
Supplementary information

Activated microglia cause metabolic disruptions in developmental cortical interneurons that persist in interneurons from individuals with schizophrenia

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Supplementary Table 1. RNA-seq Read depths. Related to Fig. 1.

Condition	Group	Sample	Batch	Input Reads	Pseudoaligned reads	Rate	Condition	Group	Sample	Batch	Input Reads	Pseudoaligned reads	Rate
Control	HC	190	a	17,363,905	14,886,042	85.73%	act.MG.	HC	190	a	16,590,278	13,463,964	81.16%
			b	15,097,267	12,613,188	83.55%				b	16,855,724	14,111,144	83.72%
			c	15,560,034	12,429,776	79.88%				c	12,639,388	10,500,443	83.08%
		226	a	11,584,641	9,992,503	86.26%			226	a	14,337,774	12,032,484	83.92%
			b	22,068,821	18,990,869	86.05%				b	15,461,241	13,113,534	84.82%
			c	14,092,097	11,997,481	85.14%				c	16,676,285	14,008,505	84.00%
		272	a	15,948,925	13,400,991	84.02%			272	a	18,845,690	15,063,706	79.93%
			b	22,408,971	18,688,367	83.40%				b	14,343,990	11,679,698	81.43%
			c	18,661,856	15,628,733	83.75%				c	15,839,313	13,056,386	82.43%
		367	a	15,535,315	12,756,213	82.11%			367	a	13,527,418	11,346,373	83.88%
			b	10,527,909	8,839,637	83.96%				b	13,801,137	11,428,810	82.81%
			c	14,649,726	12,259,978	83.69%				c	15,479,213	13,056,547	84.35%
	SCZ	67	a	27,327,936	22,865,917	79.60%		SCZ	67	a	13,400,957	11,001,785	82.10%
			b	27,043,247	21,526,307	79.60%				b	14,655,687	12,274,700	83.75%
			c	15,713,582	13,297,919	84.63%				c	14,473,824	12,394,673	85.64%
		128	a	15,269,796	12,937,516	84.73%			128	a	11,658,309	9,384,463	80.50%
			b	17,312,274	14,015,710	80.96%				b	14,100,948	11,464,008	81.30%
			c	13,662,407	11,776,383	86.20%				c	14,701,065	12,856,426	87.45%
		162	a	18,845,136	16,216,586	86.05%			162	a	15,916,366	12,883,297	80.94%
			b	18,544,714	15,292,973	82.47%				b	16,184,071	13,214,164	81.65%
			c	15,972,454	13,162,564	82.41%				c	17,060,248	13,953,655	81.79%
		212	a	14,892,747	12,953,157	86.98%			212	a	12,707,691	11,132,718	87.61%
			b	16,719,408	14,373,462	85.97%				b	14,974,305	12,066,397	80.58%
			c	18,383,393	15,124,374	82.27%				c	15,388,801	12,585,394	81.78%

Supplementary Table 2. DE gene list from RNAseq analysis of control vs. act.MG. cINs ($p < 0.005$). Differentially expressed genes were analyzed by Kallisto-Sleuth. (Wald test for two-sided significance testing, $n=24$ batches from 4 HC lines and 4 SCZ lines, each line with 3 independent differentiations), mean_obs: mean of natural log counts of observations, b:'beta' value (an estimator of the fold change). *Related to Fig.1.*

Symbol	Entrez	Name	mean_obs	b	p Value
ACTA2	59	actin, alpha 2, smooth muscle, aorta	3.949961884	0.605437316	4.27E-05
ACTN1	87	actinin alpha 1	4.995132457	0.343557935	7.07E-05
ADM5	199800	adrenomedullin 5 (putative)	3.658876566	-0.451093972	1.06E-05
ADO	84890	2-aminoethanethiol dioxxygenase	6.4056105	0.142897556	0.004885
ADRB1	153	adrenoceptor beta 1	1.771013668	0.530124024	0.002898
ADRB2	154	adrenoceptor beta 2	2.136836527	0.552581207	0.001156
AGO2	27161	argonaute 2, RISC catalytic component	4.035901849	0.247344912	0.004499
AGO3	192669	argonaute 3, RISC catalytic component	4.949997768	0.242802854	0.004585
AJUBA	84962	ajuba LIM protein	4.436979842	0.597457848	2.31E-07
ALDH1B1	219	aldehyde dehydrogenase 1 family member B1	4.758888811	0.344102934	5.24E-07
ALDH5A1	7915	aldehyde dehydrogenase 5 family member A1	5.789214025	0.166898563	0.003408
AMOTL2	51421	angiomotin like 2	5.137853006	0.173643318	0.002956
ANKHD1- EIF4EBP3	404734	ANKHD1-EIF4EBP3 readthrough	6.548808859	-0.181366806	0.00497
ANKRD33B	651746	ankyrin repeat domain 33B	3.445509375	0.995841894	9.14E-06
ANKRD45	339416	ankyrin repeat domain 45	4.761626415	0.214673597	0.00364
ANKRD63	100131244	ankyrin repeat domain 63	2.315608166	0.659046264	2.53E-05
ANKZF1	55139	ankyrin repeat and zinc finger domain containing 1	5.285136882	-0.183610431	0.002478
ARHGAP29	9411	Rho GTPase activating protein 29	4.736033413	0.296497772	0.000239
ATOX1	84913	atonal bHLH transcription factor 8	4.099919634	0.540133846	3.56E-05
BBC3	27113	BCL2 binding component 3	5.741291403	-0.327921065	8.10E-05
BICD1	636	BICD cargo adaptor 1	6.037394728	0.205741387	0.00069
BOLA2	552900	bolA family member 2	5.121991662	-0.264428969	0.001819
BTG1	694	BTG anti-proliferation factor 1	7.282916035	-0.32342843	2.29E-09
BTG2	7832	BTG anti-proliferation factor 2	6.253912049	-0.29998338	0.000234
C12orf29	91298	chromosome 12 open reading frame 29	4.842604835	0.205530825	0.003505

C2orf69	205327	chromosome 2 open reading frame 69	4.941269902	0.232131197	0.000207
C7orf55-LUC7L2	100996928	C7orf55-LUC7L2 readthrough	6.539345387	-0.171515031	0.001917
C9orf3	84909	chromosome 9 open reading frame 3	5.173290967	0.189048021	0.002781
CALD1	800	caldesmon 1	5.199869763	0.398477465	9.17E-05
CARNS1	57571	carnosine synthase 1	4.103421981	0.505174168	0.004746
CATSPER2P1	440278	cation channel sperm associated 2 pseudogene 1	3.33602023	0.546224377	7.45E-05
CCL2	6347	C-C motif chemokine ligand 2	3.412908135	0.88771245	0.000305
CCND1	595	cyclin D1	5.055310571	0.513551844	0.002888
CDK7	1022	cyclin dependent kinase 7	4.216712732	-0.448500803	0.001586
CDR1	1038	cerebellar degeneration related protein 1	5.73903936	0.268016794	0.00336
CEBPD	1052	CCAAT/enhancer binding protein delta	2.781833243	0.699137024	8.00E-05
CFTR	1080	cystic fibrosis transmembrane conductance regulator	3.659631934	0.343866365	0.002345
CLK1	1195	CDC like kinase 1	7.2019687	-0.215709964	0.001294
CNN2	1265	calponin 2	5.668317797	0.763631232	1.29E-11
CSF1	1435	colony stimulating factor 1	3.14615731	0.368899529	0.003707
CSRNP1	64651	cysteine and serine rich nuclear protein 1	5.141244575	0.537664877	0.000148
CTGF	1490	connective tissue growth factor	6.582002442	1.487887197	1.70E-07
DAPK3	1613	death associated protein kinase 3	5.75264371	0.174044739	0.001048
DBP	1628	D-box binding PAR bZIP transcription factor	4.31412573	0.428212504	1.35E-06
DDAH1	23576	dimethylarginine dimethylaminohydrolase 1	7.551827243	0.199171684	0.001267
DDIT4	54541	DNA damage inducible transcript 4	5.891043995	-0.234416331	0.003715
DDX39A	10212	DExD-box helicase 39A	6.2635915	-0.176943392	0.002565
DGKH	160851	diacylglycerol kinase eta	4.58878015	0.324613046	0.000724
DRD1	1812	dopamine receptor D1	3.011086452	0.555729501	0.001836
DRD4	1815	dopamine receptor D4	2.865332243	0.436371696	0.001421
EBP	10682	emopamil binding protein (sterol isomerase)	5.834534701	-0.176654355	0.00237
EIF5	1983	eukaryotic translation initiation factor 5	6.89707701	0.157219472	0.003619
ELL2	22936	elongation factor for RNA polymerase II 2	2.65555197	0.374092617	0.003058
ELMSAN1	91748	ELM2 and Myb/SANT domain containing 1	6.092149454	0.220345799	0.004092
ERF	2077	ETS2 repressor factor	5.118760673	0.213219385	0.001101
ETS1	2113	ETS proto-oncogene 1, transcription factor	4.544123579	0.404767141	0.000114

FAM46A	55603	family with sequence similarity 46 member A	5.307824708	0.376349651	0.001164
FAM46B	115572	family with sequence similarity 46 member B	2.886438259	0.554254177	0.000539
FAM84B	157638	family with sequence similarity 84 member B	6.198681259	0.51170631	0.000356
FAM89B	23625	family with sequence similarity 89 member B	6.783176319	-0.16686625	0.004551
FBXL17	64839	F-box and leucine rich repeat protein 17	6.802457875	0.244725376	0.002041
FERMT2	10979	fermitin family member 2	6.792937973	0.300809979	1.33E-06
FGF2	2247	fibroblast growth factor 2	5.464488561	0.220882164	0.003435
FHL2	2274	four and a half LIM domains 2	4.479307293	1.118198916	8.61E-29
FOSL2	2355	FOS like 2, AP-1 transcription factor subunit	5.675517127	0.835650799	1.88E-07
FOXO4	4303	forkhead box O4	3.506074828	-0.318215269	0.001635
FRAT2	23401	FRAT2, WNT signaling pathway regulator	4.915512165	-0.304463577	0.000111
GABRQ	55879	gamma-aminobutyric acid type A receptor theta subunit	5.558105555	0.276326304	0.000415
GLIPR1	11010	GLI pathogenesis related 1	2.685784224	0.561536315	0.000149
GMPR2	51292	guanosine monophosphate reductase 2	6.04627536	-0.165219691	0.002235
GOLGA8J	653073	golgin A8 family member J	3.266017245	0.363973645	0.002961
GPCPD1	56261	glycerophosphocholine phosphodiesterase 1	4.655269593	0.201559771	0.004819
GPR19	2842	G protein-coupled receptor 19	4.453430105	-0.207524651	0.004042
GUF1	60558	GUF1 homolog, GTPase	6.089417106	0.163445992	0.004789
H2AFB3	83740	H2A histone family member B3	1.079895599	-1.161268503	0.000123
HIST1H4E	8367	histone cluster 1 H4 family member e	1.797080122	-0.572172329	0.001311
HR	55806	HR, lysine demethylase and nuclear receptor corepressor	1.57982246	0.515321262	0.002127
ID1	3397	inhibitor of DNA binding 1, HLH protein	4.105292711	1.385388231	6.58E-08
ID2	3398	inhibitor of DNA binding 2	5.78532828	0.52090526	0.000341
ID3	3399	inhibitor of DNA binding 3, HLH protein	5.153950116	1.103489193	0.0001
ID4	3400	inhibitor of DNA binding 4, HLH protein	7.751713473	0.352761716	2.37E-08
IFT20	90410	intraflagellar transport 20	5.738931709	-0.16017228	0.004815
IGBP1	3476	immunoglobulin binding protein 1	6.557383664	-0.14875631	0.00326
IGFBP3	3486	insulin like growth factor binding protein 3	3.473734438	0.636946752	0.004209
ING4	51147	inhibitor of growth family member 4	6.348374215	-0.219023101	0.000818
IRS1	3667	insulin receptor substrate 1	6.146795029	0.404535248	7.15E-06
ITGB8	3696	integrin subunit beta 8	6.255714743	0.292606183	0.002179

KCNJ10	3766	potassium voltage-gated channel subfamily J member 10	4.185137233	-0.413965849	0.004733
KIAA1429	25962	vir like m6A methyltransferase associated	4.758488054	-0.216296187	0.001808
KLF10	7071	Kruppel like factor 10	5.337782635	0.645170456	7.79E-13
KLF16	83855	Kruppel like factor 16	4.309993771	0.229358089	0.003806
KLF9	687	Kruppel like factor 9	3.891969673	0.608913056	8.82E-06
LACC1	144811	laccase domain containing 1	2.999455488	0.390446128	0.004641
LATS2	26524	large tumor suppressor kinase 2	4.371241499	0.490226241	7.65E-07
LAYN	143903	layilin	2.623926699	0.500758702	0.002337
LIF	3976	LIF, interleukin 6 family cytokine	2.983301802	0.49778486	0.002418
LIMA1	51474	LIM domain and actin binding 1	5.561794174	0.534220479	2.08E-06
LMOD1	25802	leiomodlin 1	2.987393125	0.556240831	0.000162
LOC102724428	102724428	salt inducible kinase 1B (putative)	4.937094076	0.46847264	0.001824
LRRC8C	84230	leucine rich repeat containing 8 VRAC subunit C	3.147525914	0.385788009	0.000824
MAF1	84232	MAF1 homolog, negative regulator of RNA polymerase III	6.303091822	-0.203567209	0.000125
MAFK	7975	MAF bZIP transcription factor K	5.887220497	0.270638685	0.001116
MAP3K14	9020	mitogen-activated protein kinase kinasekinase 14	5.271285582	0.227114418	0.004442
MAPK1IP1L	93487	mitogen-activated protein kinase 1 interacting protein 1 like	5.526354947	0.20004245	0.000434
MARS2	92935	methionyl-tRNA synthetase 2, mitochondrial	4.905080131	0.182182135	0.004704
METTL12	751071	citrate synthase lysine methyltransferase	4.719734301	-0.339361064	0.000137
MOB1B	92597	MOB kinase activator 1B	4.862915514	0.289349731	0.000704
MXD4	10608	MAX dimerization protein 4	5.88956869	-0.163250799	0.001644
MYADM	91663	myeloid associated differentiation marker	5.633717692	0.302102875	5.58E-06
MYC	4609	MYC proto-oncogene, bHLH transcription factor	5.068258354	0.498500646	4.06E-06
MYH9	4627	myosin heavy chain 9	4.772839527	0.308067919	0.000213
MYO1E	4643	myosin IE	3.609903846	0.322563928	0.001701
NAB2	4665	NGFI-A binding protein 2	5.532575052	0.494249697	2.12E-09
NACC2	138151	NACC family member 2	6.941598343	0.274824315	0.002905
NEDD9	4739	neural precursor cell expressed, developmentally down-regulated 9	3.86876446	0.394176637	0.000246
NEXN	91624	nexilin F-actin binding protein	3.320528517	0.34576448	0.002145
NFATC2	4773	nuclear factor of activated T-cells 2	2.729959116	0.358569275	0.002914
NOC3L	64318	NOC3 like DNA replication regulator	5.030560445	0.252135766	0.001253

NOCT	25819	Nocturnin	4.554620717	0.247470097	0.003411
NOG	9241	Noggin	5.106137938	0.527610991	1.40E-07
NR4A1	3164	nuclear receptor subfamily 4 group A member 1	5.066636614	0.632937447	5.39E-06
NR4A3	8013	nuclear receptor subfamily 4 group A member 3	5.188158755	0.532395673	3.83E-06
OS9	10956	OS9, endoplasmic reticulum lectin	7.156425366	-0.149741544	0.003316
PALLD	23022	palladin, cytoskeletal associated protein	5.227044141	0.250756755	0.000237
PAWR	5074	pro-apoptotic WT1 regulator	4.210410656	0.232246751	0.004844
PDCD4	27250	programmed cell death 4	6.27098911	-0.193984097	0.002269
PDE4D	5144	phosphodiesterase 4D	4.702381631	0.269068379	0.000435
PDK3	5165	pyruvate dehydrogenase kinase 3	4.140729727	0.242664333	0.003765
PER2	8864	period circadian regulator 2	3.812279225	0.263835407	0.002372
PFKFB3	5209	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	6.257048941	0.188525591	0.003285
PHLDA1	22822	pleckstrin homology like domain family A member 1	6.536230306	0.272148693	0.001621
PIH1D1	55011	PIH1 domain containing 1	5.911657955	-0.21753196	0.000132
PIK3IP1	113791	phosphoinositide-3-kinase interacting protein 1	5.635279513	-0.233950479	2.55E-05
PIM1	5292	Pim-1 proto-oncogene, serine/threonine kinase	4.605029709	0.321466872	0.00362
PLAU	5328	plasminogen activator, urokinase	1.895820864	0.715075007	2.98E-05
PMEPA1	56937	prostate transmembrane protein, androgen induced 1	5.250582391	0.242615371	0.003314
PNRC1	10957	proline rich nuclear receptor coactivator 1	6.020979719	-0.364935736	8.56E-09
PODXL	5420	podocalyxin like	5.55977228	0.24086168	0.004303
PPP1R3B	79660	protein phosphatase 1 regulatory subunit 3B	3.478450274	0.393326188	0.000233
PPP2R2A	5520	protein phosphatase 2 regulatory subunit Balpha	5.196223806	0.180135546	0.001895
PTP4A1	7803	protein tyrosine phosphatase type IVA, member 1	6.37917937	0.206402504	0.003448
PTPN14	5784	protein tyrosine phosphatase, non-receptor type 14	4.027196932	0.334261817	0.000662
PTRF	284119	caveolae associated protein 1	4.800140036	1.125289535	1.24E-05
RAB33A	9363	RAB33A, member RAS oncogene family	5.513689317	-0.199608743	0.001952
RARA	5914	retinoic acid receptor alpha	6.167518341	0.233107836	0.001165
RASA2	5922	RAS p21 protein activator 2	3.710218559	0.302327995	0.001452
RCBTB2	1102	RCC1 and BTB domain containing protein 2	5.884604423	0.168305592	0.003675
RELB	5971	RELB proto-oncogene, NF-kB subunit	2.940267217	0.461680771	9.88E-05
RGPD5	84220	RANBP2-like and GRIP domain containing 5	4.376463772	0.297502213	0.004487

RNF113A	7737	ring finger protein 113A	5.177792707	-0.168926119	0.004809
ROCK2	9475	Rho associated coiled-coil containing protein kinase 2	4.779581109	0.223586198	0.003684
RPL13AP5	728658	ribosomal protein L13a pseudogene 5	1.495309956	0.920440303	0.001428
RRS1	23212	ribosome biogenesis regulator homolog	4.993673408	0.213802384	0.001147
RYBP	23429	RING1 and YY1 binding protein	6.613818719	0.199854098	0.003792
SAMD4A	23034	sterile alpha motif domain containing 4A	4.563055405	0.489292894	1.55E-05
SAT2	112483	spermidine/spermine N1-acetyltransferase family member 2	6.76394118	-0.209109186	0.001402
SERPINE1	5054	serpin family E member 1	3.339340486	0.64552838	0.003774
SERTAD4	56256	SERTA domain containing 4	2.616016513	0.394254157	0.000772
SESN2	83667	sestrin 2	6.394174862	-0.146055588	0.004033
SHROOM3	57619	shroom family member 3	3.455126615	0.345387212	0.003682
SIK2	23235	salt inducible kinase 2	6.588107534	0.200570449	0.002264
SIRT4	23409	sirtuin 4	2.581117888	-0.373333158	0.003762
SLC16A9	220963	solute carrier family 16 member 9	5.954351456	0.264594111	0.001357
SLC7A1	6541	solute carrier family 7 member 1	4.595642091	0.194517365	0.003336
SMC5	23137	structural maintenance of chromosomes 5	4.761612203	0.270918252	0.000608
SSR2	6746	signal sequence receptor subunit 2	7.215812766	-0.147962507	0.004086
SSR4	6748	signal sequence receptor subunit 4	6.8499521	-0.186492898	0.003988
STK17A	9263	serine/threonine kinase 17a	5.029567289	0.251273258	0.000462
STX11	8676	syntaxin 11	1.862672002	1.007999452	6.50E-05
SULT1A3	6818	sulfotransferase family 1A member 3	5.108310525	-0.228061633	0.003392
SYDE2	84144	synapse defective Rho GTPase homolog 2	3.857111914	0.440915963	4.07E-05
SYF2	25949	SYF2 pre-mRNA splicing factor	5.985886489	-0.170697348	0.001118
SYNJ2	8871	synaptojanin 2	3.841287354	0.550992058	7.91E-05
TACC1	6867	transforming acidic coiled-coil containing protein 1	4.980027714	0.205558641	0.004324
TAGLN	6876	transgelin	5.275299602	0.427424411	0.000369
TFAP2C	7022	transcription factor AP-2 gamma	1.858734098	0.72216228	0.000174
TFPI2	7980	tissue factor pathway inhibitor 2	2.938351115	0.722387783	0.002449
TGFB1I1	7041	transforming growth factor beta 1 induced transcript 1	4.0324406	0.494982532	0.001066
THBS1	7057	thrombospondin 1	4.361221969	1.084260336	2.52E-07
TIMM17B	10245	translocase of inner mitochondrial membrane 17B	6.331290688	-0.169495422	0.003251

TLE3	7090	transducin like enhancer of split 3	6.785314236	0.176551831	0.003482
TMEM198B	440104	transmembrane protein 198B (pseudogene)	6.122104285	-0.162878099	0.001944
TNFAIP3	7128	TNF alpha induced protein 3	3.610745782	0.363789162	0.001275
TNFRSF12A	51330	TNF receptor superfamily member 12A	4.228232984	1.109200988	6.65E-09
TOB1	10140	transducer of ERBB2, 1	5.677302914	-0.301879947	9.13E-05
TP53INP1	94241	tumor protein p53 inducible nuclear protein 1	7.308828454	-0.178721084	0.002306
TP53INP2	58476	tumor protein p53 inducible nuclear protein 2	6.549521796	0.206863074	0.000309
TPM1	7168	tropomyosin 1	7.158912007	0.319131067	0.000691
TPM4	7171	tropomyosin 4	6.532239092	0.167193173	0.001097
TPP1	1200	tripeptidyl peptidase 1	4.74260315	-0.219400382	0.001631
TRIOBP	11078	TRIO and F-actin binding protein	5.209628273	0.171594448	0.002876
TRPC3	7222	transient receptor potential cation channel subfamily C member 3	3.908582991	0.285248475	0.002826
UBALD2	283991	UBA like domain containing 2	4.849691749	-0.331858005	7.69E-05
ULK4P1	89838	ULK4 pseudogene 1	2.016562161	0.790915091	0.002701
URB2	9816	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	5.261977814	0.260659396	0.000144
USF1	7391	upstream transcription factor 1	7.062302723	-0.176377588	0.002553
USP21	27005	ubiquitin specific peptidase 21	5.735686874	-0.175220857	0.001351
VCL	7414	vinculin	6.638915923	0.771597413	3.44E-13
WDR1	9948	WD repeat domain 1	6.320749673	0.213862159	0.000105
WDR4	10785	WD repeat domain 4	4.411467423	0.27170709	0.000422
WWTR1	25937	WW domain containing transcription regulator 1	4.799406838	0.3503184	0.003124
YTHDF3	253943	YTH N6-methyladenosine RNA binding protein 3	6.404213206	0.178308009	0.00205
ZBTB9	221504	zinc finger and BTB domain containing 9	2.212041716	-0.678358607	0.004234
ZDHHC21	340481	zinc finger DHHC-type containing 21	5.920975003	0.242024494	0.00359
ZFP36L2	678	ZFP36 ring finger protein like 2	6.495026601	0.424179876	1.98E-06
ZNF581	51545	zinc finger protein 581	5.226345956	-0.181591309	0.002537
ZNF740	283337	zinc finger protein 740	5.420760225	-0.185642727	0.001795
ZYX	7791	zyxin	6.254602078	0.311955019	4.65E-06

Supplementary Table 3. The list of pathway genes. Genes that belong to GO:0019222 (regulation of metabolic process) are marked in red and are shared among top DE gene pathways: *Related to Fig.1.*

Term	Gene list
GO:0048519~negative regulation of biological process	CTGF, THBS1, NOG, LIMA1, HR, PAWR, FOXO4, MAF1, PDCD4, NOCT, LATS2, VCL, OS9, C7ORF55-LUC7L2, SERPINE1, RARA, LMOD1, ATOH8, TFPI2, FGF2, MYC, SAMD4A, ROCK2, RELB, PIM1, ACTN1, LOC102724428, PDE4D, CDK7, PIK3IP1, MYH9, H2AFB3, DAPK3, IRS1, MYADM, BICD1, DDIT4, MXD4, CCND1, ADRB2, ADRB1, PIH1D1, BTG2, BTG1, IGBP1, NAB2, TFAP2C, TGFB1I1, TNFAIP3, PMEPA1, TRIOBP, ING4, DRD1, CCL2, DRD4, FHL2, SESN2, TPM1, LIF, ZFP36L2, ITGB8, HIST1H4E, PER2, AGO2, AGO3, CNN2, NFATC2, RASA2, FAM89B, ERF, NACC2, KLF9, CEBPD, PODXL, KLF10, SIRT4, KLF16, PTPN14, RYBP, NR4A1, NR4A3, WWTR1, USF1, AJUBA, ID2, ETS1, ID1, BBC3, SYF2, ID4, ID3, IGFBP3, TP53INP2, PLAU, TP53INP1, TOB1
GO:0010629~negative regulation of gene expression	CTGF, THBS1, NOG, HR, PAWR, MAF1, PDCD4, NOCT, SERPINE1, RARA, ATOH8, MYC, SAMD4A, RELB, DAPK3, MYADM, H2AFB3, MXD4, CCND1, BTG2, NAB2, IGBP1, TFAP2C, ING4, FHL2, SESN2, ZFP36L2, ITGB8, PER2, HIST1H4E, AGO2, AGO3, NFATC2, ERF, NACC2, CEBPD, KLF10, RYBP, KLF16, SIRT4, NR4A3, WWTR1, AJUBA, ID2, ID1, ID4, ID3, TP53INP1, TOB1
GO:0009892~negative regulation of metabolic process	CTGF, THBS1, NOG, HR, PAWR, MAF1, PDCD4, LATS2, NOCT, OS9, C7ORF55-LUC7L2, SERPINE1, RARA, ATOH8, TFPI2, MYC, SAMD4A, ROCK2, RELB, LOC102724428, PDE4D, PIK3IP1, H2AFB3, DAPK3, MYADM, DDIT4, MXD4, CCND1, PIH1D1, BTG2, NAB2, IGBP1, TFAP2C, TNFAIP3, PMEPA1, ING4, DRD4, FHL2, SESN2, LIF, ZFP36L2, ITGB8, HIST1H4E, PER2, AGO2, AGO3, NFATC2, ERF, NACC2, CEBPD, KLF10, SIRT4, KLF16, RYBP, NR4A1, NR4A3, WWTR1, AJUBA, ID2, ID1, ID4, ID3, IGFBP3, TOB1, TP53INP1
GO:0048523~negative regulation of cellular process	CTGF, THBS1, NOG, LIMA1, HR, PAWR, FOXO4, MAF1, PDCD4, NOCT, LATS2, VCL, OS9, SERPINE1, RARA, LMOD1, ATOH8, TFPI2, FGF2, MYC, SAMD4A, ROCK2, RELB, PIM1, ACTN1, LOC102724428, PDE4D, CDK7, PIK3IP1, MYH9, H2AFB3, DAPK3, IRS1, MYADM, BICD1, DDIT4, MXD4, CCND1, ADRB2, PIH1D1, BTG2, BTG1, IGBP1, NAB2, TFAP2C, TGFB1I1, TNFAIP3, PMEPA1, TRIOBP, ING4, DRD1, CCL2, DRD4, FHL2, SESN2, TPM1, LIF, ZFP36L2, HIST1H4E, PER2, AGO2, AGO3, CNN2, NFATC2, RASA2, FAM89B, ERF, NACC2, KLF9, CEBPD, PODXL, KLF10, SIRT4, KLF16, PTPN14, RYBP, NR4A1, NR4A3, WWTR1, AJUBA, ID2, ETS1, ID1, BBC3, SYF2, ID4, ID3, IGFBP3, TP53INP1, TOB1
GO:0010605~negative regulation of macromolecule metabolic process	CTGF, THBS1, NOG, HR, PAWR, MAF1, PDCD4, LATS2, NOCT, OS9, SERPINE1, RARA, ATOH8, TFPI2, MYC, SAMD4A, ROCK2, RELB, PDE4D, H2AFB3, DAPK3, MYADM, DDIT4, MXD4, CCND1, PIH1D1, BTG2, NAB2, IGBP1, TFAP2C, TNFAIP3, PMEPA1, ING4, FHL2, SESN2, LIF, ZFP36L2, ITGB8, HIST1H4E, PER2, AGO2, AGO3, NFATC2, ERF, NACC2, CEBPD, KLF10, SIRT4, KLF16, RYBP, NR4A1, NR4A3, WWTR1, AJUBA, ID2, ID1, ID4, ID3, IGFBP3, TOB1, TP53INP1
GO:0019222~regulation of metabolic process	CTGF, THBS1, ZNF581, NOG, EIF5, CLK1, FOXO4, MAF1, C7ORF55-LUC7L2, SERPINE1, RARA, ATOH8, TFPI2, DDAH1, SAMD4A, DDX39A, ROCK2, RELB, PIM1, ACTN1, LOC102724428, PDE4D, PIK3IP1, MYH9, IRS1, DDIT4, ELL2, PTRF, IGBP1, TFAP2C, TGFB1I1, TNFAIP3, DRD1, CCL2, DRD4, STK17A, SESN2, LIF, PPP1R3B, ITGB8, HIST1H4E, KLF9, KLF10, PTPN14, KLF16, RYBP, NR4A1, NR4A3, MAFK, USF1, BBC3, ETS1, CSRNPI, PNRC1, FOSL2, HR, PAWR, PDCD4, NOCT, LATS2, OS9, FGF2, MYC, ELMSAN1, ACTA2, TLE3, CDK7, H2AFB3, DAPK3, MYADM, MXD4, CCND1, ADRB2, PIH1D1, ADRB1, BTG2, BTG1, NAB2, USP21, MAP3K14, ZNF740, PMEPA1, ING4, MOB1B, ZBTB9, CSF1, FHL2, FAM46A, ZFP36L2, ZDHHC21, PER2, AGO2, AGO3, CNN2, GUF1, NFATC2, ERF, NACC2, CEBPD, PDK3, SIRT4, WWTR1, AJUBA, ID2, DBP, ID1, ID4, ID3, IGFBP3, TP53INP2, TOB1, TP53INP1

Supplementary Table 4. HC DE gene list from RNAseq analysis of control vs. act.MG. cINs ($p < 0.005$). Differentially expressed genes were analyzed by DESeq2 (Wald test for two-sided significance testing, $n=24$ batches from 4 HC lines and 4 SCZ lines, each line with 3 independent differentiations). *Related to Fig. 3.*

Symbol	Entrez	Name	BaseMean	Log2FC	p Value
FHL2	2274	four and a half LIM domains 2	115.314692	1.74165985	1.85E-19
CNN2	1265	calponin 2	654.821079	1.20159674	4.57E-08
VCL	7414	vinculin	1533.70822	1.16285833	7.71E-08
TNFRSF12A	51330	TNF receptor superfamily member 12A	121.155745	1.56938648	3.71E-07
PNRC1	10957	proline rich nuclear receptor coactivator 1	423.242701	-0.63787294	8.16E-07
KLF10	7071	Kruppel like factor 10	237.683696	0.98869553	8.80E-07
THBS1	7057	thrombospondin 1	1289.15859	2.15325334	1.53E-06
IRS1	3667	insulin receptor substrate 1	906.434255	0.54691717	1.72E-06
ANKRD33B	651746	ankyrin repeat domain 33B	92.4894704	1.54384278	2.68E-06
PER2	8864	period circadian regulator 2	346.951452	0.38116133	3.63E-06
MOB1B	92597	MOB kinase activator 1B	595.761916	0.51985511	5.32E-06
ITGB8	3696	integrin subunit beta 8	1126.71056	0.37718759	5.38E-06
DBP	1628	D-box binding PAR bZIP transcription factor	86.0343476	0.55780709	7.36E-06
BTG1	694	BTG anti-proliferation factor 1	1263.13956	-0.41820039	2.84E-05
ZYX	7791	zyxin	1521.64256	0.47212595	3.70E-05
BBC3	27113	BCL2 binding component 3	318.456624	-0.46651231	4.35E-05
NAB2	4665	NGFI-A binding protein 2	1059.32284	0.66154063	4.75E-05
SYDE2	84144	synapse defective Rho GTPase homolog 2	50.2327557	0.68144852	4.87E-05
CAVIN1	284119	caveolae associated protein 1	181.153794	1.62821493	5.57E-05
AJUBA	84962	ajuba LIM protein	451.733136	0.90432149	6.65E-05
CTGF	1490	connective tissue growth factor	1911.36675	2.19096186	7.46E-05
NOG	9241	noggin	162.386828	0.78286405	8.68E-05
NOA1	84273	nitric oxide associated 1	290.339167	-0.26276161	0.00010177
ANKRD63	100131244	ankyrin repeat domain 63	12.9905226	0.94031087	0.00010577
FAM46B	115572	family with sequence similarity 46 member B	22.8506253	1.07763135	0.00012466
MYC	4609	MYC proto-oncogene, bHLH transcription factor	200.5482	0.86799975	0.00016868
ROCK2	9475	Rho associated coiled-coil containing protein kinase 2	1068.97932	0.36028108	0.00016941

SMAD7	4092	SMAD family member 7	105.063729	0.52571054	0.00019392
MAF1	84232	MAF1 homolog, negative regulator of RNA polymerase III	901.689951	-0.31155362	0.00019983
COX6B2	125965	cytochrome c oxidase subunit 6B2	15.331834	0.79185031	0.00026229
NACC2	138151	NACC family member 2	1079.17853	0.33652443	0.00026374
TIMP3	7078	TIMP metalloproteinase inhibitor 3	1707.82616	0.42672278	0.00028084
CYHR1	50626	cysteine and histidine rich 1	963.401812	-0.17905126	0.00031843
POLR2B	5431	RNA polymerase II subunit B	2819.12177	-0.22910667	0.00032001
DAPK3	1613	death associated protein kinase 3	875.67674	0.33471636	0.00032026
LATS2	26524	large tumor suppressor kinase 2	175.577409	0.78876009	0.00035099
TFAP2C	7022	transcription factor AP-2 gamma	15.7335269	1.27861728	0.00036842
NR4A3	8013	nuclear receptor subfamily 4 group A member 3	210.41404	0.9320702	0.00037207
LMOD1	25802	leiomodin 1	28.9773502	1.27019	0.00037984
CSF1	1435	colony stimulating factor 1	99.0341054	0.52806914	0.00042183
FOSL2	2355	FOS like 2, AP-1 transcription factor subunit	727.074577	1.17609173	0.00043718
EIF4ENIF1	56478	eukaryotic translation initiation factor 4E nuclear import factor 1	812.444706	-0.17791236	0.00046857
FERMT2	10979	fermitin family member 2	1071.86132	0.48159394	0.00047657
DRD4	1815	dopamine receptor D4	21.9909165	0.80941397	0.00049784
ZNF740	283337	zinc finger protein 740	1110.32844	-0.32193789	0.00051254
SERPINE1	5054	serpin family E member 1	53.8696509	1.34360877	0.00053388
CDK7	1022	cyclin dependent kinase 7	114.315961	-0.83325024	0.00055087
ALKBH3	221120	alkB homolog 3, alpha-ketoglutaratedependent dioxygenase	287.754523	-0.24344292	0.00055648
PMEPA1	56937	prostate transmembrane protein, androgen induced 1	264.599855	0.42557468	0.00057532
ACTA2	59	actin, alpha 2, smooth muscle, aorta	93.4350414	0.909926	0.00058299
RAB3GAP1	22930	RAB3 GTPase activating protein catalytic subunit 1	1055.59364	-0.14363002	0.00060605
PIGU	128869	phosphatidylinositol glycan anchor biosynthesis class U	402.253647	-0.21022804	0.00063688
PLAU	5328	plasminogen activator, urokinase	32.6833763	1.40481358	0.00065155
ISCU	23479	iron-sulfur cluster assembly enzyme	827.686277	-0.21443417	0.00070467
SYF2	25949	SYF2 pre-mRNA splicing factor	436.954213	-0.26706383	0.00070471
TBC1D7	51256	TBC1 domain family member 7	354.861386	-0.20188716	0.00070894
SYNJ2	8871	synaptojanin 2	110.840569	0.68368488	0.00071059
GLIPR1	11010	GLI pathogenesis related 1	61.1167037	0.89979646	0.00074923

PALLD	23022	palladin, cytoskeletal associated protein	1267.25323	0.35851642	0.00079604
LRP12	29967	LDL receptor related protein 12	550.006183	0.34363409	0.00081729
HOOK1	51361	hook microtubule tethering protein 1	250.872811	0.71127217	0.00081975
MIER3	166968	MIER family member 3	467.432523	0.35817335	0.0008215
PIK3R3	8503	phosphoinositide-3-kinase regulatory subunit 3	3604.93228	-0.23166408	0.00087434
L3MBTL3	84456	L3MBTL3, histone methyl-lysine binding protein	391.629	-0.23224198	0.00093262
AMOTL2	51421	angiomotin like 2	1206.75791	0.38700804	0.00104412
MARK3	4140	microtubule affinity regulating kinase 3	1864.09247	-0.13483673	0.00106959
LIMA1	51474	LIM domain and actin binding 1	635.139435	0.86784787	0.00116853
GOLPH3L	55204	golgi phosphoprotein 3 like	166.05063	-0.25417919	0.0012131
ID1	3397	inhibitor of DNA binding 1, HLH protein	113.994066	1.5024618	0.00126732
LOC100133920	100133920	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1 like pseudogene	4.37603721	2.41582799	0.00129013
HNRNPH2	3188	heterogeneous nuclear ribonucleoprotein H2	1812.34682	-0.1438278	0.00135588
NEXN	91624	nexilin F-actin binding protein	30.7615064	0.6730295	0.00136138
IGBP1	3476	immunoglobulin binding protein 1	645.785487	-0.22330796	0.00137629
WDR1	9948	WD repeat domain 1	2583.60685	0.33848327	0.00137952
TOB1	10140	transducer of ERBB2, 1	308.117481	-0.44645454	0.00140457
TACC1	6867	transforming acidic coiled-coil containing protein 1	800.672274	0.34521831	0.00144695
RBM4	5936	RNA binding motif protein 4	1717.67583	-0.16802358	0.00158453
CDKN1B	1027	cyclin dependent kinase inhibitor 1B	1040.28799	-0.28205367	0.00159425
ATOH8	84913	atonal bHLH transcription factor 8	81.2728451	0.79904453	0.00166027
NAALADL2	254827	N-acetylated alpha-linked acidic dipeptidase like 2	27.4932494	0.8851294	0.0016626
SIKE1	80143	suppressor of IKBKE 1	594.936338	0.36754137	0.0016627
ANKRD36B	57730	ankyrin repeat domain 36B	522.006031	0.46609568	0.00172039
OAS3	4940	2'-5'-oligoadenylate synthetase 3	28.2220151	0.85593875	0.00173496
NHLRC2	374354	NHL repeat containing 2	544.221446	0.20601701	0.00173894
USP21	27005	ubiquitin specific peptidase 21	510.918646	-0.22151283	0.00179894
SHC4	399694	SHC adaptor protein 4	141.933606	0.39985765	0.00181347
ZCCHC3	85364	zinc finger CCHC-type containing 3	902.432086	-0.14744825	0.00189908
TPP1	1200	tripeptidyl peptidase 1	564.653481	-0.2968389	0.00191637

TBC1D3I	102724862	TBC1 domain family member 3I	3.76405004	-2.51065618	0.00191718
RBM14-RBM4	100526737	RBM14-RBM4 readthrough	95.24425	-0.41489305	0.00207345
SLC4A7	9497	solute carrier family 4 member 7	628.202401	0.32242107	0.00211475
ACTN1	87	actinin alpha 1	686.092654	0.53321611	0.0021294
C12orf50	160419	chromosome 12 open reading frame 50	128.832675	0.40741544	0.00221558
GTF2A1	2957	general transcription factor IIA subunit 1	614.491554	0.25761402	0.00222747
SAMD4A	23034	sterile alpha motif domain containing 4A	399.951654	0.63870601	0.00225799
DLC1	10395	DLC1 Rho GTPase activating protein	245.062136	0.4613644	0.00229702
SAC3D1	29901	SAC3 domain containing 1	108.592553	-0.42440085	0.00231804
HBP1	26959	HMG-box transcription factor 1	448.447373	-0.31272155	0.00233046
DPY30	84661	dpy-30, histone methyltransferase complex regulatory subunit	303.254047	-0.21084477	0.00233446
INTS13	55726	integrator complex subunit 13	257.235555	-0.2799761	0.00234689
RPL13AP5	728658	ribosomal protein L13a pseudogene 5	7.03850567	1.41799682	0.00238037
PIH1D1	55011	PIH1 domain containing 1	531.166755	-0.22315191	0.00239433
S100A1	6271	S100 calcium binding protein A1	12.6582613	-0.8898896	0.00239794
MYH9	4627	myosin heavy chain 9	2068.28504	0.52082221	0.00239859
ICOSLG	23308	inducible T-cell costimulator ligand	18.9356097	0.55563406	0.00242748
NEDD9	4739	neural precursor cell expressed, developmentally down-regulated 9	357.255513	0.47015008	0.00242787
AHSA1	10598	activator of HSP90 ATPase activity 1	1051.1462	-0.18650868	0.00245954
CEBPD	1052	CCAAT/enhancer binding protein delta	22.1850191	1.17506308	0.00246083
FAM89B	23625	family with sequence similarity 89 member B	857.909591	-0.28687289	0.00247072
NR4A1	3164	nuclear receptor subfamily 4 group A member 1	578.105013	0.84490309	0.00249045
ZFP36L2	678	ZFP36 ring finger protein like 2	704.458039	0.54481839	0.00252259
VGLL3	389136	vestigial like family member 3	296.954541	0.70314612	0.00254089
OTOG	340990	otogelin	3.20322786	-2.98965956	0.00265927
BDP1	55814	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	1223.01043	0.29810052	0.00269369
WDR70	55100	WD repeat domain 70	405.362676	-0.32584593	0.00271399
TP53INP1	94241	tumor protein p53 inducible nuclear protein 1	1431.20388	-0.33546889	0.002717
GOLGA1	2800	golgin A1	749.498998	-0.1769029	0.00272483
ADAMTSL4	54507	ADAMTS like 4	51.5940488	0.47077205	0.00276885

IL6ST	3572	interleukin 6 signal transducer	1046.68527	0.48622855	0.00277963
BABAM2	9577	BRISC and BRCA1 A complex member 2	386.180271	-0.18885206	0.00278035
DRG1	4733	developmentally regulated GTP binding protein 1	626.690073	-0.19040938	0.00283394
NFATC2	4773	nuclear factor of activated T-cells 2	41.0644218	0.6044478	0.00286299
WDR33	55339	WD repeat domain 33	1701.87294	-0.162195	0.00286345
TATDN3	128387	TatD DNase domain containing 3	254.264132	0.25687083	0.00292406
TUBD1	51174	tubulin delta 1	69.7544071	-0.48003072	0.00294428
CDR1	1038	cerebellar degeneration related protein 1	323.33823	0.42337977	0.00296776
POLR2K	5440	RNA polymerase II subunit K	464.899194	-0.19369813	0.00304797
PIM1	5292	Pim-1 proto-oncogene, serine/threonine kinase	397.081421	0.73404365	0.00307529
SLC4A9	83697	solute carrier family 4 member 9	3.86618645	1.38807861	0.00308953
CATSPER2P1	440278	cation channel sperm associated 2 pseudogene 1	20.2971312	0.75901719	0.00311032
SCN4A	6329	sodium voltage-gated channel alpha subunit 4	6.82759865	2.01328146	0.00316736
MYADM	91663	myeloid associated differentiation marker	497.498393	0.45435611	0.00318887
AGO2	27161	argonaute 2, RISC catalytic component	1951.99438	0.36162515	0.00332387
NOCT	25819	nocturnin	109.704163	0.43910887	0.00337436
ZBTB3	79842	zinc finger and BTB domain containing 3	93.2032905	-0.37967309	0.00347873
GPR19	2842	G protein-coupled receptor 19	224.584466	-0.30074623	0.00348795
ELK4	2005	ELK4, ETS transcription factor	344.777256	0.40766511	0.00355177
PAIP2	51247	poly(A) binding protein interacting protein 2	1362.68549	-0.20371015	0.00356644
APBB1IP	54518	amyloid beta precursor protein binding family B member 1 interacting protein	2.09382233	-2.22203814	0.00357311
LSM1	27257	LSM1 homolog, mRNA degradation associated	401.31628	-0.20565478	0.00358242
RASA2	5922	RAS p21 protein activator 2	305.862719	0.47429941	0.00358463
SERTAD4	56256	SERTA domain containing 4	81.3277898	0.54222628	0.00359973
SERTAD4	56256	SERTA domain containing 4	81.3277898	0.54222628	0.00359973
TIMM8B	26521	translocase of inner mitochondrial membrane 8 homolog B	469.207454	-0.23888204	0.00360108
PPP1R35	221908	protein phosphatase 1 regulatory subunit 35	147.846522	-0.37253328	0.00360889
ZNF816	125893	zinc finger protein 816	78.1513148	0.44218975	0.00364974
PFKFB3	5209	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	915.85458	0.35785842	0.00367395
CIR1	9541	corepressor interacting with RBPJ, 1	393.523814	-0.21533659	0.00370505

PDE4D	5144	phosphodiesterase 4D	592.026728	0.37344753	0.00374621
IGSF9B	22997	immunoglobulin superfamily member 9B	509.979706	0.43770471	0.00377878
BHLHE40	8553	basic helix-loop-helix family member e40	97.3661238	0.69779364	0.00381448
CLCF1	23529	cardiotrophin like cytokine factor 1	31.5775124	0.88805428	0.0038348
SLC7A1	6541	solute carrier family 7 member 1	1308.31949	0.23053371	0.00384368
PYGO1	26108	pygopus family PHD finger 1	336.736198	0.21700398	0.00395185
CNKSR3	154043	CNKSR family member 3	138.421516	0.41698477	0.00396512
BICD1	636	BICD cargo adaptor 1	947.801725	0.32162869	0.00398461
CXCL8	3576	C-X-C motif chemokine ligand 8	4.89022779	2.02682965	0.00403807
DNAJC7	7266	DnaJ heat shock protein family (Hsp40) member C7	1592.84598	-0.12589656	0.00412467
TGFB1I1	7041	transforming growth factor beta 1 induced transcript 1	80.4864113	0.63102079	0.00412758
GOLGA8IP	283796	golgin A8 family member I, pseudogene	1.70244149	2.30158744	0.00413316
MAPK1IP1L	93487	mitogen-activated protein kinase 1 interacting protein 1 like	1301.35824	0.29662762	0.00424774
GADD45B	4616	growth arrest and DNA damage inducible beta	74.4752981	1.07542815	0.00426313
SLC11A1	6556	solute carrier family 11 member 1	29.791612	0.86739517	0.00433597
PHRF1	57661	PHD and ring finger domains 1	1.05111932	3.50813278	0.0043458
VIRMA	25962	vir like m6A methyltransferase associated	1018.72603	-0.38645377	0.00451534
SMG9	56006	SMG9, nonsense mediated mRNA decay factor	737.676545	-0.1746651	0.00454772
ALDH1B1	219	aldehyde dehydrogenase 1 family member B1	193.771116	0.4417493	0.00455028
NPIP4	440345	nuclear pore complex interacting protein family member B4	392.234565	0.26337353	0.00458906
LOC100509620	100509620	putative aquaporin-7-like protein 3	5.93066506	1.03524699	0.00459341
MZT1	440145	mitotic spindle organizing protein 1	195.258469	-0.26240465	0.00460521
SERTAD1	29950	SERTA domain containing 1	57.5947039	0.58054705	0.00462356
FAM84B	157638	family with sequence similarity 84 member B	877.407363	0.75070266	0.00466677
TPR	7175	translocated promoter region, nuclear basket protein	2816.04007	0.26714959	0.00479435
ADM5	199800	adrenomedullin 5 (putative)	37.4518906	-0.49112377	0.00481615
TNRC6B	23112	trinucleotide repeat containing 6B	1577.08319	0.26388838	0.00482324
FAM57A	79850	family with sequence similarity 57 member A	326.540122	0.20114236	0.0048843
PDLIM7	9260	PDZ and LIM domain 7	639.700024	0.32623169	0.005

Supplementary Table 5. SCZ DE gene list from RNAseq analysis of control vs. act.MG. cINs ($p < 0.005$). Differentially expressed genes were analyzed by DESeq2 (Wald test for two-sided significance testing, $n=24$ batches from 4 HC lines and 4 SCZ lines, each line with 3 independent differentiations). *Related to Fig. 3.*

Symbol	Entrez	Name	BaseMean	Log2FC	p Value
FHL2	2274	four and a half LIM domains 2	126.901011	1.48144524	1.65E-11
FOSL2	2355	FOS like 2, AP-1 transcription factor subunit	553.358067	1.57393684	1.07E-10
KLF10	7071	Kruppel like factor 10	187.775972	0.99322049	4.66E-10
ALDH1B1	219	aldehyde dehydrogenase 1 family member B1	185.715196	0.55584007	2.19E-09
ID4	3400	inhibitor of DNA binding 4, HLH protein	2574.06454	0.68918202	2.38E-09
FAM83A	84985	family with sequence similarity 83 member A	19.9230942	-2.53695378	4.30E-08
VCL	7414	vinculin	1478.62163	1.00908965	5.39E-08
THBS1	7057	thrombospondin 1	1027.69891	2.03421466	2.53E-07
KLF9	687	Kruppel like factor 9	60.0388379	0.8936987	1.30E-06
NAB2	4665	NGFI-A binding protein 2	960.562178	0.79989808	1.35E-06
BTG1	694	BTG anti-proliferation factor 1	1310.92116	-0.57736511	1.86E-06
PIK3IP1	113791	phosphoinositide-3-kinase interacting protein 1	293.112323	-0.40383043	5.99E-06
ID1	3397	inhibitor of DNA binding 1, HLH protein	71.5843057	1.97146252	6.30E-06
CTGF	1490	connective tissue growth factor	975.565864	2.06400489	1.50E-05
LATS2	26524	large tumor suppressor kinase 2	135.24129	0.76198171	1.58E-05
NR4A3	8013	nuclear receptor subfamily 4 group A member 3	209.295243	0.84712851	4.61E-05
GMPR2	51292	guanosine monophosphate reductase 2	684.499461	-0.32705001	4.71E-05
STX11	8676	syntaxin 11	10.194125	1.50596041	5.13E-05
LIMA1	51474	LIM domain and actin binding 1	688.943531	0.75551264	5.18E-05
IGFBP3	3486	insulin like growth factor binding protein 3	110.11708	1.68633547	5.80E-05
GABRQ	55879	gamma-aminobutyric acid type A receptor theta subunit	282.858545	0.53973022	6.42E-05
CNN2	1265	calponin 2	584.577252	0.87584248	7.02E-05
SPAG5	10615	sperm associated antigen 5	683.933795	-0.42618459	7.13E-05
DRD1	1812	dopamine receptor D1	22.5835374	1.28128246	9.67E-05
TSPAN12	23554	tetraspanin 12	146.196019	-0.39206749	9.77E-05
NR4A1	3164	nuclear receptor subfamily 4 group A member 1	564.029795	1.018722	0.00011326
PDK3	5165	pyruvate dehydrogenase kinase 3	64.8982355	0.58784832	0.00011585

MYC	4609	MYC proto-oncogene, bHLH transcription factor	163.733334	0.72888167	0.00012175
MYADM	91663	myeloid associated differentiation marker	458.125082	0.44047392	0.00015861
PNRC1	10957	proline rich nuclear receptor coactivator 1	484.890427	-0.48879217	0.00015956
TNFRSF12A	51330	TNF receptor superfamily member 12A	106.333665	1.4751251	0.00016611
NOG	9241	noggin	193.793658	0.70285268	0.00016672
DBP	1628	D-box binding PAR bZIP transcription factor	89.1820316	0.67258445	0.00019507
FOS	2353	Fos proto-oncogene, AP-1 transcription factor subunit	1461.46778	-2.38401475	0.00019894
DDX23	9416	DEAD-box helicase 23	1403.15834	-0.27007223	0.00023207
IFI27	3429	interferon alpha inducible protein 27	31.1702805	-0.54338746	0.00026192
CSRNP1	64651	cysteine and serine rich nuclear protein 1	200.266875	0.88368662	0.00026478
SEH1L	81929	SEH1 like nucleoporin	474.270829	0.24943725	0.00028052
RRS1	23212	ribosome biogenesis regulator homolog	139.676088	0.37514197	0.00035728
TPR	7175	translocated promoter region, nuclear basket protein	3054.16629	-0.1959587	0.00039127
ADM5	199800	adrenomedullin 5 (putative)	45.4454583	-0.89734508	0.00039955
CENPF	1063	centromere protein F	1401.09657	-0.6153753	0.00040281
ZFP36L2	678	ZFP36 ring finger protein like 2	695.186272	0.645053	0.00040941
RELB	5971	RELB proto-oncogene, NF-kB subunit	49.2723249	0.90797899	0.00041912
FERMT2	10979	fermitin family member 2	1208.63994	0.40925543	0.00042442
CAMTA1	23261	calmodulin binding transcription activator 1	1836.28494	0.18190132	0.00042689
CDCA7L	55536	cell division cycle associated 7 like	103.901566	0.65941757	0.00044464
WDR19	57728	WD repeat domain 19	1440.30482	-0.30088979	0.00044732
TOP3B	8940	DNA topoisomerase III beta	547.943328	-0.3337513	0.00050578
SAA2	6289	serum amyloid A2	8.37715665	1.49518838	0.00052269
KLF16	83855	Kruppel like factor 16	183.171293	0.44488127	0.00054507
FOXN4	121643	forkhead box N4	89.7419376	-0.60483596	0.00058554
SAMD4A	23034	sterile alpha motif domain containing 4A	360.112222	0.81626557	0.00060859
ANKRD33B	651746	ankyrin repeat domain 33B	57.7858784	1.52834014	0.00064679
ATP1B1	481	ATPase Na ⁺ /K ⁺ transporting subunit beta 1	1687.22436	0.27833326	0.00064776
NOSTRIN	115677	nitric oxide synthase trafficking	16.7574505	1.95439562	0.00067223
MXD4	10608	MAX dimerization protein 4	2348.03923	-0.29099261	0.00069571
UPF2	26019	UPF2, regulator of nonsense mediated mRNA decay	558.739101	-0.21350978	0.00070204

NUFIP1	26747	NUFIP1, FMR1 interacting protein 1	177.413995	0.32765526	0.00070484
CNOT1	23019	CCR4-NOT transcription complex subunit 1	3353.17337	-0.20437992	0.00075255
PIF1	80119	PIF1 5'-to-3' DNA helicase	77.6101962	-0.56164309	0.00075412
PLCG2	5336	phospholipase C gamma 2	30.474138	-1.48502071	0.00078275
AJUBA	84962	ajuba LIM protein	377.513326	0.72927153	0.00079583
CCDC169	728591	coiled-coil domain containing 169	72.2937539	0.65171325	0.00088705
METTL7B	196410	methyltransferase like 7B	8.50030274	2.07043368	0.00095231
DHODH	1723	dihydroorotate dehydrogenase (quinone)	173.656524	0.34288539	0.00096141
UBALD2	283991	UBA like domain containing 2	256.740935	-0.57727898	0.00097615
ZNF468	90333	zinc finger protein 468	112.720106	0.55715902	0.00100715
ISPD	729920	isoprenoid synthase domain containing	42.4093133	0.52419762	0.00103617
NUDT15	55270	nudix hydrolase 15	169.979751	0.2929144	0.00104433
C7orf55-LUC7L2	100996928	C7orf55-LUC7L2 readthrough	670.24935	-0.37708312	0.00108858
ATP10B	23120	ATPase phospholipid transporting 10B (putative)	50.3776122	0.63115926	0.00113178
IER2	9592	immediate early response 2	681.545958	-1.10952246	0.00114442
CCDC28A	25901	coiled-coil domain containing 28A	61.0384057	-0.4228422	0.00116429
ACTN1	87	actinin alpha 1	563.747023	0.51696492	0.00118334
MAPK1IP1L	93487	mitogen-activated protein kinase 1 interacting protein 1 like	1312.70394	0.31960269	0.0011879
SLU7	10569	SLU7 homolog, splicing factor	817.976642	-0.29448084	0.0012309
PPP1R13L	10848	protein phosphatase 1 regulatory subunit 13 like	19.6237202	-0.68760655	0.00123146
ETFRF1	144363	electron transfer flavoprotein regulatory factor 1	115.788593	0.5583876	0.00123335
FRAT2	23401	FRAT2, WNT signaling pathway regulator	133.25874	-0.48874861	0.00126622
TPMT	7172	thiopurine S-methyltransferase	175.030055	0.29946912	0.00131389
PAFAH2	5051	platelet activating factor acetylhydrolase 2	114.967097	-0.4852673	0.00133183
HIST1H4E	8367	histone cluster 1 H4 family member e	6.08171025	-1.29166496	0.00134081
ADRA2B	151	adrenoceptor alpha 2B	3.61538564	-1.44209215	0.00135575
ARPC5	10092	actin related protein 2/3 complex subunit 5	1218.54364	0.20372091	0.00137897
MARCKS	4082	myristoylated alanine rich protein kinase C substrate	7866.50199	0.52304684	0.00145972
TMEM41A	90407	transmembrane protein 41A	242.160609	0.22679626	0.00146269
PIH1D1	55011	PIH1 domain containing 1	564.144516	-0.44954875	0.00154268

TMEM198B	440104	transmembrane protein 198B (pseudogene)	426.43827	-0.28785085	0.00157723
TAP1	6890	transporter 1, ATP binding cassette subfamily B member	2.49190752	-1.98110226	0.00161894
NOC3L	64318	NOC3 like DNA replication regulator	196.403712	0.38827707	0.0016252
ACTA2	59	actin, alpha 2, smooth muscle, aorta	91.0545586	1.0473653	0.00165306
AKIRIN1	79647	akirin 1	1986.97333	0.28756273	0.00166131
RDH8	50700	retinol dehydrogenase 8 (all-trans)	2.52794022	1.71560768	0.00166679
CALD1	800	caldesmon 1	699.853238	0.59857858	0.00170814
TPM1	7168	tropomyosin 1	1870.73331	0.51042517	0.00171791
CCND1	595	cyclin D1	979.29512	0.80391968	0.00173113
TAF13	6884	TATA-box binding protein associated factor 13	226.809667	0.34385521	0.00176289
C9orf3	84909	chromosome 9 open reading frame 3	237.547225	0.33711357	0.00185167
PRKRA	8575	protein activator of interferon induced protein kinase EIF2AK2	872.127251	0.15573582	0.0018582
PDGFB	5155	platelet derived growth factor subunit B	56.8779132	0.76673773	0.00187938
MAP3K11	4296	mitogen-activated protein kinase kinasekinase 11	364.730969	-0.28175732	0.00193715
INPP1	3628	inositol polyphosphate-1-phosphatase	223.002704	0.31921684	0.0020112
DENND4A	10260	DENN domain containing 4A	442.710386	0.45896452	0.00204895
ADRB2	154	adrenoceptor beta 2	8.94053969	0.93463615	0.00212897
DLL1	28514	delta like canonical Notch ligand 1	534.903123	-0.40912244	0.0021889
DLL1	28514	delta like canonical Notch ligand 1	534.903123	-0.40912244	0.0021889
NUDT4	11163	nudix hydrolase 4	896.736976	0.34499392	0.00220989
PRPF4	9128	pre-mRNA processing factor 4	514.196684	0.17542524	0.00229425
BTG2	7832	BTG anti-proliferation factor 2	731.492171	-0.47087748	0.00233719
DNAH8	1769	dynein axonemal heavy chain 8	5.77595104	-2.12587359	0.00234487
SAP25	100316904	Sin3A associated protein 25	40.5803563	-0.64623975	0.00237422
ATOH8	84913	atonal bHLH transcription factor 8	69.1526261	0.75312891	0.00238201
WDR4	10785	WD repeat domain 4	96.7656112	0.39435491	0.00244866
IL1R1	3554	interleukin 1 receptor type 1	6.32915132	1.60546132	0.0024639
MAK16	84549	MAK16 homolog	237.191836	0.32624788	0.00249187
SLC7A1	6541	solute carrier family 7 member 1	1130.10101	0.33860323	0.00249392
FASTKD2	22868	FAST kinase domains 2	448.477938	0.29552443	0.00250527

ANKZF1	55139	ankyrin repeat and zinc finger domain containing 1	877.368426	-0.43635532	0.00257473
MBNL2	10150	muscleblind like splicing regulator 2	275.478604	0.42828845	0.0026368
IRS1	3667	insulin receptor substrate 1	757.369606	0.59932529	0.00267439
MANBA	4126	mannosidase beta	282.933888	-0.31755153	0.0027236
KDM4A	9682	lysine demethylase 4A	1663.08099	-0.18155609	0.00272698
RBMX2	51634	RNA binding motif protein, X-linked 2	232.288812	-0.23263109	0.00273201
FAM84B	157638	family with sequence similarity 84 member B	1013.55734	0.85452771	0.00278621
HIST1H4J	8363	histone cluster 1 H4 family member j	16.7024956	-0.84067869	0.00280867
FTCD	10841	formimidoyltransferasecyclodeaminase	8.03527763	0.90263235	0.00281192
PGAM1P5	100132594	phosphoglycerate mutase 1 pseudogene 5	5.2567914	1.55378196	0.00286256
JUN	3725	Jun proto-oncogene, AP-1 transcription factor subunit	993.388034	-0.49453814	0.0028686
CSKMT	751071	citrate synthase lysine methyltransferase	82.522987	-0.54386418	0.00317061
CCL2	6347	C-C motif chemokine ligand 2	30.2039752	1.22825698	0.00318782
BLOC1S3	388552	biogenesis of lysosomal organelles complex 1 subunit 3	140.579893	0.33637563	0.00320041
DIO3	1735	iodothyronine deiodinase 3	123.565362	0.46143285	0.00331487
PPAT	5471	phosphoribosyl pyrophosphate amidotransferase	423.460411	0.29599395	0.00335772
C2orf69	205327	chromosome 2 open reading frame 69	231.958551	0.47595492	0.00338212
ERF	2077	ETS2 repressor factor	621.448483	0.32579093	0.00338275
ABCC1	4363	ATP binding cassette subfamily C member 1	215.537657	-0.43348247	0.0034076
SC5D	6309	sterol-C5-desaturase	630.985232	0.47482226	0.00341612
SYNJ2	8871	synaptojanin 2	102.038859	0.9030198	0.0034204
SLTM	79811	SAFB like transcription modulator	1629.95363	-0.21131635	0.00343856
RYBP	23429	RING1 and YY1 binding protein	809.745214	0.4890747	0.00346658
LGALSL	29094	galectin like	437.508475	0.36574241	0.00361329
FBXO38	81545	F-box protein 38	862.700303	-0.23769091	0.00366619
SLC25A15	10166	solute carrier family 25 member 15	129.475076	0.27584081	0.00369327
C2CD2	25966	C2 calcium dependent domain containing 2	66.6868021	0.70202187	0.00383886
INPP5K	51763	inositol polyphosphate-5-phosphatase K	399.821893	-0.22881828	0.00389802
LOC102723996	102723996	ICOS ligand	2.46200921	2.68006713	0.00394836
SIK1B	102724428	salt inducible kinase 1B (putative)	306.811284	0.69780224	0.00396312
CD101	9398	CD101 molecule	86.5230517	-0.46062784	0.00396713

DDAH1	23576	dimethylarginine dimethylaminohydrolase 1	2014.56942	0.38323324	0.00408209
FZR1	51343	fizzy and cell division cycle 20 related 1	1445.90657	0.19404425	0.00417018
PPP2R2A	5520	protein phosphatase 2 regulatory subunit Balpha	728.867846	0.31518947	0.00417597
NDUFS2	4720	NADH:ubiquinone oxidoreductase core subunit S2	1527.05778	-0.2031342	0.004228
FOSB	2354	FosB proto-oncogene, AP-1 transcription factor subunit	285.789042	-1.97210691	0.00426588
ARHGAP29	9411	Rho GTPase activating protein 29	131.766506	0.48311626	0.00434753
TOB1	10140	transducer of ERBB2, 1	327.248971	-0.46223841	0.00439895
SFTPA2	729238	surfactant protein A2	3.83313336	-1.28841401	0.00440237
PARD6B	84612	par-6 family cell polarity regulator beta	93.7443569	0.40906861	0.0044289
CTRC	11330	chymotrypsin C	13.7246262	-0.9908546	0.00449443
FAM46A	55603	family with sequence similarity 46 member A transient receptor potential cation channel subfamily C member 1	172.235934	0.59189285	0.00456402
TRPC1	7220		201.142492	0.41248239	0.00466797
DDX21	9188	DExD-box helicase 21	1109.87765	0.26427751	0.00470668
MEF2B	100271849	myocyte enhancer factor 2B	19.4449759	-0.98687215	0.00477952
NAA50	80218	N(alpha)-acetyltransferase 50, NatE catalytic subunit	772.289546	0.31784548	0.00478465
CMPK1	51727	cytidine/uridine monophosphate kinase 1	1340.80807	0.29594829	0.0048606
PROSER2	254427	proline and serine rich 2	9.69011218	1.12180925	0.0048736
CLN8	2055	CLN8, transmembrane ER and ERGIC protein	197.030269	0.66582193	0.00487436
PTGES3	10728	prostaglandin E synthase 3	2398.20544	0.28846624	0.00491563

Supplementary Table 6. HC DE gene list from RNAseq analysis of control vs. IL17. cINs ($p < 0.005$). Differentially expressed genes were analyzed by DESeq2 (Wald test for two-sided significance testing, $n=8$ independent differentiations from 4 HC lines and 4 SCZ lines). *Related to Fig. 4.*

Symbol	Entrez	Name	BaseMean	Log2FC	p Value
STAB2	55576	stabilin 2	8.63271484	4.40899875	1.20E-06
CYP21A1P	1590	cytochrome P450 family 21 subfamily A member 1, pseudogene	8.07836394	-5.67724201	3.21E-06
ADNP2	22850	ADNP homeobox 2	813.454956	1.05487187	1.20E-05
IPO7	10527	importin 7	1915.65516	0.48212783	6.04E-05
RGPD1	400966	RANBP2-like and GRIP domain containing 1	12.6018659	4.24726752	6.74E-05
HLA-DQB1	3119	major histocompatibility complex, class II, DQ beta 1 transient receptor potential cation channel subfamily M member 8	15.7557574	-2.68062455	0.00017789
TRPM8	79054	member 8	31.9638925	-1.52541947	0.00020384
EXOC6	54536	exocyst complex component 6	283.603325	0.8815818	0.0002289
SLC26A1	10861	solute carrier family 26 member 1	51.9617806	-1.43442228	0.00027453
MAP7D3	79649	MAP7 domain containing 3	157.152157	0.89716156	0.00027858
DDX10	1662	DEAD-box helicase 10	256.387158	0.66455065	0.00043225
TAS2R14	50840	taste 2 receptor member 14	14.6068624	-1.91676195	0.00048828
NPIA5	100288332	nuclear pore complex interacting protein family member A5	57.0287583	1.18795228	0.00071829
POLQ	10721	DNA polymerase theta	208.603827	0.93222063	0.00099307
MALRD1	340895	MAM and LDL receptor class A domain containing 1	12.4484054	-2.26533618	0.00111952
LENG1	79165	leukocyte receptor cluster member 1	28.6181136	1.48157589	0.00112989
PRSS2	5645	protease, serine 2	19.5361013	-2.58331853	0.00120719
FAM46A	55603	family with sequence similarity 46 member A	156.833777	-0.65499441	0.00123443
MINOS1-NBL1	100532736	MINOS1-NBL1 readthrough	16.0578052	2.05566114	0.00145044
LNX1	84708	ligand of numb-protein X 1	71.6874203	-0.8004178	0.00155416
DPP4	1803	dipeptidyl peptidase 4	57.2380626	-1.67136393	0.00159973
GABBR1	2550	gamma-aminobutyric acid type B receptor subunit 1	213.593197	-0.84362712	0.0016607
ABHD1	84696	abhydrolase domain containing 1	26.586658	1.11871487	0.00200132
YARS2	51067	tyrosyl-tRNA synthetase 2	148.555881	0.65545913	0.0020339
GABBR1	2550	gamma-aminobutyric acid type B receptor subunit 1	216.205073	-0.81561296	0.00204555
RNF39	80352	ring finger protein 39	9.15606239	-2.98919138	0.00206362

CCDC169	728591	coiled-coil domain containing 169	139.027766	0.87105946	0.00211147
JCHAIN	3512	joining chain of multimeric IgA and IgM	6.09197992	-2.98013852	0.00215252
TUBB8	347688	tubulin beta 8 class VIII	9.6928254	2.05540352	0.00257666
TMEM110-					
MUSTN1	100526772	TMEM110-MUSTN1 readthrough	79.0600406	-1.46988552	0.00268069
CENPF	1063	centromere protein F	3273.23116	0.92775377	0.00272292
SCNN1D	6339	sodium channel epithelial 1 delta subunit	104.472764	0.71468985	0.00276923
ADGRF3	165082	adhesion G protein-coupled receptor F3	23.9088578	-1.89155231	0.00282983
CPZ	8532	carboxypeptidase Z	131.962482	-1.49651019	0.00287811
CNOT3	4849	CCR4-NOT transcription complex subunit 3	17.6225638	-2.68089374	0.00290608
LRRC32	2615	leucine rich repeat containing 32	40.3917252	-1.52787099	0.0030714
EPAS1	2034	endothelial PAS domain protein 1	97.6459144	-0.90201209	0.00336088
CAVIN3	112464	caveolae associated protein 3	18.4866411	-1.93082801	0.00351354
BST2	684	bone marrow stromal cell antigen 2	26.6635752	-1.84928575	0.00367159
PLCD4	84812	phospholipase C delta 4	118.913176	0.64179206	0.00368585
PIK3IP1	113791	phosphoinositide-3-kinase interacting protein 1	107.621541	-0.63472991	0.00370898
KNL1	57082	kinetochore scaffold 1	533.472703	0.80585718	0.00398082
RAD18	56852	RAD18, E3 ubiquitin protein ligase	278.544118	0.53981941	0.00432017
CFAP46	54777	cilia and flagella associated protein 46	116.662981	-0.74237559	0.00476882

Supplementary Table 7. SCZ DE gene list from RNAseq analysis of control vs. IL17. cINs ($p < 0.005$). Differentially expressed genes were analyzed by DESeq2 (Wald test for two-sided significance testing, $n=8$ independent differentiations from 4 HC lines and 4 SCZ lines). *Related to Fig. 4.*

Symbol	Entrez	Name	BaseMean	Log2FC	p Value
SLC7A5P2	387254	Solute Carrier Family 7 Member 5 Pseudogene 2	4.63266408	-5.6438031	1.79E-05
FTH1P16	2508	Ferritin Heavy Chain 1 Pseudogene 16	9.25840593	4.74522438	9.74E-05
BMS1P11	644632	BMS1 Pseudogene 11	7.12000772	6.25460842	0.00011509
SHBG	6462	sex hormone binding globulin	10.8390253	3.51197052	0.00017391
COL15A1	1306	collagen type XV alpha 1 chain	110.796487	1.04941203	0.00024619
PPT2	9374	palmitoyl-protein thioesterase 2	14.5510029	2.94583731	0.00024635
NAA16	79612	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	235.258557	0.76426862	0.00026589
PLCG2	5336	phospholipase C gamma 2	151.579784	2.02126185	0.00027314
GTF2H4	2968	general transcription factor IIH subunit 4	22.7715902	-1.93823302	0.0007703
HFM1	164045	HFM1, ATP dependent DNA helicase homolog	72.7468267	1.10129779	0.00077082
RPL10P9	389342	Ribosomal Protein L10 Pseudogene 9	25.727179	-2.19757747	0.00092108
QDPR	5860	quinoid dihydropteridine reductase	240.338294	-0.86714728	0.00130665
PRLR	5618	prolactin receptor	31.4664355	1.47599187	0.00136706
HLA-C	3107	major histocompatibility complex, class I, C	43.5885991	-1.60029812	0.0014516
HDAC8	55869	histone deacetylase 8	170.695064	-0.71268112	0.00151564
XCR1	2829	X-C motif chemokine receptor 1	5.51098915	4.53412944	0.00163084
ITPR2	3709	inositol 1,4,5-trisphosphate receptor type 2	111.146131	1.44975798	0.00177663
SLC12A1	6557	solute carrier family 12 member 1	12.2264707	2.13204316	0.00202291
SPAG17	200162	sperm associated antigen 17	20.8724741	1.66084183	0.00212148
SORCS1	114815	sortilin related VPS10 domain containing receptor 1	421.883812	-0.69909027	0.00239087
INO80B-WBP1	100532735	INO80B-WBP1 readthrough (NMD candidate)	15.7639011	-7.40806465	0.00259439
ERN1	2081	endoplasmic reticulum to nucleus signaling 1	95.643689	0.90091893	0.00272375
KIAA0586	9786	KIAA0586	209.286822	0.71512214	0.00273773
BRD2	6046	bromodomain containing 2	172.412755	-0.99237787	0.00286014
GOLGA6L10	647042	golgin A6 family-like 10	3.06600291	-5.0600475	0.00328499
LOC440434	440434	aminopeptidase puromycin sensitive pseudogene	71.9153748	1.00710113	0.00354661
GTF2H2	2966	general transcription factor IIH subunit 2	69.8885721	-1.16249527	0.00372787

HNMT	3176	histamine N-methyltransferase	19.2705405	1.31007976	0.00395754
RINT1	60561	RAD50 interactor 1	187.927983	0.83970572	0.00397329
GPR78	27201	G protein-coupled receptor 78	3.01603416	4.20077763	0.00417086
TEAD1	7003	TEA domain transcription factor 1	948.481819	0.64066427	0.00418386
DEUP1	159989	deuterosome assembly protein 1	4.71751934	2.98665644	0.00419735
PCDHGB9P	84055	Protocadherin Gamma Subfamily B, 9 Pseudogene	10.0433427	1.97103358	0.00428525
PCDHA13	56136	protocadherin alpha 13	28.1418204	1.23420207	0.00435476
CHN2	1124	chimerin 2	433.959482	-0.52240088	0.00435572
THRB	7068	thyroid hormone receptor beta	27.9882317	1.43664196	0.00443418
INO80E	283899	INO80 complex subunit E	341.836523	-0.65875845	0.00454463
DET1	55070	de-etiolated homolog 1 (Arabidopsis)	90.4807738	-0.85084194	0.00455508
ANKRD30BL	554226	ankyrin repeat domain 30B like	122.575451	1.2855802	0.0045955
IKZF2	22807	IKAROS family zinc finger 2	61.8646436	0.83520168	0.0046795
GSN	2934	gelsolin	68.6560576	0.99076388	0.00474464
ZNF19	7567	zinc finger protein 19	86.5637407	0.74424492	0.00478203
		phosphatidylinositol glycan anchor biosynthesis class			
PIGY	84992	Y	3.5845166	5.25502029	0.00480862
NDUFA6	4700	NADH:ubiquinone oxidoreductase subunit A6	384.875304	-1.05642369	0.00496183

Supplementary Table 8. HC DE gene list from RNAseq analysis of delayed control vs. delayed stress. cINs ($p < 0.005$).

Differentially expressed genes were analyzed by DESeq2 (Wald test for two-sided significance testing, $n=8$ independent differentiations from 4 HC lines and 4 SCZ lines). *Related to Fig. 5.*

Symbol	Entrez	Name	BaseMean	Log2FC	p Value
LCP1	3936	lymphocyte cytosolic protein 1	46.6994126	5.71778805	2.13E-10
RIN2	54453	Ras and Rab interactor 2	101.545705	1.12718896	4.85E-05
LGALS1	3956	galectin 1	68.9477129	2.89541441	5.51E-05
SPI1	6688	Spi-1 proto-oncogene	15.3706976	6.43087374	7.16E-05
CAPG	822	capping actin protein, gelsolin like	50.9874636	3.00746657	8.40E-05
CLIC1	1192	chloride intracellular channel 1	46.6649807	-3.16977836	0.00012061
PABPC3	5042	poly(A) binding protein cytoplasmic 3	11.6366865	4.90781872	0.00013644
CYBB	1536	cytochrome b-245 beta chain	14.9162632	4.71571133	0.00014277
SCG5	6447	secretogranin V	50.9876666	8.40131828	0.00022273
ACTBL2	345651	actin, beta like 2	7.63088559	6.36790549	0.00028942
PLEK	5341	pleckstrin	10.9944	5.24164552	0.00031694
CTSZ	1522	cathepsin Z	40.5156426	2.9296345	0.00043387
STARD5	80765	StAR related lipid transfer domain containing 5 ring finger and FYVE like domain containing E3 ubiquitin protein ligase	6.29844434	2.62707011	0.00056478
RFFL	117584	transmembrane protease, serine 11D	176.688756	0.74207392	0.00057115
TMPRSS11D	9407	BMS1, ribosome biogenesis factor pseudogene 17	3.72707269	3.79413537	0.00067942
BMS1P17	101101776	PR/SET domain 6	3.58237815	4.51819465	0.00075554
PRDM6	93166	ubiquitin B pseudogene 4	7.00292392	-2.5787792	0.00093416
UBBP4	23666	protein phosphatase 1 regulatory subunit 18	11.115129	3.67205408	0.00110972
PPP1R18	170954	calcineurin like phosphoesterase domain containing 1	9.25295763	-5.65291403	0.00115859
CPPED1	55313	insulin like growth factor 1	66.2610051	0.75545936	0.00120238
IGF1	3479	SATB homeobox 2	33.8143697	1.5348843	0.0013619
SATB2	23314	actin gamma 1 pseudogene 17	35.3744184	1.15915594	0.00164377
ACTG1P17	283693	TAM41 mitochondrial translocator assembly and maintenance homolog	10.1512788	2.26301388	0.0017468
TAMM41	132001	killin, p53-regulated DNA replication inhibitor	12.5207898	-1.76310973	0.00182885
KLLN	100144748		8.69668948	2.61002374	0.00224189

BLOC1S5-TXNDC5	100526836	BLOC1S5-TXNDC5 readthrough (NMD candidate)	15.1392495	-3.45480029	0.00242845
RPL31P11	641311	ribosomal protein L31 pseudogene 11	3.5810563	5.07900115	0.00266229
S100A4	6275	S100 calcium binding protein A4	15.741414	2.15229137	0.00274844
WDR12	55759	WD repeat domain 12	189.725672	0.86142946	0.00281902
LIPJ	142910	lipase family member J	5.65167601	2.71626481	0.00299156
RAC2	5880	Rac family small GTPase 2	3.98959327	5.43047688	0.003412
LAPTM5	7805	lysosomal protein transmembrane 5	13.4694162	3.03930069	0.00406538
IDE	3416	insulin degrading enzyme	190.202422	0.84997381	0.00416725
AZIN2	113451	antizyme inhibitor 2	60.3074197	-0.79818009	0.0046478

Supplementary Table 9. SCZ DE gene list from RNAseq analysis of delayed control vs. delayed stress. cINs ($p < 0.005$). Differentially expressed genes were analyzed by DESeq2 (Wald test for two-sided significance testing, $n=8$ independent differentiations from 4 HC lines and 4 SCZ lines). *Related to Fig. 5.*

Symbol	Entrez	Name	BaseMean	Log2FC	p Value
ZNF430	80264	zinc finger protein 430	9.8352763	2.87291345	1.18E-05
KLF5	688	Kruppel like factor 5	42.9107211	-3.11274787	0.00019033
C3orf62	375341	chromosome 3 open reading frame 62	130.692764	-0.69436714	0.0002164
PARP8	79668	poly(ADP-ribose) polymerase family member 8	180.044004	-0.65407864	0.00022893
LGALS1	29094	galectin like	146.974116	0.77222847	0.00054616
ABCC2	1244	ATP binding cassette subfamily C member 2	8.08990915	-2.38162821	0.00057028
TAF1C	9013	TATA-box binding protein associated factor, RNA polymerase I subunit C	340.853964	-0.5537708	0.00057209
ACTR3C	653857	ARP3 actin related protein 3 homolog C	6.5411726	-3.5920774	0.0007421
RAB21	23011	RAB21, member RAS oncogene family	366.512912	0.6664165	0.00078863
PLEK	5341	pleckstrin	10.7968528	5.15769727	0.00081478
PRPF40A	55660	pre-mRNA processing factor 40 homolog A SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	476.438825	0.5870678	0.00086161
SMARCA2	6595	subfamily a, member 2	215.909257	0.66704372	0.00086734
TNFAIP3	7128	TNF alpha induced protein 3	17.0549483	1.48023227	0.00089196
HMGN4	10473	high mobility group nucleosomal binding domain 4	128.03145	-0.65435646	0.00091364
UCHL5	51377	ubiquitin C-terminal hydrolase L5	146.32843	0.63397492	0.00098289
NDUFS1	4719	NADH:ubiquinone oxidoreductase core subunit S1	265.671106	0.43918695	0.00121267
NDUFS1	4719	NADH:ubiquinone oxidoreductase core subunit S1	265.671106	0.43918695	0.00121267
SPTAN1	6709	spectrin alpha, non-erythrocytic 1	5169.76515	-0.33792136	0.00156159
CCNB3	85417	cyclin B3	15.3037776	-1.85332959	0.00189341
S100A4	6275	S100 calcium binding protein A4	13.3718785	2.96807729	0.00189519
NAMPT	10135	nicotinamide phosphoribosyltransferase	143.757792	0.5016928	0.00223315
C16orf45	89927	chromosome 16 open reading frame 45	78.7930689	0.93117475	0.0024871
AZIN2	113451	antizyme inhibitor 2	50.037575	-1.00712964	0.00248876
ZNF268	10795	zinc finger protein 268	148.28664	0.71077732	0.00250043
OTUB2	78990	OTU deubiquitinase, ubiquitin aldehyde binding 2	4.83753541	-5.81396908	0.00254246
PRDM10	56980	PR/SET domain 10	152.021581	0.67750694	0.0029171

RAD51D	5892	RAD51 paralog D	104.257156	-0.61726545	0.00308803
ATP2C2	9914	ATPase secretory pathway Ca ²⁺ transporting 2	15.860005	1.51458722	0.00349343
FAAP100	80233	Fanconi anemia core complex associated protein 100	397.662782	-0.33731484	0.00358713
ITSN2	50618	intersectin 2	110.743817	0.75092741	0.00365311
SAA2	6289	serum amyloid A2	6.25220406	4.41812372	0.00370742
CAPN15	6650	calpain 15	166.963189	-0.67758713	0.00375483
PARVB	29780	parvin beta	37.9876385	1.21271293	0.00375825
PPP6R2	9701	protein phosphatase 6 regulatory subunit 2	552.218261	-0.40712349	0.00379278
RPAP1	26015	RNA polymerase II associated protein 1	171.742568	-0.52662419	0.00380813
ZBTB48	3104	zinc finger and BTB domain containing 48	113.802107	-0.74409383	0.00390064
KCMF1	56888	potassium channel modulatory factor 1	269.971351	0.47615327	0.00409951
GOSR1	9527	golgi SNAP receptor complex member 1	244.498612	0.42360563	0.0041113
FBN3	84467	fibrillin 3	252.892459	-0.64267268	0.00423739
ZBTB20	26137	zinc finger and BTB domain containing 20	274.013383	0.8071571	0.00431792
ZNF573	126231	zinc finger protein 573	32.1106557	-1.16592321	0.00435258
DIO2	1734	iodothyronine deiodinase 2	11.1613299	2.26492228	0.00443709
EFCAB14	9813	EF-hand calcium binding domain 14	172.418386	0.50905995	0.00455242
VAPB	9217	VAMP associated protein B and C	486.044686	0.39956585	0.00462867
TBPL1	9519	TATA-box binding protein like 1	120.856622	0.50371274	0.004872

Supplementary Table 10. Cell lines used for each experiment. *Related to Methods section.*

Cohort	ID	Acute RNAseq	Acute qPCR	Immunocytochemistry	Acute-Replication cohort	Acute Seahorse	Overexpression Seahorse	siRNA Seahorse	Arborization	Organoid Synapse analysis	IL17 RNAseq	IL17 qPCR	Delayed RNAseq	Delayed-Replication cohort	HMC3 Acute qPCR	HMC3 Delayed qPCR	HMC3 Acute Seahorse	HMC3 Delayed Seahorse	Glut qPCR	Glut Seahorse	iPSC Seahorse
HC	272	✓	✓	✓		✓				✓	✓	✓		✓	✓	✓	✓	✓	✓	✓	
	190	✓	✓	✓		✓	✓	✓	✓	✓	✓	✓		✓	✓	✓	✓	✓	✓		
	367	✓	✓	✓		✓	✓	✓		✓	✓	✓		✓		✓	✓	✓	✓		
	226	✓	✓	✓		✓	✓	✓	✓	✓	✓	✓		✓		✓	✓	✓	✓		
	PYAUM			✓	✓	✓	✓	✓					✓								
	317		✓	✓									✓								
	L9		✓	✓	✓	✓	✓		✓				✓	✓							✓
	L7		✓	✓	✓	✓	✓	✓					✓	✓	✓	✓	✓	✓	✓		
	L5		✓	✓									✓								
SCZ	292		✓	✓	✓								✓	✓	✓	✓	✓	✓	✓	✓	✓
	67	✓	✓	✓		✓				✓	✓	✓		✓	✓	✓	✓	✓	✓		
	128	✓	✓	✓		✓	✓	✓		✓	✓	✓		✓		✓	✓	✓	✓		
	212	✓	✓	✓		✓	✓	✓	✓	✓	✓	✓		✓		✓	✓	✓	✓		
	162	✓	✓	✓		✓	✓	✓	✓	✓	✓	✓		✓		✓	✓	✓	✓		
	58		✓	✓									✓								
	282		✓	✓									✓								
	285		✓	✓	✓	✓	✓						✓	✓	✓	✓	✓	✓	✓	✓	
	L10		✓	✓	✓	✓	✓						✓								
	689		✓	✓	✓	✓	✓	✓	✓				✓	✓	✓	✓	✓	✓	✓	✓	
	L8		✓	✓				✓					✓			✓	✓	✓	✓		✓

Supplementary Table 11. List of primers used in this study. Related to Methods section.

Gene	Primer Sequences
<i>IL-1β</i>	F 5' -TGGAGTCACAGAAGGAATGGCTAAG R 5' -GGAAGACACAGATTCCATGGTGAAG
<i>IL-6</i>	F 5' -CTGCAAGAGACTTCCATCCAGTT R 5' -GAAGTAGGGAAGGCCGTGG
<i>INOS</i>	F 5' -GGCAGCCTGTGAGACCTTTG R 5' -GCATTGGAAGTGAAGCGTTTC
<i>TNFA</i>	F 5' -ATAGCTCCCAGAAAAGCAAGC, R 5' -CACCCCGAAGTTCAGTAGACA
<i>NFKBIZ</i>	F 5' -AGAGGCCCTTTCAAGGTGT R 5' -TCCATCAGACAACGAATCGGG
<i>TNFRSF12A</i>	F 5' -AACAGAAAGGGAGCCTACG R 5' -GTGGGGCTAGTGTCAAGTC
<i>TNFAIP3</i>	F 5' -TCCTCAGGCTTTGTATTTGAGC R 5' -TGTGTATCGGTGCATGGTTTTA
<i>NFATC2</i>	F 5' -GAGCCGAATGCACATAAGGTC R 5' -CCAGAGAGACTAGCAAGGGG
<i>CTGF</i>	F 5' -AAAAGTGCATCCGTACTCCCA R 5' -CCGTCGGTACATACTCCACAG
<i>THBS1</i>	F 5' -AGACTCCGCATCGCAAAGG R 5' -TCACCACGTTGTTGTCAAGGG
<i>SOX6</i>	F 5' -ATCTCTCATCCCGACCCAAGAC R 5' -TTCCCAGGCTTCCTCCAATG
<i>GAD1</i>	F 5' -CTGCTCTTCTCTTACGCTCTCTGTC R 5' -TCTTCGGAAATGTTGCCTTAGG
<i>KLF5</i>	F 5' -TCAGTCGTAGACCAGTTCTTCA R 5' -CTGGGATTTGTAGAGGCCAGT
<i>GAPDH</i>	F 5' -GCTCAGACACCATGGGGAAGGT R 5' -GTGGTGCAGGAGGCATTGCTGA

Supplementary Table 12. List of antibodies used in the experiments. *Related to Methods section.*

Antibody	Species	Vendor	Cat. number	Dilution
GAD1	Rabbit	Millipore	AB1511	1:1,000
SOX6	Rabbit	Millipore	AB5805	1:1,000
VGAT	Rabbit	Synaptic system	131003	1:1,000
Gephyrin	Mouse	Synaptic system	147011	1:1,000
VGlut1	Mouse	UC Davis/NIH NeuroMab	73066	1:1,000
GABA	Rabbit	IMMUNOSTAR	20094	1:1,000
Glutamate	Rabbit	Sigma-Aldrich	G6642	1:1,000
β -Tubulin III	Mouse	Covance	802001	1:1,000
Iba1	Rabbit	FUJIFILM Wako	019-19741	1:1,000
OLIG2	Rabbit	Millipore	AB9610	1:1,000
GFAP	Mouse	UC Davis/NIH NeuroMab	N206A/8	1:1,000
ChAT	Mouse	Chemicon	AB114P	1:1,000
TH	Rabbit	Pel-Freez	P40101-150	1:1,000
5-HT	Rabbit	IMMUNOSTAR	20080	1:1,000
VIP	Rabbit	IMMUNOSTAR	20077	1:1,000

Supplementary Table 13. Statistical analysis used for each experiment. * indicates $p < 0.05$. *Related to Methods section.*

Figure number	Analysis ID	Normal Distribution (Shapiro Wilks test)	Statistical test used
Fig 1B	MG IL-1 β qPCR		Paired t-test
	MG IL-6 qPCR		Paired t-test
	MG iNOS qPCR		Paired t-test
	MG TNF α qPCR		Paired t-test
Fig 1G	cIN CTGF qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN THBS1 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
Fig 1H	cIN CTGF qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN THBS1 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
Fig 2A	cIN Basal Respiration	*	Paired t-test after log transformation
	cIN Maximum Respiration		Paired t-test
Fig 2B	cIN Basal Respiration		Paired t-test
	cIN Maximum Respiration		Paired t-test
Fig 2C	cIN Basal Respiration	*	Paired t-test after log transformation
	cIN Maximum Respiration	*	Paired t-test after log transformation
Fig 2F	cIN Neurite Length	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN Branch Number		Two-Level Hierarchical Mixed Effect Log- Linear Model
Fig 2H	cIN Synapse Analysis	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
Fig 3C	cIN HC CTGF qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN HC THBS1 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN SCZ CTGF qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN SCZ THBS1 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation

Fig 3D	cIN HC Basal Respiration		Paired t-test
	cIN HC Maximum Respiration		Paired t-test
	cIN SCZ Basal Respiration		Paired t-test
	cIN SCZ Maximum Respiration		Paired t-test
Fig 3E	cIN HC Neurite Length	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN HC Branch Number		Two-Level Hierarchical Mixed Effect Log-Linear Model
	cIN SCZ Neurite Length	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN SCZ Branch Number		Two-Level Hierarchical Mixed Effect Log-Linear Model
Fig 5G	cIN HC delayed KLF5 qPCR	*	Paired t-test after log transformation
	cIN SCZ delayed KLF5 qPCR	*	Paired t-test after log transformation
Fig 5H	cIN HC delayed KLF5 qPCR		Paired t-test
	cIN SCZ delayed KLF5 qPCR		Paired t-test
Fig 5I	cIN HC delayed Maximum Respiration		Paired t-test
	cIN SCZ delayed Maximum Respiration		Paired t-test
Fig 6D	cIN acute HC Basal Respiration		Paired t-test
	cIN acute HC Maximum Respiration		Paired t-test
	cIN acute SCZ Basal Respiration		Paired t-test
	cIN acute SCZ Maximum Respiration		Paired t-test
Fig 6E	cIN acute HC GABA		One-way ANOVA, followed by posthoc analysis using Dunnett's multiple comparisons test
	cIN acute SCZ GABA		One-way ANOVA, followed by posthoc analysis using Dunnett's multiple comparisons test
Fig 6F	cIN delayed HC Basal Respiration		Paired t-test
	cIN delayed HC Maximum Respiration	*	Paired t-test after log transformation
	cIN delayed SCZ Basal Respiration		Paired t-test

	cIN delayed SCZ Maximum Respiration		Paired t-test
Fig 6G	cIN delayed HC GABA		One-way ANOVA, followed by posthoc analysis using Dunnett's multiple comparisons test
	cIN delayed SCZ GABA		One-way ANOVA, followed by posthoc analysis using Dunnett's multiple comparisons test
Fig 7C	Glut HC CTGF qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	Glut SCZ CTGF qPCR		Two-Level Hierarchical Linear Mixed Effect Model
	Glut HC THBS1 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	Glut SCZ THBS1 qPCR		Two-Level Hierarchical Linear Mixed Effect Model
Fig 7D	Glut HC Basal Respiration	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	Glut HC Maximum Respiration		Two-Level Hierarchical Linear Mixed Effect Model
	Glut SCZ Basal Respiration		Two-Level Hierarchical Linear Mixed Effect Model
	Glut SCZ Maximum Respiration		Two-Level Hierarchical Linear Mixed Effect Model
Fig 7E	iPSC HC Basal Respiration		Paired t-test
	iPSC HC Maximum Respiration		Paired t-test
	iPSC SCZ Basal Respiration		Paired t-test
	iPSC SCZ Maximum Respiration		Paired t-test
eData 2D	cIN NFkBIZ qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN TNFRSF12A qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN TNFAIP3 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN NFATC2 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
eData 4C	cIN GAD1 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	cIN SOX6 qPCR	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
eData 5C	cIN CTGF O.E qPCR		Ratio paired t-test
	cIN THBS1 O.E qPCR		Ratio paired t-test

	cIN CTGF siRNA qPCR		Ratio paired t-test
	cIN THBS1 siRNA qPCR		Ratio paired t-test
eData 5D	cIN ATP Production	*	Paired t-test after log transformation
	cIN Baseline Glycolysis	*	Paired t-test after log transformation
	cIN Glycolytic Reserve		Paired t-test
eData 5E	cIN ATP Production		Paired t-test
	cIN Baseline Glycolysis	*	Paired t-test after log transformation
	cIN Glycolytic Reserve	*	Paired t-test after log transformation
eData 5F	cIN ATP Production		Paired t-test
	cIN Baseline Glycolysis	*	Paired t-test after log transformation
	cIN Glycolytic Reserve	*	Paired t-test after log transformation
eData 5G	cIN delayed HC Basal Respiration		Paired t-test
	cIN delayed HC ATP Production		Paired t-test
	cIN delayed HC Baseline Glycolysis		Paired t-test
	cIN delayed HC Glycolytic Reserve	*	Paired t-test after log transformation
eData 5H	cIN delayed SCZ Basal Respiration		Paired t-test
	cIN delayed SCZ ATP Production		Paired t-test
	cIN delayed SCZ Baseline Glycolysis		Paired t-test
	cIN delayed SCZ Glycolytic Reserve		Paired t-test
eData 6B	cIN Basal Respiration		Paired t-test
	cIN Maximum Respiration		Paired t-test
	cIN ATP Production		Paired t-test
eData 7A	cIN control CTGF qPCR	*	Unpaired t-test after log transformation
	cIN control THBS1 qPCR	*	Unpaired t-test after log transformation
	cIN act.MG CTGF qPCR		Unpaired t-test
	cIN act.MG THBS1 qPCR		Unpaired t-test

eData 7B	cIN control Basal Respiration		Unpaired t-test
	cIN control Maximum Respiration		Unpaired t-test
	cIN act.MG Basal Respiration	*	Unpaired t-test after log transformation
	cIN act.MG Maximum Respiration		Unpaired t-test
eData 7C	cIN control delayed KLF5 qPCR		Unpaired t-test
	cIN act.MG delayed KLF5 qPCR	*	Unpaired t-test after log transformation
eData 7D	cIN control delayed Maximum Respiration	*	Unpaired t-test after log transformation
	cIN act.MG delayed Maximum Respiration		Unpaired t-test
eData 7E	cIN Neurite Length	*	One-way ANOVA, followed by posthoc analysis using Dunnett's multiple comparisons test
	cIN Branch Number		One-way ANOVA, followed by posthoc analysis using Dunnett's multiple comparisons test
eData 8A	cIN NFkBIZ qPCR		Paired t-test
	cIN TNFRSF12A qPCR		Paired t-test
	cIN TNFAIP3 qPCR	*	Paired t-test after log transformation
eData 8B	cIN HC CTGF qPCR		Ratio paired t-test
	cIN HC THBS1 qPCR		Ratio paired t-test
	cIN SCZ CTGF qPCR		Ratio paired t-test
	cIN SCZ THBS1 qPCR		Ratio paired t-test
eData 8C	cIN HC delayed KLF5 qPCR	*	Paired t-test after log transformation
	cIN SCZ delayed KLF5 qPCR		Paired t-test
eData 9A	cIN acute HC ATP Production		Paired t-test
	cIN acute HC Baseline Glycolysis		Paired t-test
	cIN acute HC Glycolytic Reserve		Paired t-test
eData 9B	cIN acute SCZ ATP Production		Paired t-test

	cIN acute SCZ Baseline Glycolysis		Paired t-test
	cIN acute SCZ Glycolytic Reserve		Paired t-test
eData 9C	cIN delayed HC ATP Production		Paired t-test
	cIN delayed HC Baseline Glycolysis		Paired t-test
	cIN delayed HC Glycolytic Reserve	*	Paired t-test after log transformation
eData 9D	cIN delayed SCZ ATP Production		Paired t-test
	cIN delayed SCZ Baseline Glycolysis		Paired t-test
	cIN delayed SCZ Glycolytic Reserve		Paired t-test
eData 9E	cIN control acute Basal Respiration		Unpaired t-test
	cIN control acute Maximum Respiration		Unpaired t-test
	cIN act.MG acute Basal Respiration		Unpaired t-test
	cIN act.MG acute Maximum Respiration		Unpaired t-test
eData 9F	cIN control delayed Basal Respiration		Unpaired t-test
	cIN control delayed Maximum Respiration		Unpaired t-test
	cIN act.MG delayed Basal Respiration	*	Unpaired t-test after log transformation
	cIN act.MG delayed Maximum Respiration		Unpaired t-test
eData 9G	cIN acute control GABA		Unpaired t-test
	cIN acute act.MG GABA		Unpaired t-test
eData 9H	cIN delayed control GABA	*	Unpaired t-test after log transformation
	cIN delayed act.MG GABA		Unpaired t-test
eData 10A	Glut HC ATP Production		Two-Level Hierarchical Linear Mixed Effect Model
	Glut HC Baseline Glycolysis		Two-Level Hierarchical Linear Mixed Effect Model
	Glut HC Glycolytic Reserve		Two-Level Hierarchical Linear Mixed Effect Model

eData 10B	Glut SCZ ATP Production	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
	Glut SCZ Baseline Glycolysis		Two-Level Hierarchical Linear Mixed Effect Model
	Glut SCZ Glycolytic Reserve	*	Two-Level Hierarchical Linear Mixed Effect Model after log-transformation
eData 10C	Glut control Basal Respiration		One-Level Hierarchical Linear Mixed Effect Model
	Glut control Maximum Respiration		One-Level Hierarchical Linear Mixed Effect Model
	Glut act.MG Basal Respiration		One-Level Hierarchical Linear Mixed Effect Model
	Glut act.MG Maximum Respiration		One-Level Hierarchical Linear Mixed Effect Model