	10	52	5
TGFB1	ENSP000000221930	23	43	18	33	5
CCND1	ENSP000000227507	24	60	22	46	5
PXN	ENSP000000228307	11	30	13	11	3
IFNG	ENSP000000229135	20	38	17	31	4
GAPDH	ENSP000000229239	26	68	20	65	4
ENO2	ENSP000000229277	11	20	11	27	2
MAPK14	ENSP000000229794	20	41	11	25	6
ENO1	ENSP000000234590	11	15	11	45	4
CDKN1A	ENSP000000244741	15	42	15	43	7
RAC2	ENSP000000249071	11	31	12	13	3
MYOD1	ENSP000000250003	16	36	12	22	4
APOE	ENSP000000252486	13	26	11	18	2
EPO	ENSP000000252723	12	28	13	21	3
MX1	ENSP000000252971	21	37	13	13	0
H3F3B	ENSP000000254810	18	40	11	55	9
KRAS	ENSP000000256078	13	46	15	30	9
IL6	ENSP000000258743	19	47	15	29	5
CDH1	ENSP000000261769	23	46	16	31	2
PDGFRB	ENSP000000261799	16	24	10	16	2
N/A	ENSP000000262266	24	49	16	79	5
MAPK3	ENSP000000263025	15	38	12	27	7
TYR	ENSP000000263321	23	41	27	44	8
IL1B	ENSP000000263341	10	32	10	21	3
PIK3CA	ENSP000000263967	15	47	18	24	3
STAT3	ENSP000000264657	18	44	13	25	4
POMC	ENSP000000264708	15	36	12	17	4
N/A	ENSP000000264998	13	32	10	23	1
KNG1	ENSP000000265023	12	25	10	12	2
EGF	ENSP000000265171	30	46	19	28	7
SRF	ENSP000000265354	14	30	13	18	2
N/A	ENSP000000266427	17	19	10	20	3
RB1	ENSP000000267163	12	27	11	30	4
CDH2	ENSP000000269141	15	18	11	11	1
TP53	ENSP000000269305	28	58	21	74	9
ERBB2	ENSP000000269571	30	41	20	37	6
SOD1	ENSP000000270142	11	21	10	59	3
AKT1	ENSP000000270202	36	70	32	52	8
CALM2	ENSP000000272298	24	49	20	47	5
FTH1	ENSP000000273550	15	32	12	38	4
EGFR	ENSP000000275493	29	54	22	35	7
NOTCH1	ENSP000000277541	25	52	16	24	8
CD44	ENSP000000278385	17	45	14	16	1
N/A	ENSP000000284384	10	21	11	18	4
SST	ENSP000000287641	16	32	11	17	3

PIK3CB	ENSP00000289153	11	40	14	21	3
CALM3	ENSP00000291295	26	49	20	38	4
REL	ENSP00000295025	19	34	12	30	5
ALPPL2	ENSP00000295453	24	43	13	32	6
ALB	ENSP00000295897	33	63	27	71	8
SHH	ENSP00000297261	21	36	12	16	5
NOS3	ENSP00000297494	11	31	12	18	0
N/A	ENSP00000299293	10	18	12	12	2
CRK	ENSP00000300574	12	21	13	12	2
PRL	ENSP00000302150	18	36	11	20	1
VAV1	ENSP00000302269	10	22	11	14	3
IGF1	ENSP00000302665	20	42	14	23	6
BCR	ENSP00000303507	11	37	12	18	1
RAC3	ENSP00000304283	17	45	20	20	4
FOS	ENSP00000306245	26	62	22	42	4
CYCS	ENSP00000307786	10	41	11	46	4
HRAS	ENSP00000309845	34	65	25	50	11
CASP3	ENSP00000311032	18	46	18	42	5
LEP	ENSP00000312652	21	35	11	20	2
CDC42	ENSP00000314458	23	45	18	23	3
ZHX2	ENSP00000314709	21	37	16	21	1
MET	ENSP00000317272	11	28	12	11	1
HSD17B6	ENSP00000318631	14	15	10	11	2
POLE	ENSP00000322570	23	45	16	69	5
DNMT3B	ENSP00000328547	10	23	10	32	4
TSPO	ENSP00000328973	36	78	32	73	9
ACTG1	ENSP00000331514	12	30	11	51	5
SMAD3	ENSP00000332973	11	22	10	16	5
FGF1	ENSP00000338548	19	33	12	16	2
GRB2	ENSP00000339007	16	44	15	32	2
SMAD4	ENSP00000341551	16	34	11	30	3
ADCY2	ENSP00000342952	13	27	10	15	2
PKN1	ENSP00000343325	13	25	12	18	4
CTNNB1	ENSP00000344456	18	35	13	27	5
UBC	ENSP00000344818	42	60	37	188	16
FN1	ENSP00000346839	23	41	20	28	6
RET	ENSP00000347942	17	22	15	16	2
MBP	ENSP00000348273	10	27	10	16	2
RAC1	ENSP00000348461	19	47	20	23	6
INS-IGF2	ENSP00000348986	38	69	30	72	10
CALM1	ENSP00000349467	27	53	21	41	4
ACTB	ENSP00000349960	13	29	11	52	5
BRCA1	ENSP00000350283	13	31	11	59	3
SRC	ENSP00000350941	33	58	25	34	6
REV3L	ENSP00000351697	26	47	17	70	5
PIK3CG	ENSP00000352121	14	39	13	21	4
DNAH8	ENSP00000352312	15	42	13	45	6
MAPK8	ENSP00000353483	15	31	11	21	2
MTOR	ENSP00000354558	17	45	12	35	4
CDKN2A	ENSP00000355153	14	40	11	35	5
H3F3A	ENSP00000355778	17	40	13	59	9
PARK2	ENSP00000355865	15	37	14	25	5
PTGS2	ENSP00000356438	15	37	14	19	3

NES	ENSP00000357206	16	24	10	20	1
FYN	ENSP00000357656	14	32	12	13	1
N/A	ENSP00000358175	14	41	11	48	8
NGF	ENSP00000358525	26	44	17	33	5
NRAS	ENSP00000358548	14	42	15	36	9
JUN	ENSP00000360266	27	62	25	51	5
PTEN	ENSP00000361021	27	48	15	44	6
VEGFA	ENSP00000361125	25	54	21	36	7
CD40	ENSP00000361359	10	29	10	18	3
MMP9	ENSP00000361405	12	34	13	16	3
ALPL	ENSP00000363965	24	43	13	32	5
MYC	ENSP00000367207	29	53	16	58	6
CKAP2	ENSP00000367276	13	22	16	58	5
POLA1	ENSP00000368349	23	52	15	73	8
PCNA	ENSP00000368438	14	32	12	95	7
JAK2	ENSP00000371067	13	33	11	19	2
ALPP	ENSP00000375881	25	45	14	33	6
PAX3	ENSP00000375921	12	24	11	12	1
N/A	ENSP00000376688	12	19	11	11	5
FGFR1	ENSP00000380280	14	21	12	13	1
RELA	ENSP00000384273	12	32	11	29	4
ELAVL1	ENSP00000385269	17	33	14	60	6
CXCR4	ENSP00000386884	10	33	10	18	3
GCG	ENSP00000387662	11	36	10	12	2
UBA52	ENSP00000388107	29	73	24	104	8
N/A	ENSP00000389265	15	41	17	39	3
N/A	ENSP00000392858	17	43	17	39	3
TNF	ENSP00000398698	19	50	21	50	6
FGFR2	ENSP00000410294	16	24	12	12	3
BDNF	ENSP00000414303	16	35	13	23	3
TGFBI	ENSP00000416330	15	36	15	15	1

Table S6. Differentially expressed genes between PLX4720 sensitive and resistant BRAF V600E melanoma cell lines

Shown are gene expression measured by U219 microarray. Cell lines are sorted by PLX4720 IC50 and splitted to a sensitive group an

Gene	WM278	A375	WM35	MMAC-SF	UACC-62	IGR-37	MEL-HO
ABTB2	8.2585	6.95618	7.83118	7.2887	6.14106	4.88887	5.75692
ACAM	3.18788	4.45323	2.74345	2.7257	2.83797	2.88925	2.88759
ACAN	8.71187	8.39678	5.10148	3.20172	5.95878	3.20097	3.37094
ACP6	9.41095	8.56747	6.49242	7.43934	8.83154	7.59868	6.81361
ACPL2	10.0686	11.3344	8.81519	5.98298	9.59488	7.44799	6.00857
ACSS1	8.77134	7.11986	9.87193	7.94931	7.61095	10.3355	9.19028
ACTA2	8.83244	8.88175	7.9439	8.31004	8.53396	2.99651	6.88397
ACTG2	3.15115	3.03746	3.72235	3.46038	3.20627	4.17376	3.89697
ACTN2	5.37916	5.28188	6.39316	3.18369	5.36094	3.51866	3.186
ADAMTS5	3.10337	2.84638	2.75143	3.03019	2.79788	2.96584	2.82631
ADORA2B	8.52292	8.7806	7.69217	4.10734	9.41386	4.52739	7.08145
ADRBK2	3.95695	3.81131	4.76954	7.7916	4.69764	8.16277	5.58257
AGPAT9	8.89994	8.85594	8.72935	6.81138	7.91284	7.96381	8.51016
AHCYL2	7.63261	7.51852	6.84801	7.89043	6.96812	8.63862	8.60324
AK5	3.13991	3.46269	3.09688	4.77637	3.12049	3.24942	3.23995
AKR1C2	5.92739	10.5279	3.42945	6.7616	5.13844	3.33419	3.4159
ALCAM	9.54927	8.45375	8.1764	3.06259	9.73839	5.4516	3.69971
ALDH1A1	6.63325	3.70083	4.96361	9.40701	5.91952	5.87293	4.52941
ALDH2	4.00529	6.70421	3.3957	3.90979	3.37327	4.07939	3.69771
ALDH5A1	4.16672	6.04993	5.11052	4.04907	5.0507	6.52797	4.59138
ALDOC	7.99837	8.21539	3.31339	3.67426	9.86451	3.70414	8.03534
AMIGO2	8.32555	7.79071	3.33263	3.69777	3.64606	3.40481	5.12985
ANGPT1	9.95819	6.19931	6.45165	3.27577	9.15921	3.62	3.28766
ANGPTL2	4.22583	6.68216	6.45826	8.14525	8.23181	8.29733	7.07279
ANGPTL7	5.04071	4.26361	3.56483	3.63993	5.48637	3.52402	3.35466
ANKRD12	6.63894	6.38733	6.18818	6.10688	6.84928	3.83643	7.36904
ANLN	7.49928	6.20526	7.80264	7.17468	8.49829	6.26324	8.21604
ANO4	3.14077	4.65371	2.80431	6.69521	3.7704	2.94063	6.97283
ANP32E	3.89364	5.70769	5.34688	3.70768	6.99183	4.60904	6.67464
ANPEP	3.53035	5.32474	3.43121	3.59004	3.56258	3.31925	3.35573
APOC2	3.07412	3.26914	10.7122	4.12368	4.06168	8.96369	3.57575
APOD	6.65569	3.59603	11.8712	6.4216	8.98616	7.25809	10.8206
ARHGAP6	5.41915	5.39492	3.33287	4.18929	8.47056	3.0214	3.01554
ARNT2	9.7775	10.7444	9.35187	8.89063	9.12655	9.30936	8.26186
ASPM	6.98449	8.28634	6.90651	6.15908	8.34053	5.86312	7.67716
ATRX	7.14362	7.73714	4.7361	6.27761	8.14968	4.53632	5.59361
ATRX LOC651	8.57129	8.41176	6.44951	7.7714	8.18056	4.56441	6.03126
AZGP1	6.69023	7.23953	7.93646	3.30557	5.59347	3.88101	3.58969
AZK*	4.69982	4.75018	5.25072	4.62339	4.79145	4.62558	4.45251
B3GALNT1	4.04334	3.20585	3.85329	3.47361	3.34501	3.55427	6.86144
BAALC	4.50078	4.67595	3.43143	3.38709	8.75524	3.19337	5.75288
BASP1	4.49866	3.24208	2.97687	3.30284	3.28333	3.09031	2.95524
BAT2L2	7.19991	7.4202	6.56073	6.9273	8.04149	4.44973	7.20418
BCAN	2.76711	2.94836	3.99615	7.34395	2.80579	8.34735	4.19325
BCL2A1	7.58768	6.43054	10.2834	9.19059	9.70207	9.50122	9.80269
BDKRB1	2.93496	2.93949	2.79308	2.82247	2.69225	2.83255	2.82816
BDNF	3.7972	2.97136	3.06216	2.78025	3.00673	3.09819	3.10408
BEST1	3.71223	4.43004	6.20468	8.20479	4.0061	8.03498	6.11141
BEX1	5.61204	3.22091	3.1932	8.06528	4.85987	4.28001	3.31979

BFSP1	9.70302	8.15319	4.4421	4.5402	6.63555	4.83462	3.25423
BHLHE41	7.07243	4.44272	9.35822	9.93152	6.36853	9.59543	9.79668
BST2	11.1036	6.80162	10.7984	12.0148	10.8278	6.66044	10.7598
BTBD10	6.64637	5.83203	6.50463	7.48965	6.73706	6.53149	6.78458
BTBD16	8.75242	6.28669	4.05196	4.14529	5.13771	3.19654	3.16838
BTG2	4.50032	6.81643	5.52466	6.1254	6.77263	4.91901	6.09264
BUB1	6.21632	6.09707	7.36186	4.97389	7.83099	7.76724	8.20643
C10orf90	9.2051	8.06452	6.87362	7.4564	7.21806	5.80602	6.48847
C14orf106	3.22874	3.80551	4.18406	3.06798	5.61587	2.85805	5.06307
C14orf145	4.17577	4.00108	5.53935	4.43349	5.40144	4.25241	5.61117
C1orf59	3.62236	4.75536	3.8645	3.99349	3.42074	4.42842	3.34784
C1S	10.9289	3.7252	3.16441	9.27198	5.55986	4.66976	3.24498
C22orf9	6.42482	5.64464	9.79125	7.38687	7.369	8.41734	9.32044
C3orf70	9.25916	5.56992	7.18038	4.83969	7.94141	7.62647	6.99592
C4orf7	10.0105	10.4315	2.79988	2.98279	2.96576	3.06316	3.1166
C5orf62	3.47187	3.30335	3.53146	3.7237	7.70414	3.08762	3.57819
C6orf167	4.72609	4.78525	5.39117	3.92472	5.80863	5.58321	5.59
C6orf192	7.90293	8.80532	10.0247	9.94034	6.9973	9.47323	8.01852
CACNA1A	3.29201	5.29593	3.20028	3.34105	3.07724	5.96721	3.54277
CAPG	3.7265	8.6782	10.8589	11.2194	5.89172	11.9379	12.1787
CAPN3	5.29114	4.87662	8.45018	11.0911	8.09062	11.4542	11.5799
CASP8AP2	6.70213	7.20518	7.68547	6.65981	6.92198	5.23884	7.24925
CCDC88A	5.96478	3.39676	3.62218	3.87	5.27772	3.22674	6.12621
CD200	9.931	7.96687	9.95917	7.58754	9.19153	9.63867	7.28623
CD59	7.79907	4.40181	6.03293	5.2168	4.61485	4.14039	5.34081
CD74	9.97148	10.3956	7.92009	10.4758	8.51839	2.932	3.91288
CD9	10.2613	9.86521	9.3397	10.027	8.09842	10.3043	7.8994
CDH1	3.01485	2.79166	3.14161	9.01171	2.82625	4.69893	9.33274
CDH13	8.78142	11.2208	3.04523	3.14919	5.95074	2.99043	2.84878
CEACAM1	3.27589	3.38443	7.06754	10.0263	6.65833	8.95768	8.86807
CENPE	6.06774	5.7465	5.83922	4.27124	6.63911	3.37695	7.90655
CENPF	5.36456	5.93614	5.54656	4.3	7.86143	3.52229	7.33593
CENPV	3.57598	5.73647	3.75467	3.95819	3.44212	3.97649	3.86378
CEP152	6.71089	6.75452	6.52932	7.11797	6.92122	5.93468	7.51277
CEP55	6.60808	7.27837	7.92757	7.06607	7.35206	6.80759	8.41586
CFH	5.75758	3.28432	2.68159	3.007	5.00843	2.78859	2.63945
CFH CFHR1	6.15574	3.74464	3.66674	3.35437	5.47362	3.28736	3.36716
CHRD1	7.94198	10.7094	3.22856	3.55317	9.62219	3.37363	3.35819
CKAP2L	6.52535	6.22612	7.36646	4.94596	7.22979	5.10999	6.58226
CKB	3.49231	6.74947	4.81939	3.98592	8.16507	5.87093	6.72897
CKS1B	5.87407	8.18789	8.14767	6.70395	7.67537	8.20869	8.65142
CLCN5	6.29997	5.83349	6.36084	7.05075	6.54958	6.80208	4.73639
CMBL	8.66665	9.11423	5.99201	8.48175	8.89135	3.42697	5.82216
CNIH3	4.00276	4.9542	8.8409	4.59223	7.49959	8.47374	8.20309
CNTN3	2.90583	8.26627	2.92964	7.45796	3.30658	2.74056	2.84308
COL14A1	3.05406	2.84752	3.02959	2.96395	4.41844	3.19046	7.38014
COL16A1	8.45944	10.5734	7.58258	8.6678	9.0507	7.26527	3.8768
COL22A1	8.66164	4.34814	3.11662	7.69247	5.35972	3.28457	3.19104
COL3A1	2.86008	2.72116	2.80993	2.78973	3.30968	2.78612	2.83722
COL4A5	8.55277	6.69834	4.40207	6.37792	6.87841	4.28698	3.17089
COL5A1	4.59344	5.73455	3.5195	3.51963	6.57251	3.54382	3.93018
COL6A3	3.15489	2.99285	2.96598	2.91236	5.83356	2.89954	2.97774
COL9A1	5.76536	4.20485	3.27201	3.3179	7.40931	2.83235	3.14028

COLEC10	2.91222	2.76455	2.95429	3.07438	2.92252	2.95743	2.84227
COLEC12	6.28786	7.55537	3.67317	3.72215	4.38605	3.79397	3.87096
COPZ2	8.51268	7.74166	8.56162	8.87813	8.45581	7.60348	4.69078
CORO2B	3.71542	4.2035	7.18068	6.99951	4.69919	5.25999	3.94661
CPM	7.33507	5.1515	6.81795	7.97405	7.26098	4.23421	6.80248
CPN1	9.59088	8.81121	9.30309	9.60976	6.83171	7.34313	8.8071
CPPED1	5.39229	6.17408	7.87582	7.6741	7.6949	7.21121	8.25937
CPT1C	3.91753	3.74113	6.49772	3.15444	7.42656	7.38568	3.33224
CPXM2	3.22319	3.43267	3.32067	3.40334	3.09419	3.32112	3.33276
CRYAB	4.30404	5.45491	8.59867	12.592	10.1962	8.37825	4.43509
CRYL1	9.79107	9.1526	9.22477	8.85883	7.10864	9.81359	7.06585
CSAG3 CSAG	7.82768	10.0585	4.90049	3.11681	8.47324	3.82554	4.40234
CSPG4	8.03189	8.62419	8.01748	3.25801	6.19523	8.40574	6.93866
CT45A3 CT45	6.36594	11.525	3.18581	2.92324	11.966	3.06696	3.18603
CTAG1B CTA	3.40597	10.1414	3.43312	3.34419	3.87797	3.42076	3.56846
CTGF	10.0394	4.68981	6.77341	4.82101	11.1495	4.07671	4.71415
CTSZ	10.3575	9.14078	10.2906	10.9196	9.7428	10.8162	7.53611
CUBN	4.79598	3.28474	3.66733	4.0425	8.2404	3.60009	3.39272
CXCL1	11.8752	9.23278	7.44778	8.543	7.17706	7.17594	7.73468
CYB5R2	9.36771	3.63469	2.90671	3.80716	5.38665	3.72244	7.13055
CYP27A1	9.27298	6.37773	8.47124	8.42666	8.51493	8.67588	8.52683
CYR61	7.73891	7.68968	3.05013	4.77523	8.99128	3.45685	3.39514
DAAM2	5.94765	7.86654	9.21862	8.11483	8.24382	7.29427	7.91841
DCT	3.24345	4.23577	12.3174	12.2112	5.66867	12.742	12.3519
DDX43	3.28986	3.41495	3.51773	3.36768	6.05977	5.35709	3.13397
DEK	6.799	6.87081	8.18305	7.24214	6.61224	5.51318	8.11526
DEPDC1	7.09128	7.21381	7.54891	7.03151	8.98856	6.81584	9.00233
DEPDC6	4.11972	6.87314	6.08783	5.54354	7.80412	5.42843	2.97774
DHRS3	11.0265	11.0344	4.52268	3.79381	5.35258	3.54983	4.64069
DIAPH3	5.86756	4.73833	5.9081	5.25106	6.42906	7.09756	6.62823
DIP2B	3.99579	5.67508	7.14492	4.29341	7.01543	7.05636	7.73963
DLGAP5	6.72183	7.11712	7.92136	5.45176	8.58858	6.74591	9.00498
DLL3	5.81574	6.31289	7.18968	7.7114	7.04397	7.99427	10.0974
DNAH9	3.50369	6.25806	3.28645	3.42268	7.50178	3.20774	3.09795
DNER	7.22334	3.08092	3.66982	3.30979	6.90783	6.79859	3.69164
DSE	5.60272	4.52637	4.70059	3.87312	4.17841	5.38428	3.58803
DST	7.27013	4.499	4.96231	4.61669	7.88936	2.9649	6.46381
DTL	4.07681	5.75452	6.21837	5.65629	6.19009	6.12586	5.72952
DUSP23	7.21272	8.85671	7.77647	8.20247	8.93927	8.98477	8.67244
E2F7	5.5398	6.48083	7.48408	5.91257	7.68943	7.54111	7.11094
EBF3	7.84984	9.4417	3.34576	3.41541	6.40923	3.39336	5.8258
ECT2	5.09461	5.8244	6.89295	5.46543	7.01847	6.56713	7.38559
EDA2R	6.71997	4.4885	5.74676	6.71248	6.79049	3.14904	5.20852
EDIL3	9.15211	9.3249	3.79658	4.31683	7.90051	3.35354	3.12372
EDNRB	10.5342	9.68345	9.67577	10.2096	8.37785	10.4271	5.98769
EFHD1	3.33683	3.41065	3.50058	6.94332	3.62544	4.55856	3.60595
EFR3B	7.9205	4.68665	7.11725	8.31927	7.67186	8.48554	6.24992
EGF	5.68051	5.03226	3.03231	3.20521	4.77035	3.0692	7.25092
EGFR	4.52782	4.06115	3.06332	3.79716	4.13417	3.81922	3.19431
EGR3	8.13441	8.71783	9.25807	5.35433	8.41617	7.74522	6.69548
EIF5B	9.14979	8.98676	9.17027	8.688	10.0265	5.48233	10.2244
ELOVL2	7.08022	4.31393	6.85441	6.64995	7.60933	4.06327	8.20773
ENPP2	10.9252	10.5357	7.1856	8.77297	8.8502	5.35802	4.72248

ENSG00000188	6.7443	6.97273	7.05022	7.38575	8.09254	8.05461	7.05203
EPDR1	7.89193	6.61998	8.75497	10.1977	9.59719	9.65948	8.27635
EPHA3	8.89085	8.89312	8.37638	8.7888	9.77779	6.40354	3.10709
EPHX2	4.15671	4.52593	7.36117	4.33785	7.38222	7.46357	6.10415
ERBB3	10.4587	10.9588	9.62403	10.0861	8.70034	9.32117	9.37594
EZR	5.62071	6.54057	7.76934	4.30993	6.54473	4.2741	9.06189
FABP7	10.2424	7.78532	7.48172	3.05605	10.384	9.12176	10.971
FAM101B	6.74816	5.86912	5.36101	9.46461	7.81191	9.69306	7.47738
FAM129A	9.42357	7.42033	3.24098	2.92717	7.68298	3.58135	7.89526
FAM134B	5.76527	8.80648	6.55754	8.2606	8.10079	5.34123	5.82389
FAM167A	4.02593	3.23119	4.15102	3.6272	3.23568	6.65581	3.46577
FAM198B	8.78087	3.74976	5.64849	7.90739	7.47411	4.02917	7.15791
FAP	8.25166	5.53977	9.10307	3.17341	7.70119	5.78098	2.91244
FARP1	8.5987	8.55017	7.05735	6.52361	7.75353	8.59463	8.09797
FARP2	7.31427	4.83249	6.62465	5.85206	7.31632	6.14267	4.73774
FBXL16	5.01107	3.6577	6.76036	6.41456	3.9962	8.03478	3.39679
FCGR2A	9.43208	8.09845	5.0792	5.28395	5.65032	5.00254	6.23128
FCGR2A FCG	10.374	9.25131	6.79357	4.86487	7.9147	5.84435	8.48444
FCGR2B	4.33327	3.96414	5.19588	5.51775	5.5307	7.50104	5.18808
FCRLA	10.9185	6.61194	8.72918	6.76415	7.10649	5.69211	6.84616
FEZ1	9.11101	9.06637	7.81907	4.34845	5.15374	5.34793	3.1419
FLRT2	4.31301	4.80811	4.37102	5.29665	5.80144	7.28454	3.24982
FOSL2	4.98407	4.6102	4.29695	4.94368	5.48365	7.61478	5.32722
FREM2	8.85115	4.98277	6.29658	3.47723	6.98666	3.20013	2.96479
FST	11.0348	11.3215	8.69173	9.12016	8.06207	5.57834	4.36361
FSTL5	4.1846	2.79585	3.10348	3.13987	3.22793	3.08836	3.41364
FXD3	8.63325	11.0125	11.0367	12.0918	9.9954	3.82579	10.9336
GAB2	6.72113	5.45718	7.25181	7.54197	5.80175	6.32579	7.32354
GALC	4.36959	6.89079	4.2893	4.23594	7.37033	4.26799	3.80889
GALNT5	3.05097	4.46112	3.54826	3.2365	8.24001	2.68633	3.22285
GAPDHS	2.83354	3.07499	9.34556	9.17373	7.6913	8.49186	8.4079
GAS1	8.46387	8.16134	7.75869	9.12545	7.21768	8.72119	6.49062
GAS7	11.0433	10.4859	10.2613	10.0472	11.1713	9.14848	7.68787
GBP2	8.25999	9.03383	3.67525	6.90502	5.76995	3.72269	4.63558
GDF11	6.18872	7.4789	7.24934	8.0857	6.98717	5.70325	7.19887
GDF15	9.13398	6.66756	12.3635	12.2095	10.9599	10.2916	12.4294
GHR	8.30979	3.70618	4.21987	7.7356	8.35882	4.31125	7.79015
GIMAP2	7.8123	6.70806	7.24916	5.39763	3.60328	7.31822	6.96705
GLIPR1	5.6884	4.21662	3.41968	3.38207	6.64966	3.61606	4.95529
GNG2	11.0585	10.2898	9.27022	9.2262	10.9281	7.10288	7.7318
GNG7	9.32021	8.19211	8.81876	8.25803	6.63315	8.50392	7.10836
GOLGA4	9.17658	9.63823	9.29486	9.76025	9.07332	4.0244	10.3763
GPC4	6.13656	4.08221	2.58117	7.1191	7.20619	5.80731	2.88758
GPC6	10.4763	9.51948	7.93629	4.26213	9.17102	3.06329	5.21386
GPM6B	4.63388	3.67402	10.505	10.1151	9.72632	10.3093	10.0031
GNMB	11.091	10.5653	12.1456	11.7434	10.8869	12.0351	11.7226
GPR155	9.12864	4.80143	7.91204	4.8487	5.93714	3.76126	4.94471
GPR56	6.6263	9.24391	10.2761	11.2101	10.6092	11.7598	11.4584
GRASP	5.38996	4.63733	5.52585	5.54774	6.92857	5.77449	6.14258
GSTT1	7.14256	7.27433	3.84132	6.35991	3.59854	3.72139	7.865
HAPLN1	11.8269	11.7201	3.18331	3.26337	3.49971	2.983	3.10383
HIF1A	6.76426	6.98475	6.07266	5.9177	8.76793	5.59621	8.23601
HLA-B	11.577	11.9669	9.78573	11.3618	10.1232	10.8617	9.91742

HLA-DMA	8.95121	8.85947	8.40917	9.60448	8.88225	6.40647	4.55012
HLA-DMB	7.33849	7.16351	6.15802	8.07775	7.15028	3.98783	4.20666
HLA-DPA1	12.4631	12.2986	11.9773	12.6202	11.5597	6.72107	7.22228
HLA-DPB1	9.41197	10.356	8.54691	9.21075	8.22904	3.40147	7.78899
HLA-DQA1	7.49001	3.50269	3.97706	8.83535	8.8891	3.49134	4.39229
HLA-DQB1	7.14931	3.74978	3.84551	7.35668	7.52491	3.28378	5.67565
HLA-DRA	11.8541	12.0907	10.748	12.0841	11.4266	3.19817	5.90689
HLA-DRB1	10.6966	11.0218	9.15134	11.0163	10.3366	3.51354	3.68956
HLA-DRB4	10.4548	10.1883	8.03572	10.6093	3.65188	2.92796	3.01658
HLA-DRB5	3.39446	3.42921	7.79533	9.34126	3.58529	3.38875	3.21497
HMMR	6.33502	6.30147	8.09383	6.0027	7.21377	5.65856	8.17419
HOXA11	2.83026	3.19422	3.41029	3.30379	2.90892	4.07775	3.378
HOXB13	6.03047	5.67702	3.61399	5.48264	4.81909	7.07324	3.3764
HOXC13	6.5969	7.35954	5.34774	4.92421	5.6298	5.43004	5.84327
HSPA12A	6.58806	6.27427	7.57561	8.32983	7.33291	8.22207	6.64875
HSPA1A	10.5719	10.4154	5.02797	11.2421	9.62463	9.63324	3.14634
HSPA2	4.91636	4.44612	3.97983	7.99254	8.94519	4.8843	3.80955
HTRA1	10.4346	10.0757	9.96543	8.89764	9.99116	9.89805	8.96658
ICAM1	8.97172	8.61982	5.9736	7.48445	8.43582	4.45102	6.88071
ID3	8.11235	10.0251	7.1532	3.84342	8.25212	6.43801	7.94775
IFITM1	11.3638	9.44116	10.6245	9.86362	8.83455	6.257	5.27318
IFITM2	11.4223	10.9653	10.6969	10.5839	8.60045	5.77104	4.79648
IFT74	7.04393	7.95367	4.50187	5.21523	6.86868	4.10484	6.47166
IGFBP3	11.4146	8.02571	5.87256	7.02417	11.9363	3.66224	4.32415
IL13RA2	10.5691	12.0612	3.21809	5.12349	12.2498	3.14391	2.84758
IL24	3.08056	9.66779	3.3967	3.00533	3.04748	3.4094	3.07783
IL31RA	3.52821	3.89867	3.40543	3.13573	3.44389	3.47999	3.4982
IL6	5.1416	2.99867	3.0643	2.98601	3.16025	3.61342	3.47614
INSR	4.32033	6.30375	5.57455	5.35671	5.55351	6.51458	5.10073
IRS1	6.15054	3.94957	3.74401	5.91552	6.53845	4.88442	3.79272
IRS2	8.72457	10.0775	8.99573	9.37897	8.16947	9.46419	7.0309
ITGA1	3.7037	4.17417	3.76478	3.1384	3.24215	2.96908	3.00828
ITGA10	7.88013	8.34802	3.45716	3.58745	7.81581	2.75924	3.14076
ITGB1	6.72458	6.67689	5.48379	6.16284	8.7479	7.0183	6.32717
ITGB3	8.55881	9.17266	8.41838	8.39808	8.04767	4.12305	7.50829
ITGB8	9.69041	8.54185	8.94081	8.46326	8.93468	8.02822	5.73062
ITIH5	8.2946	8.89647	8.76466	3.97291	10.3103	7.05768	3.44529
ITIH5L	7.28066	5.63953	4.65666	3.26742	5.99431	3.05487	3.07327
ITPRIP	5.66787	6.00051	4.73971	3.6776	3.24742	7.62524	3.9167
JPH1	6.32535	7.41999	7.51281	7.77178	8.04187	6.68668	3.38582
KAT2B	9.80911	8.91353	9.91716	9.33291	8.91915	7.84707	8.12583
KCNE4	5.08177	3.21391	5.79649	6.10336	7.37134	7.30359	3.67781
KIF14	4.5899	5.35045	3.63428	3.54917	6.64965	4.07615	5.83779
KIF18A	4.04473	4.52292	5.56685	5.15207	5.77526	3.84461	6.87459
KRT27	2.80979	2.94292	4.59038	6.89435	3.01313	3.66413	5.01075
KTN1	7.53834	7.81197	6.66464	6.61345	8.52195	3.84438	8.35326
LAMA4	8.17852	6.06337	6.94651	5.70602	11.0241	4.72914	5.77547
LAPTM5	3.51174	3.06184	3.29591	3.23649	3.3581	3.38719	3.51223
LARGE	8.14894	5.76041	9.15106	8.07551	7.16709	6.94056	7.54711
LASS1	7.3262	7.78585	6.05844	6.43995	7.12849	7.09465	5.49381
LCN2	9.61713	3.26368	3.11138	3.60339	2.80589	2.63831	2.99407
LOC100131392	10.4376	3.69573	10.3885	3.73793	5.61913	3.51266	5.28663
LOC100133678	7.09166	7.74947	4.0924	8.57221	6.13722	3.61694	3.73795

LOC100290966	10.7879	10.6532	8.74912	10.9119	10.8787	3.68707	3.87222
LOC100292463	9.78709	7.50606	12.8309	12.7433	11.8545	11.066	13.1367
LOC100294036	10.7684	10.6723	8.69547	10.7333	7.09521	3.29649	3.99296
LOC100294224	9.75045	10.8107	4.17742	10.7549	8.74026	3.54668	3.82531
LOC387763	5.19059	4.99848	8.05677	8.68571	4.05842	9.73951	8.99904
LOC399940 L	8.38804	6.93041	7.83	6.9742	7.8345	4.33838	6.17677
LOC440459 S	4.12653	3.61908	11.2809	8.97603	2.88171	10.2678	9.99998
LOXL4	4.92057	12.5319	3.22784	3.0967	3.04986	3.08328	3.3756
LPCAT2	4.90372	7.10045	8.06784	5.61712	8.43621	6.82994	2.87666
LPXN	7.70315	7.15236	8.13357	8.51731	8.03013	6.7628	9.92905
LUM	2.57936	2.66148	2.82469	7.48375	7.68492	5.99651	9.84536
LY96	6.40057	3.38819	3.64913	8.64233	7.87615	7.8856	7.29646
MAF	4.43373	8.15023	6.53257	7.92911	7.59012	5.86276	6.04018
MAGEA2B M	7.60542	9.93671	5.46247	3.27391	8.95801	3.40594	5.78601
MAGEA3 MA	11.6263	11.8163	10.8929	4.38905	11.7652	10.6778	10.4305
MAGEA4	3.54131	11.1031	3.6012	3.59773	10.9282	3.32648	4.08073
MAGEB2	3.02665	2.99696	3.04199	3.01193	2.98639	2.91282	4.26483
MANSC1	6.41499	6.91894	4.32772	4.4275	4.45492	3.27867	4.86765
MCF2L	9.54354	7.06026	6.58526	5.32643	3.74111	8.24925	7.56839
MCOLN2	6.81801	6.57822	7.24833	6.75313	6.04393	7.10417	7.40506
MCTP2	3.65464	2.65991	3.05937	3.69185	2.99308	3.10973	4.04477
MDK	4.71195	8.37397	6.61766	3.60194	3.56102	3.8547	7.42733
MDM2	6.07907	5.36103	5.3266	9.25007	6.05676	3.39879	7.30899
METTL7B	2.81115	4.88561	6.9479	3.62036	6.51662	3.00704	3.53268
MFAP2	3.43654	7.16242	3.16045	3.39871	3.8983	4.00466	3.75652
MGC39393*	4.88395	8.75002	7.57392	9.77534	5.99431	10.1391	7.33806
MGP	8.67806	8.57764	4.43321	9.21279	12.548	3.2934	3.74561
MGST1	3.60595	8.72705	5.13395	3.77594	9.90875	10.3524	9.0273
MIA	11.4013	10.6137	11.1506	10.6153	10.3601	9.77909	10.3045
MICAL2	5.5694	4.21005	6.41222	4.70534	5.24766	6.00212	6.63261
MID2	6.45433	3.26673	4.07283	5.84694	4.15398	2.80038	2.7622
MKI67	6.9312	6.27362	7.82229	5.08038	7.33727	3.90417	7.64098
MLANA	3.70688	3.47238	12.6716	12.8955	10.0074	12.6046	12.8904
MME	4.01392	3.97259	5.24768	3.98779	3.35627	5.53469	5.16197
MMP1	5.45021	2.98383	4.39414	3.34339	3.78173	2.86635	3.56097
MMP8	4.45622	3.67519	6.82989	6.25777	4.70007	6.13211	7.28081
MPPED2	3.48627	4.35125	3.85379	8.50787	3.26162	5.41691	7.18115
MRAS	7.40352	5.71373	8.64601	7.17161	7.31122	7.63705	6.80651
MRC2	10.7188	9.5538	5.19572	3.07822	7.7378	3.3151	3.06991
MRPS6	8.94266	8.15075	9.48767	9.36484	9.13956	7.22565	7.12738
MTUS1	8.80331	6.36622	9.28599	7.78775	10.5911	7.23584	8.57044
MUC15	10.5476	9.09984	3.62133	3.28409	3.42572	3.44088	3.58213
MX2	9.00455	8.0197	9.0461	7.58421	3.09611	5.78191	8.12698
MYOF	8.62684	8.56075	8.29208	9.52153	9.23722	4.99349	3.97
MYOZ2	3.39774	2.97269	4.09331	2.79599	3.75744	3.34779	2.7494
NANOS1	8.036	7.52484	7.11823	9.24901	5.85512	4.30099	7.0294
NCAM1	8.09554	5.26595	8.38152	8.89976	6.43831	7.78123	4.25626
NDC80	6.04452	6.2289	6.29229	5.81014	7.35191	5.54209	7.63252
NEK2	3.28686	4.38196	4.10779	3.55532	4.62098	4.51801	4.50359
NEK9	8.10931	7.44104	7.7487	6.71659	6.80891	8.42129	7.20425
NFATC2	11.7441	11.4228	10.6774	11.5375	10.2302	5.57877	8.05797
NFIA	5.71678	5.80279	3.28415	6.159	6.70544	5.60331	5.24421
NHLRC3	7.24726	6.1053	7.63201	7.57597	6.2115	7.44447	7.31405

NINL	4.81912	3.56824	4.90448	3.6316	3.64272	3.65841	3.7912
NLGN4X	7.69822	8.75199	4.13966	2.81789	7.83711	3.07399	2.9427
NoGeneName	5.99404	4.56056	7.28701	7.38112	3.46615	9.08758	8.67646
NRCAM	6.63405	7.46366	8.00624	7.38313	8.5783	5.49926	3.41294
NRIP3	3.55767	3.91252	5.97213	3.68637	3.9405	4.83494	9.34537
NRXN3	9.42255	3.64352	5.07439	4.9252	6.98912	3.45685	5.47364
NSUN5	8.57748	8.17707	7.76728	8.39702	8.97162	8.69747	9.50311
NUF2	5.50753	6.44201	5.77274	4.66519	6.80092	5.68743	6.77856
NUPR1	3.89648	3.77781	11.2132	10.8418	8.69204	11.5051	4.31328
OAS1	5.98261	4.87297	6.6852	8.43147	5.09453	4.22442	5.34069
OLFML2B	3.6423	2.88866	3.32521	3.77116	3.97062	3.77145	3.18331
OLIG2	8.84692	6.62871	6.69056	4.77197	3.37541	6.91406	7.05628
OVOS* LOC7	13.0889	12.7386	12.7739	12.2428	11.5465	12.8309	12.2562
PABPC4L	3.10833	5.43333	3.10633	3.01838	3.02928	3.39302	2.83996
PAPPA	8.81798	6.4656	3.74601	3.80013	4.0977	3.54123	4.0407
PCDH1	5.37883	4.96431	6.59046	7.56472	4.56412	4.09171	3.32085
PCDHB16	8.55098	7.73684	6.66768	7.74066	8.05719	3.57147	3.25869
PCDHB5	7.73552	6.76681	5.56708	7.94909	8.00974	4.32413	2.92648
PCDHB6	5.96131	6.6447	4.30083	6.16625	8.16693	2.89705	2.78722
PCSK5	8.51001	4.08633	6.51736	6.96153	7.97573	3.38342	2.9403
PDE4DIP	5.13548	6.54925	4.82241	5.7535	7.05673	5.79635	5.32733
PHGDH	8.72278	9.76078	10.2414	10.8015	9.22722	11.1701	10.2458
PHIP	9.00278	8.662	8.66624	7.86399	8.4601	5.34578	9.09151
PHKA1	3.60027	5.3422	2.72047	6.29851	5.42538	4.45865	4.04209
PHLDB2	6.19545	8.49878	5.65393	7.05116	8.19373	9.42289	4.01865
PI15	7.51654	7.80768	9.80594	9.99503	9.86658	8.3006	7.56023
PIR	9.67709	7.73897	10.7761	10.897	8.89025	11.5156	9.97813
PLA1A	3.73529	3.36389	9.17261	8.40274	7.20879	10.2655	8.51766
PLAGL1	3.00407	3.07201	3.11592	2.68893	5.99933	3.35127	3.56231
PLAT	7.82801	7.44011	9.97978	10.9381	9.92143	6.3482	8.01922
PLCB4	7.57357	4.24707	3.36822	5.63384	5.73075	3.02317	7.56901
PLEKHA5	5.73973	7.40245	7.41781	7.32932	7.81824	9.33468	8.79838
PLEKHB1	3.7798	3.6957	4.42808	5.64053	5.14175	3.81713	3.39126
PLK4	3.79729	4.48117	5.6452	3.99519	4.90934	5.24628	6.20594
PLN	2.99821	2.59822	2.62949	2.76497	2.81656	2.79798	2.76478
PLOD2	6.99156	7.02864	5.63009	5.83649	7.84871	4.91437	6.70979
PLP1	11.9477	11.3283	11.5509	12.1011	11.2255	11.315	9.96741
PLXNB2	8.62418	7.15831	8.59478	7.60704	9.0162	6.23754	8.64152
PNMAL1	2.99465	9.87246	3.04415	2.98959	3.16255	4.82943	6.47171
PNPLA4	7.91648	2.59009	8.43421	9.2237	9.08831	8.60417	8.7929
POSTN	3.17992	2.97325	2.8815	2.87432	10.2184	3.10069	2.73978
PPIG	7.30027	5.69069	7.08216	5.58404	8.29645	2.76698	7.66225
PPP1R14C	5.26237	4.5861	7.58325	6.19137	5.44266	3.4489	7.83372
PPP1R3C	3.5713	3.33869	3.45972	8.81185	3.77092	3.54407	7.64989
PRDM7	2.78694	3.5026	4.84412	6.77181	3.03498	9.59355	8.98795
PRDM8	3.34109	4.32258	3.7684	4.01285	4.03631	3.76047	3.65251
PREX1	7.28097	5.89576	6.23303	7.72536	5.91143	5.39993	5.30699
PRKCD	9.28197	8.92673	7.47084	7.33186	8.56168	7.58337	7.52603
PRR4	6.66776	4.2916	4.82448	4.05753	6.2961	3.47078	4.1286
PRSS23	10.5405	9.11769	9.46471	10.7615	10.4561	4.85736	4.93702
PRSS33	3.42481	8.14379	4.09505	8.31902	3.36373	4.8377	4.49235
PTEN	8.37716	8.26202	7.80703	8.38926	7.29954	6.76116	7.66194
PTGES	4.94048	7.06696	3.67946	4.22666	4.10544	5.182	3.33739

PTGS2	8.07346	3.16856	3.0259	3.38239	6.68828	2.84759	2.80994
PTN	10.1545	7.96615	3.33507	3.30115	8.37814	3.08837	3.18877
PTPRN2	8.02637	2.92676	3.34027	3.19389	3.6129	3.44518	3.40161
PTPRZ1	10.7566	7.43443	8.44611	7.91076	9.1842	4.8643	5.30916
PYCARD	3.78477	3.09934	10.2832	10.8948	3.01229	11.8052	9.23083
PYGB	9.70351	10.1856	9.44576	7.82575	8.49704	7.17704	8.76331
PYROXD2	7.36027	7.77736	4.81706	5.78122	4.43479	3.73289	3.80036
RAB17	7.86717	8.29327	7.66118	7.91406	6.53989	9.47749	9.2903
RAB31	8.45811	6.18513	7.06867	3.99952	5.6871	4.65482	7.08095
RAB7B	3.85829	6.53615	5.13955	6.92896	6.49387	4.92979	3.08859
RAD51AP1	5.03575	6.1296	6.24648	5.46181	6.52943	6.13922	6.97952
RARB	4.99008	3.15487	3.05348	3.02895	4.39734	3.45082	4.20948
RASSF2	3.39388	3.21879	4.7638	3.35948	3.00222	3.61797	7.92987
RASSF8	6.92198	7.78812	6.68092	6.64123	6.94802	5.38866	6.54571
RBM25	7.17169	6.78695	7.18927	7.29453	7.69882	3.30151	8.09165
RCS*	8.14705	7.7976	8.23179	3.06233	8.10802	3.1634	3.18517
RFTN1	8.72962	7.57841	5.68485	7.28727	4.95718	4.44455	3.99772
RGS1	2.73728	2.721	5.19808	2.91126	2.84061	7.38276	3.16952
RGS2	7.00986	7.09701	6.35815	6.53835	8.38188	7.46266	4.35942
RHBDF1	8.73402	8.37556	8.51043	7.33188	7.51027	6.98055	7.97613
RIPK4	8.2681	9.61056	8.67332	9.95026	7.81207	10.2104	10.0012
RNF128	8.44807	7.13146	6.79831	4.39405	9.60096	2.96236	5.45349
RNF175	6.50736	5.41195	2.86685	3.32924	7.19415	2.86025	4.69433
RNLS	3.47013	3.29634	3.66535	3.52904	3.3878	9.4236	3.86172
ROPN1B ROP	8.6041	5.61142	9.34882	9.37546	8.11725	9.05432	9.58426
RPS23	9.40785	8.83902	8.55672	9.40026	5.88453	7.39691	4.6826
RPS4Y1	3.51822	3.50057	3.30393	3.43651	3.58238	12.0159	4.01156
RRAGD	8.79132	8.68073	10.3749	9.36583	8.92978	10.7003	10.8901
RUNX3	3.11176	5.73973	7.8855	7.22414	2.95102	8.29749	8.5835
RYR2	6.72143	6.28848	2.92844	2.79043	6.0457	3.08216	3.05512
S100B	11.6766	8.91269	11.3912	11.9794	11.6532	9.10189	10.4076
SAA1	6.74204	2.96782	3.3493	3.57448	3.15726	3.24633	3.25316
SAA1 SAA2	8.83776	3.30423	3.07638	3.4141	3.00055	2.82436	2.80767
SAT1	9.34184	8.54695	9.32443	10.3699	9.60369	10.4236	10.1353
SATB1	8.70044	7.24734	7.57998	6.17973	6.62224	7.87902	6.13255
SCG5	5.20993	3.00863	3.18498	2.98913	3.16954	3.25099	2.99346
SCIN	2.90819	3.23648	4.3138	5.76711	2.8158	2.95991	2.89758
SCRG1	10.477	3.47162	3.93297	3.78234	9.31207	3.10896	3.20443
SDC1	4.49453	5.21882	5.96572	4.14375	6.95442	3.96861	7.5266
SDC2	8.69748	7.94011	6.30065	7.45543	6.81196	3.08613	4.94871
SEMA3B	9.82434	8.83848	9.69112	4.75722	5.37998	4.54038	4.40638
SERPINA3	12.8469	12.4301	5.93206	7.19517	13.0129	3.71325	3.75275
SERPINB2	7.86106	2.77324	2.92954	2.81955	3.08269	3.0133	3.38048
SERPINE1	6.07035	3.08293	3.21333	2.84497	8.89472	3.28404	3.23934
SERPINE2	10.533	9.25231	10.0445	9.69067	11.296	7.0182	7.58675
SFRP1	12.3795	11.5406	10.5436	10.3856	9.53509	5.95302	8.50049
SGCD	6.66036	3.45914	6.74022	8.25613	6.10616	7.79199	4.70818
SGOL2	4.52065	4.76421	5.26914	4.38385	5.92374	3.93745	6.56261
SHANK3	7.84856	5.4494	7.37068	7.81537	6.9361	7.66594	6.78519
SHROOM4	6.61845	6.13696	5.57558	6.41874	7.2533	4.89588	3.80853
SLAIN1	4.39919	4.64855	3.43028	3.39323	5.26954	7.67946	6.28109
SLAMF7	3.3195	3.41835	3.53104	4.32139	3.69517	3.90939	8.20478
SLC14A1	3.33228	3.82546	3.00102	3.29915	2.93529	2.90518	2.79936

SLC16A3	6.3441	3.03501	4.87697	2.9003	3.34989	3.55762	2.73361
SLC16A4	9.10598	8.00772	6.87995	8.68794	8.03338	7.42399	6.26465
SLC16A6	3.24852	3.28381	10.2645	7.19276	2.93489	9.21474	8.78566
SLC1A1	9.76581	9.42596	5.4114	7.06323	7.07114	6.80127	3.80169
SLC1A4	9.45898	8.42385	10.0018	10.2797	9.31221	11.1459	7.28809
SLC26A2	11.8735	11.1046	7.18588	8.66264	10.3552	8.07588	8.20317
SLC45A2	3.30176	2.9155	8.91743	10.7356	9.10817	10.0639	10.6386
SLC5A3	10.7581	10.4542	10.6185	10.3707	10.9285	7.79555	7.53415
SLCO3A1	5.57964	4.26666	6.62673	7.98666	3.56122	6.05469	3.95096
SMC2	5.18313	7.10525	5.90719	6.23295	7.85898	5.31335	6.99179
SMC3	8.04335	8.76694	7.4263	6.89771	7.65008	4.17293	7.93123
SMC4	8.05218	8.98633	9.1432	7.22836	9.28731	6.29662	9.44806
SNAPC1	7.2684	7.40571	5.28495	5.22817	8.29003	4.91139	7.8475
SNX10	10.9207	10.2307	10.7473	10.6431	10.2703	9.27946	10.837
SOAT1	4.92471	6.00848	5.93475	6.25983	5.59867	4.74742	6.94015
SORBS2	9.86583	7.59063	9.117	6.71628	8.38775	3.93381	3.46459
SORCS1	7.86404	7.22177	7.27966	7.45043	7.14509	5.56087	4.90962
SOX10	8.24883	8.17349	8.02801	7.63945	7.49305	7.15875	7.96047
SOX6	9.0815	3.99718	7.5822	9.20654	8.51943	8.39296	8.71966
SPANXB2 SPANXB1	3.20109	3.0522	3.41231	3.25959	3.39645	3.01516	3.12861
SPANXE SPANXB1	3.03829	2.91219	2.99796	3.03465	2.97408	2.99501	3.00979
SPATS1	2.73723	2.86783	2.94833	7.78595	9.09687	6.42091	6.61008
SPESP1	2.54278	7.76702	2.66733	2.50469	2.57052	8.10025	7.63415
SPP1	10.948	4.80115	8.88176	7.95422	3.92259	5.65751	10.0724
SPRY4	10.384	10.3953	7.80282	7.81836	9.63552	6.67879	6.19945
SPRYD5	9.43561	8.71118	8.98086	8.75656	9.28499	6.16188	7.64911
SRGN	6.96045	6.36367	6.52026	5.4535	6.8937	5.98105	7.57991
STAT5A	6.39061	6.80712	5.69754	6.45076	6.21261	7.58856	6.54192
STC1	5.38697	3.89054	3.05086	3.27682	9.49114	3.63656	3.09626
STC2	4.01563	3.56293	2.79457	3.54224	3.10958	3.14986	2.9779
STK32B	9.64615	9.53981	6.63018	7.61868	9.00239	6.54706	8.64449
SYCP2	3.52958	3.28805	3.64124	4.46805	4.50697	2.92511	3.11499
TBXAS1	6.87864	5.42788	3.09426	3.09502	6.24258	2.92589	3.96822
TCN1	3.30198	3.50441	6.05916	8.60765	8.77841	9.56738	7.45653
TESK2	4.22233	5.29247	7.85569	7.30756	5.13285	8.07496	8.11106
TF	9.61957	6.17651	7.0074	9.93207	7.31954	7.36865	3.30196
TFAP2B	9.00576	12.3265	3.03391	3.22599	3.65116	2.82948	2.9901
TFAP2C	10.7354	10.7058	10.099	9.3613	9.64171	8.33676	6.83543
TFPI	9.04304	5.18851	4.87151	3.91958	8.87173	3.93864	3.43542
TFPI2	7.57775	5.53383	2.90237	3.01723	2.71765	3.12774	3.76353
TGFBI	11.9385	9.65568	11.5491	3.20578	6.98249	3.646	3.47897
THBS2	10.4488	5.49353	3.10167	2.72722	3.46119	2.90697	9.64788
TIMP3	12.1795	11.4575	11.6836	11.0263	12.0709	10.2655	8.66161
TM4SF1	10.3631	9.32608	9.02575	8.34737	10.86	4.38462	9.09523
TMEM140	8.29308	3.96168	7.83035	9.14969	5.44736	8.22247	6.28752
TMEM195	11.8345	10.2426	3.45352	3.53771	11.2076	3.9674	2.82937
TMEM200A	3.18485	2.86952	2.87604	3.3311	2.87371	2.95428	3.07058
TMEM200B	3.28987	4.27993	3.77029	3.57894	3.00423	4.347	4.91187
TMEM229B	5.80042	6.62885	6.2039	4.82176	6.08251	5.62486	7.01355
TMEM47	8.47504	7.79139	5.03499	7.50634	10.0544	3.19196	3.01495
TMEM98	9.67562	8.76282	7.43996	9.38567	5.83929	9.03218	9.73286
TMSB4X	10.8866	7.31889	3.26421	6.74464	5.75966	4.78693	11.9491
TNFRSF19	8.06865	8.38054	8.66344	6.63226	8.92657	9.86906	5.83373

TNFRSF6B	3.59765	3.53005	3.17698	3.68181	3.29614	3.57953	3.09481
TOP2A	9.90778	10.4353	10.0653	9.70927	11.1619	10.1685	10.6287
TPD52	7.21857	8.52478	8.71685	9.24658	8.28971	8.65396	9.72833
TPD52L1	6.32897	10.9676	6.70806	8.73409	9.43058	4.78336	11.0815
TPM2	5.99511	10.6234	7.00318	5.75367	6.47348	6.47553	4.34888
TPR	8.5546	9.07686	7.17823	8.07256	8.93429	4.09074	8.13194
TRIM2	10.165	8.87019	10.1932	9.44206	8.28538	7.96247	9.18192
TRIM48	9.55803	3.19167	9.43286	2.91639	4.23944	2.94573	3.48758
TRIM9	7.51513	7.23266	6.88424	3.4158	8.87422	4.13789	3.95278
TRIP11	4.9828	5.66095	5.23254	3.91138	6.66382	3.43044	6.01556
TRPM8	9.24846	5.58519	6.94213	5.91249	7.88878	5.5659	4.21028
TSPAN13	11.5654	10.9343	7.11719	6.88463	9.94955	7.21399	6.94433
TSPAN33	7.08073	6.34212	6.07358	7.23186	7.05188	7.34984	6.00941
TSPAN5	5.15738	4.4394	3.45842	4.36516	5.52995	3.32674	3.66108
TUSC1	5.66969	6.70072	5.39328	2.65963	6.26489	6.43348	6.00627
TYR	6.51961	2.83159	12.6433	11.4131	11.425	12.5496	11.644
UACA	6.65259	7.38396	7.42453	6.7488	8.7261	5.75347	7.65989
UBD	11.2544	6.69599	3.15271	3.28622	3.18956	3.06102	3.30088
UCN2	4.26018	5.97327	9.46258	5.25155	7.45957	3.38445	8.94635
UGT8	9.65586	8.02384	6.74626	4.09234	6.98597	4.07847	4.14335
UHRF1	4.63882	5.2616	6.47426	4.88763	5.72861	4.97915	5.38824
VAMP8	4.91642	7.30494	7.23519	3.83114	6.57959	7.56733	3.20429
VAV3	3.62181	3.53172	4.40998	7.54556	6.76214	8.02478	9.60056
VEGFC	6.19478	4.99374	3.77203	4.53193	7.26846	3.6771	3.57813
VGf	8.73209	10.2627	7.78202	8.35795	10.283	8.69637	11.0355
VWA5A	3.32487	7.23699	6.02757	5.96955	5.09581	3.87254	3.33173
WDR66	3.60282	3.11011	2.87243	3.22882	3.4559	3.90939	3.08143
WIPI1	9.52241	8.94689	10.6708	9.78243	9.1959	11.1801	10.485
WNK4	6.44305	7.07078	3.79175	3.17424	5.28795	3.3191	3.07521
XAGE1C XAG	2.94943	11.4359	3.13768	3.02508	7.82349	3.00083	3.16352
XIST	3.34043	11.3416	10.0641	11.3333	10.4392	3.19771	9.56088
XYLT1	6.99626	6.84974	6.40267	7.24612	8.69019	5.03954	3.3732
ZC3HAV1L	3.21883	4.62193	6.67243	3.50161	5.22409	5.36137	3.18719
ZNF83	9.17347	8.92621	8.18214	7.17876	8.80447	8.00956	7.54847
ZNF91	5.72607	8.42637	3.56649	6.96933	6.72509	5.14346	6.81433

id a resistant group (separated by a double line). Genes with expression value difference over 1 between two groups are reported.

C32	RVH-421	A101D	UACC-257	M14	HT-144	MZ7-mel	IST-MEL1
7.83281	6.38739	6.32771	6.42397	5.78613	6.94834	4.04148	6.77163
2.87807	2.8661	2.8839	2.86088	2.70124	2.84658	2.88803	6.46068
6.09589	3.36277	5.48856	3.20367	3.42781	3.29622	3.27338	4.66227
7.90053	6.94308	9.41644	7.7796	6.53038	6.71002	6.23176	8.19104
6.98608	6.88871	8.2453	6.52179	6.60869	7.00681	6.00466	9.18593
9.05906	9.03931	8.38849	9.32362	9.20336	9.22085	7.43435	8.33812
8.95778	8.53903	9.16344	8.83477	3.53347	8.78577	6.42896	4.48872
3.34361	3.30741	3.5917	3.52499	3.26338	3.07211	3.94067	4.22965
2.6916	6.61183	3.27603	3.05503	3.26686	3.64613	2.76664	3.10351
2.88397	2.86938	2.97925	2.7272	2.73487	3.07596	2.88884	3.03092
5.98622	6.68556	7.38739	5.22532	4.61812	2.8189	3.92864	7.93148
7.27382	8.07494	3.67385	7.84019	4.41951	3.89921	5.45379	3.88967
9.78526	6.98564	9.25132	5.32718	7.58948	5.59075	4.70164	9.66879
11.5272	8.08493	8.92152	7.84726	6.94044	7.38717	6.29508	6.50382
3.61585	3.38379	3.24001	2.80779	5.8656	3.40591	2.89573	4.28746
3.71334	4.92088	5.0739	3.38401	3.32799	5.16127	3.19366	6.60628
7.42316	9.83216	8.05666	4.6337	8.58584	9.33519	9.25111	8.20166
10.1008	9.69897	5.7246	7.7796	5.29339	7.97907	3.85041	3.38359
4.07677	8.70062	8.44744	10.9005	3.16568	3.54427	4.70418	7.05626
4.1757	6.27484	3.29788	5.03112	3.19929	4.62314	4.15826	2.98037
10.0578	4.50961	8.55553	7.73002	4.14885	6.51239	4.93746	7.13662
3.86096	3.8096	5.4401	4.31619	5.10907	3.88542	3.6921	9.36067
4.78901	4.08419	7.40753	3.1222	5.7094	7.05579	3.74302	8.7252
3.18223	6.47831	6.33317	7.31177	3.30697	3.22194	3.29529	6.56417
3.59009	3.51466	9.81295	3.99783	3.38663	3.51329	3.37181	3.30206
6.54162	6.9359	6.47635	3.751	7.5161	6.77184	7.72427	6.30559
7.26322	3.44183	8.64288	5.1471	9.17757	5.73681	8.33359	9.92276
3.18127	4.01445	5.08721	4.10919	6.92639	7.4376	6.45222	4.30498
5.50364	3.72304	6.24251	5.35911	7.29064	5.4108	7.80163	7.89448
3.623	3.45429	3.20149	3.3103	3.02458	3.97978	3.42667	5.2433
8.14553	3.62096	3.30813	12.2085	3.35966	3.35364	8.65677	3.23262
6.63405	9.76678	8.11518	9.1469	5.73337	5.38094	4.3187	5.95697
8.0574	3.68148	6.08163	3.04707	3.16361	6.11012	3.07148	2.7975
9.69465	8.12825	9.01804	9.92915	8.96819	9.05203	7.30758	7.39624
7.54692	3.60954	7.97321	4.45483	8.75946	6.29467	9.08204	9.30972
6.15695	7.65432	7.30603	3.61783	7.71124	7.06413	6.78294	7.98778
6.24995	8.27536	8.10555	3.3978	7.92063	7.86413	7.94745	7.84561
5.64798	4.25064	7.69131	4.83353	3.18526	4.81666	3.0548	3.71746
4.31903	4.01066	4.55475	5.10666	5.88146	5.32932	5.81132	5.19344
3.45823	5.38509	4.6994	6.43052	7.40093	3.30495	7.99485	5.2881
9.43372	6.87444	8.02022	3.23196	3.2058	6.53326	3.90972	3.41811
3.72347	3.04307	3.16376	3.7392	3.53658	3.32741	3.16467	3.43565
6.13792	7.49796	7.51678	3.7938	7.15709	7.68895	7.778	8.31715
3.53341	4.61341	2.83673	8.08255	3.20185	3.03744	5.75988	2.95938
9.94612	10.1339	9.51766	9.90648	10.355	9.54518	9.8677	7.24744
3.02742	3.39248	2.95218	2.8222	2.8868	3.06423	2.74265	2.86513
2.99505	3.06357	6.29224	3.24113	2.6306	5.47481	3.13314	4.14101
7.33447	8.6518	4.77671	8.22579	5.06272	6.67013	6.5953	3.24311
3.39363	3.36779	6.99365	4.02553	3.33802	3.54427	3.49501	6.57049

7.37207	4.67665	5.96198	4.69267	5.39191	5.80707	4.02607	5.35943
6.39993	9.40377	6.93365	10.8091	4.4257	7.15015	8.42847	6.74615
7.11952	6.72531	10.7725	10.198	10.6288	7.82237	3.94982	7.15916
6.49094	7.30195	6.26843	6.15671	7.19642	7.13595	8.97306	6.6278
4.93269	4.1863	6.87556	3.08974	3.11173	3.26103	2.84525	3.01677
8.74063	5.60461	6.91133	6.51798	3.81015	6.4987	6.01855	4.19145
6.88972	3.16598	7.92952	7.63725	8.58297	5.88959	8.34454	9.26099
7.65574	6.96752	6.89622	6.1174	6.83777	6.77541	6.58079	3.42659
4.5675	3.04223	4.04838	3.01621	6.49862	4.50598	4.15289	6.63916
4.4718	4.0624	4.64175	3.55679	5.74997	4.76131	5.01086	5.70728
3.44171	3.25955	5.87547	3.87589	3.52232	5.92862	4.05436	6.49886
3.39026	5.49526	10.6538	9.8473	2.86222	8.21274	3.25024	4.21692
7.61087	9.42527	7.317	8.94085	6.28485	7.55662	7.04188	4.57338
6.82201	6.81861	8.15189	7.85437	3.03947	8.53443	6.61299	7.02244
3.00589	3.01102	7.98615	2.81988	2.92144	2.84686	2.88076	2.99634
7.21529	3.27502	4.53761	3.44283	7.35251	4.54341	6.31828	3.43008
4.85419	3.82796	4.94592	5.56499	6.40389	5.12917	6.00192	6.45281
9.97077	8.32489	9.49095	10.5015	8.63064	9.10122	10.0596	5.80738
4.10308	3.25768	3.4007	6.30099	7.2657	5.80879	3.81841	3.86523
5.72373	4.50626	6.91542	11.5621	9.45385	8.9477	5.88337	3.29188
9.79554	8.35643	8.81675	11.9657	8.16338	9.11895	10.3371	3.02564
6.43398	6.38181	6.57897	3.14537	7.52225	6.86132	7.81563	7.55616
4.07699	4.2925	5.98052	3.5086	4.83489	4.64902	6.67351	5.5826
9.44759	8.57471	8.78618	9.61887	8.81205	8.90124	9.13915	8.11855
6.73695	4.59614	6.41707	5.44033	4.51907	6.12928	4.47549	4.75379
10.8781	6.34247	8.52831	3.97066	5.75471	10.7611	3.15821	2.73446
10.6079	7.50688	9.64254	9.5744	10.0177	7.49948	7.72215	9.78973
2.56511	3.62044	3.01947	11.2301	3.16079	2.80478	4.21122	2.88886
3.12636	2.82421	8.57286	3.02865	3.96112	6.37602	3.10123	10.5258
6.80055	4.98642	6.78984	10.6734	4.62509	3.96878	8.09224	3.46236
5.91945	2.87111	7.32336	2.85311	8.04651	5.05343	7.68584	7.13173
6.09933	3.60592	7.28803	2.71894	9.5009	6.37376	7.54408	9.21398
3.50009	4.08256	3.97717	4.52853	5.93983	3.30112	7.401	6.86891
6.76863	4.84198	6.72573	3.54097	8.13931	6.79858	7.78194	8.11629
7.63184	3.93541	8.35124	5.88915	10.1779	6.61731	9.02244	9.99038
2.86638	3.04305	2.75583	2.73937	2.8067	3.17178	4.84277	2.80304
3.52874	3.44482	3.41445	3.54938	3.49746	4.20137	6.40623	3.51822
3.75493	4.09369	7.05821	3.52159	3.3716	4.51011	3.36811	6.65341
5.63725	4.16666	7.23399	4.13904	7.76066	5.05749	7.05197	8.76131
8.34804	4.74306	4.58502	6.47083	5.94402	6.74311	7.75174	6.81039
8.51259	6.10248	7.44371	8.20524	9.06017	7.75765	9.13919	9.40072
6.60495	6.66792	7.14654	7.36493	6.60031	5.76203	5.21344	4.87265
6.60725	8.0933	8.94762	8.59522	7.3509	7.97088	7.95277	5.58519
5.96941	8.42009	6.92299	8.79647	5.53032	7.88346	3.94647	4.73858
2.57393	2.99967	3.54975	4.40893	2.65002	2.71915	2.71014	3.02711
4.65133	6.15856	3.92032	7.84744	3.17476	3.73508	3.06019	2.97786
10.1037	9.10885	9.09333	7.35228	4.47826	8.08998	4.7848	6.40854
2.97248	4.41685	5.83348	4.52668	2.89285	3.94884	3.33213	5.66217
2.77581	3.4603	3.05334	2.83032	2.8251	2.94834	2.68749	3.74105
8.08043	5.88517	6.35716	3.67936	3.02436	5.59702	5.4277	3.07708
3.62235	3.49024	3.36585	3.45826	3.83188	4.32337	3.62742	9.87828
5.29834	3.08666	2.93514	3.09694	3.29855	2.7714	3.21663	4.06101
7.85684	3.66144	3.31027	3.37747	3.89108	3.05065	3.15134	3.26281

3.07305	2.97399	3.58163	2.86004	2.94852	2.78104	2.92427	4.25232
3.62772	5.31406	3.62775	3.74515	3.51175	4.50399	3.73091	9.68214
5.83813	8.21476	7.67548	6.85616	3.78038	7.84805	6.89752	4.67834
2.87765	3.37367	3.7238	7.21397	3.35938	3.62591	3.09384	4.18496
5.68938	6.30988	8.26879	7.42486	4.33741	5.86868	3.6839	4.24303
9.5796	9.81151	7.05919	9.5317	9.54875	9.45846	11.4473	5.56597
6.57426	6.66721	6.91565	7.52499	8.14383	6.85951	7.03462	6.66821
2.92124	6.7117	6.11108	3.86624	3.83792	2.77288	2.88918	5.73891
3.51293	3.46948	3.29394	3.30524	7.63676	9.16315	9.61896	3.52862
11.112	10.8731	9.84094	10.1547	3.3987	10.5211	7.47548	5.37039
8.7134	9.25365	8.13874	9.48811	7.34785	8.84908	7.36751	7.51211
2.97438	3.1804	9.53337	5.39083	8.24183	8.72045	7.3221	8.51783
8.6232	6.2215	6.08481	8.31391	6.54487	7.49706	6.58365	6.52485
3.09902	2.97645	6.88687	3.17605	3.17555	8.01852	3.25122	3.00849
3.4189	3.3254	3.12359	10.7715	3.34189	3.43943	3.35281	3.53848
6.16439	5.69669	10.6048	5.68736	3.91174	7.22603	7.59431	10.4147
9.31329	10.462	10.2237	9.46065	9.75871	11.0132	3.61623	4.41125
5.90835	6.78257	7.62564	4.30812	3.45936	3.78579	3.13589	2.97999
3.54834	9.34328	12.5493	8.23241	3.30156	8.97306	6.38474	7.35168
3.30464	7.77585	9.0381	4.48339	3.6699	3.78844	3.34648	5.04349
9.8912	8.10505	7.91804	9.31403	7.53998	7.28929	7.38362	6.70653
5.01671	4.13676	9.67074	6.63012	5.46365	5.71648	5.85555	9.88054
9.1665	7.85089	7.54876	8.53643	8.93257	7.5468	8.01373	4.23121
12.1015	12.0737	10.1775	12.9138	12.0488	12.287	8.20287	2.65471
3.09201	3.54783	3.19858	4.85716	5.26305	6.33416	6.78747	7.14276
6.74632	6.97575	7.42912	5.47183	8.56157	7.51943	7.5738	8.42324
7.90414	3.9872	8.7456	7.8865	9.63499	6.58046	8.88343	9.45897
5.06658	5.97328	5.1449	4.24755	6.22407	5.57094	3.91948	3.86056
9.56604	8.78606	9.22046	5.70797	10.2339	10.3492	7.87324	11.3253
6.16576	3.58426	7.18411	5.84331	8.14812	5.51529	6.32278	8.36538
5.74214	6.91475	7.49714	4.60712	7.02976	7.45018	6.61487	3.36295
7.25225	4.07616	8.61194	6.15618	9.06313	7.16432	8.45147	9.59544
8.63214	10.7643	6.69756	11.2542	7.83981	6.39217	7.01107	6.16215
5.68525	3.28692	5.47462	3.42322	2.9159	3.42227	3.18801	2.85003
2.66312	3.50817	6.09072	3.26267	3.09567	3.30755	6.72759	7.18245
3.84644	4.47636	6.18105	3.45708	3.78803	5.27914	4.48209	5.35973
5.51601	5.45232	6.62061	3.34117	6.08591	6.49927	5.52477	6.61767
5.81398	3.67815	5.46088	6.32558	7.69436	5.19791	8.2282	7.79012
11.0665	9.38127	8.57805	9.71809	8.44045	8.01791	8.93615	8.20045
7.39383	3.88486	6.68997	6.81299	8.11738	5.05846	6.82172	7.53158
3.50664	3.24406	4.00431	3.24596	3.18854	8.44946	3.26525	4.46506
5.97006	3.75803	6.95151	6.28279	8.38921	5.74536	7.39126	7.68109
6.45944	5.61815	6.60697	6.82097	3.046	4.41106	5.57192	2.79411
3.59421	3.24984	3.15136	3.20533	3.19834	8.43521	6.65977	8.00077
9.94487	9.95574	8.17481	10.7798	9.33367	10.4968	9.91668	6.79642
3.34415	4.03976	3.05716	8.68585	3.01035	3.51286	10.8216	7.41166
8.90483	7.2374	7.5589	8.29219	7.31584	7.71207	6.9515	7.96373
6.78727	4.76338	5.78612	5.13189	3.09653	3.54652	2.83283	3.28455
3.73741	3.03882	5.60544	2.93135	4.09129	3.35962	3.3151	5.73785
6.09101	3.97627	5.27187	8.18411	5.32186	6.99044	4.72747	7.73153
9.0455	9.49886	9.94763	3.3676	9.85134	9.41868	9.92944	10.1414
7.41273	4.88947	7.37393	7.37024	5.31483	6.28059	3.38548	5.40677
10.295	8.08571	10.076	4.98843	6.77279	7.42063	3.01254	6.77638

7.28333	7.172	3.97525	5.81591	6.2866	6.18804	5.03438	3.71683
7.33195	8.02052	8.93657	6.54178	8.64388	9.0389	7.04965	3.26233
6.96997	5.51349	9.12133	7.07282	5.73853	7.50973	5.95722	3.82737
5.81545	5.64827	4.29901	5.97544	3.28969	4.31087	4.39643	3.60223
9.70003	9.6514	10.2463	9.77744	8.95573	10.6303	9.21101	9.55609
7.27299	7.4917	5.79945	7.97329	7.28601	6.14342	6.19511	8.52488
10.3467	11.3947	9.35154	8.64839	3.72799	10.5291	3.81867	9.41558
7.88324	8.27467	5.51849	10.1272	8.17908	6.82534	9.90687	8.37333
8.732	10.7931	10.7888	8.01788	9.28548	9.6736	10.2841	9.24852
7.81235	7.84571	7.92773	5.97492	5.58983	7.99672	8.20574	6.3559
3.206	2.90496	3.5093	3.07905	2.95653	3.4165	5.04183	3.64169
7.56908	7.96636	8.67169	7.09431	7.21462	7.88243	3.72408	3.05412
8.62954	6.40165	7.44048	4.49989	9.08436	6.11815	8.61074	8.27705
6.84826	7.96127	7.21568	8.38299	6.87389	7.01956	6.85239	8.29093
5.79141	7.21302	5.13237	7.85707	4.46896	5.72823	6.04112	4.31355
5.34094	4.46822	3.07087	5.12942	3.33418	3.78932	2.95334	2.86888
8.58443	6.00383	5.8601	7.67812	4.29187	6.92665	5.99905	4.84186
9.79473	7.47693	6.29082	8.80999	5.32463	7.98967	7.84952	6.61888
3.50735	4.04273	5.13892	7.06849	3.53501	6.32848	3.56487	3.32475
10.5614	7.42575	8.09222	9.17434	5.30964	7.20989	8.86557	6.66278
5.52013	6.34773	8.65282	4.80855	3.9886	7.4302	6.63244	7.73841
4.00973	3.19932	2.90692	4.80938	5.85444	4.45414	8.49837	8.20305
4.74577	5.09691	5.4968	4.49116	4.36738	4.74129	6.09481	6.3639
3.39827	4.12131	9.14859	4.46175	3.52788	4.22457	2.90515	8.13329
8.29714	10.1153	8.21366	4.47739	7.74314	10.2751	5.79381	8.42163
5.43532	3.23854	3.07638	3.31502	4.21166	7.6701	7.18116	3.2586
12.3022	7.65348	8.95628	11.4603	10.1928	11.6559	9.06943	6.69913
6.85866	7.56798	5.3012	7.46221	6.75989	6.56581	6.0458	4.58808
3.73013	4.1719	7.92163	3.45467	4.36855	5.27147	6.17494	6.4103
3.26675	5.25346	5.6836	2.93031	3.10982	3.22396	2.94016	2.80548
2.90669	3.46956	3.03623	9.27853	2.78052	3.74843	7.44088	2.69692
8.06831	9.0274	10.3713	7.80694	7.80236	8.64635	8.44682	7.1958
10.4844	9.63309	10.9882	10.6463	8.64653	10.5496	5.37952	10.7216
8.22685	3.49446	6.97804	3.35324	5.70565	4.91634	2.35764	5.32238
8.43707	6.10342	6.44873	6.26491	4.56567	7.91956	4.38319	5.76668
12.5231	11.8423	11.0299	12.7346	8.7756	10.9967	11.9863	6.40609
8.88054	7.73089	4.95344	7.88967	3.53087	7.63419	6.06233	2.88656
7.84547	4.23646	7.0973	5.65659	6.4231	5.1049	4.45095	3.89965
4.22449	4.07112	7.81832	3.45076	4.93337	5.15908	3.94242	5.67455
10.0324	8.84435	10.3756	8.69929	9.30844	9.49274	5.54523	10.3744
9.0042	8.99769	6.81777	8.41237	6.93166	9.10085	7.60524	7.44361
8.36231	9.72072	9.17118	3.00996	9.65512	9.81178	9.5946	8.72082
6.49819	4.14119	6.59172	6.73688	5.27125	5.76179	3.57801	4.31009
9.33886	8.25461	8.40959	5.10964	3.59686	9.32594	2.69167	6.93013
9.6336	10.4722	10.4806	10.7263	9.42519	10.1033	10.8375	3.25804
11.9011	11.9484	11.5193	12.0453	11.3685	12.3078	11.3825	7.59284
6.78375	3.86681	9.65521	4.87014	5.44637	6.41142	3.09825	4.52714
12.0295	11.2888	9.20643	11.4904	10.7326	11.4098	9.87391	8.58056
7.38464	6.1418	7.48524	5.86359	4.74877	5.76691	4.58893	4.70194
5.32823	4.06432	8.01426	7.71135	4.1616	3.56165	5.08308	6.14119
3.40337	3.27502	3.93409	3.00051	2.89173	6.47416	3.10844	6.6682
8.60124	6.9987	9.55176	6.63839	6.65399	8.77784	9.42282	9.31394
11.7474	10.8323	10.6796	7.75378	8.25296	10.9105	8.42814	7.32287

9.74034	7.67552	8.83194	6.94956	5.25837	9.6368	4.65426	3.507
8.16533	5.49435	7.4335	6.48517	5.03386	8.34307	3.78329	4.0157
12.995	11.8089	11.752	9.18542	7.81056	12.848	5.18517	3.66417
9.85722	7.73568	8.7627	8.33719	3.08078	10.1415	3.17928	4.12534
4.04821	5.32075	7.85716	3.62859	3.26093	3.76271	3.46735	3.24361
8.48728	4.07677	7.69214	3.46987	3.53154	3.51747	3.29556	3.25012
12.4061	8.75134	11.6409	3.13683	7.28695	12.2706	2.95487	3.53693
11.9308	8.43571	10.7023	3.08695	4.67887	11.7903	3.51691	2.86837
10.7411	6.98817	3.22008	3.20276	3.23267	11.4559	3.06234	2.90503
10.646	4.26518	9.4122	3.07925	3.1826	3.75279	3.12691	2.99876
6.03488	3.03784	7.08893	4.51941	8.77606	6.07864	8.21069	8.02083
2.88455	3.53851	3.74068	3.88347	2.69091	3.42239	4.28241	3.06707
6.08632	6.69928	5.32532	5.25512	2.82318	5.35435	4.35386	3.80799
5.90254	6.3411	7.20719	6.44537	5.53915	5.7029	4.09274	5.64605
7.59389	7.70583	7.10304	7.92536	6.43868	7.59172	7.54648	5.54407
11.1663	12.2663	10.5688	10.4148	10.565	9.78732	8.49736	10.8741
10.5462	3.59122	3.32022	9.38004	7.4359	8.04879	8.54514	6.65593
11.8246	9.34511	9.63915	8.85479	8.5858	9.34315	10.3421	9.02746
9.79949	6.54441	10.28	8.39073	7.40795	8.12474	6.95415	5.43477
9.18009	3.68538	9.43471	5.43952	7.85896	5.91843	6.74009	10.4411
11.2669	4.35618	7.95849	7.85035	7.87144	9.92447	3.10589	9.8385
12.7658	6.93858	8.46052	10.6925	5.42408	11.9152	7.62511	5.69664
5.07634	5.76527	7.0397	3.13398	7.04882	6.6742	7.12756	7.11752
5.93347	8.85359	10.4356	6.37853	4.01567	8.72572	3.5965	10.141
2.96864	3.42505	3.15855	8.77849	3.20371	9.43172	4.51915	2.81899
3.22668	3.14626	4.03192	3.11642	3.85089	4.9754	2.84511	4.73863
3.20835	3.77831	3.25119	3.34424	3.30376	3.36576	3.56299	3.41639
3.27117	3.10436	9.25464	3.03889	3.30071	3.36195	3.27967	3.69131
6.00274	4.70092	3.78554	6.04072	5.04742	5.33166	4.11509	4.52657
4.66236	4.62658	4.86914	5.11445	6.47172	6.29176	5.90732	6.33828
8.83326	9.13791	8.41238	8.96864	7.21387	8.10057	6.40008	7.02538
3.15874	3.3316	3.45344	3.07296	3.6585	3.06937	7.21104	5.18519
7.33096	3.21938	2.89984	6.86758	3.24773	3.62902	3.28004	4.99745
7.79231	7.30944	8.11265	7.09435	8.91753	7.66934	6.26307	9.57868
8.07526	7.44178	7.9457	7.51413	5.90745	6.14356	4.39321	7.66483
5.96092	7.61776	9.82577	6.5204	7.22941	7.00192	6.12924	7.96416
3.95819	3.7566	7.15193	3.45819	8.13691	7.8215	3.49063	3.95964
6.5735	3.10767	4.74137	3.60881	2.84509	3.71477	2.96258	2.90423
4.33483	4.04988	4.1356	4.43958	5.14596	4.14686	6.39135	6.36799
9.01985	6.7095	6.33869	5.73773	6.45621	6.66364	5.39331	5.83228
9.53938	8.85016	10.169	8.51074	9.67093	10.0306	8.13353	7.53159
5.07023	7.05278	5.71628	3.01153	3.16145	3.20193	6.28387	3.16219
6.09386	3.37217	6.18821	3.51404	7.11307	4.13467	6.77145	8.15095
4.6974	3.69569	5.81664	3.67628	7.44365	4.83384	5.54052	6.74511
6.1017	3.27665	3.22388	4.81335	3.10481	3.0996	2.92369	2.70392
7.49885	7.58433	8.11581	3.2801	7.65529	8.06864	7.99275	8.09915
8.59447	6.75651	5.49996	6.18702	6.64655	6.30494	5.67785	6.24808
3.53021	3.53695	2.91604	3.24843	3.40546	3.23538	3.18979	5.4404
8.12556	8.576	8.14959	7.93903	6.52339	7.44669	6.79767	6.91
7.87424	8.04639	4.46556	7.07101	5.69636	7.80118	7.41089	5.85157
2.71936	3.07742	10.4315	2.85946	2.6457	3.06591	2.99292	3.17817
3.78569	9.44831	3.49395	3.27075	7.21744	6.71493	3.47345	3.46757
4.80351	5.50856	5.47589	3.61502	3.17555	8.61278	3.74051	3.60327

11.5919	8.2893	10.5121	3.63475	4.94288	11.5439	3.81691	3.23021
13.2232	12.7472	11.6467	13.1294	9.7468	11.6144	12.3556	7.11917
11.4509	7.55755	8.42589	3.33407	3.73683	11.1023	3.08997	3.12419
7.22782	7.75316	7.72443	3.58743	3.18848	11.7329	3.74932	3.23447
5.90155	8.48758	4.1367	9.59528	5.89238	6.9565	9.84526	3.06001
8.51234	9.1047	4.26717	8.08825	8.07102	7.73206	4.21137	3.4333
3.5606	8.81792	5.07332	5.24709	9.09797	7.91496	11.0632	6.54949
9.90276	6.086	3.45462	8.07596	3.13618	3.23997	3.34679	2.89566
5.65803	6.05134	6.24566	2.97209	6.85347	3.75787	3.71322	7.74312
9.65143	9.99326	8.13257	8.33222	9.59405	5.11972	4.18217	3.93403
2.77549	4.30035	2.97872	6.99759	3.08946	5.89023	7.41845	2.79249
9.99479	9.68002	7.15144	8.75226	2.87647	7.47132	7.80795	2.61545
6.23015	6.46985	6.90167	8.23923	5.59324	3.981	3.79584	4.03031
3.50843	3.06139	9.56808	6.34858	9.19993	8.65679	7.74969	8.59063
6.97164	12.2158	12.199	11.1028	12.1673	11.6361	10.7821	11.5599
3.20807	3.65889	3.38046	3.38587	3.36702	3.27943	3.31443	3.07666
2.95609	2.84411	9.49709	3.05088	2.84892	10.2336	2.876	3.30071
4.47398	4.03023	6.70946	5.74783	4.73833	3.90629	4.25821	5.20799
6.28349	3.38489	3.40025	8.83669	3.32997	3.27812	3.52996	7.32036
6.13388	6.86167	7.59536	7.29741	6.57555	6.10019	4.79024	3.71065
2.86783	3.16598	4.10638	3.61811	4.14634	2.75234	4.7848	3.03422
8.36929	7.51784	5.08081	5.07668	4.46399	8.25636	6.13569	8.38441
5.46376	6.09261	8.24971	7.499	4.36943	6.27384	5.37755	4.22094
3.32859	5.13499	3.17059	5.68627	3.10633	3.44768	3.42157	2.83252
3.63689	3.51477	3.26834	4.01379	5.18662	4.37604	6.54549	4.79739
9.09162	4.12089	7.17254	7.05857	9.2427	8.98184	6.13716	5.22985
8.76135	10.0255	10.4952	9.78537	3.65362	10.2128	3.19794	12.4172
4.94448	8.79872	7.43802	11.3696	7.90052	7.36035	9.92024	10.5112
9.90679	10.8739	10.7745	10.7902	7.81724	9.95886	4.39351	11.0621
5.21722	5.05527	4.7351	5.33024	7.72921	3.49171	6.32426	7.89262
2.86698	2.92911	2.94443	4.49089	3.01042	2.99967	2.78446	2.98381
8.05669	3.64513	7.58857	3.1332	9.17884	5.91508	7.68565	9.03048
11.3903	13.0984	5.41767	12.7706	11.4256	11.1211	13.1821	3.63889
4.16927	4.07185	3.94599	9.08784	3.21074	5.66133	10.2512	3.46624
3.1566	11.6469	6.89677	3.39985	6.84684	3.32131	3.24781	11.0473
8.20662	10.0378	10.2408	6.73825	6.7502	5.46715	5.84083	3.69317
6.73783	3.78631	5.89771	7.08232	6.26774	6.37239	3.16291	3.63307
7.26454	7.5407	7.2231	6.87121	8.12493	7.14748	7.50923	5.00367
6.86779	5.35171	2.91459	2.9572	5.17333	8.58473	3.99027	9.7146
8.50731	8.67344	8.0328	8.63742	8.06287	7.47446	6.96357	7.90613
5.77513	9.20354	9.95184	7.70815	8.43801	9.04435	8.24687	4.66296
3.54824	3.61	8.15985	3.44026	3.27283	3.45662	3.47197	8.58836
3.29755	3.31302	7.66358	8.53141	7.42069	3.16454	4.17297	3.16516
8.54139	8.86024	9.39979	3.50387	10.0165	7.53286	8.86491	10.6435
3.85274	2.8987	2.98348	2.82438	2.90728	2.99993	8.42843	2.9259
5.05891	9.79004	8.30891	10.5187	5.60424	8.41229	10.1556	5.11021
7.61207	3.2214	8.24539	7.3783	6.54451	6.57187	3.24781	5.45475
6.37809	4.53184	7.43947	4.99225	9.12759	5.61298	7.99888	8.73704
4.06257	3.08059	4.55467	3.71713	5.58021	4.13784	5.68193	6.398
7.82871	7.73778	7.12705	7.99551	3.396	8.88901	7.19283	3.43759
9.99265	9.94559	9.1754	6.91924	10.0218	10.8878	5.63803	9.83735
6.37323	4.51614	5.44096	6.92574	3.33092	5.98631	4.51717	3.02489
8.40649	6.38686	5.94446	7.87515	6.28778	7.01011	7.29446	5.00273

3.63348	5.16821	4.34436	4.07187	5.0268	3.69775	5.03871	6.5741
5.00562	3.04941	9.31263	2.9093	2.93371	5.42052	2.94216	2.88684
9.28882	8.79453	7.5775	6.88405	8.78795	3.75018	8.37724	3.43362
9.01181	3.26656	7.68926	3.16289	7.69807	5.24562	3.38433	6.89033
8.26694	6.65235	6.76731	7.40243	7.25959	4.84172	5.66828	5.45664
6.58991	4.1473	8.58966	7.17306	6.41216	5.87056	3.19858	5.63127
8.74445	7.84098	8.01036	8.50165	8.34235	7.9941	8.11912	5.99498
5.79999	3.27318	6.8369	5.2251	7.51229	5.60761	7.76636	8.96375
8.47746	11.4591	6.49056	9.65516	9.18647	11.0817	9.12943	3.49332
5.80281	5.10601	5.47117	6.48143	6.39216	4.03719	4.23945	2.87112
3.20597	2.91361	3.63736	3.3673	3.10729	3.51376	4.70107	4.00346
7.86325	4.61625	4.57608	8.01389	3.69527	6.41477	3.31423	5.56187
12.6099	13.0063	12.288	12.7023	12.7905	12.6299	11.9609	12.2313
3.42242	3.36782	3.18573	3.07503	3.09687	5.29425	4.64732	3.68086
4.08647	3.5934	5.25209	3.79894	3.86037	4.08788	3.94963	5.04486
7.12752	7.39134	5.63334	5.39995	4.2328	6.13559	3.98849	5.94585
7.88286	6.9044	3.20833	4.05624	3.23075	3.51462	4.43445	5.19435
7.92297	6.58254	2.90241	4.18271	2.75	2.83877	4.5771	5.92838
6.78392	7.94086	2.78889	3.49335	3.02407	2.82143	3.09002	4.38798
3.81051	3.32088	4.78192	2.87836	2.99574	5.6272	3.18419	4.84332
5.66673	6.50054	6.55427	5.8667	6.1523	4.62983	4.84068	7.30217
10.5815	11.2844	8.89915	10.7727	10.5097	10.5418	9.24802	10.3037
6.96224	8.04549	8.05814	5.11554	8.28214	8.66141	9.16915	8.44055
5.69645	5.96918	4.48471	4.66384	2.66064	3.9828	2.43413	2.65117
7.81045	5.54875	7.95229	7.34316	5.52643	7.4443	9.59342	9.58773
10.5017	10.6859	6.86157	10.7276	8.22101	11.6073	9.0706	5.48972
10.4922	9.99773	9.3122	10.9659	10.0575	10.3803	10.3258	7.94069
10.4519	9.19181	8.26529	11.7133	3.99756	8.50286	8.27218	3.07187
3.10613	3.06496	3.21292	3.34573	3.19546	3.05687	2.93083	3.88259
8.74962	9.71111	8.36296	7.09482	5.75539	8.29339	3.95902	7.90271
3.52917	4.33046	5.57283	5.03139	5.978	5.06019	6.61437	3.78733
8.4506	7.72741	4.89316	7.4945	8.81795	6.5638	9.77921	7.36662
5.06132	4.48346	6.68998	8.65405	3.91499	4.30683	3.84449	3.42081
4.8892	3.67961	4.99035	4.06808	6.67217	4.52495	6.5053	6.87751
2.75392	3.12644	2.61907	2.64231	2.65077	2.74647	7.45557	2.77938
7.49221	5.86721	7.87967	6.21758	7.49612	6.75878	7.28466	8.4383
11.3257	11.6484	11.1645	11.1087	10.9882	11.7755	11.0717	9.29476
9.20424	8.45106	8.6469	8.2392	6.57077	7.99411	7.06334	6.73451
2.92661	5.14481	8.48485	9.14458	3.06211	3.00444	5.36679	3.10837
7.83699	8.19612	7.94173	7.9873	6.31051	7.53954	7.06298	6.40737
2.87765	8.25486	2.88044	2.89208	3.12817	4.3481	3.03529	7.93597
7.0914	7.07196	7.76034	3.09694	8.06562	7.41034	7.49743	8.30972
8.59713	4.42615	6.99472	6.54734	3.86161	6.68134	3.70419	6.06861
9.61326	10.559	8.71387	7.7111	5.97641	4.09771	8.67032	3.64839
9.06007	10.0808	3.04741	9.28176	3.60306	6.009	2.90515	3.23962
4.53566	3.74657	3.59372	3.37781	3.67299	3.71093	3.89412	7.19894
3.53895	3.99617	6.80122	5.31555	3.4853	5.50895	3.4877	6.34319
8.79462	6.61419	6.41064	6.84513	7.18351	7.2944	6.58317	5.8575
8.48332	5.15533	4.66107	4.69595	3.38698	4.32057	3.33227	5.6273
9.86152	10.1921	10.4693	7.93789	7.39663	9.2575	5.07717	9.83522
8.49669	4.98416	3.50502	10.0028	3.62428	7.10724	3.25708	5.34729
4.26038	5.31091	2.66119	7.80152	7.87815	9.16233	7.93597	7.68688
3.94219	4.5697	5.16593	4.73452	3.58249	4.99396	3.41507	7.24915

5.62496	2.82453	6.43188	2.47871	4.33824	3.032	4.91936	7.42838
3.4599	4.15776	10.199	3.60097	3.58236	3.0946	3.06504	11.7335
3.61485	3.24264	3.61748	3.38715	3.09821	3.01701	3.05318	8.27913
8.12211	8.31481	8.31858	7.04143	6.83901	8.5405	7.33224	7.96256
3.43807	9.30916	10.0447	10.3416	6.75099	6.33495	8.77973	4.24029
9.7262	10.1828	8.29302	9.35687	8.30359	7.14735	8.19746	9.44052
10.5222	3.83173	7.98485	5.20032	3.35367	8.10464	5.01344	4.89044
8.5004	9.43819	7.01551	10.7129	7.13405	8.462	10.5924	6.47738
3.11589	6.85662	8.2864	4.54498	8.90605	6.53722	6.70187	8.64162
6.94954	3.89023	5.22526	5.70574	3.25424	3.63127	3.08752	4.23151
5.33986	4.07908	6.71054	6.07745	7.98517	5.73548	7.39732	8.76113
4.70077	3.45904	5.17943	3.13181	5.56609	6.46795	4.97748	6.60825
4.80828	5.10596	3.24744	7.2637	3.2634	3.56213	4.11223	3.23594
6.79784	4.59922	6.08896	4.83405	7.06148	7.73866	7.27183	9.118
7.48473	7.59777	7.33425	3.11149	8.18717	7.5789	7.78779	8.08796
3.1906	8.37885	3.30827	3.05787	3.8379	7.11512	3.21539	3.15461
6.23302	6.1087	5.48304	8.01464	6.27094	5.73933	8.76005	8.27644
2.99505	2.93115	2.77172	7.39957	2.94263	2.88996	11.2972	3.17637
9.2903	9.44498	5.51849	4.69806	5.05185	7.13698	9.68569	9.18579
7.90597	7.23355	7.54272	7.00346	5.91299	7.09126	5.68471	7.49244
9.97043	9.97401	7.99879	9.69702	8.42016	8.65216	10.0898	6.90166
5.58999	5.72992	6.47811	5.63643	8.18046	4.15823	2.92726	2.74188
8.58408	6.55465	6.25914	2.94159	2.86112	7.27691	2.84448	5.43453
4.16327	4.1597	3.59128	5.49379	3.76755	7.976	8.96321	4.92305
10.0145	9.11716	9.56339	9.84273	9.69067	8.59774	8.75448	8.28926
8.07172	8.62204	5.95901	8.25021	6.17079	8.99481	6.0633	7.89332
10.9691	10.955	3.44121	3.65518	6.24764	12.1404	3.41411	8.35765
10.4145	10.0607	9.18435	9.85989	9.99726	10.2344	11.0612	7.0195
6.89002	5.14677	3.49456	8.30444	8.22785	5.89677	8.97323	7.25581
3.16542	2.96947	5.08561	3.13169	2.79032	2.88499	2.80069	3.52086
10.1706	10.6083	11.9688	10.552	9.55624	10.8457	10.4895	8.59337
3.07958	3.33563	12.1976	3.16926	3.42425	3.53815	3.20205	3.08096
2.70854	3.10112	12.7167	2.97954	2.56748	2.89136	3.31248	2.8498
10.2276	7.81156	9.0251	9.06443	8.48985	7.38646	8.29863	7.78371
5.36135	6.61183	6.53592	7.05564	2.99224	8.07302	6.62415	3.27059
3.41191	3.26088	4.80072	2.83847	3.04177	2.92724	3.21639	4.2311
2.69961	2.9985	3.03806	6.46874	3.20703	3.2189	9.2303	2.61764
8.90791	5.47707	7.94405	3.11981	3.11118	5.29104	3.2659	8.14058
8.63461	6.55441	5.49224	5.97278	9.2712	7.14114	7.31316	9.29108
8.22041	6.39783	7.27138	3.20018	5.13599	7.31011	2.70916	7.52649
8.91708	5.52783	8.24498	7.20409	4.24398	6.72856	4.73025	8.31677
12.687	7.09007	12.199	10.9104	3.43504	11.2002	3.56145	10.4213
2.99809	2.66567	4.15946	2.93061	3.0066	2.89114	2.68094	5.15236
4.48208	3.22406	4.15211	3.19715	2.84022	2.88037	3.02294	5.21131
10.2323	9.69776	10.7105	8.80537	8.8244	10.3134	8.63772	8.92798
9.51996	9.55304	11.2226	9.93666	10.4797	11.1303	9.49092	11.9534
6.02155	7.19099	7.00914	6.0041	6.26947	7.11287	4.15436	3.22614
4.6454	3.9863	6.56585	3.17459	7.18136	4.64898	6.27576	6.97251
7.76593	7.15812	5.09492	7.25405	5.85003	7.9945	6.39278	4.97187
5.87742	5.86815	5.38539	6.64821	5.27904	4.85217	3.15554	4.97471
4.83959	3.00559	8.16582	6.82032	3.01574	3.19668	3.32679	3.27153
3.66766	5.07232	3.57531	6.42432	6.2028	3.66883	9.82708	3.35241
2.88753	2.82469	6.77172	2.89494	3.00124	3.27071	3.10033	7.42713

3.65784	4.14131	3.48155	3.35066	6.67209	3.61915	6.8609	7.42521
7.98793	7.16293	8.28677	8.42767	4.83964	5.64499	6.17943	4.14658
3.09719	6.75187	3.61	3.60274	7.72933	6.23577	9.9924	4.80411
6.72504	5.30324	5.99308	5.5401	3.02302	6.00111	3.93483	8.73686
9.41968	9.89529	7.8635	7.20996	8.77775	9.65851	9.31017	6.76951
8.67115	8.1863	10.2851	9.40309	7.73566	9.52232	8.22956	11.0917
5.24499	9.26529	4.77736	10.1575	9.19039	4.12462	10.7382	2.91813
9.57246	9.03488	10.5367	9.50563	9.07969	9.44639	7.18938	10.171
4.00801	5.22217	4.81159	6.17356	5.92423	4.14361	3.12902	5.85019
5.96311	5.18265	7.18858	4.0547	9.06867	6.81836	7.46415	8.99866
7.27828	6.84466	7.92249	3.72527	9.12594	8.19164	8.57642	8.96926
8.1637	5.04959	9.55798	4.25128	10.6684	8.39299	10.2076	10.4947
6.41341	5.5221	8.51952	4.85532	6.80841	8.11227	7.55348	8.76813
10.5059	10.2911	11.2435	10.0329	11.2594	11.4288	9.74168	8.34726
5.36762	5.38508	6.13533	7.33896	7.3879	5.49069	8.47194	6.95576
8.93999	8.02869	10.6267	3.62481	6.13966	8.24014	4.55229	6.24507
7.14214	7.95368	8.6493	3.46392	6.66597	8.13458	3.23607	4.35709
8.72927	8.15171	7.33079	8.10924	7.51155	7.28243	7.34954	7.03815
7.81346	7.46466	8.63351	9.38329	5.97736	7.44139	7.1882	5.91133
3.10617	3.39177	4.63322	3.61268	3.07001	3.35453	3.02771	3.3456
3.05487	3.10592	3.82316	3.20353	3.30847	2.8839	2.62086	2.86608
7.18565	4.69953	5.66976	9.31555	4.80417	6.86823	3.0085	2.79587
7.71194	2.46781	2.45172	2.73047	5.89478	2.72914	10.7063	6.94921
8.52369	10.6997	9.86347	9.36458	10.7834	11.0678	10.3022	11.4152
9.26868	8.67264	7.41626	8.48862	6.73463	9.11923	6.9509	8.97481
9.60118	10.9611	6.15145	9.29699	9.54636	9.38986	6.39353	4.76939
6.2291	6.71804	10.0208	6.39895	6.57842	6.11404	4.73175	6.94533
6.92142	5.40608	5.36905	7.75172	6.1443	7.38858	6.1014	3.64169
3.47795	3.36364	5.87853	3.37265	3.04799	3.52614	3.18693	8.06754
3.51112	4.12381	4.40998	3.3835	3.31238	3.2431	3.16277	6.29578
6.84251	6.04016	9.02297	4.2233	8.7638	6.64188	5.32568	9.07254
4.43465	3.67823	4.35306	2.60046	5.49729	4.84835	6.06142	6.25821
3.90412	3.05031	9.39357	7.05706	3.02046	2.92724	2.76926	7.17585
3.26632	8.50073	7.17979	6.24897	3.51515	10.8378	3.43139	3.10169
7.15669	6.22543	4.29403	8.70476	5.99162	5.22958	6.09767	4.66789
8.71992	7.75808	11.219	7.73912	5.16611	11.74	9.8076	8.6495
3.1813	3.56685	3.60745	2.8664	9.95644	3.1671	3.07918	2.543
10.1795	9.84323	9.6513	7.09893	10.1649	10.8708	10.0437	11.1875
5.38613	5.1599	4.45212	3.28118	3.6377	4.10939	6.23087	7.49079
3.2463	3.07245	3.53695	7.14882	3.10092	3.4465	7.27131	6.18735
7.58113	10.1366	9.75963	3.54713	10.9613	10.0014	9.06423	12.078
9.60144	10.1184	9.58653	9.67233	5.09288	3.13701	3.28252	9.08183
10.651	10.7312	12.238	10.4285	9.30691	11.1934	9.13794	11.543
10.294	8.76063	9.31135	7.62844	8.93148	7.47615	2.81802	9.38144
8.95587	8.60514	7.25781	8.25584	6.59615	5.67476	5.96711	3.34073
6.25491	2.89987	2.97891	3.58712	3.13973	7.0756	3.14666	4.57028
2.99542	3.1854	2.98556	2.98093	2.94315	3.16103	3.03431	2.79714
3.49638	3.4563	3.47408	4.1885	4.80891	6.32062	3.33992	4.54546
7.8818	7.18202	7.20962	7.85822	5.63484	7.11939	6.93838	4.63365
6.67476	6.22518	9.66234	3.07782	7.32536	8.17326	3.05735	7.69091
8.40453	8.40177	7.27845	10.0696	6.86176	8.30629	9.45359	6.76693
11.2003	9.7103	11.1394	11.5495	7.4246	8.61696	11.0743	12.4845
7.95364	8.33582	8.7786	8.16346	7.5011	9.32159	7.16811	7.18899

3.07402	3.50092	3.34666	3.17604	3.42069	3.96879	3.49809	3.72009
10.0573	5.85126	10.4444	8.28079	11.8095	10.0528	10.8609	12.1376
9.5179	8.75408	8.1352	9.54288	8.59821	7.8092	7.94889	8.83817
8.74677	7.77861	8.79176	9.24018	10.1488	8.40746	4.27973	4.49906
6.32999	5.6619	6.2239	5.30748	5.42502	9.49799	5.91153	10.5412
8.96974	7.91804	8.59533	3.86936	8.49377	8.75875	9.11472	9.31568
9.40803	9.27651	10.4167	8.53595	9.32011	9.31598	7.78995	9.31557
2.87299	8.2585	2.94417	2.7523	5.94383	5.30595	2.90515	2.7895
7.72232	6.49866	6.85316	4.86583	4.67186	7.78009	3.31843	5.96758
4.01063	4.96554	5.58146	3.02818	5.29875	5.97047	6.20753	4.84322
7.94539	6.2949	8.05201	6.52687	4.21693	3.85129	4.93152	3.92905
9.57114	7.01657	10.1293	6.94069	6.68218	4.27499	5.18082	10.4216
7.92881	6.54196	7.34673	6.99633	5.15897	6.10996	4.97728	4.33388
5.82293	6.13262	4.42904	3.16927	6.01411	5.00097	7.83646	7.69767
2.91959	6.2777	4.31645	6.60764	6.1125	6.36017	6.54136	6.67881
11.9614	12.6556	2.96805	12.7099	12.1597	11.6479	12.4842	3.03406
7.0364	5.68666	6.90935	3.25885	8.74446	7.11963	8.51507	8.4688
3.26236	3.11425	10.4585	3.14685	3.31762	2.98209	3.14295	3.24639
8.96974	6.26747	3.78576	6.35174	4.07986	3.69534	5.38053	3.94867
8.88445	7.46428	8.58926	5.13702	6.35648	7.61109	6.13516	7.44167
5.72351	3.31911	5.38359	5.97071	7.53563	5.36137	6.30563	7.58537
3.05088	4.48085	8.94578	9.04397	3.30595	5.4973	3.07661	2.66397
9.23218	9.37473	6.34816	8.89478	4.62878	8.30713	8.91659	3.59936
3.54853	3.7306	6.05693	3.4294	3.4466	4.39979	5.87139	9.18576
11.6797	9.94356	4.60172	9.99465	7.62871	9.23131	4.88541	7.17844
7.32828	3.44437	4.34319	3.41775	3.1101	3.47989	2.89561	3.10291
3.37212	3.49523	3.67551	3.33352	3.16388	3.32797	3.12852	3.2716
9.75991	10.4714	9.29328	9.86477	7.34996	9.52635	10.6288	8.4209
6.94763	4.22041	5.26654	3.05741	3.26716	5.11356	3.37446	5.8703
3.08794	3.01696	11.0226	2.96159	10.0455	10.5097	3.03143	8.83121
3.05717	3.21224	9.68495	2.97954	3.22899	3.417	3.22235	3.08123
5.93813	8.01834	5.12459	5.35767	6.23356	4.30198	4.46239	3.12726
3.33609	6.69926	6.23801	7.84528	6.63316	7.0598	7.38523	7.55405
8.77729	8.67345	4.99082	5.53301	6.1844	7.36213	3.92457	8.08712
3.57293	5.59933	3.25915	4.68925	4.14153	3.59959	3.24674	4.56523

WM1552C	COLO-679	LOXIMVI	A2058	IGR-1	WM-115	SK-MEL-28
5.32692	6.66404	4.25444	6.47061	4.32008	5.95715	5.98648
3.91413	3.1748	5.97308	3.89749	2.89525	7.05778	2.8613
3.14963	3.24247	3.02236	3.33113	3.27994	6.42696	3.61993
5.81082	8.20114	7.00553	7.40789	6.3534	6.22494	7.06642
5.16107	5.71062	6.88452	6.91749	4.49654	8.05172	7.46952
5.26855	9.07006	3.96214	8.87543	7.0045	6.54175	7.72603
8.95914	7.80509	9.4685	6.46557	4.2859	8.70614	3.57867
4.07261	3.08352	3.14089	5.24361	11.9739	4.94924	3.37419
2.93662	3.25	2.90268	2.6908	3.3746	3.27733	3.98139
7.87377	2.8259	3.50721	2.56505	4.09483	7.45996	3.04805
8.44236	5.1485	5.23028	4.1562	8.54405	7.3156	4.22606
3.51742	4.49086	6.68081	4.58974	3.67282	6.15992	5.79503
5.16952	7.42745	5.30066	6.00894	7.88232	8.29699	8.13776
6.52973	7.7022	6.41715	6.66902	7.86734	6.88025	7.41456
4.8475	3.43117	8.79012	2.86895	3.09979	5.28345	4.19218
3.45114	3.23352	3.25816	3.3254	4.11477	3.67311	5.22104
10.4157	10.0856	11.6342	8.29962	4.62595	11.327	8.94786
3.31384	9.17233	3.20196	3.67402	5.42826	3.31797	9.25589
4.50659	3.28395	3.6628	3.68987	3.73389	3.67795	3.96067
3.16323	3.31264	3.1147	4.07559	4.70003	4.10686	2.99657
3.71087	5.29662	8.02005	8.0412	3.44588	8.29965	3.36622
11.2734	4.02157	9.81932	6.70288	7.51971	7.61152	3.29387
8.73446	4.0173	7.65507	7.20662	6.80509	8.93152	6.83398
7.1309	3.42917	3.0984	3.22761	7.64403	6.35823	3.50023
3.30098	3.84655	3.10126	3.55813	3.41742	3.23012	3.87151
7.75239	7.19616	6.53065	7.65247	7.21077	8.02497	6.78789
10.3874	8.8586	4.69453	8.44842	8.32433	8.43862	7.85611
2.78309	7.28094	2.82313	5.11976	3.04751	4.8038	8.02848
8.04311	7.21988	5.00213	7.12483	6.2852	5.94521	5.96585
8.7822	3.11159	5.71964	6.36554	3.23784	10.0703	3.42159
3.05337	10.4337	3.1436	3.37184	7.38845	3.26692	3.27426
3.72459	3.39597	3.13457	6.98899	4.8038	8.90139	9.96914
3.04933	3.06033	2.97443	2.90793	3.04432	3.10704	2.79626
7.39204	8.77681	3.90769	9.04162	8.88388	6.69265	9.14217
9.11313	9.17801	4.02985	8.59383	7.53827	8.08203	8.39414
6.59171	6.94062	7.23596	8.1023	8.56175	8.68684	6.09761
7.87344	7.39775	7.33229	8.30158	8.58072	8.88085	7.23161
3.10568	3.25703	3.05357	3.6051	3.21295	4.16588	3.81457
6.9635	5.27297	8.06046	5.15251	3.83963	5.24356	5.44125
9.17168	8.97025	3.2529	8.54369	2.99614	3.10493	7.41327
3.32873	8.88442	3.06449	3.27378	2.97807	6.01173	3.1906
9.28657	3.37971	9.68675	2.95732	4.96506	9.42928	3.5486
7.49749	7.86079	6.96401	8.43104	8.0096	7.95525	6.66357
2.91286	5.0535	3.74347	4.30355	2.95933	2.65866	2.90479
2.78558	7.74729	9.15874	9.41637	6.73018	6.17001	10.6
7.61529	2.74058	5.95277	2.74416	2.71236	7.36717	2.89704
8.58442	3.22801	10.28	4.68483	3.45464	7.91766	2.80581
3.01114	4.88454	3.67313	6.87683	7.3102	3.13882	7.22614
11.4686	3.57503	11.5124	3.16072	3.69049	10.8293	5.15956

4.13916	3.55985	3.15697	4.47035	3.59202	5.52631	5.14155
3.98945	6.96293	4.89946	5.41683	10.1461	6.75825	10.5529
11.4341	9.55771	8.20203	6.22392	5.93273	6.51721	11.7035
7.74343	8.50387	8.2229	6.78913	9.17878	7.16706	7.78415
2.89584	3.22178	3.23809	2.85172	3.52825	3.49965	3.19696
4.84209	5.75384	6.73429	3.94777	4.53492	5.86374	5.08753
8.51241	8.30291	4.96369	7.76034	8.7785	6.70572	8.03812
2.75823	7.30975	2.83364	4.56032	6.76836	6.24914	8.37638
4.91211	5.22998	4.69673	6.21615	5.4486	5.10285	4.79137
6.50533	6.48543	4.64178	5.23144	6.77391	4.79883	6.56135
5.41291	6.02386	5.04955	3.88371	3.72464	3.43877	7.7153
6.54463	5.74711	3.66338	3.05273	3.06119	9.82947	4.63027
7.41288	5.76795	5.60403	6.69313	8.36166	7.12901	8.60893
2.9626	7.05756	3.10578	6.72956	3.24571	7.60391	3.09664
3.23169	2.84215	2.70514	2.77543	2.6892	2.97506	2.89075
6.65624	3.86042	8.07816	3.5303	6.71745	8.40893	3.35625
6.56136	6.37553	5.93437	6.72051	5.58222	5.8364	6.22201
6.69524	7.66711	6.53716	7.57291	9.77466	6.34097	8.6136
7.23844	5.13269	6.80226	4.27726	3.45038	6.84761	3.47939
10.1659	4.87899	2.97581	4.05057	12.1744	3.64513	12.6146
3.33665	10.8856	3.26456	9.86177	12.2981	4.78812	10.8465
7.44116	7.25378	6.62541	8.29943	7.16842	8.1254	7.32167
5.54523	5.10235	4.11024	6.93656	5.77225	5.21233	6.18377
2.7656	7.68215	3.34468	9.24069	3.15159	7.98064	9.78536
3.77917	4.4352	3.61253	3.90843	4.53243	4.44205	3.81803
3.21296	3.42735	3.3397	3.30081	3.0805	9.88642	5.59236
8.9576	9.59116	4.57299	7.78598	4.97167	9.78523	8.96035
3.13946	3.57086	2.80985	3.74176	5.06106	2.90634	3.45236
9.2013	2.64884	10.5522	3.93031	3.14888	10.8362	3.13285
2.90497	6.21976	3.45059	6.83688	9.2261	4.30945	9.72508
7.58789	8.10612	3.55654	7.44995	6.67396	5.99732	6.50418
6.81899	7.17076	3.80763	8.89989	8.60509	6.49702	6.74484
8.20706	3.74568	7.86169	9.24879	4.15121	6.4422	5.93444
8.97558	6.30001	5.92709	7.50716	7.834	7.72782	7.00583
9.45705	9.12309	5.57851	8.59016	8.69213	6.51977	8.30594
9.94793	3.33223	3.03566	3.86627	2.71278	10.1319	2.64039
10.5541	3.98437	3.8153	4.76753	3.16582	10.5489	3.46199
3.20029	3.59164	3.49112	3.764	3.79207	4.05809	3.63405
7.66625	7.33863	4.9056	6.78534	7.48907	6.71586	6.78984
9.73209	7.80037	4.90117	8.82073	7.70063	5.70127	5.22938
9.98055	8.99023	8.21417	8.6501	8.34645	7.79906	8.42612
3.12051	5.82058	3.64801	5.94518	5.69766	4.31704	7.18889
7.33697	7.7218	3.60206	8.21158	3.45589	4.01629	8.23122
4.68697	5.82853	3.7461	3.89796	6.40071	8.24694	8.76577
2.8228	3.98544	2.80055	2.55405	2.58963	2.7894	2.91109
2.95597	4.65462	3.02344	3.80315	3.43338	4.01521	2.84328
4.82571	3.53217	5.09452	6.00111	3.38955	6.63909	4.65843
3.15276	3.52553	2.92396	3.17776	2.83588	2.93838	3.52913
12.1513	2.90473	2.97506	2.83417	2.95162	12.6229	2.91948
7.67414	2.97879	3.20962	3.20852	3.02406	6.92005	3.36581
11.4763	3.47257	4.81876	3.44565	4.41226	9.07486	3.83659
10.5741	3.0925	7.89011	2.89887	6.15051	3.9603	2.82045
2.96723	3.28023	2.96636	2.93146	3.05015	3.15545	3.0595

5.30688	3.03611	10.8519	2.81335	2.73543	3.62351	2.98882
11.6816	3.6739	3.61918	4.61051	3.66243	11.904	3.82835
7.81622	7.74547	3.40532	7.3947	4.51999	8.96773	7.45579
3.19072	4.20209	3.36986	3.57317	3.01691	4.61806	3.42986
2.44871	5.17704	2.82195	3.92182	3.13261	6.53595	6.77767
3.13244	8.79408	2.82099	7.22437	7.12952	4.39565	9.99915
4.64894	6.85098	3.25867	3.53598	7.20784	5.09293	6.95446
3.17606	3.03503	5.85168	2.72704	2.6892	3.53931	2.88262
3.5355	3.1723	3.50808	3.28058	3.43338	3.28629	3.33518
3.78621	6.64615	3.80101	4.47136	10.1504	9.52744	4.12971
5.62462	7.95652	7.36824	8.28395	7.53519	7.54606	9.23167
8.35377	7.83609	9.41075	8.42753	8.18322	7.58811	7.84298
4.18122	5.12448	4.01272	8.67362	4.48688	5.21654	7.13092
2.99662	2.99672	8.28901	5.60032	3.10638	3.04106	3.08216
3.47565	3.25249	3.48338	3.49115	6.47713	3.06772	3.61455
10.2021	8.4115	10.2753	5.82151	5.65059	10.3263	8.62703
10.2005	10.6908	8.61069	10.2649	10.613	3.53098	11.9203
3.37045	3.1968	3.2237	3.30674	3.35668	6.24828	4.4676
6.53055	4.07885	11.5778	7.53702	7.32336	11.0239	7.05734
3.32753	3.30535	2.9116	6.09717	5.19477	7.89228	3.05442
4.64852	8.21467	3.93494	8.27684	7.44047	7.49588	9.24999
11.443	8.77956	11.4644	5.25122	7.96855	11.7348	5.5643
7.11106	8.32577	2.9956	8.07865	6.24178	6.15667	8.08934
2.9748	12.3541	3.12659	12.8852	13.153	3.08561	11.8311
3.86817	3.21015	9.08873	2.90918	3.11683	3.07856	3.32836
9.23852	7.5182	7.9329	8.92766	7.67749	7.70263	7.59176
9.35147	9.50369	5.72204	8.79846	9.0807	7.72132	8.61625
3.79045	3.28441	4.33677	3.3899	3.66461	4.60416	3.66044
8.53147	5.89987	8.83797	7.13446	6.6541	9.59377	4.59906
7.04038	6.96285	6.02313	7.79032	7.78826	6.08888	6.64704
3.79551	4.3248	6.28746	4.28442	4.91048	4.40939	4.08341
9.43854	8.91682	4.89616	8.55273	8.36353	7.51083	8.30303
3.70189	10.0802	7.38602	7.726	6.78447	4.93822	7.39856
3.13522	3.07084	3.0108	2.93953	3.0937	3.14727	3.16987
2.71928	6.33827	8.86938	3.53739	9.80882	7.98394	4.00897
9.30751	3.84341	10.0695	6.53667	3.73257	9.38943	3.91356
6.18984	5.59852	6.26889	6.41286	7.51473	8.10437	6.26147
7.28648	6.41217	5.42969	6.99539	6.32805	4.99419	5.96796
7.82019	9.49343	3.46162	8.95716	8.45418	5.63996	8.07171
9.59504	7.81963	9.15784	6.9	7.07411	9.42093	7.03022
3.15005	3.07598	3.45956	3.20973	3.28868	3.01368	3.34674
7.5055	7.52932	5.65748	7.14813	7.3811	6.69417	7.56546
3.34157	6.03192	6.43102	3.13425	4.26389	3.08034	3.54291
11.2533	3.50856	3.22806	3.29163	5.88705	9.96282	3.27093
2.88179	10.1017	5.84183	9.71026	8.7897	8.88586	8.58961
7.45452	10.3614	3.23922	7.57548	3.83645	7.93261	4.14406
3.51144	5.63185	3.20722	7.16097	7.18342	4.87061	7.87804
2.91258	5.35049	2.7646	5.70144	4.20407	3.70213	5.99576
7.66911	3.26084	8.43549	3.01558	3.19384	8.47084	3.27767
7.17772	7.8179	3.00792	5.71706	3.99365	7.52585	4.6304
9.27499	9.75871	9.63927	9.92296	10.0004	9.70298	9.56565
8.21756	5.6704	3.27998	7.669	3.1282	3.324	6.17221
7.25061	3.53172	3.02416	4.12514	8.03877	9.88272	5.06733

5.98557	6.36886	4.56137	7.3558	5.27066	5.39085	5.72635
9.73185	9.35143	3.01781	3.38258	7.77177	9.92513	8.83223
3.26204	7.35695	2.83506	8.24106	6.68063	4.75323	4.66941
3.9353	6.91293	3.17204	3.56216	3.41946	4.08823	4.5871
4.08031	8.85601	3.15322	9.62274	9.02085	7.96364	8.84291
8.10404	8.22788	8.63805	8.02029	9.06604	7.30138	7.16719
2.69074	4.89492	2.81699	9.40296	9.1403	8.45947	10.4924
9.98578	9.0799	8.41389	9.92443	8.11112	7.7364	9.54323
6.34536	10.7299	9.26564	10.1325	9.28526	8.45715	6.23567
3.29256	4.84361	5.64047	5.97485	6.33806	7.029	3.69775
7.19331	5.60831	9.22821	3.24413	6.70755	6.50254	3.37419
3.85618	7.61349	3.22989	6.6692	6.16616	8.4038	4.7402
9.6599	9.75843	8.33497	7.34365	5.8632	10.986	3.1615
4.94283	5.64283	3.10408	8.21923	7.47763	5.94641	7.97952
3.3753	4.11393	3.82253	5.75249	4.56273	5.71121	8.23901
3.02285	3.3394	5.22587	3.55389	3.14628	3.29995	4.25675
3.22909	4.95724	2.73228	5.47303	4.24305	4.26561	6.17217
3.72839	7.11873	3.02763	7.05887	6.27088	6.49645	8.35065
3.17872	5.10086	3.39157	3.57177	4.79505	3.25346	4.64593
4.00946	7.95902	3.21959	4.05877	9.50058	7.46622	8.24666
2.86617	5.45991	2.54086	6.62628	3.10574	8.17964	3.56882
7.0676	6.82496	8.28279	9.42252	3.40694	7.99595	5.10182
7.97959	4.13861	7.41905	5.9525	8.93655	7.99725	4.90599
3.12041	3.22601	2.87203	4.69849	3.01786	7.45617	3.13878
8.28692	5.12183	6.85657	3.92541	4.34751	10.3387	5.07382
9.30164	4.34783	3.02787	3.07259	5.68467	7.48502	3.42722
2.90651	9.5751	2.70573	7.48578	6.33592	10.9369	10.2013
2.83487	4.40717	5.09085	6.19582	5.77996	4.82498	6.98784
8.27024	5.8046	8.99426	6.36517	5.34271	7.95063	4.69795
3.30418	3.04453	2.65874	2.72334	3.1462	3.23618	3.11043
2.89987	5.79483	2.75944	2.74627	7.55326	2.5021	9.61887
3.9611	7.23732	3.63356	9.3008	6.72243	8.82787	7.47083
8.84057	9.76392	3.15813	9.30431	9.35138	11.1961	8.77926
7.40281	2.64281	4.60451	4.66649	4.21521	5.72259	4.57288
5.29285	5.4601	6.05853	6.91085	3.79008	5.22201	4.79553
9.6565	12.7031	12.0237	11.4871	5.34342	8.47724	9.94622
5.10986	7.77285	4.612	6.89225	2.79645	6.06525	6.52783
5.65222	6.63271	3.40076	5.625	5.22642	5.66662	6.44506
8.99233	4.73751	8.89754	5.4441	6.75506	7.40054	3.83629
9.42952	8.04786	4.86451	8.92476	7.39846	10.6499	7.34053
3.70389	7.05541	2.59213	6.25289	4.05846	7.87471	7.52637
8.47688	9.7675	8.72607	9.5516	9.6543	10.0434	9.20929
3.02179	3.61595	2.43354	2.63437	2.29032	4.96868	4.37279
4.93363	3.3548	9.48705	3.02056	2.92026	8.67614	8.96111
3.18905	11.1029	3.03088	9.04259	8.36831	6.66097	10.429
9.52932	12.1557	4.92128	11.9455	10.7035	11.3173	11.8263
3.46287	4.31915	3.37153	3.62829	6.91992	8.09392	5.2062
3.4095	8.24263	3.51448	9.83096	11.8561	8.2636	10.9897
3.91832	5.09012	3.73897	4.9653	6.09629	5.36812	4.57386
6.41933	3.25836	3.72722	7.07554	6.28589	3.27251	3.62542
3.08295	3.08061	3.14744	2.98705	2.80899	2.90744	2.84964
8.36582	7.50133	7.31264	9.41314	8.57377	9.47855	9.12796
11.564	9.23776	11.5949	7.57694	7.45807	13.0336	9.76955

6.3365	4.6723	2.96987	5.36277	3.36738	7.30841	8.17062
4.43355	5.99931	3.75287	4.97617	3.71969	7.88072	6.35306
3.61407	8.57094	5.21705	8.73583	3.88789	12.2384	11.4746
3.31407	8.50822	3.12585	8.32199	3.12441	9.56362	3.51714
3.27058	3.68549	3.20865	3.22222	3.45941	3.12901	3.3566
3.4164	6.15797	3.31628	3.22993	2.95248	3.39781	3.88631
3.12667	4.65525	2.99564	3.01932	3.05154	12.079	7.08903
4.11677	4.21322	2.98399	3.33593	3.03476	10.725	4.58488
3.10137	3.05513	2.81264	3.00996	3.13349	10.3855	7.66663
3.1128	3.08274	3.11841	3.22986	3.2384	3.46127	3.30795
7.77457	8.02069	4.63779	7.55452	7.93195	5.04801	7.85689
5.8847	7.20406	5.30919	5.6872	4.12358	3.66027	2.8495
3.21779	4.73245	2.79496	6.1822	3.92267	4.9579	4.40616
4.90056	5.70115	4.06425	5.14863	4.56186	5.02864	4.83333
3.66693	6.2568	3.60176	6.83815	3.91713	6.23576	7.09829
11.4613	9.83918	11.2895	11.6726	10.6148	11.1779	11.3812
3.98887	9.99281	4.13972	6.77745	8.89909	8.84114	9.81141
5.68215	7.7187	3.57182	10.4794	5.07166	11.2409	11.2874
7.34268	7.88808	4.21182	5.16297	3.77291	9.08238	8.15402
9.85007	10.6836	8.80472	6.61956	8.23508	8.6975	8.79967
11.1002	3.59217	11.0143	6.87079	3.51661	7.78202	5.26848
12.2375	7.19817	10.0193	9.81855	5.87037	9.77401	4.84018
6.35779	6.91398	8.14719	6.92922	10.0208	6.45722	6.03658
9.37337	3.57101	4.95967	5.62375	3.57185	8.83258	5.54126
2.88362	3.3354	11.8591	2.99657	2.85016	7.87634	3.31215
9.33676	11.2795	9.81271	3.13552	2.90958	4.68358	3.22897
4.16809	3.21136	9.94209	3.33065	3.50052	8.75196	3.49294
10.4871	3.39323	8.86829	3.78441	3.38006	7.58304	3.19183
2.81386	3.63299	3.91032	3.11299	5.65316	3.27165	5.356
7.86628	4.7869	6.77479	3.51344	5.85851	7.03591	5.80369
5.57242	9.17854	7.93061	9.61869	8.64396	6.63228	8.07464
5.45734	3.97596	4.3342	4.27146	3.26196	8.33402	3.19273
7.16771	3.03515	2.95946	3.27494	3.03639	5.02875	3.45536
6.73021	6.84779	9.83319	8.68209	8.5751	10.4107	5.75246
4.67233	7.88314	4.17245	6.92347	6.48195	7.16012	7.73996
5.65655	6.23476	2.59009	7.12299	7.00004	9.05522	8.26017
3.02796	3.09598	3.26685	3.322	3.99134	7.03167	7.76706
3.0744	2.84636	3.06368	3.01159	2.96051	5.17298	3.96808
4.88995	4.21704	9.25867	6.09357	6.65213	6.36536	4.01679
6.26802	7.10515	3.88085	7.36869	3.7832	4.97803	5.85907
4.49511	9.23599	5.13298	8.90484	7.84375	8.61648	8.29396
3.22736	3.02712	2.87323	7.23011	2.85742	7.75336	3.10905
6.47295	6.732	3.67389	6.52177	6.86381	5.80683	4.8732
7.60025	6.60654	5.76338	6.18908	6.54118	5.487	5.84057
2.93435	3.12255	2.81703	2.96272	3.62106	2.97184	3.72832
8.3692	8.13631	7.79434	8.39547	8.54877	8.10014	7.33172
3.36247	7.36929	3.28293	5.73714	4.31201	5.99394	7.24473
9.7947	3.0153	3.04916	3.57212	10.0875	3.3312	3.23732
3.8055	6.14808	3.76869	7.22406	6.44651	3.1684	7.77857
4.46058	4.29667	3.62514	7.00541	6.02723	5.04167	6.07628
3.08898	2.84886	2.69959	2.69807	2.6892	2.5769	3.02373
3.33539	3.92714	3.61718	3.60884	5.36208	6.2	3.66491
3.59635	3.58851	3.24364	3.62563	3.38871	6.7702	3.76864

4.03556	4.36681	3.56421	3.45085	3.25672	10.5378	5.32403
10.1571	13.2978	12.6908	12.5039	5.92068	9.73897	10.5472
3.30466	4.04589	3.3266	3.15077	3.39246	11.465	4.1992
3.52684	3.3865	3.22873	3.57713	3.39687	10.6328	4.16857
3.62962	4.58682	3.10462	4.6767	8.92741	3.70752	6.88439
2.77829	7.41278	3.1737	6.12675	6.2423	4.67741	6.40711
10.6365	7.98631	2.95963	8.64188	10.2064	10.0965	10.2776
4.95322	8.13261	3.07162	3.12696	3.2823	7.25058	3.39761
4.80732	6.38289	3.86795	3.15498	3.30934	3.94035	3.23133
9.38778	6.76596	8.04177	5.90951	6.4108	9.90339	9.61166
10.4178	7.84885	2.65533	7.36833	9.22846	10.141	7.70151
6.64577	4.45314	9.29865	7.04108	6.32835	7.21126	7.20121
3.13428	9.20716	3.02263	6.23238	7.14498	4.50146	6.38875
8.17218	9.06184	9.36424	8.93882	9.52718	6.78279	7.67445
11.5986	11.3289	11.1222	11.4888	11.2562	11.0095	11.7075
3.45591	3.4354	3.24038	4.22215	4.47827	3.22864	7.37761
3.3223	2.89123	10.3369	8.1826	3.07754	2.89803	3.03691
3.20886	3.79681	3.01737	4.16633	3.35228	3.02117	3.77325
3.49223	5.99567	3.38375	3.49469	9.43717	5.48557	3.41028
3.71246	6.20479	6.37253	6.18075	4.37904	5.69663	7.76571
6.87615	2.9826	2.66121	7.04896	6.72186	5.96733	6.06449
9.30069	4.901	8.73472	9.58392	4.81799	8.05463	4.7281
4.66034	5.86876	6.24851	4.89025	5.62839	6.71499	4.2196
3.07756	4.46244	2.72915	3.39737	2.75926	2.92539	3.08091
5.4133	3.94634	6.84273	8.01686	3.97051	3.20544	3.66544
3.32514	3.72477	3.53504	8.28939	9.15497	4.07505	7.40815
3.78951	5.05712	3.1697	6.43687	3.92387	8.59458	4.71812
12.1614	10.1296	3.28312	11.5512	12.2568	10.6894	11.9902
3.34552	8.4137	3.41681	7.93885	6.03014	8.41349	10.8184
9.95353	5.68355	10.7232	7.09875	4.91392	8.58101	4.00955
2.83946	2.69888	2.76115	2.8601	2.61081	2.95936	2.83609
7.69295	8.69139	4.342	8.14822	7.42349	4.56796	8.33863
3.42511	12.2382	3.69987	10.8469	13.2189	3.51796	13.2454
9.06737	5.95645	11.0756	7.78827	10.0986	8.29561	9.43258
7.7653	12.7244	7.51414	11.6179	2.96099	11.0165	5.31692
3.11722	4.99547	3.20582	5.97978	7.38332	5.97998	8.02614
2.65253	6.72544	2.80296	6.35652	3.32606	2.72793	4.39918
4.81704	7.04016	3.97855	5.15535	4.86243	7.27635	7.21106
9.91122	3.40467	8.55056	7.5173	3.53783	10.8249	4.35067
8.02742	8.17951	7.57668	7.27027	7.01222	7.45988	6.18346
3.82915	9.1355	5.13093	9.3675	9.39473	5.70503	7.11853
3.50637	3.3125	3.4511	3.32552	3.6266	3.09295	3.28012
5.14636	3.72512	8.86568	8.08845	3.73939	8.23395	3.20643
11.4656	7.99731	9.25862	4.33796	7.08406	10.5576	9.02458
2.70758	9.1441	3.45489	2.88863	6.72422	5.08838	2.82748
4.93972	7.64633	3.82253	7.02097	4.54746	3.30018	9.06893
5.23515	4.93847	3.40965	8.6964	3.46476	7.5282	3.68637
7.99566	7.63756	6.26425	7.4432	7.17449	5.5791	6.92166
6.87124	4.63817	3.58247	5.3873	5.29433	3.66561	5.02718
8.48215	6.31085	7.12331	3.34048	5.8379	8.28347	7.6079
3.44886	8.89192	9.23048	5.08898	4.58683	9.93055	8.91993
3.09042	4.07987	5.96967	7.29557	3.09979	2.65059	3.66772
4.00817	5.71758	5.52462	6.97218	5.31556	6.71316	7.21843

6.46585	6.40713	3.51304	5.99914	6.14054	5.73413	4.69795
2.75528	2.99986	2.94907	3.02299	4.40558	7.3481	3.16984
3.6204	3.18159	3.5327	3.94405	8.25479	4.73086	6.28236
3.0014	4.11764	2.71884	6.47418	3.94335	7.93974	7.1981
7.75807	7.39075	10.0573	5.45899	9.06714	8.54077	8.55293
3.29007	3.79471	3.12882	3.50937	3.452	6.78675	4.4693
8.18955	7.64906	4.27114	8.3263	8.56621	4.64419	6.8216
8.34348	7.41151	4.41014	7.16612	7.09101	5.66801	6.8728
4.92311	4.02011	5.54983	10.5845	3.8971	8.08914	8.98147
3.77254	3.38666	8.40554	3.47378	4.5946	4.4357	6.09851
10.5774	3.62179	3.10101	3.13188	4.17263	7.36846	3.09834
3.25542	6.71139	3.4078	5.61059	4.92325	7.04217	4.15019
7.43077	12.4108	7.53289	10.5499	13.0004	11.4178	12.6658
6.25204	6.07529	3.98104	6.69728	3.15194	5.75356	2.95401
9.42114	4.13205	10.6267	4.24789	3.9039	11.04	3.78522
2.80259	5.71794	2.97366	2.95413	3.588	3.50206	3.26485
4.09417	4.05121	4.69885	3.70918	3.25802	7.30866	4.69942
3.64159	2.94241	7.22612	4.57352	2.83229	8.66441	5.37753
3.15392	3.00724	7.83851	3.37555	2.77677	7.93131	3.62847
2.7392	2.97921	2.88321	2.96359	3.08798	7.77697	2.86427
7.75528	6.97844	9.54318	6.53373	7.63941	9.14108	6.80526
6.25151	8.81792	3.20821	11.1356	9.51505	9.41257	11.5882
9.43434	8.66153	8.34494	8.78485	8.58568	9.46664	8.76267
3.87866	3.55422	2.83598	5.22666	5.00159	2.84328	4.7414
9.35824	8.94711	9.70991	8.5808	8.16383	9.34298	4.91704
2.86378	7.8553	3.37849	7.23169	6.25146	3.81642	8.4653
5.23574	9.90002	4.77465	10.7074	10.5671	7.63033	11.3507
2.93751	7.53214	3.02366	6.57094	9.12421	3.09095	11.9939
8.27624	3.41137	7.8179	3.96773	3.24656	7.75088	3.66072
6.3954	8.82679	6.17004	6.71925	6.82181	7.5713	8.07706
6.7377	8.19865	3.37736	6.43829	6.28359	5.44869	8.77068
9.37893	8.76252	9.54599	9.91856	9.78498	8.57336	8.69107
3.24388	6.45651	3.01313	4.27386	3.60023	3.43752	4.00028
6.94819	6.03363	4.10145	5.74496	5.86879	4.88319	5.34442
2.79339	10.6495	2.77021	3.97017	2.9483	2.69614	2.82432
7.61486	7.23745	7.96331	7.85142	7.50911	7.93557	7.34629
3.372	11.4434	3.56393	10.842	10.4215	10.9542	10.961
8.00069	8.31592	4.23167	6.80455	5.70266	8.45402	6.56863
3.19299	6.02375	2.57293	4.71682	7.67928	5.78043	3.18921
7.38915	8.59758	2.34853	7.04219	7.67722	4.75163	8.50982
8.44975	4.34799	9.97317	3.57896	3.22436	9.5206	2.88699
7.4207	7.49585	7.0271	7.88305	7.62528	8.15768	7.68553
3.66794	3.92063	3.57905	3.8568	3.56331	3.43027	8.21885
3.31501	8.56462	3.8282	3.45875	3.65307	3.8529	3.96574
2.86498	3.09567	2.79153	8.60029	9.92713	2.84724	9.85082
8.12465	3.97608	9.12454	3.75546	3.57503	7.23114	4.32944
4.33502	3.63162	4.35427	4.07879	4.1559	5.43092	4.76553
4.90217	7.59969	5.7771	6.49118	7.61494	5.65144	6.63689
3.89563	4.08469	4.08766	4.10306	3.99576	4.82347	3.57252
8.98914	7.27486	8.13523	7.39447	4.84192	10.3494	8.92564
2.94592	4.93877	2.98083	6.16165	3.01377	3.27015	7.14955
7.4264	8.17953	7.75705	7.51105	7.98764	7.84416	7.92708
9.13324	3.32606	8.94948	4.00321	8.22691	7.06696	3.87292

11.3917	3.17093	6.70203	4.87394	3.07331	10.0866	3.81581
3.23973	3.14899	3.70904	3.48966	3.14991	6.2618	3.12985
5.87984	3.27654	9.62621	2.80831	3.34329	9.19648	2.99674
3.05178	6.94575	2.72547	5.586	3.25889	10.0677	5.41891
5.31341	4.89963	2.82099	10.204	3.32232	2.9018	10.7651
5.48559	9.27936	6.20233	8.64283	7.76677	6.83479	9.03002
4.53633	3.68578	3.82887	6.01718	3.68162	3.43713	4.877
3.69158	7.58837	3.3736	8.81739	8.77814	5.06963	9.66089
8.64553	6.23487	8.86979	7.68038	9.0319	10.2489	4.54904
3.05957	4.37258	2.89313	3.63497	3.79759	3.48442	3.25187
7.82676	7.33646	5.16687	7.14909	7.60743	5.63621	6.71833
3.01114	6.1121	6.00375	3.17377	3.40911	7.36698	3.21356
3.43608	3.24536	2.95309	3.79374	3.94079	3.29922	3.35043
7.50699	6.39426	8.04677	6.94312	6.82727	7.33122	7.52328
7.72029	7.71646	7.28968	8.72169	7.5635	7.7888	7.18355
3.16307	6.13947	2.89661	3.02711	2.91933	3.04619	3.05627
9.46177	7.40121	9.43668	7.67759	8.58862	10.3108	4.54492
9.11528	7.28976	2.75371	2.91476	9.01782	2.95948	8.36797
10.3153	9.08583	7.90084	7.22708	11.0967	8.938	5.87453
7.24622	6.59749	6.75489	6.03482	6.57915	7.3926	6.72221
6.78406	7.63026	3.00497	10.4531	8.73449	8.09109	9.56089
3.17535	7.71465	3.35354	5.21683	2.73494	7.02502	7.25268
3.05983	3.09476	2.89499	7.4047	3.22382	2.77148	3.15843
5.56219	8.31851	5.67219	3.8007	10.0621	3.56703	5.86723
3.38546	9.31622	3.40076	9.11845	9.34818	6.41242	10.4186
7.30893	6.99901	5.84897	6.23921	4.75531	7.42013	4.93754
3.74669	3.54524	3.53504	11.269	11.701	3.33019	10.9478
3.57291	10.1112	3.40076	10.55	10.0695	7.43952	10.3997
5.57933	7.39494	6.45008	7.72922	8.77235	3.73305	8.76863
3.19228	2.87999	2.85454	3.27102	2.78639	3.01773	3.04335
2.95076	11.7102	2.92008	9.02693	8.75745	10.7324	10.9177
3.16323	3.21361	3.81559	3.14974	3.21272	3.12257	3.06445
3.16773	3.05048	4.40715	2.97183	2.81977	2.81212	2.80435
6.66085	7.5258	7.4218	8.89421	8.53284	9.84675	10.3381
4.57831	6.63125	6.94961	3.31398	3.14566	7.40572	5.4974
10.7565	3.15678	9.84902	3.31967	3.28676	9.08515	2.77331
2.77353	9.854	2.70513	2.75031	6.8107	3.42845	8.00218
3.15448	5.71867	3.02123	3.66533	3.22158	6.95018	3.8505
9.34862	4.86667	9.30132	8.25595	4.79164	9.78278	6.62376
5.45205	3.46131	2.38894	5.91543	3.48213	5.15035	5.59498
5.48079	4.83754	3.77233	6.03883	5.88129	6.57376	4.17559
3.16502	8.22409	3.44973	9.95464	3.52187	5.23141	4.43431
7.39955	3.42325	9.7125	3.03882	2.72756	9.62555	3.42438
10.9361	2.80163	10.493	3.02306	3.43403	11.5894	2.72343
4.55989	9.61656	3.20827	6.73016	6.04804	8.27726	9.04568
10.3577	6.7923	2.87075	8.11919	4.00254	11.0851	11.0763
2.8798	5.55266	2.94616	5.99989	6.1075	5.80178	6.07406
6.07648	6.77478	3.62514	6.02323	6.5331	5.26974	6.47468
3.65664	4.52039	7.18359	6.48677	5.64223	5.62178	6.21891
3.00236	3.98512	2.89548	3.8457	3.36171	5.10867	5.522
2.79464	4.11605	4.2172	6.78987	7.53961	2.89508	3.32752
3.60208	10.6319	3.31529	4.26752	5.40814	3.02753	8.23253
8.95296	3.00772	3.116	2.78811	2.79432	10.7523	2.79498

8.74792	6.1574	5.37204	6.36558	7.13205	3.59418	3.80724
9.07427	7.41596	3.13432	3.39325	4.45205	7.01545	6.91339
9.03274	6.78531	3.02926	7.12665	9.11925	8.83773	8.97285
3.8856	3.28177	3.25101	5.4512	4.5944	5.1968	6.39624
4.96741	7.19581	3.27989	9.03499	9.60858	6.98295	9.66376
6.58685	7.91165	6.90517	9.39058	7.2993	7.66167	8.05685
3.20595	10.1006	3.33433	7.43413	10.2719	3.08226	9.55338
8.09617	8.45381	8.32864	8.93954	7.82212	9.56069	7.52812
3.26704	4.86683	2.98662	4.88305	3.35317	4.50466	3.91286
6.86979	8.1567	7.00263	8.25949	7.75468	7.70033	6.82315
8.10648	8.70658	7.99739	8.94986	9.08338	7.00759	7.28401
9.69666	9.72396	8.03679	9.16763	8.99924	9.50249	9.68007
7.78869	6.53003	7.35151	8.06473	8.49135	7.49252	6.88148
5.81382	9.43255	3.16562	10.3179	9.20283	9.31992	10.1568
6.76113	7.53046	6.53064	6.53745	6.7113	6.06981	7.53449
3.77908	3.58672	3.35199	3.95389	6.15887	9.77704	4.42803
3.03577	5.60336	2.94302	8.31978	5.40262	5.1422	5.75467
3.1057	7.56056	3.39532	7.47266	7.79628	5.54156	7.90781
3.04638	8.34361	3.01067	8.27414	8.11399	6.13192	9.44425
9.28647	3.27953	3.96928	3.02402	7.30422	8.05737	3.30624
11.7223	2.88393	11.9204	3.07533	3.15584	3.26332	2.90644
2.86514	3.88605	2.71094	4.08479	6.51985	2.72837	4.08957
7.087	2.59744	6.60826	2.79339	2.70252	8.21582	7.47438
2.76567	11.2991	9.9712	10.9888	9.25214	9.71625	9.28178
5.60776	7.49577	6.74777	5.95038	5.03597	8.19861	7.59686
2.91254	8.70201	2.94775	8.04134	7.11774	6.48991	8.0676
4.08938	3.32746	3.33864	4.83977	6.85932	8.25136	7.99651
3.78794	3.57632	3.27174	6.57702	3.98925	5.92537	5.92664
9.45153	3.24833	8.66036	3.81771	5.77589	7.81396	3.30328
8.7975	2.9505	7.48744	3.70944	4.92035	3.9346	2.92599
8.22585	3.82195	3.4536	5.82126	6.80882	8.54952	4.5619
3.93175	7.22697	3.11244	4.23157	2.942	5.41124	6.69094
3.25652	2.8659	3.13573	6.66121	3.28741	3.1218	3.16075
3.41153	6.99757	3.37675	3.89655	8.48571	3.27061	4.25972
3.118	6.27726	3.4454	5.12394	6.65032	4.77236	8.32366
3.11775	3.89123	3.14914	6.94179	5.81245	3.41368	3.12421
3.02792	2.88177	2.93126	2.612	2.66154	2.66389	3.04496
8.65059	5.61522	4.18483	5.34107	5.07214	10.5087	9.83682
10.2342	5.43683	10.0212	7.45318	6.849	10.3493	6.80201
6.61921	2.80678	11.7116	9.53473	4.25821	7.76538	4.60299
10.8995	5.51614	9.62401	3.39237	10.8375	12.6656	3.58892
4.52322	10.1031	4.81889	11.0932	2.86102	3.38356	2.79775
12.1892	11.1717	2.90126	9.56283	9.33175	12.112	10.3557
4.68127	3.62785	11.024	8.47608	9.86153	8.78911	9.54342
4.28649	7.64989	4.87587	4.85591	6.84301	6.81211	8.70839
2.67459	4.29948	3.5363	3.55522	3.02938	7.84727	6.65965
8.47171	2.94825	9.77329	2.92161	3.06439	7.12343	2.87901
6.2027	3.67561	4.30904	3.72491	5.27469	7.7143	4.31534
4.39958	5.44958	3.33944	6.2234	5.46013	4.07406	5.85514
3.09533	6.98163	2.89953	2.93694	3.05698	9.86252	3.0529
3.59445	9.14158	3.13213	7.84479	8.87416	4.04216	9.3942
11.8069	10.7575	10.9353	11.0629	11.5642	11.7837	11.6178
4.8647	5.01044	3.29277	9.19431	7.75541	7.05944	6.9165

9.76613	3.26192	7.80652	3.40106	3.58958	3.60935	3.23124
11.4585	10.9015	8.5132	11.3621	10.7318	10.7205	10.1544
4.2586	8.24694	2.7359	9.96225	9.50047	3.9549	10.3068
5.28962	10.2105	6.59621	8.10133	5.2406	5.30825	8.50224
10.8366	5.03993	10.1934	8.38576	5.10161	8.68019	6.32294
9.12588	8.82318	7.44226	9.61638	8.429	8.93573	7.93529
3.53278	9.42027	3.45626	9.43533	9.69842	8.50285	8.83577
3.05243	2.99434	2.71264	2.96805	3.88977	4.50281	2.96236
3.27511	5.02173	4.52161	3.91096	4.67709	6.70437	3.85467
7.39151	6.25784	4.91205	6.35321	5.81318	6.44805	6.14075
3.33627	8.84687	2.90219	4.33318	5.63591	8.74068	3.52983
7.10338	7.75717	3.7296	7.21269	7.23841	8.40582	7.48311
4.06341	6.02763	4.37728	5.71991	5.43722	4.96294	4.83157
5.6128	4.39963	7.55278	4.69789	3.39378	9.07225	3.75572
5.6808	7.33375	7.36757	7.42458	9.12379	6.43478	6.52454
2.75847	12.7609	2.93471	12.5994	12.0786	2.84989	12.3804
8.52208	7.25219	5.72076	8.29962	9.06984	7.65737	7.70835
2.91197	3.08366	3.5141	3.16072	3.95654	3.32558	2.9241
3.68613	7.82997	3.12202	4.06231	6.84213	3.84091	8.56542
3.55732	6.14301	4.22404	7.22336	3.72896	4.69737	3.87717
6.94075	6.45848	6.2971	6.7741	5.58154	5.69541	4.62564
3.19713	8.22481	3.29527	3.28899	7.69818	3.23972	9.54418
3.30566	4.57064	3.53769	5.83755	5.38766	4.83933	11.1234
10.3683	4.22827	9.29478	6.76728	3.95114	9.90551	4.39258
5.02349	10.4357	10.5704	6.88103	7.17018	10.3382	7.86947
4.674	3.49946	3.518	3.13754	3.3119	3.60585	3.4296
6.3902	3.6077	10.8203	3.74586	7.34056	3.32828	3.06245
8.32176	9.79637	8.80836	9.66439	3.84586	9.40936	10.539
3.09767	3.50056	3.53223	3.07715	3.22997	3.32566	3.10444
11.2448	3.29924	2.91882	5.61478	10.9054	5.60894	3.228
3.03331	10.0204	2.83506	2.94906	2.87355	2.7864	3.20999
4.32501	3.67962	4.37689	3.12733	3.00242	7.8581	4.70358
7.56786	8.14649	7.41738	7.97247	8.05054	5.79971	6.63589
9.38173	5.6803	2.99541	7.06497	6.44422	9.37369	7.0726
3.79183	6.14385	3.46162	3.44916	5.69203	4.07836	5.87472

Table S7. Gene expression regulated by TAZ.

List of genes with altered expression value in A375 cells overexpressing WWTR1 (TAZ). Genes with 1.5-fold expression value changes are listed.

Gene	log2FoldChange	PValue	FDR
OLR1	8.295749723	5.61E-99	4.62E-95
KRT17	7.999507512	3.12E-50	1.84E-47
NPPB	7.883741309	5.15E-66	9.43E-63
TNNT2	7.202164658	3.94E-89	2.16E-85
MFAP5	6.446544772	9.19E-57	7.97E-54
KPRP	6.274498442	3.16E-31	5.10E-29
CDH5	6.243188881	1.36E-23	1.14E-21
SDPR	6.16365841	6.66E-12	1.55E-10
ALPP	5.987943101	1.69E-53	1.16E-50
APCS	5.549864485	6.88E-35	1.45E-32
PSG4	5.356464469	5.16E-48	2.83E-45
ANO2	5.253792612	4.48E-34	8.89E-32
NPR3	5.173511465	4.99E-11	1.05E-09
ANXA3	5.105238112	6.23E-27	7.22E-25
CCL3	5.059252073	1.59E-38	4.29E-36
KCND3	4.928089584	1.55E-65	2.56E-62
XIRP1	4.905662414	4.52E-09	7.22E-08
TNNC1	4.640529737	8.09E-18	3.79E-16
KIF17	4.564688149	8.60E-45	3.94E-42
ANKRD1	4.55405431	1.01E-33	1.93E-31
SERPINE1	4.547500596	3.02E-39	8.44E-37
DYSF	4.529680031	9.46E-44	3.80E-41
TLL1	4.488050946	1.43E-34	2.92E-32
HCLS1	4.449774922	1.07E-25	1.07E-23
KRTAP2-3	4.436129834	4.76E-21	3.16E-19
KISS1	4.368497247	1.53E-31	2.52E-29
ANKRD2	4.27348164	1.03E-26	1.17E-24
RP11-54A9.1	4.264510616	2.48E-19	1.37E-17
RP11-380J14	4.239688085	2.30E-26	2.53E-24
IL18	4.221584142	1.28E-12	3.26E-11
VSTM1	4.219731838	7.75E-33	1.33E-30
SFTA1P	4.209688786	4.71E-24	4.08E-22
CCDC148	4.143676735	9.37E-59	9.08E-56
MOB3B	4.127966293	7.60E-38	1.96E-35
MUC2	4.055689153	1.11E-06	1.16E-05
KRT34	4.03331082	4.50E-25	4.26E-23
LINC00520	3.994091812	3.66E-20	2.20E-18
CTD-2354A18	3.933871346	1.27E-25	1.27E-23
FOLR1	3.82720568	4.28E-15	1.49E-13
EDN1	3.793610814	6.43E-23	5.00E-21
UNC13D	3.722885886	1.13E-40	3.71E-38
ITGB2	3.719145896	5.04E-31	7.90E-29
ECSCR	3.710431237	4.71E-23	3.70E-21
TOX	3.635796179	2.10E-39	6.08E-37
PVRL4	3.600519091	9.30E-34	1.80E-31
TGFB2	3.591517856	1.30E-25	1.29E-23
LRRC4C	3.575160298	2.51E-29	3.51E-27
STXBP6	3.531389065	2.28E-14	7.35E-13
WNT7A	3.52063926	5.92E-33	1.04E-30
LYPD6B	3.506193617	4.01E-10	7.43E-09

CXCL14	3.502745849	0.00011164	0.000717
ADAMTS5	3.473753507	1.21E-07	1.51E-06
TMEM40	3.459036671	8.75E-23	6.73E-21
IL6	3.446263483	3.44E-07	3.99E-06
GNGT2	3.420920932	8.17E-22	5.93E-20
CLSTN2	3.413351328	3.01E-19	1.63E-17
MPP7	3.398785379	2.09E-12	5.23E-11
GBX2	3.33837745	1.73E-37	4.26E-35
PEAR1	3.285467675	1.01E-29	1.45E-27
GDF15	3.277974661	8.06E-11	1.64E-09
IGDCC4	3.262405125	1.00E-27	1.25E-25
RP3-399L15.3	3.260168163	4.14E-41	1.42E-38
NLRP10	3.240493136	4.16E-13	1.13E-11
PGM5	3.210399918	3.13E-09	5.10E-08
ALS2CL	3.194350049	2.91E-56	2.39E-53
CDH4	3.165918645	1.80E-13	5.20E-12
SYTL3	3.158298312	5.60E-21	3.62E-19
CDA	3.155533234	3.33E-27	3.98E-25
PPME1	3.088891995	5.02E-83	2.07E-79
TAGLN	3.07171079	2.34E-17	1.04E-15
MIR503HG	3.035816426	3.51E-26	3.76E-24
GFRA1	3.0315276	7.15E-15	2.44E-13
SFN	3.016695296	9.38E-20	5.36E-18
SAA1	2.962517175	9.82E-05	0.00064159
ADAMTS6	2.961519996	3.31E-24	2.93E-22
FAM155B	2.938829865	3.30E-23	2.64E-21
CTC-308K20.	2.936473775	4.82E-41	1.62E-38
LCP1	2.906207571	3.87E-21	2.58E-19
MME	2.868266589	6.64E-14	2.05E-12
ZNF542	2.867926638	9.03E-51	5.51E-48
SBSN	2.859032821	1.45E-09	2.49E-08
RAB3B	2.855026363	4.23E-37	1.03E-34
4-Mar	2.833736473	4.92E-18	2.38E-16
GOLT1A	2.818027998	1.26E-21	8.99E-20
MIR137HG	2.814876107	1.45E-32	2.44E-30
CALB1	2.809417134	4.76E-26	4.99E-24
ADM	2.801038008	2.25E-42	8.23E-40
CD274	2.76702629	2.44E-24	2.19E-22
UCA1	2.729457454	1.18E-11	2.69E-10
TMEFF2	2.706522495	0.00011321	0.00072482
APLN	2.675495467	1.66E-14	5.41E-13
ABI3	2.670343366	1.03E-16	4.37E-15
FGF5	2.664332447	1.39E-30	2.10E-28
F3	2.658192289	2.16E-67	5.09E-64
TMEM178B	2.643431486	2.42E-13	6.86E-12
GAL	2.624368385	1.20E-24	1.10E-22
KITLG	2.610832893	4.26E-17	1.85E-15
TSPAN2	2.598004099	1.25E-26	1.41E-24
GABRA5	2.595991903	1.20E-20	7.50E-19
PLEKHA7	2.581110604	1.42E-23	1.19E-21
RNF144B	2.560764295	2.02E-33	3.71E-31
MISP	2.550432418	4.81E-18	2.34E-16
DUSP8	2.546822774	8.92E-09	1.36E-07
TRIM58	2.51651337	3.13E-39	8.60E-37
PIK3AP1	2.499963187	1.67E-43	6.56E-41
CGN	2.49925825	1.28E-15	4.77E-14

OSCAR	2.480662883	2.20E-07	2.66E-06
SEMA3E	2.454563604	8.25E-08	1.07E-06
ZNF185	2.445142482	1.06E-37	2.64E-35
PCLO	2.445087483	2.44E-63	3.35E-60
PTPRR	2.431227647	7.36E-19	3.79E-17
AC073130.1	2.427627739	2.45E-14	7.87E-13
DMKN	2.426208326	7.16E-12	1.66E-10
DCLK1	2.419658314	7.97E-20	4.62E-18
TMEM45A	2.418440717	2.13E-35	4.67E-33
AOX1	2.417598845	4.49E-22	3.29E-20
HSPB8	2.409790926	8.56E-30	1.26E-27
TNFSF4	2.404877345	4.45E-07	5.04E-06
INPP5D	2.396608462	5.24E-51	3.32E-48
OR2W3	2.388281999	5.20E-33	9.21E-31
TIE1	2.377111098	2.12E-24	1.91E-22
RP11-244F12	2.376675383	3.29E-15	1.16E-13
IL2RG	2.373958336	3.71E-05	0.00027196
WWC1	2.352972947	1.44E-17	6.52E-16
RASGRF1	2.345864223	1.20E-12	3.09E-11
UPK3B	2.334883363	9.25E-07	9.83E-06
NRG1	2.330952538	2.93E-16	1.18E-14
OR51B5	2.322759467	1.14E-15	4.29E-14
THSD1	2.316896931	3.16E-19	1.70E-17
CPED1	2.304026957	1.60E-23	1.32E-21
NUAK2	2.279924628	2.43E-39	6.91E-37
AP1M2	2.269804017	2.57E-19	1.41E-17
RGS7	2.258057608	2.19E-28	2.82E-26
SH2D5	2.255799535	7.13E-27	8.21E-25
C12orf39	2.253373251	0.00015285	0.00093884
CITED2	2.245659758	1.32E-07	1.64E-06
PRR5L	2.245211213	5.42E-20	3.19E-18
PLEKHA6	2.229394198	7.73E-18	3.64E-16
ARHGDIB	2.185853975	9.43E-21	6.02E-19
NID2	2.175647013	3.25E-06	3.08E-05
RPL13AP20	2.164062725	7.20E-18	3.41E-16
PTPRB	2.161328111	7.76E-16	2.96E-14
PAQR5	2.160661775	1.95E-13	5.62E-12
PLCB4	2.145277672	2.24E-19	1.24E-17
FSTL1	2.144394917	2.71E-26	2.96E-24
MAGEC1	2.136390024	7.32E-07	7.90E-06
RP11-540A21	2.133951306	1.54E-08	2.26E-07
SPNS2	2.13356092	6.60E-19	3.41E-17
FAM49A	2.124423567	2.93E-05	0.00021987
WWTR1	2.110566515	2.11E-29	2.98E-27
FRAS1	2.094691768	3.92E-19	2.08E-17
CD33	2.093915785	7.32E-11	1.50E-09
PROSER2	2.090202393	6.88E-56	5.40E-53
S1PR1	2.087188029	9.52E-09	1.44E-07
LUM	2.086699231	6.37E-07	6.96E-06
RGS4	2.080933758	1.62E-05	0.00013007
IL7R	2.076081501	1.63E-35	3.67E-33
ROS1	2.073108207	2.81E-17	1.23E-15
MATN3	2.072939798	3.06E-13	8.51E-12
NEXN	2.064875841	2.09E-14	6.81E-13
SNAPC1	2.064087081	3.13E-22	2.32E-20
CDHR1	2.059371727	2.83E-06	2.72E-05

CA9	2.048984166	0.00181086	0.00794627
SPN	2.029303899	0.00155257	0.00697606
VGLL3	2.019542772	9.19E-20	5.28E-18
TBC1D2	2.018432162	5.93E-29	8.07E-27
HRK	2.012178073	2.07E-12	5.17E-11
SERPINB7	2.010717473	6.91E-16	2.67E-14
EPB41L3	2.007400383	5.49E-12	1.30E-10
CPA4	2.005531357	1.59E-06	1.60E-05
GADD45B	2.00459661	9.10E-43	3.41E-40
CCBE1	1.997904082	1.86E-11	4.14E-10
SLAMF7	1.997468447	6.25E-09	9.81E-08
EXPH5	1.987808461	4.94E-14	1.56E-12
CCDC80	1.976836703	1.79E-17	8.02E-16
CHST15	1.962169426	0.00040208	0.00217789
PLK2	1.953376518	9.47E-23	7.25E-21
SCG5	1.948593597	1.07E-14	3.58E-13
CYR61	1.941306958	4.04E-19	2.14E-17
NPAS1	1.936654165	5.99E-37	1.41E-34
IGFBP4	1.914205974	1.44E-28	1.88E-26
TRIML2	1.913039903	1.78E-05	0.00014129
ITGB2-AS1	1.907560271	8.73E-06	7.52E-05
POSTN	1.903894033	0.00046428	0.00246473
NUAK1	1.897488099	5.70E-55	4.09E-52
TGM1	1.893809747	4.82E-11	1.02E-09
SAMD5	1.888562941	1.73E-09	2.94E-08
CTGF	1.888195211	2.76E-29	3.82E-27
CCNA1	1.881778146	3.50E-13	9.67E-12
GDA	1.880739782	1.62E-17	7.29E-16
CYP11A1	1.859901467	5.63E-13	1.49E-11
TUFT1	1.859582741	7.33E-27	8.39E-25
CTD-2130O1	1.849230956	6.53E-06	5.85E-05
ADRB2	1.848621958	1.32E-14	4.38E-13
DGKI	1.847397121	1.94E-05	0.00015244
CD163L1	1.827463003	4.54E-06	4.19E-05
TGM2	1.823198291	7.68E-16	2.95E-14
PNMA2	1.821277136	4.37E-09	7.00E-08
SCN5A	1.817597351	1.00E-07	1.28E-06
MYO5B	1.814594642	3.87E-12	9.38E-11
MUC13	1.810793209	3.73E-07	4.29E-06
UCP2	1.79222863	1.38E-10	2.71E-09
RP1-102E24	1.790920576	4.62E-14	1.47E-12
GREB1	1.784308659	7.31E-12	1.69E-10
EPB41L4B	1.782743842	3.30E-11	7.13E-10
C20orf197	1.778773754	3.13E-06	2.99E-05
PKP2	1.778588667	1.59E-27	1.96E-25
KCNK6	1.771770668	7.05E-08	9.23E-07
UGCG	1.760340867	3.88E-13	1.06E-11
ZNF699	1.756763221	5.20E-21	3.38E-19
OR51B2	1.752791638	0.0005424	0.00282306
SAMD4A	1.749179785	3.51E-32	5.85E-30
GDPD5	1.748053637	1.85E-28	2.40E-26
KIF1A	1.742336909	9.19E-30	1.34E-27
SUGCT	1.741670956	7.78E-13	2.04E-11
RP11-245M2	1.738793881	3.56E-13	9.82E-12
NFASC	1.732962643	7.51E-09	1.16E-07
ADAMTS1	1.730764477	1.30E-15	4.85E-14

DUSP1	1.726441902	6.92E-06	6.14E-05
DDAH1	1.723432074	2.77E-44	1.17E-41
PDGFB	1.721348433	1.12E-13	3.34E-12
PRR16	1.720433416	1.89E-12	4.75E-11
KIRREL3	1.719021381	3.08E-15	1.09E-13
PLCXD2	1.716633424	3.42E-06	3.23E-05
PAGE1	1.712841083	6.06E-09	9.55E-08
SLFNL1	1.709268634	7.25E-09	1.13E-07
ARL14EPL	1.706567236	0.00011967	0.00075818
CD1D	1.704213579	8.70E-08	1.12E-06
KRT18P18	1.692444219	1.16E-12	2.98E-11
SSR3	1.683796413	4.43E-38	1.16E-35
USP2	1.680091701	2.34E-14	7.55E-13
NLRP3	1.679116263	5.52E-06	5.00E-05
FAP	1.670014347	0.0001469	0.00090607
RP11-386I14	1.667174317	1.10E-19	6.27E-18
ZNF582	1.657102296	2.12E-12	5.29E-11
RAB30	1.656101347	3.28E-29	4.50E-27
NABP1	1.653174786	1.13E-26	1.27E-24
DNAH11	1.652633343	4.04E-24	3.54E-22
TRBC2	1.652101833	0.00164904	0.00734972
LIMA1	1.648737006	2.34E-25	2.29E-23
HHAT	1.646834401	6.23E-20	3.63E-18
IGFN1	1.645789327	1.03E-05	8.74E-05
MAPK13	1.644902496	3.41E-09	5.54E-08
HES2	1.642704003	5.03E-11	1.06E-09
HES7	1.641055313	2.21E-23	1.81E-21
ANKRD33B	1.632036408	4.89E-12	1.17E-10
PDE2A	1.627083061	2.75E-06	2.65E-05
ZNF431	1.626337994	7.94E-14	2.43E-12
DOCK2	1.625287489	1.15E-07	1.45E-06
LRP3	1.620897912	4.59E-07	5.19E-06
ANKRD30A	1.619178777	4.62E-10	8.48E-09
MSX1	1.618425591	5.41E-31	8.41E-29
CYTH3	1.615668359	1.44E-46	7.42E-44
PLAC8	1.615437739	0.00024925	0.00143663
MCTP2	1.59844963	1.30E-06	1.34E-05
PRICKLE1	1.595737212	2.60E-05	0.00019826
CREB5	1.589709896	6.66E-09	1.04E-07
STC2	1.586924905	6.57E-10	1.18E-08
PRR5	1.586393658	1.22E-20	7.62E-19
KRT18	1.58608112	1.27E-28	1.69E-26
ADTRP	1.585117983	8.33E-05	0.00055807
RP11-38P22.	1.580751751	4.38E-12	1.05E-10
P2RY1	1.577587693	2.23E-10	4.26E-09
CLDN1	1.56623532	0.00083565	0.00410791
CES3	1.561761355	8.39E-10	1.49E-08
AC124789.1	1.561739159	3.29E-12	8.03E-11
CTIF	1.559551601	1.64E-66	3.37E-63
FAM196B	1.555881452	0.00123139	0.00573989
KRT18P33	1.554915853	1.58E-12	4.00E-11
OGFRL1	1.553700881	1.15E-22	8.80E-21
PLA2G4C	1.540836704	2.59E-05	0.0001978
RPS6KL1	1.537548516	7.77E-12	1.79E-10
FOXO6	1.526321163	3.17E-19	1.70E-17
C16orf74	1.520499126	3.74E-13	1.02E-11

TNS1	1.511671603	6.13E-05	0.0004238
RP11-54F2.1	1.511627074	5.55E-07	6.13E-06
MYCL	1.507185087	4.96E-07	5.56E-06
CTB-175P5.4	1.502865778	7.69E-16	2.95E-14
HMOX1	1.502769221	8.21E-09	1.26E-07
SCARA3	1.5004406	3.43E-08	4.76E-07
RHOBTB1	1.493862985	1.38E-08	2.05E-07
GPRC5B	1.492641289	6.65E-07	7.24E-06
CAV1	1.492576979	2.90E-14	9.31E-13
C19orf33	1.486428504	0.00029743	0.00167737
PDCD1LG2	1.48299546	1.18E-10	2.36E-09
PALLD	1.482098609	2.21E-16	9.05E-15
HBEGF	1.482030813	5.66E-27	6.66E-25
FGD6	1.481598702	4.97E-09	7.91E-08
CCDC85C	1.481178703	1.26E-26	1.41E-24
MBOAT2	1.479662594	8.00E-25	7.37E-23
KRT18P31	1.476175794	1.78E-15	6.50E-14
NOG	1.472319269	2.12E-06	2.08E-05
PRKCE	1.471467798	4.99E-25	4.67E-23
FAM101B	1.471292419	1.21E-21	8.69E-20
DENND2A	1.470453922	2.75E-12	6.76E-11
F2RL2	1.466410437	1.12E-05	9.41E-05
ALDOC	1.463428913	8.05E-13	2.11E-11
MAOA	1.462445623	1.85E-07	2.26E-06
SLCO1A2	1.454356009	7.55E-07	8.13E-06
DAPK1	1.449667329	5.42E-08	7.23E-07
RP5-1028K7.	1.446460041	0.00020595	0.00121774
AC104389.28	1.445940978	7.43E-06	6.55E-05
LINC00707	1.44427452	1.84E-11	4.11E-10
PDLIM1P1	1.439914977	4.81E-07	5.42E-06
NETO1	1.43955131	2.77E-11	6.03E-10
GJB3	1.435469968	1.34E-08	2.00E-07
AP001065.15	1.431668211	1.35E-08	2.00E-07
SUSD1	1.42882577	3.47E-06	3.27E-05
RAP1GAP2	1.427746561	5.43E-17	2.33E-15
BTG2	1.42698657	1.27E-13	3.78E-12
REEP1	1.424511284	3.62E-07	4.17E-06
ARC	1.423645248	1.16E-06	1.21E-05
IL32	1.422000678	0.00065591	0.00333072
PTX3	1.414984294	2.41E-06	2.35E-05
BDNF	1.414677637	2.29E-16	9.38E-15
LMO7	1.412302677	6.74E-28	8.54E-26
DKK1	1.408782113	7.37E-08	9.63E-07
EPS8L2	1.405203603	2.03E-06	2.00E-05
EFEMP1	1.404539281	2.36E-07	2.83E-06
PTPRF	1.402537389	1.45E-23	1.21E-21
FUT1	1.396992556	0.00010082	0.00065568
LSP1	1.396593757	5.01E-08	6.73E-07
RP4-555D20.	1.395697544	6.99E-05	0.00047672
RCN3	1.39431762	5.70E-20	3.34E-18
BCAM	1.394301645	2.70E-05	0.00020402
PPP1R1C	1.387856695	1.64E-09	2.80E-08
PODXL	1.384991391	5.74E-20	3.35E-18
TPM1	1.382958206	5.52E-07	6.11E-06
SRGN	1.380241984	7.01E-12	1.63E-10
COL17A1	1.379760686	0.00012387	0.00078074

JDP2	1.378805165	0.0008982	0.00437981
ETS1	1.37850426	4.28E-20	2.54E-18
FDXR	1.376987815	9.55E-19	4.87E-17
GADD45A	1.373309377	6.97E-36	1.60E-33
FAM83H	1.37050707	9.78E-06	8.32E-05
GRB14	1.370370699	0.0003235	0.00180703
RGMB-AS1	1.364005826	3.21E-10	6.04E-09
BNC1	1.36197599	1.32E-09	2.28E-08
HMGCS1	1.358220221	5.17E-08	6.92E-07
C10orf54	1.355642469	5.54E-07	6.13E-06
SLC35F3	1.355130904	3.21E-10	6.04E-09
DSC3	1.35282083	1.17E-17	5.37E-16
ADD2	1.342818688	3.23E-07	3.78E-06
RP11-879F14	1.336966903	8.95E-06	7.69E-05
ARHGAP23	1.334307659	4.00E-23	3.16E-21
GPR126	1.331107593	9.64E-38	2.44E-35
SYT17	1.330799798	1.38E-06	1.40E-05
MYLK	1.327252574	3.64E-11	7.83E-10
BCL11A	1.322171827	7.55E-08	9.84E-07
GALNT18	1.321683348	5.26E-06	4.78E-05
ADAMTSL4	1.320409623	0.00011199	0.00071841
CAV2	1.320025602	2.28E-17	1.01E-15
KLF2	1.319106944	7.58E-07	8.15E-06
ALPK2	1.317500216	0.00069968	0.00353446
IL24	1.307840384	0.00064276	0.00327201
SYNC	1.299810884	0.00015564	0.00095344
UAP1	1.296070861	3.78E-19	2.01E-17
SBF2-AS1	1.294578152	2.77E-05	0.00020907
MYPN	1.292482758	3.22E-05	0.00023966
FLRT2	1.292306987	4.01E-09	6.45E-08
CDC42EP1	1.290591933	2.51E-08	3.56E-07
KIAA1244	1.287403963	1.63E-15	5.99E-14
IL12A	1.280923146	1.34E-08	2.00E-07
C4orf36	1.277702167	3.36E-09	5.46E-08
AJUBA	1.275579727	4.96E-23	3.87E-21
CRIM1	1.271072793	3.32E-26	3.57E-24
PALD1	1.267712425	1.95E-07	2.37E-06
EEPD1	1.266796481	3.70E-06	3.47E-05
VGLL2	1.265678411	0.00040303	0.00218178
TSC22D2	1.254397974	3.07E-35	6.57E-33
NRXN3	1.254071908	1.92E-06	1.90E-05
LPAR1	1.253339525	0.00047438	0.00250704
PKP4P1	1.252670288	1.10E-09	1.94E-08
NMNAT2	1.244306499	2.75E-17	1.21E-15
NLRP2	1.242665223	0.00014484	0.00089462
PDLIM1	1.242638506	9.83E-07	1.03E-05
PPARGC1B	1.23939236	1.02E-07	1.30E-06
RBMS2	1.239247857	1.01E-16	4.30E-15
EXT1	1.23796178	2.34E-27	2.84E-25
TUBB6	1.236794595	2.96E-20	1.78E-18
GLCC1	1.234047427	5.30E-13	1.42E-11
LYPD6	1.232417086	2.34E-12	5.83E-11
JUN	1.23163188	1.53E-05	0.00012325
RP11-1002K1	1.230976004	1.29E-05	0.00010609
OSBP2	1.228918164	8.55E-07	9.13E-06
SYDE2	1.228587689	4.32E-13	1.17E-11

FADS3	1.224398385	1.08E-08	1.62E-07
ADAMTS12	1.223966062	8.94E-13	2.33E-11
SHROOM3	1.222006505	1.01E-14	3.40E-13
SEMA3F	1.219588894	4.82E-07	5.43E-06
SGK223	1.210304598	4.62E-07	5.22E-06
CISH	1.208169471	7.01E-09	1.09E-07
SCN8A	1.206207689	1.85E-12	4.66E-11
PAWR	1.205513102	5.08E-14	1.60E-12
PRKAG2	1.200697454	2.23E-13	6.39E-12
CHRN1	1.199987003	1.26E-10	2.49E-09
RBMS2P1	1.198233588	1.83E-09	3.08E-08
LACTB	1.187923528	1.31E-15	4.86E-14
XG	1.187786366	1.08E-05	9.10E-05
TXNRD2	1.187586673	1.28E-27	1.59E-25
ARHGEF28	1.186962225	1.77E-16	7.33E-15
BCL2L1	1.186524887	1.29E-26	1.43E-24
ZNF788	1.186269215	1.45E-15	5.37E-14
RP11-1100L3	1.186217147	1.18E-08	1.77E-07
PKP4	1.184417158	8.48E-24	7.20E-22
TENM2	1.183149902	0.00230423	0.00973271
WNT10B	1.182859607	2.98E-10	5.63E-09
GTF2H2	1.182225711	0.00041358	0.00223007
NEK3	1.18045109	0.00046071	0.00244894
RP11-215G15	1.179765863	2.57E-14	8.24E-13
LEPREL1	1.179029457	0.00036027	0.00197827
CHCHD10	1.177788877	5.02E-16	1.98E-14
FOSL2	1.177690161	2.68E-21	1.82E-19
WTIP	1.17629881	2.27E-13	6.46E-12
RP11-14N7.2	1.17518189	1.49E-09	2.56E-08
SAMD12	1.173569856	1.56E-13	4.54E-12
AFF1	1.171763454	8.19E-35	1.71E-32
TRPM2	1.170361965	1.15E-07	1.44E-06
CMIP	1.168872852	2.80E-35	6.07E-33
RP11-289I10	1.16561675	8.12E-09	1.25E-07
PRELP	1.161207995	0.00022077	0.0012942
TUBB4A	1.153876776	0.00010353	0.00067145
P2RX5	1.152601541	1.63E-08	2.38E-07
PAQR3	1.149225901	4.38E-31	6.94E-29
HSPA4L	1.148487993	1.71E-06	1.71E-05
LINC01021	1.148227259	2.79E-05	0.00021037
GPR160	1.143301938	0.00014976	0.00092156
MTL5	1.1413036	0.00012763	0.00080187
ERVMER34-1	1.137094196	0.00036581	0.00200666
COL4A6	1.134377518	6.06E-05	0.00041994
ZNF582-AS1	1.132033194	2.12E-05	0.00016529
CSMD3	1.130206065	8.02E-07	8.60E-06
RFTN1	1.129459922	7.53E-15	2.56E-13
KAZN	1.128964394	5.83E-13	1.54E-11
LINC00664	1.12646277	4.35E-09	6.98E-08
CTC-241F20.3	1.12046409	1.77E-09	3.00E-08
FAM212B	1.116033786	3.93E-08	5.38E-07
CARD11	1.115476125	2.63E-05	0.00020006
MPP4	1.112202876	3.38E-07	3.93E-06
RP11-673E1.1	1.110938053	2.61E-07	3.09E-06
CORO1C	1.108862346	5.88E-18	2.81E-16
RP11-30P6.6	1.102623769	1.18E-06	1.23E-05

NTN4	1.102310463	5.74E-17	2.46E-15
CDKN1A	1.100986288	1.33E-14	4.40E-13
CDC20P1	1.100729108	4.35E-07	4.95E-06
LINC00883	1.09890777	7.09E-15	2.43E-13
TRIM22	1.096664225	1.21E-05	0.00010019
ACER2	1.091941816	0.00089351	0.00436094
LATS2	1.089753651	6.36E-19	3.30E-17
ARHGAP30	1.089399999	0.00022946	0.00133896
FEM1C	1.086807304	1.43E-17	6.50E-16
COL12A1	1.086164783	1.34E-09	2.32E-08
NNMT	1.084877439	0.00156039	0.0070039
IRS1	1.084303667	5.96E-09	9.40E-08
TERT	1.08388457	4.86E-11	1.03E-09
SAV1	1.078271403	5.15E-14	1.62E-12
SHANK1	1.077981835	0.00010562	0.00068361
DSP	1.07778998	1.18E-07	1.48E-06
RP11-554I8.2	1.074447044	1.82E-07	2.22E-06
TNFAIP2	1.074344121	0.0001922	0.00114839
SLC16A10	1.070345736	1.05E-09	1.84E-08
NDRG1	1.064632599	1.33E-09	2.30E-08
CLU	1.064131858	1.06E-05	8.94E-05
RP11-255H23	1.063622555	2.12E-06	2.08E-05
GFOD1	1.063463997	3.03E-07	3.55E-06
PINK1	1.059899292	4.90E-14	1.55E-12
MAP3K1	1.059498739	1.12E-17	5.15E-16
AC027612.6	1.056778933	5.00E-05	0.00035512
DDX60L	1.05636942	2.32E-15	8.39E-14
DSE	1.056202948	5.83E-09	9.20E-08
ARVCF	1.054588287	1.01E-08	1.53E-07
ABLIM1	1.049433029	1.42E-05	0.00011527
FJX1	1.04531594	5.47E-14	1.72E-12
EVA1A	1.045111404	1.08E-10	2.17E-09
DUSP9	1.04281516	1.63E-12	4.11E-11
ARHGEF26	1.040377588	8.67E-12	1.99E-10
YOD1	1.039373082	3.30E-13	9.15E-12
CYFIP2	1.039281482	2.95E-09	4.84E-08
ALCAM	1.038707461	9.45E-14	2.87E-12
LLGL2	1.034190386	2.83E-09	4.66E-08
RAB15	1.03136351	1.53E-12	3.90E-11
GPR85	1.028667468	9.91E-07	1.04E-05
CDR2L	1.028162118	5.60E-13	1.49E-11
TRIM59	1.026669833	1.16E-06	1.21E-05
EGFR	1.023683332	3.31E-12	8.08E-11
ARID3A	1.021526416	5.92E-05	0.00041188
NEK6	1.019467364	1.38E-21	9.68E-20
TEC	1.017700545	1.74E-06	1.74E-05
RASSF2	1.01635402	2.22E-05	0.00017235
CDC20	1.014335309	7.87E-07	8.45E-06
HS3ST3B1	1.014141218	5.81E-07	6.40E-06
KLHL29	1.011151082	3.66E-11	7.86E-10
TMOD3	1.010757117	1.59E-20	9.80E-19
RP11-655M1	1.010730109	0.00235187	0.00988577
CYCSP55	1.006980292	1.80E-09	3.03E-08
ELL2P1	1.006054955	1.36E-05	0.00011078
LINC00152	1.00542148	1.28E-08	1.91E-07
EFNB1	1.003580264	1.53E-08	2.25E-07

SIK1	0.998862685	4.96E-14	1.57E-12
SEMA3G	0.993532383	1.95E-05	0.00015287
PVR	0.991934375	9.85E-16	3.73E-14
ZNF804A	0.991809449	3.69E-13	1.01E-11
GPX3	0.991367042	0.00128128	0.00593212
AMOTL2	0.989668841	2.48E-17	1.10E-15
RAB11FIP1	0.989616533	1.28E-21	9.11E-20
IGFBP3	0.986988504	0.00087276	0.00426997
GNAI1	0.98502946	4.77E-21	3.16E-19
MAP1B	0.983758295	3.20E-11	6.93E-10
MED12L	0.982904073	9.92E-06	8.43E-05
ERBB2IP	0.982584578	1.16E-21	8.35E-20
ADAMTSL1	0.981751275	0.00010657	0.00068872
FAM72C	0.978806201	0.00092254	0.00448288
TBC1D30	0.978068055	2.46E-06	2.39E-05
MAST1	0.976529988	1.31E-05	0.00010795
MB21D2	0.975531296	1.23E-08	1.84E-07
PLD6	0.97483191	6.44E-08	8.50E-07
MICAL2	0.974305999	5.17E-07	5.76E-06
GREB1L	0.971111048	2.01E-06	1.98E-05
TMEM154	0.970324845	8.59E-08	1.10E-06
SLC25A19	0.969292579	9.53E-08	1.22E-06
DUSP3	0.969265053	6.76E-26	7.00E-24
ANKRD13A	0.967083831	1.89E-19	1.05E-17
LZTS3	0.966626464	2.46E-11	5.41E-10
MYL12A	0.966570447	5.54E-08	7.38E-07
ARG2	0.961813279	3.58E-08	4.96E-07
FAM198B	0.959209433	4.74E-07	5.35E-06
BBC3	0.957457135	5.56E-07	6.14E-06
HIF1A	0.956566547	3.18E-19	1.70E-17
C3orf52	0.955216966	4.48E-08	6.08E-07
RP11-490M8	0.953925224	8.98E-06	7.70E-05
FABP5	0.953507873	0.00039516	0.00214552
PVRL2	0.952410121	1.90E-21	1.31E-19
GCLM	0.948005784	3.97E-07	4.55E-06
DNAJB6	0.947915792	9.04E-14	2.75E-12
ZNF442	0.947776885	0.00059627	0.00305896
RRAS2	0.947628945	3.54E-07	4.09E-06
RAB3IL1	0.946877855	9.48E-05	0.0006224
ST3GAL1	0.946562675	8.15E-20	4.71E-18
MSMO1	0.945611485	4.92E-05	0.00034993
FAM167A	0.943029106	3.42E-07	3.97E-06
ZNF296	0.942080979	0.00030014	0.00169033
MIR4435-1H	0.940405141	5.71E-11	1.19E-09
RP11-611D20	0.938483474	1.79E-06	1.78E-05
DUSP5	0.938465334	3.37E-05	0.0002496
BARX1	0.937728649	1.96E-05	0.00015408
MLK4	0.937504039	9.03E-11	1.82E-09
RBM38	0.935360989	6.45E-11	1.34E-09
FOXF2	0.9333714	9.05E-11	1.82E-09
CHMP4C	0.932290075	1.90E-05	0.0001493
RP11-744K17	0.930621857	0.00087997	0.0043015
RP11-671C19	0.930363476	8.03E-16	3.06E-14
FEZ2	0.929729815	6.46E-15	2.22E-13
ABL2	0.929590143	4.66E-09	7.44E-08
RASL11A	0.928905563	5.25E-06	4.78E-05

BOK	0.925808409	3.18E-16	1.28E-14
CPNE7	0.921902041	9.09E-05	0.00060102
FMNL1	0.919732431	9.45E-07	1.00E-05
GCNT1	0.918754282	5.70E-05	0.00039769
HK2P1	0.918733182	3.17E-06	3.02E-05
WWC2	0.917568971	1.47E-16	6.11E-15
LIN28B	0.915416253	7.95E-07	8.53E-06
MITF	0.915254018	5.97E-10	1.08E-08
KRT80	0.912924776	8.81E-05	0.00058676
GPR176	0.912211048	5.13E-13	1.38E-11
KCNH1	0.910399511	0.00011635	0.00074087
DIAPH3	0.910363903	1.82E-12	4.59E-11
AC005336.5	0.909199569	0.00014243	0.00088038
ADAMTS7	0.908500685	5.81E-07	6.40E-06
ZNF704	0.908455987	2.26E-06	2.22E-05
PGM2	0.906581679	5.37E-17	2.32E-15
TEAD4	0.90564336	2.48E-09	4.10E-08
BAX	0.905514786	1.85E-07	2.26E-06
BNIP3P1	0.90384355	7.33E-09	1.14E-07
FRMD6	0.903068763	1.01E-07	1.29E-06
GLIPR1	0.901586789	3.11E-05	0.00023238
PRKX	0.900894374	4.06E-13	1.11E-11
GLIPR2	0.900335865	0.00019523	0.00116394
RIN2	0.899915429	1.61E-14	5.27E-13
GATA2	0.898944886	1.20E-07	1.50E-06
WNT3	0.89813419	6.31E-10	1.14E-08
RP11-253E3.	0.897609347	2.59E-13	7.27E-12
CNN3	0.896337279	1.44E-11	3.26E-10
CYP2S1	0.896200332	0.00131281	0.00605428
PDIA5	0.893732519	7.10E-07	7.69E-06
SLC7A5	0.891716142	1.45E-08	2.14E-07
FSTL3	0.891603455	4.46E-14	1.42E-12
C2CD3	0.891182784	1.63E-14	5.33E-13
RP11-216L13	0.890575161	6.42E-05	0.00044162
RHBDF2	0.886501931	1.55E-09	2.65E-08
RASSF5	0.884763546	2.49E-08	3.53E-07
ETS2	0.884246163	1.97E-10	3.76E-09
RAB20	0.883227117	3.36E-05	0.00024855
SRXN1	0.882013156	0.00021695	0.001275
CD3EAP	0.881061576	0.00045485	0.00242094
CHKA	0.879692192	7.47E-15	2.55E-13
RP3-510D11.	0.878858799	1.38E-05	0.00011284
BOP1	0.874542241	5.47E-05	0.00038342
NRD1	0.874404099	1.80E-18	9.08E-17
ASRGL1	0.874073038	6.73E-08	8.84E-07
VOPP1	0.873469903	7.19E-12	1.67E-10
FLNB	0.87302305	3.48E-13	9.61E-12
ZNF714	0.871907211	1.96E-10	3.75E-09
TM4SF19	0.871883491	1.44E-06	1.46E-05
PROCR	0.870500248	2.49E-19	1.37E-17
MROH1	0.868491664	1.05E-07	1.34E-06
METRNL	0.86546938	2.66E-12	6.58E-11
NAV2	0.864048393	0.0007048	0.00355487
DHCR7	0.863171617	4.83E-07	5.43E-06
PCID2	0.862320994	8.70E-14	2.65E-12
ZNF488	0.862241141	0.00018272	0.00110013

RAB32	0.862173925	2.25E-13	6.43E-12
FIGN	0.861077265	5.09E-08	6.83E-07
PDGFA	0.860411858	1.53E-05	0.00012317
ERCC2	0.859949968	3.54E-14	1.13E-12
GLUL	0.855417996	5.52E-07	6.12E-06
TFRC	0.854624132	7.66E-09	1.18E-07
KLF5	0.853552418	1.28E-15	4.77E-14
NLRP1	0.85280058	7.08E-10	1.27E-08
SEC14L1	0.851866361	1.24E-19	7.04E-18
SLC9A3R1	0.845693205	3.35E-08	4.66E-07
BNIP3	0.845671634	6.55E-11	1.35E-09
STARD8	0.843893184	0.0023428	0.00986528
RP11-548L20	0.843616346	0.00158873	0.00711558
SPHK1	0.842776897	0.00037022	0.0020268
EZR	0.841870525	7.03E-14	2.16E-12
IL6R	0.841055593	0.00022788	0.0013307
USP18	0.840366464	1.77E-05	0.00014023
TMEM160	0.838865539	1.79E-09	3.03E-08
CCDC86	0.837602283	1.89E-08	2.72E-07
CHORDC1	0.837340267	0.00199717	0.00865091
SOGA2	0.83724795	3.09E-12	7.57E-11
DSEL	0.837109835	4.82E-07	5.42E-06
MRS2	0.836530096	3.74E-15	1.32E-13
TNFSF9	0.836361588	0.00047535	0.00251138
HERC5	0.835229278	0.00013585	0.00084605
RPS27L	0.834244251	1.55E-07	1.91E-06
RUSC2	0.833897379	5.35E-12	1.27E-10
MEX3B	0.830330159	5.04E-07	5.63E-06
RP11-412P11	0.830306144	0.00027538	0.00156585
RGS2	0.829296976	1.52E-05	0.00012284
PINX1	0.827935643	0.00036907	0.00202321
C12orf75	0.827835087	7.01E-15	2.41E-13
NRIP3	0.827527263	1.19E-05	9.91E-05
DLC1	0.825059352	1.20E-07	1.50E-06
BTBD10	0.823711833	1.39E-12	3.53E-11
KIAA1522	0.822902746	9.72E-06	8.28E-05
ATAD3B	0.822595631	1.72E-07	2.11E-06
DENND3	0.822440617	1.73E-08	2.50E-07
MARS2	0.820895534	1.34E-05	0.00010959
TRIO	0.820652194	1.15E-07	1.44E-06
RDM1	0.820626754	0.00110011	0.00521652
PM20D2	0.81956566	6.68E-16	2.59E-14
CHML	0.819344435	1.14E-07	1.44E-06
EBNA1BP2	0.819188872	2.50E-09	4.12E-08
IER5	0.817966905	5.65E-13	1.50E-11
FLII	0.817172393	6.12E-13	1.61E-11
CDC42EP2	0.816606831	2.50E-07	2.98E-06
RPS27P27	0.815169367	2.41E-05	0.00018582
TXNRD1	0.813391981	1.28E-13	3.78E-12
MAGEA1	0.812345223	0.00103198	0.00493606
PDGFRB	0.810489517	0.00121167	0.00566879
MPP5	0.810446876	2.95E-09	4.84E-08
LRRC20	0.809949087	6.14E-07	6.73E-06
FHL1	0.809551349	0.00164959	0.00735019
EMR2	0.809063621	0.00033302	0.00185331
ZNF331	0.809061484	1.22E-10	2.42E-09

LCAT	0.806862812	0.00042346	0.00227548
SMURF2	0.804572473	1.04E-05	8.76E-05
NT5C2	0.804213264	2.60E-12	6.45E-11
GCAT	0.803962859	2.52E-08	3.56E-07
CYP2J2	0.802881483	0.00022313	0.00130572
CHIC2	0.802103107	2.61E-10	4.94E-09
ALDH1B1	0.801928412	5.19E-12	1.23E-10
CALD1	0.801168238	9.38E-11	1.88E-09
TMSB4XP8	0.800994228	0.00023744	0.00138061
NR2F2	0.800231884	7.47E-09	1.16E-07
YDJC	0.800143284	5.03E-17	2.17E-15
RP11-676M6	0.798297073	8.55E-12	1.97E-10
PHLDA3	0.796928383	2.24E-09	3.74E-08
SERINC2	0.796120235	0.00014234	0.00088017
SIPA1L3	0.794814367	9.92E-14	2.99E-12
KCNQ5	0.794262273	9.72E-06	8.28E-05
PDLIM2	0.793629894	8.29E-11	1.68E-09
TP53INP1	0.792088813	1.14E-08	1.71E-07
MPP3	0.791451655	0.00011014	0.00070846
PNP	0.788499925	1.04E-08	1.56E-07
SLC22A15	0.787752801	0.00122495	0.00571472
CTPS1	0.786930036	4.74E-06	4.36E-05
CLUH	0.784635948	3.19E-08	4.46E-07
UNC13A	0.783229927	0.00023448	0.00136536
KBTBD8	0.780464159	0.002358	0.00990649
NBEAL2	0.779448926	5.42E-06	4.91E-05
EEF1A2	0.778712033	0.00010064	0.00065495
PPIF	0.777213475	1.23E-14	4.07E-13
BCL9L	0.776315772	1.09E-11	2.48E-10
NLN	0.77364106	2.07E-06	2.05E-05
EGFLAM	0.773347117	0.00140134	0.00639985
DRAM1	0.772906331	9.43E-09	1.43E-07
EDA2R	0.772491407	2.15E-05	0.00016725
ACTA2	0.771262292	0.00223028	0.00946649
UCHL3	0.77000616	0.00018857	0.0011312
ELL2	0.76920739	2.31E-06	2.26E-05
DUSP2	0.76874712	8.48E-07	9.08E-06
IL15RA	0.76641865	0.00039876	0.00216218
PHLPP1	0.765701434	3.73E-08	5.14E-07
STX3	0.764568368	1.92E-10	3.68E-09
BMP2K	0.761840385	1.52E-05	0.00012256
ZP3	0.761838518	0.00076045	0.00380064
RP11-660L16	0.761833856	0.00049756	0.0026096
RP11-309G3.	0.759221551	0.00227735	0.00963646
NFIA	0.758962562	1.35E-06	1.38E-05
BAG2	0.75673572	6.65E-07	7.24E-06
PEA15	0.75573536	1.46E-10	2.85E-09
SLC17A9	0.754775799	1.35E-14	4.45E-13
ZFPM2	0.754509662	4.88E-08	6.57E-07
ARID3B	0.751797196	0.00059009	0.00303766
PLK3	0.750663443	5.23E-08	7.00E-07
RINL	0.74738935	5.08E-05	0.00035962
IMPDH1	0.74665687	4.48E-06	4.13E-05
KIAA1211	0.746230054	7.04E-06	6.24E-05
DLG1	0.746033568	6.51E-14	2.02E-12
LPAR3	0.745922656	6.82E-11	1.41E-09

AC073150.6	0.745558682	0.00182947	0.00801938
OPN3	0.744954799	0.00090798	0.00441735
RP1-152L7.5	0.743912218	5.04E-07	5.63E-06
CTU1	0.743879866	3.39E-06	3.20E-05
CTDSPL	0.743877502	1.28E-09	2.23E-08
IRAK1	0.742654706	1.47E-09	2.53E-08
LRRC8E	0.741728246	0.00135709	0.00622365
ACSL1	0.741552547	1.40E-13	4.11E-12
CRY1	0.740344054	5.09E-11	1.07E-09
RP11-713C19	0.74005105	1.98E-13	5.70E-12
RELL2	0.73981677	0.00067838	0.00343636
SLC8B1	0.739399608	8.74E-09	1.34E-07
TMEM144	0.737564081	2.32E-05	0.00017994
PDGFC	0.734523783	8.49E-10	1.51E-08
ANKRD34A	0.733736819	3.03E-09	4.95E-08
EFCAB4B	0.731600788	1.46E-08	2.16E-07
RP11-564D11	0.731485788	0.00013338	0.00083255
ARHGAP29	0.731305837	4.82E-06	4.42E-05
CLTB	0.730844209	1.28E-09	2.22E-08
RPL26L1	0.730185815	4.86E-08	6.54E-07
SQLE	0.730088839	8.50E-06	7.36E-05
TAF1A	0.729856798	6.87E-06	6.11E-05
SLC29A2	0.728451519	2.70E-05	0.00020402
SCARF2	0.727273939	2.15E-07	2.59E-06
C17orf51	0.727203342	8.24E-06	7.17E-05
GET4	0.72706079	9.08E-05	0.00060054
RP11-686D22	0.726648948	0.00042141	0.00226713
POLRMTP1	0.725640998	6.38E-06	5.73E-05
ITPK1	0.724288737	8.85E-09	1.35E-07
FAM162A	0.723990941	9.46E-09	1.44E-07
CDV3	0.723592534	4.38E-11	9.32E-10
PPP1R13L	0.72341833	0.00025356	0.00145791
TBC1D23	0.722377409	5.62E-14	1.76E-12
TRIP6	0.721881351	2.80E-15	1.00E-13
GRK6P1	0.72124831	0.00019523	0.00116394
FZD4	0.720028554	9.04E-05	0.00059871
GPR63	0.718627875	0.00098954	0.00475938
CCDC69	0.718556852	9.76E-05	0.00063811
NCEH1	0.716535072	3.36E-09	5.47E-08
RASSF7	0.71630029	1.65E-06	1.65E-05
SMPD3	0.716120385	0.00087999	0.0043015
BATF2	0.715844255	0.00098055	0.00472711
NTMT1	0.715348724	9.21E-09	1.40E-07
RP11-350E12	0.713611434	9.07E-05	0.00060013
HK2	0.712710317	2.43E-06	2.37E-05
PDCD2L	0.709205652	2.46E-07	2.94E-06
COMTD1	0.707324884	0.00109295	0.00518854
JADE3	0.706509888	9.99E-06	8.48E-05
CDC25A	0.705805498	3.32E-05	0.00024618
DAB2	0.704951231	7.56E-06	6.64E-05
MESDC1	0.70480392	1.42E-07	1.76E-06
PKN1	0.70299016	2.50E-13	7.07E-12
ADA	0.701940674	2.25E-06	2.21E-05
RPL23AP82	0.700850262	0.00154899	0.00696219
SRGAP1	0.700501667	0.001026	0.00491319
GNB1L	0.700210694	7.49E-05	0.00050778

FTH1	0.699629221	0.00135453	0.00621885
ARHGEF17	0.699096763	6.44E-06	5.78E-05
CHST2	0.69894792	0.00192706	0.00839135
SPIRE1	0.69867398	9.25E-09	1.41E-07
EPG5	0.69860118	1.09E-05	9.19E-05
ATP5G1P4	0.698433963	0.00114786	0.00540557
DAPK3	0.698150477	8.09E-12	1.86E-10
SPAG1	0.697240264	1.44E-06	1.46E-05
CCDC84	0.696728508	3.76E-06	3.52E-05
QSOX1	0.696601246	6.16E-14	1.92E-12
PDXK	0.695629077	6.26E-10	1.13E-08
PRPS1	0.694596825	1.58E-10	3.06E-09
FAM117A	0.694524507	8.86E-05	0.0005887
C20orf27	0.692812522	2.74E-11	5.96E-10
NMT2	0.692705532	0.00205941	0.00887847
RPL26P30	0.692323319	8.36E-05	0.00055988
SDC1	0.692042719	2.55E-06	2.47E-05
SESN1	0.69026306	0.00021566	0.0012683
GBGT1	0.687451305	3.41E-07	3.96E-06
CTA-29F11.1	0.686545304	2.65E-05	0.00020094
ZNF25	0.685163441	0.00035802	0.00196718
SKP2	0.683305688	1.68E-08	2.44E-07
HPRT1	0.682798827	9.52E-14	2.88E-12
TSPAN33	0.682476147	0.00108641	0.00516194
TNPO1P1	0.682265018	0.00026313	0.00150402
C20orf24	0.679951318	4.41E-05	0.0003177
CTD-256I122	0.679523609	0.00010477	0.00067842
FMN2	0.67908109	2.58E-12	6.40E-11
FLI1	0.678995605	0.0012169	0.005689
UBE2J1	0.67861447	6.91E-10	1.24E-08
TXNP4	0.677712884	0.00209926	0.00901617
KIF1C	0.6773231	2.03E-08	2.90E-07
NUDCD1	0.677319966	5.81E-09	9.19E-08
ANXA2	0.677233005	8.06E-05	0.00054264
NANP	0.676692508	3.82E-11	8.16E-10
MAPK12	0.676181413	1.31E-05	0.00010731
FHL3	0.67532712	4.87E-05	0.00034695
CASP4	0.674947078	0.00017202	0.00104338
TOMM40	0.673833952	3.63E-08	5.02E-07
SLC27A5	0.671053357	2.65E-07	3.14E-06
C12orf5	0.670421494	9.58E-06	8.17E-05
TSEN15P1	0.66809401	0.0017295	0.00764015
MIEF2	0.667758629	1.41E-05	0.00011476
ZNF330	0.667103295	3.90E-12	9.45E-11
NANS	0.667091342	4.29E-12	1.03E-10
MTSS1L	0.667049321	3.04E-11	6.61E-10
PHLDB2	0.66651354	3.07E-07	3.60E-06
RRAGD	0.665813484	3.25E-06	3.08E-05
RP11-177C12	0.665798856	0.00119596	0.00560166
PDE1C	0.664864713	4.10E-06	3.81E-05
RP11-395L14	0.664344633	0.0003981	0.00215932
EPHA2	0.664028094	2.42E-05	0.0001863
HSPD1P5	0.663568385	0.00100459	0.00482043
PAICSP3	0.663532868	0.00232243	0.00979953
AC009299.5	0.663320652	3.90E-05	0.00028416
PGK1P2	0.663252127	1.28E-06	1.32E-05

SLC43A2	0.662540598	0.00109972	0.00521613
PLCD3	0.661487237	7.84E-06	6.86E-05
MVD	0.659413211	3.16E-05	0.00023564
SH3BP4	0.659158176	4.45E-08	6.04E-07
FCRLB	0.658281309	0.00040889	0.00220912
TRAP1	0.656737829	7.22E-10	1.29E-08
CCDC124	0.655615002	3.06E-07	3.59E-06
RP11-528A10	0.6543951	0.00229019	0.00968334
RP11-438N16	0.654129545	3.37E-10	6.32E-09
HDAC7	0.653346136	7.63E-09	1.18E-07
INO80C	0.653345637	2.34E-05	0.00018104
RP11-423H2.	0.652769364	0.0001058	0.00068457
HOMER2	0.652514169	4.35E-05	0.00031424
ANKZF1	0.652435307	3.57E-10	6.68E-09
PNO1	0.652211272	1.11E-05	9.32E-05
LETM2	0.651419284	0.00034228	0.00189638
GXYLT1	0.651338445	4.29E-07	4.89E-06
AC104297.1	0.651334871	1.88E-05	0.00014801
RNASET2	0.651160955	8.77E-05	0.00058495
STRIP2	0.650810826	3.06E-05	0.00022851
SGMS2	0.650793125	9.67E-05	0.00063313
VRK2	0.648515877	9.95E-07	1.05E-05
SAPCD2	0.648200166	0.00027227	0.00155144
WT1	0.647456007	4.13E-05	0.00029925
RP11-162O12	0.646493869	8.25E-06	7.17E-05
WDR77	0.646171641	0.00018996	0.00113834
UBE2SP1	0.645279644	5.59E-10	1.02E-08
FAR1P1	0.644562997	0.00170712	0.00756244
RP11-516A11	0.644423869	1.20E-05	9.97E-05
RP11-807E13	0.644081612	0.0006572	0.00333624
SMCO4	0.642367454	0.0014598	0.00661912
MYL12B	0.64149065	9.84E-11	1.97E-09
RP11-2C24.5	0.641091483	0.00161034	0.00720259
RP11-641A6.	0.641080889	0.00154718	0.00695687
UBE2S	0.640828398	1.20E-09	2.09E-08
RHOF	0.639965719	0.00058436	0.00301268
TAX1BP3	0.639216555	5.44E-06	4.93E-05
ACO1	0.639010188	1.41E-06	1.43E-05
ARRB1	0.638877016	0.00206867	0.00891139
ZFP42	0.638421923	9.89E-05	0.00064491
ASCC3	0.638019532	0.00042204	0.00226977
SLC7A6	0.637860078	2.23E-07	2.69E-06
FAM207A	0.637401844	0.000166	0.00101053
ATP5G1P5	0.637047608	0.00041229	0.00222385
GABARAPL1	0.636299154	4.73E-10	8.66E-09
TTC27	0.636285535	4.17E-05	0.00030164
LRFN4	0.635372808	5.54E-11	1.16E-09
RASAL2	0.635250106	0.00217886	0.0092865
MCC	0.635232336	5.02E-05	0.00035614
RP11-467J12	0.634876945	0.00178963	0.00787408
PROSER1	0.634623727	8.83E-10	1.57E-08
RP11-142L4.2	0.634125605	0.00081585	0.00403277
PUS1	0.63323612	1.22E-05	0.00010087
DOCK9	0.633218066	0.00033858	0.00188043
SLFN12	0.63320755	8.04E-06	7.02E-05
SPTLC2	0.633046122	4.22E-09	6.78E-08

C3orf58	0.632673491	8.42E-08	1.09E-06
RRP1B	0.631875655	6.37E-06	5.72E-05
LINC01029	0.631790646	3.14E-05	0.00023418
DSG2	0.630290146	1.56E-10	3.04E-09
AC093673.5	0.629684064	0.00075201	0.00376532
PWWP2B	0.629181564	2.64E-05	0.00020061
CCDC58	0.628705158	0.00030524	0.00171439
TRIM7	0.628697652	0.00029327	0.00165669
STRBP	0.628145714	7.41E-06	6.53E-05
ZNF598	0.627202466	2.61E-10	4.94E-09
FTLP3	0.627074807	1.62E-06	1.63E-05
RP11-365D23	0.626401661	0.00227435	0.00962624
TTC7A	0.626320464	4.02E-07	4.61E-06
FTL	0.625476733	1.58E-06	1.59E-05
POLRMT	0.623130079	3.01E-06	2.87E-05
ATAD3A	0.621823824	2.65E-08	3.74E-07
TRAM2	0.621084267	2.49E-11	5.47E-10
TNPO1	0.620825735	1.76E-10	3.39E-09
PFAS	0.620599059	7.64E-05	0.00051704
RP11-265N6	0.620444383	4.96E-07	5.56E-06
ANXA2P2	0.619697371	0.00032527	0.0018163
TMSB4X	0.619510015	0.00091128	0.00443208
AP000439.1	0.619400661	0.00024871	0.00143405
RAB11FIP5	0.617311625	7.87E-11	1.60E-09
FLNA	0.616591062	1.80E-10	3.46E-09
CECR2	0.615726013	0.00233252	0.00983469
DUSP16	0.615250769	1.42E-05	0.00011525
HAUS2	0.615219851	1.44E-08	2.13E-07
PNPT1	0.614885471	0.00019904	0.00118199
SLC7A6OS	0.613806697	0.00013073	0.00081841
PARD3B	0.613656988	0.0006712	0.003401
RP1-273G13	0.613426773	9.72E-05	0.00063618
LINC00665	0.613189432	2.29E-07	2.75E-06
PLOD2	0.612922368	1.77E-08	2.57E-07
DUSP7	0.612536832	1.31E-06	1.34E-05
STAP2	0.612188138	0.00034054	0.0018894
FTLP2	0.611969751	5.12E-06	4.68E-05
PPM1H	0.609595305	0.00048189	0.00254185
FASN	0.609406491	1.06E-06	1.10E-05
RHPN2	0.609097435	1.59E-08	2.32E-07
GRK6	0.606668325	1.57E-09	2.68E-08
GPRC5A	0.606645515	0.0019997	0.00865731
HOXA1	0.606629834	0.00220148	0.00937324
JPH1	0.605652288	7.78E-06	6.81E-05
CMSS1	0.605626133	5.13E-09	8.15E-08
LRRC8B	0.605330233	0.00032003	0.00179133
PNPT1P1	0.604901775	0.00097079	0.00468556
ZNF430	0.604012842	9.43E-05	0.00061972
KIAA1671	0.603971628	0.00066875	0.00338962
CMBL	0.60334197	9.87E-10	1.74E-08
SLC8A1	0.603283656	0.00133454	0.0061476
DYRK2	0.603136464	4.43E-09	7.08E-08
HPDL	0.602375943	8.54E-06	7.38E-05
RP11-601I15	0.602148627	0.00027722	0.00157578
ANKRD27	0.601285891	2.22E-06	2.18E-05
GCH1	0.601199025	0.00019761	0.00117602

PGAM1	0.60098549	0.00017009	0.00103238
HOXD13	0.600916805	0.00012612	0.00079357
MRPS5	0.60085806	2.21E-08	3.15E-07
SLC7A2	0.600619086	1.09E-06	1.14E-05
RP11-134G8.	0.600207212	0.00231434	0.00976789
PRDX6	0.600032814	8.63E-11	1.75E-09
PIP5K1P1	0.599408823	0.00048594	0.00256158
TRIM14	0.599174393	9.85E-08	1.26E-06
NEDD4L	0.599065921	3.19E-06	3.03E-05
ASL	0.598752604	0.00046722	0.00247475
MID1	0.597597244	1.69E-05	0.00013468
FAM160B1	0.59756021	4.31E-06	3.99E-05
TJP1	0.597537385	9.95E-08	1.27E-06
KLHL18	0.597404133	6.11E-05	0.00042315
CSRN1P1	0.597351678	0.0022148	0.00941775
MCTP1	0.596431162	2.54E-05	0.00019409
RG510	0.596216176	0.00026971	0.00153895
EHD4	0.594286593	1.79E-06	1.78E-05
RP11-567G24	0.594119006	0.00136232	0.00624591
ZNF880	0.593592146	0.00018657	0.00112092
FZD5	0.593488305	0.00013081	0.00081841
TRABD	0.592840893	5.41E-09	8.58E-08
LYN	0.592736901	4.31E-08	5.87E-07
RHOB	0.591958299	1.06E-05	8.98E-05
HEG1	0.591890824	4.95E-08	6.66E-07
NAMPTL	0.590753695	9.95E-06	8.46E-05
SOHLH2	0.589984273	2.86E-07	3.37E-06
RUVBL1	0.589341861	4.31E-07	4.91E-06
CUTC	0.588680302	1.16E-06	1.20E-05
ZNF675	0.588625956	0.00209824	0.0090152
PGK1	0.588200549	1.49E-05	0.00012055
SLC39A4	0.587873724	0.00031975	0.00179035
ANXA2P3	0.587749403	0.00100104	0.00480621
DPP9	0.587507003	1.75E-05	0.00013924
RP11-23P13.	0.587230557	0.00212384	0.00909199
SYDE1	0.585803004	3.62E-10	6.76E-09
LARP4P	0.585545807	0.00177649	0.00782253
FAM83G	0.5850699	1.28E-05	0.00010552
CTDSP1	-0.58503239	5.32E-07	5.91E-06
MFSD11	-0.585559059	2.01E-05	0.0001573
RP11-349A22	-0.586327639	1.51E-05	0.00012194
ARPC1B	-0.586592753	8.09E-08	1.05E-06
RP11-697E2.	-0.586860894	0.00012634	0.00079467
ACAP3	-0.58844186	2.03E-05	0.00015909
TMEM179B	-0.589119146	0.00010713	0.00069124
TNFRSF1A	-0.58964288	1.45E-05	0.00011756
BDH2P1	-0.589888558	0.00234789	0.00987914
LRP11	-0.589995034	0.00013905	0.00086209
IFT74	-0.590423282	6.15E-07	6.74E-06
CUX1	-0.590546978	2.30E-06	2.25E-05
NME3	-0.591447778	1.86E-07	2.26E-06
RPS6KA3	-0.591604222	5.23E-06	4.77E-05
RNF146	-0.592280343	2.43E-06	2.37E-05
STIM2	-0.59270958	1.13E-05	9.50E-05
ITPKB	-0.592779228	1.25E-06	1.29E-05
AC005789.11	-0.592831238	0.00042298	0.00227408

LBX2	-0.593280785	0.00016724	0.00101673
PREX1	-0.593390273	7.18E-07	7.75E-06
HIP1	-0.594979863	2.26E-09	3.77E-08
WAC-AS1	-0.59538391	5.37E-05	0.00037788
DDX26B	-0.595736594	0.00053285	0.0027786
NBPF10	-0.596437428	0.00032586	0.001819
HEXIM1	-0.596530711	1.19E-09	2.08E-08
TBC1D4	-0.600256019	8.50E-06	7.36E-05
SFR1	-0.60128843	0.00020819	0.00122963
TPBG	-0.601450394	9.20E-06	7.86E-05
ADD3	-0.60149805	2.48E-09	4.10E-08
RASA1	-0.602535668	3.41E-05	0.00025204
NMNAT1	-0.602681429	0.00013861	0.00085967
RP11-661A12	-0.602840659	0.00220412	0.00937961
DHTKD1	-0.603407337	1.34E-06	1.37E-05
BNC2	-0.603485462	5.13E-07	5.72E-06
NAPEPLD	-0.604480346	2.76E-06	2.66E-05
ZMYND8	-0.605263438	4.20E-10	7.75E-09
ZNF436	-0.605560478	8.51E-06	7.36E-05
FRMD5	-0.607362641	3.94E-06	3.67E-05
CDKN1B	-0.608086462	0.00011332	0.00072496
LINC00648	-0.609293537	0.0002465	0.00142329
ZKSCAN1	-0.609483243	8.57E-06	7.39E-05
HOXB7	-0.609589315	9.13E-06	7.83E-05
UGGT2	-0.61002028	3.66E-05	0.00026837
WDR91	-0.61104224	5.26E-05	0.00037047
NFATC1	-0.611421787	0.00076564	0.00382078
SSH1	-0.611857936	7.12E-07	7.70E-06
SCARB2	-0.611986128	3.49E-07	4.03E-06
MOK	-0.612826568	0.00195496	0.00849486
TIAM1	-0.613479395	1.40E-05	0.00011427
SAGE1	-0.614593188	8.54E-07	9.13E-06
USP6NL	-0.614839692	7.86E-10	1.40E-08
ARSB	-0.616119649	4.97E-07	5.56E-06
DALRD3	-0.61629349	1.16E-09	2.03E-08
RP11-221N13	-0.616776785	0.00075347	0.00377033
OPHN1	-0.616924473	0.00019739	0.00117515
KDELC2	-0.617919777	6.30E-05	0.00043416
DECR1	-0.617964641	5.17E-08	6.92E-07
POGLUT1	-0.619057239	1.43E-08	2.12E-07
SH3BGR1	-0.619120677	2.67E-05	0.00020232
MRPS6	-0.619570258	3.23E-08	4.49E-07
CEP85L	-0.61997491	1.77E-06	1.77E-05
BCAP29	-0.620617946	5.14E-06	4.69E-05
CRELD1	-0.620709596	1.29E-05	0.00010642
NRBP2	-0.620808166	0.0001459	0.00090047
LRP6	-0.62126871	1.04E-08	1.56E-07
RP1-102E24.	-0.621551625	0.00016726	0.00101673
TMEM121	-0.621705873	0.00081498	0.00403103
BAZ2B	-0.621740187	4.81E-06	4.42E-05
FAM168A	-0.623067576	2.38E-10	4.53E-09
SAP30L	-0.624592407	1.23E-08	1.84E-07
RABL5	-0.624823022	1.34E-06	1.37E-05
CALHM2	-0.626019777	0.00021394	0.00125999
AHCYL2	-0.626293371	1.47E-08	2.17E-07
TXNDC15	-0.626670232	8.48E-08	1.09E-06

ID3	-0.626875679	0.00167273	0.00744109
ZNF513	-0.627158543	1.44E-06	1.46E-05
KCTD13	-0.628464571	2.13E-05	0.00016575
SRGAP2B	-0.628759838	1.62E-05	0.00012969
WDR19	-0.628833351	2.61E-05	0.00019869
CCDC106	-0.629484533	7.18E-06	6.35E-05
OSER1-AS1	-0.629842786	0.00071233	0.00358952
STPG1	-0.630078939	3.42E-05	0.0002525
DPYSL2	-0.63198272	2.13E-09	3.58E-08
ARSA	-0.632307089	0.00122445	0.00571472
SNX21	-0.632500484	1.62E-06	1.63E-05
CREM	-0.632857587	0.00160072	0.00716541
ABHD2	-0.634074524	3.82E-09	6.17E-08
PELI2	-0.634124581	8.18E-05	0.00054938
DHRS1	-0.634250629	4.18E-05	0.0003021
LINC00341	-0.634303399	0.00131201	0.00605227
RPS4XP8	-0.635347161	0.00021817	0.00128081
IFT27	-0.635568184	0.00018868	0.00113148
TRPM4	-0.636389691	0.0002402	0.00139472
PGAP1	-0.636849282	1.33E-05	0.00010938
ACP2	-0.637139476	2.43E-05	0.00018667
RPL37P23	-0.637425617	1.30E-06	1.34E-05
CD276	-0.638075987	8.26E-08	1.07E-06
MCOLN3	-0.638313323	0.0011705	0.0055012
SMPD1	-0.639085216	5.69E-07	6.28E-06
SLC27A3	-0.639321982	0.00042538	0.00228476
CHSY1	-0.639536289	1.79E-11	4.01E-10
PRICKLE4	-0.639826958	0.00120579	0.00564609
DOPEY1	-0.639971834	0.00026559	0.0015165
CBX5	-0.642060742	1.45E-10	2.83E-09
LINC00205	-0.642125805	0.00129396	0.00597908
CREB3L4	-0.642208191	6.48E-06	5.81E-05
RPS4XP2	-0.643044273	0.0014606	0.00662092
ZNF558	-0.644041163	0.00017642	0.0010661
C9orf16	-0.644264803	6.21E-05	0.00042822
ZEB1	-0.644341745	3.61E-08	4.99E-07
MEGF9	-0.644472954	5.84E-07	6.43E-06
COL4A2	-0.645286141	9.72E-05	0.00063585
FBXL17	-0.645661752	2.10E-08	3.00E-07
NAGLU	-0.645758497	1.90E-07	2.31E-06
ETV6	-0.646901974	3.66E-09	5.92E-08
DYRK1B	-0.647110753	0.0002818	0.00159851
ARSK	-0.647362413	1.59E-05	0.00012784
TSPAN31	-0.648473669	7.58E-08	9.88E-07
FAM46A	-0.649108527	2.56E-05	0.00019563
KRT222	-0.649163598	0.00066432	0.00336927
ITGA5	-0.649287141	8.88E-05	0.00059011
AC003665.1	-0.649395923	0.00157748	0.00707198
GDF11	-0.649504781	2.53E-11	5.55E-10
CD44	-0.650370882	2.15E-09	3.61E-08
DLK2	-0.651923393	0.00073105	0.00367265
SUFU	-0.6530755	5.90E-07	6.49E-06
FAM214B	-0.653712611	2.28E-07	2.74E-06
METTL7B	-0.653793834	0.00024217	0.00140321
TMPO-AS1	-0.654149966	0.00065406	0.00332234
HAPLN3	-0.654247742	1.33E-05	0.00010938

FAM102A	-0.654695428	1.31E-06	1.34E-05
FNTB	-0.654698188	0.00029283	0.0016554
AC009245.3	-0.654726458	8.70E-05	0.00057991
ZFP14	-0.655165912	0.00055755	0.00289094
PHLDB1	-0.655489942	8.83E-09	1.35E-07
ZNF546	-0.655789493	0.00115349	0.00542744
ARID5A	-0.657347395	0.00011522	0.00073456
TNFAIP8	-0.65769231	0.00035301	0.00194352
BPHL	-0.657863107	0.00189948	0.00829316
GAB1	-0.658301028	9.67E-05	0.00063313
ZNF34	-0.658409814	0.00012337	0.00077838
ZDHHHC20	-0.658757323	3.73E-05	0.00027315
VEZF1P1	-0.659425098	3.03E-05	0.00022641
PTCH1	-0.659624399	8.66E-07	9.24E-06
PXK	-0.660068811	1.94E-09	3.27E-08
BACE1	-0.661673448	1.90E-10	3.65E-09
TBX2	-0.661734247	5.08E-06	4.64E-05
SARNP	-0.663264753	0.00015086	0.00092765
CCSAP	-0.665731372	7.32E-13	1.92E-11
TANC1	-0.665882578	5.61E-09	8.88E-08
VPS36	-0.666042839	3.60E-10	6.73E-09
PHF2P2	-0.666595299	0.00082529	0.00406792
RP11-53O19.	-0.668593501	0.00034313	0.00189806
RAB36	-0.669999572	0.00013317	0.00083187
RP11-212P7.	-0.671352891	0.00145065	0.0065885
SPATA20	-0.672887366	3.59E-08	4.98E-07
BTN2A2	-0.674331058	3.39E-05	0.00025067
AP1S2	-0.675028695	3.31E-09	5.38E-08
DZIP3	-0.675238595	3.64E-08	5.02E-07
DAG1	-0.675456597	4.24E-11	9.05E-10
ERCC1	-0.675598281	4.84E-10	8.86E-09
SIRPAP1	-0.675762174	0.00125754	0.00584356
GLCE	-0.676419869	5.28E-10	9.62E-09
TMEM67	-0.6768389	0.00124264	0.00578414
GTPBP2	-0.676953241	0.00236816	0.00994665
MPV17L	-0.676995362	0.00145259	0.00659553
S100A10	-0.677759493	6.52E-06	5.84E-05
HOXA3	-0.677800987	3.47E-06	3.26E-05
SRPX2	-0.677814026	2.33E-05	0.00018003
CMTM6	-0.677827495	2.71E-12	6.69E-11
ZMYM5	-0.67880057	5.03E-05	0.00035632
PSD4	-0.679314725	0.00045933	0.00244318
TP53	-0.679398945	5.12E-05	0.00036183
ZNF521	-0.680061274	1.97E-05	0.00015408
RP11-458F8.4	-0.680090789	0.00011389	0.00072829
PMP22	-0.680507989	1.30E-05	0.00010693
NFKB1	-0.681935061	0.00077474	0.00385686
PDE4D	-0.682877114	7.38E-07	7.96E-06
GSK3B	-0.683076267	1.67E-10	3.22E-09
EHD3	-0.68342463	1.59E-11	3.57E-10
GPR135	-0.683976847	0.00022107	0.00129552
MMD	-0.684144257	7.87E-06	6.88E-05
DCBLD2	-0.684437015	2.78E-06	2.68E-05
KIF13A	-0.685660749	1.92E-08	2.75E-07
C20orf112	-0.686760452	8.09E-09	1.24E-07
VAMP1	-0.686807375	0.00118407	0.00555229

CTSZ	-0.687089928	4.86E-07	5.46E-06
B4GALT6	-0.687667292	3.80E-08	5.23E-07
CELSR1	-0.687682343	3.43E-07	3.98E-06
TTC13	-0.687747803	6.51E-10	1.17E-08
ATG2B	-0.687909429	1.36E-09	2.35E-08
MAP1A	-0.688030682	0.00173621	0.00766566
CLHC1	-0.688223567	0.00025187	0.00144969
IRF1	-0.689035409	6.34E-06	5.70E-05
MINPP1	-0.689728979	3.07E-11	6.65E-10
ZDHH14	-0.690507282	2.43E-05	0.00018685
SLC35B2	-0.691918769	6.65E-08	8.75E-07
ABHD8	-0.692022616	1.43E-07	1.77E-06
RBM5	-0.692341139	4.25E-09	6.83E-08
RP11-57H14.1	-0.692497159	0.00104682	0.00499833
C6orf1	-0.692729223	4.63E-06	4.27E-05
ABAT	-0.693048054	0.00076215	0.00380682
ZNF821	-0.693329958	0.00176822	0.00779236
RP11-259N19	-0.694325016	1.64E-05	0.0001313
LEPROT	-0.694643827	3.24E-06	3.07E-05
PLEKHG1	-0.69494255	0.00107414	0.00511297
FAM173B	-0.69553571	5.00E-05	0.00035472
CROCCP3	-0.695591427	0.00045457	0.00242019
CCDC163P	-0.696769387	8.12E-05	0.00054581
TRNP1	-0.697909347	2.08E-11	4.61E-10
FBXO27	-0.69830168	0.00014018	0.00086788
NFE2L3	-0.698467017	5.09E-05	0.00036035
CSAD	-0.699765708	0.00057114	0.00295582
ST3GAL3	-0.70058456	4.38E-05	0.00031603
ABHD15	-0.700778476	7.75E-07	8.33E-06
RP11-820L6.1	-0.70278233	0.00024794	0.0014306
GGT7	-0.702961285	2.06E-10	3.94E-09
CNKSR2	-0.703542237	0.00013555	0.00084486
UBBP4	-0.703649847	0.00046481	0.00246595
CKAP2L	-0.704240245	1.53E-07	1.88E-06
FAM114A1	-0.705571763	0.00013839	0.000859
PLA2G6	-0.705846458	5.71E-05	0.00039826
RP11-365H23	-0.706225902	1.77E-08	2.56E-07
CIRBP	-0.706534493	0.00017902	0.00107901
RBPJ	-0.708595208	1.14E-13	3.41E-12
FLG-AS1	-0.708818953	1.85E-06	1.84E-05
NOMO2	-0.709128227	7.35E-05	0.00050035
GPAA1	-0.709738904	5.50E-13	1.46E-11
DCPS	-0.71071436	4.37E-12	1.05E-10
HDAC4	-0.710737974	5.39E-05	0.00037846
NACC2	-0.710873084	1.65E-06	1.65E-05
TCTN2	-0.712996823	0.00047156	0.00249537
FAM3C2	-0.713753789	5.93E-11	1.24E-09
AGAP2	-0.714553358	0.00102679	0.00491552
ANO8	-0.715171917	4.77E-06	4.38E-05
GABARAP	-0.715578587	2.75E-08	3.87E-07
AIF1L	-0.717963855	0.00014012	0.00086788
AC004980.7	-0.718081501	0.00202621	0.00876056
CLASP1	-0.718557241	2.31E-06	2.26E-05
AC091729.9	-0.721019563	7.24E-05	0.00049302
TMEM14A	-0.721307836	0.00061241	0.00313397
CREBL2	-0.722016424	7.12E-14	2.19E-12

SLC12A7	-0.722675684	7.91E-08	1.03E-06
UHRF2	-0.723530342	0.00215385	0.00919417
CEP70	-0.723663962	2.33E-05	0.00018014
ETV4	-0.723764731	4.48E-11	9.52E-10
ACP6	-0.724929718	1.09E-07	1.38E-06
TOM1L2	-0.725311227	1.38E-12	3.52E-11
PCDHB7	-0.725709917	6.57E-06	5.87E-05
KCNAB2	-0.727072601	3.87E-05	0.00028228
ZFYVE28	-0.727714369	0.00020049	0.00118931
ABHD6	-0.728557499	1.57E-06	1.59E-05
POPDC3	-0.728817317	1.34E-10	2.64E-09
TMEM17	-0.730059716	1.38E-06	1.41E-05
TAPT1	-0.730759023	1.67E-13	4.84E-12
TIAM2	-0.730820707	9.10E-06	7.80E-05
KCTD15	-0.73223443	8.83E-11	1.78E-09
MYO5A	-0.732611768	1.57E-10	3.05E-09
ZDHHHC20P4	-0.732794335	0.00023195	0.00135254
TEF	-0.732964954	0.0003278	0.00182612
AC012512.1	-0.733558794	1.27E-07	1.58E-06
RP11-343N15	-0.734496883	7.59E-06	6.66E-05
ARHGEF11	-0.735427513	2.99E-09	4.89E-08
SLCO4A1	-0.736080497	1.08E-11	2.47E-10
TBC1D19	-0.737801819	0.00028137	0.00159664
RP11-166D19	-0.737840544	3.28E-07	3.83E-06
BSCL2	-0.738206817	1.45E-06	1.47E-05
RP11-226L15	-0.738381577	1.47E-05	0.00011885
GPR137	-0.738544531	1.58E-08	2.32E-07
BHLHB9	-0.74027552	0.00041187	0.00222232
CD83	-0.742881038	0.00034542	0.00190755
PITPNM2	-0.743138143	6.07E-09	9.56E-08
SEC31B	-0.744609082	7.48E-05	0.00050746
LHFPL2	-0.745017205	1.79E-09	3.03E-08
VPS37D	-0.745939723	0.00053015	0.00276539
PRKACB	-0.74610221	7.55E-15	2.56E-13
ZDHHHC13	-0.7461318	3.61E-07	4.16E-06
HPS5	-0.746594005	0.00014319	0.00088478
TIMP1	-0.746845512	1.73E-08	2.51E-07
RMDN2	-0.7481103	1.34E-05	0.00010951
DNM1	-0.748593278	9.22E-10	1.63E-08
SLC44A1	-0.749726391	9.90E-14	2.99E-12
CAPN5	-0.750277373	3.13E-10	5.89E-09
FAM3C	-0.75154722	2.29E-07	2.75E-06
SESTD1	-0.751784507	6.75E-08	8.86E-07
CCDC28B	-0.751807377	1.04E-06	1.09E-05
CLDN4	-0.752103662	0.00074106	0.00371839
NET1	-0.752538395	8.47E-05	0.00056651
SLC22A4	-0.754086118	0.00090254	0.00439606
AF013593.1	-0.755325378	0.0007275	0.00365593
RP11-46C24.	-0.756287023	2.71E-06	2.62E-05
FOX2	-0.757172786	9.19E-06	7.86E-05
TMEM198	-0.758289278	0.00024505	0.00141587
SUSD5	-0.759475253	1.03E-09	1.81E-08
WNK4	-0.759633737	4.81E-11	1.02E-09
FOXF1	-0.760630003	0.00016512	0.00100631
GABRA3	-0.760721934	4.99E-05	0.00035467
ANK3	-0.76074101	0.00011462	0.00073184

NRG2	-0.76083759	9.89E-05	0.00064491
RARG	-0.76093094	1.34E-10	2.64E-09
UPP1	-0.761026586	3.20E-07	3.75E-06
SEMA4C	-0.763073733	4.87E-11	1.03E-09
IFI35	-0.763155619	5.72E-05	0.00039863
MTHFD2L	-0.763737973	4.64E-06	4.27E-05
UGT2B7	-0.764521238	0.00103406	0.00494169
DNAJC4	-0.764595792	2.96E-05	0.00022161
KIAA0513	-0.764758208	4.29E-07	4.89E-06
SLC16A9	-0.766181333	0.00041599	0.00224236
CTC-228N24.	-0.766626685	9.97E-09	1.51E-07
SLC9A7P1	-0.768174514	0.00011564	0.00073692
ING4	-0.770358851	5.78E-10	1.05E-08
ADAM23	-0.771332166	1.59E-05	0.00012756
TGFBR2	-0.771839547	6.93E-07	7.52E-06
CCDC24	-0.773021315	0.00023388	0.00136232
PCDH10	-0.773366012	0.00195474	0.00849486
FRMD4A	-0.773854438	3.25E-11	7.02E-10
ARL6IP5	-0.774370271	1.30E-06	1.34E-05
SGCB	-0.774739435	2.39E-11	5.27E-10
IGFBP7	-0.776574955	6.59E-09	1.03E-07
RP11-216N14	-0.777207591	9.92E-06	8.43E-05
IFT122	-0.777981727	2.00E-08	2.87E-07
ATP1A1	-0.778653559	1.63E-10	3.15E-09
PI15	-0.779164233	0.00072246	0.0036317
GXYLT2	-0.779171147	3.45E-06	3.25E-05
ARHGAP33	-0.779462021	0.00082078	0.00405053
EHBP1	-0.779723868	4.03E-15	1.41E-13
FAM89B	-0.779850375	7.10E-08	9.29E-07
ENDOD1	-0.780648189	2.64E-11	5.79E-10
NID1	-0.780695452	0.00049809	0.00261139
EMILIN1	-0.781411445	1.97E-07	2.39E-06
CUEDC1	-0.781601411	5.90E-15	2.05E-13
MCL1	-0.78224849	1.25E-05	0.00010349
DPY19L1	-0.782383095	3.85E-14	1.23E-12
LMLN	-0.782763682	1.40E-05	0.00011366
IFT88	-0.785567494	1.49E-07	1.84E-06
SUMF1	-0.786883628	6.40E-09	1.00E-07
SMAD6	-0.787602998	4.63E-05	0.00033202
HFE	-0.787833013	2.86E-05	0.00021521
CALB2	-0.788856008	0.00228393	0.00965934
AL109763.2	-0.789001715	0.0009595	0.00463687
SORBS1	-0.789917586	0.00163976	0.0073143
TAPT1-AS1	-0.79013302	7.70E-05	0.00052097
SPATS2L	-0.791320443	2.78E-07	3.29E-06
FAM43A	-0.791819308	2.75E-06	2.65E-05
MARCKSL1	-0.792062097	6.04E-10	1.09E-08
TESK2	-0.792412254	6.90E-06	6.13E-05
RP11-196G18	-0.792439848	3.00E-06	2.87E-05
KIAA1324L	-0.792835617	2.48E-11	5.46E-10
IDUA	-0.79290986	1.79E-06	1.78E-05
SLC4A3	-0.794158271	1.57E-07	1.93E-06
CCT6P3	-0.794759807	0.00075028	0.0037578
PLIN2	-0.794903071	4.09E-08	5.58E-07
RABL2A	-0.795147014	4.68E-05	0.00033505
CCNJL	-0.795605275	4.76E-13	1.28E-11

LPXN	-0.796357408	0.00070109	0.00353829
TGFBR3	-0.797359455	0.00114713	0.0054037
PDK2	-0.798262993	4.44E-08	6.03E-07
SLC16A4	-0.798941494	4.50E-06	4.16E-05
PDLIM4	-0.799112769	9.07E-09	1.38E-07
WWP2	-0.799373754	2.01E-07	2.44E-06
ALAD	-0.800189845	3.09E-15	1.10E-13
SSFA2	-0.803724555	0.00015792	0.00096637
BICD1	-0.803820483	3.99E-18	1.96E-16
CYB5D2	-0.804476494	0.00093221	0.00452053
TTLL3	-0.804500387	0.0002096	0.00123728
COL6A2	-0.804670824	0.0004306	0.00231049
NT5E	-0.805092989	8.19E-06	7.13E-05
LRRC73	-0.80556497	0.0001169	0.00074321
CCNG2	-0.80623197	0.00016519	0.00100635
RP11-18H7.1	-0.806274639	0.00090078	0.00438879
SIK2	-0.806675348	7.04E-17	3.01E-15
TCP11L2	-0.806753837	0.00233255	0.00983469
PLCB1	-0.807837706	6.04E-08	8.00E-07
CACNA2D1	-0.808022462	3.92E-08	5.38E-07
THBS3	-0.808622508	0.00018811	0.00112925
ANTXR2	-0.810513513	2.41E-10	4.58E-09
HPCAL1	-0.811560729	3.02E-11	6.57E-10
ADAM12	-0.812189568	0.00044467	0.00237439
OSBPL5	-0.812696006	2.04E-05	0.0001592
APOBEC3G	-0.813302685	7.64E-05	0.00051704
ANGPTL2	-0.814387811	2.03E-13	5.83E-12
HOTAIR	-0.814579017	0.00077245	0.00384659
RP5-1024G6.	-0.814677219	2.52E-07	3.00E-06
PKD2	-0.819786603	4.08E-13	1.11E-11
LMNA	-0.819806036	2.43E-11	5.35E-10
CPS1	-0.82020816	1.24E-06	1.29E-05
FZD9	-0.820425068	0.00046604	0.00247021
GNE	-0.820578082	2.43E-07	2.90E-06
RP11-445F12	-0.82081599	0.00227794	0.00963649
YPEL2	-0.823857829	0.00017438	0.0010561
HMGA2	-0.823975137	0.00094248	0.00456361
SAT1	-0.823975506	8.64E-06	7.45E-05
LAMC1	-0.82452264	1.86E-12	4.67E-11
ELOVL4	-0.826139142	2.38E-08	3.38E-07
RP11-603J24	-0.82729077	8.55E-15	2.88E-13
SLC27A1	-0.830520237	0.00048721	0.00256742
AC074212.6	-0.832534676	0.00072236	0.0036317
ZNF517	-0.832660581	9.20E-05	0.0006069
PBXIP1	-0.833374592	2.64E-13	7.40E-12
TTC30B	-0.833552509	9.18E-06	7.85E-05
SERPINB8	-0.83643028	7.54E-12	1.74E-10
TCTN1	-0.836476613	9.92E-14	2.99E-12
LGALS1	-0.837319434	2.77E-08	3.91E-07
GALNT5	-0.838072618	0.00010103	0.0006568
KIAA1755	-0.8381537	1.17E-05	9.75E-05
PRR4	-0.839243606	1.62E-06	1.63E-05
ARHGEF37	-0.839377911	0.00070075	0.0035382
RP11-541N10	-0.840206861	0.0002407	0.00139664
SOCS6	-0.840719684	5.16E-12	1.23E-10
ADAM8	-0.841357043	0.00020233	0.00119892

PLCD1	-0.841717396	0.00018917	0.00113401
CRISPLD1	-0.842165155	0.0004818	0.00254185
PAQR4	-0.844197869	7.33E-14	2.25E-12
ZBTB38	-0.84431511	1.49E-07	1.84E-06
CMPK2	-0.845690966	0.00078664	0.00390663
TAPBPL	-0.845839628	1.86E-05	0.00014657
LUCAT1	-0.847011873	0.00128717	0.00595269
ALDH3A2	-0.847255285	1.57E-11	3.53E-10
PLA2R1	-0.847324997	0.00065351	0.00332085
MOCOS	-0.847415547	2.92E-05	0.00021918
ABTB1	-0.847571281	7.69E-12	1.78E-10
PSKH1	-0.848405881	8.89E-09	1.36E-07
RAB13	-0.848475772	2.58E-15	9.26E-14
PCDHGA1	-0.84878581	0.00015399	0.00094491
GLB1L	-0.850969122	7.90E-05	0.00053338
SASH1	-0.851163773	9.94E-14	2.99E-12
CCDC159	-0.854299391	0.00011675	0.00074253
SPATA17	-0.855288335	0.00074472	0.00373219
ACVR1	-0.855316814	1.06E-12	2.76E-11
ERMAP	-0.855438267	1.37E-06	1.39E-05
RAB38	-0.856708707	1.07E-05	8.99E-05
PIR	-0.8578433	1.04E-09	1.84E-08
TNS3	-0.861369012	1.01E-06	1.06E-05
AAMDC	-0.862112699	0.00025789	0.00147613
LYST	-0.862762023	8.69E-05	0.00057965
APLP2	-0.863521111	2.47E-13	7.00E-12
BCAS3	-0.8646533	6.39E-11	1.33E-09
RP11-479G22	-0.866769284	0.00086187	0.00422172
SEZ6L2	-0.867430222	1.99E-06	1.97E-05
HGSNAT	-0.868422609	1.61E-06	1.62E-05
GNG4	-0.869787099	3.46E-07	4.01E-06
KLHL22	-0.87154065	1.00E-05	8.49E-05
CA5B	-0.871702635	6.20E-05	0.00042774
FGFR3	-0.872362744	0.00012009	0.00076029
ERVK13-1	-0.872667198	8.51E-07	9.11E-06
LMBRD1	-0.873214825	8.83E-07	9.41E-06
CABLES2	-0.874200223	3.03E-09	4.95E-08
CEP19	-0.875175469	0.00063312	0.00323091
CNR1	-0.87570591	3.85E-10	7.18E-09
RP3-368A4.5	-0.876131957	0.00012792	0.00080309
PRKAR1A	-0.87620737	5.65E-12	1.33E-10
CCDC121	-0.87818022	0.00027884	0.0015828
EPS8	-0.87830352	2.78E-09	4.58E-08
PCYOX1L	-0.878604447	8.03E-08	1.04E-06
MMP14	-0.879608465	4.05E-08	5.54E-07
PAN3-AS1	-0.879871314	0.00140544	0.006415
BAIAP2-AS1	-0.880300966	1.87E-07	2.28E-06
ID1	-0.880813538	1.85E-08	2.65E-07
DLGAP1-AS1	-0.880975544	2.83E-05	0.00021298
NDE1	-0.881383491	2.10E-15	7.59E-14
FAM107B	-0.88191492	1.48E-06	1.50E-05
SRGAP2	-0.883181256	1.12E-16	4.73E-15
TMEM158	-0.883618713	1.69E-06	1.69E-05
FMNL3	-0.884423582	4.57E-07	5.17E-06
PAG1	-0.884715515	0.00034016	0.00188794
GALNT2	-0.88553794	2.55E-10	4.83E-09

VIM	-0.885674653	2.72E-12	6.69E-11
PC	-0.887229033	7.79E-11	1.59E-09
VWA5A	-0.887785953	0.00102968	0.00492791
NPTXR	-0.892055639	0.00015401	0.00094491
PHC2	-0.89231973	1.69E-13	4.90E-12
PRKAR1AP	-0.892613646	1.78E-08	2.58E-07
C11orf35	-0.894066985	0.0011271	0.00532914
MYLIP	-0.896190425	0.00060214	0.00308717
BMP6	-0.896489434	0.00040846	0.00220812
RP11-152P17	-0.896859416	0.00033209	0.00184876
LRRC29	-0.897142099	0.00186611	0.00815828
IFT80	-0.899125671	4.39E-09	7.03E-08
HAS3	-0.899851763	2.82E-05	0.00021252
TRIOBP	-0.90047839	6.40E-08	8.45E-07
FAM184A	-0.900719287	3.56E-07	4.11E-06
C6orf141	-0.900967234	0.00127962	0.00592612
SNRPB2	-0.901844022	2.64E-13	7.40E-12
H1FX-AS1	-0.902465048	4.60E-05	0.00032939
GPC6	-0.902740555	5.35E-05	0.00037662
AP001372.2	-0.902963328	4.46E-06	4.12E-05
TSHZ3	-0.903198213	6.96E-06	6.17E-05
RP11-396K3.	-0.903541217	0.00020205	0.00119767
CTA-246H3.1	-0.907811848	0.00035348	0.00194486
LSR	-0.909384083	0.00024812	0.00143113
NOVA1	-0.909880024	1.73E-07	2.12E-06
EVA1C	-0.910619175	1.08E-06	1.13E-05
PRNP	-0.911306794	5.14E-15	1.79E-13
ZNF117	-0.911666752	1.15E-07	1.44E-06
H6PD	-0.912278524	0.00011816	0.00075037
ZNF75D	-0.912417665	0.00014544	0.00089798
FGFRL1	-0.912845528	5.30E-12	1.26E-10
C11orf80	-0.913555492	3.13E-05	0.00023398
EFCAB13	-0.914898679	9.32E-06	7.96E-05
POU3F2	-0.915421143	1.28E-09	2.22E-08
NQO1	-0.915591901	4.17E-16	1.66E-14
BTG1	-0.91663637	5.16E-10	9.40E-09
BBS12	-0.917484139	0.00020415	0.00120855
TTC28	-0.918308026	6.94E-05	0.00047415
HMG20B	-0.921406343	9.05E-15	3.04E-13
KYNU	-0.92152728	3.73E-07	4.29E-06
ABR	-0.922064776	1.37E-17	6.24E-16
GAREM	-0.922083704	2.89E-05	0.00021692
QPCT	-0.922420049	1.11E-05	9.31E-05
NAB2	-0.922660591	4.69E-13	1.27E-11
GFPT2	-0.923287635	3.69E-11	7.91E-10
LGR4	-0.923897314	0.00233639	0.00984583
MYO1E	-0.924739838	1.87E-08	2.69E-07
FARP1	-0.925188646	1.38E-10	2.71E-09
C9orf89	-0.925833437	1.25E-09	2.17E-08
CCDC40	-0.928271905	0.00034248	0.00189638
LRRC46	-0.92994543	0.00011276	0.0007222
DUSP6	-0.930683506	6.50E-06	5.82E-05
IRF2BPL	-0.931330359	8.02E-06	7.01E-05
FAM222A	-0.931510053	1.57E-05	0.00012617
CPT1A	-0.931670184	5.55E-08	7.38E-07
DUSP4	-0.93290326	2.62E-18	1.31E-16

CTD-2044J15	-0.933150655	0.00014871	0.00091647
STK17A	-0.936215877	1.74E-10	3.35E-09
RP11-37B2.1	-0.937456363	1.49E-07	1.84E-06
PHF10	-0.938387386	4.12E-09	6.62E-08
IL11RA	-0.938947608	4.76E-08	6.42E-07
VMAC	-0.943545963	1.31E-06	1.34E-05
SOS2	-0.944900428	1.72E-11	3.86E-10
LTBP3	-0.945689174	6.66E-16	2.59E-14
MBNL3	-0.946193633	3.20E-08	4.46E-07
PPFIBP1	-0.948135443	3.43E-17	1.49E-15
LRRC48	-0.948223023	1.48E-06	1.50E-05
ITFG3	-0.949770055	1.11E-11	2.53E-10
LMCD1	-0.951125012	1.24E-10	2.45E-09
MFSD12	-0.951181271	1.02E-17	4.72E-16
USP46-AS1	-0.953103357	8.54E-06	7.38E-05
HBP1	-0.953930911	2.28E-08	3.25E-07
UST	-0.956677446	2.58E-07	3.07E-06
DLG3	-0.956855997	2.27E-11	5.02E-10
RP5-882C2.2	-0.956954249	0.00047243	0.00249835
PLEKHH2	-0.958220161	6.66E-07	7.25E-06
MEGF8	-0.958421788	3.99E-10	7.41E-09
SNX10	-0.958916265	8.22E-05	0.00055155
CYP27A1	-0.960175716	2.14E-05	0.00016648
EMP2	-0.965120839	3.95E-10	7.34E-09
EFNB2	-0.966087929	1.13E-05	9.45E-05
CDC42EP3	-0.966423139	3.16E-16	1.27E-14
RGS17	-0.966727776	5.12E-06	4.68E-05
SEMA3A	-0.966810471	1.74E-09	2.95E-08
RP11-277P12	-0.96731693	0.00138508	0.00633439
CRLF1	-0.968790875	1.29E-06	1.33E-05
S100A4	-0.969801505	0.00019183	0.0011466
ITGAV	-0.97047427	3.92E-12	9.48E-11
B3GNT5	-0.970841511	1.74E-07	2.13E-06
ROM1	-0.97140654	0.00011436	0.00073043
NBEA	-0.972222221	4.18E-08	5.70E-07
CDK19	-0.972420397	1.36E-11	3.09E-10
FMNL2	-0.973034212	2.51E-13	7.07E-12
THSD4	-0.973484211	8.35E-07	8.95E-06
ARHGAP5	-0.974018518	8.41E-18	3.93E-16
AC010904.1	-0.974140941	2.37E-07	2.83E-06
ARHGEF9	-0.97420946	0.00175006	0.00772062
CNIH3	-0.974953154	0.00013852	0.00085947
RP13-228J13	-0.975052726	5.96E-05	0.00041436
LINC00963	-0.975264024	2.90E-08	4.05E-07
CDKN2C	-0.975299082	0.00010381	0.00067296
ETV5	-0.976335832	1.62E-12	4.11E-11
AQP3	-0.97658643	0.00027795	0.00157882
RCBTB2	-0.98132057	7.69E-07	8.27E-06
ARHGEF6	-0.982319136	1.00E-05	8.49E-05
ACSL3	-0.984091614	3.58E-18	1.77E-16
ATP7A	-0.985728347	3.35E-11	7.22E-10
CTA-217C2.1	-0.986151137	5.84E-05	0.0004067
GNAS	-0.987196104	6.47E-12	1.51E-10
ST6GALNAC3	-0.988119399	1.11E-07	1.40E-06
IL22RA1	-0.989220316	6.29E-05	0.00043377
CDH12	-0.989225074	8.93E-10	1.58E-08

KALRN	-0.990289232	0.00081596	0.00403277
TMEM164	-0.990765771	6.02E-12	1.41E-10
MRC2	-0.991057908	3.74E-11	8.00E-10
TTLL7	-0.991071892	1.30E-05	0.00010693
FHDC1	-0.991342678	9.26E-05	0.00061003
FRMD3	-0.99392781	0.00137014	0.00627826
RP11-108P20	-0.994744221	1.23E-05	0.00010197
S100A6	-0.99566465	4.14E-16	1.65E-14
SALL1	-0.995882007	8.75E-06	7.52E-05
RP11-496I9.1	-0.995962771	0.00200116	0.00865906
FAXDC2	-0.996123902	4.81E-07	5.42E-06
COL16A1	-0.996666261	1.75E-09	2.96E-08
CXXC5	-0.997439708	3.41E-10	6.39E-09
C2orf81	-0.999222663	2.18E-08	3.11E-07
SYNJ2	-1.000147359	0.00026757	0.00152726
TBC1D8	-1.002963481	1.52E-11	3.44E-10
SFT2D2	-1.004744654	6.20E-19	3.22E-17
SCN1B	-1.005510618	1.60E-05	0.00012817
LNX1	-1.009834688	4.41E-07	5.01E-06
KIAA1549L	-1.011291172	7.08E-05	0.00048284
MUC15	-1.014504708	0.00020403	0.00120854
SHISA4	-1.014929036	6.42E-08	8.48E-07
MXD3	-1.015038895	4.33E-08	5.89E-07
PRKCDBP	-1.016151027	4.17E-10	7.70E-09
BMP8B	-1.016834503	6.01E-12	1.41E-10
CRYL1	-1.017059451	0.00234561	0.00987206
ETFB	-1.019298232	4.13E-19	2.18E-17
GPT	-1.021383005	5.41E-05	0.00038014
SEMA3C	-1.02167646	3.90E-10	7.26E-09
SAMD14	-1.021810193	6.67E-06	5.95E-05
TPT1-AS1	-1.023169991	0.00149275	0.00674256
ST6GAL1	-1.023978378	9.48E-12	2.18E-10
RP11-549B18	-1.027310196	5.63E-05	0.00039358
DLX2	-1.027616338	0.00077634	0.00386131
RP11-477D19	-1.027702987	2.72E-08	3.83E-07
AGA	-1.028288554	2.04E-10	3.90E-09
TLE2	-1.029657985	0.0008932	0.00436094
ICK	-1.030214986	8.74E-06	7.52E-05
DIXDC1	-1.030608934	3.71E-07	4.27E-06
SNTB2	-1.030839647	4.82E-18	2.34E-16
SLFN5	-1.031095316	6.64E-09	1.04E-07
AHRR	-1.031250657	1.53E-12	3.88E-11
RAP1GAP	-1.031306735	3.02E-05	0.00022599
ZNF385A	-1.032338956	8.81E-16	3.34E-14
CNTRL	-1.032984532	2.26E-14	7.32E-13
ARSE	-1.034145438	2.77E-07	3.27E-06
IFNAR2	-1.035532068	2.66E-10	5.02E-09
TBX19	-1.035565436	3.55E-07	4.10E-06
CADM1	-1.037075063	8.19E-10	1.46E-08
LAMA2	-1.039748921	0.00058331	0.00300841
SDHAP3	-1.041766419	0.00103263	0.0049363
JADE2	-1.042233715	1.35E-13	3.98E-12
CNP	-1.042239395	6.07E-22	4.42E-20
RBM47	-1.042459152	0.00011899	0.00075444
RP11-551L14	-1.043062298	0.00079833	0.00395874
PPP4R4	-1.043241807	0.000339	0.00188217

ACSS2	-1.044600803	5.31E-05	0.00037411
STK32B	-1.049595554	5.30E-12	1.26E-10
SH3PXD2A	-1.050153621	3.01E-15	1.07E-13
KAT2B	-1.050406117	0.00018658	0.00112092
ZNF235	-1.051882704	6.73E-07	7.32E-06
KCNIP3	-1.05407733	9.53E-07	1.01E-05
TGFB3	-1.054102524	3.63E-06	3.40E-05
RPGR	-1.056237212	3.97E-09	6.40E-08
RHPN1-AS1	-1.056655946	1.00E-07	1.28E-06
SPATA13	-1.057056044	1.65E-13	4.81E-12
PRKG1	-1.057738651	2.21E-05	0.00017194
PDE9A	-1.060120137	3.44E-06	3.24E-05
SFMBT2	-1.061964444	6.37E-08	8.43E-07
CYP1B1	-1.06210693	2.40E-05	0.00018496
RP11-50E11.1	-1.062505474	0.00051296	0.0026834
PLAT	-1.062528009	7.79E-18	3.66E-16
RP11-244O19	-1.063530157	4.27E-07	4.88E-06
ARHGAP26	-1.064129402	2.89E-13	8.04E-12
CPE	-1.066531449	6.57E-07	7.18E-06
CAT	-1.067673292	4.66E-25	4.39E-23
CAMK4	-1.068400299	1.25E-07	1.56E-06
RP11-359B12	-1.068533544	0.00145508	0.00660317
TP73	-1.068915235	6.16E-11	1.28E-09
ST3GAL4	-1.069851645	3.16E-17	1.38E-15
FAM155A	-1.072892733	1.70E-08	2.47E-07
MYH15	-1.07303246	0.00137073	0.00627922
NIPAL3	-1.073644921	2.19E-16	8.98E-15
NCOA7	-1.073753657	0.00034501	0.00190666
RP11-282O18	-1.073945432	7.42E-08	9.69E-07
WNT5A	-1.074533855	3.83E-06	3.57E-05
TRIB1	-1.075015518	0.00016318	0.00099592
PIP5KL1	-1.07606845	0.00041994	0.00225992
ICOSLG	-1.076379602	3.97E-08	5.44E-07
PCDH9	-1.078355576	1.56E-12	3.97E-11
PIK3R3	-1.078783197	2.49E-09	4.11E-08
TLR6	-1.080018936	1.58E-10	3.07E-09
SEMA3B	-1.080054182	1.85E-11	4.13E-10
GPR110	-1.084408469	0.00113896	0.00537906
OSBPL10	-1.08446563	4.16E-15	1.46E-13
MF12-AS1	-1.087143859	5.42E-07	6.00E-06
PHYHIP	-1.08728855	5.51E-06	4.99E-05
RCAN3	-1.089669156	4.62E-10	8.48E-09
NRP2	-1.090960121	1.22E-13	3.64E-12
CDK2AP1	-1.090990606	1.86E-24	1.69E-22
LHX1	-1.091194981	0.0001764	0.0010661
PLD1	-1.091718744	1.68E-08	2.45E-07
ZNF827	-1.093666302	6.85E-26	7.06E-24
GULP1	-1.093743515	2.65E-21	1.81E-19
GPR37	-1.094356213	0.00198695	0.00861341
PGAP3	-1.094772468	6.38E-08	8.44E-07
SULF2	-1.094805723	1.49E-09	2.56E-08
DOCK4	-1.097654154	2.06E-13	5.92E-12
FAM46B	-1.097888817	0.00076911	0.00383344
CMTM7	-1.098829023	1.13E-15	4.26E-14
SLC5A3	-1.09947016	1.95E-05	0.00015287
WBP1	-1.102430305	2.38E-09	3.94E-08

ABCA1	-1.106156544	2.66E-08	3.75E-07
SPARC	-1.108258024	2.68E-12	6.63E-11
S100A13	-1.10969994	2.10E-19	1.16E-17
SYNE2	-1.113708388	6.47E-08	8.52E-07
STON1	-1.116378975	9.35E-05	0.0006152
LINC00886	-1.117490764	4.54E-05	0.00032608
DISP1	-1.120062322	2.04E-13	5.86E-12
UBE2F	-1.122572017	3.76E-13	1.03E-11
DUSP10	-1.124956853	5.77E-08	7.66E-07
SLCO3A1	-1.126376615	1.14E-12	2.95E-11
RP11-284F21	-1.126723632	3.17E-12	7.76E-11
LINC00622	-1.127116752	0.00013335	0.00083255
PLXNB3	-1.129206994	1.40E-10	2.75E-09
C9orf3	-1.131074487	6.07E-07	6.67E-06
HIPK2	-1.134280418	1.33E-13	3.93E-12
LYPD3	-1.134796553	7.45E-05	0.00050612
GOLGA7B	-1.136225609	0.00211654	0.00907253
PPARG	-1.136541711	2.10E-14	6.82E-13
DMRTA1	-1.136593074	4.32E-06	4.00E-05
FUT8	-1.137508516	2.28E-07	2.74E-06
WDR72	-1.137651371	4.11E-16	1.64E-14
PHLDA1	-1.138092975	2.63E-13	7.37E-12
SH3KBP1	-1.139377696	2.58E-19	1.41E-17
IFNGR2	-1.139654634	4.30E-22	3.16E-20
SIPA1L2	-1.139688963	0.00137447	0.00629284
MOXD1	-1.144482446	0.00095393	0.00461227
FHOD3	-1.145892283	1.27E-05	0.00010498
PBX1	-1.148259318	8.23E-08	1.07E-06
RP11-558F24	-1.149874309	7.88E-05	0.00053239
VIM-AS1	-1.150399126	4.39E-08	5.97E-07
CCDC92	-1.152073885	9.56E-10	1.69E-08
DYNLT3P1	-1.153405294	4.02E-07	4.60E-06
KHDRBS3	-1.154832387	2.87E-08	4.02E-07
CTSF	-1.156549811	4.11E-06	3.82E-05
C1orf106	-1.156597958	3.27E-12	8.00E-11
MAP2K6	-1.158867264	3.19E-05	0.00023729
PCDHGA7	-1.160428881	3.56E-06	3.34E-05
B4GALNT1	-1.160939458	2.56E-15	9.20E-14
ACOX2	-1.162153956	7.66E-06	6.72E-05
ALG1L6P	-1.162909831	0.00032739	0.00182512
RHBDF1P1	-1.163028964	1.31E-06	1.34E-05
PAX8-AS1	-1.164827966	0.00013768	0.00085551
SLC7A11	-1.168391688	0.00052159	0.0027244
CARF	-1.168870298	1.22E-08	1.83E-07
ZNF608	-1.168878697	8.06E-05	0.00054264
PAPSS2	-1.171561044	1.54E-21	1.08E-19
KCNQ1OT1	-1.175186048	7.06E-06	6.25E-05
RHBDF1	-1.178231897	2.79E-17	1.23E-15
ENC1	-1.178260735	0.00010347	0.00067134
GSAP	-1.179389282	4.56E-10	8.39E-09
RNF157	-1.182122424	3.68E-13	1.01E-11
PPP1R3F	-1.183402473	6.82E-08	8.94E-07
LCTL	-1.184157269	2.37E-05	0.000183
WIPF1	-1.184699622	5.19E-21	3.38E-19
AHR	-1.189954801	7.50E-11	1.53E-09
TMEM117	-1.191205932	1.10E-05	9.26E-05

ZNF365	-1.197445326	7.04E-11	1.45E-09
PROX1	-1.19749615	3.04E-07	3.57E-06
TBXAS1	-1.203394031	1.80E-08	2.60E-07
MEOX2	-1.203445961	0.00130033	0.00600685
TSC22D1	-1.203501746	2.77E-12	6.81E-11
MMP2	-1.205502298	4.15E-12	1.00E-10
SPATA6	-1.206649766	2.13E-20	1.30E-18
MXRA8	-1.207214617	8.16E-09	1.25E-07
S1PR2	-1.207544507	1.24E-07	1.55E-06
PHLDA2	-1.208619075	2.58E-16	1.05E-14
LTBP1	-1.210159307	3.39E-08	4.71E-07
SLC12A2	-1.210628787	1.36E-17	6.23E-16
DAAM2	-1.211492845	6.01E-05	0.00041726
RP4-792G4.2	-1.211509704	8.00E-05	0.00053932
PTHLH	-1.214558374	5.01E-05	0.00035551
SMIM14	-1.215700317	4.62E-06	4.25E-05
C1QTNF1	-1.21579415	7.59E-06	6.66E-05
TMCC3	-1.217838419	2.63E-09	4.33E-08
HTR7	-1.218848483	1.13E-16	4.75E-15
RP11-460N16	-1.220186562	6.12E-05	0.00042329
MAML2	-1.222443467	3.91E-28	4.99E-26
HS3ST1	-1.223031638	8.44E-06	7.31E-05
ESPN	-1.22438873	1.36E-06	1.39E-05
LPP-AS2	-1.224538276	1.82E-07	2.22E-06
AP3B2	-1.226061218	0.00012389	0.00078074
FAM78B	-1.226763492	6.35E-10	1.14E-08
PCDHB11	-1.22784978	0.00027817	0.00157957
AC138123.2	-1.231386167	4.36E-06	4.03E-05
C16orf52	-1.232188446	1.46E-25	1.44E-23
C19orf57	-1.236498474	3.35E-07	3.91E-06
RAB17	-1.236514355	6.54E-06	5.85E-05
RNF125	-1.237270532	5.91E-07	6.49E-06
ELTD1	-1.238641488	0.00034151	0.00189419
RASSF8	-1.241269511	1.01E-11	2.32E-10
DYNLT3P2	-1.241548202	5.77E-07	6.36E-06
ABCC3	-1.243693185	3.38E-07	3.93E-06
TCF7L2	-1.244351568	9.42E-13	2.45E-11
RNF144A-AS1	-1.245506228	0.00034503	0.00190666
MEF2C	-1.247292084	1.03E-05	8.70E-05
SLC22A17	-1.249400884	1.15E-05	9.58E-05
PCDHGC3	-1.250030355	1.97E-06	1.95E-05
DCHS1	-1.25004154	1.83E-05	0.00014489
XYLT1	-1.250974894	0.00011516	0.00073444
RP11-6N17.4	-1.253259386	5.29E-07	5.88E-06
ANKRD50	-1.253383647	2.15E-17	9.57E-16
RP11-1055B8	-1.254289746	1.50E-06	1.52E-05
LEMD1	-1.255831014	0.00024035	0.00139508
DYNLT3	-1.259861264	1.37E-19	7.66E-18
NTM	-1.260001342	1.45E-08	2.14E-07
CLMP	-1.26296947	1.21E-12	3.11E-11
CDON	-1.264121449	8.69E-23	6.72E-21
ZNF362	-1.264313037	8.86E-18	4.12E-16
SH3TC2	-1.264549366	5.40E-21	3.50E-19
ANPEP	-1.265995934	3.16E-06	3.01E-05
C19orf71	-1.267099635	2.48E-09	4.10E-08
TLR4	-1.268741217	2.65E-11	5.81E-10

GRK5	-1.270626804	1.22E-13	3.62E-12
RTKN	-1.273599461	4.16E-23	3.28E-21
CYP4X1	-1.275840234	6.85E-07	7.45E-06
LPAR6	-1.276569642	6.56E-14	2.03E-12
ADAMTS9	-1.279956265	5.80E-05	0.00040401
SSBP2	-1.280873351	2.64E-05	0.00020054
RASSF8-AS1	-1.282044222	2.33E-08	3.31E-07
RNF144A	-1.282726354	1.60E-10	3.10E-09
DHRS3	-1.283871107	5.82E-07	6.41E-06
MF12	-1.287395247	1.49E-16	6.18E-15
ATXN1	-1.289108294	6.22E-12	1.46E-10
KLF12	-1.290832771	7.55E-16	2.90E-14
PDZD2	-1.290840501	3.77E-07	4.33E-06
CLMN	-1.292820669	6.30E-06	5.66E-05
EYA4	-1.294025614	8.55E-15	2.88E-13
SRPX	-1.294530153	1.07E-30	1.64E-28
BIN3	-1.29565421	9.56E-26	9.66E-24
ARHGAP12	-1.298344515	2.24E-22	1.68E-20
RP11-66B24.	-1.299709105	5.15E-12	1.23E-10
LIMCH1	-1.300063454	8.53E-14	2.61E-12
SECTM1	-1.304681698	5.49E-05	0.00038479
MFAP2	-1.306608654	1.83E-17	8.21E-16
SLC25A45	-1.307376059	4.90E-09	7.81E-08
SPRY1	-1.308626675	8.46E-06	7.32E-05
PITPNC1	-1.30996918	7.96E-08	1.04E-06
KCNN4	-1.310672197	2.50E-27	3.00E-25
C16orf45	-1.31403995	1.47E-15	5.41E-14
AC007362.1	-1.32037854	2.54E-12	6.32E-11
CEND1	-1.322191699	7.10E-07	7.69E-06
ARRDC3	-1.323880467	4.33E-06	4.00E-05
KANK1	-1.327204092	1.22E-34	2.50E-32
FAM84B	-1.328228296	8.75E-34	1.72E-31
ZNF469	-1.336072161	1.91E-12	4.78E-11
CTD-2369P2.	-1.346225879	1.31E-09	2.27E-08
CYB5R2	-1.350650399	0.00044835	0.00239098
GAS1	-1.3540319	9.46E-07	1.00E-05
UGT8	-1.355398763	4.23E-19	2.23E-17
ATP2B4	-1.355629478	2.67E-18	1.33E-16
SLC22A18	-1.358950442	6.59E-11	1.36E-09
CD58	-1.359009729	2.43E-25	2.36E-23
TTLL1	-1.362614642	8.35E-08	1.08E-06
RP11-582J16	-1.362750241	1.53E-14	5.02E-13
TRPV4	-1.365625069	3.32E-22	2.45E-20
ARHGEF40	-1.366295001	4.18E-31	6.68E-29
TNFRSF9	-1.366757787	2.73E-05	0.00020676
TIGD4	-1.367378226	1.40E-07	1.74E-06
TNFRSF21	-1.367447536	1.97E-11	4.39E-10
PIANP	-1.370304385	1.14E-08	1.71E-07
COL6A1	-1.370527471	1.42E-10	2.78E-09
EDNRA	-1.372434429	0.00010703	0.00069086
TMEM47	-1.379388712	0.00169376	0.00752058
ISG20	-1.383853638	1.17E-18	5.96E-17
ATP6V0A4	-1.39152146	0.00074423	0.0037309
AMOTL1	-1.392614978	5.09E-27	6.03E-25
PXDN	-1.392958655	1.19E-18	6.03E-17
FAM86DP	-1.404389082	8.95E-20	5.15E-18

IL8	-1.405498611	0.00038584	0.00210186
PRSS12	-1.406933165	4.49E-26	4.77E-24
ABTB2	-1.407057444	7.41E-19	3.80E-17
TMTC2	-1.409653305	6.07E-11	1.27E-09
ST8SIA4	-1.410019549	1.89E-05	0.0001492
CCDC149	-1.41214378	7.20E-06	6.37E-05
PRRT2	-1.412676902	1.18E-08	1.76E-07
ERRFI1	-1.415945707	1.11E-13	3.32E-12
KLF9	-1.416746297	0.00182645	0.00800828
GRAMD1B	-1.418244117	8.82E-05	0.00058688
COL18A1	-1.425611548	2.51E-10	4.76E-09
CTNNBIP1	-1.427604103	3.29E-18	1.63E-16
RAB4B	-1.428023281	6.12E-16	2.39E-14
SEC14L2	-1.430847932	4.53E-18	2.21E-16
RCAN1	-1.43161897	2.68E-05	0.00020344
DNAH10OS	-1.431657998	3.36E-07	3.92E-06
FAM134B	-1.432673861	1.84E-05	0.00014568
PYROXD2	-1.441214464	1.61E-11	3.63E-10
KCNS3	-1.441471678	9.17E-07	9.75E-06
VAT1L	-1.448361342	0.00018515	0.00111392
SH2B3	-1.453563764	1.57E-21	1.09E-19
LINC00460	-1.455855124	7.83E-10	1.40E-08
IGSF3	-1.45803276	4.57E-26	4.83E-24
FAM20C	-1.460310572	5.15E-13	1.38E-11
RP4-758J24.5	-1.463683148	1.63E-08	2.38E-07
IL1RAP	-1.464916059	3.73E-07	4.29E-06
CTD-2207A17	-1.466863956	1.59E-06	1.60E-05
ST8SIA1	-1.471687985	0.00086016	0.00421457
SLC20A1	-1.472039336	2.91E-25	2.79E-23
AC079922.3	-1.477284505	9.14E-13	2.38E-11
MDGA1	-1.47807867	8.73E-07	9.31E-06
TANC2	-1.482484184	2.08E-20	1.28E-18
U73166.2	-1.482774659	2.64E-05	0.00020059
NPAS2	-1.484239907	2.04E-48	1.16E-45
SPOCK1	-1.487757688	1.53E-10	2.98E-09
EDNRB	-1.491076265	4.86E-13	1.31E-11
GPR56	-1.504154884	2.52E-23	2.04E-21
PCDH18	-1.504242958	4.17E-10	7.70E-09
INHBA	-1.504400312	9.78E-07	1.03E-05
GRIK2	-1.504696751	1.76E-14	5.73E-13
CNTN3	-1.507147638	2.14E-09	3.59E-08
GLT8D2	-1.508572771	0.00023693	0.00137817
GNG7	-1.509076147	5.51E-08	7.34E-07
MAB21L1	-1.510939678	0.00021278	0.00125453
IL1A	-1.511305273	0.00080201	0.00397577
EGR2	-1.511880965	0.00090754	0.00441654
ANKH	-1.512927979	1.70E-33	3.18E-31
ADAM19	-1.515341	0.00010443	0.00067647
ARHGAP31	-1.516421244	6.60E-11	1.36E-09
C3orf70	-1.519109889	1.17E-07	1.46E-06
LINC00461	-1.525724073	2.16E-08	3.09E-07
EPHA7	-1.527898833	1.09E-16	4.60E-15
SPRY2	-1.530385187	1.25E-17	5.71E-16
ANO1-AS2	-1.530876789	8.09E-06	7.05E-05
SLC5A12	-1.535616583	8.96E-05	0.00059485
LINC00327	-1.53699587	1.85E-09	3.12E-08

DEPTOR	-1.542894602	4.44E-07	5.04E-06
CSPG4	-1.549922571	5.40E-18	2.60E-16
CNTNAP3B	-1.557828713	3.74E-09	6.04E-08
DLGAP1-AS2	-1.558385968	1.66E-08	2.42E-07
ZCCHC24	-1.558734664	2.09E-15	7.58E-14
SERPINA1	-1.558935301	4.48E-05	0.00032234
TXK	-1.561995738	1.72E-11	3.87E-10
MAF	-1.562279829	7.61E-11	1.55E-09
CBR3	-1.564701903	4.59E-13	1.24E-11
RAB9B	-1.569971865	1.12E-10	2.23E-09
BEND6	-1.570207486	6.13E-11	1.28E-09
RNF182	-1.570880412	9.50E-14	2.88E-12
CNIH2	-1.571863043	5.98E-19	3.11E-17
TRIM62	-1.575286946	6.27E-33	1.09E-30
ASAP3	-1.577830964	1.19E-06	1.23E-05
STX1A	-1.586025817	6.00E-10	1.09E-08
RLBP1	-1.597067314	9.04E-07	9.63E-06
DNM3	-1.598641786	8.70E-08	1.12E-06
IKZF2	-1.600636139	0.00127732	0.00592086
SYNM	-1.601740624	2.29E-08	3.26E-07
FGF12	-1.601898071	4.50E-13	1.22E-11
FZD7	-1.606141804	6.19E-14	1.93E-12
NRP1	-1.606566469	5.81E-14	1.82E-12
GBP2	-1.617573329	0.00039797	0.00215932
PAQR8	-1.623449901	1.57E-14	5.16E-13
ADAMTS3	-1.624375532	2.75E-16	1.11E-14
TMX4	-1.629573028	2.48E-31	4.04E-29
HEY1	-1.629787047	6.16E-07	6.75E-06
PRR7-AS1	-1.629877587	1.71E-15	6.26E-14
RELL1	-1.644428138	2.36E-15	8.51E-14
ETV1	-1.648084719	2.77E-25	2.67E-23
TRIB2	-1.648753904	1.81E-08	2.62E-07
CXCL1	-1.649449804	1.81E-08	2.61E-07
P2RX6	-1.649794725	5.03E-07	5.63E-06
LRAT	-1.653454727	2.33E-23	1.89E-21
NOX4	-1.653552805	6.24E-16	2.43E-14
NHSL1	-1.654556233	2.12E-44	9.18E-42
IL13RA2	-1.6549522	5.88E-58	5.38E-55
PDE4B	-1.655197273	1.11E-07	1.40E-06
LPCAT2	-1.657585016	3.62E-33	6.56E-31
TFAP2C	-1.659249367	2.88E-55	2.15E-52
GJB1	-1.659982988	1.98E-09	3.33E-08
COLEC12	-1.663603712	1.68E-06	1.68E-05
KIAA0040	-1.667589807	1.00E-08	1.52E-07
PPAPDC1A	-1.669057659	0.00050007	0.00261914
KIAA1217	-1.669183523	3.88E-33	6.96E-31
ARHGAP5-AS	-1.669520296	1.16E-11	2.64E-10
SLC26A4	-1.670784813	7.46E-05	0.00050633
AIM1	-1.679315636	5.52E-19	2.89E-17
PDK4	-1.67952479	3.79E-06	3.54E-05
LOXL4	-1.683867085	6.12E-06	5.52E-05
MMP17	-1.68751469	4.96E-21	3.27E-19
PCDH1	-1.689461354	4.14E-20	2.46E-18
PLEKHA4	-1.690779893	4.94E-13	1.33E-11
DACT1	-1.691739935	0.00083599	0.00410837
TSPAN13	-1.693651642	1.00E-20	6.37E-19

UNC5D	-1.695206593	5.24E-06	4.77E-05
BFSP1	-1.698768314	9.14E-05	0.00060365
TRIM2	-1.700646246	1.09E-20	6.91E-19
TRAF1	-1.700700506	1.49E-08	2.19E-07
TRIM9	-1.70278266	9.43E-05	0.00061972
KRCC1	-1.709180989	2.96E-19	1.61E-17
TMEM2	-1.720111396	4.50E-11	9.55E-10
LRP1B	-1.722522001	0.00087622	0.00428562
SETBP1	-1.72420276	8.05E-09	1.24E-07
SORCS1	-1.725363969	3.99E-07	4.58E-06
LPHN3	-1.726769307	8.27E-08	1.07E-06
VGF	-1.729748972	1.56E-17	7.06E-16
SCG2	-1.731308768	3.66E-25	3.49E-23
AIM2	-1.73154144	1.17E-15	4.41E-14
GLDCP1	-1.734920051	1.84E-05	0.0001453
CD109	-1.737030199	2.69E-30	3.99E-28
MIR146A	-1.739406894	2.53E-05	0.00019382
FXYD3	-1.743511496	0.00197636	0.00857429
ST3GAL5	-1.748344901	1.17E-16	4.91E-15
PHEX	-1.749351412	0.00016789	0.00102015
RP13-735L24	-1.7496417	7.82E-15	2.65E-13
SHROOM4	-1.752372177	1.06E-19	6.03E-18
PDGFRA	-1.755896213	1.09E-07	1.38E-06
LOXL3	-1.758303441	3.80E-23	3.02E-21
LINC01059	-1.758525593	0.00145861	0.00661556
ITGA6	-1.758557903	9.45E-61	1.04E-57
RP11-59D5	-1.763246993	2.36E-20	1.44E-18
PCSK1	-1.763733348	0.00082673	0.00407135
S100A1	-1.765020768	7.09E-11	1.45E-09
RP11-93B14	-1.770448064	4.87E-11	1.03E-09
FBXO32	-1.772196209	6.09E-29	8.22E-27
RFTN2	-1.77467352	5.10E-05	0.00036057
MAML3	-1.776309184	3.25E-44	1.34E-41
FRMPD4	-1.776902309	2.81E-06	2.70E-05
LINC00473	-1.780541742	1.04E-15	3.92E-14
RP11-726G1	-1.781291927	6.27E-12	1.46E-10
AMOT	-1.78152471	7.10E-25	6.57E-23
AATK	-1.783674949	9.08E-05	0.00060047
RIPK4	-1.785468758	1.28E-21	9.11E-20
GPR153	-1.786141963	2.39E-18	1.21E-16
SNTB1	-1.788910354	2.42E-07	2.89E-06
NR4A2	-1.790984214	3.16E-09	5.15E-08
B3GAT1	-1.792317574	3.09E-10	5.83E-09
FAM19A2	-1.7936857	7.22E-06	6.37E-05
SLC1A1	-1.796424125	5.71E-24	4.92E-22
ADAMTS15	-1.798060291	9.56E-07	1.01E-05
OLFML2A	-1.799730587	0.00011262	0.00072158
ERO1LB	-1.802121986	3.74E-20	2.24E-18
MSC	-1.802859692	2.61E-07	3.09E-06
C10orf90	-1.802865458	1.22E-09	2.12E-08
LRIG3	-1.804312538	8.17E-15	2.76E-13
ISLR	-1.80479786	3.71E-05	0.00027182
CIITA	-1.81004833	2.48E-09	4.10E-08
ALDH1A3	-1.810533749	3.31E-62	3.93E-59
LONRF2	-1.810979451	1.27E-12	3.26E-11
EYS	-1.813795906	6.58E-18	3.13E-16

THBS2	-1.815955304	5.32E-13	1.42E-11
NTSR1	-1.818305363	3.00E-16	1.21E-14
PYGB	-1.820261896	1.01E-39	3.08E-37
STRA6	-1.821303468	5.99E-21	3.85E-19
C15orf48	-1.825088367	0.00210001	0.00901617
LRRK2	-1.828085053	1.08E-13	3.23E-12
PFKFB4	-1.832656304	1.23E-10	2.45E-09
BRINP2	-1.836356018	0.00025517	0.00146514
SOX6	-1.838784338	5.91E-13	1.56E-11
AGPAT9	-1.843906135	2.59E-15	9.28E-14
FOLH1	-1.847407827	1.44E-08	2.13E-07
MANSC1	-1.849122808	1.51E-46	7.55E-44
EPHA4	-1.856516337	3.44E-11	7.40E-10
NES	-1.857837405	2.41E-16	9.79E-15
DMRT2	-1.861687168	1.32E-13	3.89E-12
SHC4	-1.865029497	1.16E-10	2.31E-09
SVIL	-1.867812129	5.61E-42	2.01E-39
TMEM229B	-1.868898987	1.35E-16	5.65E-15
NLGN1	-1.877715948	7.11E-18	3.37E-16
AC020907.1	-1.878629959	2.14E-06	2.10E-05
MRGPRX4	-1.882935376	1.83E-06	1.82E-05
JAG1	-1.88563035	0.00018106	0.00109054
CD74	-1.888982617	7.25E-18	3.42E-16
SIRPB1	-1.889339089	1.83E-16	7.54E-15
PLP1	-1.89993675	7.54E-05	0.00051116
BAMBI	-1.900955288	2.78E-21	1.88E-19
SLITRK6	-1.906328815	1.75E-09	2.97E-08
ITGA10	-1.906348982	3.16E-05	0.00023564
ARNT2	-1.907824182	8.60E-24	7.26E-22
HLA-DRB5	-1.921099339	3.57E-09	5.78E-08
PTGES	-1.921574373	1.34E-06	1.37E-05
FAM19A3	-1.921812626	8.97E-06	7.70E-05
CHST6	-1.929756126	1.08E-12	2.79E-11
SERPINE2	-1.933037478	2.71E-11	5.91E-10
ITGB8	-1.935598781	3.21E-17	1.40E-15
PLA2G7	-1.938930527	6.16E-11	1.28E-09
FREM2	-1.94655965	3.31E-21	2.23E-19
COL9A2	-1.966755011	1.20E-16	5.01E-15
RNF150	-1.97168217	5.34E-11	1.12E-09
CXCL3	-1.974904317	5.05E-09	8.03E-08
TRPM8	-1.975645769	0.00031771	0.00178077
ABHD17C	-1.98001446	1.22E-28	1.64E-26
CTHRC1	-1.980111787	1.30E-19	7.30E-18
NREP	-1.985592846	6.94E-26	7.10E-24
INPP5F	-1.987561808	1.20E-47	6.36E-45
TIMP3	-1.991218279	1.82E-46	8.81E-44
CYP27C1	-1.991473077	1.54E-13	4.50E-12
CD200	-1.997431055	1.22E-05	0.00010156
FGF13	-2.001336811	4.64E-16	1.84E-14
FZD1	-2.004955037	1.50E-40	4.83E-38
LINC01060	-2.006515644	7.00E-16	2.70E-14
LINC00511	-2.00751653	1.85E-19	1.03E-17
KIAA1199	-2.010230015	2.79E-05	0.0002104
ITGA1	-2.017864685	6.24E-12	1.46E-10
MUC5B	-2.021703634	8.68E-16	3.30E-14
RP11-599J14	-2.021775885	2.86E-18	1.43E-16

RHOJ	-2.035250017	1.64E-08	2.39E-07
GSN	-2.037670486	1.36E-07	1.69E-06
RP11-472N13	-2.041212892	2.89E-08	4.05E-07
PTN	-2.042260294	1.25E-22	9.46E-21
TMPRSS5	-2.052192358	1.07E-20	6.77E-19
SHROOM2	-2.061508802	4.21E-34	8.45E-32
RP11-390P2.	-2.062213608	6.01E-14	1.87E-12
SDC3	-2.064081957	1.11E-09	1.95E-08
PRSS33	-2.072616831	1.43E-05	0.00011559
AC145436.1	-2.087050461	5.15E-10	9.40E-09
SERPINF1	-2.09023766	0.00230687	0.00974137
IL18R1	-2.097165393	1.73E-05	0.0001373
GLDC	-2.099955895	1.58E-10	3.07E-09
GNG2	-2.103581173	1.43E-44	6.39E-42
OPRD1	-2.104044152	5.26E-12	1.25E-10
STARD4-AS1	-2.108352018	3.16E-15	1.12E-13
SOX10	-2.112284703	1.49E-39	4.40E-37
RP11-34A14.	-2.1209423	1.24E-05	0.00010281
RP4-718J7.4	-2.121467927	2.37E-09	3.93E-08
LINGO2	-2.121986282	2.61E-18	1.31E-16
SOBP	-2.131320383	2.94E-26	3.19E-24
CPN1	-2.137310035	1.33E-10	2.61E-09
FLT1	-2.147749463	6.68E-09	1.04E-07
ANO1	-2.164135129	1.52E-30	2.28E-28
CDH19	-2.16641223	8.80E-11	1.78E-09
CAPS	-2.167627209	4.76E-20	2.81E-18
HEY2	-2.169428413	3.25E-05	0.00024123
LINC00326	-2.170546099	2.67E-20	1.62E-18
BCL2A1	-2.173280349	0.00013763	0.00085551
COL6A3	-2.180489652	0.0007415	0.00371945
FCGR2A	-2.181479651	6.67E-09	1.04E-07
SLC26A2	-2.187670868	1.69E-35	3.77E-33
WSCD1	-2.187705089	0.0001308	0.00081841
NRCAM	-2.192105387	2.40E-16	9.79E-15
TGFA	-2.202426875	1.01E-16	4.30E-15
SFRP1	-2.203077995	2.82E-43	1.08E-40
PMEPA1	-2.212418681	2.33E-05	0.00018014
CTC-529P8.1	-2.215247042	2.10E-16	8.66E-15
GAS7	-2.220709774	5.68E-12	1.34E-10
COL22A1	-2.224473487	0.00032322	0.00180623
AFAP1L2	-2.224617588	4.17E-10	7.70E-09
HIVEP3	-2.227234489	2.41E-73	6.61E-70
SLC24A3	-2.228492177	2.16E-09	3.61E-08
CHRM3	-2.24571852	1.04E-10	2.07E-09
CORO2B	-2.254623371	1.36E-21	9.59E-20
EXTL1	-2.26779066	1.16E-32	1.97E-30
ABCA10	-2.269698509	0.00114172	0.00538744
LYPD1	-2.27889099	2.26E-13	6.44E-12
SERPIND1	-2.280937381	9.16E-06	7.84E-05
ID4	-2.280987543	1.68E-05	0.00013392
S100B	-2.288348333	2.08E-13	5.95E-12
AGMO	-2.290850792	3.39E-06	3.20E-05
RAMP1	-2.291580167	6.57E-36	1.52E-33
AMACR	-2.298884455	1.51E-14	4.98E-13
ACAN	-2.301085433	2.55E-13	7.19E-12
EPHB3	-2.30376181	1.18E-20	7.40E-19

MIA	-2.305010276	7.19E-28	9.04E-26
RP11-399D6.	-2.314543627	1.85E-27	2.25E-25
PRRX1	-2.325751585	1.99E-11	4.41E-10
LSAMP	-2.337180761	6.31E-10	1.14E-08
ACPL2	-2.338261478	2.97E-22	2.22E-20
FZD8	-2.351071619	1.20E-13	3.59E-12
MGC4294	-2.352642562	9.90E-09	1.50E-07
PLEKHB1	-2.354834648	5.05E-16	1.99E-14
HTRA1	-2.367817353	4.94E-18	2.38E-16
SHISA2	-2.368339763	2.78E-07	3.28E-06
FAM65B	-2.371237698	1.24E-10	2.45E-09
CD96	-2.380899073	3.31E-24	2.93E-22
PART1	-2.390967245	5.42E-17	2.33E-15
MMP16	-2.406196164	3.34E-62	3.93E-59
CNTNAP3	-2.414984995	5.51E-26	5.75E-24
TNFRSF19	-2.419251209	9.15E-40	2.84E-37
CTD-2023N9.	-2.42086427	1.59E-08	2.32E-07
CHST1	-2.426748146	2.13E-23	1.75E-21
DNAH9	-2.443797386	2.09E-07	2.53E-06
COL9A3	-2.448185513	2.09E-53	1.38E-50
FLRT3	-2.457162521	1.36E-15	5.04E-14
VIT	-2.464075835	3.17E-05	0.00023631
SERPINA5	-2.473504114	1.12E-41	3.91E-39
FCRLA	-2.475860738	1.55E-29	2.20E-27
PTPRZ1	-2.480812826	9.92E-08	1.27E-06
B3GNT7	-2.492995824	7.18E-26	7.30E-24
SNED1	-2.495946866	1.29E-19	7.26E-18
SYTL5	-2.496238463	2.26E-21	1.55E-19
AC017104.6	-2.499187565	1.98E-24	1.79E-22
UCN2	-2.541785567	1.42E-13	4.17E-12
HR	-2.551818341	4.14E-64	6.20E-61
AL121578.2	-2.567063012	6.57E-14	2.03E-12
IGFBP5	-2.573225123	1.64E-05	0.00013116
GRM8	-2.576404935	2.03E-17	9.05E-16
SOX5	-2.5765761	1.95E-33	3.60E-31
EPHA3	-2.590877579	1.65E-33	3.13E-31
EGR3	-2.596800336	1.24E-17	5.71E-16
RP11-370B11	-2.63434927	2.38E-20	1.45E-18
LAMA4	-2.643069602	2.13E-59	2.20E-56
HES1	-2.65067795	4.75E-12	1.14E-10
FABP7	-2.653394261	3.16E-08	4.42E-07
CSGALNACT1	-2.67272024	5.54E-37	1.32E-34
SERPINA3	-2.673875227	2.26E-09	3.76E-08
SPRY4	-2.677006054	3.04E-22	2.26E-20
ITIH6	-2.678615155	1.33E-05	0.00010938
CDKN1C	-2.704260791	5.87E-27	6.86E-25
RP11-277B15	-2.725820084	5.16E-07	5.75E-06
SOX5P	-2.733101222	1.17E-22	8.89E-21
ATOH8	-2.739329287	1.44E-13	4.23E-12
RP1-212P9.2	-2.74457678	3.67E-19	1.96E-17
NFATC2	-2.759091175	1.95E-07	2.37E-06
TESC	-2.763201687	4.26E-19	2.23E-17
ERBB3	-2.778704945	1.14E-39	3.40E-37
ENPP2	-2.795471997	6.91E-05	0.0004724
HILS1	-2.804607481	1.36E-15	5.04E-14
CTD-2023N9.	-2.829626425	1.23E-45	5.79E-43

COL15A1	-2.848038779	9.49E-05	0.0006229
ZP4	-2.849177585	1.53E-10	2.99E-09
CHRD1	-2.856743257	8.21E-13	2.15E-11
PDE3A	-2.882450375	3.45E-15	1.22E-13
TFAP2B	-2.91486089	5.86E-08	7.77E-07
RXRG	-2.960655416	3.61E-05	0.00026522
COL19A1	-2.974268578	5.03E-21	3.30E-19
ARPP21	-3.010876131	9.78E-30	1.41E-27
ITGA9	-3.014858709	1.40E-06	1.42E-05
PKNOX2	-3.031950179	1.58E-15	5.82E-14
ITGB3	-3.173822451	1.11E-100	1.83E-96
APOD	-3.1899115	7.77E-08	1.01E-06
RP11-408N14	-3.200162298	4.47E-24	3.90E-22
ART3	-3.23083861	3.02E-40	9.57E-38
ITIH5	-3.252141131	9.83E-05	0.00064232
TNC	-3.376372547	1.22E-76	4.01E-73
EYA1	-3.42608129	1.08E-30	1.65E-28
HMCN1	-3.428972573	3.51E-11	7.54E-10
SOD3	-3.449552178	1.02E-08	1.53E-07
NPPC	-3.50025496	5.11E-08	6.86E-07
HPN-AS1	-3.514370088	3.91E-15	1.37E-13
SLC24A2	-3.600536498	5.35E-07	5.95E-06
ABCA6	-3.618578981	1.55E-05	0.00012445
MGP	-4.684127849	1.48E-05	0.00011993

Table S8. NEDD4L, WWTR1 and EGFR expression across cell lines.

Expression values of NEDD4L, WWTR1 and EGFR in a panel of cancer cell lines. Gene expression values were measured by U219 microarray.

Cell line	NEDD4L	WWTR1	EGFR
PL-21	2.29175	3.14747	3.08188
A204	2.46693	9.76958	2.96693
MC116	2.54269	2.55284	3.18262
Ramos-2G6-4C10	2.5779	2.53478	6.63972
G-402	2.63731	8.01423	3.04396
KARPAS-231	2.64618	2.80359	3.21789
H-EMC-SS	2.71171	5.84024	2.94718
HL-60	2.72787	2.70074	3.14476
MONO-MAC-6	2.7746	2.7232	2.84806
OCI-LY-19	2.79175	2.67394	3.40683
G-401	2.82343	5.83319	3.16732
EoL-1-cell	2.85012	3.06937	2.94594
L-363	2.86067	2.65865	3.25626
MV-4-11	2.86962	2.72333	3.0987
KCL-22	2.90695	4.18698	3.14445
OACM5-1	2.91929	6.46573	3.38265
MEC-1	2.93905	3.09251	3.3709
BV-173	2.98501	2.61102	3.16617
K052	3.05215	3.14375	2.8366
KYM-1	3.08404	8.43412	3.19788
MONO-MAC-1	3.12507	2.92721	2.94759
P12-ICHIKAWA	3.1771	3.19293	2.88247
MOLM-13	3.19557	2.68904	3.43888
OCI-AML5	3.2346	2.83405	3.14259
MOLT-13	3.24741	3.06261	3.23675
EM-2	3.29223	2.97651	2.86686
SW1573	3.29984	6.68208	7.41624
SU-DHL-8	3.31909	2.66084	3.04439
SU-DHL-10	3.36307	2.8242	3.2845
KOPN-8	3.37767	3.08347	3.3129
KY821	3.3792	2.65768	2.93901
NB12	3.38383	2.88889	3.18327
EW-7	3.38847	6.15968	4.29662
NCI-SNU-1	3.41904	3.67536	8.31838
CTV-1	3.43954	3.46741	3.15467
NCI-H661	3.4717	6.65515	5.65966
GI-1	3.52318	7.57045	5.1899
SK-N-FI	3.58173	2.90908	4.95306
TE-8	3.61225	7.64022	10.3142
MOLT-4	3.61819	2.84584	3.31428
THP-1	3.66676	3.36618	3.30791
YKG-1	3.67156	8.82111	6.07505
RS4-11	3.67658	2.5773	2.78862
PFSK-1	3.72409	7.38534	3.79638
MOLT-16	3.75874	3.09166	3.04515
SK-N-SH	3.79025	5.89253	5.55912
NBsusSR	3.81285	6.81668	3.2286
ML-2	3.85776	2.71967	3.15017
JEKO-1	3.87626	2.83461	3.11932
NB10	3.88277	2.71143	3.49471
MDA-MB-157	3.88394	8.39938	5.50282

CCRF-CEM	3.90922	2.44938	2.82998
DND-41	3.98335	2.62751	3.30207
SBC-3	3.98431	6.63784	3.50979
NCI-H28	3.99419	9.09851	8.68852
HARA	4.00568	7.33234	8.0758
LU-165	4.02867	3.06078	3.64416
ST486	4.03976	2.7282	2.78877
A172	4.0425	9.213	7.31012
VAL	4.05575	2.97463	2.95198
D-263MG	4.05821	6.78869	6.49302
OCI-AML2	4.12048	4.77586	4.40405
ES4	4.12296	6.23549	5.49444
U251	4.13378	8.91668	6.49193
RPMI-2650	4.15091	6.35833	2.8809
OPM-2	4.18273	2.87842	3.43432
NB69	4.22115	3.15014	7.30148
BT-549	4.24169	8.98339	7.63612
LAN-6	4.24752	2.85826	3.32244
D-502MG	4.2476	9.78209	5.65669
CHP-212	4.26475	6.53659	4.47928
SW962	4.27282	7.74197	7.549
KE-37	4.28375	2.75053	3.11442
AMO-1	4.30056	2.8729	3.35934
NU-DUL-1	4.30063	2.62976	2.96971
HOP-62	4.31282	8.01497	5.50918
NCI-H929	4.35669	3.64348	2.97655
HAL-01	4.36055	2.60411	2.61569
KMRC-20	4.36218	8.32604	8.8028
PF-382	4.36364	3.05208	3.23562
NCI-H1155	4.37014	2.57208	4.77053
JJN-3	4.38113	2.87475	3.44359
D-542MG	4.38948	7.38474	7.13914
NH-12	4.40022	5.6352	7.2398
MFE-280	4.4018	8.3614	5.03862
KP-4	4.43518	9.55462	5.21188
IST-MES1	4.44324	7.10899	9.01044
TUR	4.44622	2.74552	3.02749
BE2-M17	4.45599	3.08325	5.49529
H2804	4.46916	7.92369	8.5183
FADU	4.4786	6.43074	9.46033
COLO-678	4.48605	4.82674	8.50743
DK-MG	4.5243	8.96146	6.18631
NCI-H1563	4.52758	8.46215	8.49442
LC4-1	4.5293	3.07578	3.1732
ALL-PO	4.54368	3.07563	3.25777
SK-PN-DW	4.56308	5.74135	3.08068
HCC1569	4.59069	7.42777	3.46292
EFM-19	4.59083	6.85815	3.08339
CA46	4.59114	3.08209	3.08189
P30-OHK	4.59682	2.81926	3.78332
RH-1	4.60948	6.99193	3.75947
ES1	4.63581	6.39388	5.09958
NCI-H810	4.63804	2.64863	2.85083
HCC1937	4.65254	8.25699	7.19141
MHH-PREB-1	4.68175	2.91734	3.2699
P32-ISH	4.68332	2.88229	3.09492

KURAMOCHI	4.69273	8.39407	4.14552
KINGS-1	4.69955	9.86846	5.68036
CGTH-W-1	4.73972	8.32427	7.1593
A673	4.74203	7.71803	3.13048
SNB75	4.74622	8.49853	5.84854
A498	4.74833	7.13026	9.40476
EB-3	4.78485	2.95038	2.70046
EW-16	4.78671	6.06726	4.19937
A4-Fuk	4.79244	4.57474	3.01248
KELLY	4.83067	2.62696	6.37542
COLO-320	4.85323	7.77404	3.14818
H513	4.87835	6.8554	6.40164
J-RT3-T3-5	4.88431	2.55306	3.11966
REH	4.9001	2.42217	3.10732
SUP-T1	4.90423	3.01531	3.14032
BEN	4.90966	4.46975	3.54948
NCI-H196	4.9232	7.85755	7.01138
ES3	4.92354	4.7664	3.03392
D-336MG	4.92452	6.50463	5.99601
MMAC-SF	4.925	8.63661	3.58639
697	4.9361	3.75562	3.24559
KMRC-1	4.94316	9.1018	9.4841
HCC2157	4.94593	4.72114	4.16288
NB5	4.94605	6.32454	5.37258
SCC-3	4.95723	4.28656	2.95485
SW872	4.96772	8.98897	6.86514
KLE	4.97009	8.14805	5.99241
U-698-M	4.97389	3.04043	3.52197
LU-135	4.97659	2.55893	5.7856
BE-13	4.97897	2.80591	3.26343
SF539	4.98471	7.60296	6.04184
EC-GI-10	5.0105	6.57508	9.10897
HT-1197	5.0105	6.16083	8.88638
HeLa	5.01418	7.79611	6.08517
MG-63	5.01776	9.53436	6.39713
SNU-C2B	5.02725	7.1244	4.26119
ECC10	5.03612	2.40184	3.01966
NB14	5.03907	2.62423	4.13021
OSC-20	5.04084	6.51039	9.22686
COLO-320-HSR	5.05601	7.70817	2.82907
KNS-81-FD	5.07266	9.84247	6.18764
HCE-T	5.08053	6.36388	8.3841
SR	5.08602	3.02538	3.11115
MS-1	5.10893	6.70379	5.53786
KARPAS-620	5.12691	4.39789	3.19795
NOMO-1	5.13536	2.6546	2.79275
U-87-MG	5.15378	6.001	6.9932
T98G	5.16365	7.62437	7.60866
QIMR-WIL	5.16438	4.56544	2.99087
HeLaSF	5.16529	6.72412	6.37834
SNU-182	5.16771	6.59486	5.37347
NCI-H1651	5.17527	7.64164	6.74322
OVCAR-8	5.20582	6.20367	6.61121
NAMALWA	5.2167	2.71512	3.49143
OVCAR-4	5.21976	6.59668	8.57621
23132-87	5.22015	3.09578	4.35822

A253	5.2256	6.68796	9.52141
NCI-H1666	5.23906	6.9699	7.19487
NCI-H378	5.24534	2.76289	4.46161
BB49-HNC	5.24746	7.91625	6.1319
OVCAR-3	5.24991	7.51934	7.7836
NCI-H1623	5.25099	4.17032	6.65772
BC-1	5.25673	5.22867	3.0135
LNZTA3WT4	5.25827	9.23904	7.14863
HEL	5.2627	2.47175	2.89179
H2731	5.26884	7.50747	9.05592
EW-11	5.2747	2.7937	3.01558
EW-13	5.28209	4.32472	3.03632
LOUCY	5.2976	2.6898	3.34979
MRK-nu-1	5.29844	5.29774	3.21191
KNS-62	5.31131	7.43849	9.36684
PCI-6A	5.31248	6.22844	9.79409
RERF-GC-1B	5.31366	6.04707	9.34654
OCUB-M	5.32039	5.292	3.90137
ES8	5.3296	5.81778	5.53451
HOS	5.3392	7.49372	7.07811
WSU-NHL	5.34652	2.92175	2.82436
TCCSUP	5.37698	6.94573	7.01006
SiHa	5.38149	5.55585	6.85575
RERF-LC-MS	5.38155	8.2791	6.78074
PSN1	5.38275	9.04026	7.00509
D-392MG	5.39426	7.26899	6.0756
Ca9-22	5.39624	8.28727	10.7995
SUIT-2	5.40086	8.20236	8.40323
Becker	5.41718	8.23924	7.03194
WIL2-NS	5.41987	4.55662	3.16275
NCI-H1581	5.42393	4.92422	3.44919
JURL-MK1	5.42675	4.9151	2.6808
SNU-398	5.43158	6.05349	3.90346
PC-14	5.43982	7.41507	9.13002
DOHH-2	5.45129	2.68207	3.35024
OS-RC-2	5.46525	9.33599	9.76297
SUP-B15	5.46564	4.13493	3.36003
SNU-387	5.46807	8.91374	6.20876
ES5	5.46851	6.80381	3.24684
BT-20	5.50868	6.99045	10.1916
T-T	5.51056	7.13014	9.13496
SW837	5.51664	2.88468	6.53656
OVK-18	5.51981	8.51903	3.36716
EFM-192A	5.5293	5.8701	3.16134
HUTU-80	5.53253	5.74435	3.24836
EW-1	5.53428	6.47233	3.49532
KARPAS-422	5.54456	2.72735	2.99503
BFTC-905	5.54781	8.40233	8.90341
RH-41	5.54868	7.35466	4.00121
G-292-Clone-A141B1	5.55538	8.04635	8.01802
UMC-11	5.56006	2.85002	3.0813
KP-1N	5.57664	7.84552	7.74798
SJRH30	5.57989	7.49481	4.30875
HD-MY-Z	5.58042	9.35813	6.30322
SK-MM-2	5.58715	2.72137	3.16557
NB7	5.58921	6.39011	3.56709

SBC-1	5.58957	2.95922	3.42169
PE-CA-PJ15	5.59579	8.41695	7.91411
BHY	5.60181	7.19584	8.44688
GI-ME-N	5.60402	8.00317	7.86231
CAL-27	5.6124	6.62308	10.1814
SKM-1	5.61673	2.61425	2.75886
NCI-H3122	5.61756	6.57262	6.81077
A427	5.62146	6.3588	5.08734
AU565	5.62601	6.3237	7.9903
T84	5.63883	3.51897	7.30176
ECC12	5.65016	4.19944	2.81146
D-247MG	5.65467	8.37341	7.36559
HA7-RCC	5.65905	9.61235	8.67852
no-11	5.66044	8.38706	8.18232
ML-1	5.66897	7.05994	8.32865
KM-H2	5.6779	4.71383	3.45748
OAW-42	5.67863	8.01162	7.09008
KYSE-450	5.67931	7.09816	11.061
SBC-5	5.68117	2.53093	2.88345
SW13	5.69341	3.25798	3.20295
TE-1	5.6973	6.72062	8.34397
HGC-27	5.70376	6.10208	2.96515
NCI-H1092	5.71392	2.81803	3.05986
NCI-H841	5.71533	4.59537	7.30871
SW48	5.71669	4.20891	7.44937
TT2609-C02	5.71931	8.97808	7.28577
SK-NEP-1	5.7261	4.42518	2.96786
HCE-4	5.72713	7.2461	6.85643
NCI-H838	5.73288	7.98298	4.75851
LU-65	5.73851	9.74349	9.84195
I-9-2	5.7402	2.85495	3.62295
NALM-6	5.74752	2.73307	3.04507
PA-TU-8988T	5.7548	6.29048	8.86472
EW-22	5.76319	5.58403	3.1178
KYSE-70	5.77292	7.16682	9.56195
NCI-H2405	5.77486	8.34393	8.51049
EW-3	5.78173	4.73554	2.90329
Saos-2	5.78807	7.82526	5.73986
RKN	5.7886	7.85253	9.09782
COR-L88	5.80204	2.94448	3.33703
SW1990	5.80957	7.64419	7.99624
NTERA-S-cl-D1	5.81932	5.84412	4.19988
SK-OV-3	5.81977	6.75602	6.42783
IMR-5	5.82053	2.5251	4.93895
CAMA-1	5.82557	4.68743	3.23032
OCI-M1	5.82606	2.80531	3.08935
LAMA-84	5.82913	4.25023	3.1344
LS-123	5.83687	7.12854	7.81526
SW900	5.83692	8.23998	7.08875
ABC-1	5.83891	4.57672	9.01771
OE21	5.84455	6.32022	11.915
SNU-475	5.84462	7.69618	5.6343
TOV-112D	5.84662	7.11627	3.31006
GOTO	5.85333	2.58087	3.18937
NCI-H64	5.85605	3.0546	3.99295
KS-1	5.86523	8.26189	6.44079

TE-12	5.86776	6.44161	9.3965
HCC-15	5.87101	6.41733	7.00614
OACp4C	5.87309	6.04569	6.45099
KYSE-510	5.87489	5.95044	7.90173
A549	5.87886	8.61249	7.10468
CCK-81	5.88063	2.69999	4.87149
EN	5.88302	7.97789	3.16365
NCI-H1648	5.88599	7.36447	7.80803
NCC021	5.88751	8.92224	8.56289
SW684	5.89294	7.41317	5.85284
NCI-H2126	5.90892	4.85497	3.09406
PCI-15A	5.91545	7.18663	12.2089
NCI-H596	5.91623	7.05981	8.67262
H3255	5.9214	7.83414	11.4202
RD	5.92522	9.58012	6.39012
A2780	5.926	7.1155	4.34682
GAMG	5.93064	8.15308	8.98281
WM-115	5.93616	8.15921	8.26874
MFH-ino	5.9433	7.32546	7.30088
RT-112	5.94809	6.67088	8.16805
NCI-H2452	5.9613	7.57147	9.0994
SW1463	5.96276	2.79399	5.19226
SK-MEL-24	5.96353	9.28432	4.57151
ES7	5.96406	7.02696	3.48609
HT-1376	5.96822	7.24591	8.91936
HCT-116	5.9689	7.74398	6.29801
JEG-3	5.97213	6.02361	6.92064
NCI-H747	5.9753	6.13576	8.29484
MDST8	5.98046	7.85055	7.59859
EPLC-272H	5.98134	7.68971	8.24645
OVKATE	5.98456	7.97	8.88737
CAKI-1	5.99333	9.03007	8.34201
HCC1954	5.99697	6.27978	7.63363
RPMI-8226	6.0014	2.90755	3.72054
GA-10	6.00587	2.77701	2.83303
CAL-85-1	6.01376	7.77573	8.53613
CAPAN-1	6.01444	6.83701	6.67662
MCF7	6.01512	4.47626	3.00531
U-266	6.01594	2.5482	3.21925
KYSE-50	6.01709	7.05965	10.0711
CAL-39	6.01864	8.10311	7.72383
SU-DHL-1	6.03089	3.03037	3.10627
WM278	6.04124	10.6664	5.22566
OC-314	6.04153	8.1222	6.9802
ONS-76	6.04215	8.14964	7.58398
H2795	6.04695	7.17294	7.18745
WSU-DLCL2	6.05051	2.93654	3.05869
HCC1428	6.05198	6.86238	4.78574
DoTc2-4510	6.05676	7.66644	8.82908
COLO-680N	6.05921	6.64453	8.96541
MES-SA	6.06154	8.39511	3.16412
EW-24	6.07343	5.73538	3.22884
NCI-H520	6.0767	6.04229	3.16403
RH-18	6.08376	7.33177	6.50779
NCI-H1688	6.08515	5.43618	5.60108
NCI-H1944	6.08723	7.00062	5.53735

ChaGo-K-1	6.08736	6.31863	9.10108
LXF-289	6.08798	8.29143	8.5695
NCI-H1573	6.09658	6.22229	9.9264
SKN	6.09699	7.25769	7.19246
NCI-H740	6.10431	2.92152	3.40226
H3118	6.10779	8.45293	9.82657
KNS-42	6.11104	7.99448	3.94277
BHT-101	6.11735	8.10168	7.52453
NCI-H1299	6.11774	7.76498	6.32932
NCI-H209	6.12659	3.23397	4.24549
H2803	6.13719	8.04877	8.36295
EW-18	6.14287	5.19991	3.17045
TE-6	6.14395	8.6487	9.77706
ME-180	6.1443	7.85416	9.43498
HSC-3	6.14479	7.5271	10.2997
769-P	6.15124	9.73249	7.86166
SUP-B8	6.15138	2.99659	3.20607
JHH-6	6.15212	5.35336	8.18678
MEG-01	6.15555	4.44703	3.14892
HCC2218	6.15898	4.00502	6.17912
A388	6.16997	7.90866	11.1064
OVISE	6.17056	10.1091	8.75893
JHU-011	6.17178	6.43624	7.90499
CTB-1	6.17549	2.47833	3.00299
NCI-H2085	6.17738	7.34566	8.79045
MEC-2	6.17827	3.11051	3.22395
SW780	6.18029	6.15961	7.86847
SCC-15	6.18395	6.96235	9.64705
NCI-H522	6.19178	5.65124	2.98464
GCT	6.19311	7.3906	7.64721
U-118-MG	6.20143	8.15552	7.20175
LS-1034	6.20497	3.15591	4.51008
Calu-6	6.2072	9.58922	6.27162
HCC1500	6.20797	2.76959	3.52942
PC-3_[JPC-3]	6.21062	6.15865	9.05356
PCI-38	6.22054	7.61243	10.4373
IGROV-1	6.22424	8.58241	5.46431
HCC-56	6.22616	6.66912	4.83864
NCI-H2029	6.23539	3.23207	4.20703
H2722	6.243	8.14627	8.45025
T47D	6.24402	6.29811	5.00086
OV-90	6.25283	7.45794	5.11507
NB13	6.25364	2.75494	4.6602
TGBC11TKB	6.26141	5.54354	4.02511
RPMI-7951	6.26668	7.23284	7.02202
MKN1	6.26684	6.82154	7.03405
CL-11	6.28007	2.70852	7.47165
NCI-H835	6.28582	3.07439	3.00539
MFE-319	6.28582	6.11942	5.27536
SW620	6.29024	3.87248	3.15177
PCI-30	6.29846	6.43146	9.02884
Hs-766T	6.30006	6.37546	6.90691
HCC1187	6.30151	5.12829	6.63342
NCI-H1694	6.3035	2.50817	4.78869
WM-266-4	6.30536	8.48319	3.01344
SCC-4	6.30674	7.40238	10.4508

CHP-134	6.31048	2.55296	3.3412
OE33	6.31227	7.6766	8.17612
NCI-H2342	6.31676	7.00106	9.75984
LU-99A	6.32509	6.68	9.50909
RCC-MF	6.33546	8.64418	8.67728
NCI-H1755	6.33584	7.29904	6.69962
NCI-H2227	6.34162	2.86822	3.03444
LS-513	6.34342	2.57413	7.00787
OAW-28	6.34873	7.86434	7.20271
KALS-1	6.35826	7.71951	5.01585
DEL	6.36457	3.22404	3.11612
NCI-H1568	6.38701	6.22239	11.4626
RCM-1	6.38949	2.90263	6.37983
LU-134-A	6.39084	2.39606	3.17615
BB30-HNC	6.39335	6.63852	9.36668
T-24	6.39555	8.42309	7.68006
EMC-BAC-2	6.40758	8.68015	7.36242
ES-2	6.40814	6.04338	8.38473
ARH-77	6.4312	2.88253	3.47117
DMS-114	6.43492	5.16045	3.41544
DOK	6.43742	6.40429	11.7614
SW954	6.43783	7.96871	9.02009
BCPAP	6.44187	6.86331	7.67462
NMC-G1	6.44491	8.62825	8.4013
A101D	6.44575	9.85043	5.60378
OE19	6.45166	2.51379	6.80961
KYSE-410	6.46078	7.68888	8.27597
UACC-62	6.46571	10.5339	4.92297
NCI-H1355	6.46705	7.68804	6.41626
SK-ES-1	6.48238	5.65396	2.82005
TE-15	6.49583	7.62856	8.13079
CAL-120	6.50345	6.85677	8.00876
BOKU	6.51063	11.6518	7.61939
HDQ-P1	6.51689	7.3317	7.94311
C2BBe1	6.51936	7.43927	6.83505
DB	6.52037	3.00938	3.24372
NCI-H1963	6.53342	2.39816	3.10083
COLO-205	6.53632	4.702	5.58331
SKN-3	6.54839	6.35483	9.82087
VA-ES-BJ	6.54841	8.90604	7.08147
NCI-H23	6.54933	7.31702	5.84449
HH	6.55651	5.46887	3.13218
BPH-1	6.55924	7.0015	8.95723
SISO	6.56568	7.02231	8.50434
Daoy	6.56581	8.01003	7.25393
CAL-72	6.5663	6.50288	6.0464
A431	6.56883	7.62881	11.1723
NCI-H2228	6.56967	8.03896	8.52948
Hs-683	6.57368	7.48488	7.35251
KATOIII	6.57991	2.6564	6.23702
639-V	6.58169	8.43867	7.04036
OVMIU	6.58588	8.35354	7.87365
NCI-H1304	6.58937	2.89933	3.13748
LN-405	6.59282	7.65574	6.00121
IM-9	6.59616	3.68249	3.40642
MKN28	6.59816	4.88102	9.26521

YAPC	6.61703	8.80872	8.175
NCI-H358	6.61995	8.14634	6.12374
TE-5	6.62757	7.61224	9.51009
HCC1419	6.62873	4.96666	3.44802
TE-9	6.63029	7.25119	8.74673
OVCAR-5	6.63134	8.80474	8.36464
H2595	6.6368	7.9014	7.22068
YH-13	6.65237	8.82107	8.01683
LOU-NH91	6.65854	4.74913	9.1052
FU-OV-1	6.67133	7.58307	7.87348
BT-483	6.6795	3.91261	2.98145
HCC1806	6.68061	7.23256	9.03041
NCI-H1734	6.68105	6.9475	6.10234
PANC-10-05	6.68256	6.24651	8.51209
JHH-7	6.68759	5.47621	5.9312
NCI-H1993	6.68789	7.83168	7.18913
SN12C	6.68871	5.91429	8.27968
NCI-H647	6.68973	7.87521	5.28961
JHH-4	6.6908	9.02197	8.64762
HPAC	6.69742	7.09192	7.55941
H2869	6.70388	7.08723	8.09477
HN	6.71513	6.49417	9.26557
RC-K8	6.71749	3.20534	2.96765
HCC202	6.71803	4.96102	4.8024
NCI-H2444	6.71937	7.60735	8.62379
C-33-A	6.72159	4.7959	3.053
IST-SL2	6.72295	6.10604	4.83471
H2810	6.72538	6.25373	8.05211
SNU-449	6.72621	8.45293	8.1491
A375	6.72641	11.116	3.58785
CAL-33	6.7295	8.16634	10.497
L-1236	6.73079	6.43394	3.24532
OSC-19	6.73139	7.18735	9.33391
CAL-29	6.7365	8.37025	9.52144
KYSE-150	6.74924	6.19528	8.92779
NCI-H1395	6.74969	8.21479	6.23945
NCI-H322M	6.75034	6.49436	7.28031
KP-3	6.75894	8.09	8.32956
PA-1	6.7597	5.92814	3.8482
no-10	6.76126	7.44921	6.59983
42-MG-BA	6.76212	7.80571	7.96754
HSC-4	6.76477	7.55372	10.1719
SHP-77	6.76713	2.45328	6.79564
ZR-75-30	6.76997	5.28788	3.89638
CAL-78	6.77441	7.60568	4.85138
HCC2998	6.7852	2.97471	6.45844
JHH-2	6.78648	8.7858	8.34296
NCI-H727	6.78886	6.07407	7.8562
NCI-H2023	6.7964	7.63017	7.09997
RCC-AB	6.80067	9.27776	7.12022
HPAF-II	6.80826	6.41131	8.03045
TE-10	6.81307	7.83892	8.34394
M14	6.82792	8.56651	3.86145
TGBC24TKB	6.82995	3.51183	5.34895
NCI-H1915	6.84951	7.97284	6.78147
LB647-SCLC	6.84971	2.65954	2.96952

PL18	6.85045	7.90456	6.57121
SW1710	6.85573	8.82773	7.62284
SF126	6.85803	8.66301	7.30197
NB17	6.86187	2.7327	5.77513
H4	6.87734	7.37287	6.77383
UACC-893	6.87824	6.16309	7.15514
RCC-JW	6.88632	8.71828	9.04942
HT-115	6.89037	4.76546	5.85671
DAN-G	6.89885	9.24045	8.49277
HT-29	6.89987	2.60853	5.97077
ETK-1	6.90393	6.34668	8.11432
SW982	6.91062	8.57538	6.07235
SW1088	6.9109	7.63525	7.21327
CAS-1	6.91319	8.14881	5.43786
EMC-BAC-1	6.91484	7.11454	7.88769
IST-SL1	6.93685	3.74108	3.05453
HT-3	6.93937	5.84975	7.81318
NCI-H1793	6.94064	8.57462	6.69037
HCC-44	6.94461	7.09531	6.30246
NCI-H630	6.94527	3.23899	4.86226
NCI-H510A	6.94563	2.83713	3.89048
HCC-827	6.947	6.1163	10.0566
NCI-H1650	6.94895	7.39554	8.16808
KYSE-140	6.95006	6.23116	10.1254
U031	6.95574	7.96737	8.03781
LN-18	6.96289	5.63079	7.31959
EHEB	6.96326	4.22152	3.10797
RF-48	6.96445	4.25103	3.36329
HuO9	6.97409	7.51009	3.25646
LS-411N	6.97667	4.41599	6.08188
SCC-25	6.98009	6.98626	9.14915
MS751	6.98197	7.42418	9.98452
HCT-15	6.98377	4.38509	5.79304
H2461	6.98504	6.66096	9.1761
S-117	6.9938	6.52406	6.34228
TOV-21G	6.99664	7.37932	5.30101
AN3-CA	6.9994	7.13967	7.57215
IST-MEL1	7.00248	9.58076	5.93493
EB2	7.00301	3.00703	3.99624
NCI-SNU-16	7.00975	2.54275	6.8355
MDA-MB-361	7.02109	4.73915	4.15373
RKO	7.0247	6.91223	4.10275
ESO26	7.02702	5.439	6.24147
J82	7.03186	6.55433	6.36117
NCI-H187	7.03775	2.8129	3.36014
SCC-9	7.03989	6.79303	8.40028
SW948	7.04981	2.9643	6.35903
786-o	7.06584	7.73891	9.20224
LU-139	7.07255	2.91566	3.66463
RXF393	7.07266	8.89928	7.98856
NCI-H650	7.07425	7.97188	5.99996
NCI-H1975	7.08366	7.46717	7.56072
KOSC-2	7.08727	7.45041	9.55989
RMG-I	7.08832	8.10155	7.88603
MDA-MB-453	7.11053	4.44602	3.46733
RL	7.11395	2.55814	3.27241

SU-DHL-4	7.11914	2.95332	3.28524
MZ2-MEL	7.12857	10.7312	3.18317
JAR	7.12876	5.83638	6.78345
KYSE-520	7.13432	6.89454	12.2212
BICR78	7.13555	6.67256	9.34861
EFO-27	7.14428	7.03272	6.27845
647-V	7.15344	6.74686	8.54274
NCI-H2135	7.15471	8.10766	6.94659
SNU-423	7.15913	6.59627	6.63647
NCI-H1838	7.1606	6.74757	9.26529
DSH1	7.17281	3.46103	6.60434
GP5d	7.17456	4.32451	6.6775
HCC70	7.17553	7.55572	7.77452
NCI-H1869	7.18415	7.04378	7.17914
NCI-H2291	7.18711	7.07593	7.69875
SCH	7.19351	6.89681	7.23663
CPC-N	7.20407	5.8492	3.10559
Hs-633T	7.20839	7.86799	7.28398
GB-1	7.21014	7.29873	5.36547
CAL-54	7.23044	8.81778	9.43504
SKG-IIIa	7.23156	7.85663	7.56888
SK-UT-1	7.23829	7.1947	4.68555
HuH-7	7.2392	6.11998	8.41523
IM-95	7.24099	2.4541	6.40401
SF268	7.24581	4.55173	6.90245
NY	7.24726	6.44081	7.60553
LN-229	7.25234	9.54254	6.06343
CFPAC-1	7.25592	9.65191	7.7158
SW1116	7.2582	4.32313	7.25387
JHU-022	7.26	6.12304	7.37642
COLO-668	7.2621	4.3707	5.17182
Detroit562	7.27738	8.39898	9.88616
BICR22	7.29045	7.90959	8.9347
MFM-223	7.29687	6.71019	2.98584
NCI-H146	7.31763	2.75028	3.22856
H9	7.34026	3.13408	3.31969
HT55	7.34273	5.02868	5.63879
RPMI-8866	7.34426	2.36006	3.18678
HDLM-2	7.35397	4.78797	3.00348
Capan-2	7.35958	7.47496	7.52188
ESO51	7.37359	7.35636	6.00478
PANC-08-13	7.37617	8.46415	7.72122
ATN-1	7.3764	4.08203	2.97739
IHH-4	7.38702	7.35697	7.52167
NCI-H1792	7.39284	8.01114	7.55389
HCC-78	7.39286	7.43598	6.15221
COLO-824	7.40784	6.61505	5.76266
DG-75	7.40988	2.97486	2.9557
VCaP	7.41596	3.9071	5.01519
CAL-51	7.42142	8.45772	5.32267
EVSA-T	7.43	5.73966	4.18427
MKN7	7.43018	6.01617	7.419
NCI-H1048	7.44338	7.13187	7.2481
Ca-Ski	7.44997	5.17917	9.41067
KGN	7.45275	6.88941	8.30496
EKVX	7.45636	7.25247	7.56653

WM35	7.46126	9.71119	3.43283
HEC-1	7.46717	7.91315	6.54755
MPP-89	7.46737	8.03936	5.54188
PANC-03-27	7.47795	8.16984	8.17096
WM1552C	7.48394	8.32636	7.50685
SK-LMS-1	7.48769	9.06293	8.32452
NCI-H2009	7.4928	5.33257	5.08033
NCI-H526	7.49449	2.95297	2.9554
M059K	7.49716	7.79407	6.59717
KYSE-270	7.52352	8.54419	9.54786
LCLC-97TM1	7.52888	9.45026	8.18275
JVM-3	7.53213	2.75031	2.95262
C8166	7.53384	4.00271	3.47105
SK-LU-1	7.53837	6.46881	6.03435
NCI-H2347	7.57743	7.55113	7.38096
LS-180	7.57999	5.22845	7.16801
SK-MES-1	7.58012	8.17993	8.498
H290	7.59034	7.326	6.71407
NCI-H1781	7.6072	5.91866	6.31139
RERF-LC-Sq1	7.61221	7.29273	8.87593
COLO-684	7.61767	3.16443	2.74805
MZ1-PC	7.6284	7.32382	8.43244
SK-MG-1	7.63822	7.09673	7.04222
JHH-1	7.67177	10.1397	8.06302
COLO-792	7.67265	8.28091	3.28165
SAT	7.6794	6.04442	9.73127
AM-38	7.69065	5.34152	8.22171
H2369	7.69585	6.71648	8.83124
JiyoyeP-2003	7.70158	2.88561	3.15277
QGP-1	7.71006	3.22111	6.14681
JSC-1	7.71344	2.84071	3.12835
BALL-1	7.73452	2.60809	2.99984
LB2241-RCC	7.73815	8.82177	9.18531
201T	7.74144	7.83406	7.2053
GMS-10	7.74166	7.62097	7.24156
TE-11	7.76035	6.95182	9.09108
HuCCT1	7.76714	7.08992	9.10108
SLVL	7.78411	3.81656	3.20555
DU-4475	7.78934	2.50192	3.19442
HT-144	7.80437	10.2998	3.03779
OCUM-1	7.81221	6.33343	9.54516
FU97	7.82912	4.7289	6.67193
KON	7.83162	6.89001	8.8263
COLO-800	7.85215	9.55209	2.93196
HuP-T3	7.85244	7.67361	7.35548
SW1783	7.87508	6.02284	7.57884
H2591	7.8761	6.01161	8.31348
SW1417	7.90578	6.56752	8.07915
BB65-RCC	7.90598	8.21929	7.70675
HuP-T4	7.9236	6.42363	5.7123
RPMI-6666	7.94519	3.70862	3.00535
NCI-H441	7.96092	7.51324	7.25831
SK-MEL-1	7.96871	9.83174	3.47823
HO-1-N-1	7.99765	6.55597	8.88704
SCaBER	8.00648	7.54101	9.99952
NCI-H2052	8.01395	5.20625	7.27062

SAS	8.01697	6.58405	9.99697
COLO-679	8.03297	9.01601	2.94234
Hs746T	8.03794	7.06749	6.21223
NCI-H69	8.06651	2.76481	3.04721
NCI-H211	8.09329	2.78969	3.1231
IGR-1	8.10748	7.05833	3.04271
C3A	8.11634	7.02957	3.37738
EGI-1	8.13511	7.28743	7.36196
CRO-AP2	8.16418	2.82015	3.02159
DU-145	8.17604	7.07786	8.00041
Mewo	8.1882	7.44397	3.48765
HOP-92	8.23771	7.10246	7.77807
G-MEL	8.24189	7.66913	3.86564
MEL-JUSO	8.2648	9.68625	3.38982
SH-4	8.2836	9.88913	3.42613
IA-LM	8.29516	8.69623	8.6407
H2818	8.30025	6.4524	8.88633
NCI-H1703	8.30357	8.3519	6.90962
BT-474	8.31185	5.28139	5.60326
CP66-MEL	8.32333	10.2813	3.10287
5637	8.33373	5.57463	9.12172
GCIY	8.34806	8.39923	8.87534
GAK	8.35305	9.24208	3.84626
LCLC-103H	8.3614	6.21909	7.38795
EFO-21	8.36716	8.27209	6.09686
NCI-H82	8.3767	2.69141	2.91497
VM-CUB-1	8.37827	6.98025	8.30773
HLE	8.39955	7.67923	7.11844
SK-MEL-3	8.41362	7.54634	3.7036
C32	8.41979	8.87284	3.83382
8305C	8.43423	7.56793	9.31241
ASH-3	8.49397	6.56798	6.90605
COR-L105	8.49695	7.97371	9.08088
MDA-MB-231	8.553	6.27124	7.75613
DMS-79	8.56821	2.617	6.2535
MZ7-mel	8.57412	7.68197	3.20973
HTC-C3	8.588	6.98804	6.60085
RVH-421	8.6292	8.91381	3.55494
NCI-H2030	8.655	7.27525	7.35353
RT4	8.70732	5.73217	7.71938
451Lu	8.73591	8.74712	3.15106
CHL-1	8.7364	6.13536	3.65379
HT-1080	8.74479	9.04744	7.00548
IPC-298	8.76217	6.71894	3.01614
UM-UC-3	8.79107	8.15783	7.23648
Hs-944-T	8.79545	8.28207	3.2912
SK-MEL-5	8.79856	8.57057	3.67394
GT3TKB	8.80424	6.69426	8.95896
HMV-II	8.86767	9.42482	4.2442
SK-MEL-28	8.8855	9.47798	3.49545
A2058	8.91199	8.88747	3.53598
LOXIMVI	8.91679	7.22021	7.26013
Mo-T	8.95362	2.76117	3.15439
NCI-H1693	8.96045	4.20302	8.48689
DJM-1	8.97009	7.63068	8.75106
NUGC-3	9.0076	5.19675	8.62371

D-283MED	9.11192	7.08141	2.93053
SK-HEP-1	9.1143	6.62532	8.60087
H2373	9.11435	5.98409	7.89281
WM793B	9.12145	8.20376	7.19387
MEL-HO	9.14272	7.90761	3.03935
EBC-1	9.15328	8.23697	7.76145
RO82-W-1	9.19641	5.51826	5.15562
UACC-257	9.24477	8.20484	2.82874
G-361	9.27926	8.02832	3.72157
SK-MEL-30	9.32927	8.11061	3.45604
CaR-1	9.33483	8.47066	8.50633
IGR-37	9.56842	7.44125	4.01854
CESS	9.95113	4.46382	2.94334
COR-L23	10.0948	7.31989	8.04282

SUPPLEMENTARY METHODS

Transposon mutagenesis library construction and screen. To construct transposon mutagenesis libraries, cells were seeded in ten T175 culture flasks at cell density of 2.5×10^6 cells per flask. After 24-hour incubation, each flask was transfected with 12 μ g pPB-SB-CMV-puro-SD, 12 μ g transposase plasmid pCMV-hyPBase, 48 μ l X-tremeGENE 9 DNA transfection reagent (Roche) and 1.5 ml OPTI-MEM (Thermo Fisher Scientific). After three days, cells were selected using 2 μ g/ml puromycin with medium refreshment every 4 days and cryo-preserved after 8 days of treatment. To screen for survivors of PLX4720 treatment, 3×10^6 cells from each library was plated on a 15 cm tissue culture dish, and treated with 10 μ M PLX4720 for three weeks, with fresh medium and drug replacement twice a week. A control dish seeded with the same number of untransfected parental cells was treated in parallel to monitor selection. After this screen, 30-50 colonies emerged from each library while no colonies were found on the control plate. Clearly isolated founder colonies were randomly picked from screening plates using cloning discs (Sigma-Aldrich) and remaining cells were then trypsinized and expanded to $2\text{--}10 \times 10^6$ cells for each resistant pool. Additional colonies were collected by seeding a pool of resistant cells on 96-well culture plates at 0.5 cells per well.

PCR and sequencing for insert site identification. Genomic DNA was prepared using Qiagen DNeasy Blood & Tissue kit. 170 ng of genomic DNA was digested using 2 units of Csp6I in 15 μ l reaction at 37°C for 2 hours, followed by 65°C heat inactivation for 20 minutes, then ligated to 10 picomole indexed adapters with 100 units of T4 DNA ligase in 20 μ l reaction at 16°C overnight. Double-stranded adapters were generated by annealing two sets of oligonucleotides (GTAATACGACTCACTATAGGGCACGCGTGGTTCGACTGCGCATDDDDDDDC and TAGUUUUUUATGCGCAGTTTTTTTGCAAAAA) whereas DDDDDD and UUUUUU denote complementary nucleotides for sample indexing [1]. Genomic DNA flanking the insert was amplified by two rounds of PCRs, with the first round in a 50 μ l reaction with primers GTAATACGACTCACTATAGGGCACG and CGCTATTTAGAAAGAGAGAGCAATATTTC respectively matching the adapters and the PB 5'-LTR, and with 0.2 μ l PlatinumTaq DNA polymerase. Thermo-cycling conditions were 94°C/3'; 10 cycles of 94°C/15", 72°C/30" with -1°C/cycle touchdown, 72°C/1'; 20 cycles of 94°C/15", 62°C/30", 72°C/1'; followed by 72°C/2' extension. Second PCR was performed in a

10 µl reaction with 0.2 µl of first-round PCR product input and nested primers AATGATACGGCGACCACCGACACTCTactatagggcacgcgtggt and CAAGCAGAAGACGGCATAACGAGCTCTTCagaatgcatgcgtcaattttacgcagac whereas uppercases matched Illumina P5 and P7 adapters and lowercases matched the first round of amplicons. Indexed PCR products were pooled, purified using Qiagen PCR purification columns and diluted to 2.5 ng/µl for Illumina sequencing. Up to 10 samples from resistant pools or 96 samples from clones were combined to be sequenced in a single channel. Sequencing was performed for single-end 50-cycle reactions (SR50) with custom sequencing primer ACTATAGGGCACGCGTGGTCGACTGCGCAT, following standard protocol except that sample loading density was reduced by half to avoid over-clustering.

Lentiviral cDNA plasmid construction. ORF (open reading frame) entry clones of *TRPS1* (HsCD00365530), *ESRRG* (HsCD00296449), *BRAF* (HsCD00379096), *ARHGEF28* (HsCD00295151), *YES1* (HsCD00376153), *DCN* (HsCD00044608), *WWTR1* (HsCD00045395), *RAPGEF6* (HsCD00379344), *USP25* (HsCD00372810), *SOX5* (HsCD00000303), *EYA1* (HsCD00376948), *NEDD4L*-dWW2 (HsCD00045367), *POU2F1* (HsCD00365256), *ZFHX3* (HsCD00365522), and *AKAP13* (HsCD00399180) were obtained from DF/HCC DNA Resource Core (<http://horfdb.dfci.harvard.edu/index.php?page=home>), and subcloned to lentiviral vectors pLENTI6.2/V5-DEST (Thermo Fisher Scientific) and pLENTI-puromycin (Addgene #39481) using Gateway L/R cloning. Both ends of the ORFs in the destination plasmids were verified by Sanger sequencing. cDNA plasmids of *NEDD4L*-WT (#27000), DD (#27001), SASA (#27003), S382A (#27036), and S468A (#27037) were obtained from Addgene [2]. *NEDD4L* ORFs were PCR-amplified using primers CACCATGGATTATCCGTATGATGTTC and TTAATCCACCCCTTCAAATCCTTG, subcloned to the entry vector pENTR/SD/D-TOPO (Thermo Fisher Scientific), and then to lentiviral vectors using Gateway L/R cloning. Full sequences of *NEDD4L* ORFs in lentiviral vectors were verified by sequencing. *ABCB1* plasmid purchased from Origene was amplified with primers CACCATGGATCTTGAAGGGGACCG and TCACTGGCGCTTTGTTCCAG and similarly subcloned to pENTR/SD/D-TOPO and then to lentiviral vectors.

Cellular assays. For short-term viability assays, cells were seeded in 96-well plates at 1250 cells per well in 100 µl growth media one day before treatment with 11-point/2-fold dilution series of compounds and assayed by adding 50 µl/well CellTiter-Glo (Promega) 5 days post treatment.

For apoptosis assays, caspase 3/7 (Promega) was added 24 hours after drug treatment, and signal was normalized to untreated cells. For cell growth assays, cells were plated at 1250 cells per well in 96-well plates, treated by compound one day after seeding, and assayed by CellTiter-Glo every day. For clonogenic assays, cells were plated at low density in clear 6-well or 96-well plates and drug-treated for 14 days, then were either stained with 1% Methylene Blue in 70% ethanol for 30 minutes or fixed with 12% glutaraldehyde for ten minutes then stained with 0.1% Crystal Violet for 30 minutes.

qPCR. Total RNA was prepared using Qiagen RNeasy mini kit and reverse-transcribed using iScript Supermix (Biorad) in 20 µl reactions. Quantitative PCR was performed with iTaq Universal SYBR Green Supermix using the Roche LightCycler LC480 system. Primers for each gene are listed below:

TRPS1: AGCCCCAGTAAGGGAGGAAA; GGGTGCAGGCCATATCTTGAG.

ESRRG: GCCCTCACTACACTGTGTGAC; CCTGCTAATTTGGACTGGTCTT.

BRAF: AATACACCAGCAAGCTAGATGC; AATCAGTTCCGTTCCCCAGAG.

ARHGEF28: AGGTGATGAAGTCTACGCTAACT; AGTGGCAGTGATTCCCTCTAT.

YES1: GCCTGTCAGTACAAGTGTGAG; AAAGGCGTTACCCCTGAGGAT.

DCN: ATGAAGGCCACTATCATCCTCC; GTCGCGGTCATCAGGAAGTT.

WWTR1: GATCCTGCCGGAGTCTTTCTT; CACGTCGTAGGACTGCTGG.

RAPGEF6: CAGGCGTTGAGGAAGAAGC; TCTGGCAATCGTTTCTGAACAA.

USP25: GCACCAGCAGACGTTTTTGA; AGCATTCTTCGCAGTAAGGAAA.

SOX5: CAGCCAGAGTTAGCACAATAGG; CTGTTGTTCCCGTCGGAGTT.

EYAI: CACCACAGATTTACCCTTCCAAC; GTACGTGGCATAGGCTGTAGC.

NEDD4L: GACATGGAGCATGGATGGGAA; GTTCGGCCTAAATTGTCCACT.

POU2F1: ATGAACAATCCGTCAGAAACCAG; GATGGAGATGTCCAAGGAAAGC.

ZFHX3: CAAGTTCACGACGGACAACCT; GCTTGCACTGGTATGAGTCCC.

AKAP13: GTCAACGGGCACACTTTCAG; GGAGGCTAGACTTTCTCGGC.

siRNA transfection. For samples used in the immunoblotting assays, cells were suspended in growth media at 1×10^5 cells/ml, and 2 ml of cells were reverse-transfected with 100 nM siRNA, 20 µl Lipofectamine RNAiMax (Thermo Fisher), and 0.5 ml OPTI-MEM in 6-well culture plates. After 48 hours of transfection, cells were treated with inhibitors for an additional 48 hours and cell lysates were collected. For samples used for viability assays, 100 µl of cells were

transfected with 100 nM of siRNA, 0.2 μ l Lipofectamine RNAiMax, and 25 μ l OPTI-MEM in 96-well microplates. After 24 hours, cells were treated with inhibitors for 72 hours before subjecting to CellTiter-Glo analysis.

Immunoblotting. Cultured cells were lysed on plates with cell lysis buffer (20 mM Tris, pH7.4, 150 mM NaCl, 1% Nonidet-P40 (Sigma-Aldrich), 1 mM EDTA, 1 mM EGTA, 10% glycerol), and quantified by Pierce BCA protein assay. Samples were balanced in NuPAGE LDS sample buffer (Thermo Fisher Scientific) and reducing agent, fractionated in 4-12% Bis-Tris SDS-PAGE gel, and transferred to polyvinylidene fluoride membranes. Samples were blocked with 5% non-fat milk and blotted in primary antibodies at 4°C overnight. Membranes were washed in TBST (50 mM Tris, pH7.6, 150 mM NaCl, 0.1% Tween 20) three times. Secondary antibodies were used at 1:20000 dilution followed by washing in TBST. Signals were detected using SuperSignal West Femto substrate (Thermo Fisher) and imaged with a G-box imager (Syngene). To re-probe, membranes were treated with stripping buffer (GM Biosciences) and then processed as above. Phospho-MEK (Ser217/221) (#9154), phospho-ERK (Thr202/204) (#9101), total ERK (#9102), phospho-AKT (Thr308) (#4056), phospho-AKT (Ser473) (#4060), phospho-S6K (Thr389) (#9205), phospho-S6 (Ser235/236) (#2211), phospho-4EBP (Thr37/46) (#2855), GAPDH (#2118), phospho-Gab1 (Tyr627) (#3233), phospho-IGF1R β (Tyr1135/1136) (#3024), TAZ (#2149), phospho-SMAD2/3 (#9510), total SMAD2/3 (#8685), TEAD1 (#8526), Phospho-YAP1 (Ser127) (#4911), BRAF (#9002), and YES1 (#3201) antibodies were purchased from Cell Signaling Technology. NEDD4L (ab46521), ESRRG (ab49129), POU2F1 (ab15112), and phospho-EGFR (Tyr1068) (ab5644) were from Abcam. Total GAB1 (sc-9049) and total EGFR (sc-03) were from Santa Cruz Biotechnology. Phospho-RSK (Thr359/Ser363) (04-419) was from Millipore. YAP antibody (#13584) was from Proteintech. Peroxidase-conjugated goat anti-rabbit IgG (#31460) and anti-mouse IgG (#31430) were from Thermo Scientific.

Permutation tests for STRING analysis. We performed significance tests (permutation tests) to test whether the null hypothesis (H_0 : there is no relationship between the two genesets) could be rejected. Permutation tests were set so that an equal number of random genes to the number of query screen genes were drawn from the query library and projected to the object geneset with the same STRING criteria used to test connections between hit lists. The direction of STRING analysis from queries to objects are indicated as arrows in corresponding graphs. Random draw was performed using the initial libraries corresponding to: 169 genes out of 14,457 candidate

genes for the ORF screen[3], 31 genes out of 16,601 for the shRNA screen[4], 263 genes out of 18,080 for the CRISPR screen[5], and 186 out of 23,430 candidates for the dCAS9 library[6]. The number of permutations varied between 10^5 and 10^6 to confer statistical power. STRING and permutation tests were also performed between screened genesets and a set of MAPK pathway components (GRB2, SOS1, KRAS, NRAS, BRAF, CRAF, MEK, ERK, S6K, RSK, CREB1, FOS, JUN), with the above library background for each screen geneset plus all RefSeq genes as the library background for the transposon geneset. These analyses were run using scripts written both in R and Matlab (for random permutations, the built-in ‘randperm’ Matlab function was used). p-values were calculated as the number of random instances reaching the connectivity level vs. total permutations.

Patient samples. Patients with metastatic melanoma containing BRAF^{V600E} mutation enrolled on clinical trials for treatment with a BRAF inhibitor vemurafenib or combined BRAF + MEK inhibitor (dabrafenib + trametinib or LGX818 + MEK162) were reported previously [7]. Tumor biopsies were performed pre-treatment (day 0), at 10-14 days on treatment, and/or at time of progression if applicable. Formalin-fixed tissue was analyzed to confirm that viable tumor was present via hematoxylin and eosin (H&E) staining. Additional tissue was snap-frozen and stored in liquid nitrogen or was immediately processed for purification of RNA. To assess therapy response, patients underwent computed tomography every 3 months. Responses were determined according to the Response Evaluation Criteria in Solid Tumors (RECIST), version 1.1. Samples were homogenized and disrupted using a mortar and pestle followed by use of a QIAshredder (Qiagen). A QIAcube was used to harvest RNA using the RNeasy Mini Protocol (Qiagen). Starting with about 700 ng of total RNA, poly-A containing mRNA molecules were converted into libraries suitable for next generation sequencing approaches using reagents and the protocol provided by Illumina TruSeq RNA Sample Prep Kit v2, and sequenced paired-end 2x75 bp using HiSeq 2000.

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4. Whittaker, S.R., et al., *A genome-scale RNA interference screen implicates NF1 loss in resistance to RAF inhibition*. Cancer Discov, 2013. **3**(3): p. 350-62.
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6. Konermann, S., et al., *Genome-scale transcriptional activation by an engineered CRISPR-Cas9 complex*. Nature, 2015. **517**(7536): p. 583-8.
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SUPPLEMENTARY TEXT

>pPB-SB-CMV-puro plasmid with degenerate 5 bp barcodes 7101 bp

ATTGCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCC
TGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTGCGCCAGCTGGCGTAATAGCGAAGAGGCC
CGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGGACGCGCCCTGTAGCGGCGCAT
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TCATCGTCTAAAGAACTACCCATTTTATTATATATTAGTCACGATATCTATAACAAGAAAATATATATAT
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CGCTATTTAGAAAGAGAGCAATATTTCAAGAATGCATGCGTCAATTTTACGCAGACTATNNNNNTAGG
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Figure 3D original

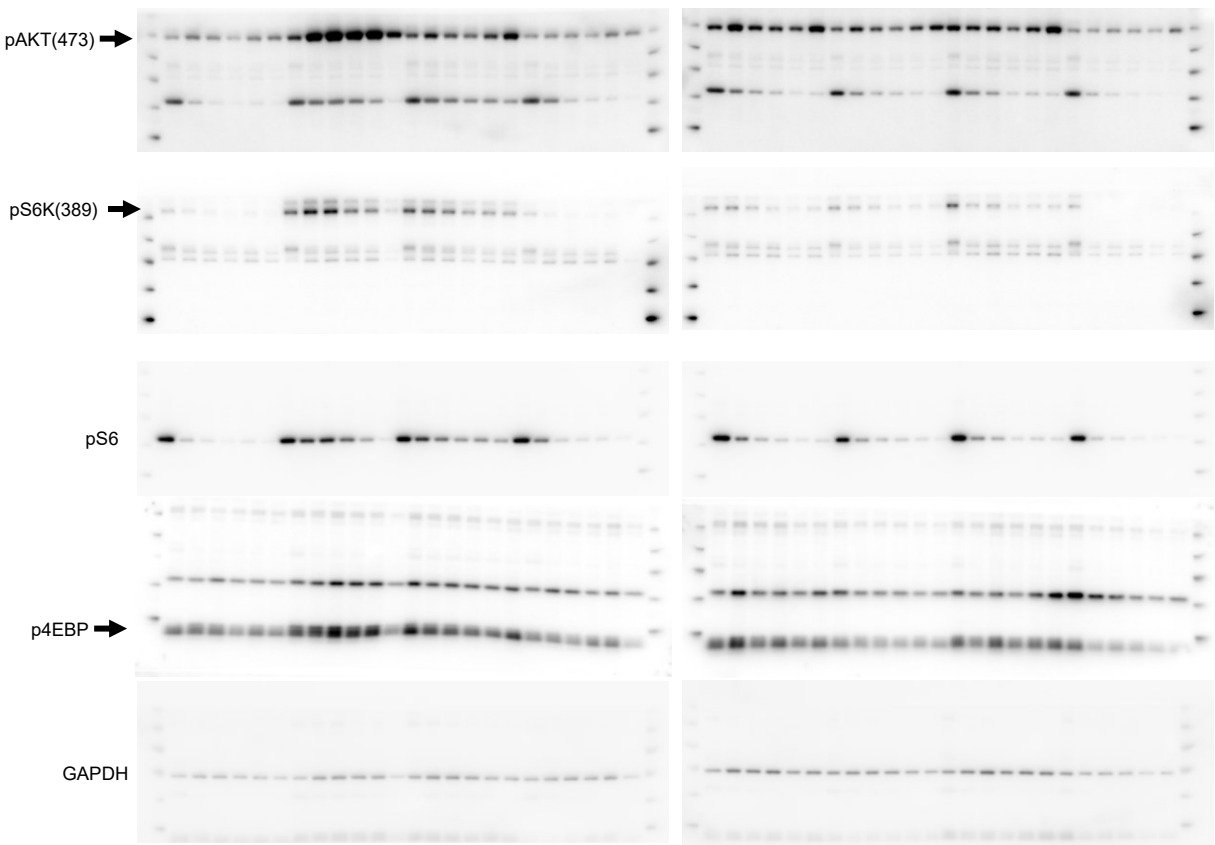
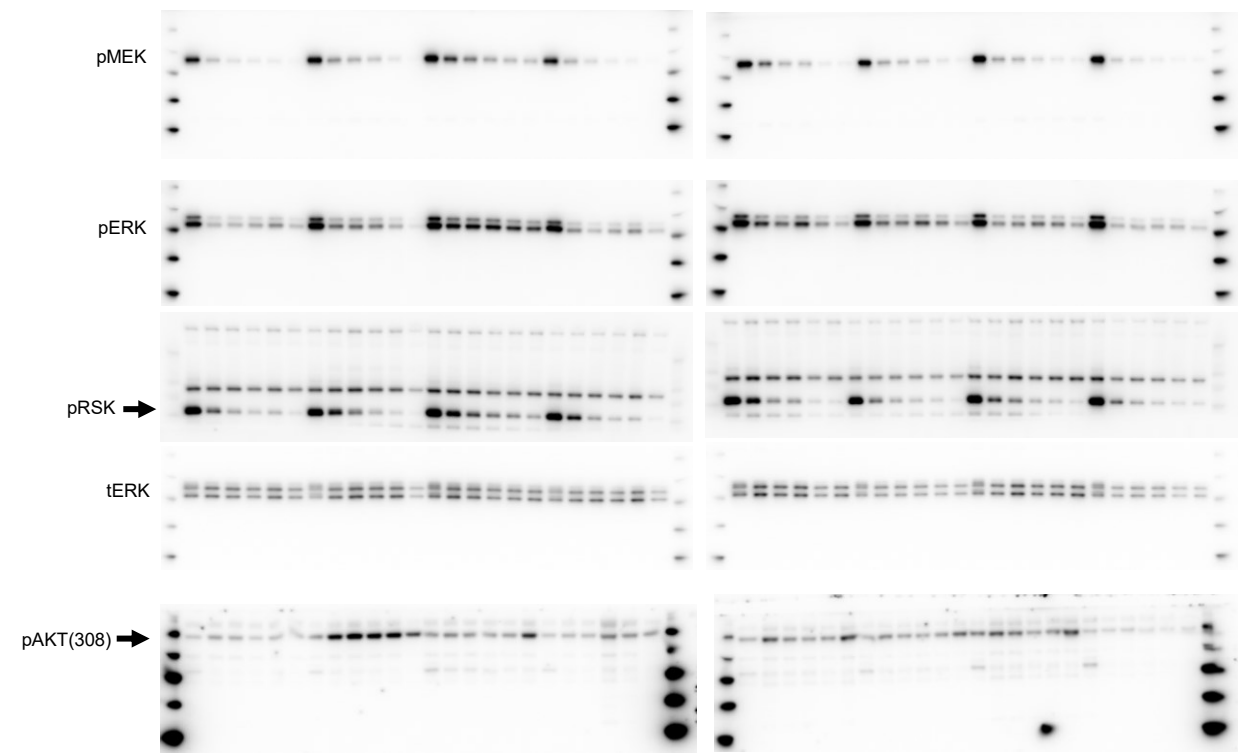
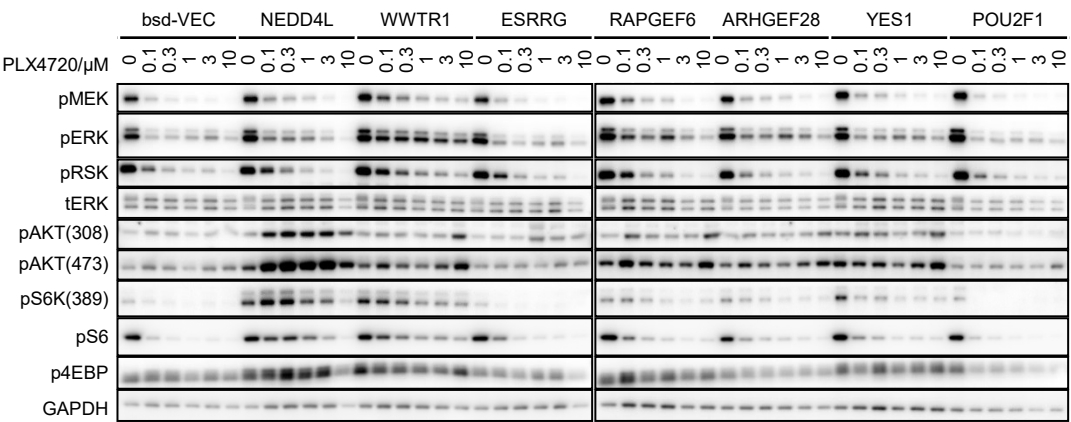


Figure 4B original

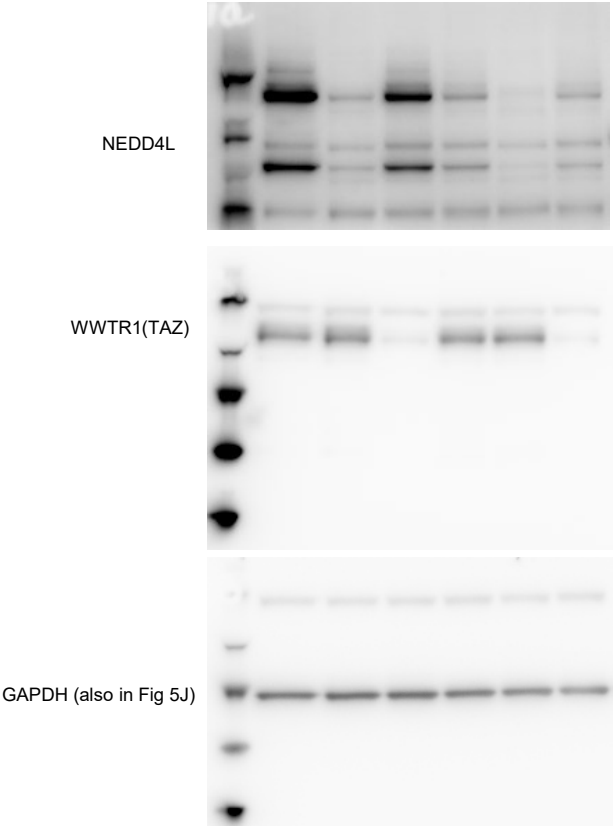
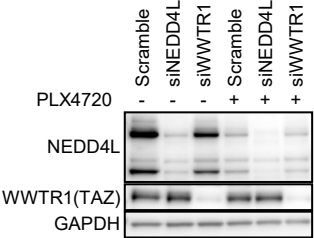
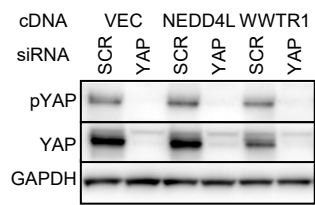
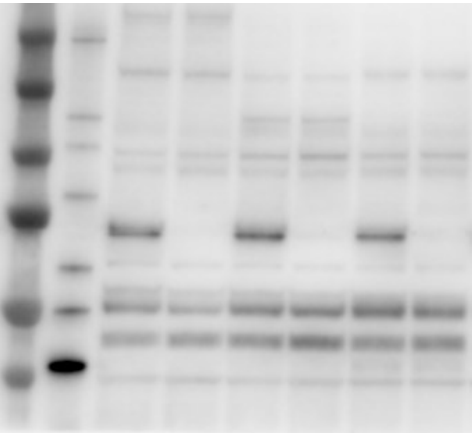


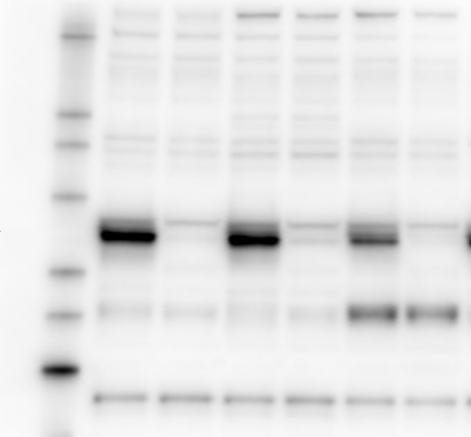
Figure 4D original



pYAP →



YAP →



GAPDH

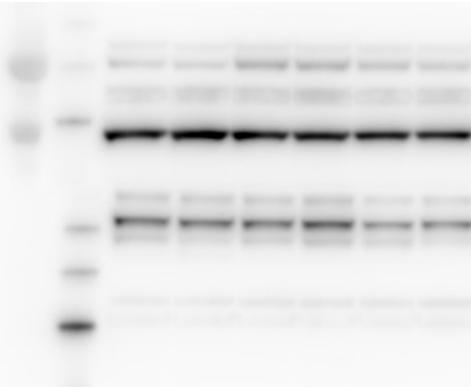


Figure 4F original

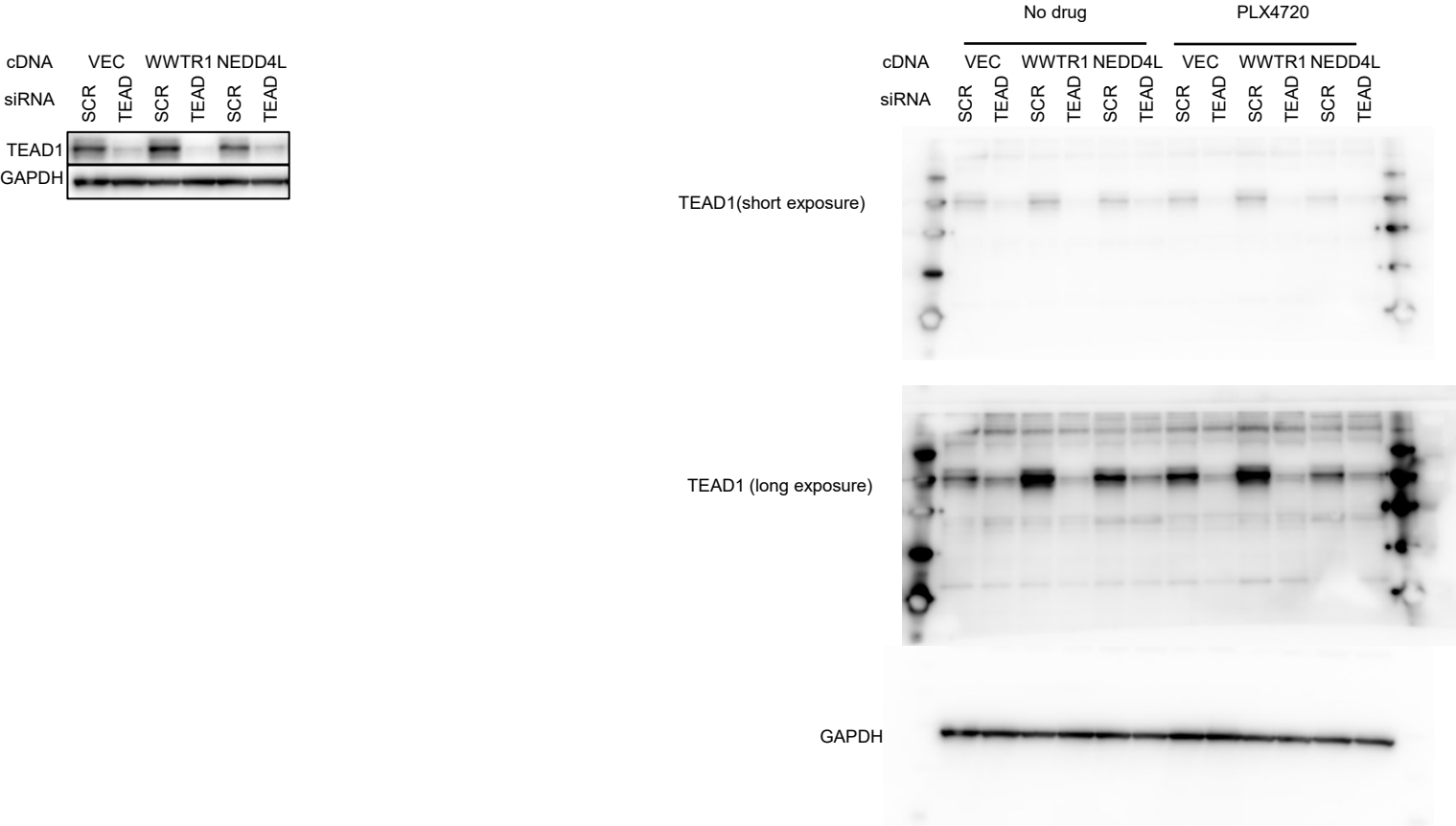


Figure 5C original

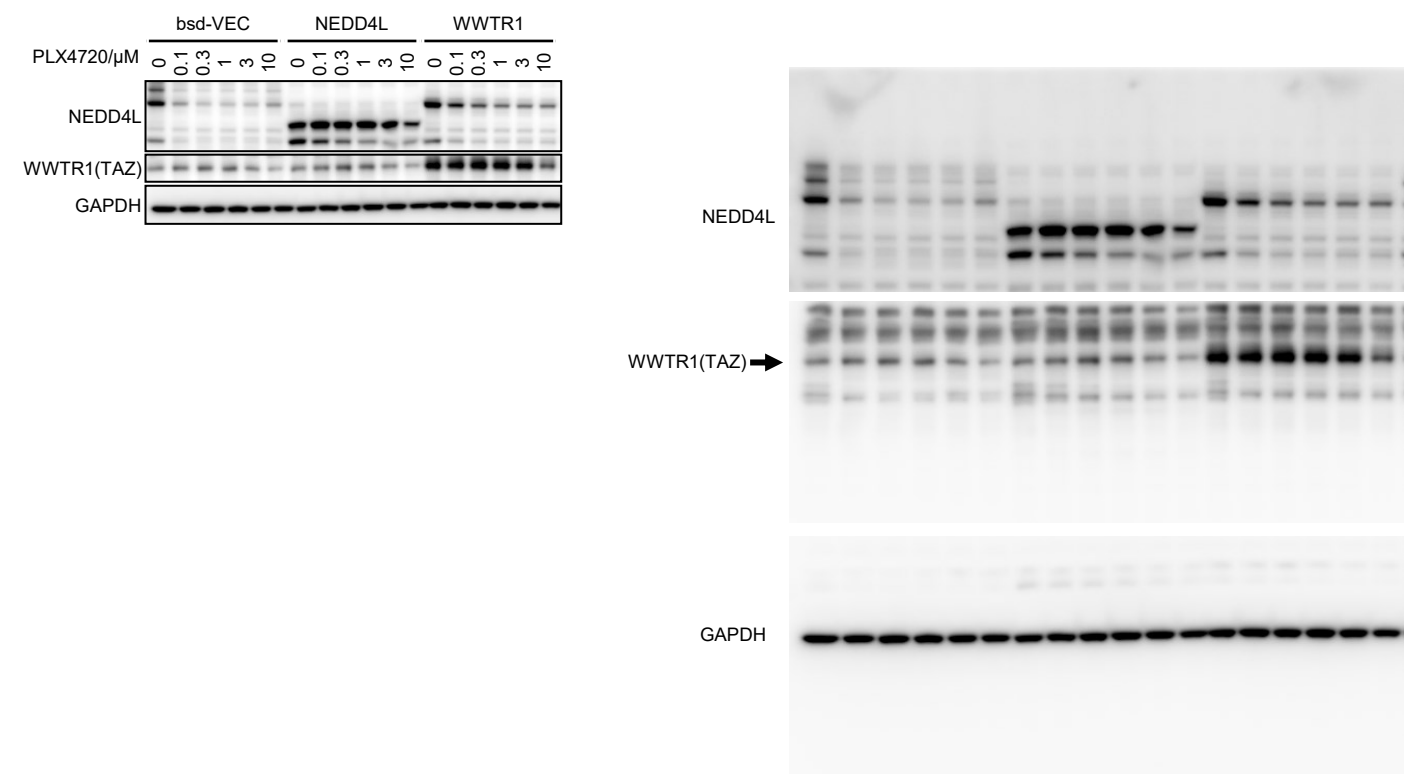


Figure 5F original

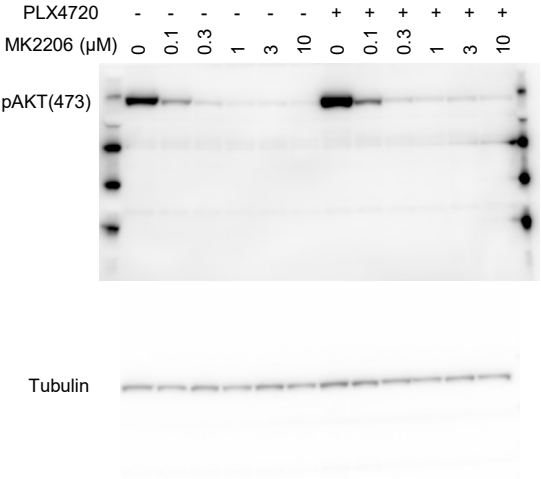
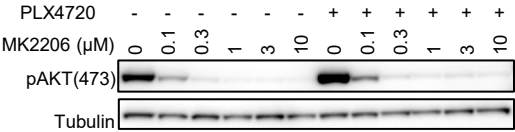


Figure 5H original

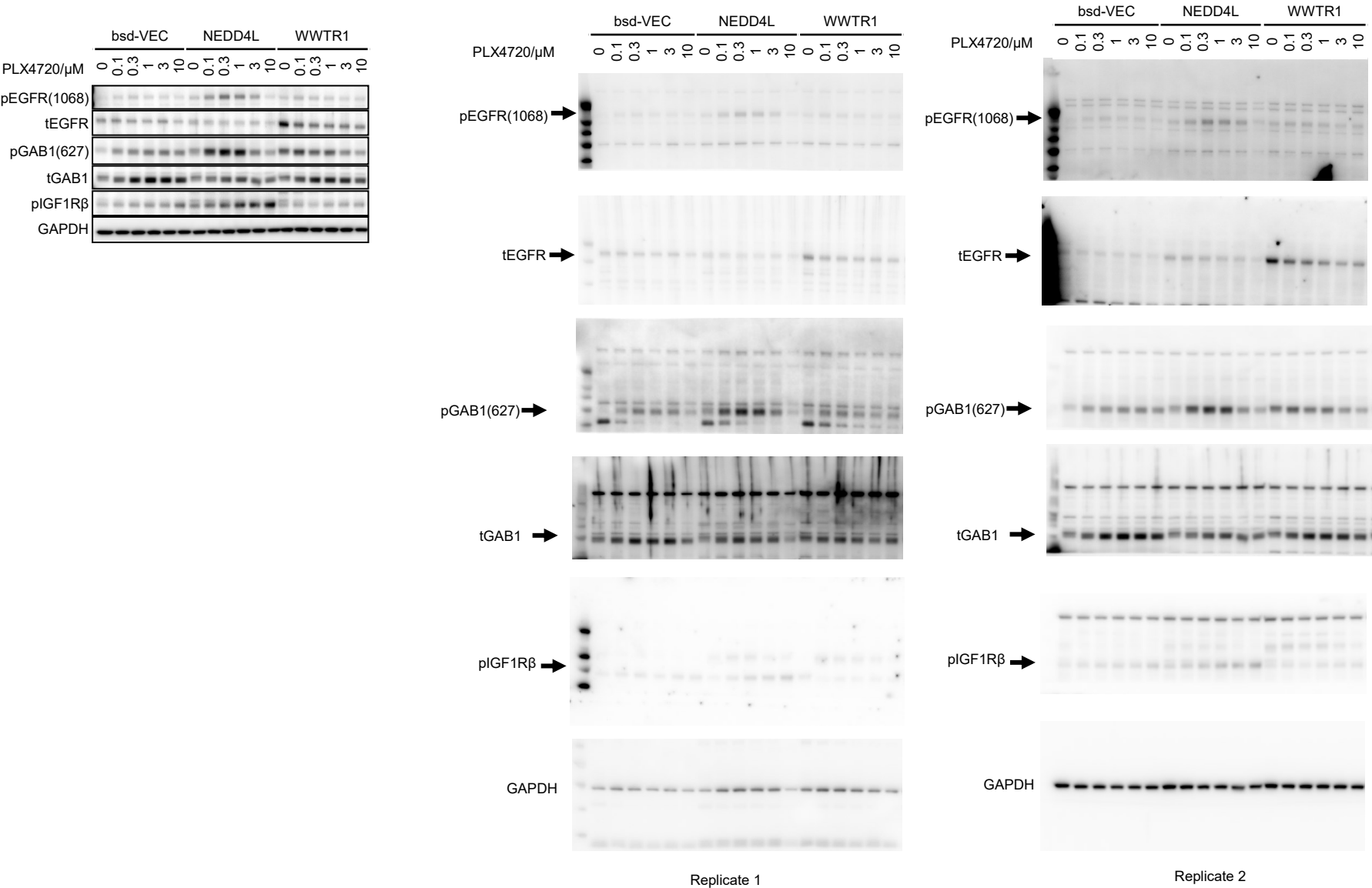
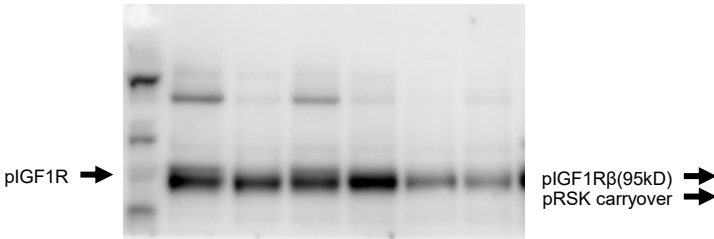
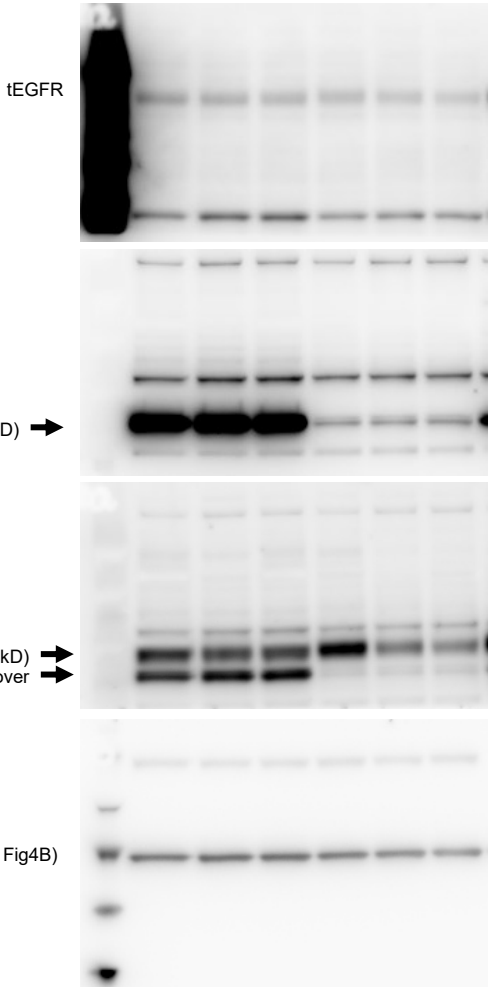
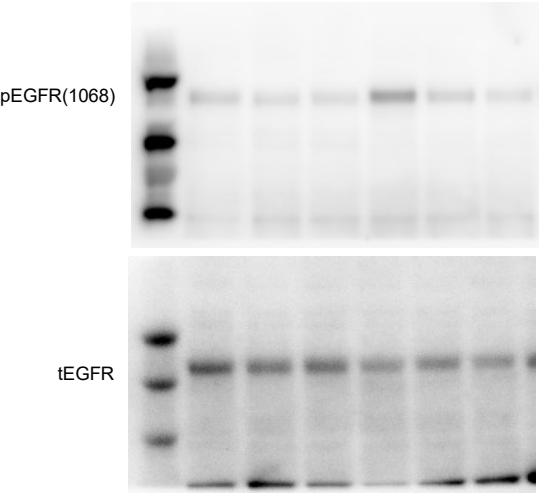
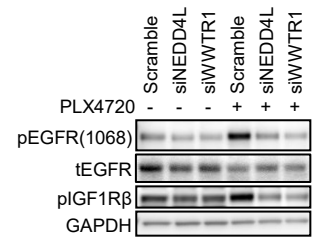
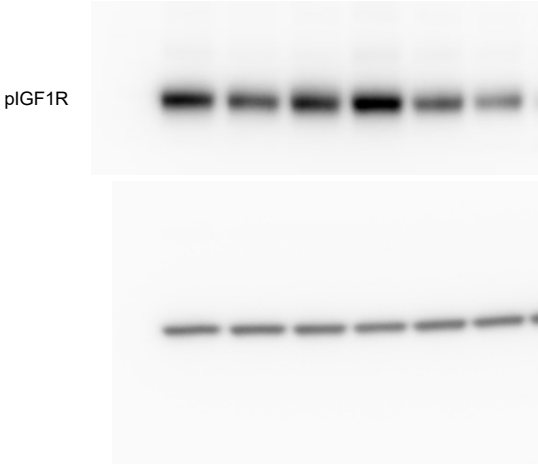
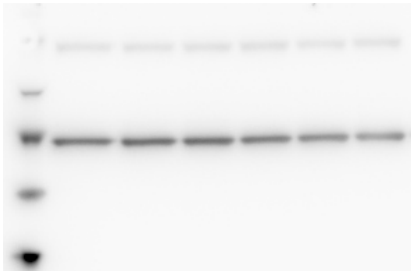


Figure 5J original



GAPDH(also in Fig4B)



Replicate1-gel1

Replicate1-gel2

Replicate2

Figure S2D original

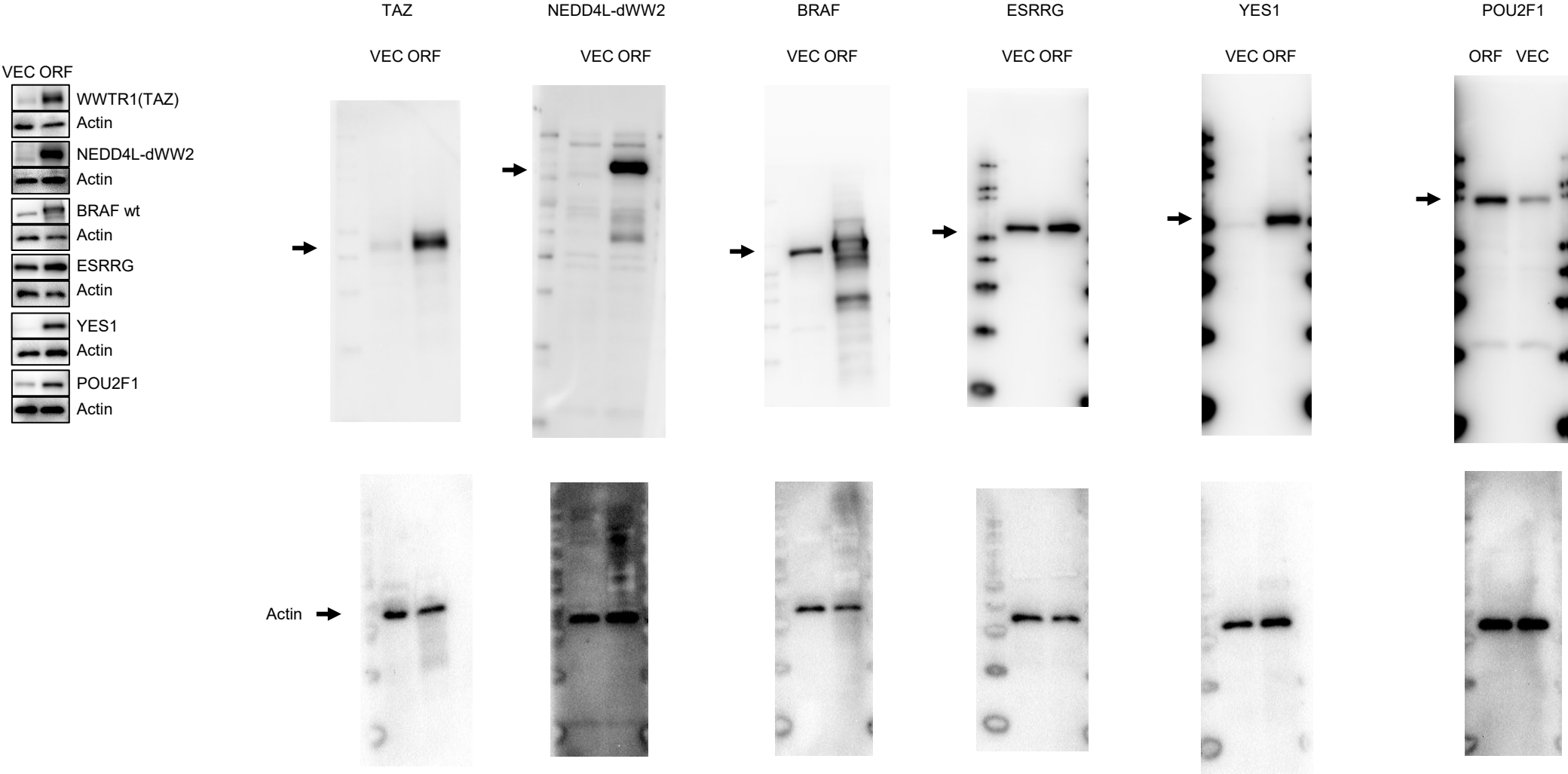


Figure S4A original

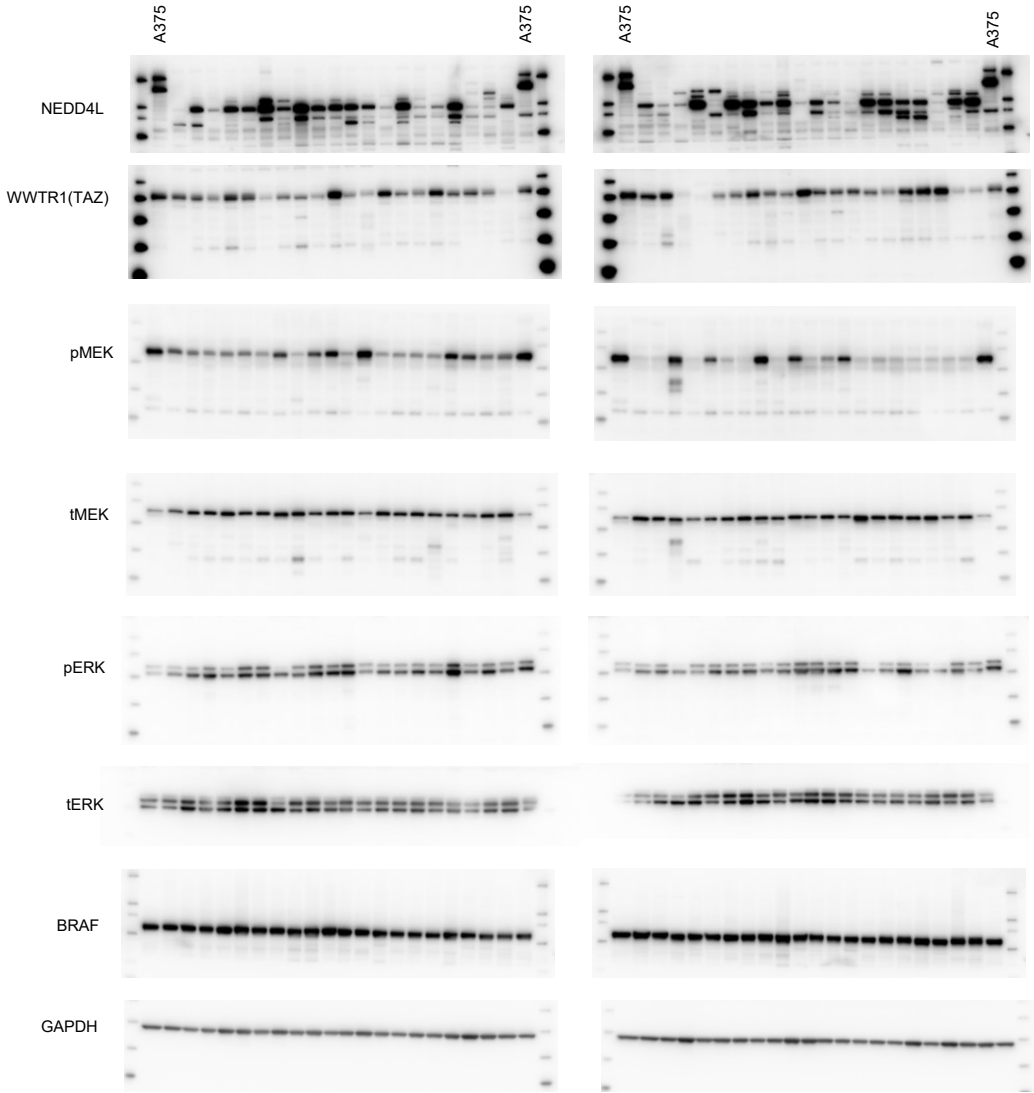
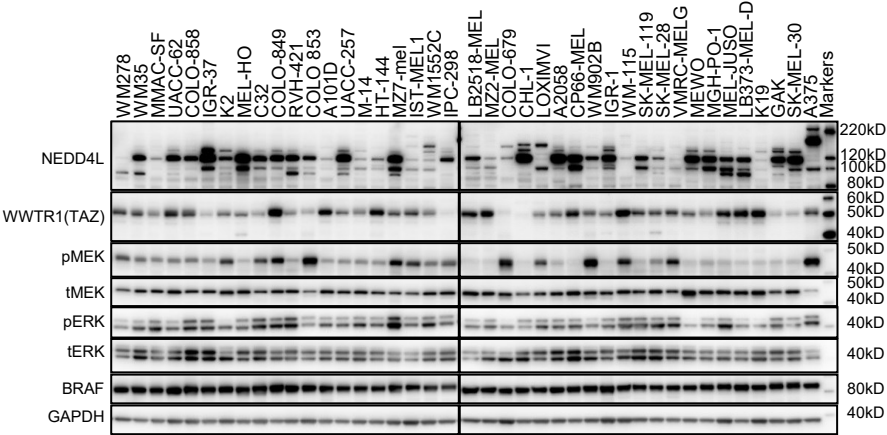


Figure S5A original

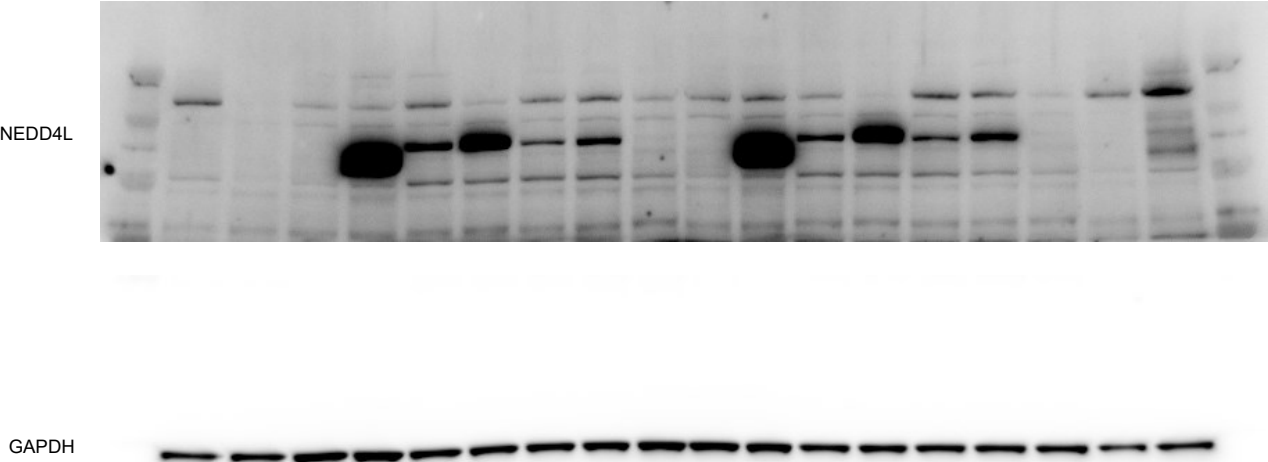
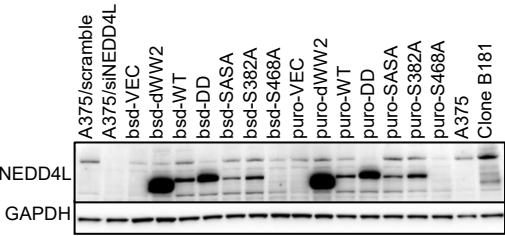


Figure S5E original

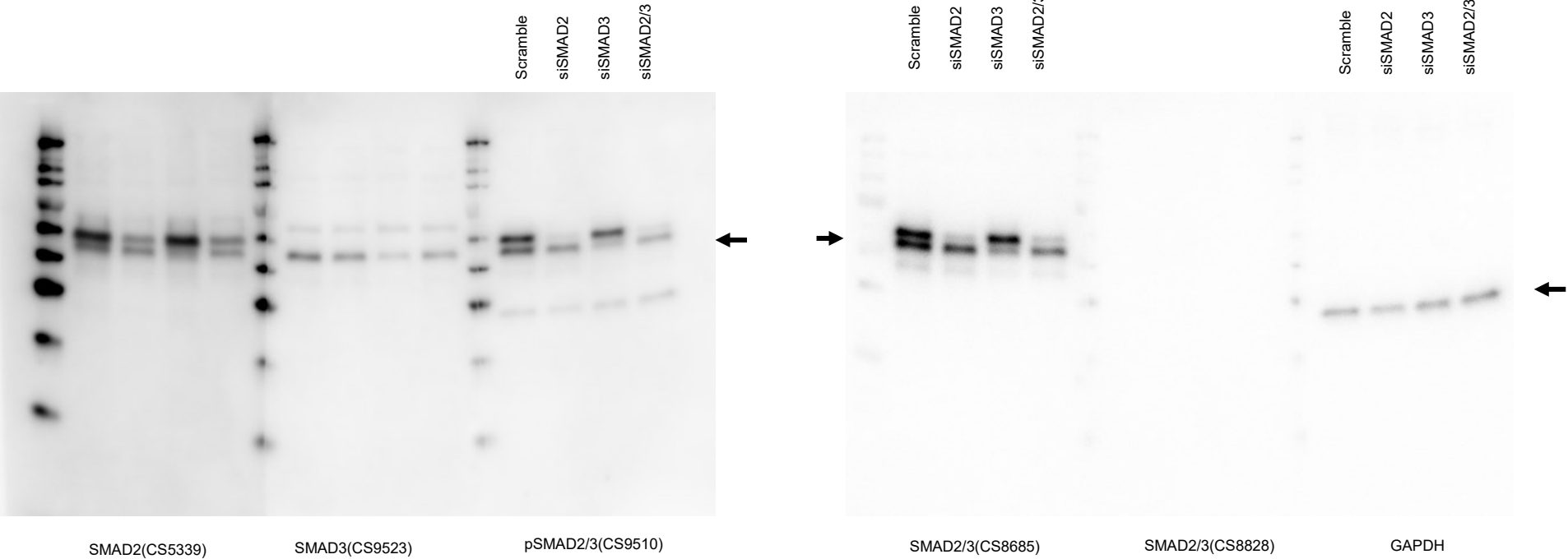
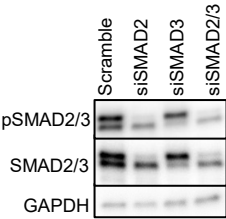
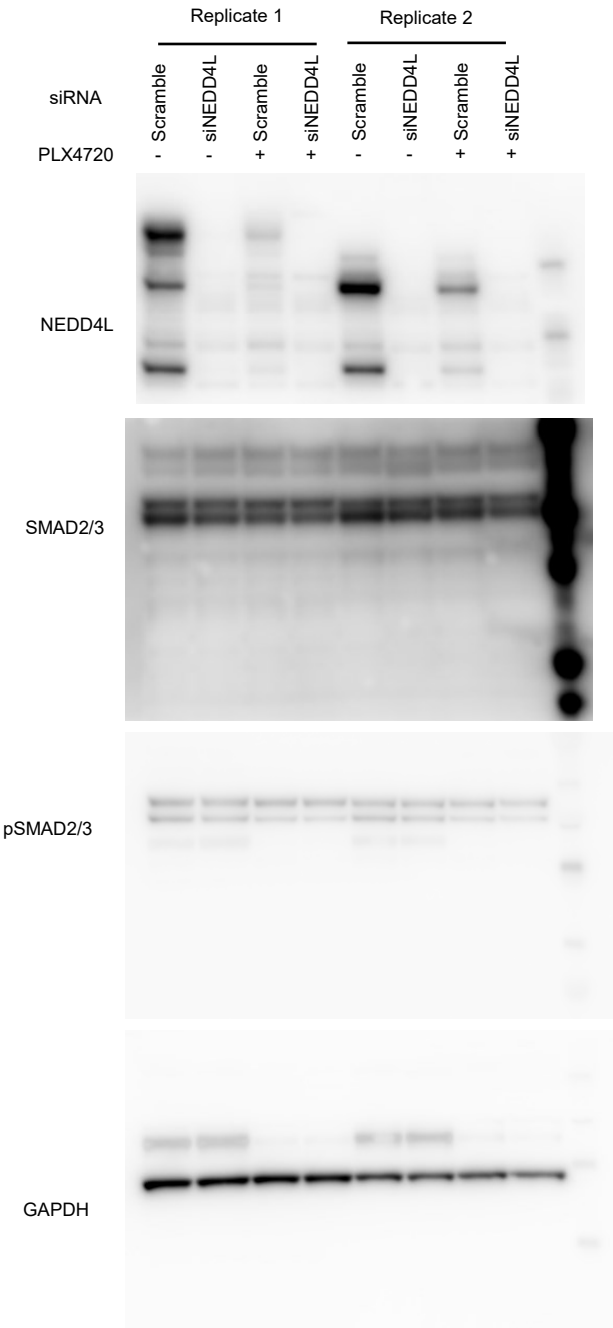
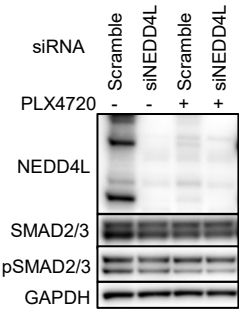
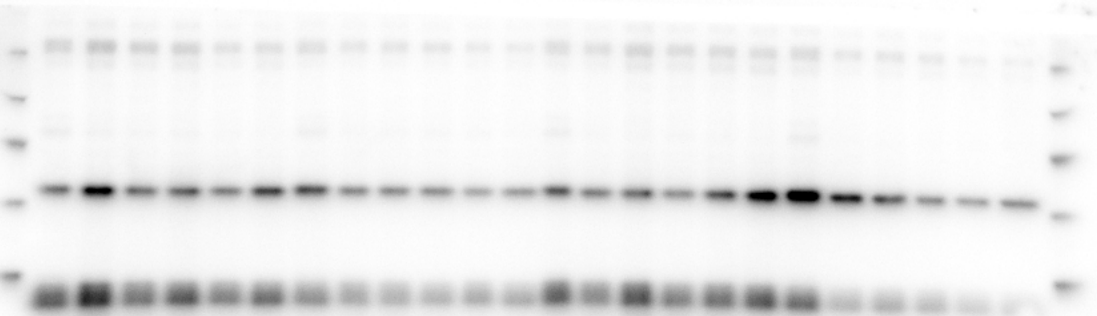
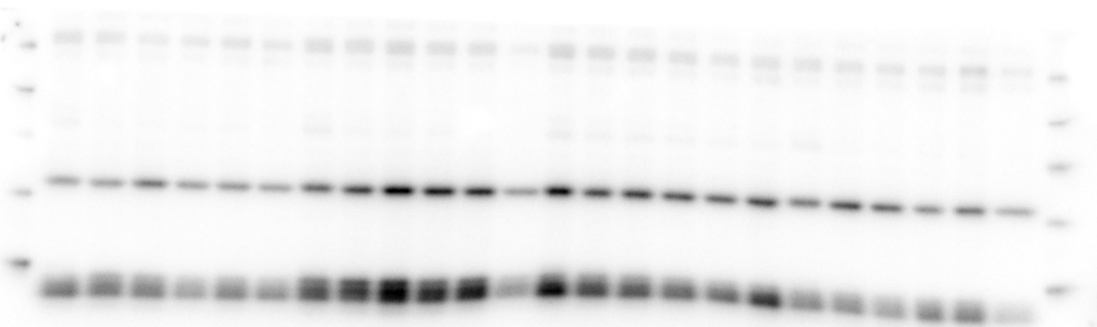
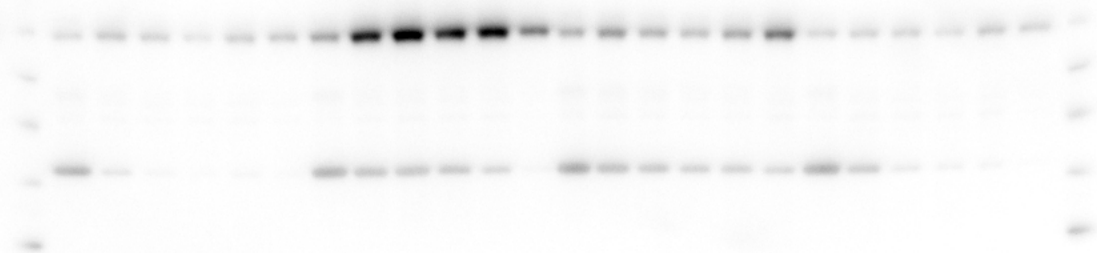
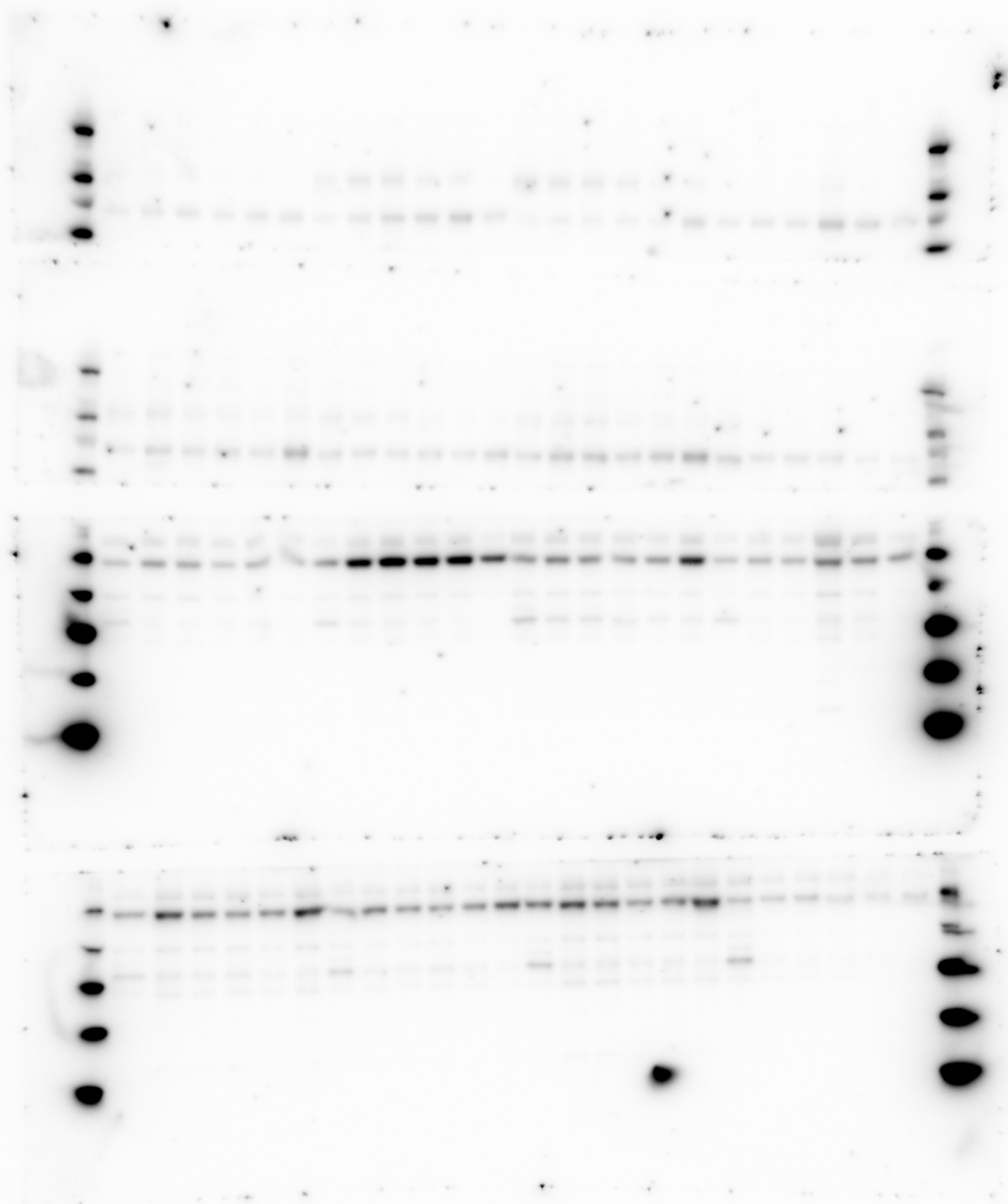
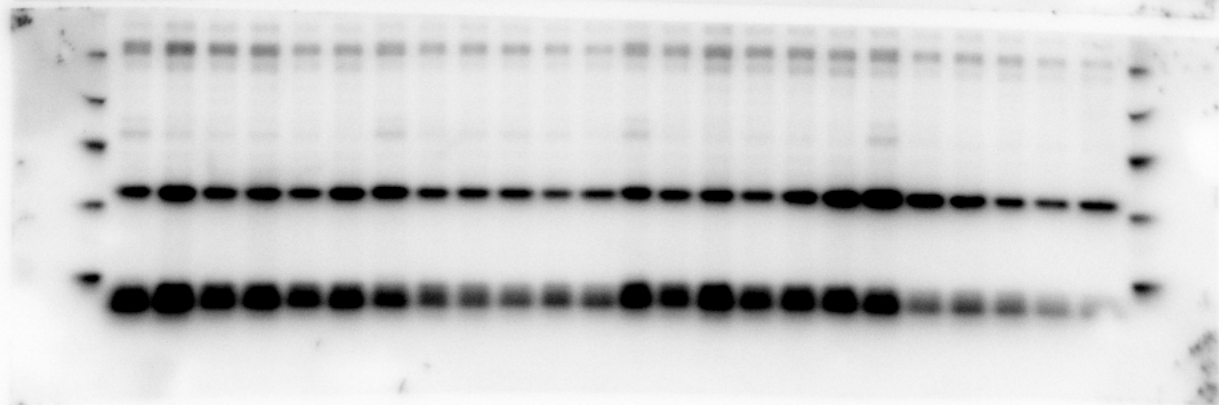
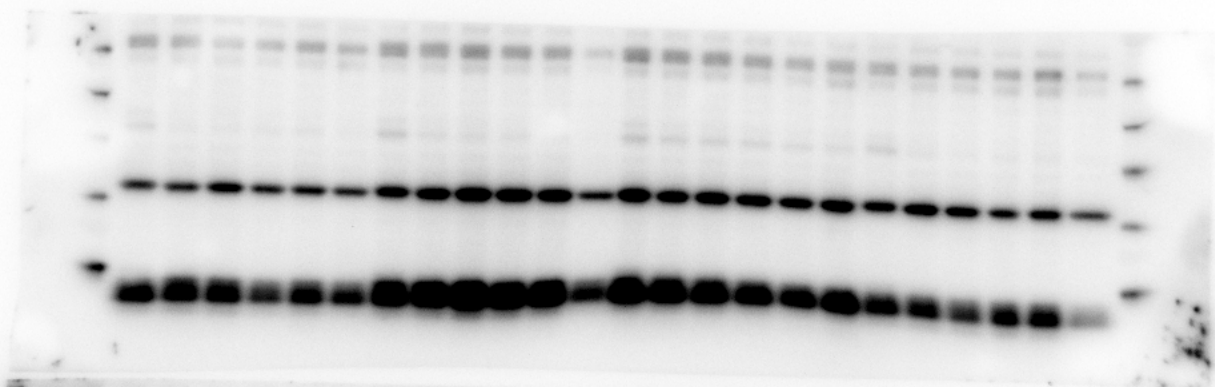
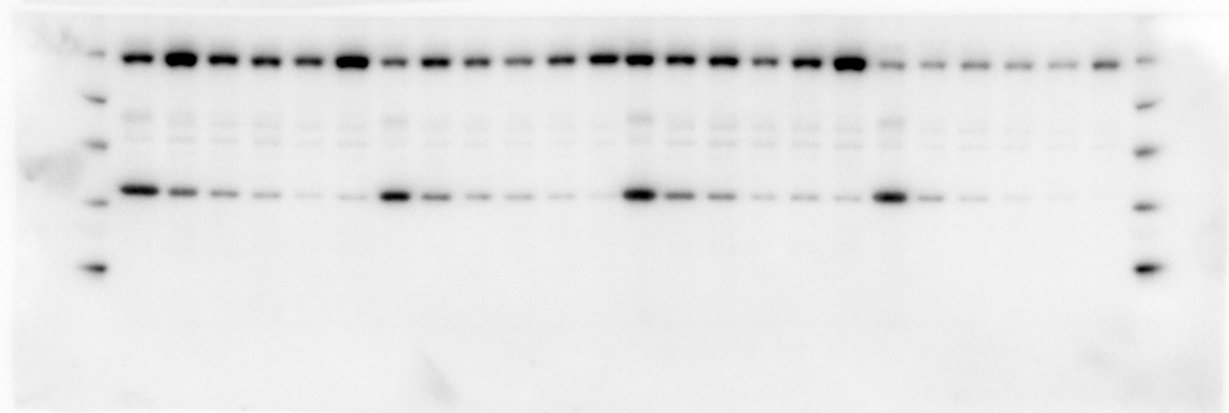
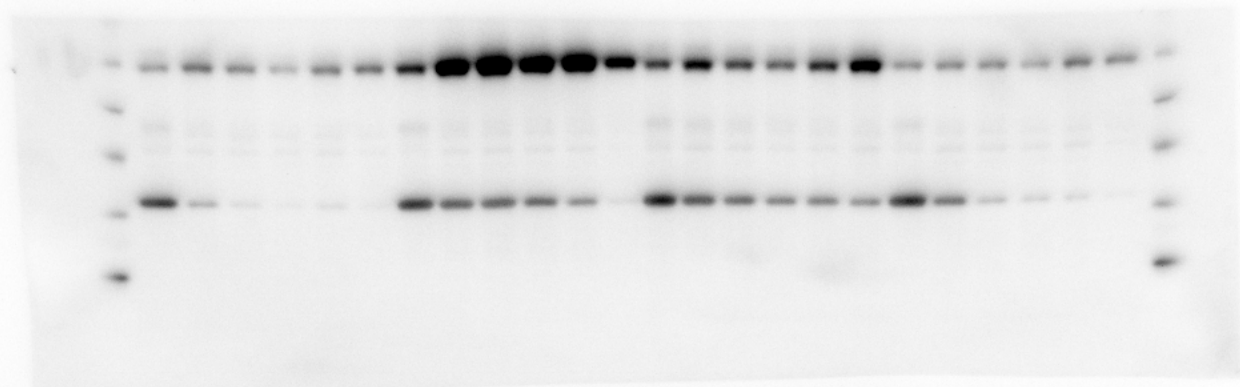


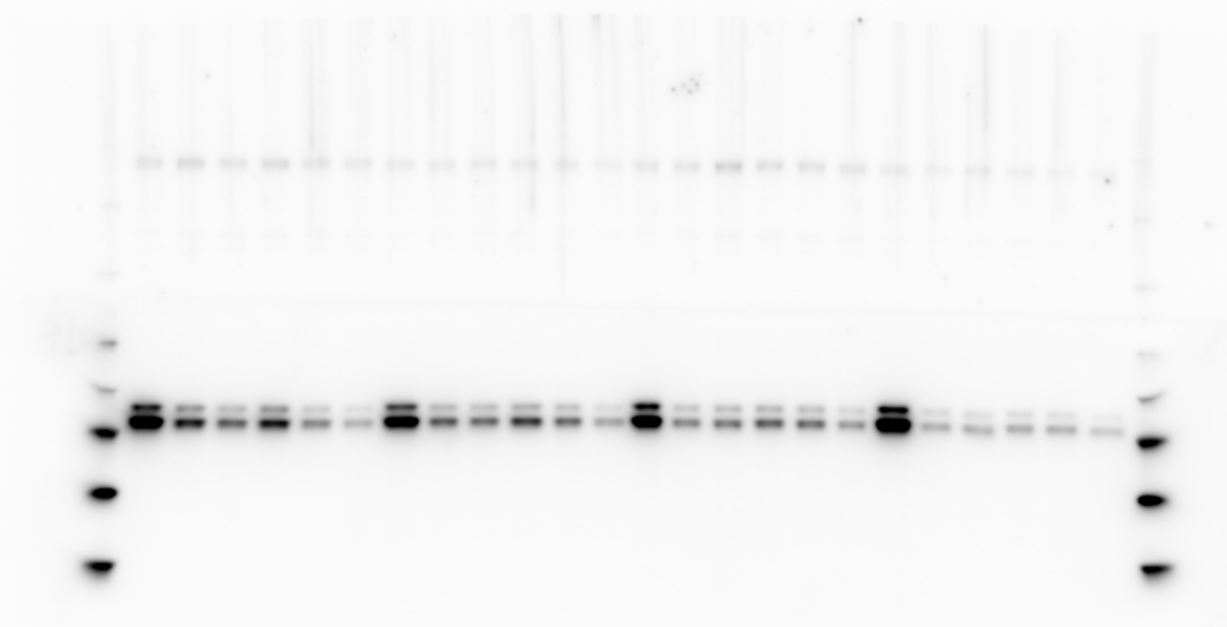
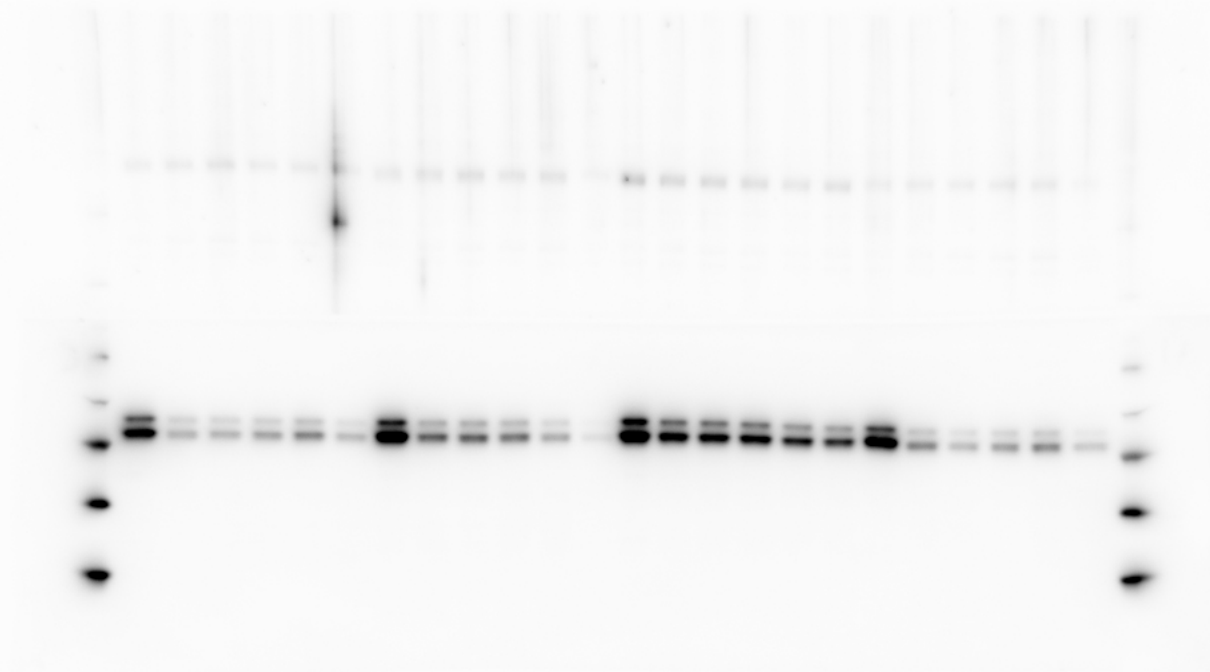
Figure S5F original

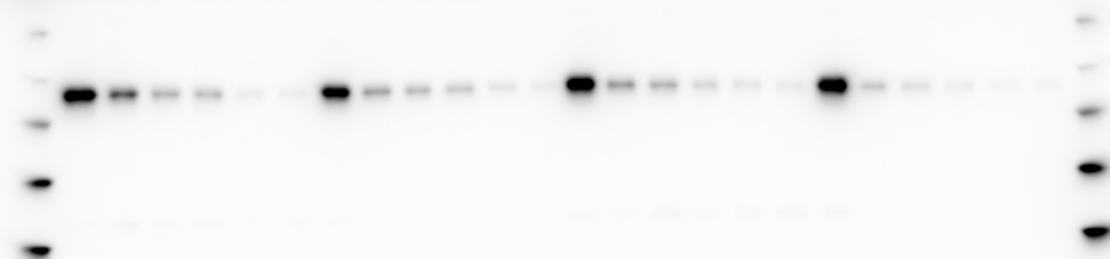
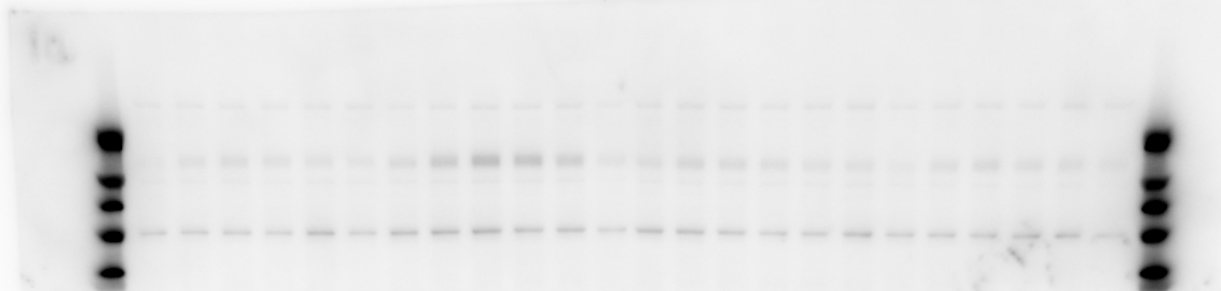


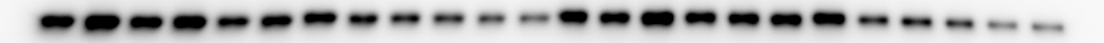
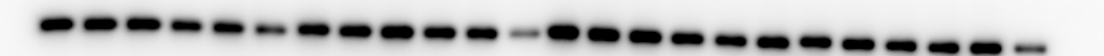
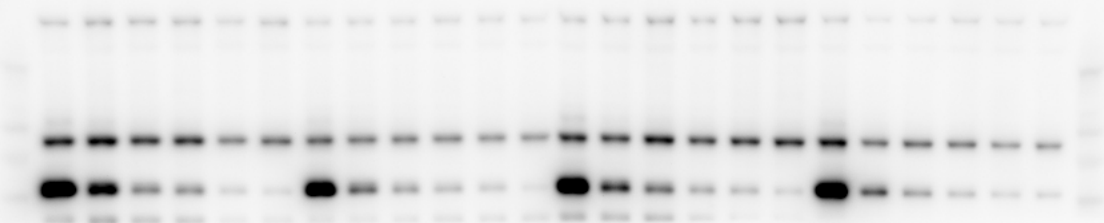
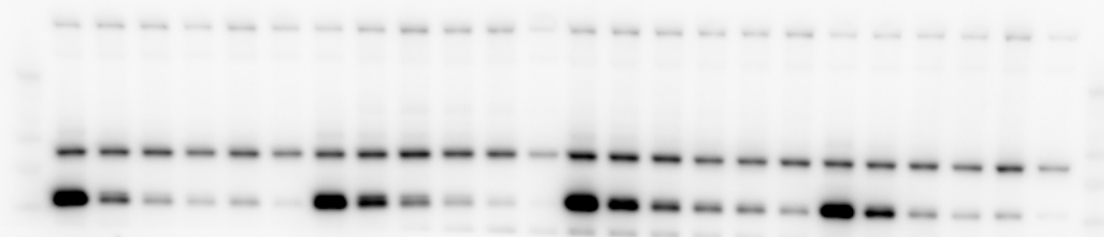


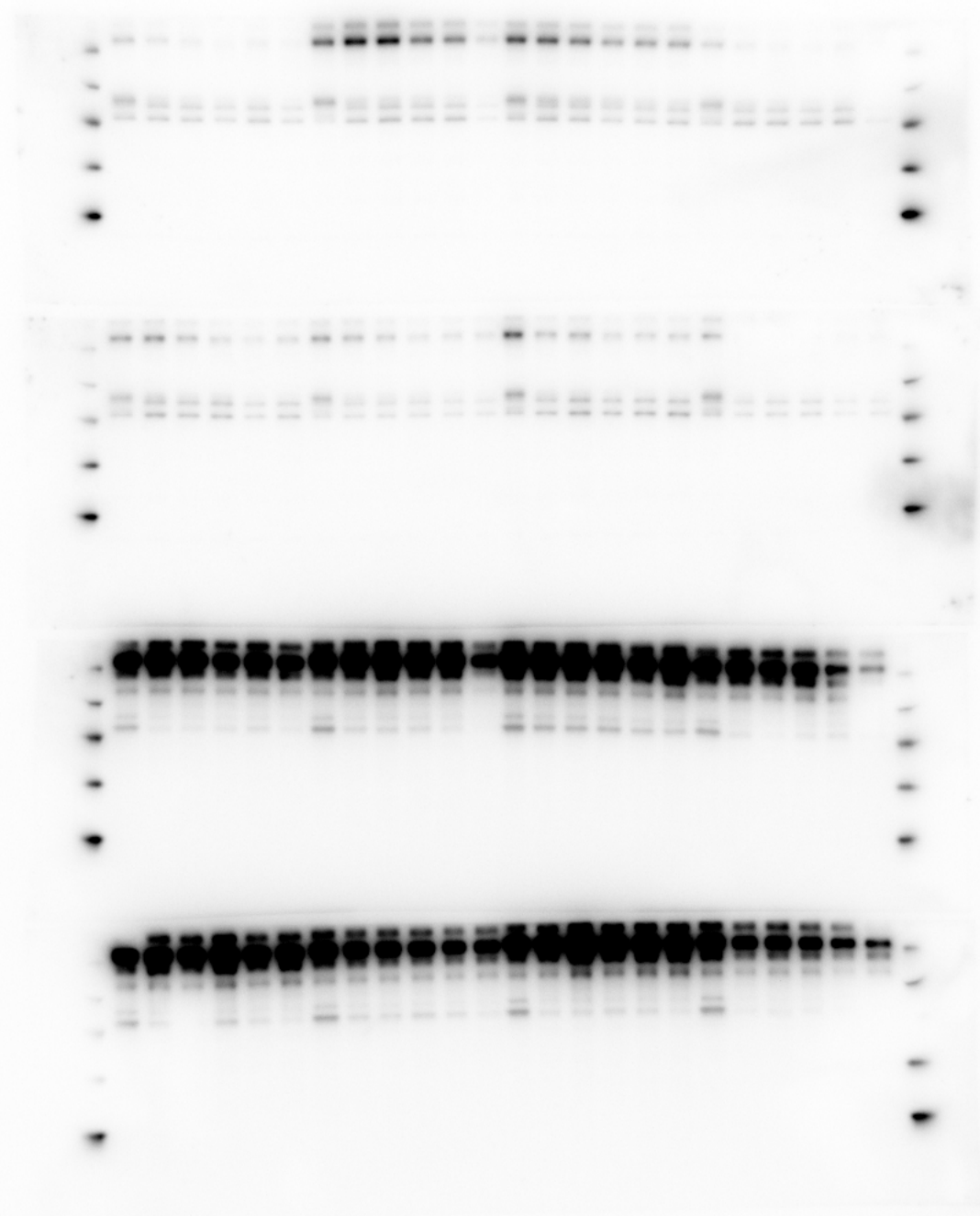


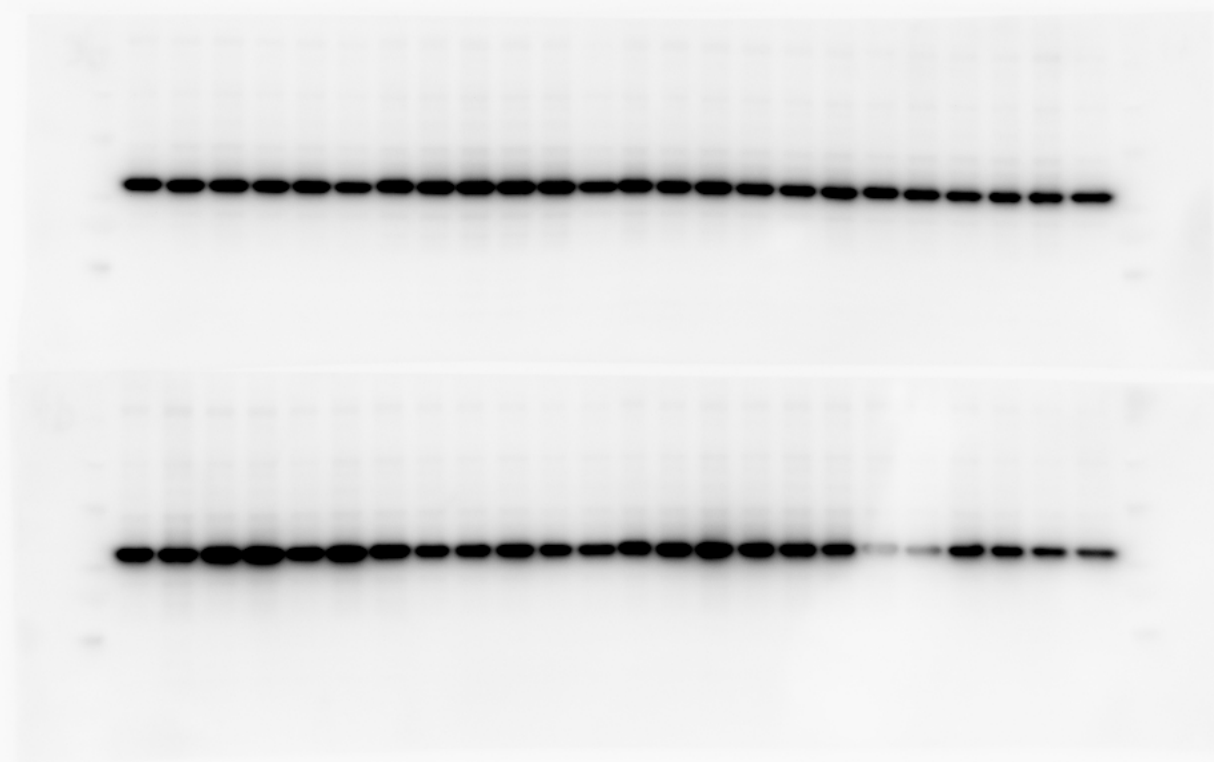
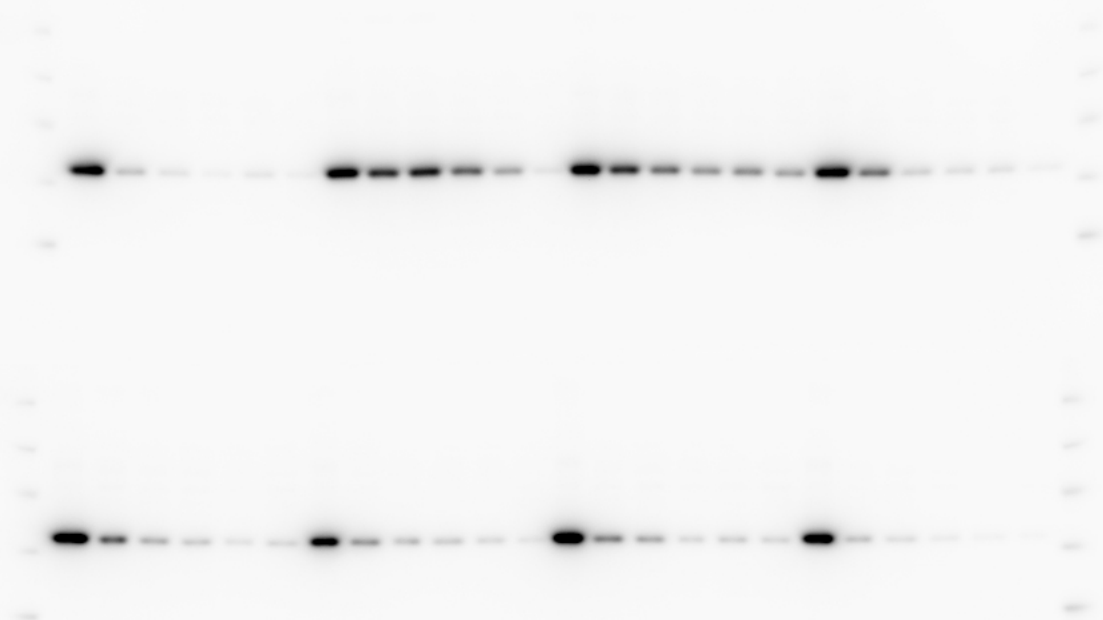


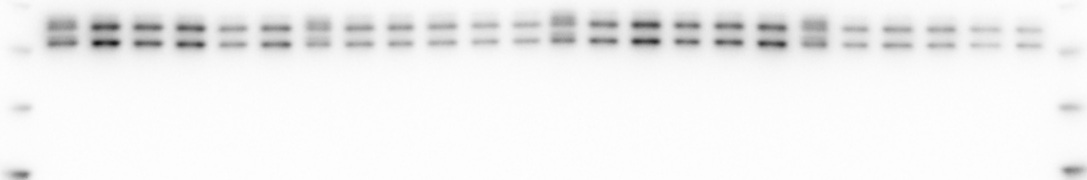
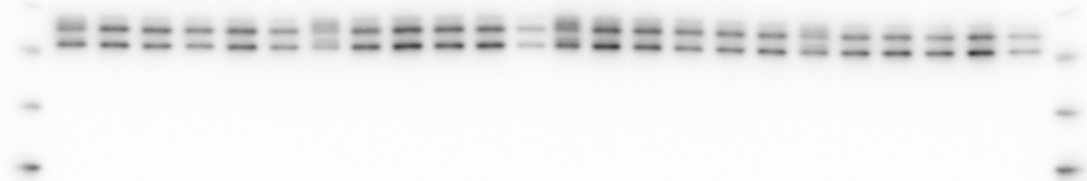
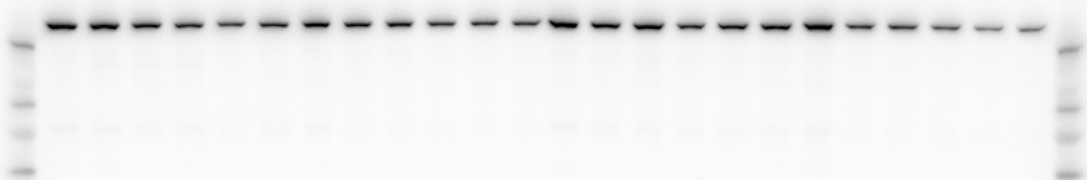
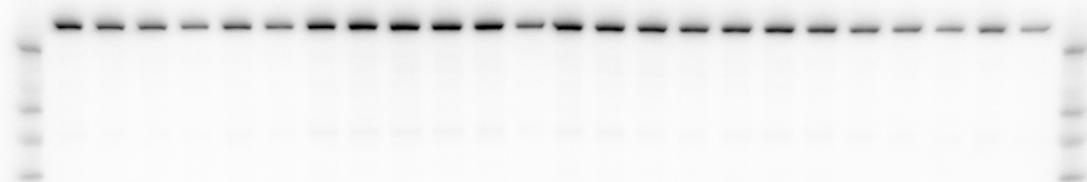


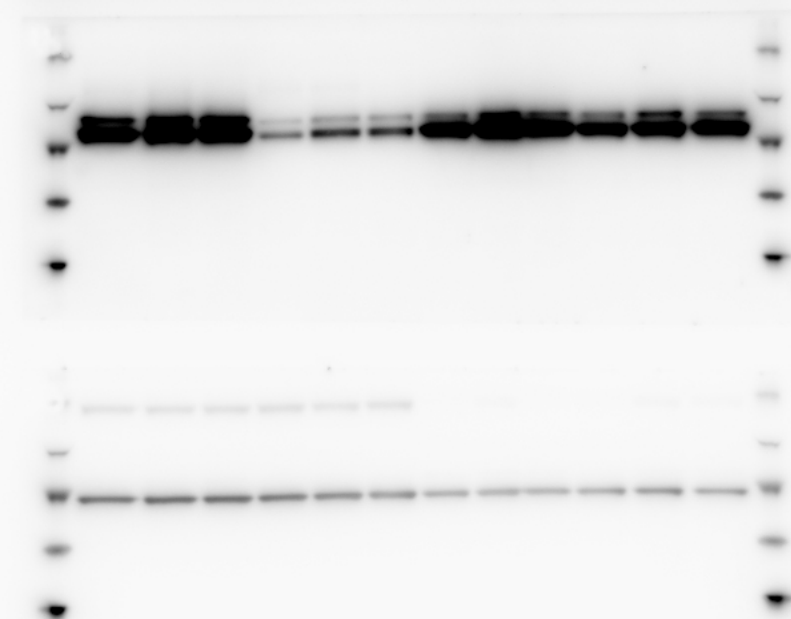
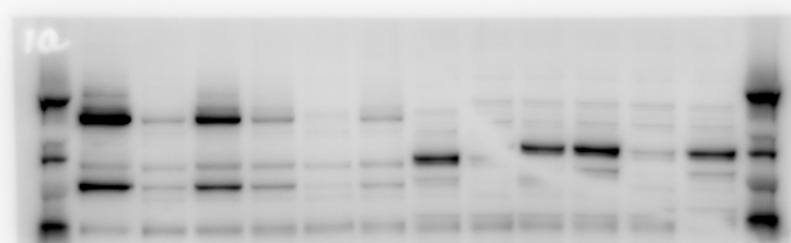


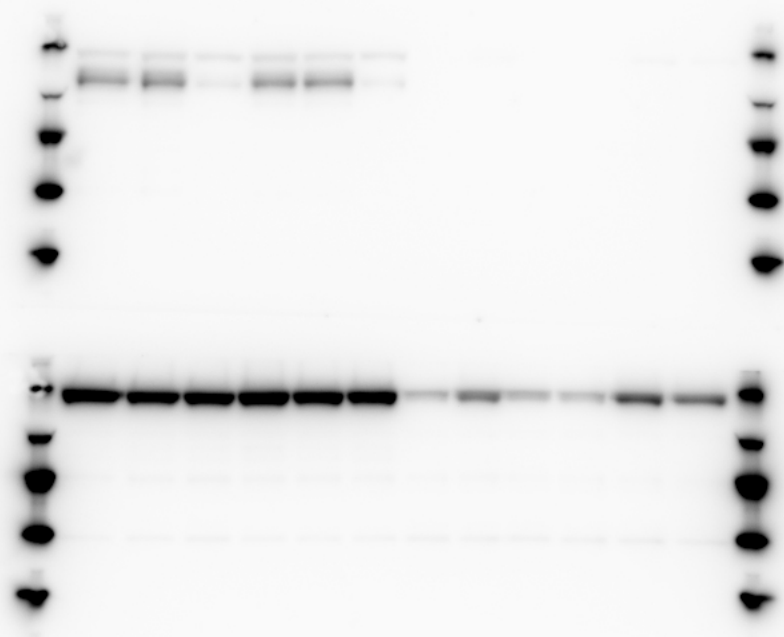


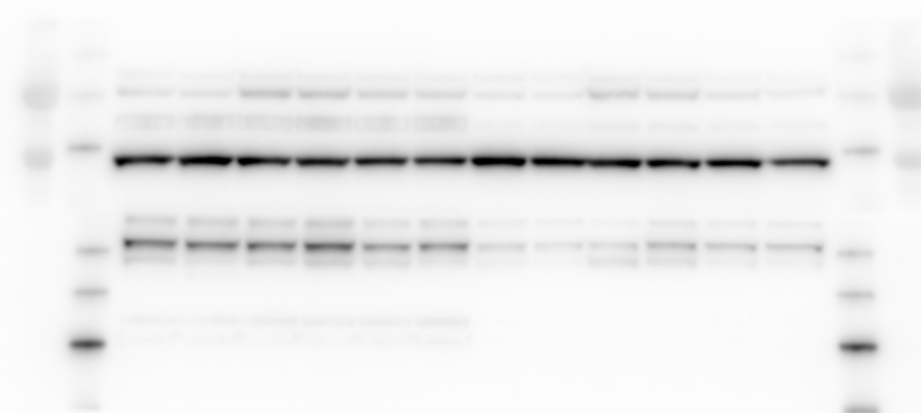


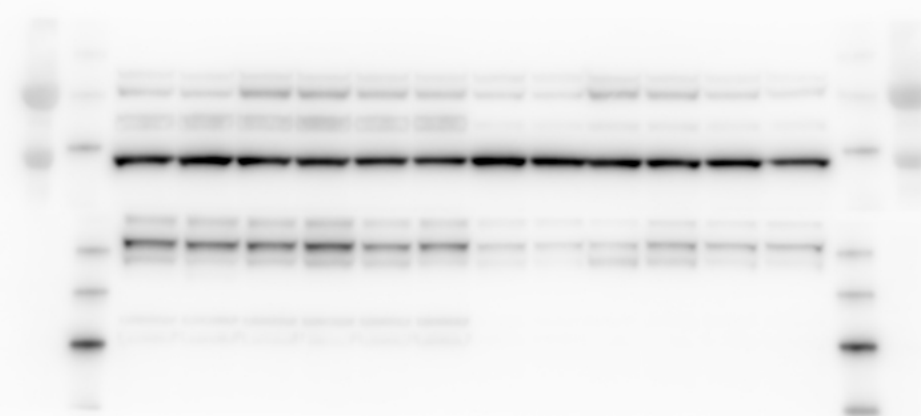


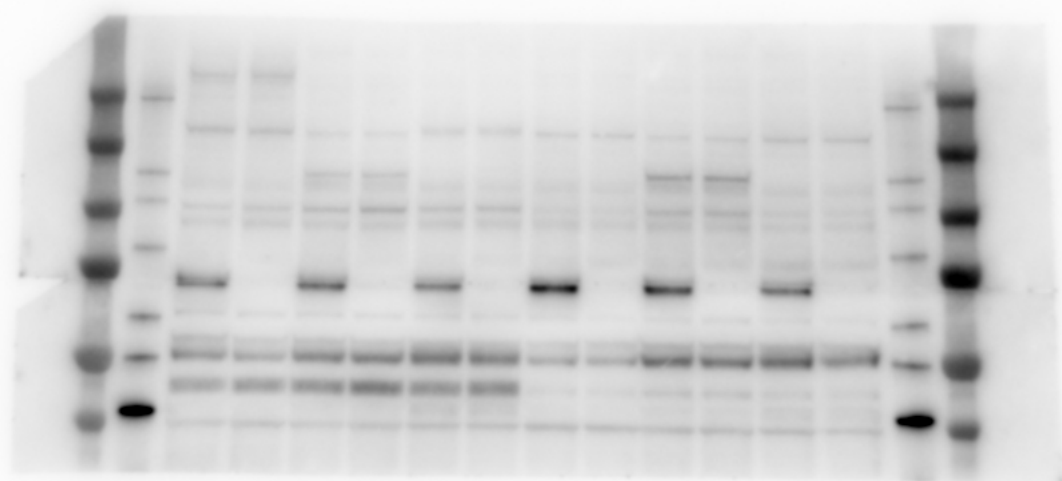


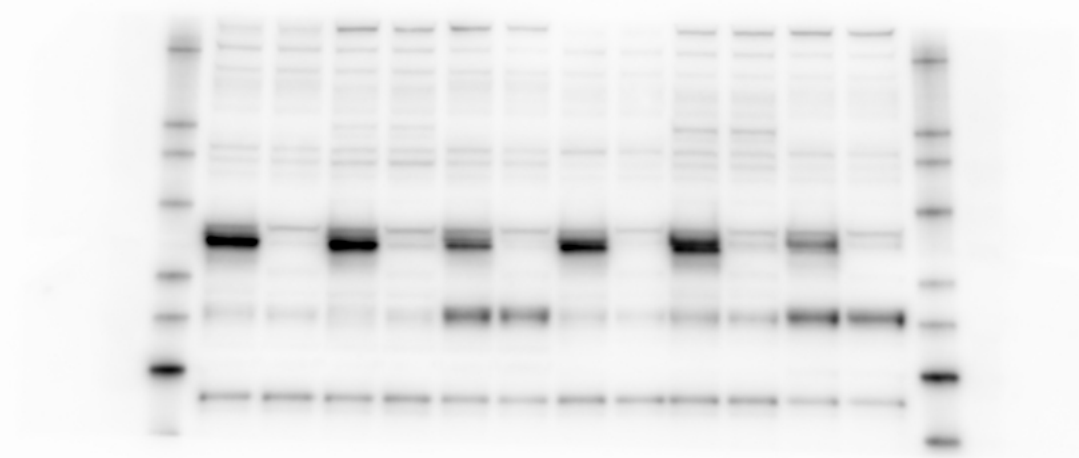


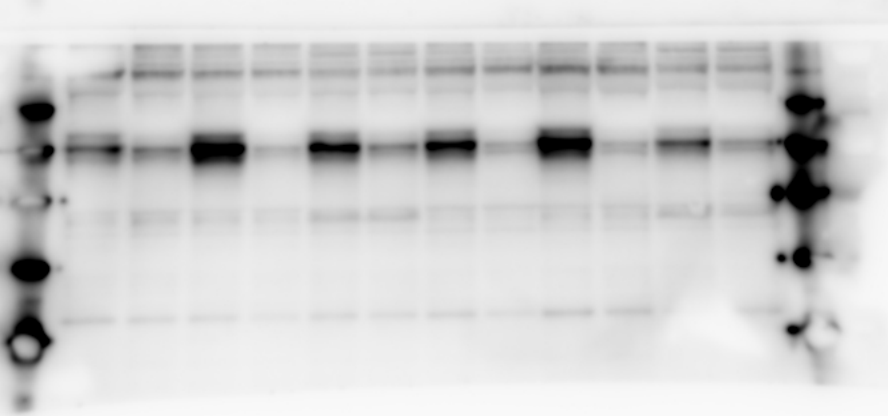






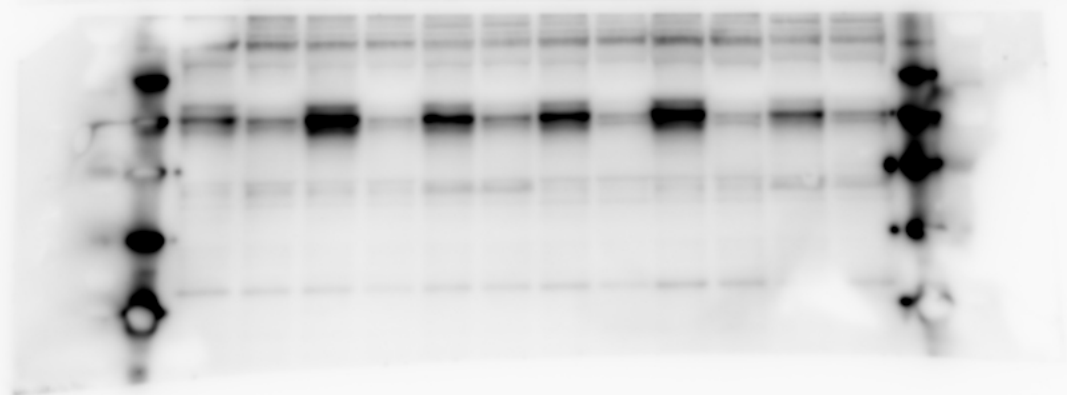
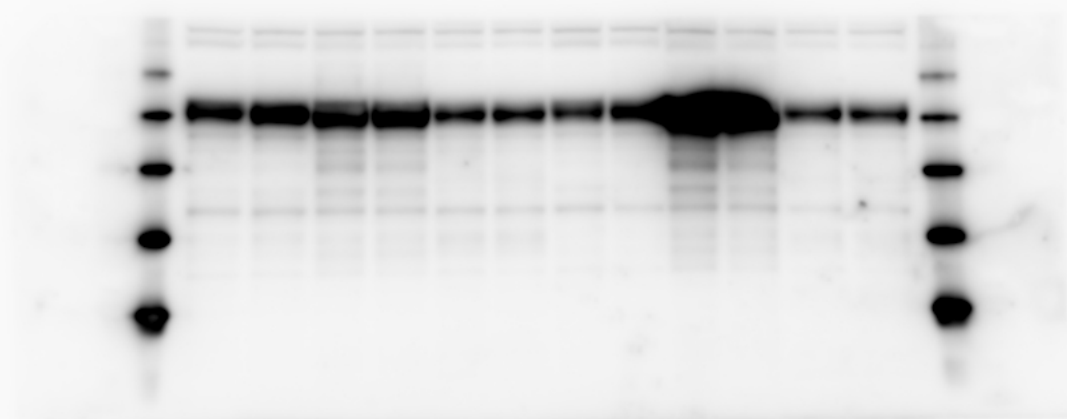


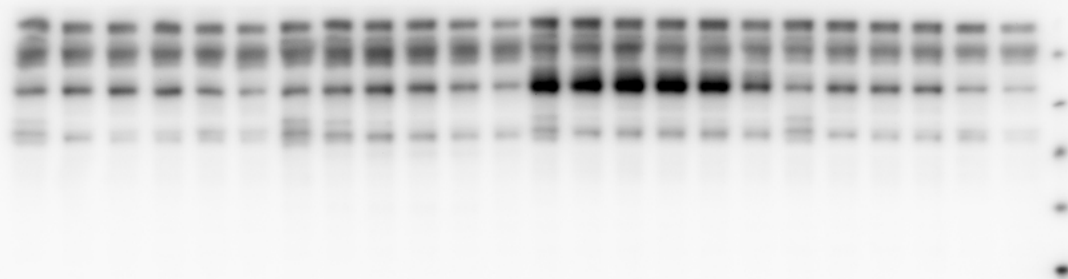
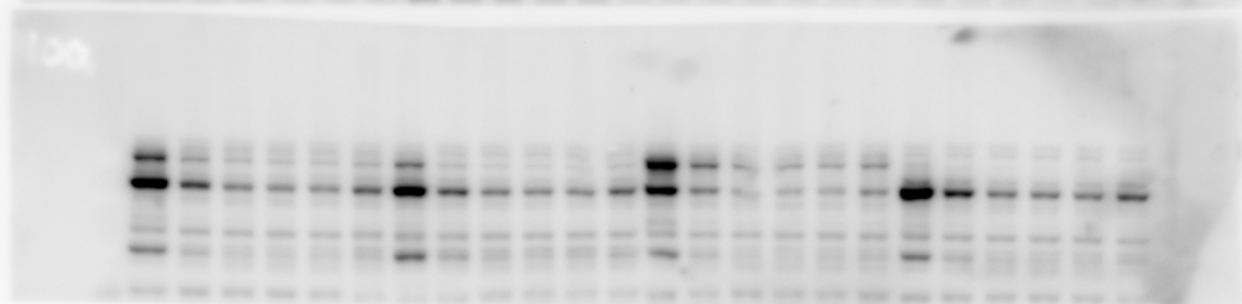
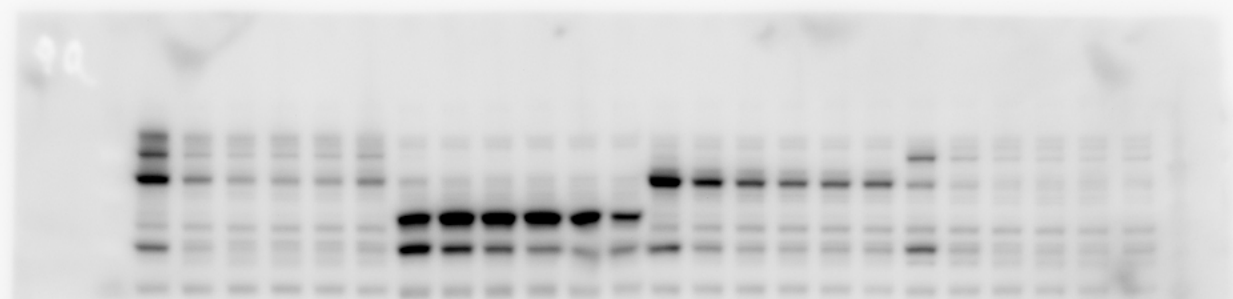


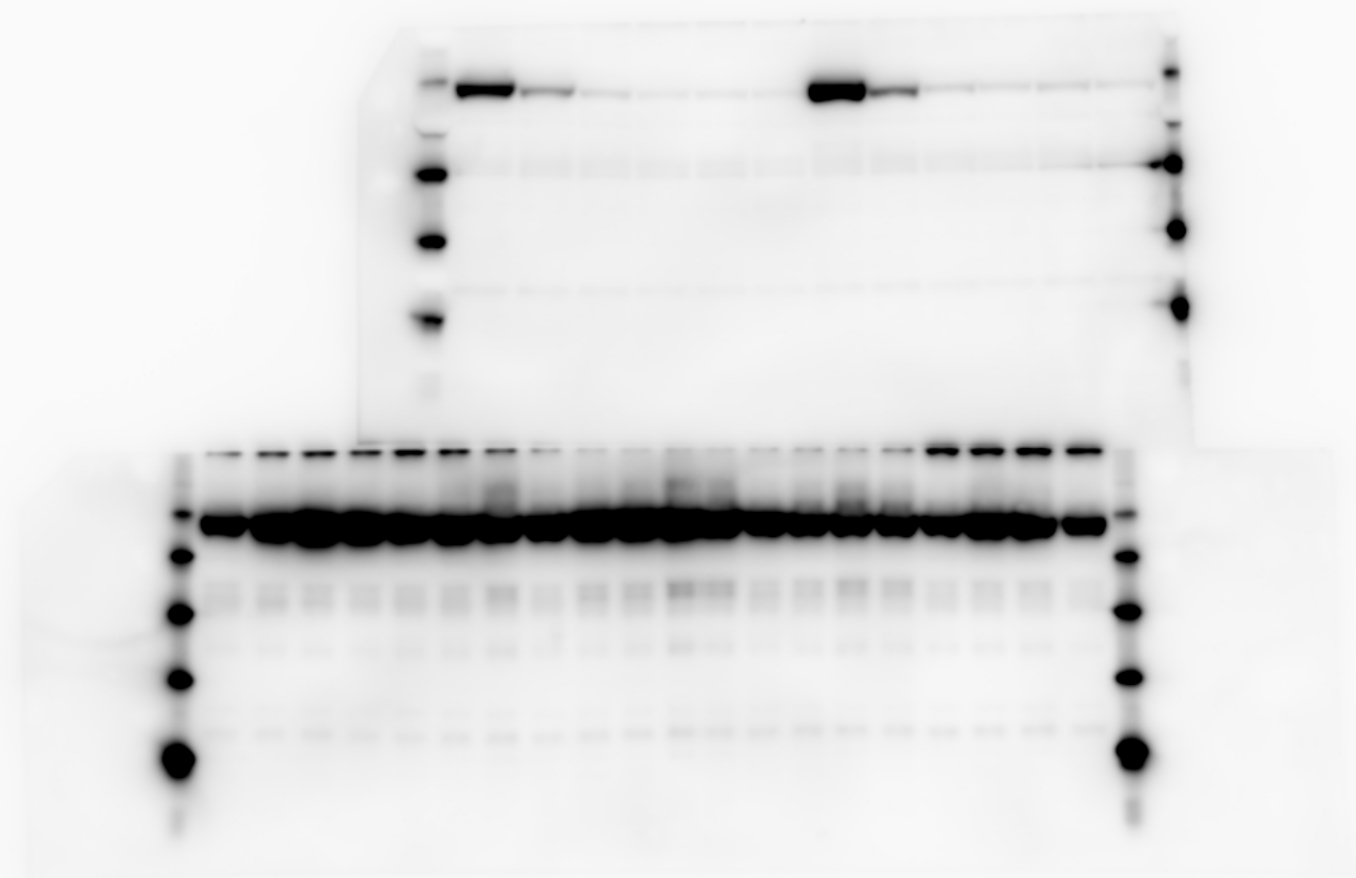


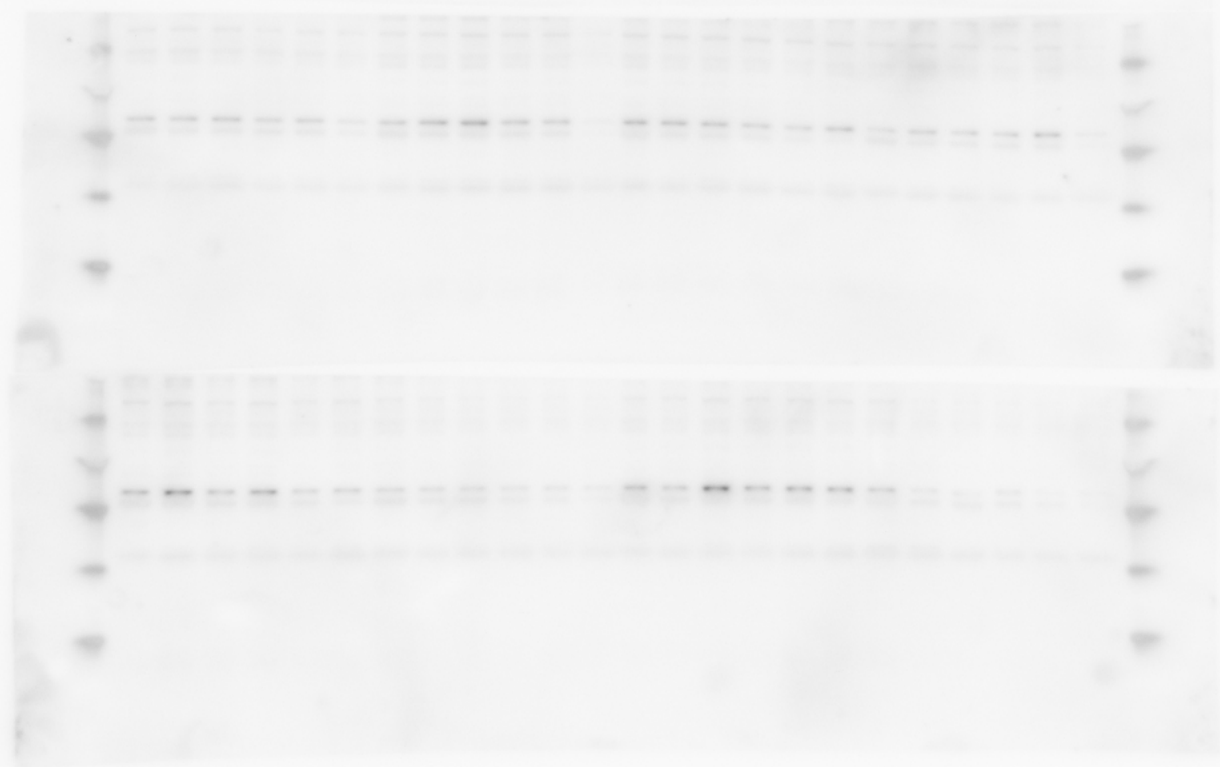
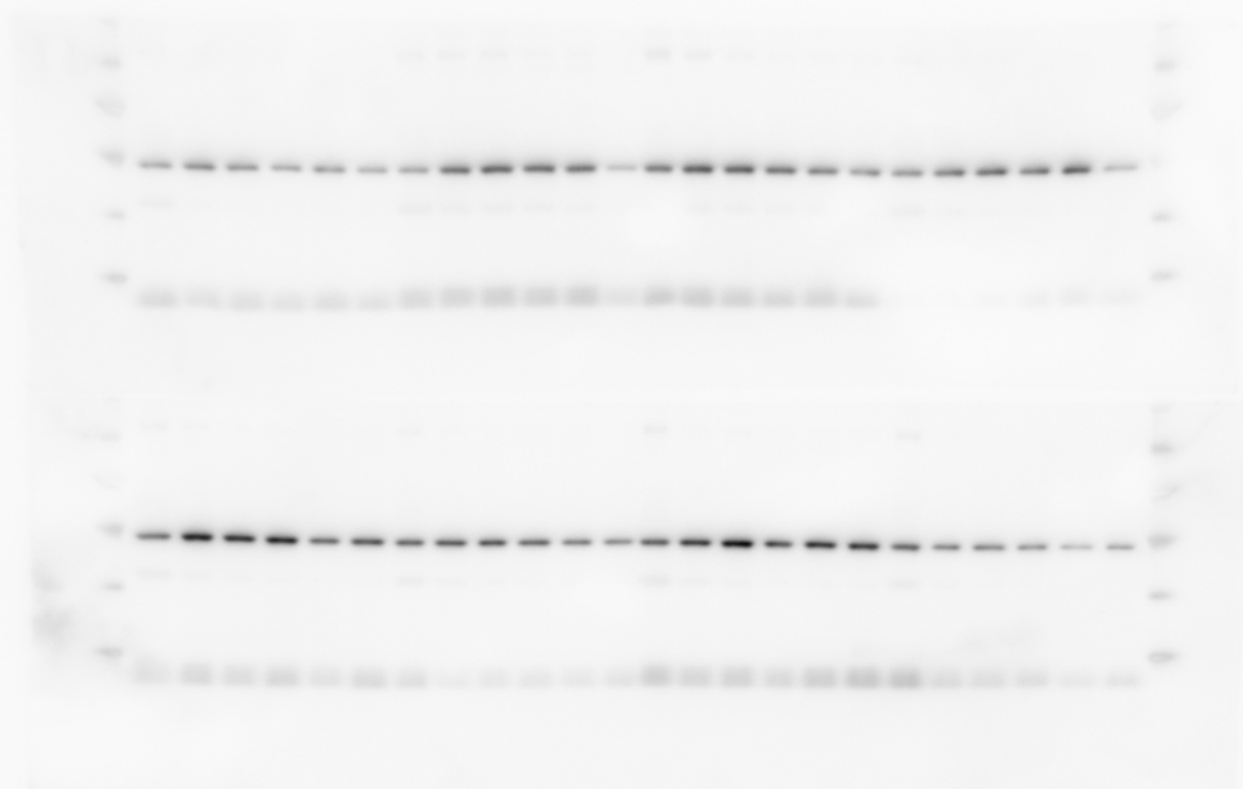


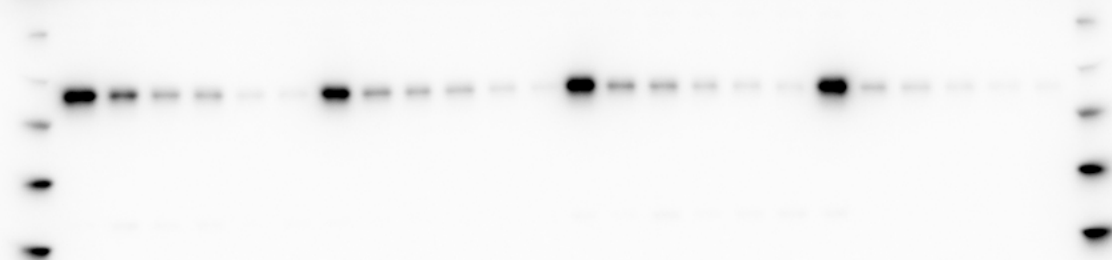
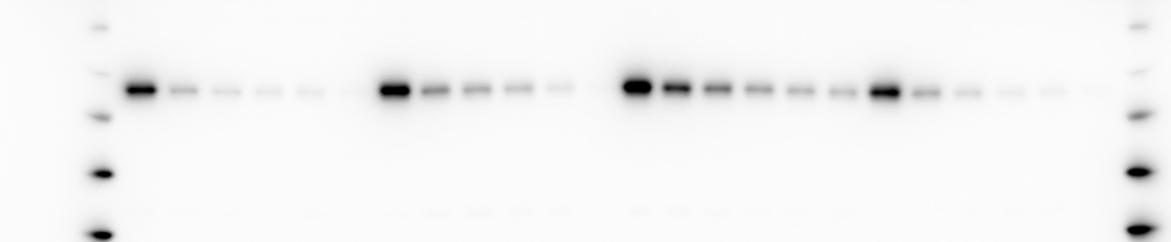
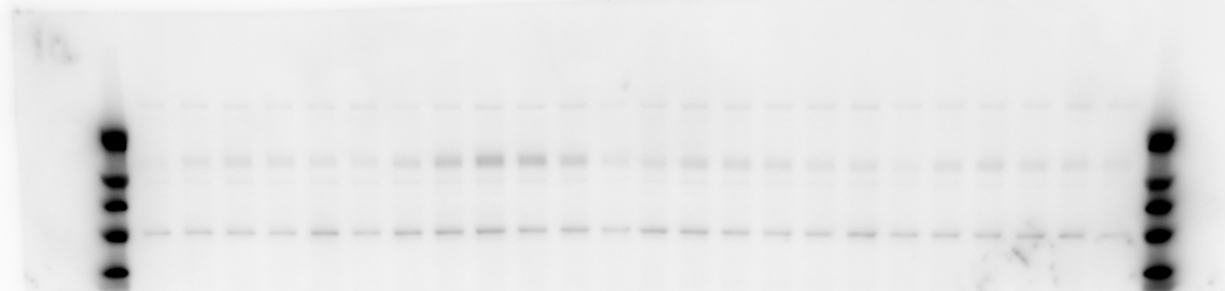


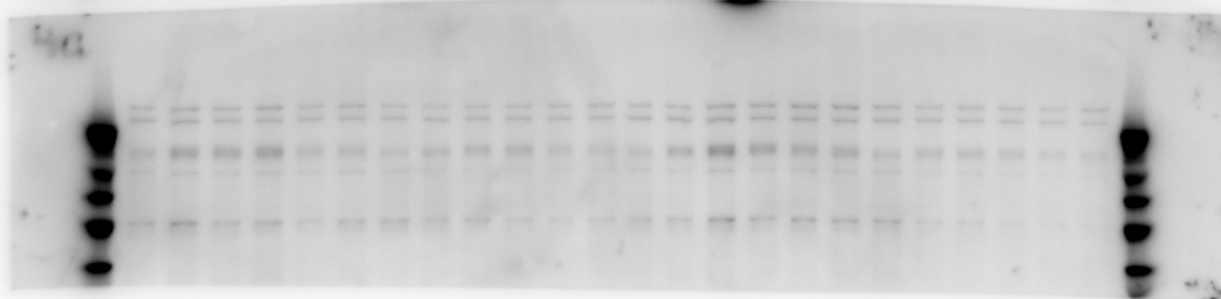
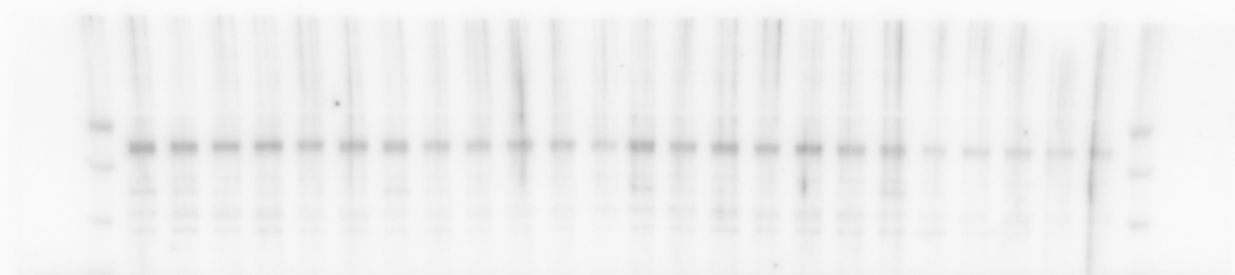
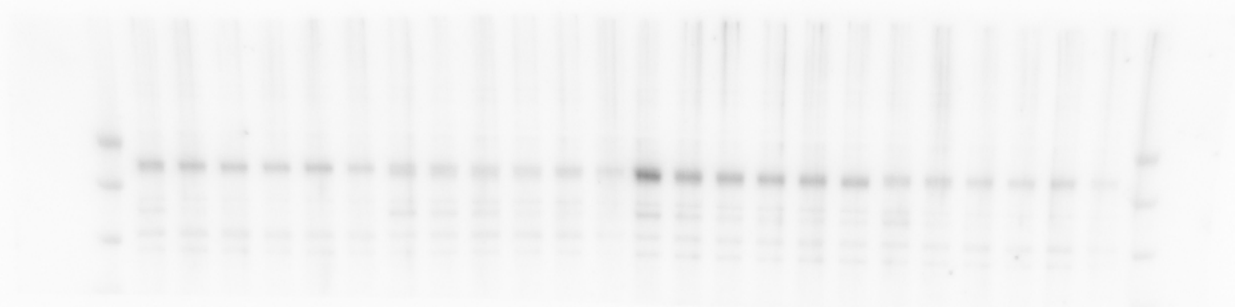


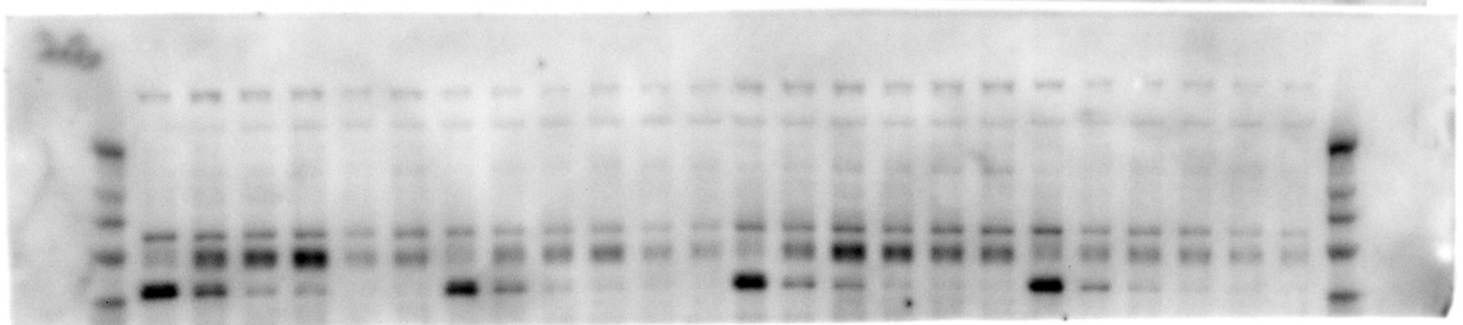
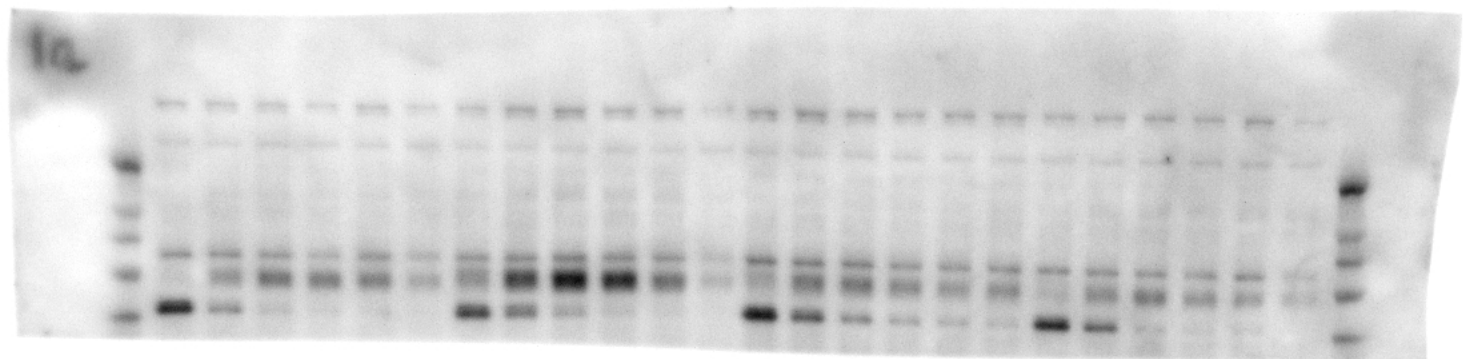


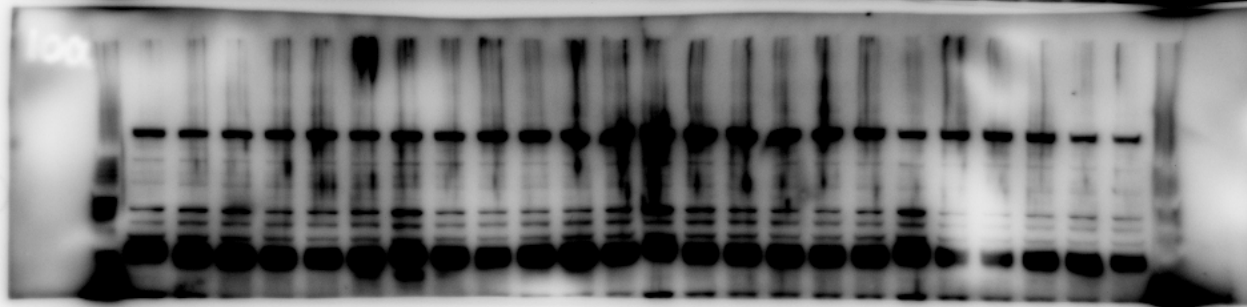
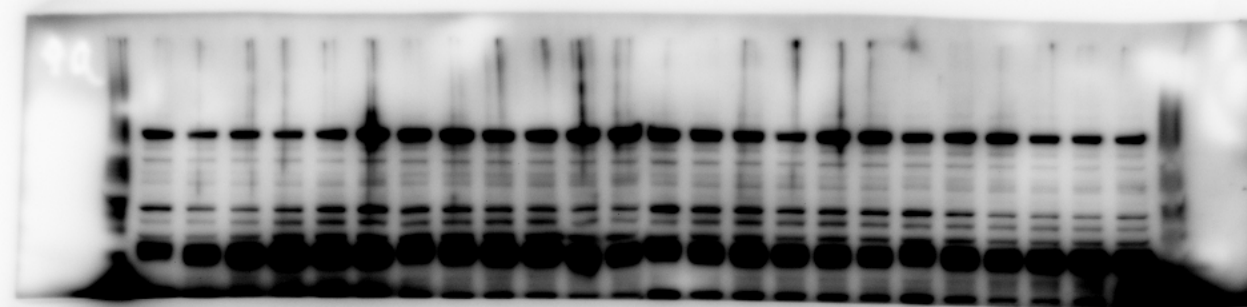
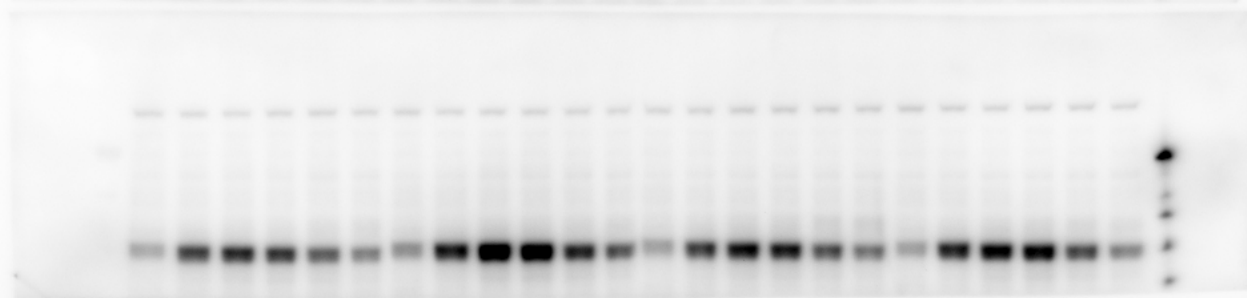
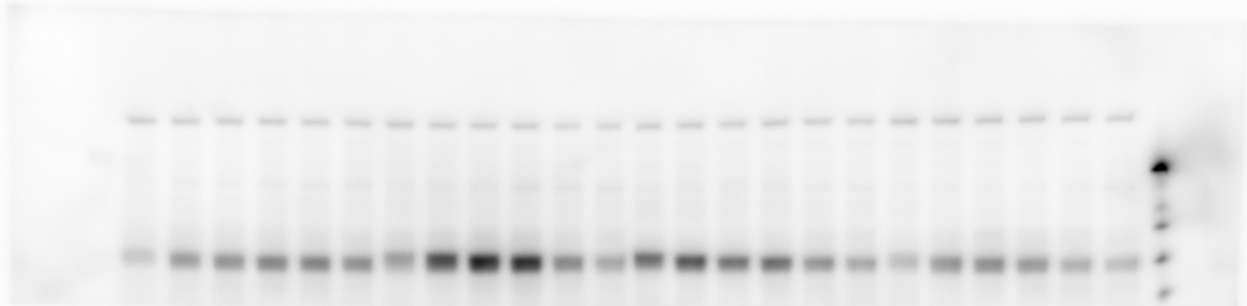


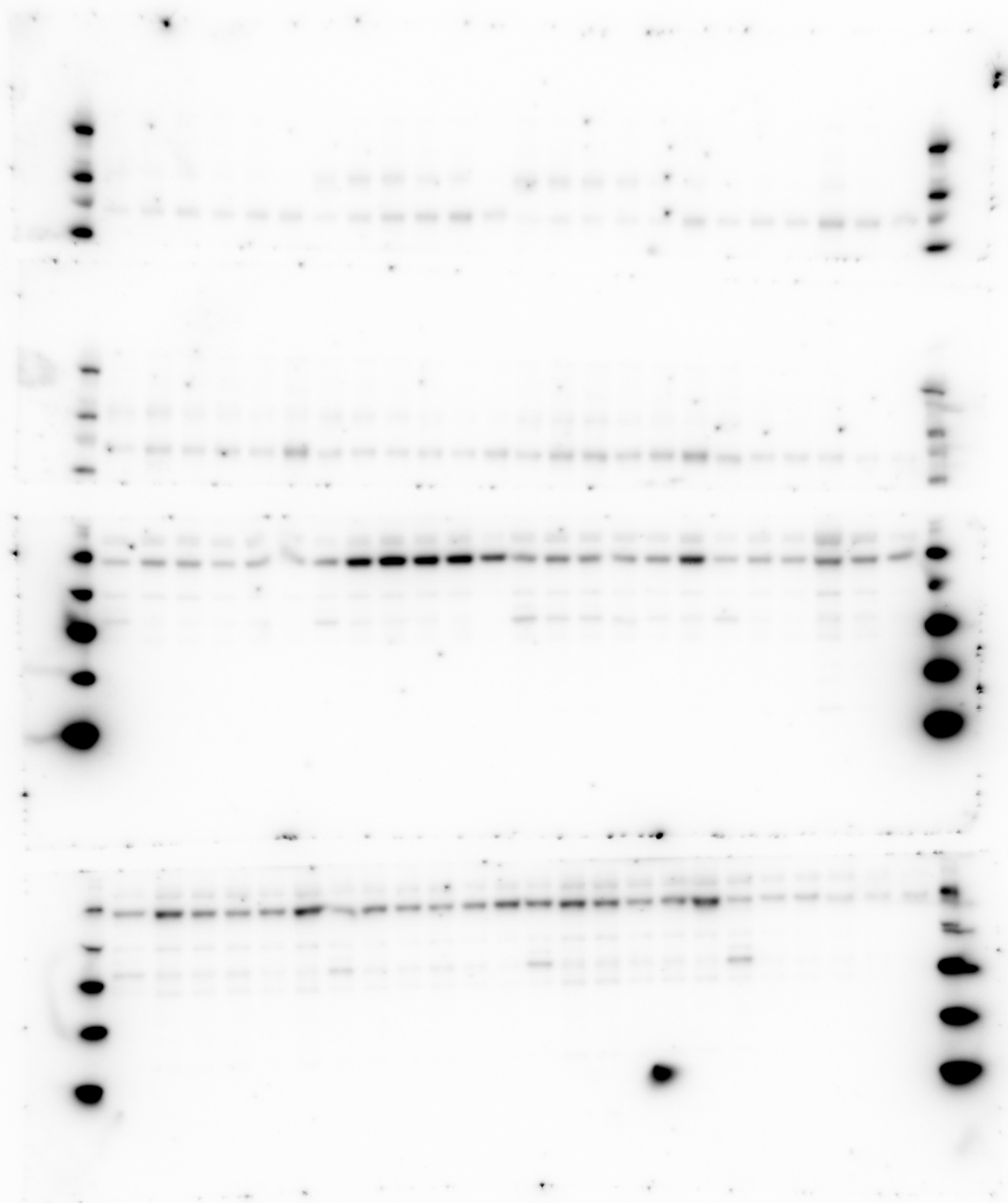


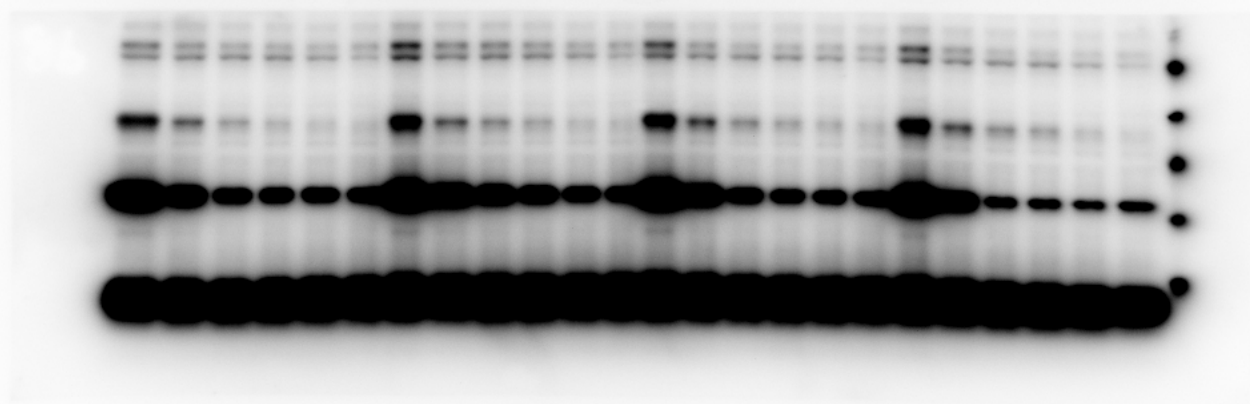
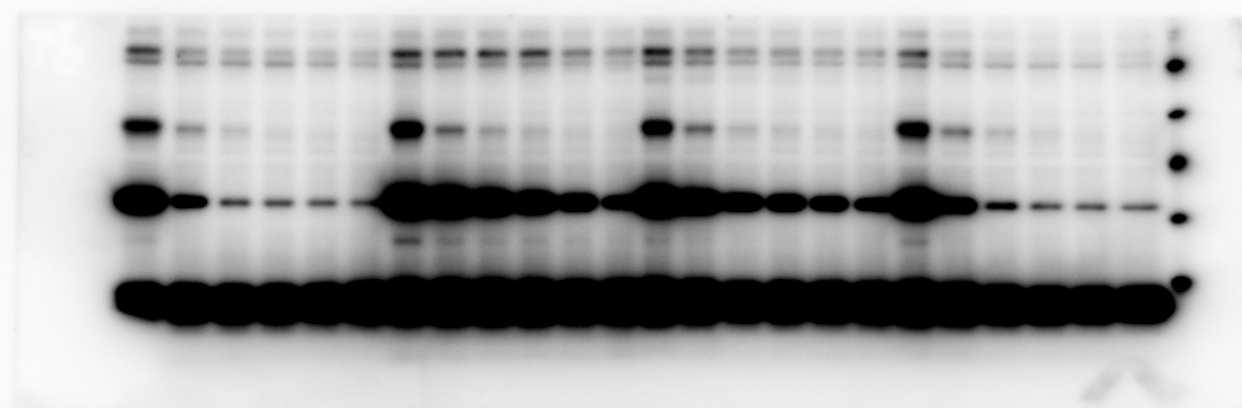
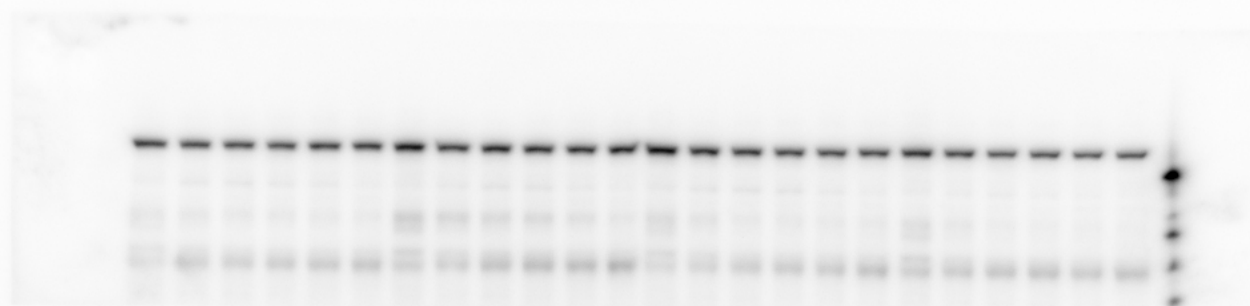
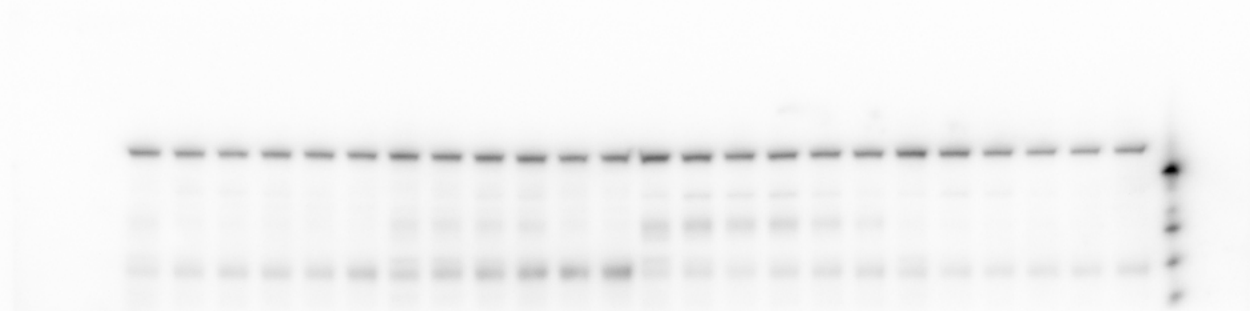


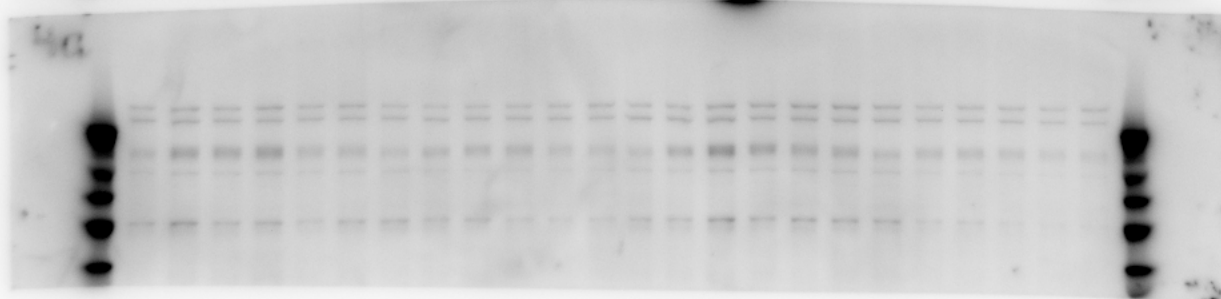
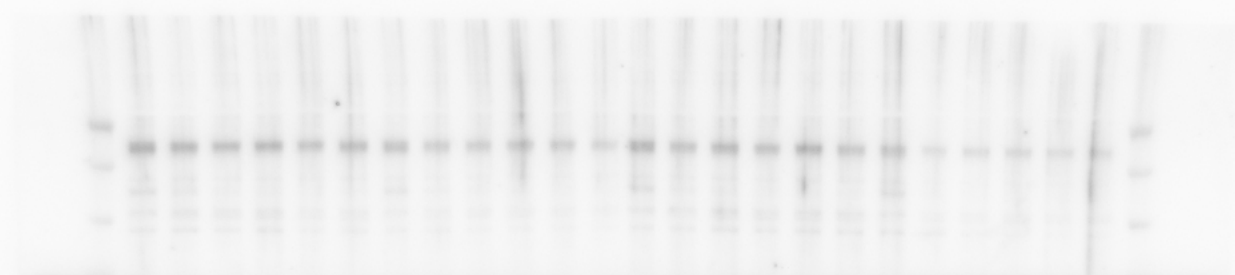
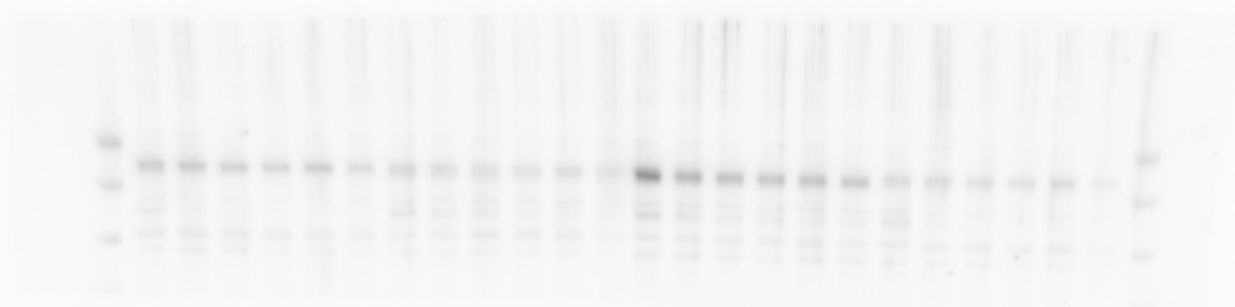


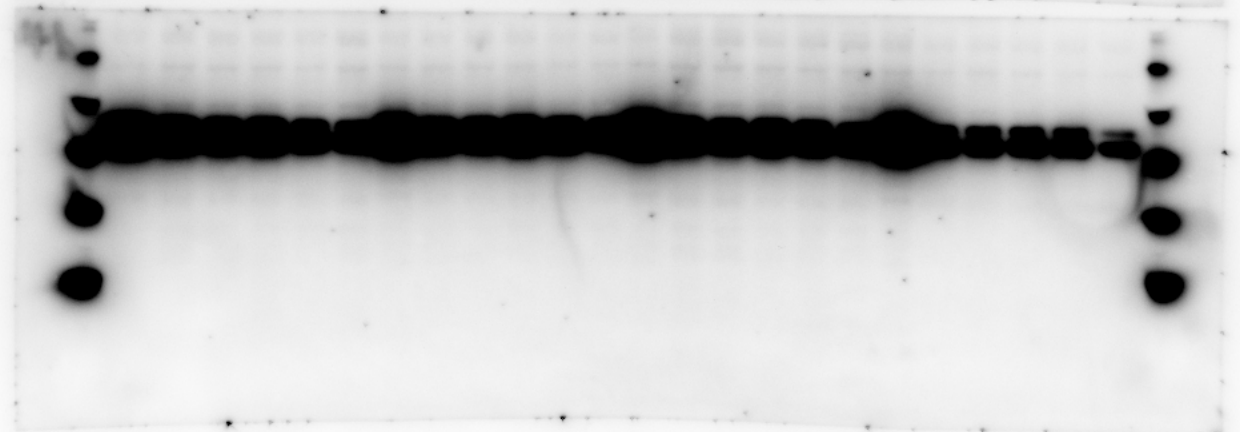
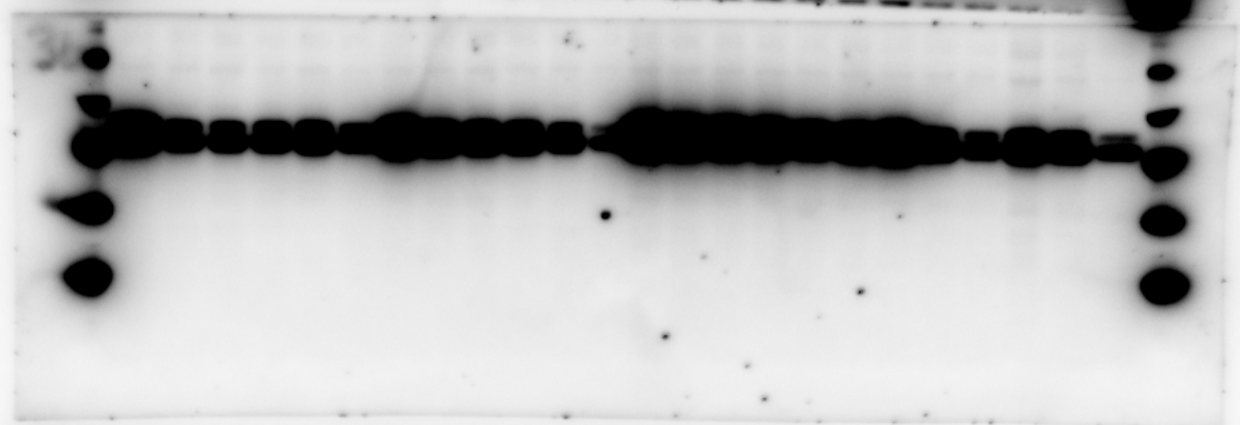
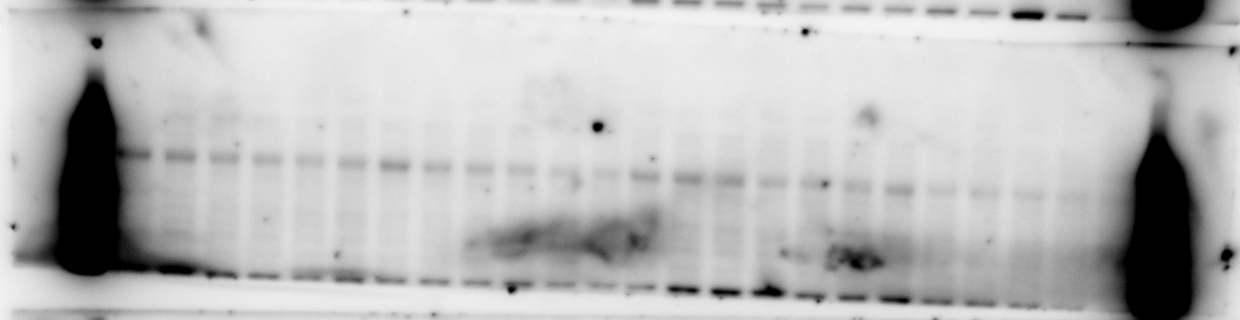
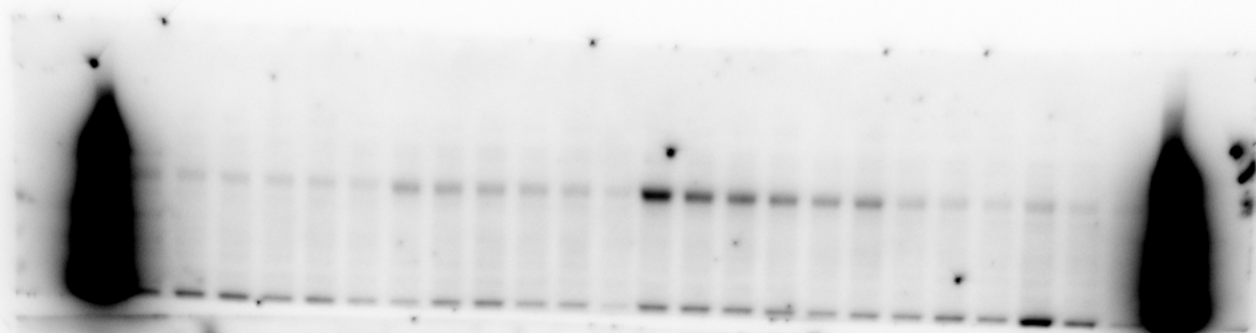


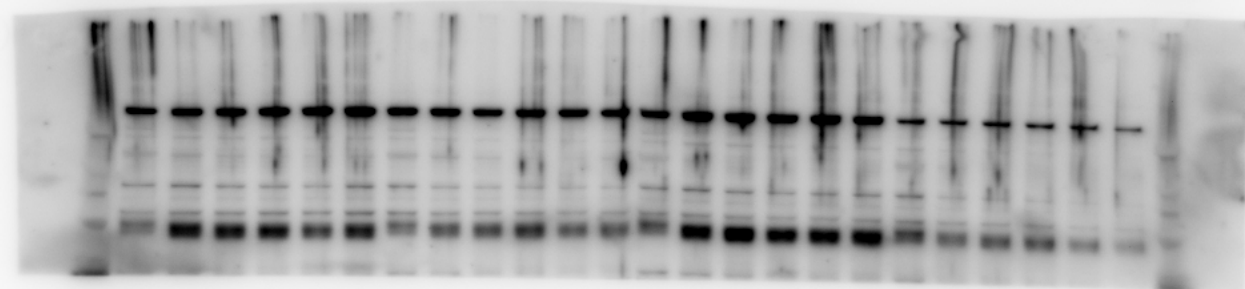
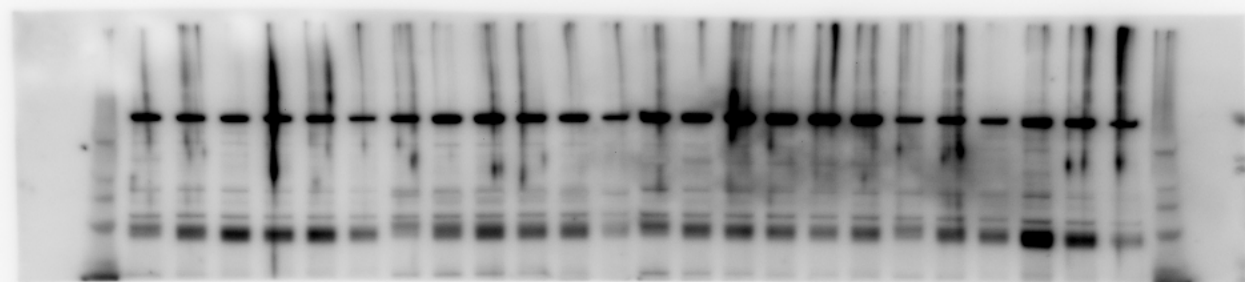










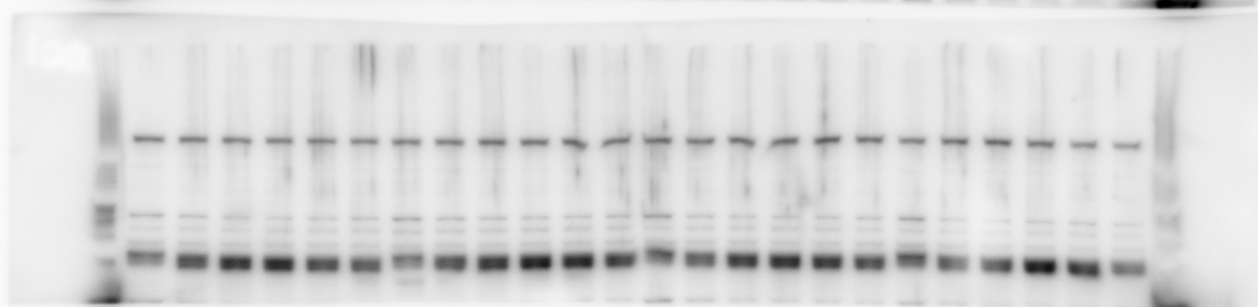
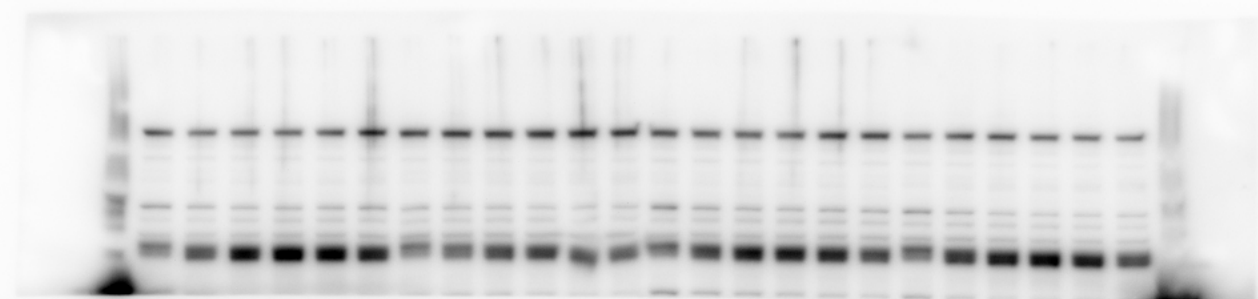


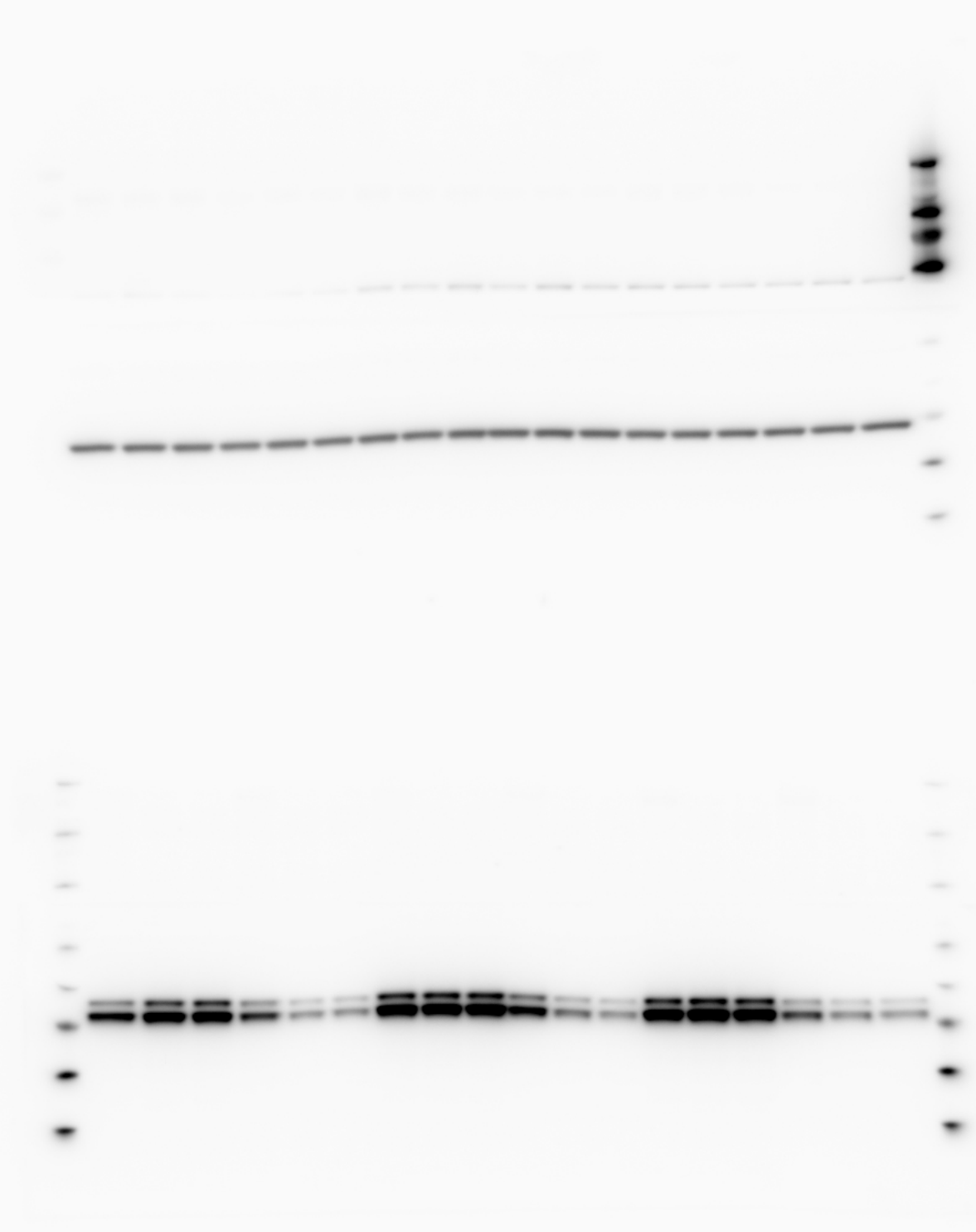
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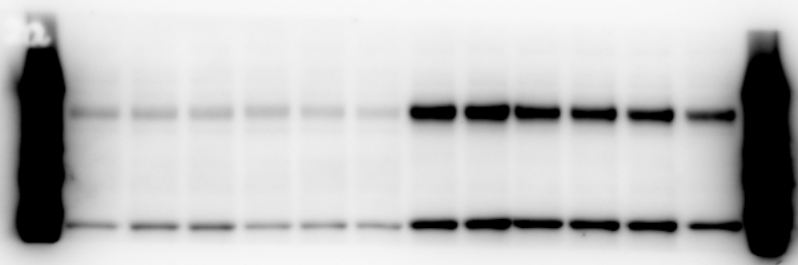
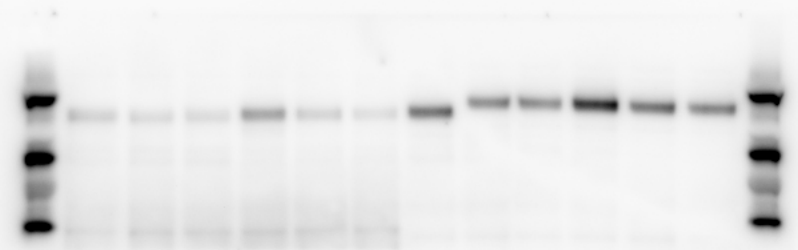
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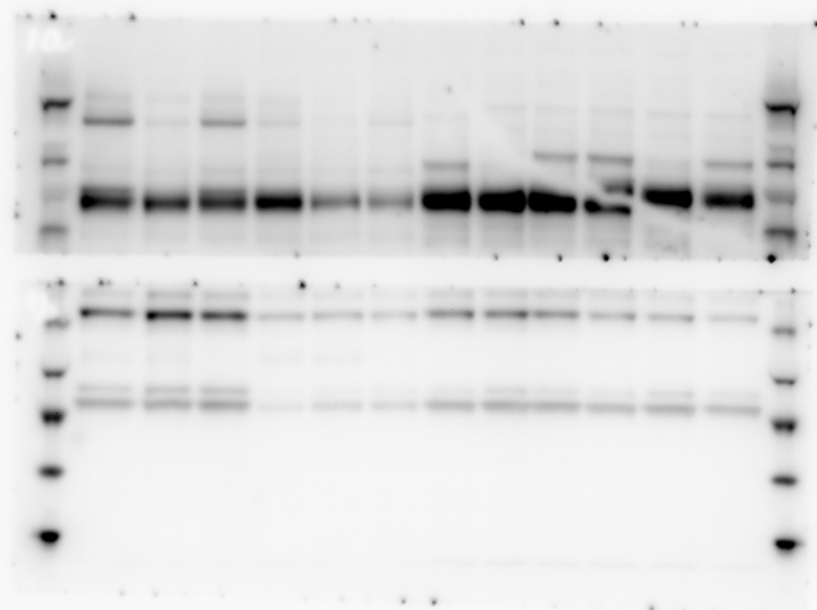
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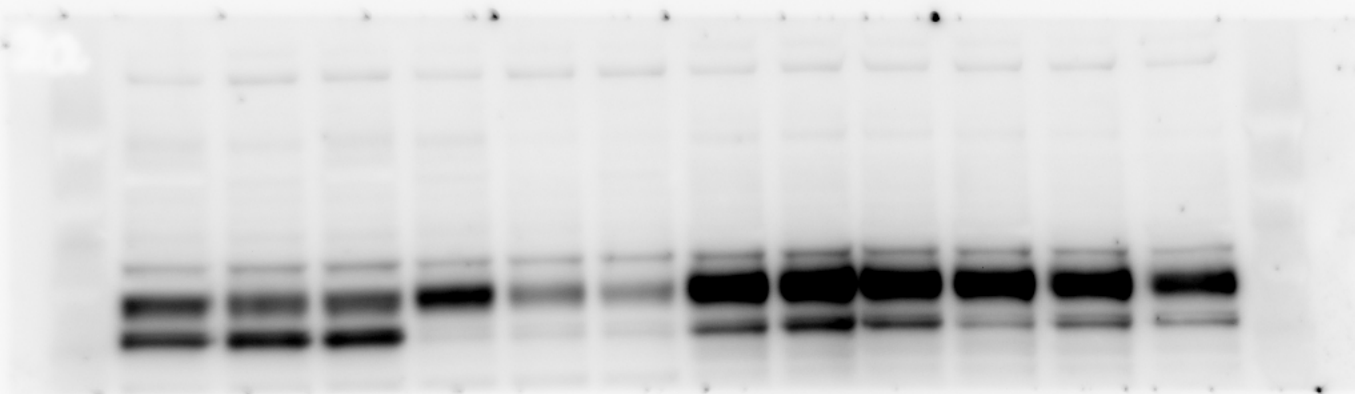
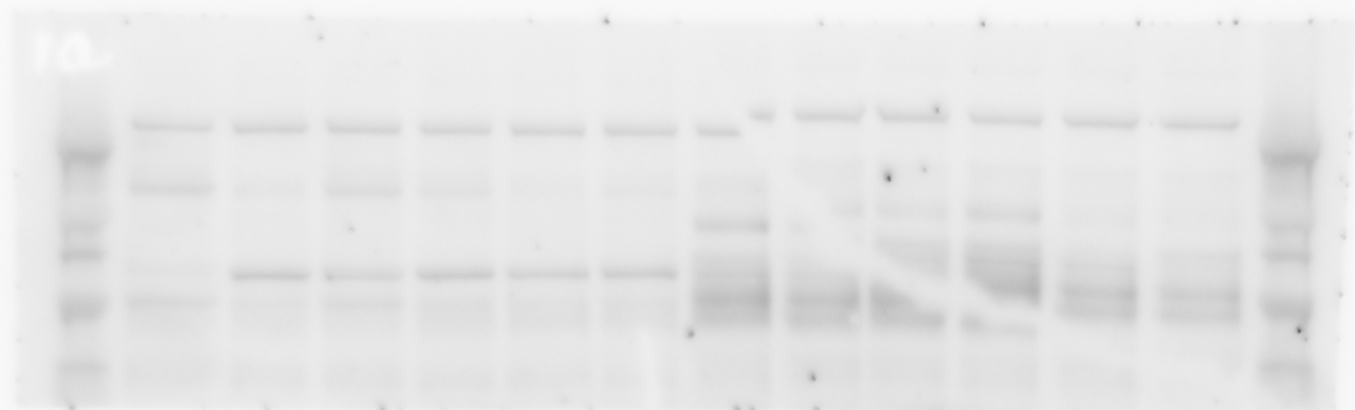
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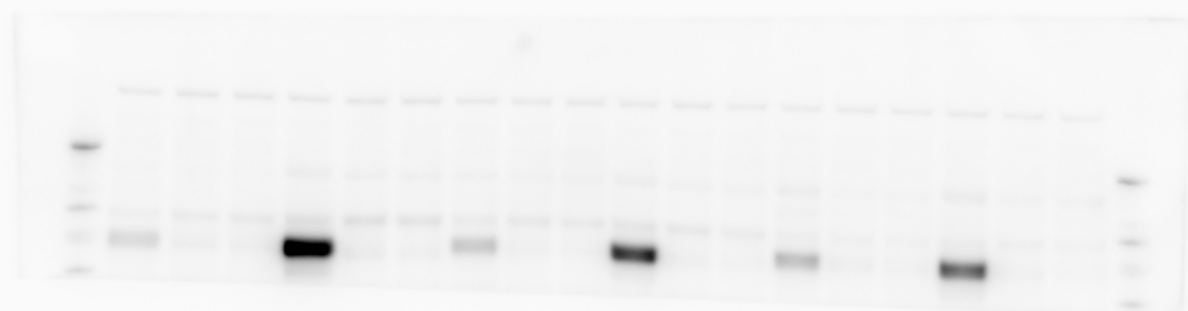
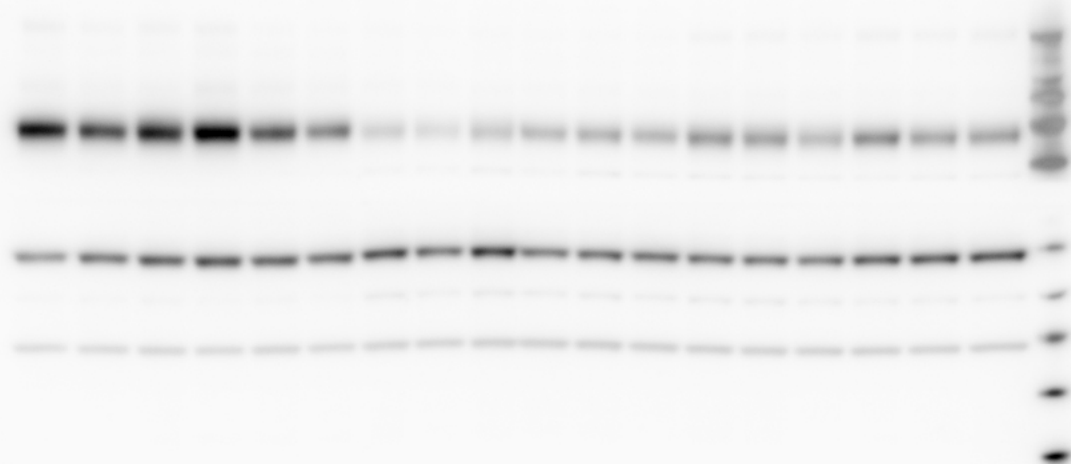


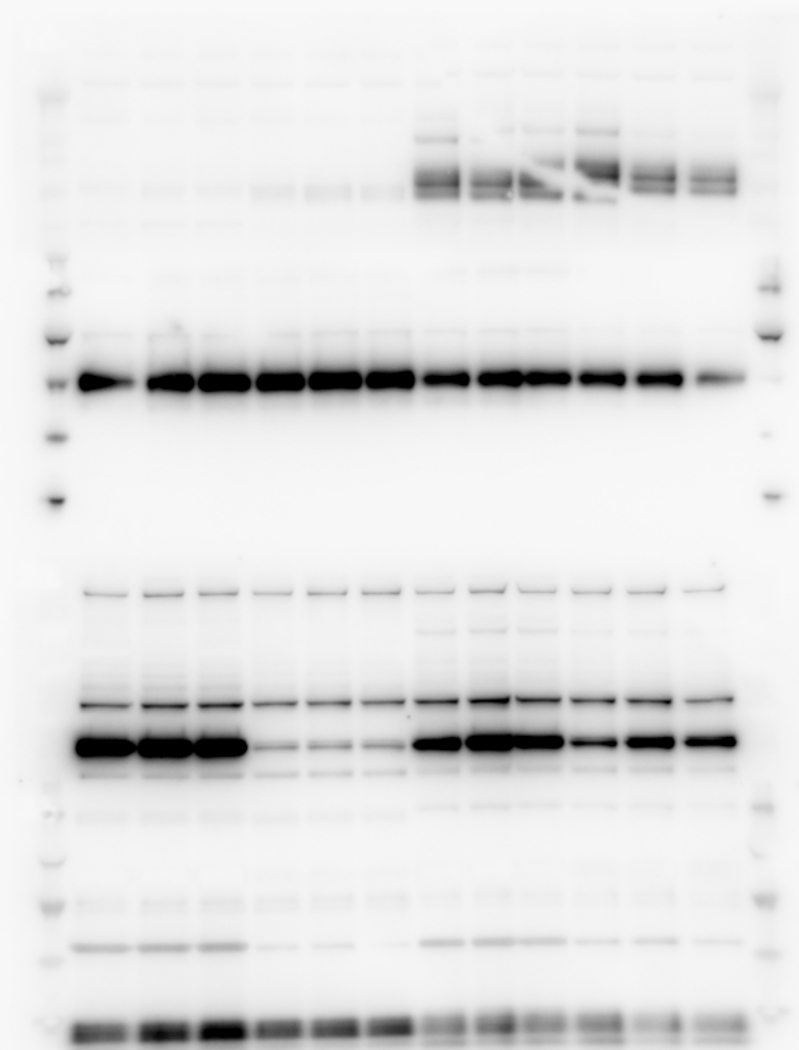


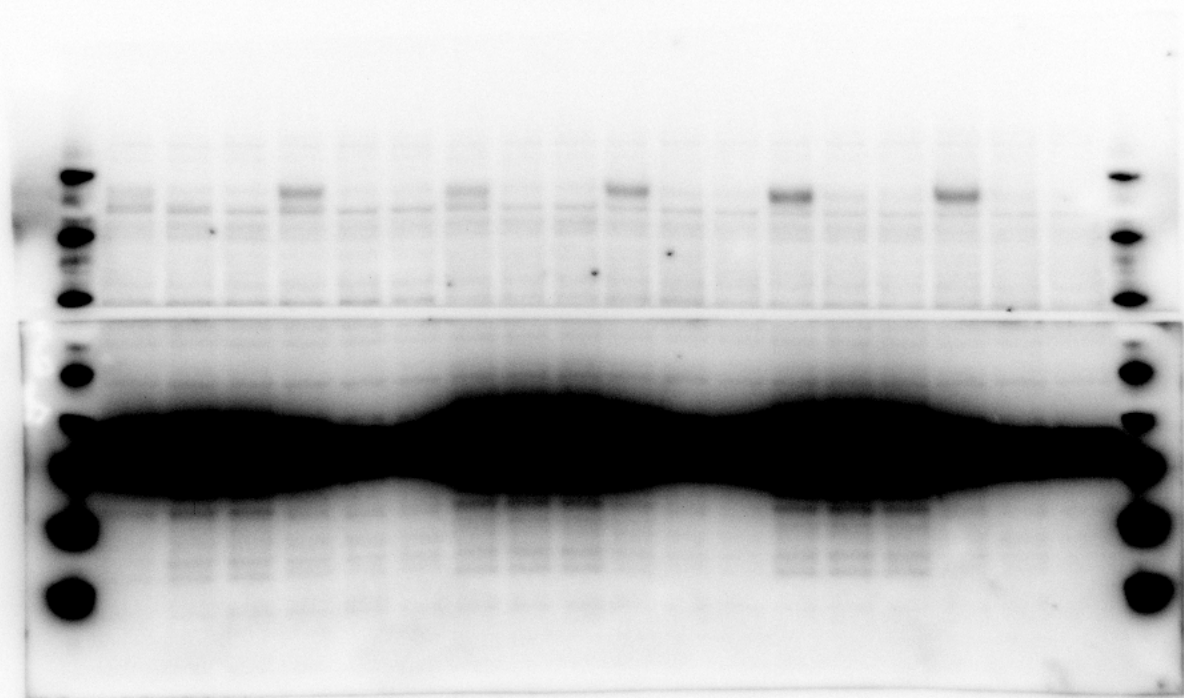
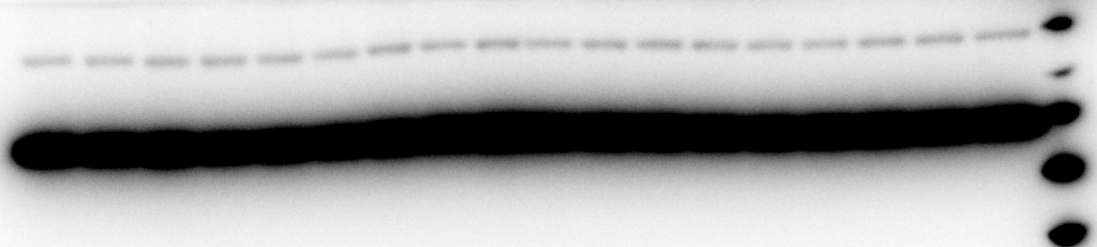
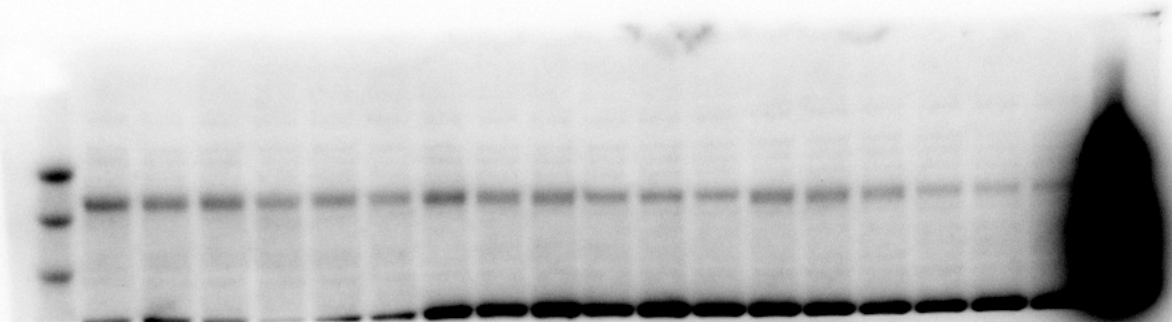


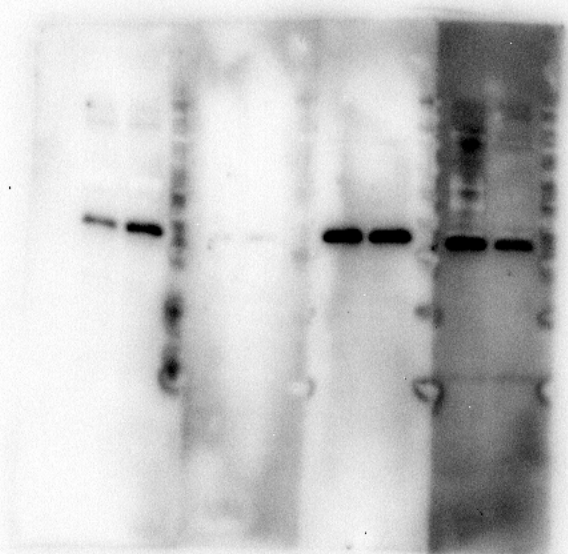
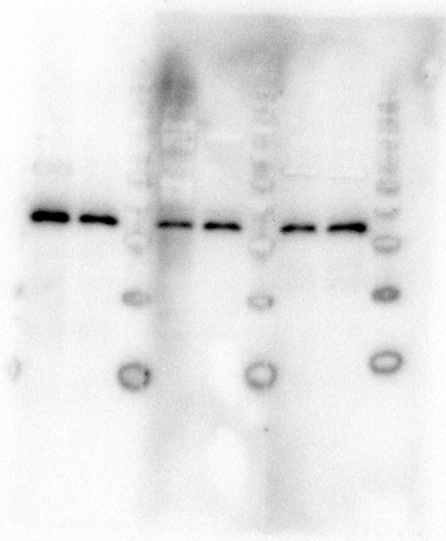
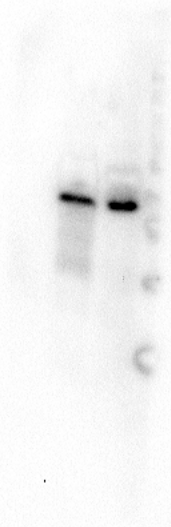


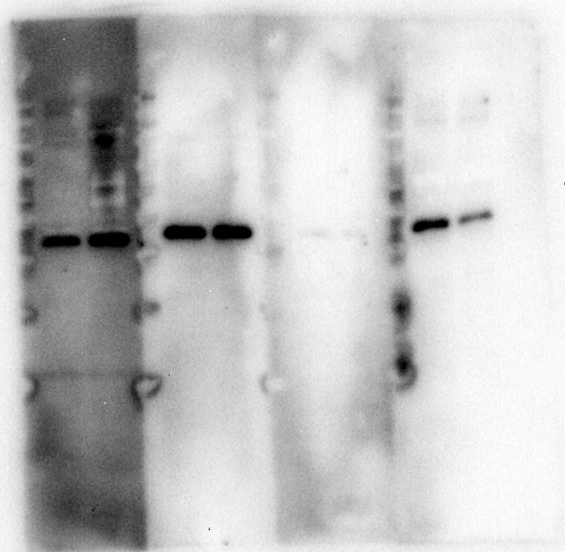
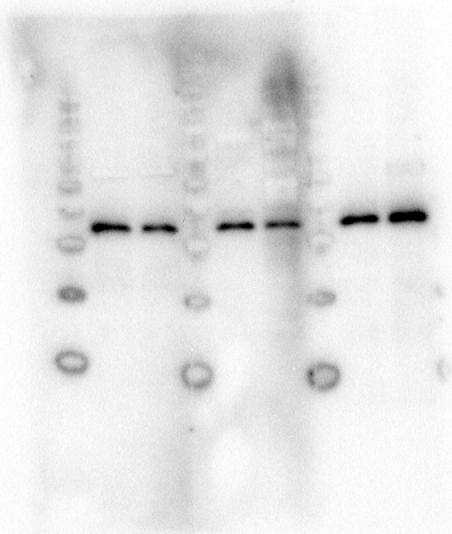


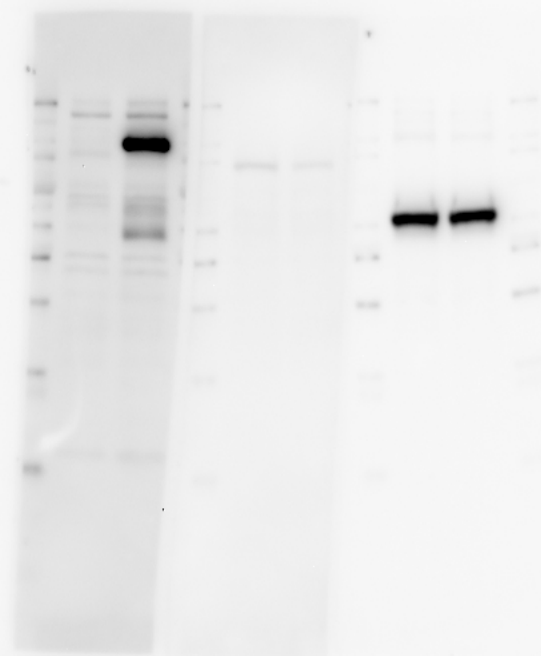
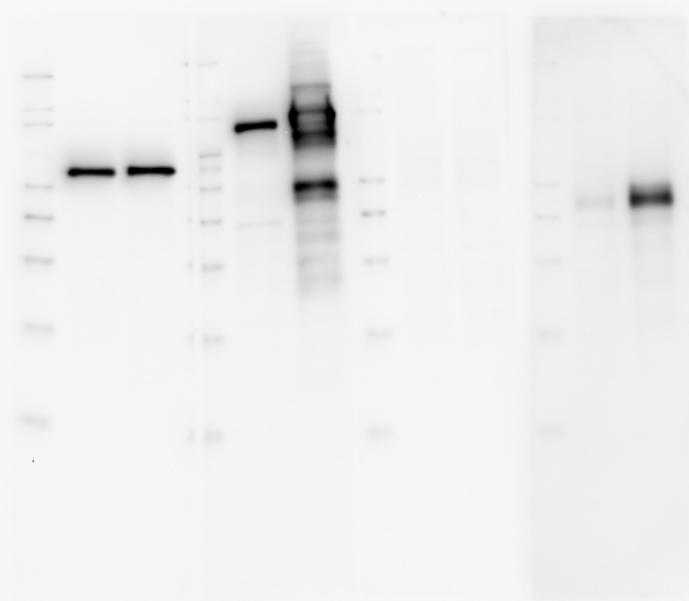


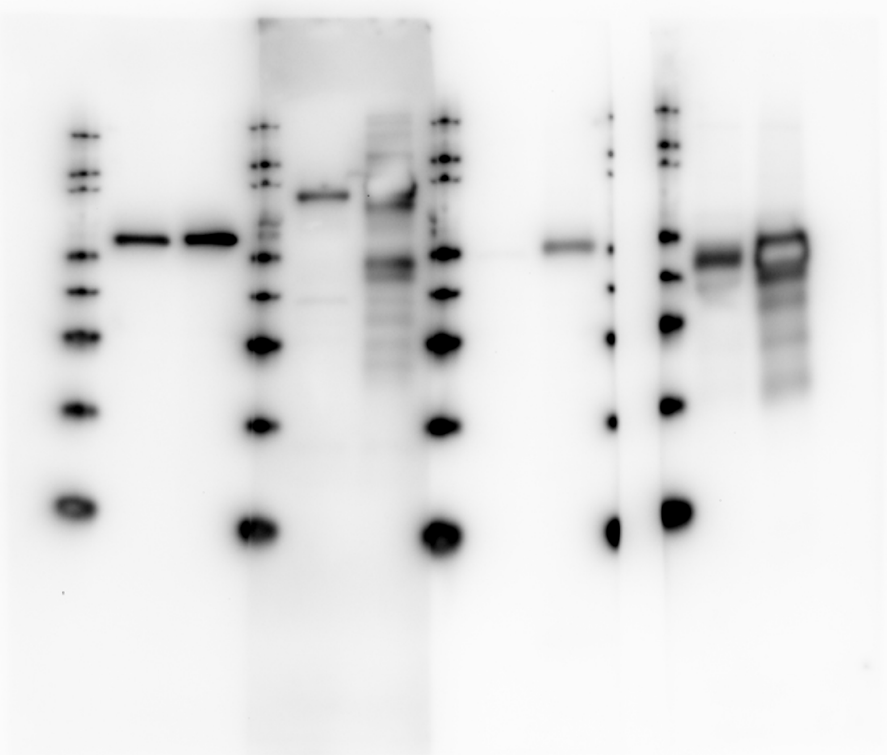
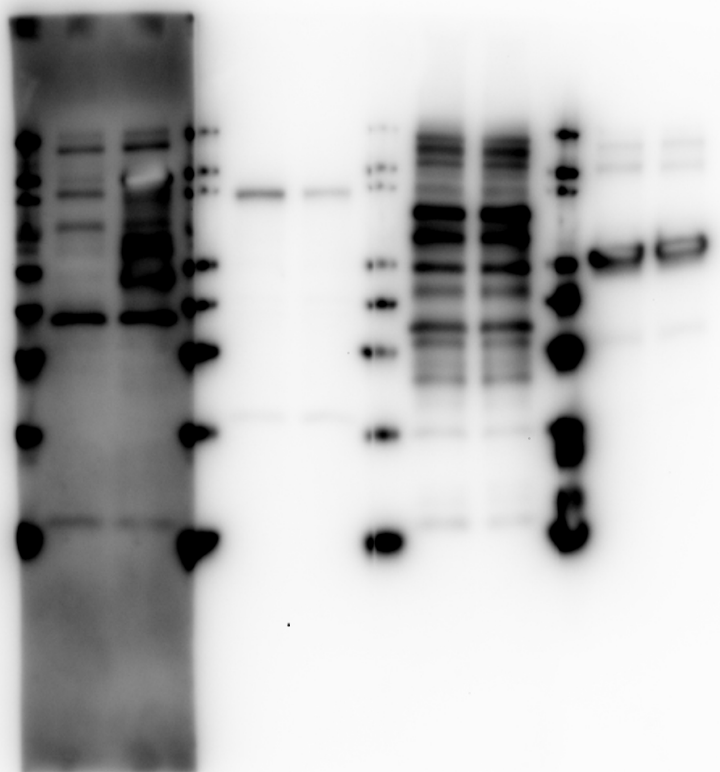


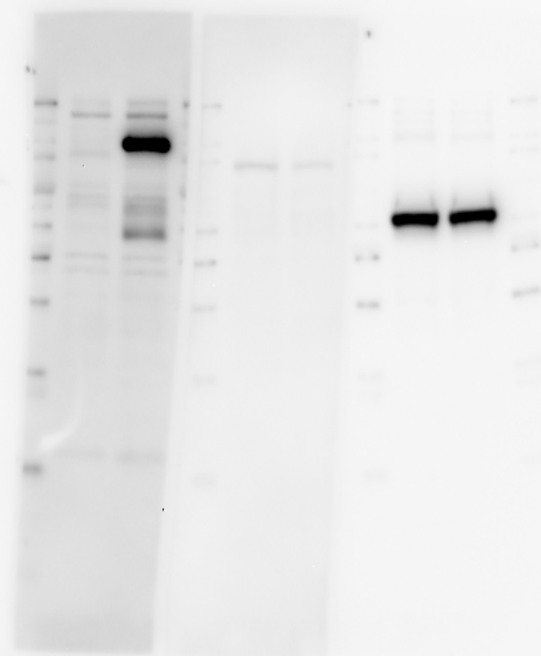
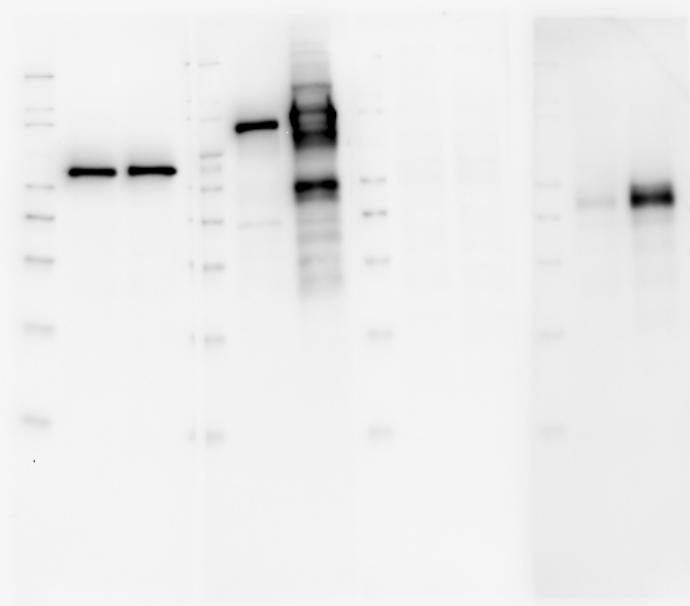


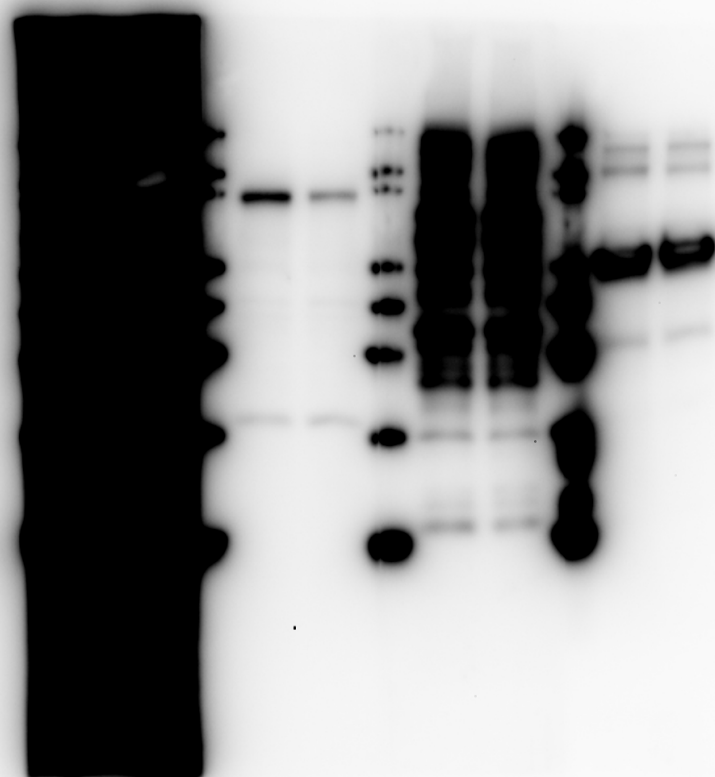
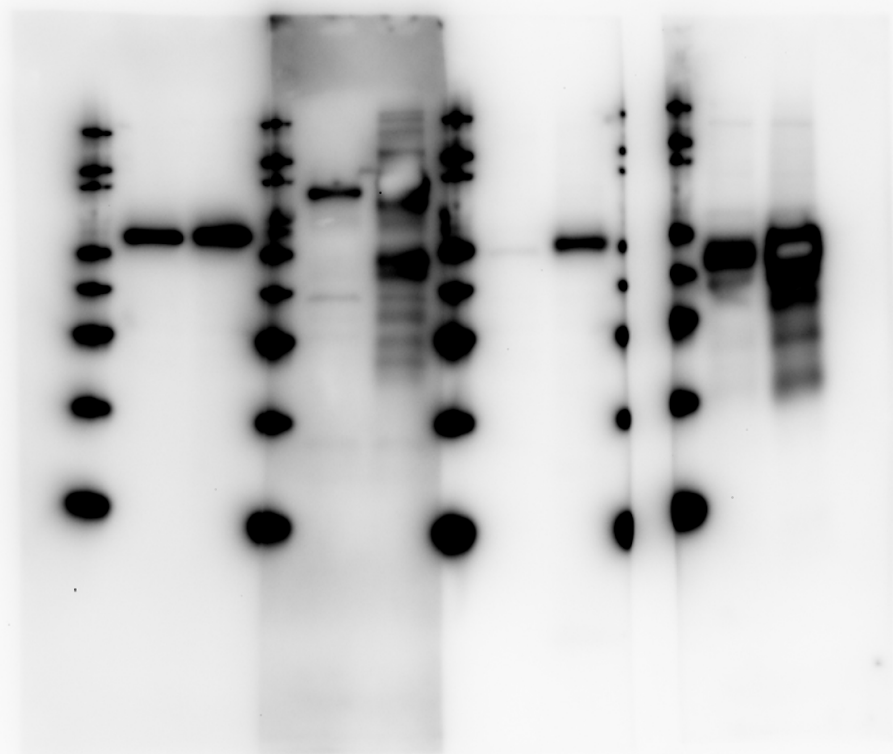


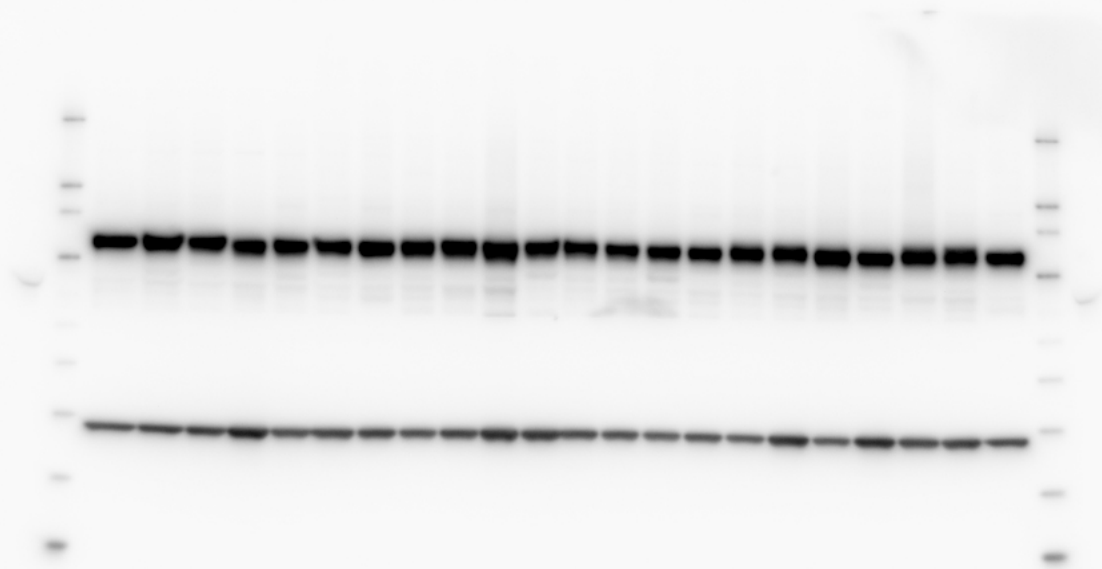
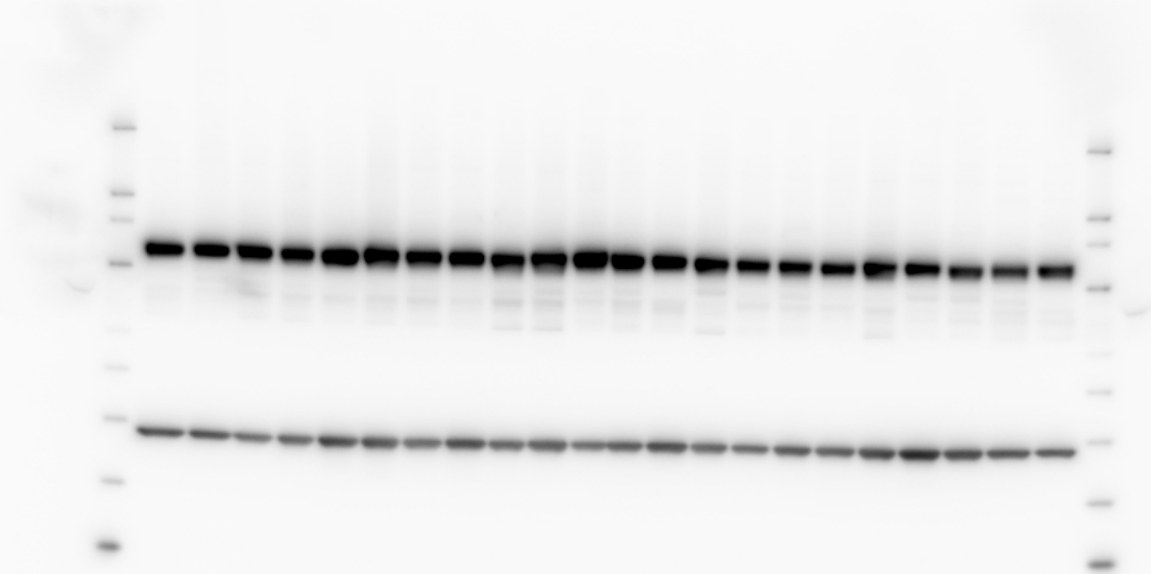


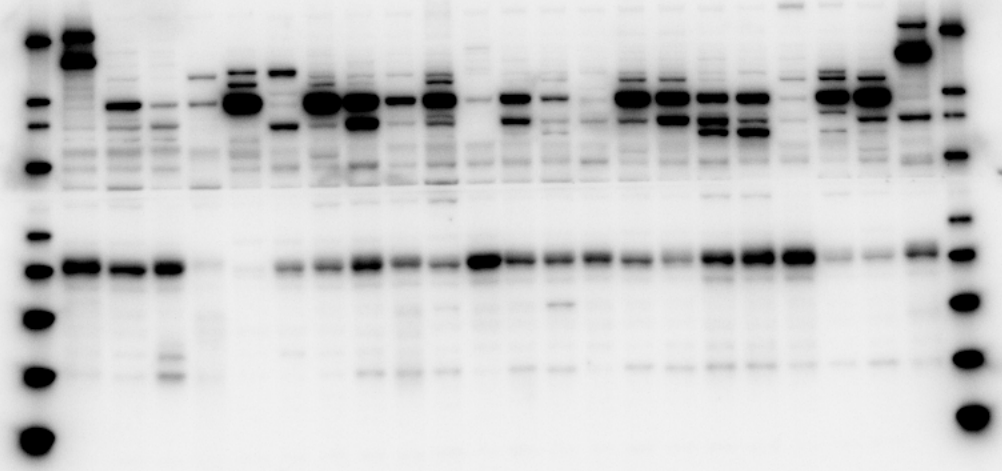
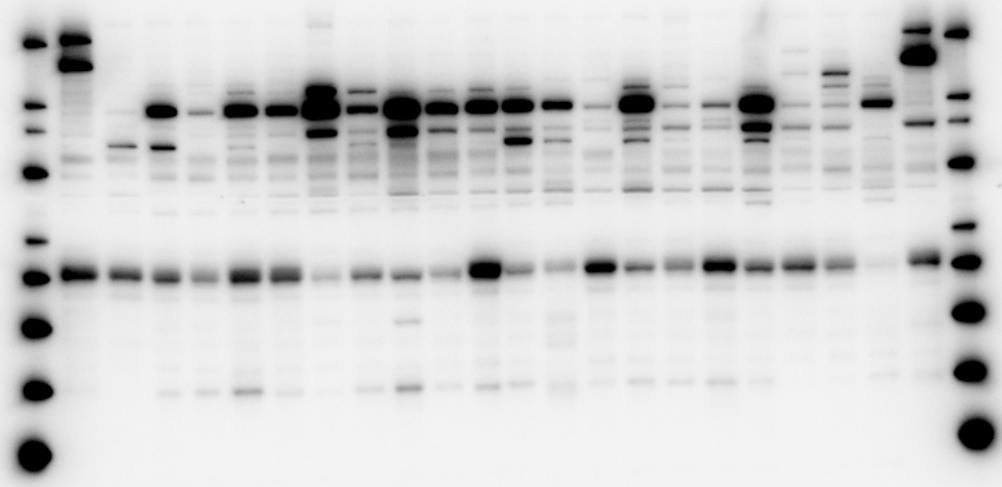


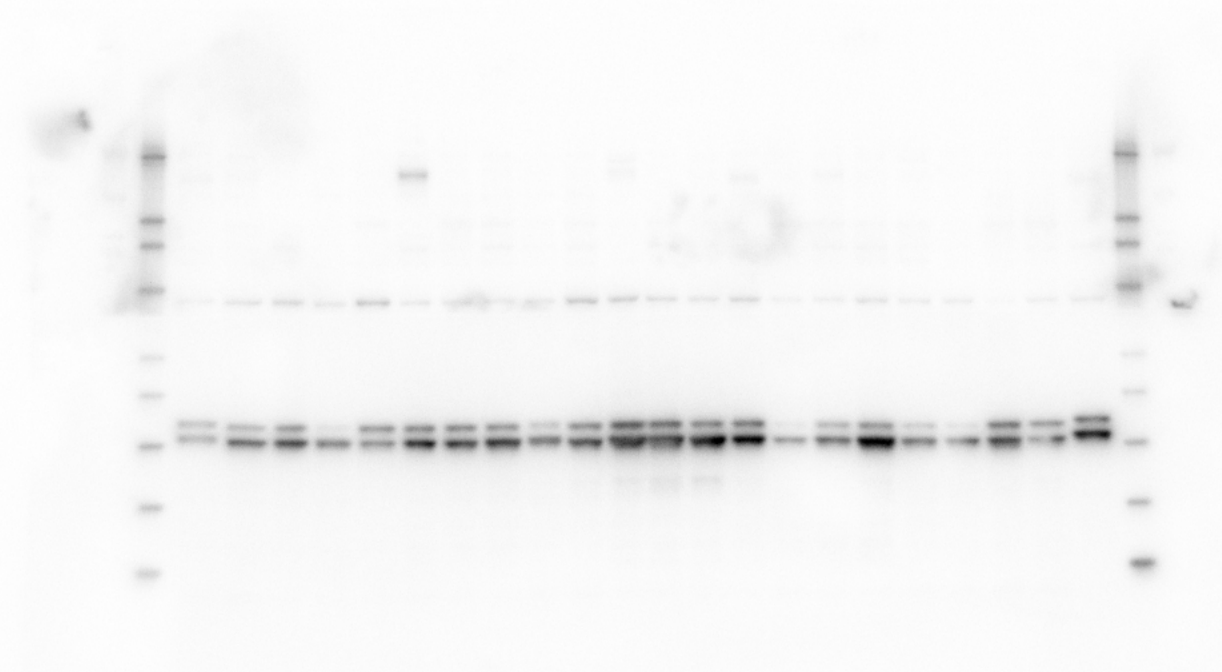
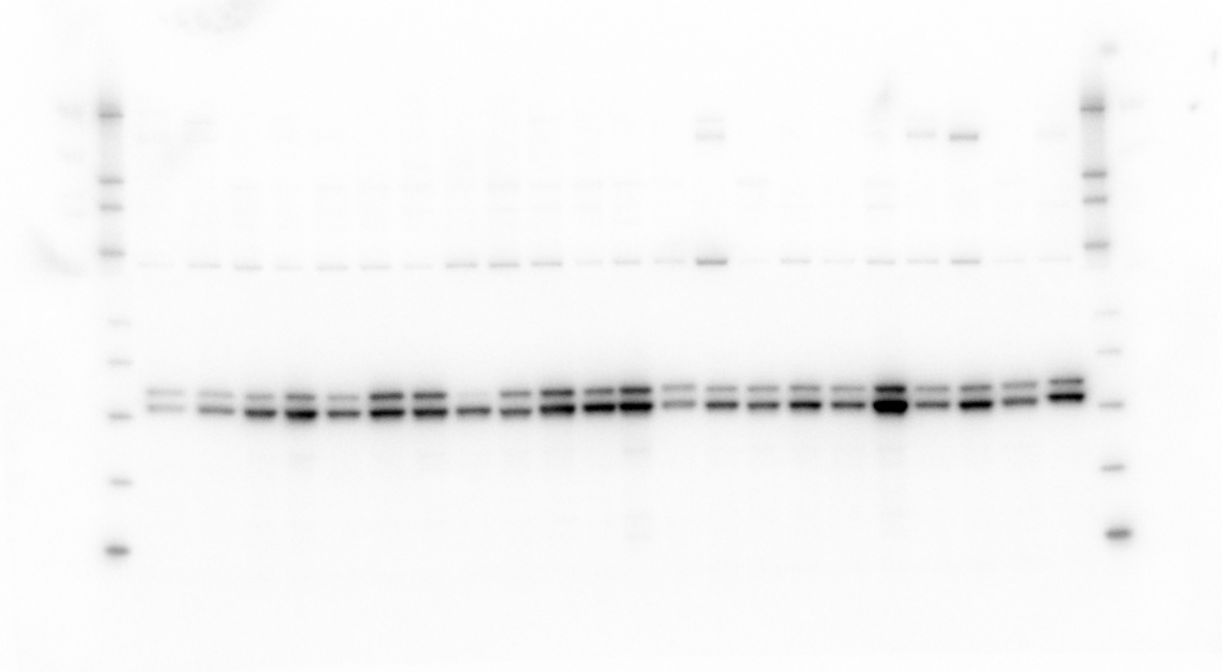


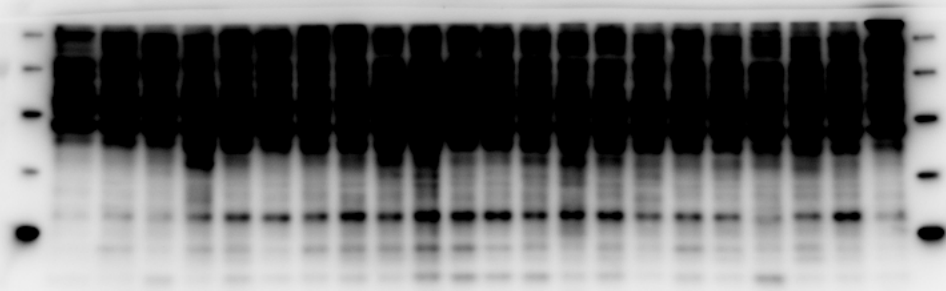
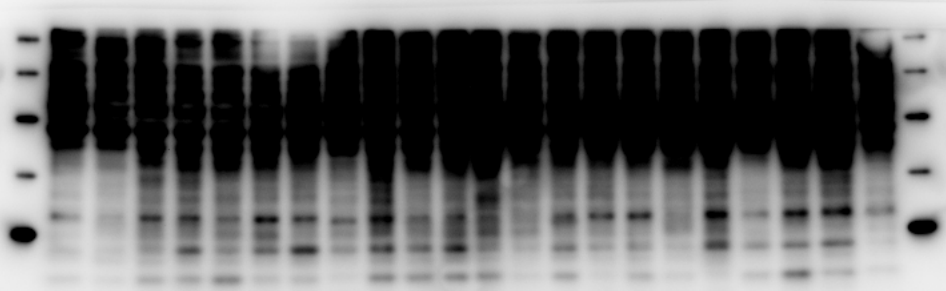
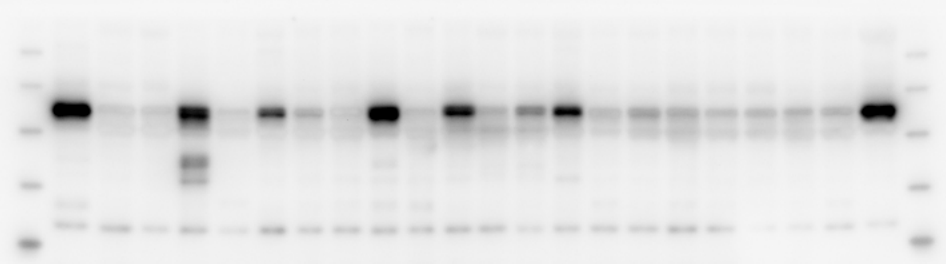
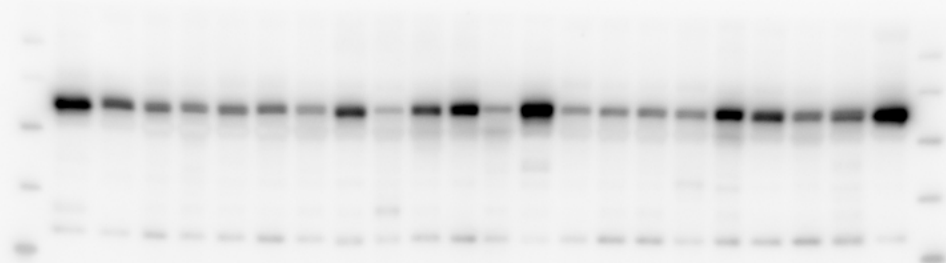


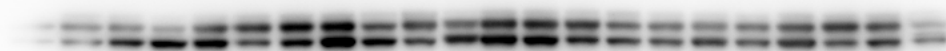
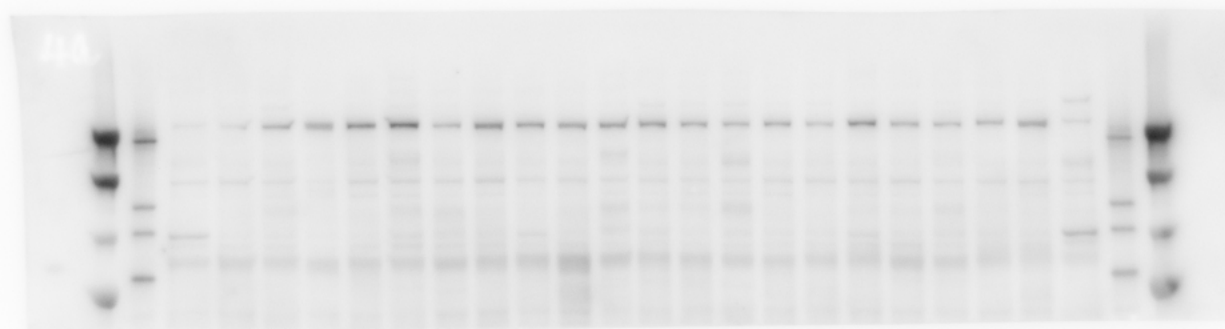
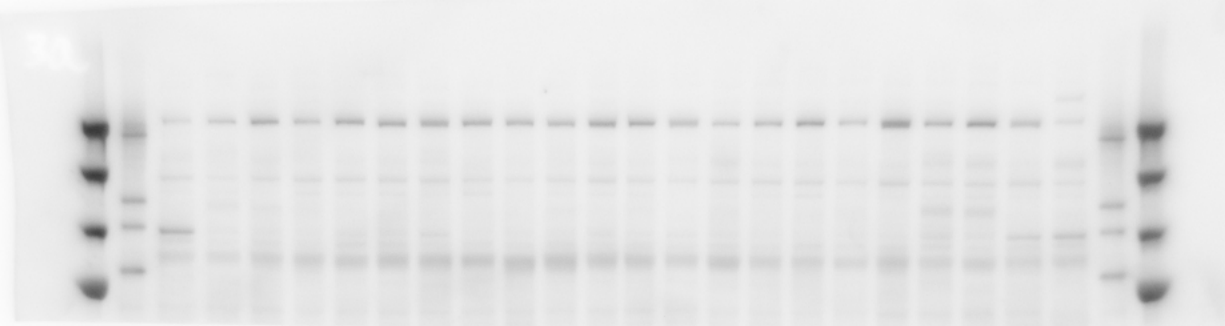


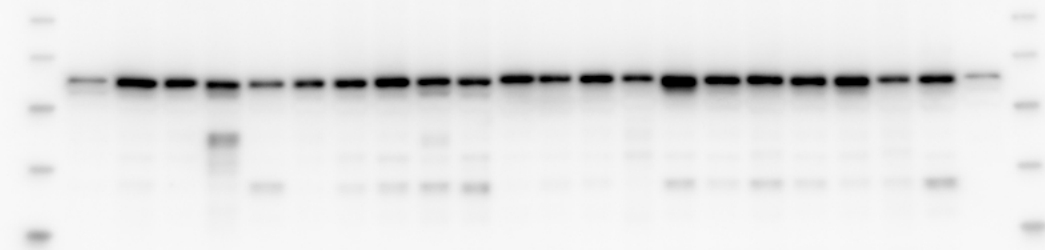
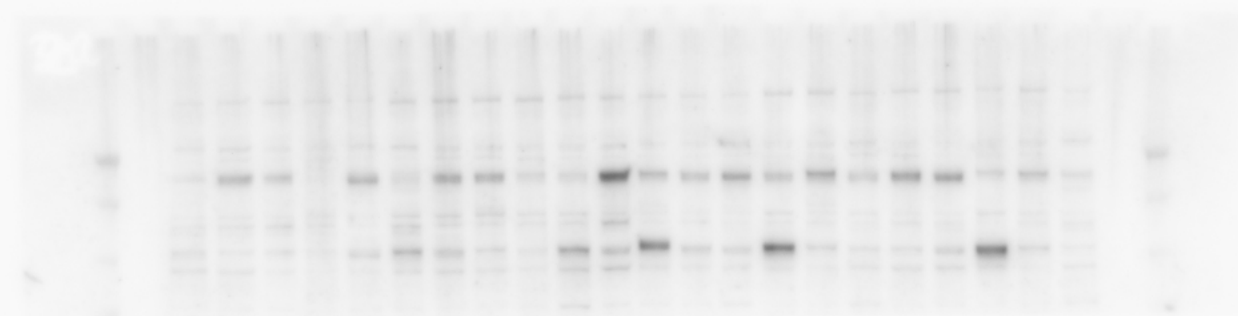
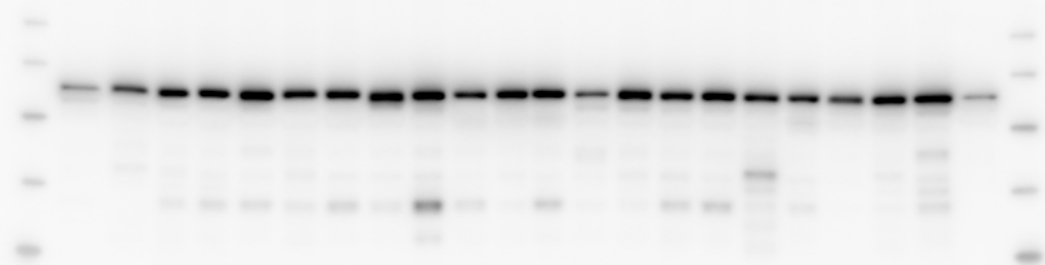












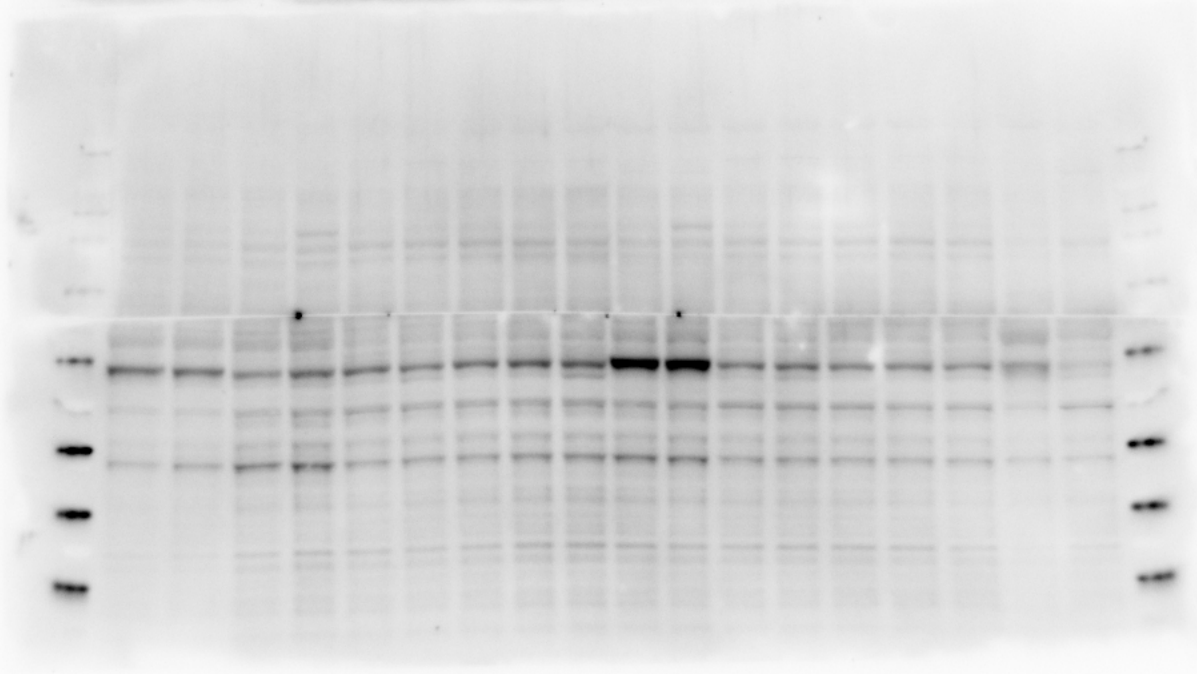
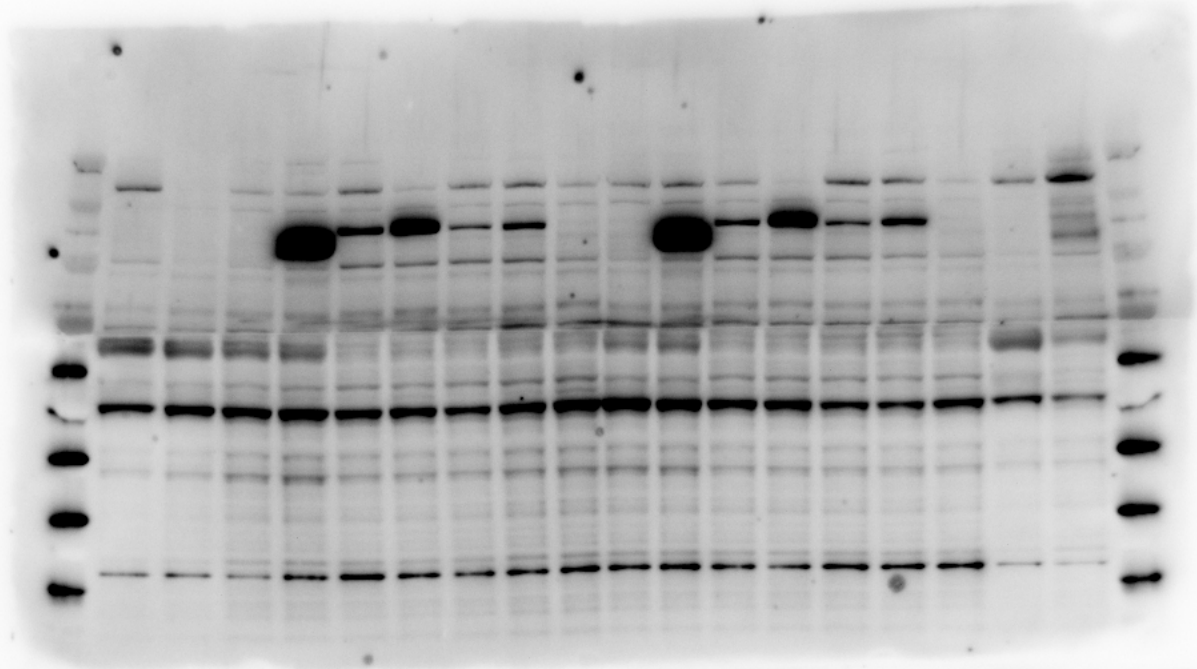
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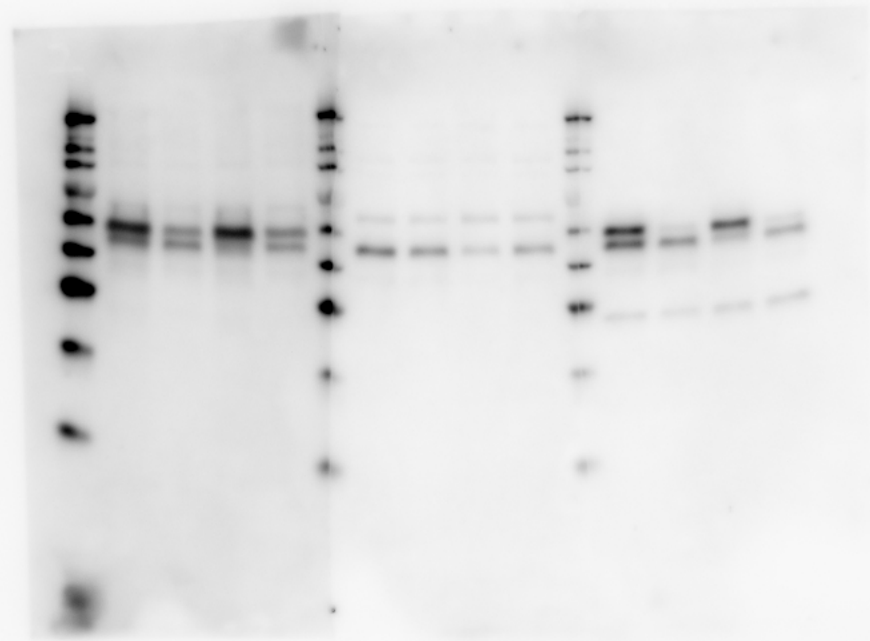
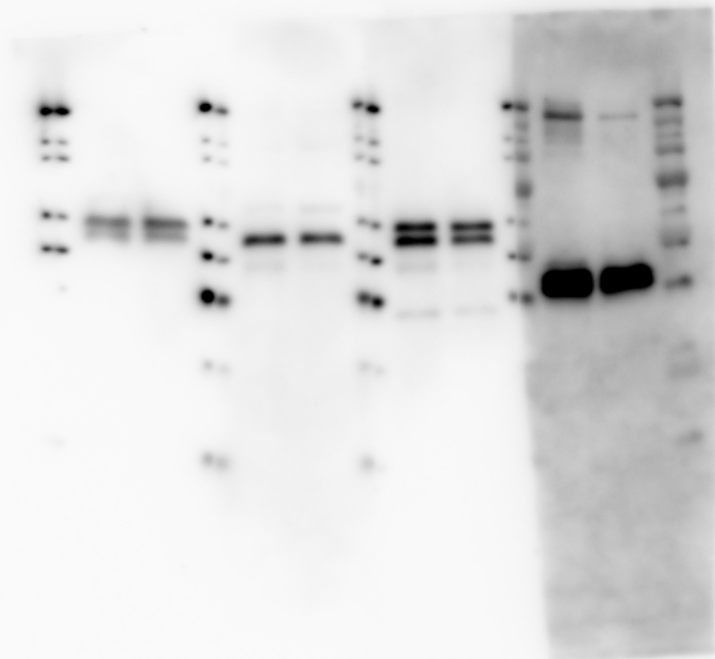
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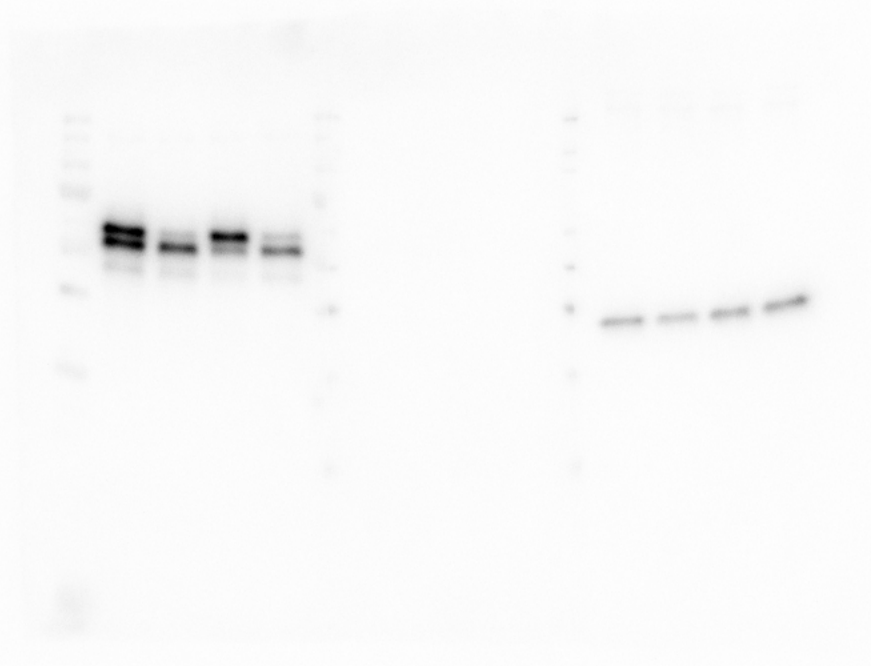
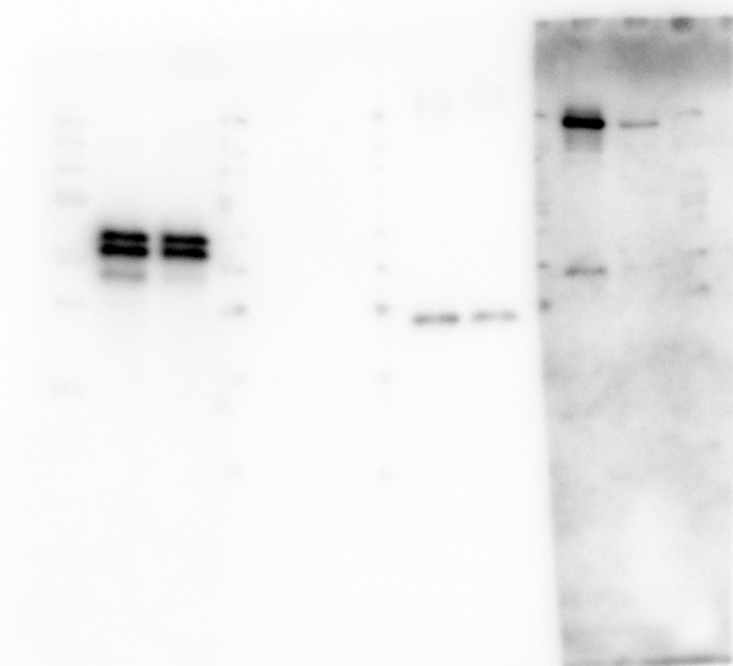
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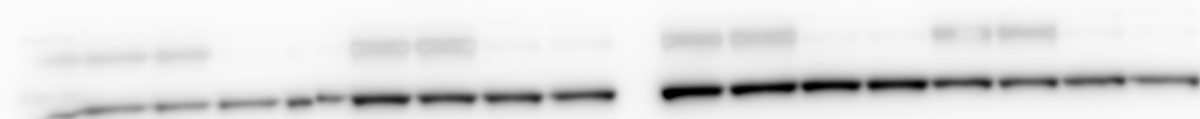
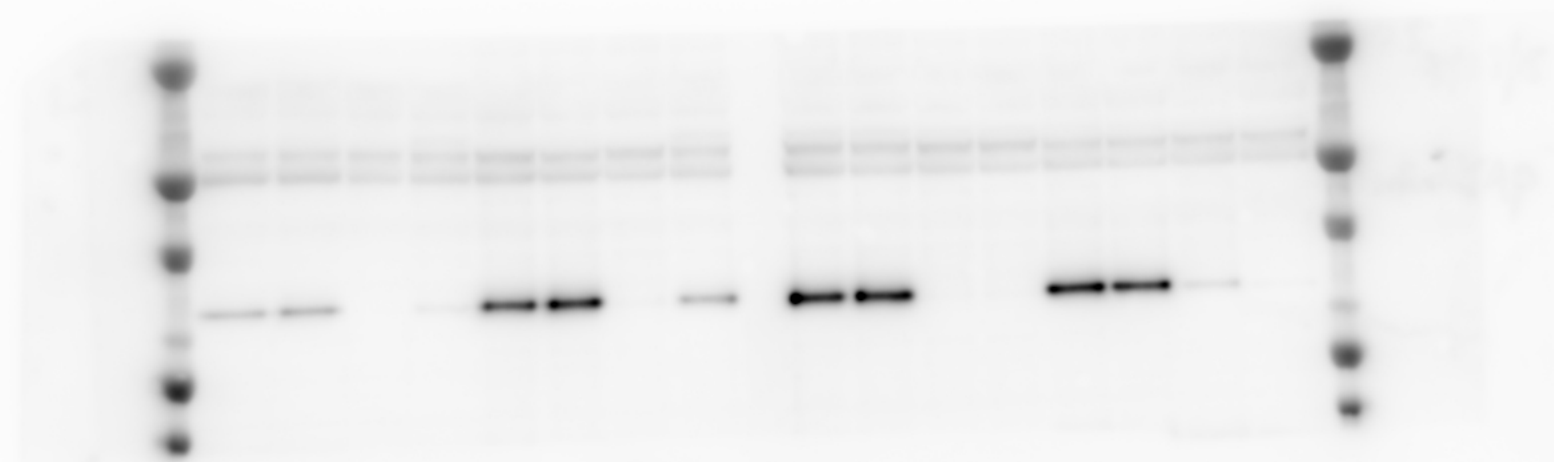
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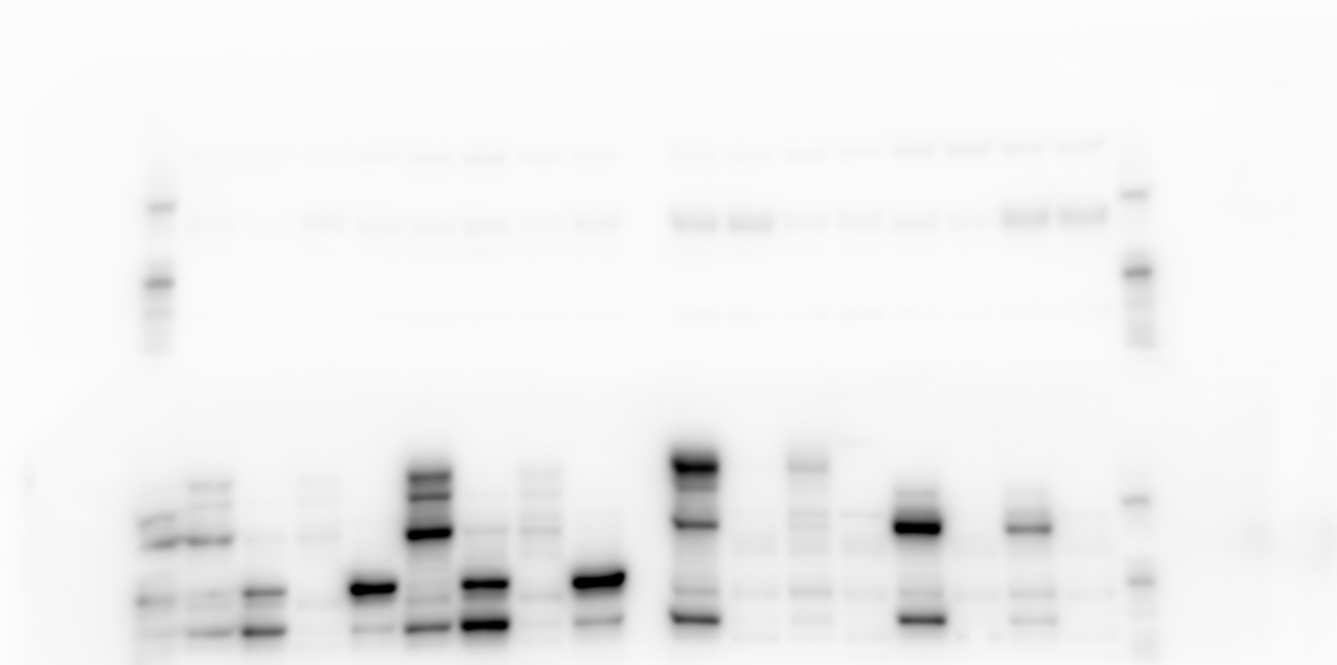


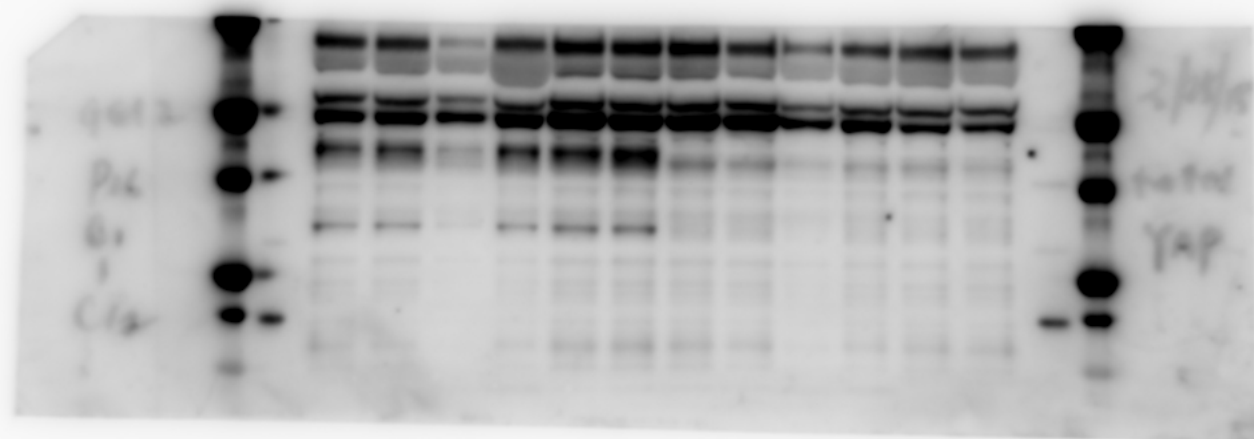


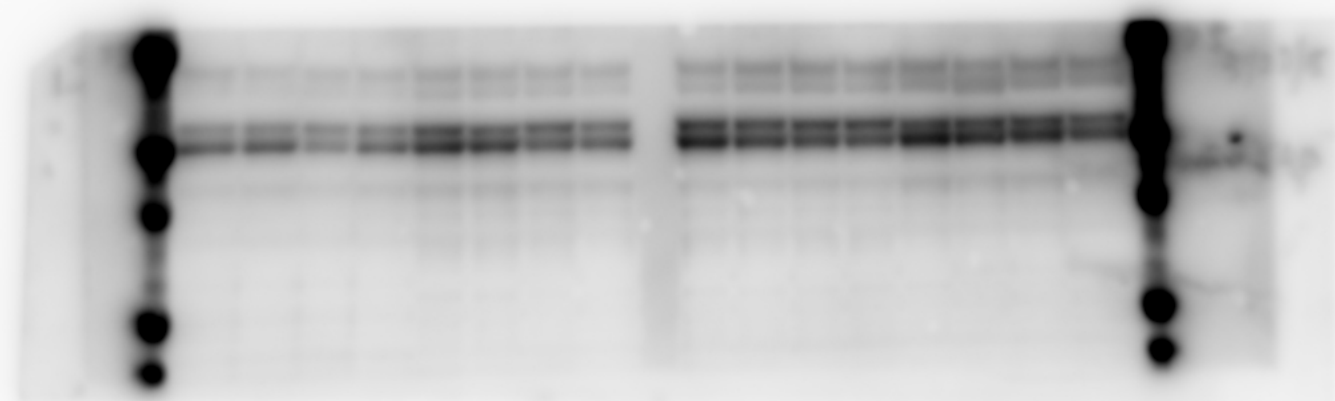












list of original immunoblot image files

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166	Fig3D_pAKT308_WBS140506_WB140508_pIGF1Rb pAKT308 exp2 #8
167	Fig3D_pAKT473_WBS131017_WB140114a_WB140114 pAKT p4EBP #5
168	Fig3D_pERK_WBS131017_WB140108b_tEGFR pERK #5
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171	Fig3D_pS6_WBS131017_WB140113a_WB140113 pS6 tS6 #3
172	Fig3D_pS6k_WBS131017_WB140110a_pS6K tS6K #5
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174	Fig4B_WWTR1_WBS140415_WB140424_WWTR1 pAKT473 #5
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177	Fig4D_GAPDH_WBS150323_WB04102015_top(GAPDH)_bot(pS6K)#5
178	Fig4D_pYAP_WBS150323_WB04132015_plate 16 E1-E12_p-YAP#5
179	Fig4D_tYAP_WBS150323_WB04132015_plate 16 E1-E12_total-YAP#4
180	Fig4F_GAPDH_WBS150521_WB05282015_17E1-E12_GAPDH#2
181	Fig4F_TEAD1_WBS150521_WB05262015_17E1-E12_top(WWTR1)-bot(TEAD1)#3
182	Fig4F_TEAD1_WBS150521_WB05262015_17E1-E12_top(WWTR1)-bot(TEAD1)#5
183	Fig4F_TEAD1_WBS150521TEAD1_WB05252015_17E1-E12_top(WWTR1)-bot(TEAD1)#5
184	Fig4F_TEAD1_WBS150521TEAD1_WB05262015_17E1-E12_top(WWTR1)-bot(TEAD1)#3
185	Fig5C_GAPDH_WBS140519_WB140530_gel 9a10a-tRSK 9b10b-GAPDH#4
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187	Fig5F_pAKT473_WBS150506MKsIPLEK_WB05082015_top(16H1-H12)-bot(17C1-D8)_pAKT473#5
188	Fig5F_tubulin_WBS150521_WB05272015_top(16H1-H12)_bot(17C1-D8)_tubulin#4
189	Fig5H_GAPDH_WBS131017_WB140124a_WB140124a GAPDH#8
190	Fig5H_GAPDH_WBS140519_WB140530_gel 9a10a-tRSK 9b10b-GAPDH#4
191	Fig5H_pEGFR1068_WBS131017_WB140108b_pEGFR pMEK #5
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205	Fig5J_pIGF1RbetaGel2_WBS140415_WB140508_pPDGFRa pIGF1Rb #8
206	Fig5J_pRSKgel2_WBS140415_WB140507_pGAB1 pPRAS40 pRSK p4EBP #5
207	Fig5J_tEGFR_WBS140512_WB140514b_gel 5a-tEGFR 5b-GAPDH 6a-pEGFR1068 6b-pERK #8
208	FigS2D_ACTB_of_POU2F1_WBS130422_WB130514actb_130513actb7flip
209	FigS2D_ACTB_of_TAZ_NEDD4L_BRAF_ESRRG_YES1_WBS130422_WB130514actb_130513actb7
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214	FigS4A_BRAF_GAPDH_WBS131202_WB131206_gel 3 4 BRAF GAPDH #4
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216	FigS4A_pERK_WBS131202_WB131209_WB131209 tEGFR pERK #1
217	FigS4A_pMEK_WBS131202_WB140106_sublImage5

218	FigS4A_tERK_WBS131202_WB140102_gel 3 4 #3
219	FigS4A_tMEK_WBS131202_WB140102_gel 1 2 #4
220	FigS5A_GAPDH_WBS130904_WB130910_t-mTOR p-AKTS473 p-mTOR GAPDH_invert
221	FigS5A_NEDD4L_WBS130904_WB130906_NEDD4L_WBS_WB_5
222	FigS5E_pSMAD2_3_WBS130729_WB130731_subImage8
223	FigS5E_SMAD2_3_GAPDH_WBS130729_WB130730_subImage2
224	FigS5F_GAPDH_WBS150323_WB04032015_RerunP10+P12 samples_top(pS6+p4EBP1)_bot(GAPDH) (5)
225	FigS5F_NEDD4L_WBS150323_WB03302015_RerunP10+P12 samples_top(p_EGFR)_bot(NEDD4L) #5
226	FigS5F_pSMAD2_3_WBS150323_WB04082015_top(P16C1-C12)_total smad23_bot(return p10+P12)_p-smad23#5
227	FigS5F_SMAD2_3_WBS150323_WB04022015_top(psmad_C1-C12)_bot(total smad_rerunP10+P12)#4