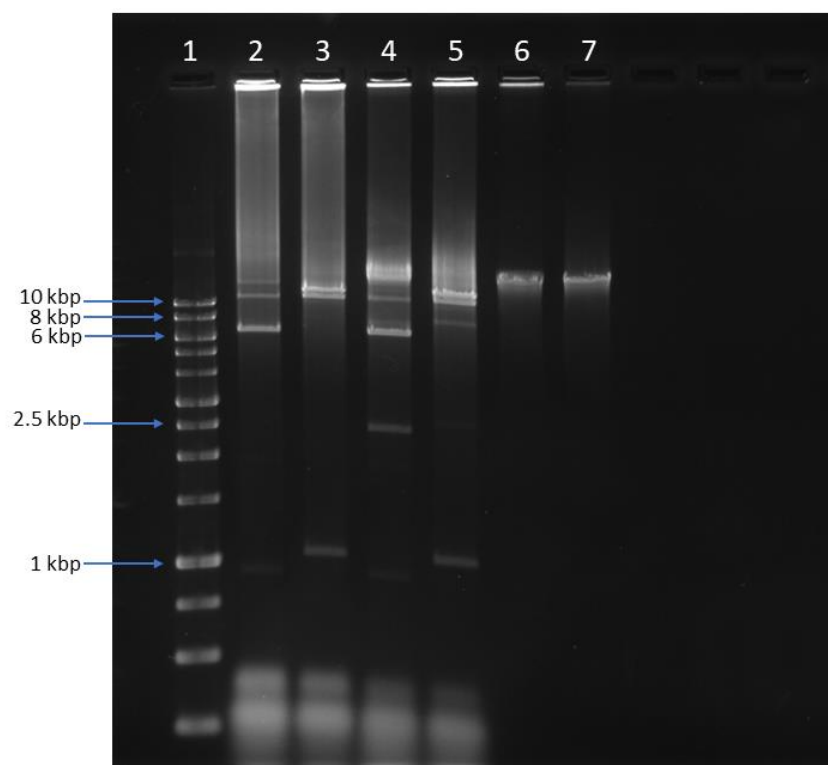
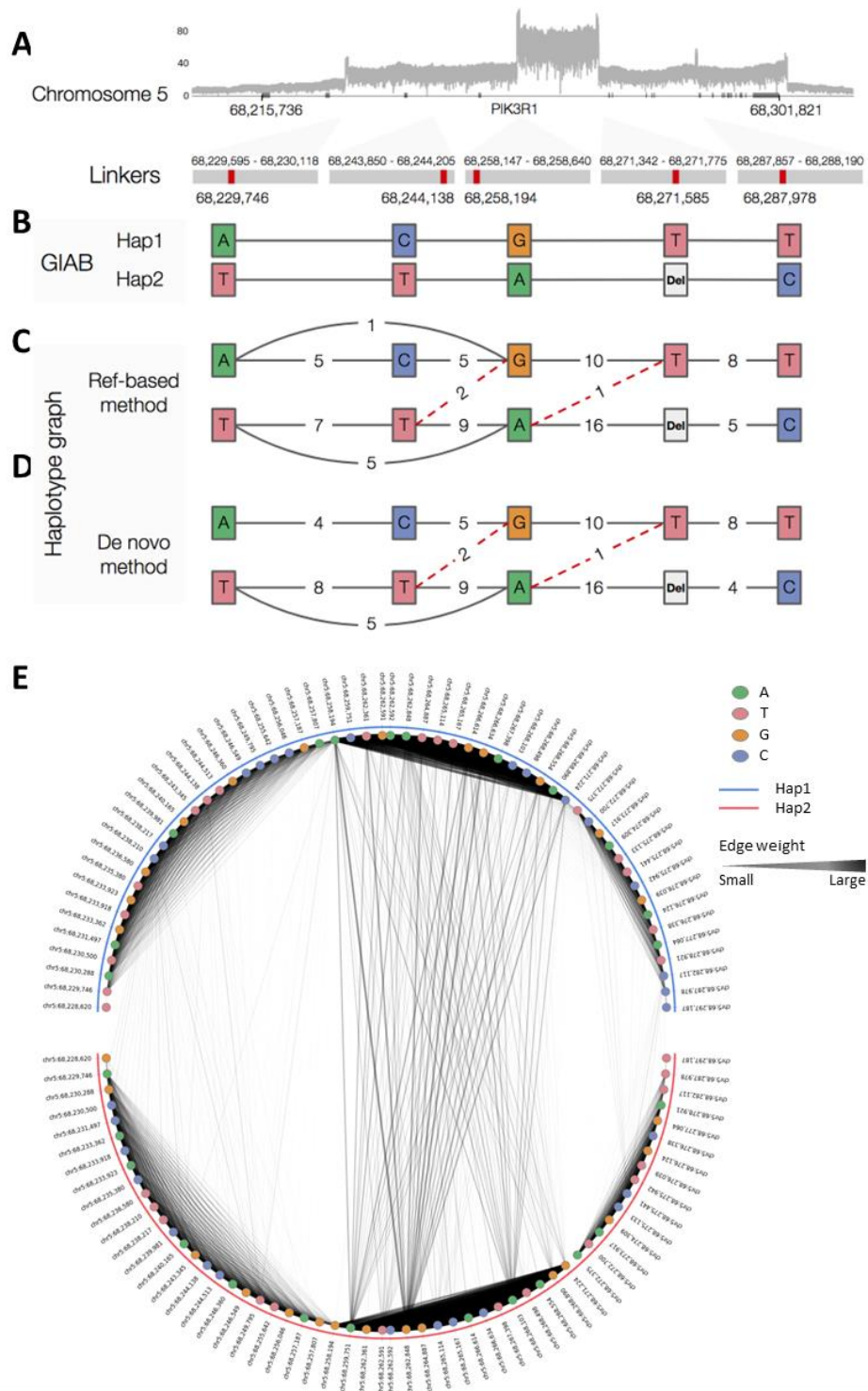
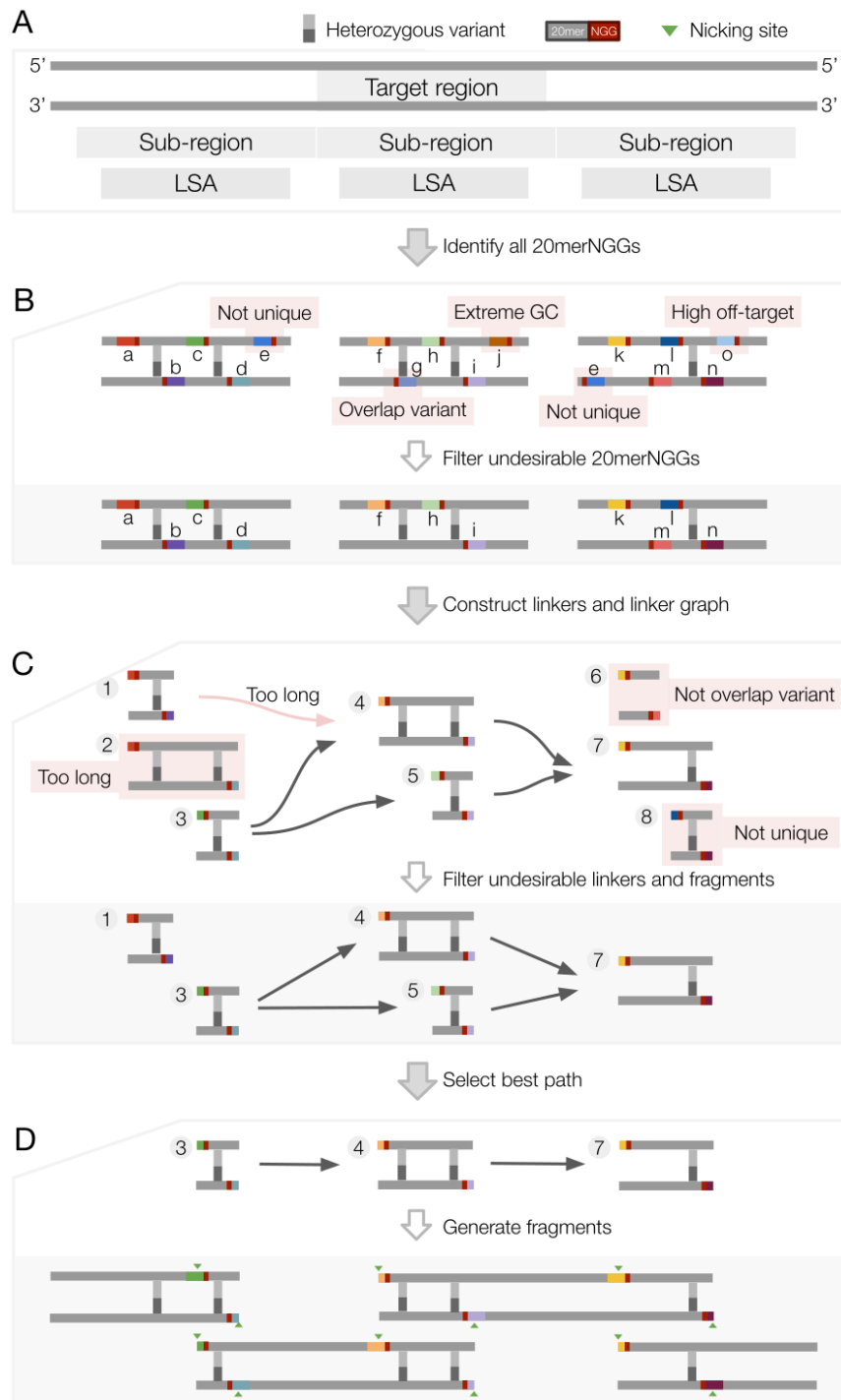




Supplementary Figure 1. Gel image containing Lambda DNA linked-fragments. Lane 1 has a 10 kbp ladder. Lanes 2, 3 and 5 have digestion products from a different sgRNA design. Lane 4 shows the sequenced product following protocol and the sgRNAs designed for Lambda linker generation. Lanes 6 and 7 contain replicates of Lambda DNA as temperature controls without any enzymes or sgRNAs.



Supplementary Figure 2. Haplotype phasing of the heterozygous variants within the linker regions of the gene PIK3R1. (A) Depth of sequencing reads aligned to the gene region. (B) The six heterozygous SNVs within the four linkers and the corresponding haplotypes phased by GIAB. (C-D) Haplotype graphs constructed (C) by aligning the sequencing reads to the reference genome and (D) by multiple sequence alignment of the sequencing reads. Each solid black line indicates two alleles found on the same read that are from the same GIAB haplotype, and each dotted red line indicates two alleles found on the same read that are from different GIAB haplotypes. Each of these two types of lines is labeled by the number of supporting reads. (E) Haplotype phasing of all heterozygous SNVs within the genes. In each panel, the variant sites are ordered from left to right according to their genomic locations. The two alleles from each variant site are placed at either the upper or lower semi-circle, according to the haplotype that it was assigned to by our method. Both the width and darkness of each edge reflect the number of reads in which the two alleles that define the edge co-appear.



Supplementary Figure 3. The basic workflow of sgRNA design method. (A) In order to cover target regions, we first define a list of sub-regions and further define LSAs within them. (B) The 20merNGGs (a-o) within the LSAs are collected. The ones that are not unique in the genome (e), overlapping a genetic variant (g), having an extreme GC content (j) or having a high off-target score (o) are removed. (C) For the remaining 20merNGGs, each pair of them from the same LSA located on opposite strands form a candidate linker. The candidate linkers with the two 20merNGGs too close or too far away from each other (2), not overlapping any heterozygous variants (6) or not unique in the genome (8) are removed. For the remaining candidate linkers, a graph is formed by connecting linkers that are located within a suitable range of distance from each other. Edges are not drawn for linker pairs that are not (e.g., 1 or 4). (D) Finally, the best path that starts from a node within the first LSA to a node within the last LSA is chosen. The corresponding DNA fragments can then be inferred from the linkers on this path.

Supplementary Table 1: Lambda OLAF-Seq guideRNAs

Target Genome	sgRNA ID	sgRNA sequence	start position	gRNA strand
Lambda	sgRNA1	AGCGCCATGTTTACCAGTCC	6270	+
Lambda	sgRNA2	TCCACCTCTGAATTTACGCC	6339	-
Lambda	sgRNA3	AGGTCTTCATCGTCCACCTC	13090	+
Lambda	sgRNA4	TTCGGTCCCTTCTGTAAGAA	13144	-
Lambda	sgRNA5	TGAATGACTTCCCCAATTAT	24569	+
Lambda	sgRNA6	CTGTAGCTGCTGAAACGTTG	24629	-
Lambda	sgRNA7	CCATGCAACATGAATAACAG	27154	+
Lambda	sgRNA8	CGCCGAACGATTAGCTCTTC	27221	-
Lambda	sgRNA9	CGACTATTGATAAAAAATCAA	34261	+
Lambda	sgRNA10	CAGTTTGATGAGTATAGAAA	34478	-
Lambda	sgRNA11	GAAGGTTTTACCAATGGCTC	47446	+
Lambda	sgRNA12	ATGTTTTCACTTAATAGTAT	47556	-
Lambda	sgRNA13	CTGTAGCTGCTGAAACGTTG	24629	+
Lambda	sgRNA14	ACAGGTATCGTTTGGAGGCA	24722	-
Lambda	sgRNA15	AGTTACCCCTCTAAGTAATG	26560	+
Lambda	sgRNA16	CCATGCAACATGAATAACAG	27154	-
Lambda	sgRNA17	TCAGAATGAGTGAACAACCA	21980	+
Lambda	sgRNA18	AAGCAGATAAATATATTTTT	23004	-
Lambda	sgRNA19	CTGTAGCTGCTGAAACGTTG	24629	+
Lambda	sgRNA20	ACAGGTATCGTTTGGAGGCA	24719	-

Supplementary Table 2. Cancer genes loci in the human genome targeted with OLAF-Seq

Gene name	Chromosome	Start position	End position	Length	Category
ARFRP1	chr20	63698641	63708013	9372	Short
B2M	chr15	44711486	44718159	6673	Short
BAP1	chr3	52401003	52410105	9102	Short
BCL2A1	chr15	79960889	79971301	10412	Short
BCL2L2	chr14	23306761	23311759	4998	Short
BRCA2	chr13	32315479	32399672	84193	Long
BTG1	chr12	92140277	92145897	5620	Short
CCND1	chr11	69641104	69654474	13370	Short
CCNE1	chr19	29811993	29824317	12324	Short
CD79A	chr19	41877119	41881372	4253	Short
CD79B	chr17	63928735	63932354	3619	Short
CDKN1A	chr6	36676459	36687339	10880	Short
CDKN1B	chr12	12717269	12722383	5114	Short
CDKN2B	chr9	22002902	22009313	6411	Short
CDKN2C	chr1	50968694	50974637	5943	Short
CIC	chr19	42268536	42295796	27260	Long
CNOT3	chr19	54137688	54155708	18020	Short
COL2A1	chr12	47972964	48006212	33248	Long
CRCT1	chr1	152514501	152516010	1509	Short
CRKL	chr22	20917406	20953749	36343	Long
CSF3R	chr1	36466042	36483314	17272	Short
CTNNB1	chr3	41199421	41240453	41032	Long
CXCR4	chr2	136114348	136118155	3807	Short
DAXX	chr6	33318557	33323016	4459	Short
DDX41	chr5	177511576	177517326	5750	Short
DIS3	chr13	72755401	72782128	26727	Long
DUSP4	chr8	29333061	29350750	17689	Short
EME2	chr16	1773221	1776714	3493	Short
EPCAM	chr2	47369147	47387028	17881	Short
EPHA2	chr1	16124336	16156109	31773	Long
EPOR	chr19	11377204	11384342	7138	Short
ERBB3	chr12	56080024	56103507	23483	Long
ERRFI1	chr1	8011718	8026333	14615	Short
ESPL1	chr12	53268256	53293643	25387	Long
FAM46C	chr1	117605981	117628389	22408	Long
FANCE	chr6	35452338	35467106	14768	Short
FANCG	chr9	35073837	35080016	6179	Short
FGF3	chr11	69809967	69819424	9457	Short
FGF4	chr11	69771015	69775403	4388	Short
FGF6	chr12	4434141	4445799	11658	Short

FGFR3	chr4	1793298	1808872	15574	Short
FOXA1	chr14	37589551	37595120	5569	Short
FUS	chr16	31180109	31194871	14762	Short
GATA1	chrX	48786539	48794311	7772	Short
GATA2	chr3	128479421	128493187	13766	Short
GATA3	chr10	8045419	8075201	29782	Long
GLI1	chr12	57460134	57472451	12317	Short
H3F3B	chr17	75776433	75779935	3502	Short
HNF1A	chr12	120977682	121002512	24830	Long
HOXB13	chr17	48724762	48728749	3987	Short
HRAS	chr11	532241	535567	3326	Short
HSP90AB1	chr6	44246165	44253888	7723	Short
HSPA5	chr9	125234847	125241387	6540	Short
IDH2	chr15	90083977	90102554	18577	Short
IGF2	chr11	2129111	2149603	20492	Long
IKBKE	chr1	206470242	206496890	26648	Long
KNSTRN	chr15	40382720	40394288	11568	Short
LZTR1	chr22	20982268	20999037	16769	Short
MALAT1	chr11	65497737	65506516	8779	Short
MAP3K1	chr5	56815072	56896152	81080	Long
MCL1	chr1	150574550	150579738	5188	Short
MEN1	chr11	64803513	64811294	7781	Short
MPL	chr1	43336874	43354464	17590	Short
MUTYH	chr1	45329241	45340470	11229	Short
MYC	chr8	127735433	127742951	7518	Short
MYCL	chr1	39895423	39902015	6592	Short
MYCN	chr2	15940437	15947007	6570	Short
MYD88	chr3	38137438	38143022	5584	Short
NBN	chr8	89933335	89984724	51389	Long
NF2	chr22	29603555	29698600	95045	Long
NFKBIE	chr6	44258165	44265788	7623	Short
NKX2-1	chr14	36516396	36520225	3829	Short
NOTCH1	chr9	136494432	136545786	51354	Long
NRAS	chr1	114704463	114716894	12431	Short
OR5L1	chr11	55811366	55812476	1110	Short
PHOX2B	chr4	41744081	41748970	4889	Short
PIK3R1	chr5	68215736	68301821	86085	Long
PIK3R2	chr19	18153177	18170533	17356	Short
POLD1	chr19	50384290	50418018	33728	Long
POLR2L	chr11	839720	842529	2809	Short
PTCH2	chr1	44819843	44842944	23101	Long
RAD51C	chr17	58692139	58734342	42203	Long

RIT1	chr1	155897807	155911402	13595	Short
RNF43	chr17	58352499	58418894	66395	Long
RPL10	chrX	154398064	154402339	4275	Short
RRAS	chr19	49635291	49640143	4852	Short
SDHD	chr11	112086823	112095801	8978	Short
SH2B3	chr12	111405106	111451623	46517	Long
SHH	chr7	155799983	155812273	12290	Short
SMARCA4	chr19	10960921	11062282	1E+05	Long
SMARCB1	chr22	23786930	23834518	47588	Long
SOX2	chr3	181711923	181714436	2513	Short
SPRY1	chr4	123396790	123403760	6970	Short
SPRY2	chr13	80335975	80341115	5140	Short
SPRY4	chr5	142310426	142325055	14629	Short
STK11	chr19	1205798	1228435	22637	Long
TBX3	chr12	114670253	114684164	13911	Short
TFE3	chrX	49028725	49043517	14792	Short
TMPRSS2	chr21	41464550	41508158	43608	Long
TP53	chr17	7668401	7687550	19149	Long
VEGFA	chr6	43770208	43786487	16279	Short
VHL	chr3	10141634	10153670	12036	Short
ZNF703	chr8	37695750	37700021	4271	Short

Supplementary Table 3: guideRNAs designed for targeted sequencing of NA12878 genome

Gene	gRNA ID	gRNA sequence	gRNA chromosome	gRNA start position	gRNA strand
ARFRP1	ARFRP1+1	TGCCCAGGACGGTGTCTTCG	chr20	63696239	+
ARFRP1	ARFRP1+2	GGAAGTCCAAGTCCGATGTG	chr20	63710748	+
B2M	B2M+1	TTAACACTGATTACTCATAG	chr15	44706493	+
B2M	B2M+2	TGTCAGATCCCCTGTTGA	chr15	44720639	+
BAP1	BAP1+1	ACCCAGCACAGACCGTGACC	chr3	52395900	+
BAP1	BAP1+2	GGTCGGTTTCTACTAACGGT	chr3	52410577	+
BCL2A1	BCL2A1+1	ACCTGAAAGGGTCTACCGTG	chr15	79960749	+
BCL2A1	BCL2A1+2	GTGAAAGGACTGGTGCGGGG	chr15	79975903	+
BCL2L2	BCL2L2+1	TGGTGTCTGCTAGCCCCATA	chr14	23306413	+
BCL2L2	BCL2L2+2	CGGTGAGGCGATCGGAAGAT	chr14	23321098	+
BRCA2	BRCA2+1	AATGCAAAGTTAGCCGTGCG	chr13	32314693	+
BRCA2	BRCA2-1	TCACTTAGTGGTAGTGGGCG	chr13	32315054	-
BRCA2	BRCA2+2	CCACCTGTGAGTAGTACTA	chr13	32329230	+
BRCA2	BRCA2-2	ACCCCATGAATAGGGGACTA	chr13	32329721	-
BRCA2	BRCA2+3	TGAGCCACTGTGCCTAATCA	chr13	32344760	+
BRCA2	BRCA2-3	AGTGACAATACTATTGCCG	chr13	32345132	-
BRCA2	BRCA2+4	ACAAGTCATCGGCATATAGA	chr13	32361109	+
BRCA2	BRCA2-4	TGCCTACAAGGCCAACGATC	chr13	32361635	-
BRCA2	BRCA2+5	TTTCCTGGAATACTTATAGC	chr13	32376219	+
BRCA2	BRCA2-5	TGTCTTGTTAGTGACGTGA	chr13	32376714	-
BRCA2	BRCA2+6	CACTATGCCAGCGTGTCTT	chr13	32388404	+
BRCA2	BRCA2-6	ACTCACTTTAAATTCGACAA	chr13	32388805	-
BRCA2	BRCA2+7	CTCATTTGTAAATCCACCGT	chr13	32402983	+
BRCA2	BRCA2-7	TCTTGAAGCACGTAATTGAG	chr13	32403473	-
BTG1	BTG1+1	AAAAAATCAATCTAGCCGTT	chr12	92136055	+
BTG1	BTG1+2	AGATGAGTAGAGATAGTAGT	chr12	92150192	+
CCND1	CCND1+1	TTAGTAATCCTAATCCCGG	chr11	69639581	+
CCND1	CCND1+2	AGGCTGGTGGCAAGTGCACG	chr11	69654274	+
CCNE1	CCNE1+1	TTTGCCGCTCCAGCGCCGCT	chr19	29811607	+
CCNE1	CCNE1+2	CAAATTTGAAAGTACGTTTG	chr19	29828817	+
CD79A	CD79A+1	CAAGGAAGAGCTAGCCGGGG	chr19	41868851	+
CD79A	CD79A+2	ATCACTACCATTGTACGGGT	chr19	41883559	+
CD79B	CD79B+1	ACGCCGAAAGATGCTCTATC	chr17	63919667	+
CD79B	CD79B+2	ACACACACATCCCGTGGACA	chr17	63934327	+
CDKN1A	CDKN1A+1	ATGCTGCTCCACCGCACTCT	chr6	36676302	+
CDKN1A	CDKN1A+2	TAAGACCTGACCTAATTAC	chr6	36690896	+
CDKN1B	CDKN1B+1	GAAGAGTCTTTGGTTGCTCG	chr12	12709297	+
CDKN1B	CDKN1B+2	GCTGGTGCCTCGGACGAGA	chr12	12723947	+
CDKN2B	CDKN2B+1	GGACCTCCAAGATCTCGGAA	chr9	21994542	+
CDKN2B	CDKN2B+2	TCAAAGCCGCTCTGGCCGCA	chr9	22009233	+

CDKN2C	CDKN2C+1	CCACTGCAGCGTTCAAACGC	chr1	50959670	+
CDKN2C	CDKN2C+2	AATCTTCAATAAACGTGGGG	chr1	50974258	+
CIC	CIC+1	GCCGCTGCTGATTGGCTGCG	chr19	42268473	+
CIC	CIC-1	TGGCCCGAACGTTTGTTGAC	chr19	42268817	-
CIC	CIC+2	CAGGGCTCAGGAAGCGAGTG	chr19	42285129	+
CIC	CIC-2	GGGAGCTCTGTGCGAGGCAC	chr19	42285565	-
CIC	CIC+3	AGCACCACAACCCGGGCCTG	chr19	42299970	+
CIC	CIC-3	AATGGCATTGTTGTTAACACC	chr19	42300385	-
CNOT3	CNOT3+1	ATCACCCAATCCGCGAAAGG	chr19	54137587	+
CNOT3	CNOT3+2	CACCTTTGAGTACCGCTACC	chr19	54155364	+
COL2A1	COL2A1+1	TCCCACGTCTCCGATCCAGC	chr12	47972596	+
COL2A1	COL2A1-1	CCATTAATCTCCGTTCTGT	chr12	47972930	-
COL2A1	COL2A1+2	GGGTCTCCTTCACCCGGCTC	chr12	47988541	+
COL2A1	COL2A1-2	CCAACAGCTGAGCAAGCTCG	chr12	47988888	-
COL2A1	COL2A1+3	ACTGGAATTAGACCTATATG	chr12	48006996	+
COL2A1	COL2A1-3	CTGTAGATCGGGATATTCCC	chr12	48007450	-
CRCT1	CRCT1+1	CCATCAGAGGGGAGGCGTAA	chr1	152502685	+
CRCT1	CRCT1+2	GGAAGAGACACTCGGGTCTC	chr1	152517212	+
CRKL	CRKL+1	TAGCTGTACCTAAACCTATT	chr22	20908188	+
CRKL	CRKL-1	TTTGATACAAGAACGTGCAT	chr22	20908684	-
CRKL	CRKL+2	CTGTGGAACCTCTACTGTAG	chr22	20921443	+
CRKL	CRKL-2	AATTTGCCCGGCATGGTTGC	chr22	20921876	-
CRKL	CRKL+3	AAAAGACAGTGAGGTTGATC	chr22	20940235	+
CRKL	CRKL-3	GATGTAATCCAAATTACTAC	chr22	20940755	-
CRKL	CRKL+4	GACAGGATCGTTGTCCCTAC	chr22	20953354	+
CRKL	CRKL-4	TGAACTGCCAGGAGGCTAGT	chr22	20953801	-
CSF3R	CSF3R+1	TAACCTATGTGGGCCCTGTA	chr1	36464863	+
CSF3R	CSF3R+2	GGCAAGACAGGAGGACGTCT	chr1	36483433	+
CTNNB1	CTNNB1+1	TGCAGACCACAGCGCCCTCA	chr3	41199225	+
CTNNB1	CTNNB1-1	GTCCGACCGTCTCGACCTG	chr3	41199638	-
CTNNB1	CTNNB1+2	TGCTTAATCAGTTCATCGAT	chr3	41218025	+
CTNNB1	CTNNB1-2	AGATACATACGAGAGTAAAT	chr3	41218451	-
CTNNB1	CTNNB1+3	CAGGGAGGTCTGTAGATAGC	chr3	41230362	+
CTNNB1	CTNNB1-3	GCCAAAAGACTGGATATCCC	chr3	41230828	-
CTNNB1	CTNNB1+4	TCCCAGACAGGCAACACCG	chr3	41244830	+
CTNNB1	CTNNB1-4	ACTTAGTGCCACGGTGAGG	chr3	41245275	-
CXCR4	CXCR4+1	TTTTATTTCCTCTTTTGCGA	chr2	136106742	+
CXCR4	CXCR4+2	TGGCCTGTGACCCCGGAATG	chr2	136121312	+
DAXX	DAXX+1	TTCCTCAAAGGGCGGCATG	chr6	33314095	+
DAXX	DAXX+2	CAGATACCTGAGGTGCGAGT	chr6	33328662	+
DDX41	DDX41+1	TTACAGAGCATGTTTGCGTG	chr5	177502376	+
DDX41	DDX41+2	GGAGTTCCGGATCGCGCAGA	chr5	177517047	+

DIS3	DIS3+1	CATAATTTTCAGGCACTAGTC	chr13	72754101	+
DIS3	DIS3-1	AGAAACTGGCATATAACAGC	chr13	72754490	-
DIS3	DIS3+2	TACTTTGGCTTGGTACTAGC	chr13	72770514	+
DIS3	DIS3-2	TAATTCAAAGGTTTCGTTTCA	chr13	72770912	-
DIS3	DIS3+3	GAGTGATTTAAACGTAGATA	chr13	72784794	+
DIS3	DIS3-3	AACAAACAAATTCAGTCCGA	chr13	72785298	-
DUSP4	DUSP4+1	ATCTCCACTGCGCTATTAAG	chr8	29332947	+
DUSP4	DUSP4+2	GGAGAGTGTGTTTACGAGAG	chr8	29350537	+
EME2	EME2+1	GTGTACGTGGGTTACGGGG	chr16	1767961	+
EME2	EME2+2	GTGACAAAGCTATTGCCGAG	chr16	1782657	+
EPCAM	EPCAM+1	AAAGATCCCTAACGCCGCCA	chr2	47369056	+
EPCAM	EPCAM+2	CTGCAGGCCCAGAAGCGTCC	chr2	47388318	+
EPHA2	EPHA2+1	GATCTATTTTCGACAGCTCCG	chr1	16124004	+
EPHA2	EPHA2-1	CAGATGATTCAAACCGATCT	chr1	16124352	-
EPHA2	EPHA2+2	TCCATGCAGACTAGCCTGTC	chr1	16138810	+
EPHA2	EPHA2-2	AGGAAGAAGCCCCGGAGTC	chr1	16139185	-
EPHA2	EPHA2+3	TCAAGGAGCGCCGGGCTCTA	chr1	16155777	+
EPHA2	EPHA2-3	GGCGTTGGTGACGTCACGCA	chr1	16156127	-
EPOR	EPOR+1	AGCTCTGAACTGGTTCATCC	chr19	11375396	+
EPOR	EPOR+2	ATGACACAAATTGGCCCAAT	chr19	11390573	+
ERBB3	ERBB3+1	GAATGCATAGCTCAAACGGG	chr12	56068709	+
ERBB3	ERBB3-1	AATTGGCCGGGCGCGGTGTC	chr12	56069234	-
ERBB3	ERBB3+2	GGTGTCTGTGGATAGTGCA	chr12	56084124	+
ERBB3	ERBB3-2	GGGTCTCGCTCTGTTACGAG	chr12	56084588	-
ERBB3	ERBB3+3	GATCTTCACTCCTTATCCGA	chr12	56103271	+
ERBB3	ERBB3-3	ATGAAAAGGACTATGCGCTA	chr12	56103678	-
ERRFI1	ERRFI1+1	TGCCCCGATGAAGTCTGTGGA	chr1	8011107	+
ERRFI1	ERRFI1+2	ATCCCAGAGACTCCGCGTCG	chr1	8025997	+
ESPL1	ESPL1+1	AAGGTGAGCGGATGACTCAA	chr12	53262845	+
ESPL1	ESPL1-1	TGCACAGGTGAACTTACGTG	chr12	53263274	-
ESPL1	ESPL1+2	TCCAGGGTATCGAGCGGGAT	chr12	53277464	+
ESPL1	ESPL1-2	GCTGGAGACACCGTACAGCT	chr12	53277906	-
ESPL1	ESPL1+3	CCGCGACATTGACCGCTACA	chr12	53293308	+
ESPL1	ESPL1-3	TCAGATAAACTACGCAAAAC	chr12	53293661	-
FAM46C	FAM46C+1	GGGTTGGAAGAGTAGGGCGG	chr1	117604869	+
FAM46C	FAM46C-1	TCCATTCTAACATAGCGAG	chr1	117605276	-
FAM46C	FAM46C+2	TGGATAAAAATGATACGTTG	chr1	117619307	+
FAM46C	FAM46C-2	TGCCAAACTAAGATCTAGAT	chr1	117619707	-
FAM46C	FAM46C+3	AATGAAAGGTACTGCTCCGG	chr1	117633858	+
FAM46C	FAM46C-3	TAATTGGTTTCCACCGTGGT	chr1	117634350	-
FANCE	FANCE+1	GAGAGGGTTGGGGTCGTCAG	chr6	35452088	+
FANCE	FANCE+2	CAGGGACAAACTTTCCGATA	chr6	35466911	+

FANCG	FANCG+1	GTAATCATAAAATCGGATAC	chr9	35065208	+
FANCG	FANCG+2	GTCTGACTGGGGCAGTCGCA	chr9	35079868	+
FGF3	FGF3+1	AGAACGTGAAATGGCGAGAT	chr11	69806930	+
FGF3	FGF3+2	AAAGGTGACCCCTCTATAGG	chr11	69821429	+
FGF4	FGF4+1	TTATTGTTATTTCCATCCCG	chr11	69760397	+
FGF4	FGF4+2	AGCAAGGCCAGCAGGACCGC	chr11	69775025	+
FGF6	FGF6+1	GATTTTAGCCCTCGTTTGAA	chr12	4434025	+
FGF6	FGF6+2	TTTTATCGGGTGATGCGATG	chr12	4448658	+
FGFR3	FGFR3+1	GAGCCACCGAGTCGGCACAG	chr4	1792084	+
FGFR3	FGFR3+2	CAGGCAGGGAGACGGTTTCC	chr4	1808461	+
FOXA1	FOXA1+1	GAAGGTGTGCACTCGTCAAG	chr14	37584769	+
FOXA1	FOXA1+2	ACAGAGTCCTAACCCGTAAC	chr14	37599370	+
FUS	FUS+1	TCCCCCTGCTCTTCGCGTT	chr16	31180052	+
FUS	FUS+2	ATGGAGCACTAGGCGTAAAT	chr16	31194909	+
GATA1	GATA1+1	ACGGGAGCCTAGGTCGAGCG	chrX	48786349	+
GATA1	GATA1+2	GCAGTGTTACCCGTTGGAG	chrX	48800901	+
GATA2	GATA2+1	TGAGAAGAGATACTATGATC	chr3	128478724	+
GATA2	GATA2+2	TTTCGACATCACTTTGCGGG	chr3	128493228	+
GATA3	GATA3+1	AACAGGAGAAATAGTCGGAA	chr10	8044864	+
GATA3	GATA3-1	AACAGGCAAACCGCACATCA	chr10	8045197	-
GATA3	GATA3+2	GCATATTCTCTGCGTGGAAA	chr10	8059389	+
GATA3	GATA3-2	CTCTGAAATGGACACGCCTA	chr10	8059898	-
GATA3	GATA3+3	CTAAGGTGGTTGTGCTCGGA	chr10	8074890	+
GATA3	GATA3-3	AGAAGAGCTCGGCCACCACG	chr10	8075236	-
GLI1	GLI1+1	AACTTCGAGACGTAGAGCCG	chr12	57459339	+
GLI1	GLI1+2	CCAAGGGCAGCACGGAAATG	chr12	57474040	+
H3F3B	H3F3B+1	TATCTTGCTGATTATCACGT	chr17	75771628	+
H3F3B	H3F3B+2	ATCTGGAACTTCACGTAAT	chr17	75786302	+
HNF1A	HNF1A+1	GAGAAGTGGGGTCGTATGT	chr12	120970724	+
HNF1A	HNF1A-1	CCAACACCCTGCAAGCGGCC	chr12	120971125	-
HNF1A	HNF1A+2	TCCTAGGAGCCCCGAAAGA	chr12	120984687	+
HNF1A	HNF1A-2	ATCTCTTGAGCCCAGAGGT	chr12	120985050	-
HNF1A	HNF1A+3	CTGCAGCTTGAGCCAGCCG	chr12	121002435	+
HNF1A	HNF1A-3	CATGGTAGTGAGCGCCTGTG	chr12	121002854	-
HOXB13	HOXB13+1	TCGAAGCGCCCCACGCCAGA	chr17	48719035	+
HOXB13	HOXB13+2	CTGAACTGCTTGGGGTCGCC	chr17	48733551	+
HRAS	HRAS+1	CTCTGTGGGTGAGGGTGCG	chr11	529541	+
HRAS	HRAS+2	GGCTGGGGCGTGCAGTGATC	chr11	544168	+
HSP90AB1	HSP90AB1+1	CCCGTGCTCCGTGTACGTGG	chr6	44246131	+
HSPA5	HSPA5+1	TCAAGCTGTGAGGTCCATTA	chr9	125229868	+
HSPA5	HSPA5+2	GTGCTTCTCAAAGGTTAGAC	chr9	125243413	+
IDH2	IDH2+1	GTGTCCGAGAACTCCGCAGT	chr15	90083790	+

IDH2	IDH2+2	AGCTGGAGAGCGAACGAGCA	chr15	90102394	+
IGF2	IGF2+1	GTCTCCCCGGCAAGCTAACC	chr11	2122958	+
IGF2	IGF2-1	CATGGTCCCAAGACGCCTGC	chr11	2123375	-
IGF2	IGF2+2	ATCCCGTAGCGAAGTGCCAT	chr11	2137462	+
IGF2	IGF2-2	TGTCTGCAGGGGCGACTTCC	chr11	2137966	-
IGF2	IGF2+3	AAAGCGGAGATTTCTAATC	chr11	2152106	+
IGF2	IGF2-3	TGTGAACTGGGTTAGCCCCC	chr11	2152494	-
IKBKE	IKBKE+1	TTCTGGGAGGGTCTTGCATC	chr1	206468844	+
IKBKE	IKBKE-1	GTTGGTGAGGTGGATTGAAC	chr1	206469222	-
IKBKE	IKBKE+2	TATCTTATTGTGTCGAGGA	chr1	206483188	+
IKBKE	IKBKE-2	TGTCTCTAGATAGTAGGTTA	chr1	206483714	-
IKBKE	IKBKE+3	TTATTTGGGCCTCAAGCCCG	chr1	206497741	+
IKBKE	IKBKE-3	TTGATCACTACAGTGAGTCG	chr1	206498227	-
KNSTRN	KNSTRN+1	AACACTGTTGGGTAATCAGC	chr15	40382362	+
KNSTRN	KNSTRN+2	TGCACTAACCTTAAGTGAC	chr15	40396961	+
LZTR1	LZTR1+1	AGAGCTGGAGGGCGCAAGTG	chr22	20982226	+
LZTR1	LZTR1+2	TTCATTTGTGCTCCTCGGCA	chr22	20999073	+
MALAT1	MALAT1+1	TCAGTTTCCTCATCGTCTA	chr11	65492506	+
MALAT1	MALAT1+2	TGTCCCTTTGAACGTGCTGT	chr11	65507189	+
MAP3K1	MAP3K1+1	TTGCAGCAGGCGACGGTCCC	chr5	56814937	+
MAP3K1	MAP3K1-1	AGTGGGCTGTGCTCTCCGCC	chr5	56815349	-
MAP3K1	MAP3K1+2	TTGTAAGAAGTTTCTGCGTA	chr5	56830986	+
MAP3K1	MAP3K1-2	TGGAGTTCACTGGTTTGC GA	chr5	56831388	-
MAP3K1	MAP3K1+3	TGGCAAAGACAGTATGTCTC	chr5	56849679	+
MAP3K1	MAP3K1-3	AAAACAATCCTAGTCCATTG	chr5	56850160	-
MAP3K1	MAP3K1+4	TATTTACACAAGTAGTCCAC	chr5	56868229	+
MAP3K1	MAP3K1-4	TTTAAGAAACCATTACGGCC	chr5	56868698	-
MAP3K1	MAP3K1+5	AGGCATGATAGTGACACCT	chr5	56883046	+
MAP3K1	MAP3K1-5	TGTTTTGCTTTGGTATGTCC	chr5	56883563	-
MAP3K1	MAP3K1+6	TTCTATGTCATGACGTGGTT	chr5	56898080	+
MAP3K1	MAP3K1-6	TTGCTGGGGATCTAGTCCCA	chr5	56898452	-
MCL1	MCL1+1	AACAAGGTATGCACGAGATA	chr1	150563774	+
MCL1	MCL1+2	GTAGCCAAAAGTCGCCCTCC	chr1	150579417	+
MEN1	MEN1+1	CTCACACTGGATCTCCGAGG	chr11	64799599	+
MEN1	MEN1+2	TCTTCTCTCCAGATGTCTAC	chr11	64814162	+
MPL	MPL+1	TCACCCAGGCTGGCGTACCG	chr1	43336331	+
MPL	MPL+2	CACCCCATAGAGTTGTGACG	chr1	43354044	+
MUTYH	MUTYH+1	CTGTCCCTCCCGTTGCGTG	chr1	45327455	+
MUTYH	MUTYH+2	CAAGGCATCCCCTACCATAA	chr1	45342074	+
MYC	MYC+1	GGACAATTGCTTCAGGCCGG	chr8	127731754	+
MYC	MYC+2	GAAAGCATGTAACCAATGTC	chr8	127746329	+
MYCL	MYCL+1	GATGAAGAGACTCGTTACCA	chr1	39887086	+

MYCL	MYCL+2	GGGAAGCCAATCGCAGCGCG	chr1	39901617	+
MYCN	MYCN+1	TGCAAGCCCGGGGTCCAAA	chr2	15940283	+
MYCN	MYCN+2	AGGTGCAGGTCTCCCACCT	chr2	15954908	+
MYD88	MYD88+1	CTTTTCTTGTTGCACCTGAC	chr3	38128902	+
MYD88	MYD88+2	GTCTATCTGCTGCCACGTCC	chr3	38143559	+
NBN	NBN+1	TCTACTCAAGCCTAATCAGT	chr8	89932987	+
NBN	NBN-1	GCATAGATGCTCCTTAAGTT	chr8	89933386	-
NBN	NBN+2	GCACAGCTATCATTCTGATA	chr8	89949564	+
NBN	NBN-2	TCCATCAACCTTACTCAATG	chr8	89949975	-
NBN	NBN+3	CCAAAAAACCATATTGTAAAC	chr8	89968271	+
NBN	NBN-3	GAAGCAGTAACCCGGCAGTG	chr8	89968740	-
NBN	NBN+4	TGAAATGTGCTGCGTTAAAA	chr8	89984767	+
NBN	NBN-4	GACTACATTATGTGGGACGT	chr8	89985242	-
NF2	NF2+1	TAGTGGTCTGGGCGACCTGA	chr22	29603497	+
NF2	NF2-1	GACCCTGCCTGAGCGGAAAG	chr22	29603830	-
NF2	NF2+2	ACTGGGTGCCCACGTTGACC	chr22	29620866	+
NF2	NF2-2	CTGCCTCAGCGGCCCCAACA	chr22	29621217	-
NF2	NF2+3	GATTTGGTGTGCCGACTCT	chr22	29636777	+
NF2	NF2-3	GCAATCAGGCTGGTAACAAT	chr22	29637138	-
NF2	NF2+4	TTCCAAGTCATTGTCCCCGG	chr22	29654015	+
NF2	NF2-4	ACAAGAATGTGACACTTGTA	chr22	29654425	-
NF2	NF2+5	GAGAAGGAAAGCCGATTCTT	chr22	29668373	+
NF2	NF2-5	AAGAAAGCAAGCTAGCTAGC	chr22	29668769	-
NF2	NF2+6	CACTGAGCCCTTACGAGGGC	chr22	29683158	+
NF2	NF2-6	AGAGGCTGTCAACGCATAAA	chr22	29683497	-
NF2	NF2+7	CCCTGCTAGATAGCACCCCG	chr22	29698188	+
NF2	NF2-7	CCGTGTTCTTGACGCCTCAA	chr22	29698659	-
NFKBIE	NFKBIE+1	GAGGACAAGGTTCTGGAGCGC	chr6	44265506	+
NKX2-1	NKX2-1+1	ACTCAAATGCTGGCGGCCTC	chr14	36505530	+
NKX2-1	NKX2-1+2	GAACCCTGGGGCCGCACTGT	chr14	36520186	+
NOTCH1	NOTCH1+1	GTGGTCTCCAGCCGTAGAG	chr9	136493969	+
NOTCH1	NOTCH1-1	CTGCTGGGAGAGTGACGGTG	chr9	136494344	-
NOTCH1	NOTCH1+2	CAAACAAGGGCTGCGATGGA	chr9	136511762	+
NOTCH1	NOTCH1-2	GCTTCCTTTTCGACAATTGT	chr9	136512095	-
NOTCH1	NOTCH1+3	TGGTTTAAATGTGCGAAGG	chr9	136530277	+
NOTCH1	NOTCH1-3	CACACTCCAAACAGCCTGCG	chr9	136530610	-
NOTCH1	NOTCH1+4	AACTCGGCTCCAGGCACGGG	chr9	136545491	+
NOTCH1	NOTCH1-4	GCGCAGCGAAGGAACGAGCC	chr9	136545982	-
NRAS	NRAS+1	TTCCTCTTTCCGTTATTAG	chr1	114703666	+
NRAS	NRAS+2	GTAAGCAACCATTAGGTTAG	chr1	114718437	+
OR5L1	OR5L1+1	AGAAGCAATGGCCCTCCAAT	chr11	55809084	+
OR5L1	OR5L1+2	GGATACAGTCACCGAGATAC	chr11	55820525	+

PHOX2B	PHOX2B+1	TCCTGCCTGTTGATCTAATG	chr4	41740060	+
PHOX2B	PHOX2B+2	TTGGGCTCAATTGTGGCACG	chr4	41754715	+
PIK3R1	PIK3R1+1	AAACTCTCTCCCTTCTCGC	chr5	68215058	+
PIK3R1	PIK3R1-1	GCTCTGGCTCTACACGTCCC	chr5	68215487	-
PIK3R1	PIK3R1+2	CAGGGTAGACAGAGGGTGCG	chr5	68229595	+
PIK3R1	PIK3R1-2	GGGAAGAGCTGTACTAGCAG	chr5	68230118	-
PIK3R1	PIK3R1+3	AAATGGCTCCTTAAGCTTCG	chr5	68243850	+
PIK3R1	PIK3R1-3	TTTTTCTTCTACCTAACTGG	chr5	68244205	-
PIK3R1	PIK3R1+4	AGAAAACATCTGACAGCACG	chr5	68258147	+
PIK3R1	PIK3R1-4	AGACAGAAGGTTCAATGATC	chr5	68258640	-
PIK3R1	PIK3R1+5	AAGTCACTCAGGAAATCGAG	chr5	68271342	+
PIK3R1	PIK3R1-5	ATTAGCCATTGCAACTACCC	chr5	68271775	-
PIK3R1	PIK3R1+6	TGGGGTTTAATATTCTGCCG	chr5	68287857	+
PIK3R1	PIK3R1-6	TCACTGGCTGCTGAGCGCGC	chr5	68288190	-
PIK3R1	PIK3R1+7	AAGACATAGTCTAGTAGTAG	chr5	68302723	+
PIK3R1	PIK3R1-7	GGAATTACCCTAGCTCTTAC	chr5	68303159	-
PIK3R2	PIK3R2+1	TGCGCTCGGGCATTTCGCC	chr19	18153131	+
PIK3R2	PIK3R2+2	GGAATCACAGCTCCCCGTAC	chr19	18170256	+
POLD1	POLD1+1	GGTGAGATTAGACCCCATT	chr19	50379686	+
POLD1	POLD1-1	CCTCCTCAGCCTCGAGTGGC	chr19	50380080	-
POLD1	POLD1+2	CCCTCCTGGCAGCGCACACT	chr19	50394260	+
POLD1	POLD1-2	GGCAGATCCTAGATGCGGCT	chr19	50394775	-
POLD1	POLD1+3	GGTCTCAATCTCCGTTCTTC	chr19	50406106	+
POLD1	POLD1-3	TCAAAGAGTGAGGTCAGACG	chr19	50406623	-
POLD1	POLD1+4	ACTCAACTGACTCGCCACCA	chr19	50419606	+
POLD1	POLD1-4	AGACATCAAAAATACGGATG	chr19	50420138	-
POLR2L	POLR2L+1	AGTGCGCGGCCACGACAGCT	chr11	833029	+
POLR2L	POLR2L+2	AGGGGGTGGGAGGGGTCTTA	chr11	847728	+
PTCH2	PTCH2+1	GCAGGACAGGTGCCCGACTC	chr1	44813336	+
PTCH2	PTCH2-1	GGCCTCATCCCTCTCCGCA	chr1	44813693	-
PTCH2	PTCH2+2	CTGGCCTAGAAGGTCCCGTG	chr1	44827956	+
PTCH2	PTCH2-2	CCATCCTCAGCCTGGACCTA	chr1	44828361	-
PTCH2	PTCH2+3	TACACACACCTGTCGTCGGG	chr1	44842612	+
PTCH2	PTCH2-3	ATGGGAGCGCCCAGATAACG	chr1	44842988	-
RAD51C	RAD51C+1	AAAAAAAATCGCCAATAGGT	chr17	58691677	+
RAD51C	RAD51C-1	CGGGAGTCGTATCCCGAGCA	chr17	58692018	-
RAD51C	RAD51C+2	GCAAATTTTCATTGGACCATA	chr17	58706103	+
RAD51C	RAD51C-2	GGGCAATGCTATGTCGCTCT	chr17	58706595	-
RAD51C	RAD51C+3	GATTAATTGGTATAACCTAG	chr17	58724801	+
RAD51C	RAD51C-3	TAAAGCACTACGTATTGTGG	chr17	58725144	-
RAD51C	RAD51C+4	CCTCATCCACCCGCGTAGCT	chr17	58739887	+
RAD51C	RAD51C-4	TAGAGGTGTGGTACTACCTT	chr17	58740252	-

RIT1	RIT1+1	ACTTTAAGTAACCCCTTGATC	chr1	155897528	+
RIT1	RIT1+2	CTTAAATTAACAACCTACCG	chr1	155911631	+
RNF43	RNF43+1	GACAGACACAATGGGCCAAT	chr17	58344093	+
RNF43	RNF43-1	GCTGTCCTGGGTGTCTGACC	chr17	58344588	-
RNF43	RNF43+2	GGTTCTTGGAAGATCGAGA	chr17	58358771	+
RNF43	RNF43-2	CCTTTTCTAAGGTACCCAC	chr17	58359126	-
RNF43	RNF43+3	TCTCCATGCTAATGATAGTC	chr17	58373959	+
RNF43	RNF43-3	TTAGTAAATGAGTTCGGGGA	chr17	58374293	-
RNF43	RNF43+4	GTAAAGCCAATAGTCTCTAC	chr17	58388673	+
RNF43	RNF43-4	ATCGTGCAGTACTAGATTAC	chr17	58389171	-
RNF43	RNF43+5	TCTGGCAACACTTACGAGGC	chr17	58401430	+
RNF43	RNF43-5	TAGGAAGGTAAGGTAGGATC	chr17	58401949	-
RNF43	RNF43+6	TTCCTGCTTAAACGTGCAA	chr17	58419493	+
RNF43	RNF43-6	TTTAAATGCCGTTAGGGATA	chr17	58420009	-
RPL10	RPL10+1	CCCGGGTTGACAAAGGAACG	chrX	154397893	+
RPL10	RPL10+2	CTTACAGCTCCTTTAACGTC	chrX	154412452	+
RRAS	RRAS+1	CCTCAGGTGATCCATCCGCG	chr19	49634164	+
RRAS	RRAS+2	GGGCTCTTTGGGGGCGAATG	chr19	49650066	+
SDHD	SDHD+1	ATCAGCAAGATATTACCAAC	chr11	112082469	+
SDHD	SDHD+2	CAGGAGTTTAAAACCAGCGT	chr11	112097248	+
SH2B3	SH2B3+1	CTCCTCTTCACAACCTCGA	chr12	111401533	+
SH2B3	SH2B3-1	TGAATATAGTGCAGGCTCGG	chr12	111401899	-
SH2B3	SH2B3+2	GAAGCATTTTCTACGTTCTA	chr12	111416318	+
SH2B3	SH2B3-2	ATCCCAGCACCAGCCACGCG	chr12	111416803	-
SH2B3	SH2B3+3	AATGCTGCTATGAACATTCG	chr12	111432949	+
SH2B3	SH2B3-3	GGAGTCTCTCACGCAATGA	chr12	111433452	-
SH2B3	SH2B3+4	TTTGATCATTTCTGGACCGT	chr12	111451179	+
SH2B3	SH2B3-4	CAAAGGGAAGAGCGAGTATT	chr12	111451710	-
SHH	SHH+1	GGCCTTGACGCTCCTCGCAG	chr7	155798283	+
SHH	SHH+2	GA CTCAGCCTCTGTGGACCG	chr7	155812947	+
SMARCA4	SMARCA4+1	CTCCTTCCCCACTAGACCGA	chr19	10960333	+
SMARCA4	SMARCA4-1	CGCGGTGACGATGGGGCAAC	chr19	10960672	-
SMARCA4	SMARCA4+2	GCTGGGGGGAGGCTGCGTTA	chr19	10977282	+
SMARCA4	SMARCA4-2	CACGTGAAAGGTATCGCACT	chr19	10977736	-
SMARCA4	SMARCA4+3	CAGAGAGAGAAAACCAACCG	chr19	10993962	+
SMARCA4	SMARCA4-3	AAAACCTAGAATATCGCTTT	chr19	10994321	-
SMARCA4	SMARCA4+4	TTAGAGCTGTCCTATCCAAT	chr19	11003542	+
SMARCA4	SMARCA4-4	AAAAAATCATAAGTCGGACG	chr19	11004021	-
SMARCA4	SMARCA4+5	TATTGGCTGTGCCGCTGGT	chr19	11018041	+
SMARCA4	SMARCA4-5	TGCCACCCTCCAGCCACGGA	chr19	11018535	-
SMARCA4	SMARCA4+6	TTAGCCTCCTCGTACTGTGC	chr19	11032336	+
SMARCA4	SMARCA4-6	GTGCACACAGAACCGGAACC	chr19	11032860	-

SMARCA4	SMARCA4+7	CACATAGGGCACATCAACTC	chr19	11046623	+
SMARCA4	SMARCA4-7	TAGAGAATGACGGCACTTGA	chr19	11047149	-
SMARCA4	SMARCA4+8	GCATAGGCCTTAGCAGTAAC	chr19	11061867	+
SMARCA4	SMARCA4-8	CTCCTGCTGGCAGAAACGGT	chr19	11062332	-
SMARCB1	SMARCB1+1	GGAAGGCTTCCCCGTCTCG	chr22	23783474	+
SMARCB1	SMARCB1-1	GTTTGCCAGGACCTGCATAG	chr22	23783820	-
SMARCB1	SMARCB1+2	CTTGAGTTGATAGCTAGACC	chr22	23798013	+
SMARCB1	SMARCB1-2	GGTCCCCTCTACAACCTATC	chr22	23798481	-
SMARCB1	SMARCB1+3	CACAGGCTTGAAATCGCTG	chr22	23816301	+
SMARCB1	SMARCB1-3	AGCCAAACATCTCCGGATGC	chr22	23816685	-
SMARCB1	SMARCB1+4	ACTCCTCTCCAGGCGGATG	chr22	23834127	+
SMARCB1	SMARCB1-4	CATACCACCTTCGTCCCCC	chr22	23834604	-
SOX2	SOX2+1	GGAAGAGCGCAGTACGGGAG	chr3	181711380	+
SOX2	SOX2+2	GACAAGGAGGCGAGCCACGC	chr3	181726076	+
SPRY1	SPRY1+1	CACCAATTTAGACACGTCC	chr4	123393547	+
SPRY1	SPRY1+2	ACTTGCTGCATTTGTACACG	chr4	123408338	+
SPRY2	SPRY2+1	TAAGAATAAACATAGCGACT	chr13	80330585	+
SPRY2	SPRY2+2	GCGGGTCTGGTTTTTCCGG	chr13	80345366	+
SPRY4	SPRY4+1	TGGGGGCAATCGGGACATAA	chr5	142310082	+
SPRY4	SPRY4+2	TGCCCAGGGGTCGGAACGG	chr5	142324606	+
STK11	STK11+1	TCGCCCCAAGGGGGATGCG	chr19	1205322	+
STK11	STK11-1	AGGACGACGTGCCACCCGT	chr19	1205714	-
STK11	STK11+2	CACCCACTGAGACCGGCTCT	chr19	1222517	+
STK11	STK11-2	CTGGGACCAGGCCGTGCAAG	chr19	1222878	-
STK11	STK11+3	TTCCGCCACACGCGACAGC	chr19	1237168	+
STK11	STK11-3	GTGAGGTCGGGCGAGGACGA	chr19	1237553	-
TBX3	TBX3+1	GTGACACAGCTAAGTTTTCG	chr12	114669533	+
TBX3	TBX3+2	AGAAGGTCGGGCTGCGCTGT	chr12	114684188	+
TFE3	TFE3+1	TAGCACAGAAAAGACGTTAG	chrX	49025079	+
TFE3	TFE3+2	GCCGCATGAGACATGACGCC	chrX	49043212	+
TMPRSS2	TMPRSS2+1	TGAGGCAGGAAAATCGAGTC	chr21	41461344	+
TMPRSS2	TMPRSS2-1	TGGTTTGTTCAATACTACC	chr21	41461877	-
TMPRSS2	TMPRSS2+2	TGAGCCAGCCCTGCCGGAT	chr21	41475893	+
TMPRSS2	TMPRSS2-2	GCCCTGGCAGCCACCTAACG	chr21	41476246	-
TMPRSS2	TMPRSS2+3	AATTGGTGCTACTCAATAAC	chr21	41492485	+
TMPRSS2	TMPRSS2-3	AAGTCAGCATCTCCAGACGG	chr21	41492853	-
TMPRSS2	TMPRSS2+4	CCAACTGGCTAGGGACTCGC	chr21	41507774	+
TMPRSS2	TMPRSS2-4	CTGAGATTAAAGCGAGAGCC	chr21	41508192	-
TP53	TP53+1	TTCCTGCACCCGCCCTACCA	chr17	7657641	+
TP53	TP53-1	TCACTGTACAAAAGGGACGT	chr17	7658007	-
TP53	TP53+2	CATCTCATGGGGTTATAGGG	chr17	7674734	+
TP53	TP53-2	GAGCGCTGCTCAGATAGCGA	chr17	7675073	-

TP53	TP53+3	GTAAGGATAACAACGGGGCA	chr17	7689322	+
TP53	TP53-3	CACTTTTCCATCTCCACGA	chr17	7689771	-
VEGFA	VEGFA+1	GCTGGTAGCGGGGAGGATCG	chr6	43770191	+
VEGFA	VEGFA+2	GGGAGTGGGAGTTGTATTGG	chr6	43787353	+
VHL	VHL+1	AAAAATTCAGTTAGTCCACC	chr3	10141257	+
VHL	VHL+2	ACACATACCCAGTAGTCCAT	chr3	10155938	+
ZNF703	ZNF703+1	CAAAGGACCAACTTCGCCTC	chr8	37694611	+
ZNF703	ZNF703+2	CCCACTGAGCCCTATCTACC	chr8	37709182	+

** SMARCB1-4 sgRNA was omitted accidentally in experiments