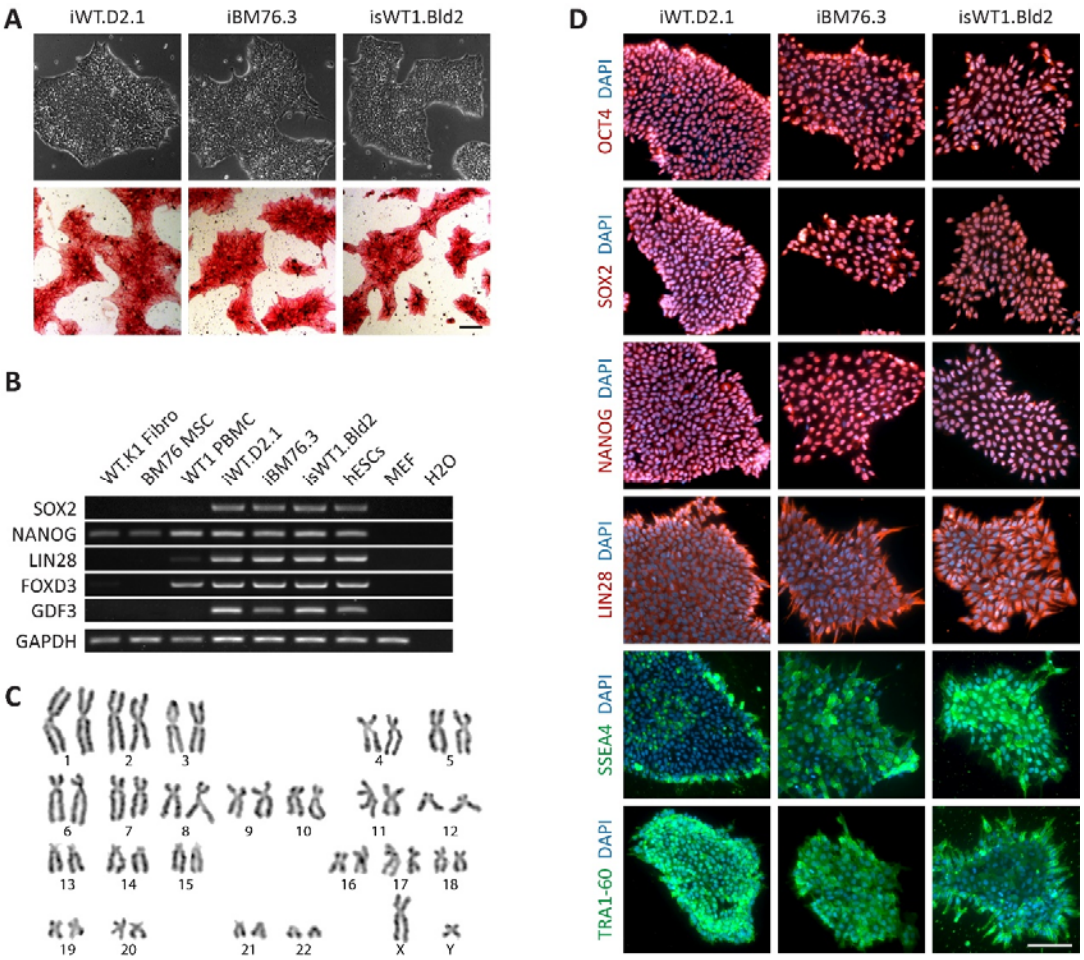
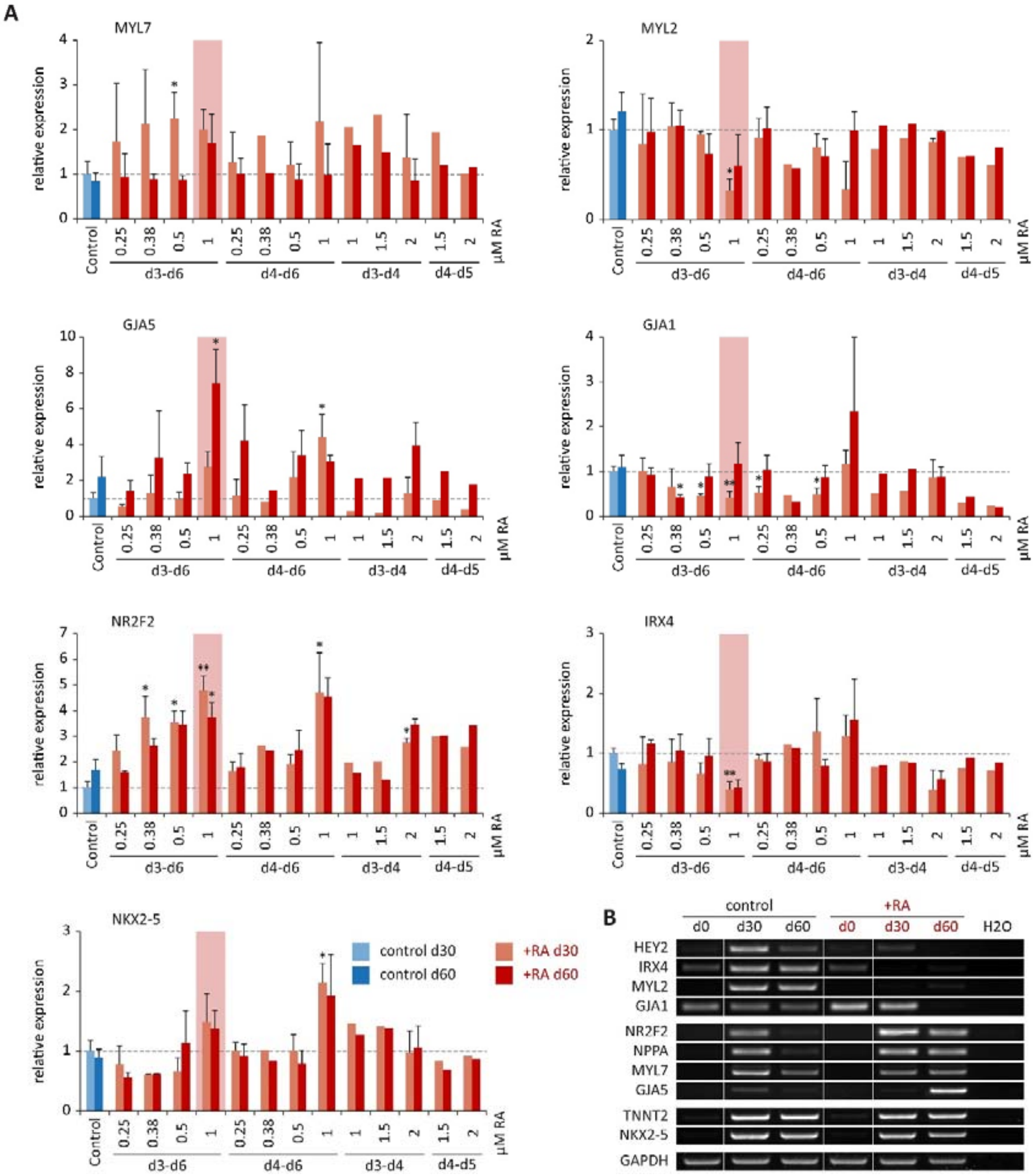
Supplemental Data

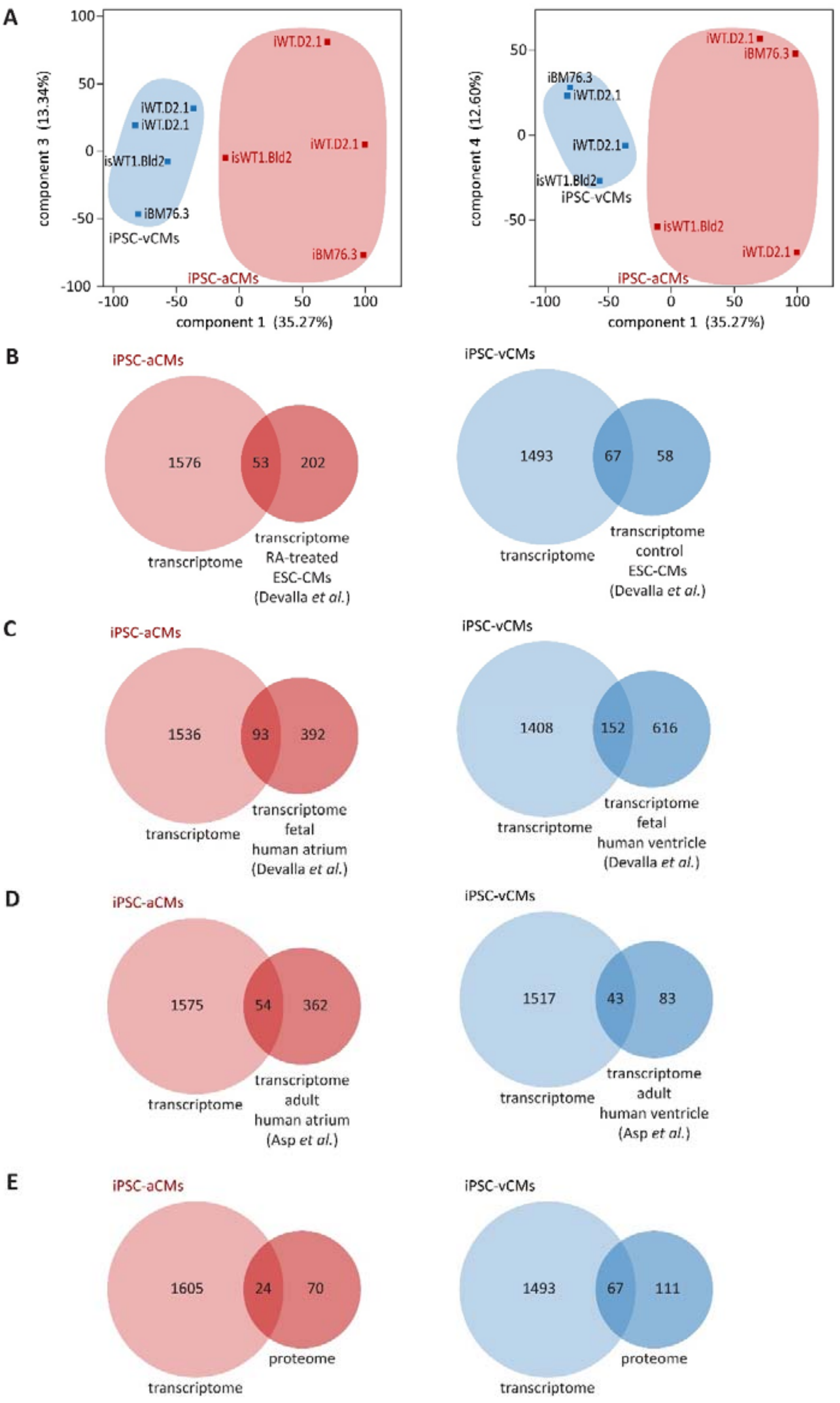
Supplemental Figures



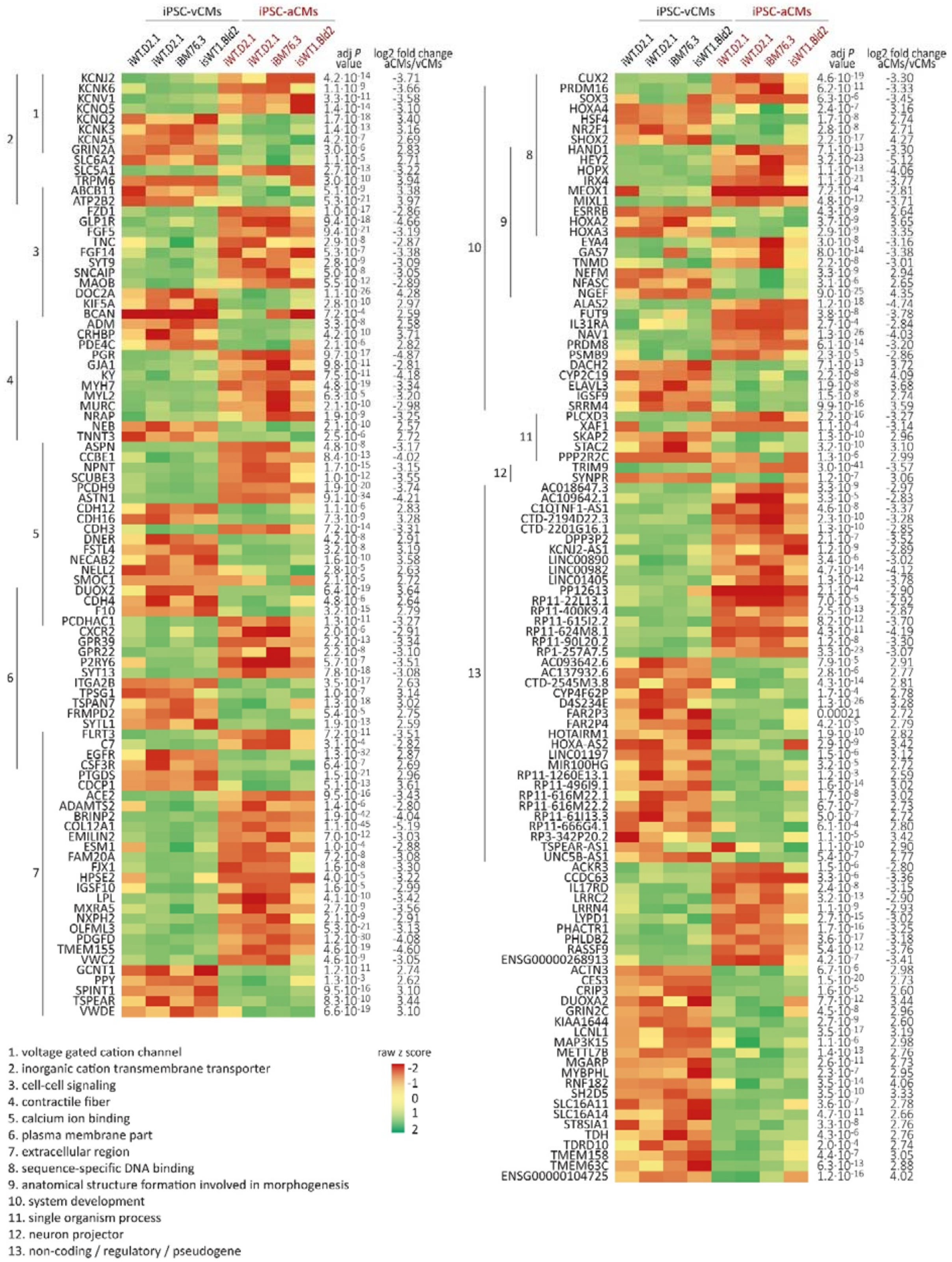
Supplemental Figure 1: Pluripotency characterization of human iPSC lines from three healthy donors. iWT.D2.1 and iBM76.3 were reprogrammed from dermal fibroblasts and mesenchymal stem cells, respectively, by using the STEMCCA lentivirus system; and isWT1.Bld2 was reprogrammed from peripheral blood mononuclear cells (PBMCs) by using the Sendai virus system. (**A**) All three analyzed iPSC lines display typical morphology of human pluripotent stem cells (upper panel) and are positive for alkaline phosphatase (lower panel); scale bar, 100 µm. (**B**) Expression of endogenous pluripotency markers (*SOX2*, *NANOG*, *LIN28*, *FOXD3*, *GDF3*) in iPSC lines compared to primary cultures of dermal fibroblasts (WT.K1 Fibro), mesenchymal stem cells (BM76 MSC) and PBMCs (WT1 PBMC) was assessed by reverse transcriptase-PCR; human embryonic stem cells (hESCs) were used as positive control; mouse embryonic fibroblasts (MEF) were used as negative control. (**C**) The analyzed iPSC lines show normal karyotype (iPSC line isWT1.Bld2). (**D**) Immunofluorescence staining for pluripotency markers (OCT4, SOX2, NANOG, LIN28, SSEA4, and TRA1-60); nuclei were count-stained with DAPI (blue); scale bar, 100 µm.



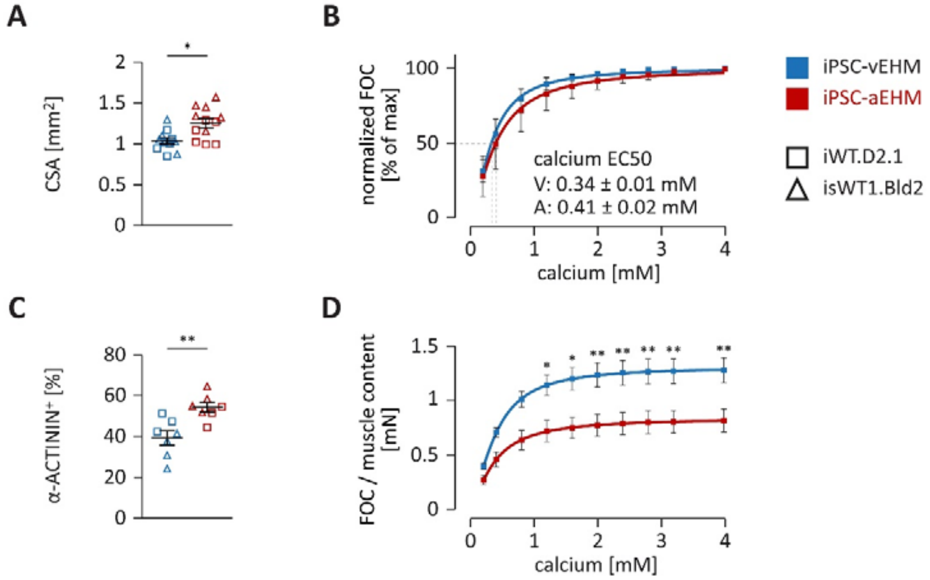
Supplemental Figure 2: Screening of retinoic acid treatments for directed differentiation of iPSCs into atrial cardiomyocytes. (**A**) Cultures during differentiation were exposed to retinoic acid (RA) at concentrations of 0.25, 0.38, 0.5 and 1 µM between day 3-6, 0.25, 0.38, 0.5 and 1 µM between day 4-6, 1, 1.5 and 2 µM between day 3-4 and 1.5 and 2 µM between day 4-5 (n=1-4 independent differentiation experiments from 3 iPSC lines, n < 3 for certain conditions due to detachment of cultures). Differentiated iPSC-derived cardiomyocytes (iPSC-CMs) were analyzed by reverse transcriptase-PCR for expression of atrial markers (*MYL7*, *GJA5*, and *NR2F2*), ventricular markers (*MYL2*, *GJA1*, and *IRX4*) and general cardiac marker *NKX2-5* at days 30 and 60 compared to untreated control. Results were quantified according to intensity and normalized to *TNNT2* expression and to controls at day 30. Treatment with 1 µM RA at day 3-6 (highlighted in red) resulted in highest expression levels of the atrial and lowest levels of the ventricular markers. Data are presented as mean ± SEM; $^{**}P < 0.01$, $^{*}P < 0.05$, by nonparametric Mann-Whitney U test. (**B**) Representative images of reverse transcriptase-PCR analysis of ventricular (*HEY2*, *IRX4*, *MYL2*, *GJA1*), atrial (*NR2F2*, *NPPA*, *MYL7*, *GJA5*) and general cardiac markers (*TNNT2*, *NKX2-5*) at day 30 and day 60 in 1 µM RA-treated cultures and controls (iPSC line WT.D2.1). d0, undifferentiated iPSCs. Lanes were run on the same gel but were noncontiguous.



Supplemental Figure 3: Comparison of transcriptomic analysis of iPSC-derived atrial or ventricular cardiomyocytes. (**A**) Principal component analysis of component 1 versus component 3 and component 1 versus component 4 of the global gene expression data of iPSC-derived atrial and ventricular cardiomyocytes (iPSC-aCMs, iPSC-vCMs) at day 90 (n = 4 iPSC-vCM and n = 4 iPSC-aCM independent differentiation experiments from 3 iPSC lines). (**B**) Comparison of significantly higher expressed genes in iPSC-aCMs or iPSC-vCMs from the RNA-seq data (log2-fold > 0.5; *P*< 0.05) with published transcriptomic data for RA-treated and control human ESC-derived CMs (1). (**C, D**) Comparison of significantly higher expressed genes in iPSC-aCMs or iPSC-vCMs from the RNA-seq data (log2-fold > 0.5; *P*< 0.05) with published transcriptomic data for human fetal (**C**) and adult heart tissues (**D**) (1, 2). (**E**) Comparison of significantly higher expressed genes in the RNA-seq data (at day 90) with proteins in the SILAC data (at day 68) in iPSC-aCMs or iPSC-vCMs.



Supplemental Figure 4: Heat map of Top200 differentially expressed transcripts in iPSC-derived atrial compared to ventricular cardiomyocytes. The genes are clustered according to biological protein function from total RNA sequencing data of iPSC-derived atrial and ventricular cardiomyocytes (iPSC-aCMs, iPSC-vCMs) at day 90 (n = 4 iPSC-vCM and n = 4 iPSC-aCM independent differentiation experiments from 3 iPSC lines); adjusted *P*-value and log2 fold change of iPSC-aCMs/iPSC-vCMs are indicated; color code according to z raw score.



Supplemental Figure 5: Generation and analysis of iPSC-derived atrial and ventricular engineered heart muscle. (**A**) Analysis of cross-sectional area (CSA) of iPSC-derived atrial and ventricular engineered heart muscle (iPSC-aEHM and iPSC-vEHM). (**B**) Determination of half maximal effective concentration (EC_{50}) for calcium of individual iPSC-EHM by analysis of normalized force of contraction (FOC) in response to increasing extracellular calcium from 0.2-4 mM. (**C**) Analysis of iPSC-CM content after enzymatic dispersion of iPSC-EHM, measured by flow cytometry for α-actinin^{+} cells. (**D**) Analysis of FOC in relation to muscle content of iPSC-EHM in response to increasing extracellular calcium from 0.2-4 mM. n = 11 iPSC-vEHM and n = 12 iPSC-aEHM from iPSC lines iWT.D2.1 and isWT1.Bld2 were analyzed. Data are presented as mean ± SEM; $**P < 0.01$, $*P < 0.05$, by nonparametric Mann-Whitney U test (**A**, **C**) or by two-way ANOVA with Sidak corrections (**B**, **D**).

Supplemental Videos

Supplemental Video 1: Representative video of an iPSC-derived ventricular engineered heart muscle (iPSC line iWT.D2.1).

Supplemental Video 2: Representative video of an iPSC-derived atrial engineered heart muscle (iPSC line iWT.D2.1).

Supplemental Tables

Supplemental Table 1: Differentially expressed genes in iPSC-derived atrial (aCMs) and ventricular cardiomyocytes (vCMs) with log2 fold changes (aCMs/vCMs) < -1 (A) or > 1 (B). n = 4 iPSC-vCM and n = 4 iPSC-aCM independent differentiation experiments at day 90 from 3 iPSC lines.

(A) List of 865 transcripts with significantly lower expression in iPSC-aCMs compared to iPSC-vCMs.

Ensembl ID	Gene name	Base mean	log2 (aCMs/ vCMs)	adj *P* value		Ensembl ID	Gene name	Base mean	log2 (aCMs/ vCMs)	adj *P* value
ENSG00000111799	COL12A1	2251.3	-5.19	1.1E-45		ENSG00000112319	EYA4	131.9	-3.16	3.0E-08
ENSG00000135547	HEY2	1060.2	-5.12	3.2E-23		ENSG00000144730	IL17RD	1629.9	-3.15	2.4E-08
ENSG00000082175	PGR	130.2	-4.87	9.7E-17		ENSG00000168743	NPNT	5746.1	-3.15	1.7E-15
ENSG00000158578	ALAS2	594.3	-4.74	1.2E-18		ENSG00000132530	XAF1	22.1	-3.14	1.1E-04
ENSG00000112164	GLP1R	87.7	-4.66	9.4E-18		ENSG00000116774	OLFML3	307.7	-3.13	5.3E-21
ENSG00000164112	TMEM155	131.2	-4.60	4.6E-19		ENSG00000172209	GPR22	349.2	-3.10	2.2E-08
ENSG00000152092	ASTN1	634.6	-4.21	9.1E-34		ENSG00000185760	KCNQ5	370.4	-3.10	1.4E-14
ENSG00000237742	RP11-624M8.1	25.1	-4.19	4.3E-11		ENSG00000170743	SYT9	191.0	-3.09	2.8E-09
ENSG00000174611	KY	37.4	-4.18	7.5E-11		ENSG00000108950	FAM20A	107.6	-3.08	7.2E-08
ENSG00000177133	LINC00982	1055.6	-4.12	4.7E-14		ENSG00000019505	SYT13	978.1	-3.08	7.8E-18
ENSG00000170962	PDGFD	1590.6	-4.08	1.2E-30		ENSG00000272379	RP1-257A7.5	181.0	-3.07	3.3E-23
ENSG00000171476	HOPX	711.7	-4.06	1.1E-13		ENSG00000064692	SNCAIP	333.7	-3.05	5.0E-08
ENSG00000198797	BRINP2	159.5	-4.04	1.9E-42		ENSG00000188730	VWC2	237.1	-3.05	4.6E-09
ENSG00000134369	NAV1	10090.6	-4.03	1.3E-26		ENSG00000132205	EMILIN2	2546.9	-3.03	7.0E-12
ENSG00000183287	CCBE1	240.5	-4.02	8.4E-13		ENSG00000150551	LYPD1	127.1	-3.02	2.7E-15
ENSG00000185847	LINC01405	200.5	-3.78	1.3E-12		ENSG00000260802	LINC00890	55.7	-3.02	3.4E-06
ENSG00000172461	FUT9	21.8	-3.78	3.8E-08		ENSG00000000005	TNMD	438.9	-3.01	2.2E-08
ENSG00000113430	IRX4	1045.1	-3.77	1.1E-21		ENSG00000152580	IGSF10	42.5	-2.99	1.6E-05
ENSG00000198774	RASSF9	42.4	-3.76	5.4E-12		ENSG00000170681	MURC	944.5	-2.98	2.1E-10
ENSG00000184226	PCDH9	95.0	-3.74	1.9E-20		ENSG00000227544	AC018647.3	119.4	-2.97	3.3E-09
ENSG00000123700	KCNJ2	85.2	-3.71	4.2E-14		ENSG00000125872	LRRN4	269.7	-2.93	1.1E-09
ENSG00000185155	MIXL1	67.6	-3.71	4.8E-12		ENSG00000272235	RP11-22L13.1	11.4	-2.92	7.0E-05
ENSG00000260577	RP11-615I2.2	59.4	-3.70	8.2E-12		ENSG00000144227	NXPH2	65.4	-2.91	2.1E-09
ENSG00000099337	KCNK6	408.5	-3.66	1.1E-09		ENSG00000180871	CXCR2	29.1	-2.91	2.0E-06
ENSG00000164794	KCNV1	49.5	-3.58	3.3E-11		ENSG00000163827	LRRC2	296.7	-2.90	3.2E-13
ENSG00000100505	TRIM9	426.1	-3.57	3.0E-41		ENSG00000226757	PP12613	9.3	-2.90	2.1E-04
ENSG00000101825	MXRA5	162.2	-3.56	2.7E-09		ENSG00000069535	MAOB	246.5	-2.89	5.5E-12
ENSG00000146197	SCUBE3	3179.9	-3.55	1.0E-12		ENSG00000267365	KCNJ2-AS1	42.6	-2.89	1.2E-09
ENSG00000221844	DPP3P2	20.2	-3.52	2.1E-07		ENSG00000164283	ESM1	21.2	-2.88	1.0E-04
ENSG00000125848	FLRT3	153.2	-3.51	7.2E-11		ENSG00000237807	RP11-400K9.4	69.3	-2.87	2.5E-13
ENSG00000171631	P2RY6	37.6	-3.51	5.7E-07		ENSG00000041982	TNC	252.6	-2.87	2.9E-08
ENSG00000134595	SOX3	37.8	-3.45	6.3E-06		ENSG00000240065	PSMB9	67.8	-2.86	2.3E-05
ENSG00000130234	ACE2	144.3	-3.43	9.5E-16		ENSG00000157240	FZD1	8716.4	-2.86	1.0E-17
ENSG00000175445	LPL	985.2	-3.42	4.1E-10		ENSG00000258444	CTD-2201G16.1	56.5	-2.85	1.3E-10
ENSG00000268913		69.2	-3.41	4.2E-07		ENSG00000164509	IL31RA	11.5	-2.84	2.7E-04
ENSG00000007237	GAS7	546.9	-3.38	8.0E-14		ENSG00000235997	AC109642.1	71.6	-2.83	3.3E-05
ENSG00000102466	FGF14	45.1	-3.38	5.3E-07		ENSG00000112936	C7	1808.8	-2.82	3.1E-04
ENSG00000265096	C1QTNF1-AS1	27.3	-3.37	4.6E-08		ENSG00000152661	GJA1	2247.2	-2.81	9.8E-11
ENSG00000173093	CCDC63	12.8	-3.36	3.3E-06		ENSG00000005102	MEOX1	8.4	-2.81	7.2E-04
ENSG00000183840	GPR39	108.0	-3.34	2.2E-13		ENSG00000144476	ACKR3	219.8	-2.80	1.5E-06
ENSG00000092054	MYH7	172994.6	-3.34	4.8E-19		ENSG00000087116	ADAMTS2	123.8	-2.80	1.4E-06
ENSG00000142611	PRDM16	969.7	-3.33	6.2E-11		ENSG00000180287	PLD5	23.0	-2.77	7.0E-07
ENSG00000062038	CDH3	838.2	-3.31	7.2E-14		ENSG00000204291	COL15A1	460.2	-2.75	3.5E-06
ENSG00000235121	RP11-90L20.2	31.8	-3.30	1.2E-08		ENSG00000223923	AC010136.2	16.1	-2.75	4.1E-05
ENSG00000113196	HAND1	275.4	-3.30	7.1E-13		ENSG00000182747	SLC35D3	128.2	-2.74	3.4E-06
ENSG00000179431	FJX1	146.4	-3.30	1.6E-08		ENSG00000260918	RP11-731J8.2	34.1	-2.72	1.2E-05
ENSG00000111249	CUX2	317.4	-3.30	4.6E-19		ENSG00000213626	LBH	4908.1	-2.72	7.3E-08
ENSG00000249116	CTD-2194D22.3	62.5	-3.28	2.3E-10		ENSG00000000971	CFH	100.3	-2.70	5.8E-05
ENSG00000182836	PLCXD3	4231.6	-3.27	2.2E-16		ENSG00000132953	XPO4	5229.7	-2.69	9.7E-14
ENSG00000248383	PCDHAC1	78.6	-3.27	1.3E-11		ENSG00000132031	MATN3	56.1	-2.68	1.4E-06
ENSG00000197893	NRAP	887.7	-3.25	1.9E-09		ENSG00000156427	FGF18	640.3	-2.67	7.1E-11
ENSG00000112137	PHACTR1	867.3	-3.25	1.7E-16		ENSG00000132464	ENAM	14.1	-2.67	6.6E-05
ENSG00000172987	HPSE2	15.1	-3.22	4.0E-05		ENSG00000135298	ADGRB3	55.0	-2.67	2.8E-06
ENSG00000100170	SLC5A1	687.6	-3.22	2.7E-13		ENSG00000162618	ADGRL4	8.0	-2.66	7.2E-04
ENSG00000111245	MYL2	18694.1	-3.20	6.3E-05		ENSG00000154258	ABCA9	15.3	-2.66	3.8E-04
ENSG00000152784	PRDM8	174.2	-3.20	6.1E-14		ENSG00000106829	TLE4	201.9	-2.65	8.9E-16
ENSG00000138675	FGF5	419.8	-3.19	9.4E-21		ENSG00000109205	ODAM	15.0	-2.65	1.1E-03
ENSG00000144824	PHLDB2	2990.0	-3.18	3.6E-17		ENSG00000101098	RIMS4	160.3	-2.62	1.4E-06
ENSG00000106819	ASPN	557.1	-3.17	4.8E-08		ENSG00000137801	THBS1	2455.8	-2.62	7.1E-06

ENSG00000127241	MASP1	1738.0	-2.61	6.2E-07
ENSG00000154856	APCDD1	732.6	-2.61	3.1E-09
ENSG00000136859	ANGPTL2	196.6	-2.60	1.2E-04
ENSG00000185774	KCNIP4	160.0	-2.59	3.8E-12
ENSG00000182463	TSHZ2	375.1	-2.59	8.6E-10
ENSG00000184937	WT1	361.9	-2.59	4.8E-06
ENSG00000261265	CTD-2515H24.4	11.8	-2.58	9.7E-04
ENSG00000016402	IL20RA	74.0	-2.57	5.8E-05
ENSG00000165186	PTCHD1	56.8	-2.56	1.1E-05
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ENSG00000079308	TNS1	5960.6	-2.55	2.2E-10
ENSG00000236333	TRHDE-AS1	9.4	-2.55	1.4E-03
ENSG00000114279	FGF12	2062.0	-2.54	2.1E-07
ENSG00000128849	CGNL1	5307.8	-2.54	1.1E-03
ENSG00000177459	ERICH5	81.5	-2.53	2.6E-06
ENSG00000203706	SERTAD4-AS1	35.3	-2.53	7.7E-05
ENSG00000108576	SLC6A4	72.4	-2.53	9.4E-06
ENSG00000164035	EMCN	8.5	-2.53	2.3E-03
ENSG00000138166	DUSP5	1054.2	-2.52	1.3E-10
ENSG00000185046	ANKS1B	73.2	-2.52	2.3E-07
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ENSG00000046653	GPM6B	252.2	-2.48	4.0E-17
ENSG00000143196	DPT	8.5	-2.47	3.1E-03
ENSG00000206384	COL6A6	113.2	-2.47	7.1E-06
ENSG00000169851	PCDH7	2099.2	-2.47	1.3E-11
ENSG00000182771	GRID1	344.5	-2.46	1.4E-07
ENSG00000249307	LINC01088	49.8	-2.45	3.8E-05
ENSG00000165124	SVEP1	86.8	-2.45	5.0E-06
ENSG00000178031	ADAMTSL1	612.9	-2.44	2.9E-03
ENSG00000145675	PIK3R1	2223.6	-2.43	2.2E-16
ENSG00000120217	CD274	160.5	-2.43	2.7E-07
ENSG00000189184	PCDH18	75.9	-2.42	9.7E-05
ENSG00000138685	FGF2	208.6	-2.42	3.9E-06
ENSG00000120278	PLEKHG1	421.9	-2.42	4.7E-13
ENSG00000125430	HS3ST3B1	16.7	-2.42	1.0E-03
ENSG00000179284	DAND5	36.1	-2.42	1.4E-07
ENSG00000146674	IGFBP3	1935.2	-2.41	2.2E-07
ENSG00000164220	F2RL2	31.2	-2.41	1.5E-04
ENSG00000176204	LRRTM4	15.5	-2.40	2.4E-03
ENSG00000074706	IPCEF1	8.8	-2.40	3.3E-03
ENSG00000139629	GALNT6	78.5	-2.40	8.1E-04
ENSG00000164128	NPY1R	59.3	-2.39	5.0E-08
ENSG00000139117	CPNE8	61.2	-2.39	5.8E-05
ENSG00000164116	GUCY1A3	2299.0	-2.39	2.3E-17
ENSG00000157399	ARSE	8.9	-2.38	2.2E-03
ENSG00000096968	JAK2	1360.4	-2.37	2.8E-14
ENSG00000148848	ADAM12	60.3	-2.36	9.3E-04
ENSG00000135604	STX11	134.7	-2.35	2.0E-07
ENSG00000080224	EPHA6	12.8	-2.35	1.1E-03
ENSG00000144285	SCN1A	16.3	-2.34	1.9E-03
ENSG00000126709	IFI6	2372.7	-2.34	6.0E-03
ENSG00000168672	FAM84B	3451.5	-2.34	3.9E-08
ENSG00000049130	KITLG	141.8	-2.33	6.5E-08
ENSG00000152402	GUCY1A2	319.1	-2.33	6.0E-08
ENSG00000180785	OR51E1	17.3	-2.33	1.2E-03
ENSG00000136630	HLX	48.0	-2.32	1.3E-05
ENSG00000134183	GNAT2	13.8	-2.30	1.2E-03
ENSG00000198846	TOX	216.3	-2.30	1.2E-05
ENSG00000205488	CALML3-AS1	10.3	-2.30	2.8E-03
ENSG00000011638	TMEM159	878.2	-2.29	5.0E-07
ENSG00000113396	SLC27A6	2190.0	-2.28	2.2E-08
ENSG00000180611	MB21D2	467.2	-2.28	7.6E-13
ENSG00000189221	MAOA	265.7	-2.28	4.3E-04
ENSG00000172380	GNG12	2094.3	-2.27	5.0E-10
ENSG00000168077	SCARA3	139.3	-2.27	3.3E-05
ENSG00000112782	CLIC5	1313.6	-2.27	8.4E-10
ENSG00000183242	WT1-AS	69.2	-2.26	1.4E-04
ENSG00000082497	SERTAD4	202.5	-2.26	8.0E-05
ENSG00000101680	LAMA1	34.1	-2.26	2.6E-04
ENSG00000169855	ROBO1	1679.1	-2.26	2.3E-06
ENSG00000076706	MCAM	1971.5	-2.26	8.5E-10
ENSG00000145423	SFRP2	369.5	-2.25	5.6E-03
ENSG00000162722	TRIM58	84.6	-2.25	3.3E-09
ENSG00000163406	SLC15A2	254.5	-2.24	2.8E-10
ENSG00000123610	TNFAIP6	9.0	-2.24	5.4E-03
ENSG00000135842	FAM129A	2592.6	-2.24	8.6E-07
ENSG00000182533	CAV3	166.2	-2.24	4.1E-06
ENSG00000168785	TSPAN5	1387.8	-2.23	6.1E-20
ENSG00000164761	TNFRSF11B	145.0	-2.23	1.7E-03
ENSG00000205413	SAMD9	20.4	-2.23	9.3E-03
ENSG00000107738	C10orf54	111.3	-2.23	4.9E-08
ENSG00000230928	RP11-34A14.3	11.0	-2.23	6.8E-03
ENSG00000039560	RAI14	613.8	-2.22	1.8E-06
ENSG00000110693	SOX6	173.3	-2.21	3.5E-06
ENSG00000182752	PAPPA	102.5	-2.21	4.2E-04
ENSG00000106571	GLI3	215.7	-2.20	4.9E-04
ENSG00000243232	PCDHAC2	467.9	-2.20	1.4E-04
ENSG00000139329	LUM	193.8	-2.19	1.2E-02
ENSG00000241732		47.8	-2.19	2.4E-03
ENSG00000138829	FBN2	9163.7	-2.18	6.9E-11
ENSG00000249693	THEGL	10.1	-2.18	5.8E-03
ENSG00000080573	COL5A3	50.4	-2.18	3.2E-03
ENSG00000152822	GRM1	193.4	-2.18	3.1E-05
ENSG00000112769	LAMA4	1102.0	-2.17	1.9E-08
ENSG00000151892	GFRA1	296.3	-2.17	9.3E-04
ENSG00000167912	RP11-25K19.1	36.8	-2.17	4.8E-05
ENSG00000185070	FLRT2	552.1	-2.17	1.6E-04
ENSG00000164741	DLC1	2554.5	-2.16	6.5E-12
ENSG00000091704	CPA1	15.4	-2.16	6.2E-03
ENSG00000132854	KANK4	45.2	-2.15	5.6E-03
ENSG00000206579	XKR4	12.6	-2.15	6.6E-03
ENSG00000152268		2535.9	-2.15	5.4E-03
ENSG00000163638	ADAMTS9	1200.7	-2.14	3.6E-09
ENSG00000150938	CRIM1	569.3	-2.14	4.3E-04
ENSG00000111913	FAM65B	325.9	-2.14	5.8E-05
ENSG00000038427	VCAN	1785.4	-2.14	5.6E-03
ENSG00000174473	GALNTL6	11.7	-2.13	5.0E-03
ENSG00000141441	GAREM	841.6	-2.13	1.8E-07
ENSG00000165071	TMEM71	332.8	-2.12	3.9E-04
ENSG00000150722	PPP1R1C	133.8	-2.12	5.8E-05
ENSG00000150394	CDH8	154.5	-2.12	6.5E-11
ENSG00000197993	KEL	135.9	-2.11	8.0E-07
ENSG00000236751	LINC01186	15.6	-2.11	5.6E-03
ENSG00000189108	IL1RAPL2	9.3	-2.11	9.7E-03
ENSG00000203688	RP11-351J23.1	8.4	-2.10	1.3E-02
ENSG00000177508	IRX3	345.0	-2.10	5.9E-05
ENSG00000169860	P2RY1	67.2	-2.10	5.2E-03
ENSG00000065361	ERBB3	728.3	-2.10	4.7E-14
ENSG00000163661	PTX3	85.4	-2.10	3.5E-05
ENSG00000140795	MYLK3	3130.9	-2.09	8.5E-10
ENSG00000197506	SLC28A3	695.8	-2.09	2.3E-05
ENSG00000173193	PARP14	747.0	-2.09	9.0E-03
ENSG00000111145	ELK3	128.7	-2.08	1.4E-04
ENSG00000119917	IFIT3	246.4	-2.08	1.9E-02
ENSG00000197555	SIPA1L1	843.1	-2.08	1.2E-05
ENSG00000197442	MAP3K5	172.5	-2.08	1.4E-05
ENSG00000179776	CDH5	17.5	-2.08	8.4E-03
ENSG00000137077	CCL21	156.4	-2.08	4.2E-03
ENSG00000174059	CD34	54.2	-2.08	9.4E-03
ENSG00000103381	CPPED1	114.8	-2.08	2.6E-10
ENSG00000184374	COLEC10	9.7	-2.07	7.2E-03
ENSG00000198929	NOS1AP	45.1	-2.07	2.7E-04
ENSG00000137968	SLC44A5	594.0	-2.07	1.2E-08
ENSG00000106366	SERPINE1	234.4	-2.06	2.4E-03
ENSG00000196136	SERPINA3	11.4	-2.06	1.3E-02
ENSG00000238243	OR2W3	54.1	-2.06	1.3E-05
ENSG00000154415	PPP1R3A	1226.3	-2.06	1.1E-06
ENSG00000239887	C1orf226	109.3	-2.05	6.6E-04
ENSG00000108405	P2RX1	827.4	-2.04	1.4E-04
ENSG00000126878	AIF1L	792.2	-2.04	6.2E-07
ENSG00000129038	LOXL1	521.6	-2.04	1.7E-06

ENSG00000181195	PENK	21.5	-2.04	1.6E-02	ENSG00000117600	LPPR4	12.6	-1.87	1.4E-02
ENSG00000039537	C6	12.3	-2.03	7.7E-03	ENSG00000122176	FMOD	138.0	-1.87	1.3E-02
ENSG00000183230	CTNNA3	933.6	-2.02	4.7E-09	ENSG00000156966	B3GNT7	213.2	-1.86	1.6E-03
ENSG00000124749	COL21A1	1075.0	-2.02	7.8E-06	ENSG00000124942	AHNAK	12304.5	-1.86	5.7E-10
ENSG00000057294	PKP2	5767.5	-2.01	2.0E-10	ENSG00000107742	SPOCK2	1315.3	-1.86	3.4E-02
ENSG00000166828	SCNN1G	8.0	-2.01	2.1E-02	ENSG00000008517	IL32	8.6	-1.86	3.6E-02
ENSG00000231013	AC013275.2	7.2	-2.01	1.6E-02	ENSG00000260641	RP11-1299A16.3	149.2	-1.86	1.3E-11
ENSG00000003137	CYP26B1	266.5	-2.01	1.2E-03	ENSG00000179241	LDLRAD3	210.7	-1.86	7.8E-04
ENSG00000134323	MYCN	84.4	-2.01	5.5E-06	ENSG00000162636	FAM102B	651.1	-1.86	4.6E-09
ENSG00000170961	HAS2	8.7	-2.00	2.2E-02	ENSG00000185745	IFIT1	1412.8	-1.85	9.2E-04
ENSG00000204248	COL11A2	5777.8	-2.00	4.3E-05	ENSG00000121898	CPXM2	26.8	-1.85	3.4E-02
ENSG00000176842	IRX5	78.1	-2.00	5.2E-05	ENSG00000250072	CTC-529P8.1	10.1	-1.84	1.5E-02
ENSG00000151224	MAT1A	206.1	-2.00	7.5E-05	ENSG00000187123	LYPD6	72.2	-1.84	1.8E-03
ENSG00000165895	ARHGAP42	380.8	-2.00	8.3E-06	ENSG00000186197	EDARADD	18.5	-1.84	2.7E-03
ENSG00000082293	COL19A1	110.9	-2.00	3.1E-06	ENSG00000058085	LAMC2	18.8	-1.84	1.3E-02
ENSG00000069122	ADGRF5	16.6	-2.00	1.0E-02	ENSG00000180801	ARSJ	63.7	-1.83	5.5E-04
ENSG00000255103		201.1	-2.00	1.2E-06	ENSG00000156486	KCNS2	190.5	-1.83	1.9E-06
ENSG00000231776	LINC01611	25.1	-1.99	2.4E-02	ENSG00000003096	KLHL13	613.6	-1.83	6.6E-07
ENSG00000074590	NUAK1	740.0	-1.99	4.6E-11	ENSG00000164300	SERINC5	187.4	-1.83	6.3E-04
ENSG00000260512		407.8	-1.98	1.5E-05	ENSG00000225706	PTPRD-AS1	29.6	-1.82	1.5E-03
ENSG00000225485		1717.6	-1.98	5.7E-18	ENSG00000048707	VPS13D	5197.1	-1.82	5.4E-07
ENSG00000169306	IL1RAPL1	42.2	-1.98	1.9E-06	ENSG00000199550	Y_RNA	31.1	-1.81	1.0E-04
ENSG00000144642	RBMS3	678.6	-1.98	4.8E-08	ENSG00000141753	IGFBP4	2952.3	-1.81	6.5E-04
ENSG00000153976	HS3ST3A1	15.6	-1.98	1.5E-02	ENSG00000140285	FGF7	236.6	-1.81	4.7E-06
ENSG00000078401	EDN1	33.4	-1.97	5.1E-03	ENSG00000137965	IFI44	141.7	-1.81	4.3E-02
ENSG00000139289	PHLDA1	356.3	-1.97	2.9E-03	ENSG00000215991	MIR208B	7.0	-1.81	3.5E-02
ENSG00000163947	ARHGEF3	531.4	-1.97	3.3E-08	ENSG00000019991	HGF	18.3	-1.81	2.9E-02
ENSG00000188452	CERKL	12.1	-1.97	1.2E-02	ENSG00000101311	FERMT1	122.2	-1.80	7.1E-04
ENSG00000102359	SRPX2	10.7	-1.96	2.8E-02	ENSG00000177409	SAMD9L	14.7	-1.80	4.5E-02
ENSG00000244405	ETV5	202.7	-1.96	2.5E-03	ENSG00000022267	FHL1	4050.8	-1.80	1.4E-05
ENSG00000204282	TNRC6C-AS1	198.5	-1.95	1.4E-11	ENSG00000113578	FGF1	496.5	-1.80	2.3E-07
ENSG00000122861	PLAU	46.6	-1.95	3.3E-04	ENSG00000146592	CREB5	537.5	-1.80	1.4E-06
ENSG00000137752	CASP1	17.6	-1.95	8.6E-04	ENSG00000188313	PLSCR1	318.0	-1.80	5.0E-03
ENSG00000154928	EPHB1	20.3	-1.95	3.4E-03	ENSG00000137959	IFI44L	47.3	-1.79	4.6E-02
ENSG00000168309	FAM107A	124.2	-1.95	6.8E-03	ENSG00000182255	KCNA4	175.9	-1.79	3.4E-05
ENSG00000165300	SLITRK5	76.5	-1.95	3.8E-05	ENSG00000166741	NNMT	34.7	-1.79	2.6E-02
ENSG00000178996	SNX18	560.9	-1.94	1.5E-09	ENSG00000108691	CCL2	47.9	-1.79	2.2E-02
ENSG00000166546	BEAN1	64.3	-1.94	3.0E-05	ENSG00000157514	TSC22D3	1148.7	-1.79	1.1E-03
ENSG00000151702	FLI1	7.5	-1.94	2.9E-02	ENSG00000100504	PYGL	1215.1	-1.79	2.5E-05
ENSG00000128052	KDR	107.4	-1.94	1.1E-02	ENSG00000133110	POSTN	1157.0	-1.78	5.6E-04
ENSG00000138131	LOXL4	631.5	-1.94	2.0E-02	ENSG00000116183	PAPPA2	94.4	-1.78	5.9E-04
ENSG00000065320	NTN1	177.6	-1.93	4.8E-04	ENSG00000143768	LEFTY2	231.2	-1.77	4.3E-02
ENSG00000143816	WNT9A	87.6	-1.93	1.5E-06	ENSG00000169122	FAM110B	555.8	-1.77	1.8E-04
ENSG00000056998	GYG2	178.3	-1.92	9.4E-05	ENSG00000130300	PLVAP	9.4	-1.77	3.8E-02
ENSG00000179921	GPBAR1	14.1	-1.92	1.9E-02	ENSG00000114529	C3orf52	149.8	-1.77	1.3E-02
ENSG00000140968	IRF8	56.1	-1.92	2.5E-04	ENSG00000180875	GREM2	22.9	-1.77	7.2E-03
ENSG00000259146	RP1-261D10.2	21.8	-1.92	2.4E-03	ENSG00000091986	CCDC80	708.7	-1.77	1.8E-03
ENSG00000139567	ACVRL1	8.5	-1.92	2.4E-02	ENSG00000185013	NT5C1B	15.2	-1.77	6.9E-03
ENSG00000260025	RP11-490M8.1	7.5	-1.92	2.2E-02	ENSG00000196628	TCF4	241.3	-1.77	1.8E-06
ENSG00000197614	MFAP5	17.3	-1.92	2.5E-02	ENSG00000228956	SATB1-AS1	6.9	-1.76	2.8E-02
ENSG00000111846	GCNT2	1113.3	-1.91	7.2E-19	ENSG00000134548	SPX	239.3	-1.76	1.7E-15
ENSG00000235357	RP1-159G19.1	8.0	-1.91	1.7E-02	ENSG00000112530	PACRG	140.2	-1.76	3.9E-06
ENSG00000183654	MARCH11	434.4	-1.91	3.2E-15	ENSG00000157654	PALM2-AKAP2	36.8	-1.76	4.1E-03
ENSG00000138080	EMILIN1	353.7	-1.91	1.8E-03	ENSG00000156103	MMP16	114.4	-1.76	1.6E-03
ENSG00000130635	COL5A1	3372.9	-1.90	1.8E-02	ENSG00000133985	TTC9	113.4	-1.76	2.7E-06
ENSG00000151834	GABRA2	65.9	-1.90	6.8E-03	ENSG00000144724	PTPRG	375.4	-1.76	5.1E-07
ENSG00000117595	IRF6	351.7	-1.90	2.4E-04	ENSG00000147234	FRMPD3	31.9	-1.75	4.2E-02
ENSG00000164176	EDIL3	595.3	-1.90	1.9E-03	ENSG00000162894	FCMR	31.3	-1.75	2.0E-03
ENSG00000165474	GJB2	21.0	-1.90	2.3E-02	ENSG00000212993	POU5F1B	8.2	-1.75	2.4E-02
ENSG00000135919	SERPINE2	857.4	-1.90	3.5E-02	ENSG00000139517	LNX2	933.3	-1.75	1.1E-07
ENSG00000017427	IGF1	31.0	-1.89	1.0E-02	ENSG00000168952	STXBP6	585.4	-1.75	1.3E-03
ENSG00000162444	RBP7	29.3	-1.89	2.4E-03	ENSG00000141524	TMC6	1125.4	-1.74	7.5E-11
ENSG00000112541	PDE10A	301.2	-1.89	1.3E-03	ENSG00000149090	PAMR1	26.7	-1.74	4.1E-02
ENSG00000061337	LZTS1	34.6	-1.89	1.1E-04	ENSG00000171517	LPAR3	376.1	-1.74	1.3E-11
ENSG00000185477	GPRIN3	1125.0	-1.89	1.3E-04	ENSG00000004799	PDK4	67.5	-1.74	5.1E-06
ENSG00000224940	PRRT4	146.4	-1.89	5.8E-05	ENSG00000170647	TMEM133	138.9	-1.74	2.0E-07
ENSG00000235902	RP11-626E13.1	180.4	-1.88	2.8E-05	ENSG00000163577	EIF5A2	381.3	-1.74	1.8E-07
ENSG00000120594	PLXDC2	49.3	-1.88	3.8E-04	ENSG00000145506	NKD2	47.8	-1.73	9.4E-03
ENSG00000069702	TGFBR3	422.9	-1.88	6.4E-06	ENSG00000072657	TRHDE	12.3	-1.73	4.3E-02
ENSG00000178776	C5orf46	17.5	-1.87	1.4E-02	ENSG00000163171	CDC42EP3	3325.2	-1.73	4.9E-07
ENSG00000156395	SORCS3	217.7	-1.87	7.7E-03	ENSG00000266208	CTD-2267D19.3	30.8	-1.73	1.2E-03
ENSG00000110492	MDK	5246.6	-1.87	2.1E-14	ENSG00000271803	RP1-63M2.5	21.7	-1.73	1.1E-02

ENSG00000155130		1467.8	-1.72	4.1E-05		ENSG00000267744	RP11-799D4.1	18.6	-1.60	1.0E-02
ENSG00000101892	ATP1B4	11.1	-1.72	4.1E-02		ENSG00000134531	EMP1	42.3	-1.60	1.7E-03
ENSG00000061918	GUCY1B3	584.6	-1.72	8.4E-05		ENSG00000120885	CLU	1091.2	-1.59	5.8E-04
ENSG00000186867	QRFPR	20.3	-1.72	1.9E-02		ENSG00000115593	SMYD1	20255.2	-1.59	2.1E-11
ENSG00000088888	MAVS	1107.0	-1.72	1.8E-04		ENSG00000179083	FAM133A	58.8	-1.59	1.1E-04
ENSG00000206052	DOK6	189.0	-1.72	1.1E-04		ENSG00000170561	IRX2	79.3	-1.59	3.6E-03
ENSG00000183814	LIN9	636.7	-1.71	3.6E-13		ENSG00000167173	C15orf39	928.9	-1.59	2.1E-04
ENSG00000259370	RP11-1069G10.1	31.8	-1.71	4.5E-04		ENSG00000197415	VEPH1	30.0	-1.59	3.4E-02
ENSG00000153993	SEMA3D	97.8	-1.71	9.5E-04		ENSG00000151458	ANKRD50	1291.3	-1.58	1.2E-09
ENSG00000120318	ARAP3	265.8	-1.71	2.6E-03		ENSG00000129595	EPB41L4A	293.5	-1.58	2.4E-06
ENSG00000093072	CECR1	141.8	-1.71	2.4E-03		ENSG00000142627	EPHA2	637.9	-1.58	1.3E-03
ENSG00000163297	ANTXR2	2259.4	-1.71	4.2E-11		ENSG00000107147	KCNT1	27.2	-1.58	2.2E-03
ENSG00000107521	HPS1	1259.9	-1.70	4.9E-13		ENSG00000143320	CRABP2	2681.5	-1.57	7.4E-03
ENSG00000115415	STAT1	3177.1	-1.70	3.8E-03		ENSG00000197405	C5AR1	15.8	-1.57	3.6E-02
ENSG00000235535	RP11-532N4.2	501.6	-1.70	3.0E-05		ENSG00000125675	GRIA3	255.2	-1.57	4.3E-03
ENSG00000138061	CYP1B1	50.6	-1.70	1.4E-02		ENSG00000165379	LRFN5	27.0	-1.57	1.4E-02
ENSG00000177189	RPS6KA3	898.6	-1.70	1.8E-05		ENSG00000239445	ST3GAL6-AS1	34.6	-1.57	2.7E-03
ENSG00000260244	RP11-588K22.2	713.5	-1.70	4.1E-12		ENSG00000185518	SV2B	59.6	-1.56	1.5E-02
ENSG00000010319	SEMA3G	265.6	-1.70	1.0E-04		ENSG00000102362	SYTL4	37.6	-1.56	1.3E-03
ENSG00000187398	LUZP2	12.3	-1.69	4.3E-02		ENSG00000169604	ANTXR1	1829.2	-1.56	3.5E-04
ENSG00000136040	PLXNC1	387.0	-1.69	2.8E-04		ENSG00000072786	STK10	137.6	-1.55	1.5E-03
ENSG00000177191	B3GNT8	112.1	-1.69	7.6E-04		ENSG00000246082	NUDT16P1	45.8	-1.55	3.1E-02
ENSG00000156466	GDF6	137.6	-1.69	1.6E-02		ENSG00000259498	RP11-244F12.3	480.5	-1.55	1.1E-03
ENSG00000181826	RELL1	107.7	-1.69	2.3E-04		ENSG00000223518	CSNK1A1P1	18.3	-1.54	1.9E-02
ENSG00000169184	MN1	213.0	-1.68	9.9E-03		ENSG00000180233	ZNRF2	495.7	-1.54	1.2E-03
ENSG00000230992	FAM201B	21.0	-1.68	1.9E-02		ENSG00000197826	C4orf22	11.2	-1.54	3.8E-02
ENSG00000244161	FLNB-AS1	29.0	-1.68	3.1E-03		ENSG00000258376	RP4-647C14.2	33.8	-1.54	1.6E-02
ENSG00000196353	CPNE4	120.0	-1.68	6.4E-04		ENSG00000183580	FBXL7	2975.1	-1.54	1.6E-06
ENSG00000154678	PDE1C	698.2	-1.68	3.4E-05		ENSG00000106034	CPED1	22.3	-1.54	3.7E-02
ENSG00000203952	CCDC160	55.5	-1.68	1.5E-03		ENSG00000183166	CALN1	584.3	-1.54	2.0E-02
ENSG00000197852	FAM212B	852.9	-1.67	3.7E-11		ENSG00000250448	RP11-19O2.2	24.3	-1.53	1.8E-02
ENSG00000120937	NPPB	2368.8	-1.67	4.0E-02		ENSG00000162595	DIRAS3	349.7	-1.53	1.8E-03
ENSG00000205213	LGR4	4771.3	-1.67	4.1E-09		ENSG00000139926	FRMD6	73.5	-1.53	2.5E-03
ENSG00000129474	AJUBA	1342.6	-1.67	3.9E-10		ENSG00000260837	RP11-434B12.1	474.5	-1.53	8.4E-11
ENSG00000151572	ANO4	51.0	-1.66	9.5E-03		ENSG00000168140	VASN	471.5	-1.52	5.3E-04
ENSG00000164099	PRSS12	109.4	-1.66	5.8E-04		ENSG00000162520	SYNC	141.6	-1.52	2.2E-05
ENSG00000143179	UCK2	482.2	-1.66	4.1E-05		ENSG00000114737	CISH	344.8	-1.51	8.7E-10
ENSG00000267848		11.6	-1.66	2.2E-02		ENSG00000164056	SPRY1	256.3	-1.51	1.4E-03
ENSG00000134602	STK26	401.0	-1.66	3.8E-05		ENSG00000102554	KLF5	52.5	-1.51	1.1E-02
ENSG00000110841	PPFIBP1	2834.2	-1.66	2.6E-07		ENSG00000159176	CSRP1	991.8	-1.51	4.5E-03
ENSG00000246090	RP11-696N14.1	62.5	-1.66	1.4E-03		ENSG00000146242	TPBG	50.1	-1.51	1.2E-03
ENSG00000131634	TMEM204	9.2	-1.66	3.4E-02		ENSG00000166974	MAPRE2	2883.1	-1.51	4.9E-11
ENSG00000165072	MAMDC2	16.2	-1.65	1.9E-02		ENSG00000230910	RP3-525N10.2	18.1	-1.50	3.9E-02
ENSG00000110400	PVRL1	1832.3	-1.65	6.9E-07		ENSG00000086289	EPDR1	328.5	-1.50	3.2E-03
ENSG00000135312	HTR1B	21.7	-1.65	1.8E-03		ENSG00000103184	SEC14L5	208.7	-1.50	5.2E-04
ENSG00000105810	CDK6	2342.3	-1.64	4.7E-11		ENSG00000013016	EHD3	2162.1	-1.49	4.9E-04
ENSG00000119943	PYROXD2	701.5	-1.64	1.4E-14		ENSG00000184349	EFNA5	524.2	-1.49	1.1E-07
ENSG00000259886		10.2	-1.64	4.3E-02		ENSG00000109436	TBC1D9	497.9	-1.49	1.9E-03
ENSG00000124813	RUNX2	39.5	-1.64	6.8E-03		ENSG00000179954	SSC5D	57.5	-1.49	4.2E-02
ENSG00000169439	SDC2	717.8	-1.63	1.8E-04		ENSG00000006468	ETV1	1301.1	-1.49	2.1E-05
ENSG00000172164	SNTB1	19.1	-1.63	1.3E-02		ENSG00000217165	ANKRD18EP	53.8	-1.48	1.6E-03
ENSG00000186073	C15orf41	1541.0	-1.63	1.2E-06		ENSG00000114019	AMOTL2	1194.6	-1.48	1.3E-09
ENSG00000250392	RP11-700N1.1	31.0	-1.62	1.6E-02		ENSG00000102547	CAB39L	706.2	-1.48	5.1E-06
ENSG00000129009	ISLR	107.3	-1.62	3.5E-02		ENSG00000174348	PODN	684.2	-1.48	1.6E-05
ENSG00000164484	TMEM200A	8.8	-1.62	4.6E-02		ENSG00000167244	IGF2	38473.8	-1.48	1.0E-02
ENSG00000233280		321.1	-1.62	1.5E-03		ENSG00000231419	LINC00689	13.8	-1.48	4.9E-02
ENSG00000166482	MFAP4	4814.5	-1.61	1.3E-05		ENSG00000100605	ITPK1	958.3	-1.48	8.6E-06
ENSG00000136158	SPRY2	733.1	-1.61	9.5E-07		ENSG00000169174	PCSK9	22.9	-1.47	3.5E-02
ENSG00000226403	RP11-31F19.1	116.1	-1.61	2.7E-05		ENSG00000143799	PARP1	3610.3	-1.47	4.0E-08
ENSG00000128283	CDC42EP1	64.7	-1.61	2.0E-02		ENSG00000162383	SLC1A7	24.0	-1.47	3.4E-02
ENSG00000242265	PEG10	10933.1	-1.61	6.1E-04		ENSG00000158966	CACHD1	957.4	-1.47	1.1E-02
ENSG00000134954	ETS1	148.8	-1.61	2.9E-04		ENSG00000269952	RP11-324I22.3	10.9	-1.47	4.3E-02
ENSG00000130055	GDPD2	23.8	-1.61	4.1E-03		ENSG00000129538	RNASE1	19.4	-1.47	3.0E-02
ENSG00000115963	RND3	575.3	-1.61	5.2E-07		ENSG00000151388	ADAMTS12	233.3	-1.46	1.5E-02
ENSG00000138758	SEPT11	1150.5	-1.61	5.8E-04		ENSG00000146386	ABRACL	40.1	-1.46	1.0E-02
ENSG00000031081	ARHGAP31	3731.5	-1.60	1.5E-04		ENSG00000150760	DOCK1	1212.6	-1.46	1.0E-06
ENSG00000112419	PHACTR2	974.9	-1.60	3.4E-14		ENSG00000120833	SOCS2	155.1	-1.46	6.9E-04
ENSG00000163288	GABRB1	10.2	-1.60	4.5E-02		ENSG00000214357	NEURL1B	685.1	-1.46	1.3E-04
ENSG00000095794	CREM	653.9	-1.60	7.5E-08		ENSG00000170571	EMB	132.7	-1.45	5.7E-03
ENSG00000163380	LMOD3	1154.8	-1.60	8.0E-03		ENSG00000246662	LINC00535	21.9	-1.45	3.7E-02
ENSG00000206538	VGLL3	66.1	-1.60	4.0E-02		ENSG00000076356	PLXNA2	660.7	-1.45	2.9E-06
ENSG00000186340	THBS2	296.8	-1.60	1.8E-02		ENSG00000116132	PRRX1	543.5	-1.44	2.8E-02

ENSG00000149591	TAGLN	1061.2	-1.44	1.7E-02		ENSG00000121577	POPDC2	8656.4	-1.32	8.7E-07
ENSG00000115841	RMDN2	73.6	-1.44	2.1E-03		ENSG00000091656	ZFHX4	143.2	-1.32	2.2E-02
ENSG00000182263	FIGN	898.8	-1.43	2.6E-09		ENSG00000184838	PRR16	82.6	-1.32	3.3E-02
ENSG00000163092	XIRP2	945.7	-1.43	7.3E-03		ENSG00000099139	PCSK5	80.3	-1.32	8.9E-03
ENSG00000157502	MUM1L1	1582.1	-1.43	4.2E-07		ENSG00000178665	ZNF713	136.4	-1.32	1.7E-06
ENSG00000162493	PDPN	917.9	-1.43	5.1E-12		ENSG00000132938	MTUS2	2247.8	-1.31	9.3E-07
ENSG00000107201	DDX58	473.6	-1.43	3.9E-02		ENSG00000006756	ARSD	426.9	-1.31	1.2E-05
ENSG00000153071	DAB2	120.7	-1.43	2.4E-03		ENSG00000197702	PARVA	843.9	-1.31	3.6E-06
ENSG00000068079	IFI35	172.2	-1.42	2.3E-02		ENSG00000166128	RAB8B	282.2	-1.31	4.9E-02
ENSG00000019549	SNAI2	33.1	-1.42	4.5E-02		ENSG00000131094	C1QL1	687.3	-1.31	6.3E-05
ENSG00000198771	RCSD1	2320.5	-1.42	7.5E-11		ENSG00000135835	KIAA1614	63.7	-1.31	1.2E-03
ENSG00000114738	MAPKAPK3	2937.7	-1.42	4.6E-08		ENSG00000134986	NREP	20905.0	-1.31	3.0E-13
ENSG00000070193	FGF10	58.9	-1.42	2.7E-02		ENSG00000102780	DGKH	228.0	-1.31	3.7E-04
ENSG00000131969	ABHD12B	19.6	-1.41	2.4E-02		ENSG00000250981	RP11-19O2.1	144.7	-1.30	1.6E-04
ENSG00000021826	CPS1	215.0	-1.41	2.5E-05		ENSG00000127955	GNAI1	393.7	-1.30	6.0E-03
ENSG00000184384	MAML2	237.7	-1.41	2.7E-04		ENSG00000047365	ARAP2	128.7	-1.30	2.1E-03
ENSG00000122012	SV2C	159.2	-1.41	9.4E-03		ENSG00000145632	PLK2	692.4	-1.30	3.6E-03
ENSG00000100100	PIK3IP1	282.5	-1.41	2.8E-03		ENSG00000154556	SORBS2	15315.2	-1.30	2.2E-05
ENSG00000223652	AC106786.1	20.9	-1.41	2.3E-02		ENSG00000147606	SLC26A7	50.6	-1.30	9.7E-03
ENSG00000122863	CHST3	367.0	-1.41	2.6E-03		ENSG00000116991	SIPA1L2	5692.4	-1.30	2.0E-04
ENSG00000109881	CCDC34	558.5	-1.41	1.4E-04		ENSG00000101463	SYNDIG1	438.4	-1.29	3.2E-03
ENSG00000171914	TLN2	1859.4	-1.41	8.8E-12		ENSG00000138646	HERC5	152.4	-1.29	4.6E-02
ENSG00000213694	S1PR3	792.6	-1.41	2.6E-03		ENSG00000214262	ANKRD36BP1	56.8	-1.29	3.3E-02
ENSG00000261553	RP11-29G8.3	35.8	-1.41	2.8E-03		ENSG00000077684	JADE1	693.9	-1.29	2.9E-06
ENSG00000120658	ENOX1	173.3	-1.41	6.5E-03		ENSG00000122779	TRIM24	2675.2	-1.28	1.2E-05
ENSG00000227885	RP11-79N23.1	25.8	-1.40	4.1E-03		ENSG00000215218	UBE2QL1	126.2	-1.28	1.3E-02
ENSG00000204682	CASC10	484.4	-1.40	2.5E-04		ENSG00000134138	MEIS2	3897.4	-1.28	2.4E-05
ENSG00000117289		6291.8	-1.40	3.0E-02		ENSG00000179277	MEIS3P1	32.8	-1.28	1.1E-02
ENSG00000227028	SLC8A1-AS1	32.4	-1.40	2.5E-02		ENSG00000071205	ARHGAP10	486.5	-1.28	3.8E-09
ENSG00000149212	SESN3	803.3	-1.40	2.9E-03		ENSG00000176887	SOX11	655.2	-1.28	6.4E-06
ENSG00000198324	FAM109A	384.7	-1.40	6.2E-09		ENSG00000156052	GNAQ	558.8	-1.27	2.6E-04
ENSG00000168135	KCNJ4	425.1	-1.40	3.4E-04		ENSG00000141338	ABCA8	620.5	-1.27	6.1E-04
ENSG00000130600	H19	34593.2	-1.40	1.0E-02		ENSG00000198842	DUSP27	2362.0	-1.27	1.1E-07
ENSG00000049323	LTBP1	6069.3	-1.40	2.8E-06		ENSG00000151693	ASAP2	158.8	-1.27	1.8E-03
ENSG00000185737	NRG3	28.2	-1.40	4.2E-02		ENSG00000146859	TMEM140	89.8	-1.27	1.7E-02
ENSG00000114450	GNB4	246.8	-1.40	1.4E-03		ENSG00000196376	SLC35F1	261.9	-1.27	3.1E-03
ENSG00000116783	TNNI3K	563.1	-1.39	1.7E-03		ENSG00000092531	SNAP23	614.8	-1.27	3.4E-07
ENSG00000145284	SCD5	518.9	-1.39	6.1E-04		ENSG00000188215	DCUN1D3	92.0	-1.26	1.1E-03
ENSG00000106018	VIPR2	262.1	-1.39	2.0E-02		ENSG00000152503	TRIM36	121.8	-1.26	1.9E-02
ENSG00000102271	KLHL4	487.7	-1.39	1.2E-06		ENSG00000198756	COLGALT2	428.2	-1.26	4.7E-04
ENSG00000186354	C9orf47	74.5	-1.39	8.9E-04		ENSG00000114554	PLXNA1	2148.6	-1.26	1.1E-09
ENSG00000260604	RP1-140K8.5	1198.1	-1.39	1.1E-02		ENSG00000136720	HS6ST1	306.7	-1.26	1.7E-03
ENSG00000097096	SYDE2	436.6	-1.39	1.4E-05		ENSG00000106078	COBL	661.8	-1.26	3.0E-02
ENSG00000018699	TTC27	247.8	-1.38	2.6E-06		ENSG00000168246	UBTD2	533.4	-1.26	3.1E-06
ENSG00000137331	IER3	469.5	-1.38	8.5E-04		ENSG00000175920	DOK7	607.9	-1.26	1.7E-06
ENSG00000124920	MYRF	873.1	-1.38	3.0E-03		ENSG00000198088	NUP62CL	29.1	-1.25	1.9E-02
ENSG00000177374	HIC1	68.2	-1.38	2.9E-02		ENSG00000058091	CDK14	1560.1	-1.25	1.2E-05
ENSG00000204764	RANBP17	82.5	-1.38	2.3E-04		ENSG00000164024	METAP1	1222.8	-1.25	1.7E-06
ENSG00000196562	SULF2	214.2	-1.38	3.1E-02		ENSG00000027075	PRKCH	343.6	-1.25	2.6E-03
ENSG00000042781	USH2A	27.9	-1.38	2.7E-02		ENSG00000163431	LMOD1	1157.5	-1.25	1.3E-03
ENSG00000214711	CAPN14	48.3	-1.38	4.1E-03		ENSG00000139174	PRICKLE1	1115.7	-1.25	1.3E-09
ENSG00000164932	CTHRC1	29.8	-1.37	2.4E-02		ENSG00000153561	RMND5A	2826.8	-1.25	1.7E-08
ENSG00000112182	BACH2	268.4	-1.37	1.1E-04		ENSG00000177311	ZBTB38	612.4	-1.25	4.5E-06
ENSG00000107562	CXCL12	1878.8	-1.37	3.4E-02		ENSG00000151320	AKAP6	2277.4	-1.25	1.0E-04
ENSG00000004776	HSPB6	1764.3	-1.37	1.1E-02		ENSG00000138771	SHROOM3	1172.5	-1.25	1.9E-03
ENSG00000152642	GPD1L	3022.2	-1.37	3.5E-05		ENSG00000144908	ALDH1L1	53.8	-1.24	7.6E-03
ENSG00000163492	CCDC141	1727.5	-1.36	3.6E-04		ENSG00000165675	ENOX2	147.8	-1.24	8.6E-04
ENSG00000029153	ARNTL2	65.5	-1.36	2.0E-04		ENSG00000183688	FAM101B	65.8	-1.24	3.3E-03
ENSG00000271155	RP11-435O5.5	22.9	-1.35	1.7E-02		ENSG00000233836	RP11-255H23.2	39.9	-1.24	3.0E-02
ENSG00000251216	RP11-161D15.3	25.4	-1.35	1.1E-02		ENSG00000140416	TPM1	86002.2	-1.24	5.7E-06
ENSG00000078053	AMPH	215.3	-1.35	1.5E-04		ENSG00000183853	KIRREL	679.6	-1.24	5.5E-03
ENSG00000121039	RDH10	379.3	-1.34	5.0E-03		ENSG00000130119	GNL3L	139.4	-1.24	4.9E-03
ENSG00000171681	ATF7IP	810.3	-1.34	2.0E-06		ENSG00000122591	FAM126A	436.3	-1.24	6.6E-08
ENSG00000184697	CLDN6	290.5	-1.34	5.2E-03		ENSG00000137198	GMPR	561.8	-1.23	3.9E-04
ENSG00000188778	ADRB3	103.0	-1.34	2.9E-02		ENSG00000250899	RP11-253E3.3	162.3	-1.23	7.1E-04
ENSG00000156219	ART3	379.8	-1.34	3.7E-03		ENSG00000253846	PCDHGA10	65.8	-1.23	7.5E-03
ENSG00000168405	CMAHP	164.1	-1.33	1.6E-02		ENSG00000268358		28.1	-1.23	2.3E-02
ENSG00000059378	PARP12	405.0	-1.33	1.4E-02		ENSG00000178385	PLEKHM3	80.4	-1.23	2.7E-02
ENSG00000168477	TNXB	141.8	-1.33	2.0E-02		ENSG00000138316	ADAMTS14	1015.7	-1.22	6.3E-03
ENSG00000103994	ZNF106	2598.0	-1.33	2.4E-07		ENSG00000073711	PPP2R3A	1842.0	-1.22	1.1E-10
ENSG00000270959	LPP-AS2	126.9	-1.33	4.0E-05		ENSG00000197894	ADH5	2056.5	-1.22	3.1E-12
ENSG00000247081	BAALC-AS1	42.4	-1.33	7.9E-03		ENSG00000172159	FRMD3	972.8	-1.22	1.0E-06

ENSG00000260398	RP11-594N15.3	171.2	-1.22	7.3E-04		ENSG00000158008	EXTL1	323.1	-1.11	1.9E-02
ENSG00000242539	AC007620.3	58.3	-1.22	4.9E-03		ENSG00000112218	GPR63	111.6	-1.11	3.9E-04
ENSG00000124406	ATP8A1	435.8	-1.22	1.4E-02		ENSG00000171357	LURAP1	86.3	-1.11	4.5E-03
ENSG00000237463	RP11-280O1.2	71.8	-1.22	1.0E-02		ENSG00000177098	SCN4B	51.3	-1.11	2.4E-02
ENSG00000245694	CRNDE	236.1	-1.22	6.0E-05		ENSG00000270504	RP11-420L9.5	93.9	-1.11	1.9E-02
ENSG00000185483	ROR1	1845.0	-1.22	3.5E-03		ENSG00000143067	ZNF697	579.8	-1.11	1.2E-03
ENSG00000155034	FBXL18	120.0	-1.21	3.7E-03		ENSG00000074416	MGLL	333.6	-1.11	3.6E-03
ENSG00000071967	CYBRD1	189.4	-1.21	2.7E-02		ENSG00000123124	WWP1	1335.9	-1.11	6.1E-06
ENSG00000111912	NCOA7	159.5	-1.21	1.1E-03		ENSG00000170456	DENND5B	4246.7	-1.11	3.6E-05
ENSG00000115902	SLC1A4	2613.1	-1.21	1.3E-03		ENSG00000157350	ST3GAL2	1099.3	-1.10	2.4E-06
ENSG00000169247	SH3TC2	313.3	-1.21	2.9E-03		ENSG00000145375	SPATA5	52.2	-1.10	9.9E-03
ENSG00000149575	SCN2B	233.5	-1.21	4.0E-03		ENSG00000235162	C12orf75	778.0	-1.10	7.7E-05
ENSG00000166073	GPR176	114.8	-1.20	2.6E-03		ENSG00000260214		287.9	-1.10	9.1E-04
ENSG00000185630	PBX1	4819.7	-1.20	3.1E-06		ENSG00000184557	SOCS3	317.3	-1.10	4.6E-02
ENSG00000067798	NAV3	276.4	-1.20	1.0E-03		ENSG00000132256	TRIM5	278.4	-1.10	1.1E-03
ENSG00000250588	IQCJ-SCHIP1	120.2	-1.20	3.2E-03		ENSG00000112852	PCDHB2	295.1	-1.10	4.4E-03
ENSG00000140557	ST8SIA2	208.4	-1.20	1.8E-02		ENSG00000213853	EMP2	3043.1	-1.10	7.3E-07
ENSG00000137266	SLC22A23	229.6	-1.19	4.9E-02		ENSG00000196159	FAT4	466.0	-1.10	2.0E-04
ENSG00000158435	CNOT11	2701.5	-1.19	5.4E-04		ENSG00000081377	CDC14B	1417.3	-1.10	3.0E-07
ENSG00000163293	NIPAL1	158.0	-1.19	9.4E-03		ENSG00000109686	SH3D19	1786.7	-1.10	9.1E-04
ENSG00000138193	PLCE1	383.4	-1.19	4.0E-02		ENSG00000109458	GAB1	3509.0	-1.09	1.2E-09
ENSG00000100320	RBFOX2	3546.9	-1.19	6.0E-04		ENSG00000151773	CCDC122	62.4	-1.09	2.4E-03
ENSG00000183690	EFHC2	44.5	-1.19	2.1E-02		ENSG00000186615	KTN1-AS1	97.8	-1.09	7.4E-04
ENSG00000265356	RP11-17M24.1	44.5	-1.19	1.8E-02		ENSG00000157927	RADIL	338.3	-1.09	3.4E-03
ENSG00000186591	UBE2H	5342.2	-1.18	2.4E-05		ENSG00000162757	C1orf74	70.5	-1.09	2.2E-03
ENSG00000198399	ITSN2	3190.4	-1.18	4.1E-04		ENSG00000166343	MSS51	532.0	-1.09	2.8E-06
ENSG00000006007	GDE1	1175.5	-1.18	9.9E-10		ENSG00000109452	INPP4B	1518.7	-1.09	3.0E-02
ENSG00000100767	PAPLN	248.0	-1.18	3.4E-02		ENSG00000128578	STRIP2	5048.5	-1.09	2.9E-05
ENSG00000123689	G0S2	1646.2	-1.18	2.6E-02		ENSG00000171444	MCC	2803.0	-1.09	1.4E-03
ENSG00000075073	TACR2	50.1	-1.18	7.3E-03		ENSG00000196588	MKL1	1165.6	-1.09	4.2E-04
ENSG00000173705	SUSD5	151.8	-1.17	2.6E-02		ENSG00000234961	RP11-124N14.3	30.5	-1.09	4.1E-02
ENSG00000258987	RP11-131H24.4	46.0	-1.17	2.4E-02		ENSG00000150347	ARID5B	420.2	-1.09	1.2E-02
ENSG00000168334	XIRP1	8142.0	-1.17	2.3E-06		ENSG00000164684	ZNF704	2076.9	-1.08	1.1E-03
ENSG00000247934	RP11-967K21.1	21.1	-1.17	3.8E-02		ENSG00000138604	GLCE	437.7	-1.08	1.1E-05
ENSG00000113749	HRH2	603.8	-1.17	2.0E-02		ENSG00000165617	DACT1	855.3	-1.08	8.1E-03
ENSG00000138642	HERC6	360.9	-1.17	4.4E-02		ENSG00000177354	C10orf71	585.8	-1.08	3.8E-05
ENSG00000169871	TRIM56	183.5	-1.17	3.3E-02		ENSG00000118922	KLF12	1247.1	-1.08	2.6E-04
ENSG00000166326	TRIM44	802.1	-1.17	1.9E-03		ENSG00000096060	FKBP5	973.2	-1.08	1.9E-02
ENSG00000089472	HEPH	6699.5	-1.17	3.0E-08		ENSG00000189409	MMP23B	108.0	-1.08	1.2E-02
ENSG00000162924	REL	56.5	-1.16	6.8E-03		ENSG00000141627	DYM	685.4	-1.08	2.0E-04
ENSG00000172954	LCLAT1	591.1	-1.16	1.2E-04		ENSG00000152492	CCDC50	1494.4	-1.07	1.7E-08
ENSG00000180914	OXTR	298.3	-1.16	2.8E-06		ENSG00000136153	LMO7	4701.7	-1.07	4.7E-05
ENSG00000157216	SSBP3	711.6	-1.16	2.3E-03		ENSG00000111077	TNS2	1441.5	-1.07	3.7E-03
ENSG00000135074	ADAM19	1348.8	-1.16	1.4E-02		ENSG00000154122	ANKH	3384.2	-1.07	1.2E-05
ENSG00000197991	PCDH20	1296.8	-1.16	4.4E-04		ENSG00000143384	MCL1	2483.4	-1.07	9.7E-05
ENSG00000067082	KLF6	753.6	-1.16	2.2E-03		ENSG00000122550	KLHL7	1794.9	-1.07	1.1E-07
ENSG00000130429	ARPC1B	266.5	-1.15	1.7E-02		ENSG00000134313	KIDINS220	5926.2	-1.06	1.4E-03
ENSG00000107771	CCSER2	2130.9	-1.15	1.9E-05		ENSG00000198964	SGMS1	939.3	-1.06	2.6E-03
ENSG00000177570	SAMD12	479.7	-1.15	8.9E-06		ENSG00000143466		54.6	-1.06	2.4E-02
ENSG00000111371	SLC38A1	5041.4	-1.15	5.5E-03		ENSG00000165806	CASP7	471.3	-1.06	6.0E-04
ENSG00000182985	CADM1	1814.3	-1.15	1.3E-06		ENSG00000168675	LDLRAD4	804.1	-1.06	7.5E-06
ENSG00000184304	PRKD1	158.4	-1.15	4.7E-03		ENSG00000137962	ARHGAP29	1182.6	-1.06	2.5E-03
ENSG00000168487	BMP1	725.9	-1.14	1.4E-04		ENSG00000113248	PCDHB15	186.0	-1.06	3.0E-03
ENSG00000146151	HMGCLL1	368.1	-1.14	3.3E-03		ENSG00000109670	FBXW7	713.5	-1.06	6.4E-06
ENSG00000213190	MLLT11	1544.6	-1.14	1.5E-03		ENSG00000139350	NEDD1	614.2	-1.06	1.6E-07
ENSG00000172458	IL17D	117.2	-1.13	1.5E-02		ENSG00000139116	KIF21A	2027.5	-1.05	1.3E-04
ENSG00000225345	SNX18P3	38.9	-1.13	1.6E-02		ENSG00000082781	ITGB5	1343.2	-1.05	6.2E-03
ENSG00000155380	SLC16A1	6329.2	-1.13	1.0E-04		ENSG00000164576	SAP30L	847.1	-1.05	6.5E-07
ENSG00000163075	CFAP221	68.9	-1.13	2.2E-03		ENSG00000165118	C9orf64	129.8	-1.05	9.2E-04
ENSG00000127946	HIP1	937.6	-1.13	1.3E-02		ENSG00000070778	PTPN21	2428.3	-1.04	2.8E-05
ENSG00000143499	SMYD2	1489.4	-1.12	4.8E-04		ENSG00000104313	EYA1	240.0	-1.04	2.6E-02
ENSG00000174306	ZHX3	488.7	-1.12	1.0E-04		ENSG00000162692	VCAM1	1706.6	-1.04	3.5E-02
ENSG00000162783	IER5	282.7	-1.12	7.6E-05		ENSG00000113580	NR3C1	1026.3	-1.04	9.3E-04
ENSG00000196154	S100A4	233.4	-1.12	1.9E-02		ENSG00000105559	PLEKHA4	1123.1	-1.04	9.2E-03
ENSG00000152779	SLC16A12	686.2	-1.12	5.2E-05		ENSG00000166317	SYNPO2L	9059.2	-1.04	2.5E-02
ENSG00000105926	MPP6	106.7	-1.12	3.6E-02		ENSG00000128656	CHN1	498.4	-1.04	2.2E-04
ENSG00000128274	A4GALT	1889.1	-1.12	9.0E-07		ENSG00000166173	LARP6	646.8	-1.04	2.0E-05
ENSG00000175115	PACS1	3734.8	-1.11	2.5E-06		ENSG00000115896	PLCL1	669.0	-1.04	1.2E-03
ENSG00000107438	PDLIM1	3587.0	-1.11	1.1E-05		ENSG00000152104	PTPN14	455.9	-1.03	3.6E-03
ENSG00000272373		33.2	-1.11	4.5E-02		ENSG00000182247	UBE2E2	856.5	-1.03	1.3E-03
ENSG00000251664	PCDHA12	117.5	-1.11	1.1E-02		ENSG00000265519	CTD-3157E16.1	26.9	-1.03	4.9E-02
ENSG00000018408	WWTR1	2390.5	-1.11	2.4E-07		ENSG00000119471	HSDL2	1964.5	-1.03	3.7E-06

ENSG00000176771	NCKAP5	60.3	-1.03	9.7E-03		ENSG00000153721	CNKSR3	399.2	-1.02	2.8E-03
ENSG00000079150	FKBP7	71.1	-1.03	3.4E-02		ENSG00000101605	MYOM1	21491.6	-1.02	1.0E-04
ENSG00000164211	STARD4	6338.9	-1.03	3.8E-07		ENSG00000196843	ARID5A	411.2	-1.01	2.2E-02
ENSG00000119699	TGFB3	124.4	-1.03	3.6E-02		ENSG00000132819	RBM38	2375.9	-1.01	6.4E-06
ENSG00000164574	GALNT10	278.4	-1.03	1.1E-02		ENSG00000168502	MTCL1	146.4	-1.01	4.1E-02
ENSG00000261788		1041.3	-1.03	5.3E-03		ENSG00000186187	ZNRF1	446.2	-1.01	2.6E-05
ENSG00000260482	CTD-2196E14.9	77.9	-1.03	4.0E-02		ENSG00000153814	JAZF1	1075.4	-1.01	8.6E-05
ENSG00000160392	C19orf47	551.9	-1.03	3.6E-06		ENSG00000140600	SH3GL3	245.7	-1.01	3.7E-02
ENSG00000121210	KIAA0922	552.8	-1.02	2.0E-04		ENSG00000065882	TBC1D1	2052.6	-1.01	1.4E-05
ENSG00000068697	LAPTM4A	5317.1	-1.02	1.7E-08		ENSG00000132669	RIN2	804.5	-1.01	4.3E-03
ENSG00000119866	BCL11A	412.8	-1.02	1.3E-05		ENSG00000169926	KLF13	1296.9	-1.00	1.2E-02
ENSG00000137575	SDCBP	2335.6	-1.02	3.0E-04		ENSG00000175155	YPEL2	1391.0	-1.00	4.2E-03
ENSG00000113272	THG1L	130.6	-1.02	2.4E-03		ENSG00000180263	FGD6	966.0	-1.00	1.5E-05
ENSG00000077522	ACTN2	31470.5	-1.02	5.7E-04						

(B) List of 1,037 transcripts with significantly higher expression in iPSC-aCMs compared to iPSC-vCMs.

Ensembl ID	**Gene name**	**Base mean**	**log2 (aCMs/ vCMs)**	**adj *P* value**		**Ensembl ID**	**Gene name**	**Base mean**	**log2 (aCMs/ vCMs)**	**adj *P* value**
ENSG00000066248	NGEF	88.2	4.35	9.0E-25		ENSG00000235890	TSPEAR-AS1	197.9	2.90	1.1E-10
ENSG00000149927	DOC2A	195.3	4.28	1.1E-26		ENSG00000165548	TMEM63C	77.1	2.88	6.3E-13
ENSG00000168779	SHOX2	971.6	4.27	2.2E-17		ENSG00000146648	EGFR	616.7	2.87	1.3E-32
ENSG00000165841	CYP2C19	12.8	4.09	2.2E-08		ENSG00000183454	GRIN2A	27.3	2.83	3.0E-06
ENSG00000180537	RNF182	158.3	4.06	3.5E-14		ENSG00000154162	CDH12	223.3	2.83	1.1E-06
ENSG00000104725		184.2	4.02	1.2E-16		ENSG00000233429	HOTAIRM1	128.0	2.82	1.9E-10
ENSG00000157087	ATP2B2	210.4	3.97	5.3E-21		ENSG00000105650	PDE4C	265.0	2.82	2.1E-06
ENSG00000119121	TRPM6	25.8	3.94	3.0E-10		ENSG00000268518	CTD-2545M3.8	32944.6	2.81	4.3E-14
ENSG00000126733	DACH2	32.2	3.72	7.1E-13		ENSG00000229031	RP11-666G4.1	20.4	2.80	6.1E-04
ENSG00000145708	CRHBP	37.8	3.71	4.2E-10		ENSG00000126218	F10	167.1	2.79	3.2E-15
ENSG00000196361	ELAVL3	14.8	3.68	1.9E-08		ENSG00000231431	FAR2P4	16.9	2.79	4.2E-05
ENSG00000105996	HOXA2	66.1	3.65	3.7E-09		ENSG00000174326	SLC16A11	19.9	2.78	3.6E-07
ENSG00000140279	DUOX2	318.0	3.64	6.4E-19		ENSG00000239402	CYP4F62P	9.6	2.78	1.7E-04
ENSG00000163814	CDCP1	213.4	3.61	5.1E-13		ENSG00000261253	AC137932.6	65.2	2.77	2.8E-06
ENSG00000139767	SRRM4	129.4	3.59	9.9E-16		ENSG00000237512	UNC5B-AS1	446.8	2.77	5.4E-07
ENSG00000103154	NECAB2	45.6	3.58	1.6E-10		ENSG00000154316	TDH	14.4	2.76	4.3E-06
ENSG00000175894	TSPEAR	912.0	3.44	8.3E-10		ENSG00000170439	METTL7B	206.3	2.76	1.4E-13
ENSG00000140274	DUOXA2	42.9	3.44	7.7E-12		ENSG00000111728	ST8SIA1	70.6	2.76	3.3E-08
ENSG00000253552	HOXA-AS2	75.9	3.42	2.9E-09		ENSG00000170324	FRMPD2	85.4	2.75	5.4E-05
ENSG00000228477	RP3-342P20.2	15.5	3.42	1.1E-05		ENSG00000085552	IGSF9	2004.8	2.74	1.5E-08
ENSG00000075043	KCNQ2	209.1	3.40	1.7E-18		ENSG00000163239	TDRD10	11.8	2.74	2.0E-04
ENSG00000073734	ABCB11	25.1	3.38	5.1E-09		ENSG00000102878	HSF4	870.3	2.74	1.7E-08
ENSG00000105997	HOXA3	221.5	3.35	2.9E-09		ENSG00000187210	GCNT1	135.8	2.74	1.2E-11
ENSG00000189410	SH2D5	22.5	3.33	3.5E-10		ENSG00000137463	MGARP	272.1	2.73	2.6E-11
ENSG00000166589	CDH16	21.9	3.28	7.3E-09		ENSG00000259910	RP11-616M22.2	24.4	2.73	6.7E-07
ENSG00000168824	D4S234E	415.6	3.28	1.3E-26		ENSG00000172828	CES3	189.8	2.73	1.5E-20
ENSG00000053108	FSTL4	34.9	3.19	3.2E-08		ENSG00000255090	MIR100HG	21.1	2.72	3.2E-05
ENSG00000214402	LCNL1	360.9	3.19	3.5E-17		ENSG00000235033	RP11-61I13.3	33.3	2.72	5.0E-07
ENSG00000197576	HOXA4	74.7	3.16	2.4E-07		ENSG00000130595	TNNT3	48.7	2.72	2.5E-06
ENSG00000171303	KCNK3	548.8	3.16	1.4E-13		ENSG00000198732	SMOC1	83.3	2.72	2.1E-05
ENSG00000260403	RP11-616M22.1	44.0	3.15	1.7E-08		ENSG00000240253	FAR2P3	11.1	2.72	2.1E-04
ENSG00000116176	TPSG1	49.0	3.14	1.0E-07		ENSG00000103546	SLC6A2	46.5	2.71	1.1E-05
ENSG00000248441	LINC01197	25.8	3.12	1.5E-06		ENSG00000175745	NR2F1	484.9	2.71	2.8E-08
ENSG00000166145	SPINT1	605.8	3.10	9.5E-16		ENSG00000119535	CSF3R	35.2	2.69	6.4E-07
ENSG00000141750	STAC2	141.4	3.10	3.2E-10		ENSG00000130037	KCNA5	1013.5	2.69	4.2E-07
ENSG00000146530	VWDE	1284.4	3.10	6.6E-19		ENSG00000163053	SLC16A14	321.2	2.66	4.7E-11
ENSG00000163630	SYNPR	27.7	3.06	1.2E-07		ENSG00000163531	NFASC	1144.4	2.65	3.1E-06
ENSG00000249992	TMEM158	17.4	3.05	4.4E-07		ENSG00000179242	CDH4	154.0	2.64	4.8E-06
ENSG00000156298	TSPAN7	410.1	3.02	1.3E-18		ENSG00000119715	ESRRB	232.9	2.64	4.3E-09
ENSG00000254815	RP11-496I9.1	195.6	3.02	1.6E-14		ENSG00000184613	NELL2	297.9	2.63	2.8E-05
ENSG00000074211	PPP2R2C	99.6	2.99	1.3E-06		ENSG00000005961	ITGA2B	155.3	2.63	3.5E-17
ENSG00000248746	ACTN3	193.8	2.98	6.7E-06		ENSG00000108849	PPY	9.6	2.62	1.3E-03
ENSG00000180815	MAP3K15	194.5	2.98	1.1E-06		ENSG00000138944	KIAA1644	289.9	2.60	2.7E-09
ENSG00000155980	KIF5A	76.0	2.97	2.8E-10		ENSG00000146215	CRIP3	189.6	2.60	1.6E-05
ENSG00000161509	GRIN2C	25.1	2.96	4.5E-08		ENSG00000262920	RP11-1260E13.1	8.7	2.59	1.2E-03
ENSG00000005020	SKAP2	488.1	2.96	1.3E-10		ENSG00000132692	BCAN	8.0	2.59	7.2E-04
ENSG00000107317	PTGDS	3700.7	2.96	1.5E-21		ENSG00000142765	SYTL1	132.1	2.59	1.9E-13
ENSG00000221986	MYBPHL	898.4	2.95	2.3E-07		ENSG00000148926	ADM	2016.2	2.58	3.3E-08
ENSG00000104722	NEFM	54.4	2.94	3.3E-09		ENSG00000183091	NEB	288.9	2.57	2.1E-10
ENSG00000232002	AC093642.6	27.8	2.91	7.9E-05		ENSG00000130558	OLFM1	191.8	2.57	2.3E-06
ENSG00000187957	DNER	85.3	2.91	4.2E-08		ENSG00000106004	HOXA5	40.1	2.57	2.7E-04

ENSG00000076864	RAP1GAP	473.2	2.57	1.7E-15		ENSG00000136542	GALNT5	275.7	2.26	8.2E-07
ENSG00000060709	RIMBP2	37.5	2.56	2.8E-05		ENSG00000132872	SYT4	7.7	2.26	8.1E-03
ENSG00000199157	MIR208A	8.0	2.54	5.4E-04		ENSG00000140961	OSGIN1	43.2	2.23	1.8E-04
ENSG00000165899	OTOGL	561.2	2.54	3.9E-07		ENSG00000164078	MST1R	7.9	2.23	5.4E-03
ENSG00000102924	CBLN1	119.8	2.54	1.0E-04		ENSG00000102003	SYP	38.3	2.23	1.8E-04
ENSG00000150045	KLRF1	20.6	2.54	1.1E-04		ENSG00000183914	DNAH2	154.5	2.22	1.2E-05
ENSG00000136999	NOV	60.3	2.53	1.1E-08		ENSG00000091409	ITGA6	278.3	2.22	3.2E-13
ENSG00000259666	LINGO1-AS1	50.5	2.51	3.4E-04		ENSG00000181773	GPR3	38.6	2.22	5.6E-04
ENSG00000157388	CACNA1D	923.2	2.51	4.7E-12		ENSG00000261159	RP11-723O4.9	10.3	2.22	4.3E-03
ENSG00000112232	KHDRBS2	28.0	2.49	6.5E-06		ENSG00000145808	ADAMTS19	931.9	2.22	2.1E-08
ENSG00000164683	HEY1	210.8	2.49	2.2E-18		ENSG00000108924	HLF	24.9	2.21	5.4E-04
ENSG00000157093	LYZL4	21.5	2.48	3.7E-04		ENSG00000170074	FAM153A	154.0	2.21	7.0E-08
ENSG00000118702	GHRH	128.7	2.48	3.7E-03		ENSG00000157445	CACNA2D3	114.2	2.21	1.7E-06
ENSG00000168071	CCDC88B	218.9	2.48	2.6E-13		ENSG00000165973	NELL1	152.6	2.20	9.4E-05
ENSG00000117834	SLC5A9	48.1	2.48	2.6E-05		ENSG00000171798	KNDC1	213.6	2.20	7.8E-14
ENSG00000174640	SLCO2A1	119.4	2.48	5.4E-05		ENSG00000167617	CDC42EP5	286.7	2.19	2.2E-13
ENSG00000260682	RN7SKP176	151.4	2.48	5.8E-05		ENSG00000162782	TDRD5	57.3	2.19	1.7E-03
ENSG00000174429	ABRA	161.7	2.47	9.8E-06		ENSG00000003987	MTMR7	124.7	2.19	1.3E-09
ENSG00000231443	AC024937.6	16.6	2.46	8.3E-05		ENSG00000223764	RP11-54O7.3	103.8	2.18	8.0E-08
ENSG00000181085	MAPK15	38.1	2.45	5.1E-08		ENSG00000235407	RP11-470L19.2	91.6	2.18	1.7E-03
ENSG00000105251	SHD	2452.2	2.45	2.1E-06		ENSG00000169291	SHE	33.3	2.17	4.5E-04
ENSG00000115705	TPO	58.3	2.45	3.1E-05		ENSG00000185522	LMNTD2	178.0	2.17	2.6E-08
ENSG00000153237	CCDC148	72.4	2.45	5.8E-09		ENSG00000087085	ACHE	164.9	2.17	1.1E-08
ENSG00000166763	STRCP1	11.7	2.45	2.9E-04		ENSG00000142606	MMEL1	9.9	2.15	4.5E-03
ENSG00000165863	C10orf82	20.5	2.44	2.1E-03		ENSG00000101180	HRH3	8.9	2.15	8.3E-03
ENSG00000182511	FES	49.6	2.43	2.9E-10		ENSG00000175147	TMEM51-AS1	25.4	2.14	2.2E-03
ENSG00000139219	COL2A1	16323.8	2.42	3.5E-03		ENSG00000124507	PACSIN1	360.1	2.13	3.4E-14
ENSG00000115457	IGFBP2	6773.9	2.42	1.1E-15		ENSG00000170091	HMP19	24.6	2.13	1.3E-04
ENSG00000079101	CLUL1	31.6	2.42	1.2E-06		ENSG00000184058	TBX1	41.2	2.13	2.6E-03
ENSG00000186994	KANK3	24.5	2.41	2.8E-05		ENSG00000266714	MYO15B	2356.6	2.13	9.6E-09
ENSG00000198915	RASGEF1A	7.1	2.41	2.6E-03		ENSG00000237940	AC093642.3	21.6	2.12	3.1E-04
ENSG00000142408	CACNG8	44.8	2.41	7.7E-07		ENSG00000240194	CYMP	70.1	2.12	5.6E-03
ENSG00000117115	PADI2	1895.3	2.40	1.3E-05		ENSG00000197467	COL13A1	473.8	2.12	3.5E-06
ENSG00000125895	TMEM74B	391.3	2.39	9.5E-08		ENSG00000066468	FGFR2	553.7	2.11	1.3E-04
ENSG00000125378	BMP4	243.7	2.39	5.0E-10		ENSG00000142621	FHAD1	9.4	2.11	4.7E-03
ENSG00000232176	RP11-146N23.1	12.7	2.39	5.3E-04		ENSG00000095397	DFNB31	537.2	2.11	1.8E-14
ENSG00000197943	PLCG2	803.4	2.39	1.2E-06		ENSG00000105376	ICAM5	843.9	2.11	7.4E-08
ENSG00000174672	BRSK2	348.6	2.39	3.0E-16		ENSG00000214140	PRCD	81.1	2.10	1.2E-06
ENSG00000105825	TFPI2	419.3	2.38	3.7E-08		ENSG00000124429	POF1B	214.4	2.09	1.2E-05
ENSG00000196668	LINC00173	80.8	2.38	3.6E-12		ENSG00000254561	RP11-196E1.3	11.0	2.09	7.8E-03
ENSG00000144596	GRIP2	45.4	2.38	2.2E-05		ENSG00000100024	UPB1	125.9	2.09	8.5E-05
ENSG00000137204	SLC22A7	22.4	2.37	1.7E-03		ENSG00000157693	C9orf91	165.8	2.09	9.8E-10
ENSG00000128564	VGF	15.2	2.37	2.5E-03		ENSG00000085741	WNT11	331.6	2.08	2.2E-10
ENSG00000141655	TNFRSF11A	46.6	2.37	2.8E-08		ENSG00000107623		84.0	2.08	2.0E-03
ENSG00000260001	TGFBR3L	51.7	2.37	8.0E-06		ENSG00000179915	NRXN1	653.4	2.08	1.3E-05
ENSG00000260284	TPSP2	10.7	2.37	1.5E-03		ENSG00000179111	HES7	101.5	2.07	1.4E-07
ENSG00000197971	MBP	143.7	2.37	5.8E-05		ENSG00000099994	SUSD2	606.2	2.07	1.6E-16
ENSG00000148798	INA	47.9	2.36	2.8E-04		ENSG00000186297	GABRA5	7.0	2.07	1.1E-02
ENSG00000197471	SPN	77.9	2.35	1.9E-08		ENSG00000156299	TIAM1	267.4	2.07	1.4E-08
ENSG00000255020	AF131216.5	17.8	2.35	2.7E-05		ENSG00000261143	ADAMTS7P3	68.0	2.07	7.7E-05
ENSG00000248309	MEF2C-AS1	12.8	2.35	2.5E-04		ENSG00000149926	FAM57B	11.7	2.06	6.7E-03
ENSG00000253807	LINC01170	24.9	2.35	3.8E-04		ENSG00000165868	HSPA12A	249.0	2.06	1.1E-06
ENSG00000052344	PRSS8	214.0	2.35	7.4E-08		ENSG00000244459	RP11-1398P2.1	12.1	2.06	1.2E-02
ENSG00000074317	SNCB	20.9	2.35	1.7E-03		ENSG00000105696	TMEM59L	147.2	2.06	7.8E-08
ENSG00000160712	IL6R	262.1	2.34	5.7E-11		ENSG00000168993	CPLX1	14.7	2.06	9.2E-03
ENSG00000090539	CHRD	23.7	2.34	1.8E-05		ENSG00000229759	MRPS18AP1	9.3	2.06	1.2E-02
ENSG00000110675	ELMOD1	21.0	2.33	3.7E-05		ENSG00000112812	PRSS16	32.2	2.05	2.9E-04
ENSG00000170049	KCNAB3	156.4	2.33	3.1E-10		ENSG00000181408	UTS2R	9.3	2.05	1.7E-02
ENSG00000225968	ELFN1	655.7	2.33	3.6E-07		ENSG00000204928	GRXCR2	7.1	2.05	1.9E-02
ENSG00000134853	PDGFRA	841.2	2.32	2.4E-07		ENSG00000127585	FBXL16	56.6	2.05	2.1E-04
ENSG00000101204	CHRNA4	8.2	2.31	6.9E-03		ENSG00000109832	DDX25	12.8	2.05	1.3E-03
ENSG00000134594	RAB33A	196.9	2.31	6.5E-10		ENSG00000105639	JAK3	84.9	2.05	4.3E-06
ENSG00000260432		6.8	2.31	4.3E-03		ENSG00000269113	TRABD2B	218.3	2.04	2.7E-05
ENSG00000181031	RPH3AL	83.2	2.30	2.5E-05		ENSG00000169918	OTUD7A	12.8	2.04	4.9E-03
ENSG00000017373		235.9	2.30	1.4E-13		ENSG00000177989	ODF3B	52.2	2.04	5.5E-07
ENSG00000196358	NTNG2	160.6	2.30	4.1E-07		ENSG00000254154	RP4-798P15.3	11.1	2.04	2.7E-03
ENSG00000103175	WFDC1	14.5	2.29	4.2E-04		ENSG00000228923	AP000355.2	7.8	2.04	1.9E-02
ENSG00000163235	TGFA	159.0	2.29	7.4E-03		ENSG00000178038	ALS2CL	561.1	2.03	3.5E-09
ENSG00000134317	GRHL1	44.5	2.28	8.1E-06		ENSG00000227184		149.2	2.03	2.2E-16
ENSG00000164076	CAMKV	7.4	2.28	8.3E-03		ENSG00000119547	ONECUT2	20.6	2.03	5.3E-03
ENSG00000102109	PCSK1N	588.5	2.27	1.6E-07		ENSG00000145358	DDIT4L	281.4	2.02	7.8E-04
ENSG00000131459	GFPT2	163.6	2.26	3.7E-14		ENSG00000261183	RP11-532F12.5	33.1	2.02	2.2E-03

ENSG00000269028	MTRNR2L12	61.9	2.01	1.9E-04		ENSG00000231663	RP5-827C21.4	30.7	1.84	5.1E-05
ENSG00000197616	MYH6	243348.1	2.01	1.7E-02		ENSG00000229344	RP5-857K21.7	54.6	1.84	3.9E-04
ENSG00000157214	STEAP2	664.3	2.01	1.1E-06		ENSG00000119283	TRIM67	11.2	1.84	1.2E-02
ENSG00000271387	RP11-382D12.2	9.1	2.01	7.3E-03		ENSG00000205517	RGL3	20.7	1.83	1.4E-03
ENSG00000081479	LRP2	188.9	2.01	1.3E-03		ENSG00000040608	RTN4R	132.4	1.83	1.7E-05
ENSG00000087250	MT3	255.2	2.00	3.3E-03		ENSG00000185551	NR2F2	3152.9	1.83	2.5E-04
ENSG00000196557	CACNA1H	926.6	2.00	4.2E-08		ENSG00000102934	PLLP	24.0	1.83	3.3E-03
ENSG00000137936	BCAR3	166.2	2.00	1.2E-06		ENSG00000156535	CD109	1746.0	1.83	1.8E-05
ENSG00000151025	GPR158	69.0	1.99	4.4E-05		ENSG00000264329	MIR3911	13.8	1.83	4.1E-03
ENSG00000260807	RP11-161M6.2	396.7	1.99	1.9E-06		ENSG00000163462	TRIM46	36.4	1.83	8.0E-04
ENSG00000109472	CPE	2305.6	1.99	1.6E-10		ENSG00000050767	COL23A1	1632.8	1.82	1.1E-05
ENSG00000100604	CHGA	16.7	1.99	2.0E-02		ENSG00000100842	EFS	314.5	1.82	1.3E-10
ENSG00000185924	RTN4RL1	270.7	1.98	4.6E-07		ENSG00000116661	FBXO2	194.1	1.82	4.9E-10
ENSG00000130649	CYP2E1	183.7	1.98	4.5E-09		ENSG00000155760	FZD7	738.7	1.82	5.1E-05
ENSG00000083067	TRPM3	36.9	1.98	2.9E-05		ENSG00000105792	CFAP69	122.7	1.81	2.0E-06
ENSG00000138670	RASGEF1B	159.4	1.98	4.2E-08		ENSG00000005059	CCDC109B	21.0	1.81	4.9E-03
ENSG00000185988	PLK5	13.3	1.97	3.6E-03		ENSG00000105991	HOXA1	25.4	1.81	3.7E-03
ENSG00000236714	AC005592.1	159.3	1.97	4.3E-03		ENSG00000271086	NAMA	6.9	1.81	2.3E-02
ENSG00000167525	PROCA1	256.1	1.97	6.0E-07		ENSG00000186715	MST1L	23.9	1.81	3.1E-04
ENSG00000214290	COLCA2	23.1	1.96	2.0E-03		ENSG00000178222	RNF212	60.2	1.81	2.0E-05
ENSG00000142235	LMTK3	153.4	1.96	4.3E-08		ENSG00000109610	SOD3	688.5	1.81	2.7E-05
ENSG00000114638	UPK1B	107.4	1.96	9.8E-06		ENSG00000176692	FOXC2	23.3	1.81	1.7E-02
ENSG00000068831	RASGRP2	584.8	1.96	3.5E-12		ENSG00000163873	GRIK3	8.0	1.81	4.4E-02
ENSG00000188993	LRRC66	23.9	1.96	1.5E-03		ENSG00000134253	TRIM45	411.9	1.81	1.4E-08
ENSG00000101282	RSPO4	19.2	1.96	1.7E-03		ENSG00000105278	ZFR2	26.6	1.80	1.2E-04
ENSG00000186326	RGS9BP	39.8	1.95	2.8E-06		ENSG00000126217	MCF2L	715.4	1.80	2.7E-08
ENSG00000225889	AC074289.1	9.8	1.94	5.8E-03		ENSG00000101096	NFATC2	658.3	1.80	5.3E-10
ENSG00000196155	PLEKHG4	61.2	1.94	1.7E-08		ENSG00000258947	TUBB3	22.2	1.80	1.4E-03
ENSG00000230006	ANKRD36BP2	9.8	1.94	4.9E-03		ENSG00000183615	FAM167B	28.3	1.80	1.0E-04
ENSG00000176678	FOXL1	17.7	1.94	7.6E-03		ENSG00000167964	RAB26	168.5	1.80	5.4E-07
ENSG00000178162	FAR2P2	39.7	1.93	4.8E-04		ENSG00000188672	RHCE	14.9	1.79	3.8E-03
ENSG00000100968	NFATC4	1120.0	1.93	8.3E-10		ENSG00000141639	MAPK4	1169.8	1.79	5.4E-05
ENSG00000181652	ATG9B	344.9	1.93	4.3E-03		ENSG00000186301	MST1P2	27.8	1.79	1.7E-04
ENSG00000253304	TMEM200B	52.8	1.93	3.8E-03		ENSG00000170545	SMAGP	27.3	1.78	8.5E-05
ENSG00000074047	GLI2	148.8	1.93	7.9E-11		ENSG00000167680	SEMA6B	512.8	1.78	3.7E-12
ENSG00000205786	LINC01531	113.9	1.92	3.8E-03		ENSG00000162989	KCNJ3	965.8	1.78	2.3E-04
ENSG00000183837	PNMA3	71.1	1.92	1.2E-03		ENSG00000126583	PRKCG	12.9	1.78	5.3E-03
ENSG00000198590	C3orf35	37.6	1.92	8.5E-05		ENSG00000164588	HCN1	240.9	1.78	1.9E-06
ENSG00000101197	BIRC7	16.0	1.92	1.9E-02		ENSG00000141404	GNAL	1117.1	1.78	4.2E-02
ENSG00000164199	ADGRV1	101.4	1.92	1.4E-03		ENSG00000133808	MICALCL	51.5	1.77	1.4E-05
ENSG00000159409	CELF3	12.6	1.91	1.9E-02		ENSG00000160111	CPAMD8	113.6	1.77	2.4E-05
ENSG00000122035	RASL11A	115.6	1.91	2.0E-06		ENSG00000166979	EVA1C	51.6	1.77	4.7E-03
ENSG00000106948	AKNA	563.5	1.91	8.0E-10		ENSG00000087258	GNAO1	977.1	1.77	1.2E-03
ENSG00000166002	SMCO4	296.8	1.91	1.2E-08		ENSG00000210100	MT-TI	69.7	1.76	1.3E-03
ENSG00000116254	CHD5	13.7	1.90	6.3E-03		ENSG00000215529	EFCAB8	7.2	1.76	4.9E-02
ENSG00000185818	NAT8L	605.5	1.90	1.3E-11		ENSG00000198719	DLL1	74.8	1.76	2.1E-03
ENSG00000198547	C20orf203	41.1	1.90	1.4E-03		ENSG00000168350	DEGS2	31.2	1.76	3.5E-02
ENSG00000128683	GAD1	76.7	1.89	4.6E-03		ENSG00000162998	FRZB	282.3	1.76	1.5E-08
ENSG00000182912	TSPEAR-AS2	166.2	1.89	4.4E-05		ENSG00000214279	SCART1	203.8	1.75	7.1E-09
ENSG00000007402	CACNA2D2	1198.3	1.89	9.5E-04		ENSG00000126259	KIRREL2	10.9	1.75	1.6E-02
ENSG00000170382	LRRN2	234.2	1.88	1.8E-03		ENSG00000215018	COL28A1	28.5	1.75	1.4E-03
ENSG00000127561	SYNGR3	340.8	1.88	5.6E-08		ENSG00000007001	UPP2	7.2	1.74	4.9E-02
ENSG00000113231	PDE8B	644.6	1.88	2.9E-04		ENSG00000230970	HHATL-AS1	14.2	1.74	6.7E-03
ENSG00000242866	STRC	13.5	1.88	1.5E-02		ENSG00000142609	CFAP74	16.2	1.74	1.8E-02
ENSG00000105717	PBX4	29.9	1.88	2.4E-04		ENSG00000249626	RP11-496H1.1	16.0	1.73	1.0E-02
ENSG00000182230	FAM153B	196.6	1.88	2.4E-03		ENSG00000156886	ITGAD	18.6	1.73	1.3E-02
ENSG00000125510	OPRL1	102.2	1.87	3.6E-05		ENSG00000143994	ABHD1	21.0	1.73	6.7E-03
ENSG00000104848	KCNA7	21.2	1.87	5.7E-03		ENSG00000182472	CAPN12	47.6	1.73	2.3E-03
ENSG00000180447	GAS1	481.2	1.87	2.6E-03		ENSG00000188522	FAM83G	93.3	1.72	1.1E-04
ENSG00000142634	EFHD2	677.2	1.87	8.1E-05		ENSG00000155974	GRIP1	277.1	1.72	2.1E-07
ENSG00000163536	SERPINI1	1392.2	1.87	1.8E-05		ENSG00000179023	KLHDC7A	8.6	1.71	4.2E-02
ENSG00000010282	HHATL	5122.9	1.87	3.3E-10		ENSG00000074966	TXK	15.1	1.71	5.3E-03
ENSG00000105255	FSD1	53.9	1.86	1.5E-04		ENSG00000183508	FAM46C	63.6	1.71	6.0E-03
ENSG00000159248	GJD2	33.8	1.86	1.3E-02		ENSG00000092529	CAPN3	257.9	1.71	8.6E-06
ENSG00000232237	ASCL5	8.1	1.85	1.7E-02		ENSG00000223756	TSSC2	34.0	1.70	2.0E-04
ENSG00000185669	SNAI3	67.3	1.85	1.3E-05		ENSG00000204018		168.1	1.70	4.6E-03
ENSG00000183421	RIPK4	77.5	1.85	6.6E-05		ENSG00000177108	ZDHHC22	23.3	1.70	1.3E-02
ENSG00000178718	RPP25	138.6	1.85	1.1E-06		ENSG00000257556	RP11-44N21.1	33.2	1.70	3.7E-04
ENSG00000271952	RP11-245G13.2	36.5	1.85	9.3E-03		ENSG00000204442	FAM155A	175.2	1.70	2.7E-05
ENSG00000148600	CDHR1	42.6	1.85	2.7E-05		ENSG00000182389	CACNB4	21.3	1.69	1.5E-02
ENSG00000107968	MAP3K8	71.7	1.84	1.9E-07		ENSG00000073737	DHRS9	170.7	1.69	1.6E-02
ENSG00000131242	RAB11FIP4	101.0	1.84	2.5E-04		ENSG00000203301		6.8	1.69	3.2E-02

ENSG00000161270	NPHS1	99.4	1.69	5.1E-05		ENSG00000229727	AC013460.1	11.2	1.58	4.2E-02
ENSG00000155511	GRIA1	19.5	1.69	3.8E-02		ENSG00000159214	CCDC24	192.5	1.58	3.7E-09
ENSG00000124602	UNC5CL	173.7	1.69	1.3E-06		ENSG00000250511	RP11-380D23.1	13.5	1.58	3.7E-02
ENSG00000095383	TBC1D2	64.7	1.69	5.8E-06		ENSG00000259895	RP11-715J22.2	18.1	1.58	1.5E-02
ENSG00000198753	PLXNB3	402.1	1.69	4.0E-05		ENSG00000116852	KIF21B	79.3	1.58	2.1E-03
ENSG00000179008	C14orf39	14.0	1.68	1.1E-02		ENSG00000269935	RP11-482M8.3	10.8	1.57	4.1E-02
ENSG00000161328	LRRC56	80.4	1.68	5.0E-04		ENSG00000060718	COL11A1	1846.0	1.57	1.1E-02
ENSG00000184925	LCN12	466.9	1.68	8.4E-05		ENSG00000111775	COX6A1	621.4	1.57	1.1E-04
ENSG00000103723	AP3B2	7.6	1.68	4.3E-02		ENSG00000185567	AHNAK2	1767.5	1.57	1.4E-03
ENSG00000237429	RP1-159A19.4	27.9	1.68	2.6E-03		ENSG00000104814	MAP4K1	10.8	1.57	2.7E-02
ENSG00000130653	PNPLA7	301.1	1.68	4.3E-06		ENSG00000166823	MESP1	86.6	1.57	1.9E-02
ENSG00000170412	GPRC5C	358.1	1.68	2.9E-08		ENSG00000132702	HAPLN2	46.6	1.57	2.3E-04
ENSG00000164659	KIAA1324L	1266.1	1.67	7.3E-06		ENSG00000214595	EML6	46.3	1.57	9.3E-04
ENSG00000117245	KIF17	13.9	1.67	1.3E-02		ENSG00000091536	MYO15A	69.5	1.57	1.2E-03
ENSG00000169783	LINGO1	434.5	1.67	1.4E-06		ENSG00000251429	RP11-597D13.7	25.6	1.56	1.2E-02
ENSG00000196126	HLA-DRB1	34.7	1.67	3.2E-03		ENSG00000188677	PARVB	267.4	1.56	1.8E-05
ENSG00000196189	SEMA4A	243.0	1.67	6.0E-08		ENSG00000243811	APOBEC3D	25.1	1.56	1.4E-02
ENSG00000108370	RGS9	60.3	1.67	1.7E-03		ENSG00000210191	MT-TL2	268.2	1.56	4.3E-03
ENSG00000130208	APOC1	16.7	1.67	3.6E-02		ENSG00000140465	CYP1A1	59.8	1.56	5.2E-04
ENSG00000199038	MIR210	24.7	1.67	4.0E-03		ENSG00000236830	CBR3-AS1	15.8	1.56	4.6E-02
ENSG00000100351	GRAP2	7.2	1.66	4.0E-02		ENSG00000105976	MET	440.2	1.56	5.2E-04
ENSG00000245213	RP11-10K16.1	7.5	1.66	4.3E-02		ENSG00000261377	PDCD6IPP2	13.1	1.55	1.5E-02
ENSG00000142347	MYO1F	21.4	1.66	8.8E-03		ENSG00000157851	DPYSL5	338.5	1.55	1.3E-08
ENSG00000143590	EFNA3	132.0	1.66	8.6E-06		ENSG00000089820	ARHGAP4	496.3	1.55	3.9E-04
ENSG00000235326		12.2	1.66	2.5E-02		ENSG00000167311	ART5	41.4	1.55	7.1E-04
ENSG00000163932	PRKCD	335.9	1.66	1.2E-05		ENSG00000061938	TNK2	3786.7	1.55	5.0E-25
ENSG00000231305	RP11-723O4.2	12.1	1.66	2.5E-02		ENSG00000157617	C2CD2	203.3	1.55	2.8E-06
ENSG00000117480	FAAH	398.7	1.66	3.2E-11		ENSG00000134222	PSRC1	190.3	1.55	3.7E-07
ENSG00000170893	TRH	827.5	1.65	1.2E-02		ENSG00000176658	MYO1D	1053.7	1.55	6.9E-07
ENSG00000223573	TINCR	25.7	1.65	1.3E-02		ENSG00000225213	RP11-197M22.2	7.9	1.55	4.5E-02
ENSG00000088726	TMEM40	156.6	1.65	3.1E-05		ENSG00000046889	PREX2	11.2	1.55	1.9E-02
ENSG00000187634	SAMD11	92.9	1.64	7.1E-03		ENSG00000109771	LRP2BP	194.3	1.55	4.8E-05
ENSG00000270087	RP11-399K21.11	14.2	1.64	2.7E-02		ENSG00000025708	TYMP	40.6	1.54	1.7E-04
ENSG00000162975	KCNF1	20.1	1.64	2.3E-02		ENSG00000143127	ITGA10	1099.5	1.54	4.0E-06
ENSG00000174514	MFSD4	75.5	1.63	9.2E-04		ENSG00000136002	ARHGEF4	178.1	1.53	2.8E-05
ENSG00000003989	SLC7A2	1635.6	1.63	3.1E-10		ENSG00000115257	PCSK4	211.9	1.53	4.3E-06
ENSG00000261693	RP13-467H17.1	11.4	1.63	2.3E-02		ENSG00000056736	IL17RB	469.9	1.53	2.2E-05
ENSG00000237886	LINC01573	145.1	1.62	8.1E-10		ENSG00000144331	ZNF385B	1397.2	1.53	1.5E-03
ENSG00000163354	DCST2	67.3	1.62	6.8E-06		ENSG00000135596	MICAL1	225.1	1.53	3.5E-04
ENSG00000245532	NEAT1	9824.8	1.62	2.7E-06		ENSG00000179296		17.0	1.53	6.8E-03
ENSG00000157782	CABP1	9.6	1.62	4.3E-02		ENSG00000180999	C1orf105	742.2	1.53	1.4E-03
ENSG00000133433	GSTT2B	14.7	1.62	2.3E-02		ENSG00000175352	NRIP3	52.9	1.53	1.7E-03
ENSG00000133083	DCLK1	190.1	1.62	1.5E-03		ENSG00000233585	AC115617.2	11.0	1.53	2.4E-02
ENSG00000187554	TLR5	63.0	1.62	2.5E-03		ENSG00000141744	PNMT	268.9	1.53	8.9E-06
ENSG00000232224	LINC00202-1	104.0	1.62	1.1E-03		ENSG00000114859	CLCN2	240.7	1.53	3.9E-06
ENSG00000237187	NR2F1-AS1	27.7	1.62	1.2E-02		ENSG00000012779	ALOX5	30.0	1.53	3.5E-02
ENSG00000166473	PKD1L2	315.3	1.61	1.5E-04		ENSG00000138821	SLC39A8	610.9	1.52	2.6E-05
ENSG00000149243	KLHL35	26.6	1.61	7.6E-04		ENSG00000243225	RP11-7F17.1	27.0	1.52	1.2E-02
ENSG00000187772	LIN28B	18.4	1.61	7.2E-03		ENSG00000239677	PDZRN3-AS1	49.8	1.52	3.3E-02
ENSG00000166450	PRTG	140.3	1.61	2.7E-03		ENSG00000149922	TBX6	28.4	1.52	6.1E-03
ENSG00000140939	NOL3	1679.4	1.61	6.0E-05		ENSG00000073670	ADAM11	7862.5	1.52	7.5E-05
ENSG00000270906	RP11-475J5.6	39.9	1.61	1.3E-02		ENSG00000072952	MRVI1	193.8	1.52	1.8E-02
ENSG00000254206	NPIPB11	19.7	1.60	8.9E-03		ENSG00000213443	RP11-75L1.2	104.5	1.52	3.8E-03
ENSG00000161544	CYGB	151.9	1.60	3.8E-05		ENSG00000111729	CLEC4A	20.1	1.52	5.8E-03
ENSG00000215039	CD27-AS1	876.1	1.60	1.4E-13		ENSG00000171219	CDC42BPG	297.2	1.52	5.3E-07
ENSG00000129667	RHBDF2	60.2	1.60	1.1E-03		ENSG00000006453	BAIAP2L1	135.5	1.52	5.8E-04
ENSG00000130762	ARHGEF16	90.4	1.59	2.2E-04		ENSG00000164604	GPR85	94.1	1.52	1.0E-03
ENSG00000116544	DLGAP3	7.6	1.59	4.1E-02		ENSG00000204314	PRRT1	76.2	1.52	1.1E-06
ENSG00000136883	KIF12	20.9	1.59	2.3E-02		ENSG00000247809	NR2F2-AS1	76.9	1.52	9.6E-03
ENSG00000204241	RP11-713P17.3	36.6	1.59	6.7E-04		ENSG00000068903	SIRT2	809.7	1.52	8.0E-04
ENSG00000225882	LINC01456	21.1	1.59	6.7E-03		ENSG00000185664	PMEL	209.5	1.51	1.2E-02
ENSG00000248527	MTATP6P1	59.9	1.59	6.2E-03		ENSG00000018625	ATP1A2	1932.5	1.51	7.9E-04
ENSG00000225783	MIAT	21.7	1.59	2.2E-02		ENSG00000118369	USP35	578.7	1.51	2.7E-08
ENSG00000198203	SULT1C2	8.8	1.59	3.6E-02		ENSG00000123095	BHLHE41	664.4	1.51	4.2E-04
ENSG00000246982	RP1-179N16.6	45.9	1.59	5.8E-05		ENSG00000187699	C2orf88	260.8	1.51	3.9E-03
ENSG00000170616		15.0	1.59	8.1E-03		ENSG00000260196	RP1-239B22.5	90.3	1.51	2.8E-03
ENSG00000230537	RP11-305L7.1	14.7	1.59	1.4E-02		ENSG00000177685	CRACR2B	765.4	1.50	2.1E-03
ENSG00000210184	MT-TS2	153.9	1.58	3.8E-03		ENSG00000139625	MAP3K12	582.7	1.50	4.1E-10
ENSG00000259344		39.0	1.58	7.1E-03		ENSG00000248603		111.9	1.50	1.2E-06
ENSG00000271858	CYB561D2	16.1	1.58	6.1E-03		ENSG00000185615	PDIA2	25.7	1.50	4.3E-02
ENSG00000113361	CDH6	44.2	1.58	2.5E-02		ENSG00000091622	PITPNM3	282.9	1.50	1.8E-02
ENSG00000228376	GAS2L1P2	24.8	1.58	9.3E-03		ENSG00000187164	SHTN1	160.1	1.50	5.4E-04

ENSG00000163931	TKT	1597.9	1.50	5.3E-07		ENSG00000196547	MAN2A2	5068.8	1.41	1.9E-07
ENSG00000139194	RBP5	31.1	1.50	3.7E-03		ENSG00000137101	CD72	18.5	1.41	2.7E-02
ENSG00000110900	TSPAN11	285.2	1.50	1.3E-05		ENSG00000196104	SPOCK3	48.1	1.41	1.3E-02
ENSG00000210112	MT-TM	23.5	1.50	7.8E-03		ENSG00000056558	TRAF1	345.5	1.41	1.7E-05
ENSG00000255458	RP11-539G18.3	15.6	1.50	2.1E-02		ENSG00000196739	COL27A1	1455.0	1.41	1.6E-12
ENSG00000146122	DAAM2	247.4	1.49	1.9E-08		ENSG00000196586	MYO6	833.6	1.41	1.1E-05
ENSG00000031544		25.5	1.49	1.4E-02		ENSG00000168907	PLA2G4F	76.1	1.41	3.5E-03
ENSG00000141756	FKBP10	2879.1	1.49	8.8E-09		ENSG00000228109	MFI2-AS1	100.7	1.41	3.0E-04
ENSG00000210174	MT-TR	111.9	1.49	1.7E-02		ENSG00000239713	APOBEC3G	45.2	1.41	3.9E-02
ENSG00000105464	GRIN2D	72.7	1.49	3.7E-04		ENSG00000170011	MYRIP	67.5	1.41	1.1E-02
ENSG00000006047	YBX2	574.7	1.49	5.8E-06		ENSG00000185128		33.7	1.41	5.3E-03
ENSG00000064547	LPAR2	161.7	1.48	8.9E-06		ENSG00000236255	AC009404.2	24.3	1.40	9.6E-03
ENSG00000120729	MYOT	76.0	1.48	1.2E-02		ENSG00000175449	RFESD	40.9	1.40	2.0E-03
ENSG00000258461	RP11-164J13.1	198.3	1.48	1.9E-05		ENSG00000120149	MSX2	58.0	1.40	8.1E-03
ENSG00000185482	STAC3	29.0	1.48	4.7E-03		ENSG00000230453	ANKRD18B	50.0	1.40	1.1E-02
ENSG00000249421	ADAMTS19-AS1	30.6	1.48	1.5E-02		ENSG00000267355	RPL9P29	16.9	1.40	3.5E-02
ENSG00000174945	AMZ1	39.2	1.48	1.0E-02		ENSG00000140181		1073.5	1.40	2.8E-07
ENSG00000106976	DNM1	482.4	1.48	3.4E-06		ENSG00000134508	CABLES1	70.4	1.40	3.6E-05
ENSG00000225630	MTND2P28	61.5	1.47	1.7E-02		ENSG00000241288	RP11-379B18.5	29.0	1.40	1.5E-02
ENSG00000214456	PLIN5	287.3	1.47	8.2E-03		ENSG00000017621		70.7	1.40	8.9E-04
ENSG00000272223	RP1-20C7.6	17.5	1.47	2.3E-02		ENSG00000260077	RP11-254F7.2	105.2	1.40	2.3E-05
ENSG00000197457	STMN3	81.0	1.47	1.3E-02		ENSG00000141068	KSR1	650.6	1.40	5.7E-05
ENSG00000135519	KCNH3	39.3	1.47	8.9E-03		ENSG00000260394	LA16c-313D11.9	16.5	1.39	3.1E-02
ENSG00000059804	SLC2A3	4446.5	1.47	2.2E-03		ENSG00000243230	RP11-286H14.8	26.1	1.39	2.1E-02
ENSG00000265487	RP11-793A3.1	13.8	1.47	2.4E-02		ENSG00000047634	SCML1	315.0	1.39	1.4E-05
ENSG00000240875	LINC00886	15.7	1.47	1.4E-02		ENSG00000005513	SOX8	49.3	1.39	3.1E-03
ENSG00000235706	DICER1-AS1	188.4	1.47	3.4E-07		ENSG00000186231	KLHL32	40.4	1.39	1.4E-02
ENSG00000210077	MT-TV	32.3	1.46	8.2E-03		ENSG00000002587	HS3ST1	16.2	1.39	3.7E-02
ENSG00000196660	SLC30A10	13.3	1.46	4.4E-02		ENSG00000225177	RP11-390P2.4	18.1	1.39	2.2E-02
ENSG00000064687	ABCA7	1544.2	1.46	1.6E-06		ENSG00000147010	SH3KBP1	1124.0	1.39	2.8E-08
ENSG00000089847	ANKRD24	33.5	1.46	3.7E-03		ENSG00000197355	UAP1L1	1384.0	1.38	3.4E-04
ENSG00000162407	PPAP2B	1275.1	1.46	8.3E-05		ENSG00000197558	SSPO	379.3	1.38	2.6E-05
ENSG00000151012	SLC7A11	75.3	1.46	8.4E-05		ENSG00000101638	ST8SIA5	170.6	1.38	5.0E-03
ENSG00000157833	GAREML	61.0	1.46	1.4E-02		ENSG00000179532	DNHD1	579.2	1.38	2.1E-09
ENSG00000072182	ASIC4	34.3	1.46	4.7E-03		ENSG00000092295	TGM1	35.5	1.38	3.0E-03
ENSG00000184985	SORCS2	635.1	1.46	9.7E-06		ENSG00000159640	ACE	98.5	1.38	1.3E-03
ENSG00000197181	PIWIL2	12.7	1.46	4.6E-02		ENSG00000167654	ATCAY	35.6	1.38	2.9E-03
ENSG00000072858	SIDT1	12.6	1.45	4.0E-02		ENSG00000161681	SHANK1	60.4	1.38	6.9E-03
ENSG00000088387	DOCK9	1471.7	1.45	1.2E-07		ENSG00000168917	SLC35G2	43.4	1.38	9.0E-04
ENSG00000197191	CYSRT1	77.2	1.45	2.2E-04		ENSG00000134533	RERG	63.9	1.37	3.3E-03
ENSG00000183117	CSMD1	33.0	1.45	3.9E-02		ENSG00000166165	CKB	2640.8	1.37	1.4E-10
ENSG00000255837	TAS2R20	13.5	1.45	4.3E-02		ENSG00000210164	MT-TG	112.1	1.37	2.7E-02
ENSG00000148803	FUOM	145.3	1.45	7.8E-03		ENSG00000100285	NEFH	27.6	1.37	1.3E-02
ENSG00000114631	PODXL2	139.1	1.44	3.2E-02		ENSG00000077009	NMRK2	1257.1	1.37	4.2E-02
ENSG00000204103	MAFB	80.6	1.44	6.5E-04		ENSG00000106617	PRKAG2	4608.9	1.37	2.3E-04
ENSG00000170579	DLGAP1	21.1	1.44	2.3E-02		ENSG00000241528		31.0	1.36	9.6E-03
ENSG00000162777	DENND2D	20.9	1.44	3.8E-02		ENSG00000247627	MTND4P12	7369.3	1.36	6.7E-03
ENSG00000157119	KLHL40	57.3	1.44	4.5E-02		ENSG00000145721	LIX1	179.9	1.36	1.4E-02
ENSG00000105290	APLP1	526.2	1.44	3.2E-05		ENSG00000171992	SYNPO	4930.7	1.36	2.0E-02
ENSG00000183324	REC114	84.9	1.43	3.0E-03		ENSG00000165359	DDX26B	2622.3	1.36	2.4E-05
ENSG00000167191	GPRC5B	2043.1	1.43	9.2E-05		ENSG00000209082	MT-TL1	432.9	1.36	2.6E-04
ENSG00000196074	SYCP2	61.2	1.43	4.0E-03		ENSG00000117425	PTCH2	61.0	1.36	4.3E-04
ENSG00000211459	MT-RNR1	60185.8	1.43	1.3E-03		ENSG00000113240	CLK4	1229.8	1.36	1.9E-06
ENSG00000162572	SCNN1D	677.7	1.43	3.9E-04		ENSG00000137868	STRA6	439.5	1.36	2.0E-03
ENSG00000128802		48.2	1.43	1.7E-03		ENSG00000248923	MTND5P11	44.2	1.35	2.6E-02
ENSG00000178803	ADORA2A-AS1	67.7	1.43	3.3E-03		ENSG00000176170	SPHK1	101.4	1.35	6.6E-04
ENSG00000267385	CTB-50L17.14	19.8	1.42	2.6E-02		ENSG00000184009	ACTG1	20139.5	1.35	6.8E-18
ENSG00000214827	MTCP1	73.9	1.42	1.7E-03		ENSG00000166839	ANKDD1A	124.1	1.35	7.8E-05
ENSG00000132386	SERPINF1	491.9	1.42	2.3E-03		ENSG00000227398	KIF9-AS1	144.5	1.35	2.1E-05
ENSG00000198879	SFMBT2	535.9	1.42	9.8E-05		ENSG00000197696	NMB	110.9	1.35	1.1E-03
ENSG00000115657	ABCB6	214.6	1.42	1.4E-03		ENSG00000211445	GPX3	3054.6	1.35	1.6E-03
ENSG00000172346	CSDC2	134.7	1.42	6.3E-05		ENSG00000105649	RAB3A	295.6	1.35	4.7E-04
ENSG00000133069	TMCC2	419.1	1.42	2.3E-04		ENSG00000152061	RABGAP1L	3413.7	1.35	7.1E-06
ENSG00000119686	FLVCR2	54.0	1.42	1.1E-02		ENSG00000187783	TMEM72	201.2	1.34	5.7E-03
ENSG00000099984	GSTT2	67.2	1.42	2.0E-03		ENSG00000262902	RP11-750B16.1	56.9	1.34	2.1E-02
ENSG00000164620	RELL2	34.7	1.42	2.4E-03		ENSG00000267750	RUNDC3A-AS1	28.8	1.34	8.5E-03
ENSG00000237753	AC079922.3	68.1	1.42	4.8E-04		ENSG00000130540	SULT4A1	49.1	1.34	2.0E-02
ENSG00000243449	C4orf48	198.3	1.42	1.5E-04		ENSG00000228727	SAPCD1	16.5	1.34	2.7E-02
ENSG00000184305	CCSER1	43.7	1.42	2.1E-03		ENSG00000069696	DRD4	51.1	1.34	2.7E-03
ENSG00000205678	TECRL	17103.6	1.42	8.1E-03		ENSG00000166793	YPEL4	123.4	1.34	3.7E-07
ENSG00000156885	COX6A2	1589.3	1.42	4.7E-03		ENSG00000204851	PNMAL2	36.4	1.34	5.1E-03
ENSG00000111452	ADGRD1	1347.8	1.41	2.9E-04		ENSG00000002016	RAD52	542.4	1.34	7.9E-10

ENSG00000162426	SLC45A1	38.4	1.34	3.1E-03		ENSG00000185100	ADSSL1	2063.3	1.25	2.3E-03
ENSG00000256967	RP11-273B20.1	15.9	1.33	4.7E-02		ENSG00000204052	LRRC73	117.2	1.25	2.1E-04
ENSG00000262772	RP11-353N14.2	30.1	1.33	7.4E-03		ENSG00000139631	CSAD	651.8	1.25	4.1E-10
ENSG00000261452		76.8	1.33	1.2E-04		ENSG00000236266	RP3-467L1.4	14.8	1.25	4.3E-02
ENSG00000248019	FAM13A-AS1	230.2	1.33	2.1E-05		ENSG00000198938	MT-CO3	274468.8	1.25	3.8E-02
ENSG00000109046	WSB1	16623.4	1.33	6.8E-04		ENSG00000163376	KBTBD8	95.7	1.25	9.2E-03
ENSG00000214870	AC004540.5	40.4	1.33	3.8E-03		ENSG00000134917	ADAMTS8	2665.4	1.25	1.5E-02
ENSG00000269996		109.2	1.33	3.9E-06		ENSG00000187994	RINL	27.8	1.25	1.4E-02
ENSG00000233175	CTD-2020K17.3	27.5	1.32	4.5E-02		ENSG00000149557	FEZ1	631.0	1.25	4.3E-04
ENSG00000188042	ARL4C	60.6	1.32	6.0E-03		ENSG00000198804	MT-CO1	660131.0	1.25	9.2E-03
ENSG00000073417	PDE8A	833.4	1.32	2.2E-06		ENSG00000069974	RAB27A	754.6	1.25	2.8E-04
ENSG00000258602	RP11-7F17.7	37.1	1.32	1.9E-02		ENSG00000260415		19.2	1.25	2.4E-02
ENSG00000235194	PPP1R3E	1195.8	1.32	1.0E-03		ENSG00000227082	CH17-437K3.1	55.8	1.24	1.6E-03
ENSG00000141505	ASGR1	52.9	1.32	3.1E-03		ENSG00000213903	LTB4R	121.7	1.24	5.8E-04
ENSG00000184544	DHRS7C	150.6	1.32	1.3E-03		ENSG00000069493	CLEC2D	463.4	1.24	9.1E-03
ENSG00000185404	SP140L	26.9	1.32	2.4E-02		ENSG00000166548	TK2	505.6	1.24	2.8E-05
ENSG00000142178	SIK1	356.3	1.32	1.8E-02		ENSG00000135119	RNFT2	76.4	1.24	6.7E-04
ENSG00000063761	ADCK1	385.2	1.31	3.1E-03		ENSG00000042980	ADAM28	35.2	1.24	2.7E-02
ENSG00000237973	RP5-857K21.6	61660.1	1.31	7.4E-03		ENSG00000136490	LIMD2	73.9	1.24	2.4E-03
ENSG00000206077	ZDHHC11B	401.1	1.31	1.8E-03		ENSG00000196123	KIAA0895L	2139.7	1.24	2.1E-07
ENSG00000141401	IMPA2	58.8	1.31	1.1E-03		ENSG00000188385	JAKMIP3	97.8	1.24	9.8E-04
ENSG00000128298	BAIAP2L2	93.8	1.31	7.5E-04		ENSG00000117479	SLC19A2	932.1	1.23	1.3E-02
ENSG00000188322	SBK1	209.1	1.31	2.6E-06		ENSG00000172819	RARG	237.9	1.23	5.4E-04
ENSG00000112715	VEGFA	18981.8	1.31	1.8E-02		ENSG00000184371	CSF1	833.4	1.23	2.8E-03
ENSG00000222020	AC062017.1	28.1	1.31	1.2E-02		ENSG00000171729	TMEM51	286.1	1.23	4.8E-05
ENSG00000182118	FAM89A	45.7	1.31	8.3E-03		ENSG00000143110	C1orf162	117.9	1.23	1.4E-04
ENSG00000167676	PLIN4	72.2	1.30	4.8E-03		ENSG00000091129	NRCAM	90.6	1.23	2.0E-02
ENSG00000092929	UNC13D	405.3	1.30	1.8E-10		ENSG00000146966	DENND2A	221.2	1.23	7.2E-06
ENSG00000259425	RP11-566K19.5	58.3	1.30	3.0E-02		ENSG00000163794	UCN	67.1	1.23	1.7E-03
ENSG00000060656	PTPRU	2876.7	1.30	5.3E-07		ENSG00000188004	C1orf204	45.2	1.23	1.2E-02
ENSG00000162650	ATXN7L2	257.5	1.30	6.7E-05		ENSG00000242759	LINC00882	27.6	1.23	9.9E-03
ENSG00000250891	CTD-2281M20.1	115.0	1.30	1.3E-02		ENSG00000198832	SELM	971.8	1.23	4.8E-04
ENSG00000056487	PHF21B	145.7	1.30	1.7E-05		ENSG00000183963	SMTN	2701.2	1.22	9.2E-05
ENSG00000271959	CTD-3064M3.7	1148.1	1.30	1.3E-02		ENSG00000166206	GABRB3	403.1	1.22	4.8E-02
ENSG00000099999	RNF215	509.9	1.29	2.8E-10		ENSG00000228594	C1orf233	706.7	1.22	2.1E-04
ENSG00000198003	CCDC151	37.9	1.29	4.6E-03		ENSG00000181577	C6orf223	33.3	1.22	2.8E-02
ENSG00000260261	RP11-480A16.1	45.5	1.29	6.6E-03		ENSG00000249119	MTND6P4	15575.6	1.22	1.6E-02
ENSG00000138744	NAAA	168.7	1.29	1.7E-05		ENSG00000136274	NACAD	329.3	1.22	2.4E-04
ENSG00000112559	MDFI	166.4	1.29	4.9E-03		ENSG00000163393	SLC22A15	108.2	1.22	1.8E-04
ENSG00000177106	EPS8L2	296.9	1.29	1.1E-03		ENSG00000178623	GPR35	146.6	1.22	2.5E-04
ENSG00000078814	MYH7B	18076.4	1.29	6.1E-04		ENSG00000198695	MT-ND6	176797.7	1.22	1.9E-02
ENSG00000235092	ID2-AS1	31.8	1.28	1.3E-02		ENSG00000250222	CTC-338M12.5	44.7	1.22	2.4E-02
ENSG00000125454	SLC25A19	102.5	1.28	2.9E-04		ENSG00000250508	RP11-757G1.6	32.8	1.22	2.0E-02
ENSG00000109063	MYH3	67.3	1.28	2.2E-03		ENSG00000248698	LINC01085	53.9	1.22	4.4E-02
ENSG00000270028	RP11-380L11.4	35.5	1.28	6.5E-03		ENSG00000260793	RP5-882C2.2	122.3	1.21	5.8E-04
ENSG00000184185	KCNJ12	360.5	1.28	5.8E-05		ENSG00000105419	MEIS3	308.8	1.21	2.7E-05
ENSG00000157890	MEGF11	77.8	1.28	5.3E-03		ENSG00000111666	CHPT1	698.0	1.21	8.9E-06
ENSG00000242686	RP11-1191J2.2	96.4	1.28	2.4E-03		ENSG00000260912	RP11-363E7.4	50.4	1.21	1.0E-02
ENSG00000260121	RP5-1142A6.9	79.8	1.28	9.3E-03		ENSG00000176490	DIRAS1	685.6	1.21	3.9E-06
ENSG00000137872	SEMA6D	3586.5	1.28	1.5E-04		ENSG00000206567	AC022007.5	80.7	1.21	1.7E-03
ENSG00000105516	DBP	467.2	1.28	1.4E-05		ENSG00000243927	MRPS6	2001.4	1.21	5.7E-04
ENSG00000198886	MT-ND4	618768.2	1.27	1.3E-02		ENSG00000224729	PCOLCE-AS1	68.5	1.21	2.1E-02
ENSG00000213983	AP1G2	665.3	1.27	6.5E-12		ENSG00000138434	SSFA2	4062.1	1.21	6.5E-08
ENSG00000110628	SLC22A18	586.0	1.27	3.1E-10		ENSG00000163517	HDAC11	1254.9	1.21	2.7E-05
ENSG00000210176	MT-TH	107.0	1.27	2.8E-02		ENSG00000103740	ACSBG1	31.5	1.21	2.2E-02
ENSG00000224699	LAMTOR5-AS1	21.1	1.27	2.4E-02		ENSG00000160678	S100A1	60.1	1.21	8.9E-03
ENSG00000036448	MYOM2	2900.1	1.27	1.0E-02		ENSG00000163032	VSNL1	655.7	1.20	3.6E-02
ENSG00000112394	SLC16A10	357.9	1.27	1.3E-03		ENSG00000099282	TSPAN15	70.4	1.20	3.9E-02
ENSG00000139200	PIANP	63.8	1.27	4.7E-02		ENSG00000245248	USP2-AS1	22.2	1.20	4.0E-02
ENSG00000172594	SMPDL3A	142.1	1.27	1.9E-03		ENSG00000138823	MTTP	22.7	1.20	2.2E-02
ENSG00000126822	PLEKHG3	1092.4	1.26	1.9E-05		ENSG00000130700	GATA5	194.6	1.20	1.3E-05
ENSG00000143140		2882.5	1.26	1.9E-03		ENSG00000182109	RP11-69E11.4	39.6	1.20	3.9E-03
ENSG00000008283	CYB561	366.1	1.26	3.5E-05		ENSG00000180448	HMHA1	1125.0	1.20	4.2E-02
ENSG00000154134	ROBO3	36.9	1.26	2.1E-02		ENSG00000171163	ZNF692	1312.4	1.20	1.5E-08
ENSG00000255153	TOLLIP-AS1	15.4	1.26	4.8E-02		ENSG00000154118	JPH3	471.4	1.20	5.2E-06
ENSG00000198870	STKLD1	30.9	1.26	7.0E-03		ENSG00000102032	RENBP	304.1	1.20	1.1E-03
ENSG00000110013	SIAE	602.3	1.26	2.6E-03		ENSG00000260293	RP11-715J22.6	24.1	1.20	2.9E-02
ENSG00000079691	LRRC16A	417.7	1.26	9.9E-04		ENSG00000225138	CTD-2228K2.7	1033.4	1.20	4.8E-05
ENSG00000164742	ADCY1	861.8	1.25	1.6E-04		ENSG00000112695	COX7A2	1951.3	1.20	8.6E-04
ENSG00000166562	SEC11C	188.3	1.25	3.3E-03		ENSG00000085514	PILRA	42.0	1.20	8.3E-03
ENSG00000173531	MST1	492.8	1.25	3.6E-06		ENSG00000136449	MYCBPAP	27.9	1.19	2.4E-02
ENSG00000228203	RNF144A-AS1	14.8	1.25	4.9E-02		ENSG00000198934	MAGEE1	312.0	1.19	2.5E-07

ENSG00000197140	ADAM32	33.2	1.19	3.4E-02		ENSG00000092096	SLC22A17	1546.8	1.13	4.1E-06
ENSG00000130294	KIF1A	3680.2	1.19	8.5E-03		ENSG00000155324	GRAMD3	466.0	1.13	3.9E-06
ENSG00000114948	ADAM23	6955.2	1.19	1.4E-04		ENSG00000105479	CCDC114	47.1	1.13	1.3E-02
ENSG00000160469	BRSK1	780.6	1.19	2.9E-09		ENSG00000186603	HPDL	29.0	1.13	2.0E-02
ENSG00000205464	ATP6AP1L	146.5	1.19	7.2E-06		ENSG00000089225	TBX5	3651.3	1.13	1.6E-03
ENSG00000110723	EXPH5	46.1	1.19	9.3E-03		ENSG00000057252	SOAT1	527.0	1.13	1.3E-07
ENSG00000153982	GDPD1	153.5	1.19	4.1E-06		ENSG00000172893	DHCR7	1240.2	1.12	4.0E-05
ENSG00000102349	KLF8	188.7	1.19	8.5E-06		ENSG00000164951	PDP1	656.1	1.12	2.8E-04
ENSG00000147155	EBP	703.0	1.19	8.8E-03		ENSG00000154265	ABCA5	418.5	1.12	6.8E-04
ENSG00000135722	FBXL8	152.6	1.19	4.8E-03		ENSG00000188818	ZDHHC11	224.3	1.12	9.0E-03
ENSG00000264469		63.1	1.19	3.6E-03		ENSG00000233621	LINC01137	29.7	1.12	2.1E-02
ENSG00000167100	SAMD14	67.0	1.19	2.4E-02		ENSG00000159314	ARHGAP27	262.5	1.12	3.6E-03
ENSG00000146067	FAM193B	1939.8	1.18	6.8E-08		ENSG00000088340	FER1L4	984.3	1.12	4.6E-02
ENSG00000260193	RP11-83N9.5	39.4	1.18	1.3E-02		ENSG00000135605	TEC	131.4	1.12	4.4E-04
ENSG00000147174	ACRC	31.9	1.18	2.9E-02		ENSG00000165061	ZMAT4	157.1	1.12	3.6E-04
ENSG00000172824	CES4A	350.5	1.18	8.2E-06		ENSG00000188176	SMTNL2	1733.8	1.12	1.8E-03
ENSG00000166592	RRAD	6005.5	1.18	7.0E-05		ENSG00000198780	FAM169A	165.0	1.12	1.7E-03
ENSG00000215375	MYL5	311.6	1.18	3.3E-05		ENSG00000106336	FBXO24	40.1	1.12	2.0E-02
ENSG00000177614	PGBD5	307.4	1.18	6.5E-03		ENSG00000120889	TNFRSF10B	2284.9	1.12	2.0E-05
ENSG00000184005	ST6GALNAC3	313.7	1.18	2.8E-03		ENSG00000174437	ATP2A2	70197.4	1.12	1.4E-04
ENSG00000224389	C4B	180.4	1.18	5.9E-03		ENSG00000177595	PIDD1	913.0	1.12	6.7E-04
ENSG00000114270	COL7A1	4508.7	1.17	9.1E-06		ENSG00000167216	KATNAL2	67.9	1.12	4.5E-03
ENSG00000142910	TINAGL1	1279.8	1.17	1.8E-03		ENSG00000175395	ZNF25	372.0	1.11	3.7E-07
ENSG00000131979	GCH1	45.3	1.17	1.5E-02		ENSG00000167280	ENGASE	1951.4	1.11	3.8E-10
ENSG00000014914	MTMR11	103.1	1.17	9.8E-03		ENSG00000078596	ITM2A	580.7	1.11	7.2E-03
ENSG00000204311	DFNB59	88.9	1.17	9.7E-04		ENSG00000140057	AK7	47.8	1.11	5.1E-03
ENSG00000144935	TRPC1	915.1	1.17	5.4E-08		ENSG00000167037	SGSM1	119.3	1.11	4.5E-02
ENSG00000181097	RP11-429J17.2	25.0	1.17	2.3E-02		ENSG00000175229	GAL3ST3	309.7	1.11	1.0E-04
ENSG00000140332	TLE3	513.7	1.17	1.6E-04		ENSG00000165338	HECTD2	904.7	1.11	9.1E-05
ENSG00000212907	MT-ND4L	81374.2	1.17	2.6E-02		ENSG00000105613	MAST1	54.5	1.11	2.5E-02
ENSG00000185187	SIGIRR	289.3	1.17	3.3E-06		ENSG00000105281	SLC1A5	643.2	1.11	4.6E-02
ENSG00000139899	CBLN3	50.7	1.17	1.7E-02		ENSG00000103160	HSDL1	2650.1	1.11	6.9E-03
ENSG00000103253	HAGHL	408.9	1.16	2.0E-06		ENSG00000155016	CYP2U1	213.8	1.11	6.4E-06
ENSG00000137393	RNF144B	170.1	1.16	1.2E-02		ENSG00000261087	KB-1460A1.5	52.7	1.10	1.5E-02
ENSG00000227195	MIR663AHG	79.4	1.16	2.9E-02		ENSG00000267980	AC007292.6	18.7	1.10	4.9E-02
ENSG00000145882	PCYOX1L	505.6	1.16	1.2E-05		ENSG00000172232	AZU1	27.3	1.10	2.8E-02
ENSG00000114779	ABHD14B	427.6	1.16	5.1E-06		ENSG00000213213	CCDC183	1052.8	1.10	1.0E-04
ENSG00000173715	C11orf80	146.1	1.16	2.1E-04		ENSG00000099260	PALMD	189.3	1.10	8.4E-03
ENSG00000228252	COL6A4P2	86.7	1.16	4.3E-02		ENSG00000054983	GALC	1271.6	1.10	1.8E-03
ENSG00000210196	MT-TP	6378.1	1.16	2.7E-02		ENSG00000197291	RAMP2-AS1	31.2	1.10	1.3E-02
ENSG00000160460	SPTBN4	72.0	1.16	2.4E-02		ENSG00000140876	NUDT7	58.5	1.10	2.4E-02
ENSG00000111885	MAN1A1	1240.3	1.15	2.1E-02		ENSG00000099822	HCN2	150.8	1.10	3.0E-03
ENSG00000104888	SLC17A7	43.7	1.15	6.0E-03		ENSG00000141140		790.8	1.10	2.1E-08
ENSG00000167107	ACSF2	1812.4	1.15	6.9E-04		ENSG00000100003	SEC14L2	126.6	1.10	3.0E-04
ENSG00000184451	CCR10	100.5	1.15	7.0E-04		ENSG00000205560	CPT1B	114.0	1.10	1.3E-02
ENSG00000176749	CDK5R1	108.5	1.15	2.8E-03		ENSG00000260000	RP3-467N11.1	41.3	1.09	2.1E-02
ENSG00000050555	LAMC3	82.7	1.15	1.8E-02		ENSG00000206344	HCG27	76.1	1.09	7.8E-03
ENSG00000130433	CACNG6	35.2	1.15	2.8E-02		ENSG00000135541	AHI1	473.0	1.09	4.8E-04
ENSG00000063180	CA11	443.6	1.15	9.1E-06		ENSG00000174628	IQCK	87.9	1.09	2.8E-03
ENSG00000261051	RP11-274H2.5	42.4	1.15	4.4E-02		ENSG00000129951	LPPR3	195.2	1.09	7.4E-03
ENSG00000184828	ZBTB7C	72.0	1.15	2.9E-02		ENSG00000121057	AKAP1	3339.0	1.09	7.3E-04
ENSG00000129295	LRRC6	26.9	1.15	3.1E-02		ENSG00000258301	RP11-488C13.5	36.2	1.09	2.3E-02
ENSG00000100321	SYNGR1	1326.4	1.15	4.4E-05		ENSG00000074855	ANO8	1171.3	1.09	5.2E-06
ENSG00000148288	GBGT1	31.1	1.15	3.0E-02		ENSG00000155367	PPM1J	143.6	1.08	1.2E-04
ENSG00000132016	C19orf57	63.0	1.14	7.3E-03		ENSG00000107821	KAZALD1	164.3	1.08	1.3E-03
ENSG00000240038	AMY2B	689.3	1.14	3.0E-06		ENSG00000173457	PPP1R14B	552.7	1.08	1.2E-04
ENSG00000163618	CADPS	1080.1	1.14	9.8E-04		ENSG00000244731	C4A	206.8	1.08	1.2E-02
ENSG00000168528	SERINC2	112.5	1.14	2.7E-02		ENSG00000136866	ZFP37	60.1	1.08	9.0E-03
ENSG00000182379	NXPH4	431.2	1.14	3.3E-02		ENSG00000173947	PIFO	505.3	1.08	5.2E-04
ENSG00000089060	SLC8B1	110.5	1.14	1.6E-03		ENSG00000160360	GPSM1	2087.8	1.08	6.8E-04
ENSG00000184402	SS18L1	968.3	1.14	6.6E-04		ENSG00000167766	ZNF83	1750.8	1.08	6.0E-12
ENSG00000171310	CHST11	358.8	1.14	5.3E-03		ENSG00000272288	RP11-140K17.3	67.3	1.08	3.5E-02
ENSG00000210195	MT-TT	136.3	1.14	1.4E-02		ENSG00000232442	CTD-3184A7.4	74.7	1.08	2.7E-03
ENSG00000157992	KRTCAP3	23.9	1.14	3.9E-02		ENSG00000116883	RP11-268J15.5	570.8	1.08	4.9E-02
ENSG00000054967	RELT	71.3	1.14	2.7E-02		ENSG00000137819	PAQR5	80.6	1.08	3.8E-02
ENSG00000165495	PKNOX2	95.8	1.14	1.3E-02		ENSG00000074800	ENO1	53075.0	1.08	2.0E-02
ENSG00000158716	DUSP23	148.0	1.14	4.1E-02		ENSG00000106772	PRUNE2	388.0	1.08	1.4E-02
ENSG00000099251	HSD17B7P2	57.7	1.13	5.5E-03		ENSG00000178573	MAF	305.5	1.07	2.1E-02
ENSG00000271971	CTD-2006H14.2	37.8	1.13	2.9E-02		ENSG00000198185	ZNF334	238.3	1.07	1.6E-03
ENSG00000111674	ENO2	8317.9	1.13	1.9E-02		ENSG00000236901	MIR600HG	456.6	1.07	8.3E-03
ENSG00000163040	CCDC74A	56.8	1.13	2.8E-02		ENSG00000144118	RALB	872.7	1.07	7.2E-04
ENSG00000198794	SCAMP5	356.9	1.13	1.0E-04		ENSG00000158292	GPR153	390.3	1.07	2.1E-03

ENSG00000153933	DGKE	201.6	1.07	2.9E-03		ENSG00000137857	DUOX1	56.2	1.04	2.0E-02
ENSG00000163050	ADCK3	2942.1	1.07	1.3E-04		ENSG00000224165	DNAJC27-AS1	35.7	1.03	3.4E-02
ENSG00000259291	RP11-617F23.1	362.3	1.07	6.9E-05		ENSG00000157470	FAM81A	235.4	1.03	2.0E-02
ENSG00000161653	NAGS	100.7	1.07	7.8E-03		ENSG00000187609	EXD3	601.6	1.03	6.5E-06
ENSG00000204084	INPP5B	426.5	1.07	1.6E-05		ENSG00000210049	MT-TF	251.4	1.03	4.7E-02
ENSG00000139974	SLC38A6	73.5	1.07	1.5E-03		ENSG00000170919	TPT1-AS1	392.8	1.03	9.5E-04
ENSG00000089723	OTUB2	39.4	1.06	1.2E-02		ENSG00000108474	PIGL	213.7	1.03	3.6E-05
ENSG00000168000	BSCL2	55.4	1.06	7.5E-03		ENSG00000132906	CASP9	953.1	1.03	6.2E-04
ENSG00000136404	TM6SF1	152.0	1.06	8.2E-05		ENSG00000101384	JAG1	1322.6	1.03	3.2E-03
ENSG00000072310	SREBF1	2914.2	1.06	4.6E-03		ENSG00000162946	DISC1	95.1	1.03	2.5E-02
ENSG00000270419	CAHM	72.1	1.06	1.0E-02		ENSG00000155066	PROM2	132.9	1.02	8.8E-03
ENSG00000136378	ADAMTS7	622.1	1.06	4.2E-03		ENSG00000099977	DDT	107.5	1.02	2.1E-03
ENSG00000145911	N4BP3	243.7	1.06	9.5E-03		ENSG00000166762	CATSPER2	108.4	1.02	4.5E-02
ENSG00000203485	INF2	1240.4	1.06	7.0E-04		ENSG00000143502	SUSD4	397.3	1.02	1.6E-03
ENSG00000174669	SLC29A2	1622.0	1.06	2.9E-04		ENSG00000138111	TMEM180	71.8	1.02	3.1E-03
ENSG00000187672	ERC2	216.9	1.05	7.4E-04		ENSG00000156804	FBXO32	5742.8	1.02	6.8E-04
ENSG00000132718	SYT11	253.5	1.05	4.4E-03		ENSG00000186577	C6orf1	171.6	1.02	5.0E-04
ENSG00000198786	MT-ND5	408701.5	1.05	2.9E-02		ENSG00000196757	ZNF700	212.5	1.02	3.4E-02
ENSG00000204054	LINC00963	364.6	1.05	6.5E-06		ENSG00000124772	CPNE5	16717.9	1.02	1.8E-02
ENSG00000196876	SCN8A	64.6	1.05	2.4E-03		ENSG00000183569	SERHL2	54.4	1.02	4.8E-03
ENSG00000136267	DGKB	122.9	1.05	2.0E-02		ENSG00000091262	ABCC6	36.4	1.02	2.3E-02
ENSG00000197565	COL4A6	3126.6	1.05	1.3E-05		ENSG00000225313	RP11-415J8.3	35.7	1.01	2.9E-02
ENSG00000143801	PSEN2	511.4	1.05	6.2E-04		ENSG00000103227	LMF1	417.8	1.01	6.0E-03
ENSG00000220785	MTMR9LP	102.0	1.05	2.9E-03		ENSG00000163617	KIAA1407	88.9	1.01	4.1E-03
ENSG00000223802	CERS1	80.4	1.04	4.3E-03		ENSG00000072201	LNX1	110.5	1.01	2.9E-02
ENSG00000111490	TBC1D30	53.4	1.04	2.8E-02		ENSG00000215788	TNFRSF25	243.4	1.01	6.9E-04
ENSG00000175197	DDIT3	349.7	1.04	1.4E-02		ENSG00000162769	FLVCR1	369.7	1.01	3.8E-05
ENSG00000013523	ANGEL1	980.9	1.04	8.7E-07		ENSG00000259605	AC074212.5	80.6	1.01	1.6E-03
ENSG00000186532	SMYD4	510.7	1.04	1.7E-04		ENSG00000069424	KCNAB2	191.3	1.00	1.1E-03
ENSG00000148187	MRRF	600.2	1.04	2.8E-03		ENSG00000108773	KAT2A	2107.3	1.00	4.1E-07
ENSG00000025434	NR1H3	118.2	1.04	6.1E-04		ENSG00000184916	JAG2	801.7	1.00	1.3E-04
ENSG00000181418	DDN	384.2	1.04	1.5E-03		ENSG00000260563	RP13-516M14.1	55.7	1.00	1.3E-02
ENSG00000227855	DPY19L2P3	92.5	1.04	3.8E-02		ENSG00000235280	MCF2L-AS1	55.0	1.00	9.0E-03
ENSG00000115318	LOXL3	293.7	1.04	4.3E-02		ENSG00000129244	ATP1B2	2515.5	1.00	7.9E-04
ENSG00000065833	ME1	253.1	1.04	1.3E-02		ENSG00000131435	PDLIM4	418.1	1.00	2.6E-03
ENSG00000189157	FAM47E	30.8	1.04	3.5E-02						

Supplemental Table 2: Correlation of our RNA sequencing data of human iPSC-derived atrial (iPSC-aCMs) and ventricular cardiomyocytes (iPSC-vCMs) with published transcriptomic data of human RA-treated and control ESC-derived cardiomyocytes (RA-CMs/CT-CMs). RNA sequencing: n = 4 iPSC-vCM and n = 4 iPSC-aCM independent differentiation experiments at day 90 from 3 iPSC lines. Microarray: RA-CMs vs. CT-CMs at day 31 post-differentiation (1).

(A) List of 67 overlapping genes, which are significantly lower expressed both in iPSC-aCMs from our study (1.560 differential genes vs. iPSC-vCMs; log2 fold < -0.5; *P*< 0.05) and in RA-CMs from the published data set (125 differential genes vs. CT-CMs).

Gene name	**Gene name**	**Gene name**	**Gene name**	**Gene name**	**Gene name**	**Gene name**
HEY2	MYL2	FAM84B	MARCH11	ART3	CHN1	SGCE
ALAS2	NPNT	TSPAN5	PLXDC2	MTUS2	UBE2E2	CORIN
PDGFD	EMILIN2	LAMA4	AHNAK	SORBS2	SH3GL3	TNFRSF19
NAV1	FZD1	DLC1	SPOCK2	NUP62CL	RHOQ	CITED2
IRX4	FGF18	VCAN	IFIT1	SLC1A4	ABLIM1	FZD8
TRIM9	TLE4	TMEM71	PYGL	PCDH20	JPH1	FHOD3
MYH7	ODAM	KEL	PACRG	S100A4	KCTD12	TGFBR2
PRDM16	MASP1	ERBB3	STXBP6	A4GALT	FHL2	
HAND1	TSHZ2	PKP2	PEG10	MMP23B	AP1S2	
PLCXD3	GUCY1A3	MYCN	CACHD1	VCAM1	UBE2E1	

(B) List of 53 overlapping genes, which are significantly higher expressed both in iPSC-aCMs from our study (1.629 differential genes vs. iPSC-vCMs; log2 fold > 0.5; *P*< 0.05) and in RA-CMs from the published data set (255 differential genes vs. CT-CMs).

Gene name	**Gene name**	**Gene name**	**Gene name**	**Gene name**	**Gene name**	**Gene name**
SHOX2	SMOC1	PRSS8	NR2F2	C1orf105	ADAMTS8	SLIT2
DACH2	NR2F1	PDGFRA	FZD7	SERPINF1	FEZ1	PKDCC
KCNQ2	KCNA5	RAB33A	KCNJ3	RERG	DENND2A	COL6A1
D4S234E	NOV	WFDC1	DHRS9	PRKAG2	VSNL1	ADCY5
PTGDS	SHD	NELL1	KIAA1324L	ACTG1	JAG1	ACTB
MYBPHL	BMP4	BCAR3	SAMD11	GPX3	FBXO32	
EGFR	PLCG2	CPE	PSRC1	SBK1	TMEM141	
F10	MBP	GAD1	ZNF385B	MYOM2	A2M	

Supplemental Table 3: Correlation of our RNA sequencing data of human iPSC-derived atrial (iPSC-aCMs) and ventricular cardiomyocytes (iPSC-vCMs) with published transcriptomic data of human fetal atrial and ventricular tissues. RNA sequencing: n = 4 iPSC-vCM and n = 4 iPSC-aCM independent differentiation experiments at day 90 from 3 iPSC lines. Microarray: 15-week-old human fetal atrial and ventricular tissues (1).

(A) List of 152 overlapping genes, which are significantly lower expressed both in iPSC-aCMs from our study (1.560 differential genes vs. iPSC-vCMs; log2 fold < -0.5; *P*< 0.05) and in human fetal atrial tissue from the published data set (768 differential genes vs. ventricular tissue).

Gene name		Gene name		Gene name		Gene name		Gene name		Gene name		Gene name
HEY2		EMILIN2		DLC1		LEFTY2		SORBS2		SLC44A1		STMN1
TMEM155		LYPD1		KANK4		TCF4		COBL		BMP7		BBS9
PDGFD		MURC		ADAMTS9		TMC6		METAP1		PGRMC2		SNX6
HOPX		MAOB		TMEM71		PDK4		ROR1		LYRM1		FASTKD1
NAV1		FZD1		PPP1R1C		LIN9		SLC1A4		FHL2		TNFRSF19
IRX4		GJA1		IRX3		ARAP3		XIRP1		GJA3		EIF3M
KCNJ2		COL15A1		CCL21		C15orf41		HEPH		RASD2		TRIM2
MXRA5		LBH		CD34		SPRY2		LCLAT1		PPP2R5C		SLC2A8
ACE2		XPO4		P2RX1		ETS1		PCDH20		CD58		SLC38A2
LPL		FGF18		PENK		RND3		SLC38A1		SRP14		FRMD5
GAS7		MASP1		PKP2		GABRB1		MLLT11		RAMP1		FHOD3
MYH7		HECW2		MYCN		SMYD1		SMYD2		AP1S2		CSRP2
PRDM16		DUSP5		IRX5		EPDR1		S100A4		C14orf180		CTNNB1
HAND1		RGS5		ARHGEF3		SEC14L5		A4GALT		CACNB2		SLC25A46
PLCXD3		GPM6B		ACVRL1		CAB39L		C1orf74		OSBPL8		CYFIP2
PHACTR1		PCDH7		MARCH11		PRRX1		KIDINS220		UBE2E1		RPL13
SLC5A1		GUCY1A3		RBP7		MAPKAPK3		FBXW7		HIGD1A		DTNA
MYL2		KITLG		C5orf46		CCDC34		HSDL2		PPP2R5A		RAB3IP
PRDM8		TMEM159		MDK		TNNI3K		BCL11A		PRKCDBP		STOM
PHLDB2		SLC27A6		IL32		HSPB6		ABLIM1		ZNF622		NT5DC2
GPR22		FAM129A		KLHL13		GPD1L		JPH1		PERP		
VWC2		CAV3		PYGL		ART3		CCNG1		NDRG4		

(B) List of 93 overlapping genes, which are significantly higher expressed both in iPSC-aCMs from our study (1.629 differential genes vs. iPSC-vCMs; log2 fold > 0.5; *P*< 0.05) and in human fetal atrial tissue from the published data set (485 differential genes vs. ventricular tissue).

Gene name		Gene name		Gene name		Gene name		Gene name		Gene name		Gene name
DUOXA2		COL2A1		GAS1		MYOT		CHPT1		INPP1		SAT1
D4S234E		PLCG2		HHATL		SH3KBP1		VSNL1		CAMK1D		MTHFR
TSPAN7		MBP		NR2F2		TGM1		ST6GALNAC3		COL9A1		PKDCC
MYBPHL		INA		PLLP		PRKAG2		SLC22A17		TMEM141		PIGP
DNER		PDGFRA		MAPK4		GPX3		ZDHHC11		PLOD2		PGM5
METTL7B		RAB33A		KCNJ3		RABGAP1L		SMTNL2		COL4A5		MATN2
IGSF9		SYT4		GNAO1		DHRS7C		ATP2A2		LHPP		H2AFY
SMOC1		UPB1		FAM46C		MYH3		NUDT7		SCD		PABPN1
NR2F1		DDIT4L		CAPN3		MYOM2		SYT11		ARHGAP24		SPATS2L
KCNA5		MYH6		DHRS9		SEC11C		COL4A6		MPP3		
ADM		STEAP2		KIAA1324L		KBTBD8		ANGEL1		DSC2		
RAP1GAP		CACNA2D2		TNK2		ADAMTS8		ME1		C1QTNF3		
SLCO2A1		LRRN2		ZNF385B		FEZ1		JAG1		ATP6V1G2		
SHD		PDE8B		C1orf105		GABRB3		FBXO32		DAPK1		

Supplemental Table 4: Correlation of our RNA sequencing data of iPSC-derived atrial (aCMs) and ventricular cardiomyocytes (vCMs) with published transcriptomic data of human adult atrial (A) and ventricular (V) tissues. RNA sequencing: n = 4 iPSC-vCM and n = 4 iPSC-aCM independent differentiation experiments at day 90 from 3 iPSC lines. Microarray: n=5 human adult right atrial and n =5 left ventricular tissues (2).

(A) List of 43 overlapping genes, which are significantly lower expressed both in iPSC-aCMs from our study (1.560 differential genes vs. iPSC-vCMs; log2 fold < -0.5; *P*< 0.05) and in human adult atrial tissue from the published data set (126 differential genes vs. ventricular tissue).

	RNAseq	**Asp et al.**			**RNAseq**	**Asp et al.**			**RNAseq**	**Asp et al.**
Gene name	**log2 (aCMs/ vCMs)**	**log2 (A/V)**		**Gene name**	**log2 (aCMs/ vCMs)**	**log2 (A/V)**		**Gene name**	**log2 (aCMs/ vCMs)**	**log2 (A/V)**
HEY2	-5.12	-1.83		OR51E1	-2.33	-1.49		INPP4B	-1.09	-2.04
NAV1	-4.03	-1.63		FBN2	-2.18	-2.33		C10orf71	-1.08	-1.52
KCNJ2	-3.71	-1.96		TMEM71	-2.12	-1.18		CHN1	-1.04	-1.13
LPL	-3.42	-3.16		GCNT2	-1.91	-1.73		PLCL1	-1.04	-1.18
MYH7	-3.34	-2.24		GUCY1B3	-1.72	-1.02		BCL11A	-1.02	-1.02
NRAP	-3.25	-1.46		PDE1C	-1.68	-1.55		MYOM1	-1.02	-1.25
PHACTR1	-3.25	-1.48		PPFIBP1	-1.66	-1.14		RHOQ	-0.98	-1.15
MYL2	-3.20	-7.15		C15orf41	-1.63	-2.97		RAPGEF1	-0.96	-1.11
PHLDB2	-3.18	-2.05		SMYD1	-1.59	-1.70		MPPED2	-0.88	-1.08
MURC	-2.98	-1.23		SV2B	-1.56	-1.59		ASB2	-0.85	-1.28
LRRC2	-2.90	-2.45		XIRP2	-1.43	-3.32		NDRG4	-0.74	-1.78
LBH	-2.72	-1.10		HSPB6	-1.37	-2.15		FHOD3	-0.62	-1.78
XPO4	-2.69	-1.51		LCLAT1	-1.16	-1.08		PTPRM	-0.61	-1.25
GRAMD1B	-2.51	-1.07		SLC38A1	-1.15	-1.28				
GUCY1A2	-2.33	-1.28		SMYD2	-1.12	-2.90				

(B) List of 54 overlapping genes, which are significantly higher expressed both in iPSC-aCMs from our study (1.629 differential genes vs. iPSC-vCMs; log2 fold > 0.5; *P*< 0.05) and in human adult atrial tissue from the published data set (416 differential genes vs. ventricular tissue).

	RNAseq	**Asp et al.**			**RNAseq**	**Asp et al.**			**RNAseq**	**Asp et al.**
Gene name	**log2 (aCMs/ vCMs)**	**log2 (A/V)**		**Gene name**	**log2 (aCMs/ vCMs)**	**log2 (A/V)**		**Gene name**	**log2 (aCMs/ vCMs)**	**log2 (A/V)**
D4S234E	3.28	1.31		MYH6	2.01	3.18		RERG	1.37	1.45
VWDE	3.10	3.18		STEAP2	2.01	1.16		LRRC16A	1.26	1.42
SYNPR	3.06	2.75		LRP2	2.01	3.14		KIF1A	1.19	1.05
TSPAN7	3.02	1.96		CPE	1.99	1.35		C4A	1.08	1.74
SKAP2	2.96	1.18		RASGEF1B	1.98	1.15		PRUNE2	1.08	1.70
MYBPHL	2.95	3.71		UPK1B	1.96	2.81		TM6SF1	1.06	1.29
DNER	2.91	2.35		PDE8B	1.88	2.34		INPP1	1.00	1.07
METTL7B	2.76	1.67		FAM153B	1.88	1.64		CAMK1D	0.99	2.01
GCNT1	2.74	1.24		PLLP	1.83	1.70		L3MBTL4	0.85	1.61
SMOC1	2.72	2.01		CCDC109B	1.81	1.53		SMPD3	0.85	1.18
KCNA5	2.69	1.80		KCNJ3	1.78	2.83		DAPK1	0.84	2.70
ADM	2.58	1.57		HCN1	1.78	1.74		SAT1	0.84	1.44
NEB	2.57	2.28		GNAO1	1.77	1.52		CLSTN2	0.81	1.40
ELMOD1	2.33	1.40		ZNF385B	1.53	2.12		NSUN7	0.80	1.31
SYT4	2.26	2.40		SLC39A8	1.52	3.33		PGRMC1	0.79	1.26
FGFR2	2.11	1.24		SLC7A11	1.46	3.18		SEMA3A	0.73	1.64
POF1B	2.09	1.55		MYRIP	1.41	1.13		PRCP	0.70	1.56
TIAM1	2.07	1.53		TGM1	1.38	1.32		MATN2	0.68	1.89

Supplemental Table 5: Stable isotope labeling by amino acids in cell culture (SILAC)-based proteomic data of iPSC-derived atrial (aCMs) compared to ventricular cardiomyocytes (vCMs). n = 4 vCM and n = 4 aCM independent differentiation experiments at day 68 from iPSC line isWT1.Bld2.

(A) 1,442 proteins with log2 fold < 0, of which 178 were significantly lower expressed in iPSC-aCMs.

Gene name	**log10 intensity**	**log2 (aCMs /vCMs)**	**Significance B**		**Gene names**	**log10 intensity**	**log2 (aCMs /vCMs)**	**Significance B**
DCN	8.66	-3.69	**1.2E-08**		G6PD	9.30	-1.88	**1.1E-03**
SULT1E1	10.82	-3.65	**4.9E-15**		HSPB3	10.02	-1.87	**2.0E-04**
DCD	9.43	-3.64	**1.3E-09**		FBN2	9.15	-1.87	**2.4E-03**
KCTD12	10.17	-3.58	**2.0E-12**		S100A6	10.39	-1.84	**1.7E-04**
MYL3	11.27	-3.50	**5.6E-14**		NRAP	9.10	-1.84	**2.7E-03**
BGN	8.67	-3.39	**1.5E-07**		CDH3	8.70	-1.83	**3.4E-03**
S100A4	9.65	-3.36	**1.7E-09**		SPON1	9.62	-1.81	**5.9E-04**
MYL2	11.49	-3.22	**4.0E-12**		COL6A6	8.62	-1.81	**3.8E-03**
COL12A1	9.47	-3.22	**6.6E-08**		EPB41L2	9.17	-1.78	**3.5E-03**
ANXA1	10.48	-3.17	**3.9E-10**		GBE1	10.91	-1.76	**9.3E-05**
PLS3	10.03	-3.07	**2.3E-09**		PDE1C	9.00	-1.73	**4.6E-03**
MYL5	10.48	-3.01	**2.6E-09**		PSMB9	9.41	-1.72	**2.4E-03**
AIF1L	9.28	-3.00	**4.3E-07**		CSRP1	10.63	-1.71	**4.5E-04**
PSAT1	10.30	-2.84	**1.7E-08**		MYO1B	8.50	-1.71	**5.8E-03**
BCAT1	8.99	-2.79	**1.1E-05**		SERPINE2	9.14	-1.70	**5.3E-03**
NNMT	9.16	-2.72	**1.7E-05**		REEP6	8.65	-1.68	**6.6E-03**
FLNB	9.71	-2.69	**9.1E-07**		FAM84B	9.11	-1.68	**5.7E-03**
IQGAP1	9.85	-2.69	**1.4E-07**		CAB39L	9.91	-1.68	**7.9E-04**
MDK	10.00	-2.68	**1.6E-07**		POMP	9.01	-1.66	**6.4E-03**
ARG2	9.73	-2.61	**1.8E-06**		COL1A2	9.62	-1.65	**1.5E-03**
COL3A1	10.07	-2.52	**7.7E-07**		PRKCA	9.30	-1.65	**3.6E-03**
RAB8B	8.61	-2.50	**8.6E-05**		AHNAK	11.97	-1.64	**2.6E-04**
TPM4	10.62	-2.49	**6.4E-07**		SNX18	8.94	-1.61	**7.8E-03**
FTL	8.93	-2.47	**8.2E-05**		MAOB	9.47	-1.56	**5.5E-03**
PNP	9.25	-2.45	**2.8E-05**		HEPH	9.40	-1.56	**5.5E-03**
TAGLN2	10.33	-2.44	**1.0E-06**		FSCN1	10.96	-1.55	**5.3E-04**
CLDN6	9.07	-2.41	**1.2E-04**		COL5A1	9.11	-1.55	**1.0E-02**
FLNA	11.08	-2.36	**2.6E-07**		HSPG2	10.06	-1.54	**2.0E-03**
COL1A1	9.98	-2.33	**4.6E-06**		ASS1	10.53	-1.51	**1.8E-03**
LAMB1	9.34	-2.32	**7.1E-05**		IKBIP	8.26	-1.51	**1.4E-02**
COL6A3	10.11	-2.31	**5.3E-06**		CGNL1	8.50	-1.50	**1.5E-02**
RCN3	9.11	-2.31	**2.2E-04**		GAK	9.09	-1.50	**1.3E-02**
COL15A1	8.65	-2.30	**2.7E-04**		ANKRD50	8.17	-1.49	**1.5E-02**
MST4	9.03	-2.29	**2.5E-04**		GUCY1A3	9.11	-1.47	**1.4E-02**
NDRG1	9.57	-2.25	**2.9E-05**		DSG1	7.93	-1.45	**1.8E-02**
TPM3;DKFZp686J1372	9.43	-2.24	**1.2E-04**		ITGA1	7.97	-1.44	**1.8E-02**
NAV1	9.66	-2.23	**3.4E-05**		FAM114A1	9.55	-1.44	**4.9E-03**
COTL1	10.06	-2.23	**1.1E-05**		KIF21A	9.22	-1.43	**1.0E-02**
MYH9	11.55	-2.21	**1.4E-06**		ABRACL	9.23	-1.42	**1.1E-02**
CAPZB	9.13	-2.20	**4.2E-04**		LTBP1	8.44	-1.41	**2.1E-02**
SLC1A3	8.58	-2.20	**5.0E-04**		MGP	8.49	-1.37	**2.4E-02**
LMCD1	9.13	-2.17	**5.0E-04**		RCSD1	9.92	-1.37	**5.6E-03**
GPNMB	8.60	-2.16	**6.2E-04**		FAM129B	9.55	-1.35	**7.5E-03**
ARPC1B	9.94	-2.15	**2.2E-05**		LAMA4	8.49	-1.35	**2.6E-02**
ACTB	9.50	-2.15	**2.1E-04**		COL6A2	9.27	-1.35	**1.5E-02**
CNTN1	7.98	-2.15	**6.7E-04**		PPP3CA	10.09	-1.34	**6.3E-03**
THY1	9.43	-2.13	**2.3E-04**		MYL6	10.59	-1.34	**5.0E-03**
ACTG1	11.52	-2.11	**3.6E-06**		PPL	8.95	-1.34	**2.4E-02**
ACTA1	8.82	-2.11	**8.1E-04**		ACLY	9.83	-1.33	**6.9E-03**
ENPEP	8.20	-2.10	**8.8E-04**		PLOD2	9.55	-1.33	**8.5E-03**
DHX40	9.75	-2.09	**9.7E-05**		MYL12A/B	9.88	-1.32	**7.4E-03**
MYLK3	9.78	-2.07	**1.1E-04**		PLCXD3	10.48	-1.30	**6.5E-03**
PYGL	11.07	-2.06	**6.1E-06**		FGF1	9.14	-1.29	**2.9E-02**
CYGB	8.34	-2.04	**1.2E-03**		CAP1	10.48	-1.27	**7.4E-03**
S100A11	9.69	-2.04	**1.3E-04**		SORBS2	9.42	-1.27	**2.0E-02**
ARHGDIB	9.69	-2.03	**1.4E-04**		ISG15	9.40	-1.27	**2.1E-02**
PHLDB2	8.85	-1.97	**1.6E-03**		S100A10	10.36	-1.26	**8.0E-03**
FGF12;FGF14	8.91	-1.95	**1.5E-03**		XIRP1	10.67	-1.24	**4.9E-03**
DLGAP4	8.64	-1.95	**1.9E-03**		RAI14	10.08	-1.22	**1.2E-02**
ASNS	9.32	-1.94	**7.5E-04**		NDUFA4L2	8.66	-1.22	**4.3E-02**
CALD1	10.37	-1.92	**9.3E-05**		APOE	9.95	-1.20	**1.4E-02**
FABP5	10.93	-1.92	**2.4E-05**		BIN1	9.10	-1.20	**4.1E-02**
HSPB2	10.42	-1.91	**1.0E-04**		PGK2	9.63	-1.19	**1.6E-02**
POTEE;POTEF;POTEJ	10.20	-1.91	**1.0E-04**		TLN2	10.72	-1.19	**6.8E-03**

ANXA2;ANXA2P2	11.79	-1.18	**7.1E-03**		AGRN	8.80	-0.92	1.1E-01
TTC27	8.18	-1.17	5.0E-02		PGM2	9.86	-0.92	5.4E-02
AHNAK2	10.08	-1.17	**1.6E-02**		TSC22D2	9.85	-0.92	5.4E-02
COL18A1	9.98	-1.17	**1.6E-02**		LIMS2	9.09	-0.92	1.0E-01
HECW2	8.50	-1.17	5.1E-02		CCDC40	9.03	-0.91	1.0E-01
TNS1	9.83	-1.17	**1.7E-02**		PSPH	9.86	-0.91	5.6E-02
PRKAG1	9.84	-1.15	**1.8E-02**		PAWR	8.87	-0.91	1.1E-01
PSMG1	9.23	-1.15	**3.3E-02**		PTGIS	9.43	-0.91	8.2E-02
UBE2E2;UBE2E3;UBE2E1	9.12	-1.15	**4.8E-02**		SH3BGRL3	10.01	-0.91	5.7E-02
METAP1	9.73	-1.15	**2.0E-02**		PIN4	9.13	-0.90	1.1E-01
ANXA3	11.33	-1.15	**8.7E-03**		MAP4	11.72	-0.90	**3.5E-02**
LXN	9.15	-1.14	**4.9E-02**		FTH1	9.92	-0.89	6.0E-02
NDRG3	9.38	-1.14	**3.5E-02**		SLC2A1	10.06	-0.89	6.1E-02
GUCY1B3	9.52	-1.14	**2.0E-02**		ZYX	10.40	-0.89	5.1E-02
COL14A1	9.80	-1.14	**2.0E-02**		DYNLT3	9.04	-0.89	1.1E-01
UCHL1	10.14	-1.14	**1.9E-02**		STXBP6	9.26	-0.89	8.8E-02
SPARC	9.27	-1.13	**3.6E-02**		FHL1	11.22	-0.88	**3.8E-02**
RAB6B	9.46	-1.13	**3.6E-02**		ADH5	11.13	-0.88	**3.8E-02**
VAT1	10.45	-1.13	**1.6E-02**		UBE2H	9.57	-0.88	6.0E-02
SORBS2	8.80	-1.12	6.0E-02		P4HA2	10.35	-0.87	5.5E-02
LGALS1	10.64	-1.11	**1.1E-02**		WASF2	9.64	-0.87	6.2E-02
COL6A1	10.12	-1.11	**2.2E-02**		TP53I3	9.81	-0.86	6.4E-02
SDCBP	9.57	-1.10	**2.4E-02**		UBE2G1	9.37	-0.86	9.7E-02
PPP3R1;HZGJ	9.61	-1.10	**2.4E-02**		SEPT2	11.01	-0.86	**4.3E-02**
DIAPH1	9.68	-1.09	**2.5E-02**		MLIP	8.63	-0.86	1.4E-01
TWF2	9.20	-1.08	**4.5E-02**		UXT	8.57	-0.85	1.4E-01
ARG1	8.84	-1.08	6.9E-02		MAPRE2	9.98	-0.85	7.1E-02
TNKS1BP1	9.17	-1.08	6.2E-02		GCN1L1	10.33	-0.85	6.0E-02
TLN1	11.19	-1.07	**1.4E-02**		PGK1	12.20	-0.85	**4.5E-02**
RPS6KA3	9.58	-1.07	**2.8E-02**		EIF4A1	10.41	-0.85	6.1E-02
GPD1L	10.42	-1.06	**2.3E-02**		GAB1	9.10	-0.85	1.3E-01
UGDH	9.89	-1.06	**2.9E-02**		TKT	10.87	-0.85	**4.5E-02**
HSPB6	11.36	-1.05	**1.5E-02**		PTPN12	8.56	-0.84	1.4E-01
LRRFIP1	8.61	-1.05	7.5E-02		CHN1	9.10	-0.84	1.3E-01
LEPRE1	9.66	-1.05	**3.0E-02**		HDAC6	9.06	-0.84	1.3E-01
WARS	10.48	-1.05	**2.4E-02**		GARS	10.61	-0.84	6.3E-02
PPP1R9B	9.61	-1.05	**3.0E-02**		GAPVD1	9.54	-0.84	6.9E-02
FKBP15	9.12	-1.05	6.8E-02		CPPED1	9.19	-0.84	1.3E-01
DPYSL5	9.86	-1.04	**3.1E-02**		SORBS2	11.02	-0.84	**4.7E-02**
ITGA5	8.69	-1.04	7.7E-02		PGM3	10.05	-0.84	7.6E-02
SNX24	8.58	-1.04	7.9E-02		ANKFY1	9.68	-0.84	6.9E-02
NFKB2	9.13	-1.03	7.2E-02		KPRP	7.74	-0.83	1.5E-01
CYFIP1	9.88	-1.02	**3.4E-02**		CHORDC1	9.49	-0.83	1.1E-01
PPFIBP1	9.67	-1.01	**3.5E-02**		TXNDC9	8.98	-0.83	1.3E-01
CAST	10.24	-1.01	**2.9E-02**		ZNF259	8.48	-0.83	1.5E-01
TPM3	10.34	-1.01	**2.9E-02**		NAMPT	10.51	-0.82	6.9E-02
PDLIM1	10.78	-1.01	**1.9E-02**		MYH10	11.08	-0.82	5.2E-02
MYO1E	9.10	-1.00	7.9E-02		KIAA0196	9.51	-0.82	1.1E-01
GFPT1	10.13	-0.99	**3.9E-02**		SELENBP1	10.25	-0.81	7.1E-02
LLGL2	8.80	-0.99	9.1E-02		GNL1	8.66	-0.81	1.5E-01
PMM2	9.42	-0.99	6.2E-02		GYG1	9.23	-0.81	1.1E-01
GPHN	9.52	-0.98	**3.9E-02**		APOBEC2	10.83	-0.81	5.4E-02
ACTN4	9.28	-0.98	6.4E-02		TUBA4A	10.63	-0.81	5.5E-02
PPP2R5C	8.44	-0.98	9.5E-02		XPOT	9.30	-0.81	1.2E-01
ITSN2	8.40	-0.98	9.6E-02		PPIP5K2	8.35	-0.81	1.6E-01
KPNA2	9.12	-0.97	8.6E-02		PXDN	9.45	-0.80	1.2E-01
ARHGEF2	9.65	-0.97	**4.2E-02**		XPO4	9.94	-0.80	8.8E-02
TWF1	9.14	-0.96	8.9E-02		MARCKS	10.44	-0.80	7.4E-02
PYCR1	9.63	-0.95	**4.5E-02**		ATOX1	9.05	-0.80	1.5E-01
CRTAP	9.35	-0.95	7.2E-02		PLCL2	9.66	-0.80	8.0E-02
EML4	8.88	-0.94	9.5E-02		SH3PXD2A	8.42	-0.80	1.6E-01
AKAP13	10.06	-0.94	**4.9E-02**		CASP7	8.74	-0.79	1.6E-01
SEPT9	10.90	-0.94	**2.8E-02**		TGFB1I1	10.02	-0.79	9.3E-02
ACOT7	8.83	-0.94	1.1E-01		PLOD1	10.26	-0.78	8.1E-02
CYTH2;CYTH1;CYTH3	8.59	-0.94	1.1E-01		CLIC1	10.78	-0.78	6.2E-02
MALT1	8.02	-0.93	1.1E-01		CDC34	8.58	-0.78	1.7E-01
ABCF3	8.53	-0.93	1.1E-01		GLUL	9.05	-0.78	1.5E-01
TANC1	9.22	-0.93	7.6E-02		PFKP	12.18	-0.78	6.3E-02
SEC24D	9.20	-0.93	7.6E-02		MVB12B	8.53	-0.78	1.7E-01
VCAN	8.98	-0.92	1.0E-01		PPM1G	9.22	-0.77	1.3E-01
NT5C2	10.04	-0.92	5.3E-02		CLTA	9.60	-0.77	8.9E-02
RECQL	9.29	-0.92	7.9E-02		DCTPP1	8.95	-0.76	1.6E-01

PHLDB1	9.11	-0.76	1.6E-01	PCK2	9.19	-0.65	2.1E-01
BROX	9.48	-0.76	1.3E-01	PAFAH1B2	10.21	-0.65	1.3E-01
SYAP1	8.81	-0.75	1.8E-01	IKBKAP	9.45	-0.64	1.9E-01
VCL	11.93	-0.75	7.1E-02	HSP90AB1	11.67	-0.64	1.1E-01
RTCA	9.57	-0.75	9.5E-02	GGCT	10.02	-0.64	1.6E-01
A0A096LP25;A0A096LNZ0;Q6ZSR9	9.03	-0.75	1.7E-01	MVP	10.16	-0.64	1.6E-01
				FLII	10.00	-0.64	1.6E-01
TSC22D3	9.35	-0.75	1.4E-01	FNTB;CHURC1-FNTB	9.36	-0.64	1.9E-01
SH3BGR	10.32	-0.75	9.2E-02	CPVL	10.61	-0.64	1.4E-01
ARL2BP	8.94	-0.75	1.7E-01	THOP1	9.61	-0.64	1.4E-01
PEA15	10.30	-0.75	9.3E-02	ROCK2	9.85	-0.64	1.6E-01
ABI2	8.54	-0.75	1.9E-01	NCKAP1	10.53	-0.64	1.4E-01
SDK2	8.06	-0.74	1.9E-01	IFITM3;IFITM2;IFITM1	9.68	-0.63	1.4E-01
CRYAB	11.96	-0.74	7.4E-02	RNF213	9.13	-0.63	2.3E-01
LAMC1	9.96	-0.74	1.1E-01	MAPKAPK3	8.53	-0.63	2.5E-01
HBS1L	8.53	-0.73	1.9E-01	NUDCD1	9.09	-0.62	2.3E-01
DIP2B	9.45	-0.73	1.4E-01	ISOC1	11.18	-0.62	1.2E-01
FBXL18	8.60	-0.73	1.9E-01	SERPINH1	11.31	-0.62	1.2E-01
VPS4B	8.99	-0.73	1.8E-01	TARS	10.21	-0.62	1.5E-01
ZNF622	8.24	-0.73	1.9E-01	PPME1	9.79	-0.62	1.5E-01
ENO1	12.44	-0.73	7.9E-02	ACACA	8.86	-0.61	2.4E-01
PARVA	10.38	-0.72	1.0E-01	MAP2K1	10.13	-0.61	1.8E-01
REPS1	8.79	-0.72	2.0E-01	IPO9	10.15	-0.61	1.8E-01
CASP3	9.98	-0.72	1.2E-01	IPO4	8.53	-0.61	2.6E-01
CD2AP	8.91	-0.72	1.8E-01	PTK2	8.93	-0.61	2.4E-01
RPAP1	10.35	-0.72	1.0E-01	AAK1	9.27	-0.61	2.1E-01
FOCAD	8.62	-0.72	2.0E-01	PKN1	8.50	-0.61	2.6E-01
CYFIP2	10.41	-0.72	1.0E-01	UBAC1	8.73	-0.60	2.6E-01
PTPN11	10.14	-0.71	1.2E-01	CSRP2	9.55	-0.60	1.6E-01
SERPINB9	9.90	-0.71	1.2E-01	COMMD4	9.32	-0.60	2.1E-01
PGM2L1	9.46	-0.71	1.5E-01	DYSF	10.02	-0.60	1.8E-01
AEBP1	8.79	-0.71	2.0E-01	P4HA1	10.60	-0.60	1.6E-01
FKBP7	8.88	-0.71	1.9E-01	EIF5B	9.98	-0.60	1.9E-01
SWAP70	9.35	-0.71	1.6E-01	GALE	9.97	-0.60	1.9E-01
ANTXR2	9.00	-0.70	1.9E-01	PGD	11.07	-0.60	1.4E-01
SPATA5	8.30	-0.70	2.1E-01	SH3GLB1	10.46	-0.60	1.6E-01
PDLIM5	9.52	-0.70	1.6E-01	CRK	9.33	-0.59	2.2E-01
PLOD3	9.31	-0.70	1.6E-01	HEMK2;N6AMT1	8.65	-0.59	2.7E-01
VARS	10.33	-0.70	1.1E-01	HDDC2	9.39	-0.59	2.2E-01
ARF4	10.45	-0.70	1.1E-01	MYH14	10.17	-0.59	1.7E-01
KIAA1279	8.58	-0.69	2.1E-01	PPP4R1	9.00	-0.59	2.5E-01
ABI1	9.42	-0.69	1.6E-01	CCDC6	9.81	-0.59	1.6E-01
OSTF1	9.11	-0.69	1.9E-01	NAGLU	8.76	-0.58	2.8E-01
PTPN9	8.39	-0.69	2.1E-01	KIAA1033	9.38	-0.58	2.2E-01
PFKL	10.78	-0.69	9.3E-02	MYH13	10.81	-0.58	1.5E-01
PHGDH	11.11	-0.69	9.3E-02	SRM	9.28	-0.58	2.2E-01
CRABP2	10.96	-0.69	9.4E-02	UNC45B	11.37	-0.58	1.5E-01
RNASET2	9.78	-0.69	1.2E-01	URM1	8.89	-0.58	2.6E-01
HSPH1	9.93	-0.69	1.4E-01	CCDC93	8.81	-0.58	2.8E-01
CPNE3	10.53	-0.69	1.2E-01	SOS1	8.12	-0.58	2.8E-01
TSC22D1	9.16	-0.69	2.0E-01	FABP3	12.08	-0.57	1.5E-01
ANXA5	11.78	-0.69	9.5E-02	PTMA	9.06	-0.57	2.6E-01
ATXN7L3B	8.54	-0.68	2.2E-01	CPQ	9.29	-0.57	2.3E-01
RICTOR	9.17	-0.68	2.0E-01	PPID	9.48	-0.57	2.3E-01
ARHGAP35;GRLF1	8.72	-0.68	2.2E-01	AKT1	9.35	-0.57	2.3E-01
KIF13A	9.57	-0.68	1.2E-01	PHYHD1	9.44	-0.57	2.3E-01
ATL3	8.90	-0.68	2.0E-01	GART	10.10	-0.57	2.1E-01
STAT1	10.23	-0.68	1.2E-01	PLCG1	9.04	-0.56	2.7E-01
CARS	9.40	-0.68	1.7E-01	VPS13C	9.86	-0.56	2.1E-01
CDK6	9.23	-0.68	1.7E-01	EIF4EBP1	8.83	-0.56	2.9E-01
TTC38	8.62	-0.68	2.2E-01	SEPT10	10.35	-0.56	1.8E-01
PLCL1	9.66	-0.68	1.2E-01	C9orf64	9.64	-0.56	1.8E-01
CNN2	9.69	-0.67	1.2E-01	CHMP4B	9.89	-0.56	2.1E-01
COMMD8	9.11	-0.67	2.0E-01	ARHGDIA	10.74	-0.56	1.6E-01
HNRNPC	8.93	-0.67	2.1E-01	HSP90AB2P	10.24	-0.56	1.9E-01
UTRN	10.35	-0.66	1.3E-01	CHMP1B	9.13	-0.55	2.7E-01
ICAM1	8.72	-0.66	2.3E-01	MAGED2	10.43	-0.55	1.9E-01
PYGM	10.96	-0.66	1.1E-01	DNAJB4	8.63	-0.55	3.0E-01
MIF4GD	8.84	-0.66	2.3E-01	STAMBPL1	9.49	-0.55	2.5E-01
PACS1	9.95	-0.66	1.5E-01	EPS15	9.23	-0.55	2.5E-01
RPS4Y1	8.99	-0.65	2.1E-01	COMMD3;BMI1	9.51	-0.55	2.5E-01
TTC37	9.82	-0.65	1.5E-01	BZW1	9.84	-0.54	2.2E-01

SEC31A	10.35	-0.54	2.0E-01		COPG1	10.41	-0.48	2.4E-01
DAB2IP	8.65	-0.54	3.1E-01		SCRN2	9.77	-0.48	2.2E-01
UBXN7	8.78	-0.54	3.1E-01		SNW1	9.01	-0.48	3.3E-01
USP15	9.43	-0.54	2.5E-01		SLK	10.32	-0.48	2.4E-01
GPI	12.08	-0.54	1.7E-01		LYPLA2	9.94	-0.48	2.7E-01
RCC2	9.17	-0.54	2.8E-01		VPS35	10.50	-0.48	2.4E-01
PPP2CB	8.97	-0.54	2.8E-01		APRT	10.14	-0.48	2.7E-01
CDK2;CDK3	8.86	-0.54	2.8E-01		TRIP10	8.86	-0.47	3.3E-01
PDCD10	10.12	-0.54	2.2E-01		MROH1	9.24	-0.47	3.0E-01
COMMD2	9.34	-0.54	2.5E-01		CSK	9.45	-0.47	3.0E-01
CBFB	8.99	-0.54	2.9E-01		SRP54	9.61	-0.47	2.3E-01
RGL1	8.86	-0.54	2.9E-01		NRBP1	10.43	-0.47	2.5E-01
PACSIN3	9.75	-0.54	1.9E-01		NUP214	8.68	-0.47	3.6E-01
LDHA	12.45	-0.53	1.8E-01		TRIOBP	9.90	-0.47	2.8E-01
EXOC6B	9.48	-0.53	2.5E-01		UBR4	10.48	-0.47	2.5E-01
CD63	9.37	-0.53	2.5E-01		LMNA	9.76	-0.47	2.3E-01
TBC1D15	9.63	-0.53	1.9E-01		PFN2	10.48	-0.47	2.5E-01
FKBP10	10.20	-0.53	2.0E-01		ARPC5	10.34	-0.47	2.5E-01
PPM1F	9.28	-0.53	2.6E-01		SEPT7	11.15	-0.47	2.2E-01
TPD52;MRPS28	8.78	-0.53	3.2E-01		DHX36	9.07	-0.47	3.4E-01
FNTA	9.35	-0.53	2.6E-01		TBCD	9.98	-0.46	2.8E-01
UBA6	10.16	-0.53	2.3E-01		EIF1	9.96	-0.46	2.8E-01
MTMR2	8.45	-0.53	3.2E-01		GDI2	11.20	-0.46	2.3E-01
LAMP2	10.11	-0.53	2.4E-01		REXO2	9.57	-0.46	2.3E-01
FERMT2	10.75	-0.52	1.8E-01		UBQLN1	9.61	-0.46	2.4E-01
STK39	10.28	-0.52	2.1E-01		AP3M1	9.38	-0.46	3.1E-01
PPP2R3A	8.72	-0.52	3.2E-01		NAA25	9.23	-0.46	3.1E-01
ISYNA1	10.87	-0.52	1.9E-01		WBP2	9.00	-0.46	3.4E-01
RCN1	10.23	-0.52	2.1E-01		BOLA2;BOLA2B;LOC101060252	9.83	-0.46	2.9E-01
MEMO1	9.13	-0.51	3.0E-01					
NUTF2	10.77	-0.51	1.9E-01		MOB1A;MOB1B	9.58	-0.46	2.4E-01
TSC22D4	9.22	-0.51	2.7E-01		PELO	8.99	-0.45	3.4E-01
MLLT4	9.59	-0.51	2.0E-01		YWHAH	11.01	-0.45	2.4E-01
ITGB1BP2	9.78	-0.51	2.0E-01		BRK1	9.51	-0.45	3.1E-01
GGPS1	9.43	-0.51	2.7E-01		MTOR	9.83	-0.45	2.9E-01
ABHD14B	9.51	-0.51	2.7E-01		AARS	10.80	-0.45	2.4E-01
NME1	10.06	-0.51	2.5E-01		GLRX3	10.30	-0.45	2.6E-01
DPP3	10.07	-0.51	2.5E-01		CORO1B	9.00	-0.45	3.5E-01
SCYL1	8.63	-0.51	3.3E-01		PRRC1	9.25	-0.45	3.1E-01
EIF4G1	10.35	-0.51	2.2E-01		XPO5	8.91	-0.45	3.5E-01
ARIH2	9.22	-0.51	2.7E-01		LRP1	9.96	-0.45	3.0E-01
RAP1GDS1	10.33	-0.51	2.2E-01		UBE2L3	10.63	-0.45	2.7E-01
CDV3	9.84	-0.51	2.5E-01		SEPT11	10.75	-0.45	2.4E-01
ALPK3	9.00	-0.51	3.1E-01		C17orf49;BAP18;RNASEK-C17orf49	9.11	-0.45	3.5E-01
DNAJC7	9.67	-0.51	2.1E-01					
L3HYPDH	9.06	-0.51	3.1E-01		ARIH1	8.85	-0.44	3.8E-01
GSTP1	11.50	-0.51	2.0E-01		TAGLN	11.24	-0.44	2.4E-01
KANK2	10.22	-0.51	2.2E-01		WASL	9.42	-0.44	3.2E-01
C16orf80	9.18	-0.51	3.1E-01		SRP68	9.94	-0.44	3.0E-01
HDLBP	10.26	-0.50	2.2E-01		TPT1	10.82	-0.44	2.5E-01
TOM1L2	9.50	-0.50	2.7E-01		STARD7	8.64	-0.44	3.8E-01
PSMD9	9.80	-0.50	2.1E-01		NANS	9.84	-0.44	3.1E-01
COG6	8.98	-0.50	3.1E-01		CHMP1A	9.36	-0.44	3.2E-01
SORBS1	8.67	-0.50	3.4E-01		SNX1	9.80	-0.44	2.5E-01
NEK7	10.18	-0.50	2.3E-01		SNX3	10.16	-0.44	3.1E-01
EGLN1	8.66	-0.50	3.4E-01		NUDC	10.36	-0.44	2.7E-01
DST	9.64	-0.49	2.1E-01		AP3B1	9.94	-0.44	3.1E-01
AKR1B1	11.79	-0.49	2.0E-01		VPS26A	9.93	-0.43	3.1E-01
DCTD	9.16	-0.49	3.2E-01		XPNPEP1	10.57	-0.43	2.8E-01
GCLC	9.13	-0.49	3.2E-01		HERC4	9.40	-0.43	3.2E-01
ENO3	11.59	-0.49	2.1E-01		MON2	8.89	-0.43	3.6E-01
RSU1	10.50	-0.49	2.3E-01		FAM21A;FAM21B;FAM21C	8.84	-0.43	3.9E-01
ROCK1	10.09	-0.49	2.6E-01		EFTUD1	9.47	-0.43	3.3E-01
IKBKB	8.38	-0.49	3.5E-01		RRBP1	9.71	-0.43	2.5E-01
CLIP1	9.04	-0.49	3.2E-01		CYP2J2	9.15	-0.43	3.6E-01
COPA	10.80	-0.48	2.1E-01		RNF123	9.19	-0.43	3.6E-01
MYO6	8.60	-0.48	3.5E-01		STK24	9.70	-0.43	2.6E-01
KANK1	8.49	-0.48	3.5E-01		DDX19B;DDX19A	8.49	-0.43	3.9E-01
HN1L	8.56	-0.48	3.5E-01		DNAJA1	10.17	-0.43	3.1E-01
ERO1L	10.45	-0.48	2.4E-01		CLIC4	11.31	-0.43	2.5E-01
OBSL1	9.99	-0.48	2.7E-01		EXOC7	9.72	-0.43	2.6E-01
ANXA4	10.38	-0.48	2.4E-01		RANBP1	10.19	-0.43	2.8E-01

ILK	10.59	-0.43	2.8E-01		UBAP2	8.51	-0.38	4.4E-01
STMN1	11.08	-0.43	2.6E-01		RABEP1	9.29	-0.38	3.7E-01
GSPT1	9.95	-0.43	3.2E-01		RAN	11.05	-0.38	3.0E-01
FASN	10.65	-0.43	2.6E-01		CNOT11	8.62	-0.38	4.4E-01
DPCD	9.28	-0.42	3.3E-01		CACYBP	10.26	-0.38	3.3E-01
LIMS1	9.76	-0.42	2.6E-01		DHX57	7.91	-0.37	4.4E-01
SKIV2L	9.67	-0.42	2.6E-01		MMS19	9.45	-0.37	3.7E-01
EIF5A;EIF5AL1;EIF5A2	11.04	-0.42	2.6E-01		PDLIM5	11.37	-0.37	3.1E-01
AKAP12	10.26	-0.42	2.9E-01		PNMA3	9.24	-0.37	3.8E-01
MARK3	8.73	-0.42	4.0E-01		TIGAR	8.67	-0.37	4.4E-01
GBF1	9.74	-0.42	2.6E-01		NDE1;NDEL1	8.76	-0.37	4.4E-01
COPB1	10.54	-0.42	2.9E-01		DDAH2	10.65	-0.37	3.1E-01
RPS15A	9.19	-0.42	3.7E-01		TNNC1	10.42	-0.37	3.4E-01
HK2	9.81	-0.42	2.6E-01		EIF2B5	9.04	-0.37	4.1E-01
ZC3HAV1L	9.71	-0.42	2.7E-01		IPO11	8.88	-0.37	4.1E-01
ASPSCR1	8.68	-0.42	4.0E-01		ACADS	10.31	-0.37	3.4E-01
SMPX	9.30	-0.42	3.4E-01		LASP1	10.10	-0.37	3.8E-01
A0A075B730;A0A087X1U6	9.94	-0.42	3.3E-01		ETF1	10.01	-0.36	3.8E-01
RTN4	9.17	-0.41	3.8E-01		SEPT6	9.88	-0.36	3.8E-01
EEF2	11.64	-0.41	2.7E-01		TSC2	8.47	-0.36	4.5E-01
TRAF6	8.80	-0.41	4.1E-01		HSP90AA1	12.00	-0.36	3.2E-01
HEATR6	7.81	-0.41	4.1E-01		PTPN23	9.33	-0.36	3.8E-01
IST1	10.07	-0.41	3.3E-01		C12orf57	8.73	-0.36	4.5E-01
COMMD1	9.06	-0.41	3.8E-01		EIF2AK4	9.63	-0.36	3.1E-01
SPTAN1	9.20	-0.41	3.4E-01		ASMTL	9.76	-0.36	3.1E-01
CFL1	11.78	-0.41	2.7E-01		MBNL1;MBLL;MBNL2	9.18	-0.36	4.2E-01
PPP6R1	8.81	-0.41	4.1E-01		GEMIN5	8.54	-0.36	4.5E-01
MICAL3	9.74	-0.41	2.7E-01		PSMD5	10.27	-0.36	3.4E-01
RAPGEF1	8.51	-0.41	4.1E-01		MCAM	9.92	-0.36	3.8E-01
YKT6	9.84	-0.41	3.4E-01		IDI1	9.10	-0.36	4.2E-01
SNX6	10.08	-0.41	3.4E-01		LRRC57	9.38	-0.36	3.9E-01
PFAS	10.25	-0.41	3.0E-01		LRRC40	9.54	-0.36	3.1E-01
FLNC	12.46	-0.41	2.8E-01		UBLCP1	9.09	-0.36	4.2E-01
STIP1	11.24	-0.41	2.8E-01		CNBP	9.66	-0.36	3.1E-01
DPP9	9.07	-0.40	3.8E-01		TPI1	12.36	-0.36	3.2E-01
TUBB	11.65	-0.40	2.8E-01		BIRC6	9.16	-0.36	4.2E-01
PITPNA	10.20	-0.40	3.0E-01		EXOC4	9.83	-0.36	3.8E-01
CALCOCO1	8.20	-0.40	4.1E-01		NUDT1	9.21	-0.36	3.9E-01
VPS29	10.12	-0.40	3.4E-01		TUBB4B	12.24	-0.36	3.2E-01
TXN	10.61	-0.40	3.0E-01		S100A13	10.01	-0.36	3.9E-01
PM20D2	9.25	-0.40	3.5E-01		FKBP3	10.63	-0.36	3.5E-01
IFI16	8.87	-0.40	3.9E-01		HGS	9.98	-0.36	3.9E-01
ARAP1	8.17	-0.40	4.2E-01		COMMD10	8.51	-0.36	4.6E-01
TUBA1A;TUBA3C;TUBA3E	11.25	-0.40	2.8E-01		GLMN	8.92	-0.35	4.3E-01
DYNC1H1	11.85	-0.40	2.8E-01		FBXO2	9.31	-0.35	3.9E-01
TSR1	8.31	-0.40	4.2E-01		NAA15	9.84	-0.35	3.9E-01
NID1	9.27	-0.40	3.5E-01		STAM	9.81	-0.35	3.1E-01
CLASP1	9.84	-0.40	3.5E-01		NRD1	8.86	-0.35	4.3E-01
INF2	9.41	-0.40	3.6E-01		PDE6D	9.03	-0.35	4.3E-01
SAE1	9.89	-0.39	3.5E-01		NME2;NME1-NME2;NME1	11.34	-0.35	3.3E-01
TUBA1B	12.41	-0.39	2.9E-01		NUDT5	10.36	-0.35	3.5E-01
YWHAG	11.37	-0.39	2.9E-01		TJP1	9.88	-0.35	3.9E-01
IARS	10.65	-0.39	2.9E-01		ENAH	9.75	-0.35	3.2E-01
DENND5B	8.96	-0.39	4.0E-01		NAA10	10.16	-0.35	3.9E-01
NMT1	9.69	-0.39	2.9E-01		TAOK1	8.50	-0.35	4.6E-01
LARP1	9.65	-0.39	2.9E-01		CMPK1	10.17	-0.35	3.6E-01
FAM50A	9.14	-0.39	4.0E-01		ELP3	9.13	-0.35	4.3E-01
UBE2Z	9.56	-0.39	2.9E-01		AKT2	8.43	-0.35	4.6E-01
SRP72	9.77	-0.39	2.9E-01		TMX1	9.47	-0.35	4.0E-01
PPIC	9.55	-0.39	2.9E-01		FHIT	9.79	-0.34	3.2E-01
SBDS	10.11	-0.39	3.5E-01		EEF1A1P5;EEF1A1	12.19	-0.34	3.4E-01
FBXL8	8.32	-0.39	4.3E-01		PEF1	9.65	-0.34	3.2E-01
HPRT1	10.49	-0.39	3.2E-01		ENO2	11.04	-0.34	3.4E-01
DNAJC9	9.15	-0.39	4.0E-01		C1orf123	9.87	-0.34	4.0E-01
HSPA14	8.82	-0.38	4.3E-01		FKBP5	9.07	-0.34	4.4E-01
CNOT1	9.65	-0.38	2.9E-01		C16orf13	9.36	-0.34	4.0E-01
ACSS2	9.84	-0.38	3.6E-01		PARP1	10.13	-0.34	4.0E-01
TES	10.11	-0.38	3.6E-01		ARFGAP1	8.95	-0.34	4.4E-01
SLC3A2	9.31	-0.38	3.7E-01		TCEA3	8.51	-0.34	4.7E-01
CIAPIN1	9.96	-0.38	3.6E-01		PPP6R3	9.62	-0.34	3.3E-01
COMMD6	8.88	-0.38	4.0E-01		SEC13	10.20	-0.34	3.7E-01
IRGQ	9.35	-0.38	3.7E-01		ARPC4;ARPC4-TTLL3	10.82	-0.34	3.5E-01

SRP19	9.39	-0.34	4.1E-01		DYNC1I2	10.58	-0.30	4.1E-01
COPB2	10.41	-0.34	3.7E-01		TRIM25	9.56	-0.30	3.6E-01
DAK	9.35	-0.33	4.1E-01		ABI2	9.26	-0.30	4.4E-01
TUBB8	10.53	-0.33	3.7E-01		VWA5A	9.02	-0.30	4.8E-01
ARHGAP17	9.12	-0.33	4.4E-01		MPDZ	8.17	-0.30	5.1E-01
SNX2	10.26	-0.33	3.7E-01		DRAP1	8.95	-0.30	4.8E-01
DPYSL2	11.10	-0.33	3.5E-01		UBE2L6	9.16	-0.30	4.8E-01
PIK3C3	8.67	-0.33	4.8E-01		PPP6C	9.90	-0.29	4.5E-01
GANAB	9.46	-0.33	4.1E-01		RPE	9.31	-0.29	4.5E-01
ARPC3	10.60	-0.33	3.7E-01		SNX12	9.89	-0.29	4.5E-01
EIF6	10.03	-0.33	4.1E-01		CARM1	9.54	-0.29	3.7E-01
ACTR2	10.59	-0.33	3.7E-01		CTTN	10.18	-0.29	4.1E-01
UBE3A	9.75	-0.33	3.3E-01		PPP3CC	8.94	-0.29	4.8E-01
IPO7	10.49	-0.33	3.7E-01		EML1	9.67	-0.29	3.7E-01
PDXDC1	9.12	-0.33	4.5E-01		OARD1	9.20	-0.29	4.5E-01
RBM8A	9.44	-0.33	4.1E-01		MTHFD1	10.64	-0.29	4.0E-01
CCDC22	9.27	-0.33	4.1E-01		PRMT5	10.22	-0.29	4.2E-01
NUP155	8.78	-0.33	4.8E-01		CTPS1	9.68	-0.29	3.7E-01
ARAF	8.31	-0.33	4.8E-01		TARSL2	9.24	-0.29	4.5E-01
DCLK2	9.55	-0.33	3.3E-01		AIP	9.30	-0.29	4.5E-01
UBE2I	10.07	-0.32	4.2E-01		DCTN1;DKFZp686E0752	10.71	-0.29	4.0E-01
PDCD6	9.99	-0.32	4.2E-01		COMMD9	9.63	-0.28	3.7E-01
SLC27A6	10.16	-0.32	4.2E-01		ABCF2	8.97	-0.28	4.9E-01
PDCD6IP	10.85	-0.32	3.6E-01		VBP1	10.25	-0.28	4.2E-01
PRKG1	9.65	-0.32	3.4E-01		KIAA1468	8.49	-0.28	5.2E-01
LARS	10.50	-0.32	3.8E-01		P4HB	11.54	-0.28	4.0E-01
NAA50	9.71	-0.32	3.4E-01		SPAG9	9.40	-0.28	4.6E-01
CIAO1	9.13	-0.32	4.5E-01		VPS52	9.34	-0.28	4.6E-01
DDX3Y	8.47	-0.32	4.9E-01		DNAJB1	9.68	-0.28	3.7E-01
BLVRA	10.47	-0.32	3.8E-01		TRAPPC11	8.27	-0.28	5.3E-01
MURC	10.18	-0.32	3.8E-01		H2AFV;H2AFZ	9.26	-0.28	4.6E-01
CELF1	8.89	-0.32	4.6E-01		TNNI1	10.86	-0.28	4.1E-01
AP3D1	9.74	-0.32	3.4E-01		CAPN2	10.43	-0.28	4.3E-01
NPEPL1	8.96	-0.32	4.6E-01		CSRP3	11.83	-0.28	4.1E-01
TTC28	8.90	-0.32	4.6E-01		AASDHPPT	10.03	-0.28	4.7E-01
ATXN2	8.70	-0.32	4.9E-01		DBN1	9.80	-0.28	3.8E-01
EXOC3	9.42	-0.32	4.3E-01		PFN1	11.70	-0.28	4.1E-01
EIF2B1	9.88	-0.32	4.3E-01		ECM29;KIAA0368	9.98	-0.28	4.7E-01
ESYT1	9.80	-0.32	3.5E-01		SEC23IP	9.60	-0.28	3.8E-01
MYL9	10.57	-0.31	3.9E-01		CDC37	10.21	-0.28	4.3E-01
LUC7L2	8.63	-0.31	4.9E-01		PABPC1	10.66	-0.28	4.1E-01
MVD	9.15	-0.31	4.6E-01		HECTD1	9.33	-0.28	4.6E-01
C19orf10	10.19	-0.31	3.9E-01		ADSSL1	9.62	-0.28	3.8E-01
ACTC1	10.85	-0.31	3.7E-01		MAP2K2	10.27	-0.28	4.3E-01
COPE	10.00	-0.31	4.3E-01		MCMBP	8.85	-0.28	5.3E-01
PIK3R4	8.58	-0.31	5.0E-01		C15orf38	8.99	-0.28	5.0E-01
NEDD8	8.15	-0.31	5.0E-01		ACP1	10.49	-0.27	4.3E-01
TFG	10.38	-0.31	3.9E-01		FKBP1A	10.50	-0.27	4.3E-01
AHSA1	10.05	-0.31	4.4E-01		FKBP4	10.35	-0.27	4.3E-01
PEX19	9.17	-0.31	4.7E-01		VPS26B	9.21	-0.27	4.6E-01
PCLO	9.11	-0.31	4.7E-01		DYNC1LI1	10.71	-0.27	4.2E-01
USP9X;USP9Y	10.13	-0.31	4.4E-01		UBA2	9.73	-0.27	3.8E-01
LRRFIP1	9.14	-0.31	4.7E-01		STOM	9.65	-0.27	3.8E-01
DDX3X	10.07	-0.31	4.4E-01		ACTN1	10.54	-0.27	4.3E-01
HACE1	8.45	-0.31	5.0E-01		PTGES3	10.50	-0.27	4.3E-01
C5orf51	9.20	-0.31	4.3E-01		CUL2	10.03	-0.27	4.8E-01
C1orf198	9.12	-0.31	4.7E-01		PFDN2	10.10	-0.27	4.8E-01
NDRG2	10.39	-0.30	4.0E-01		UBR3	9.22	-0.27	4.7E-01
EXOC5	9.50	-0.30	4.4E-01		SARS	10.40	-0.27	4.4E-01
UBE2D2	10.09	-0.30	4.4E-01		FEN1	9.56	-0.27	3.8E-01
MAPKAP1	8.52	-0.30	5.0E-01		TRAPPC5	9.64	-0.27	3.9E-01
ARHGEF7	9.49	-0.30	4.4E-01		COPZ1	10.08	-0.27	4.8E-01
PCNP	9.73	-0.30	3.6E-01		SEPT8	10.17	-0.27	4.4E-01
CTSC	10.15	-0.30	4.4E-01		AKAP2	10.62	-0.27	4.4E-01
ERC1	9.94	-0.30	4.4E-01		MYO9B	9.12	-0.27	5.0E-01
PPM1B	9.46	-0.30	4.4E-01		PITHD1	9.56	-0.27	3.9E-01
PPP2R5A	9.95	-0.30	4.4E-01		CNDP2	10.63	-0.27	4.4E-01
RAF1	9.46	-0.30	4.4E-01		MAGOHB	9.66	-0.27	3.9E-01
PHLDA3	8.86	-0.30	4.7E-01		NARS	10.62	-0.27	4.4E-01
PFDN6	9.90	-0.30	4.5E-01		ZC3H15	9.09	-0.27	5.1E-01
PALLD	10.39	-0.30	4.0E-01		ANKRD17	8.40	-0.27	5.4E-01
UBE2K	10.06	-0.30	4.5E-01		EIF2A	9.47	-0.27	4.7E-01

HYPK	9.18	-0.27	5.1E-01		ATXN10	10.02	-0.23	5.3E-01
ACTR3	10.80	-0.26	4.3E-01		HIST1H2AJ;HIST1H2AH;H2AFJ;HIST2H2AC;HIST1H2AC;HIST3H2A;HIST2H2AA3;HIST1H2AD;HIST1H2AG;HIST1H2AB	10.66	-0.23	4.7E-01
MAP1S	9.67	-0.26	3.9E-01					
STAU1	9.46	-0.26	4.8E-01					
HMGB1;HMGB1P1	11.28	-0.26	4.3E-01					
GLRX2	8.86	-0.26	5.4E-01		EIF2B3	9.06	-0.23	5.4E-01
ANP32A	10.96	-0.26	4.3E-01		GMPS	10.05	-0.23	5.3E-01
SNX9	9.59	-0.26	3.9E-01		SUMO3	10.10	-0.23	5.3E-01
KLC4	9.46	-0.26	4.8E-01		MTR	9.95	-0.23	5.3E-01
ITGA9	8.66	-0.26	5.4E-01		SYNCRIP	10.15	-0.23	5.3E-01
RAB3GAP2	9.53	-0.26	3.9E-01		HIST2H2BE;HIST1H2BB;HIST1H2BO;HIST1H2BJ	9.37	-0.23	5.1E-01
PROSC	10.16	-0.26	4.9E-01					
PSME2	10.85	-0.26	4.3E-01		ILKAP;ILKAP3	9.26	-0.22	5.1E-01
RIC8A	9.77	-0.26	3.9E-01		TRIM23	8.87	-0.22	5.5E-01
C11orf68	9.17	-0.26	5.1E-01		PBDC1	9.50	-0.22	5.1E-01
DRG1	9.62	-0.26	3.9E-01		PRKCSH	10.72	-0.22	4.8E-01
NSUN2	9.19	-0.26	5.1E-01		EDF1	9.92	-0.22	5.4E-01
TPM2	9.55	-0.26	4.0E-01		ECE1	9.07	-0.22	5.5E-01
HUWE1	10.70	-0.26	4.4E-01		TCEA1	9.54	-0.22	4.3E-01
TSC1	8.50	-0.26	5.5E-01		COMMD7	9.03	-0.22	5.5E-01
EIF1AY	10.25	-0.26	4.5E-01		A0A0A0MS51	11.85	-0.22	4.8E-01
MSN	11.00	-0.25	4.4E-01		SMYD5	8.97	-0.22	5.5E-01
PAICS	10.77	-0.25	4.4E-01		CKAP5	10.12	-0.22	5.4E-01
RILPL1	8.44	-0.25	5.5E-01		XPO7	10.38	-0.22	4.9E-01
ARHGAP5	8.53	-0.25	5.5E-01		CHMP2A	9.38	-0.22	5.2E-01
CAND2	9.97	-0.25	5.0E-01		PSME4	8.36	-0.22	5.9E-01
PDXP	10.16	-0.25	5.0E-01		PRPSAP2	10.01	-0.22	5.4E-01
BTF3L4	9.79	-0.25	4.0E-01		UBA1	11.16	-0.22	4.9E-01
RAB3GAP1	9.36	-0.25	4.9E-01		ATG4B	8.69	-0.22	5.9E-01
MYOF	9.02	-0.25	5.2E-01		GPRIN3	8.81	-0.22	5.9E-01
PAFAH1B1	10.62	-0.25	4.6E-01		SEC24A	8.67	-0.22	5.9E-01
FAM127A;FAM127C	9.80	-0.25	4.0E-01		MAPK3	9.44	-0.22	5.2E-01
KIAA1143	8.47	-0.25	5.6E-01		ATRIP	9.75	-0.22	4.4E-01
ARCN1	10.53	-0.25	4.6E-01		USP24	9.70	-0.21	4.4E-01
RASA1	8.70	-0.25	5.6E-01		WDR77	9.88	-0.21	5.5E-01
MOB2	9.32	-0.25	4.9E-01		PKN2	9.16	-0.21	5.6E-01
NQO2	10.05	-0.25	5.1E-01		SEC24C	9.95	-0.21	5.5E-01
PICALM	9.72	-0.25	4.1E-01		ACTR1B	10.01	-0.21	5.5E-01
TBCC	9.07	-0.24	5.3E-01		RABGAP1	9.60	-0.21	4.4E-01
CHMP5	9.60	-0.24	4.1E-01		SFN	10.93	-0.21	4.9E-01
UBA5	9.44	-0.24	4.9E-01		ATG3	9.42	-0.21	5.3E-01
NCAPG	8.02	-0.24	5.6E-01		HMGB2	10.85	-0.21	4.9E-01
STAT3	10.55	-0.21	5.0E-01		PSME1	11.17	-0.21	4.9E-01
CAPNS1	10.71	-0.24	4.5E-01		BAG5	8.69	-0.21	5.9E-01
CAP2	11.13	-0.24	4.5E-01		CSE1L	10.72	-0.21	4.9E-01
UBL5	9.49	-0.24	5.0E-01		EEA1	10.43	-0.21	5.0E-01
RABGGTB	8.82	-0.24	5.6E-01		VPS4A	10.11	-0.21	5.5E-01
LZTFL1	8.98	-0.24	5.3E-01		GGA2	9.01	-0.21	5.6E-01
TRIO	8.29	-0.24	5.6E-01		RNPEP	10.13	-0.21	5.5E-01
ARPC2	10.82	-0.24	4.5E-01		EIF4E	10.04	-0.21	5.6E-01
TXNDC5	10.42	-0.24	4.7E-01		CAPN1	10.69	-0.21	5.0E-01
RABGGTA	9.58	-0.24	4.1E-01		PTBP1	10.20	-0.21	5.1E-01
MAP4K4	9.71	-0.24	4.1E-01		RHOC	9.86	-0.21	5.6E-01
SEC23A	10.53	-0.24	4.7E-01		GYS1	10.80	-0.21	5.0E-01
PRPSAP1	9.18	-0.24	5.3E-01		PFDN5	10.13	-0.21	5.6E-01
ANKZF1	9.25	-0.24	5.0E-01		C12orf10	9.78	-0.21	4.5E-01
ATP6V1G1	9.18	-0.24	5.3E-01		NISCH	8.66	-0.21	6.0E-01
KIF5B	10.84	-0.24	4.6E-01		RELA	9.75	-0.21	4.5E-01
GSTT1	10.23	-0.24	4.7E-01		SOD1	10.74	-0.20	5.0E-01
DBI	10.62	-0.24	4.7E-01		MIF	11.52	-0.20	5.0E-01
CCDC124	9.22	-0.24	5.0E-01		ANP32B	10.32	-0.20	5.1E-01
HTT	9.05	-0.23	5.3E-01		PCBP1	10.96	-0.20	5.0E-01
TPM1	11.44	-0.23	4.6E-01		MACF1	10.66	-0.20	5.0E-01
PLXNA1	8.62	-0.23	5.7E-01		CROCC	10.37	-0.20	5.1E-01
PXN	9.51	-0.23	5.0E-01		HIST1H2BM;HIST1H2BN;HIST1H2BH;HIST2H2BF;HIST1H2BC;HIST1H2BD;H2BFS;HIST1H2BK	10.83	-0.20	5.0E-01
ACSL3	9.83	-0.23	5.2E-01					
CAD	9.85	-0.23	5.2E-01					
UFM1	9.60	-0.23	4.2E-01					
SLC16A1	9.94	-0.23	5.3E-01		PSMF1	9.24	-0.20	5.4E-01
CARHSP1	10.06	-0.23	5.3E-01		CPT1B	8.70	-0.20	6.0E-01
HSPB7	11.32	-0.23	4.7E-01		HOOK3	8.64	-0.20	6.0E-01
PLIN3	10.93	-0.23	4.7E-01		CAND1	11.04	-0.20	5.1E-01

NXN	9.79	-0.20	4.5E-01
NAP1L1	10.42	-0.20	5.1E-01
EXOC8	9.48	-0.20	5.4E-01
COPS7B	9.74	-0.20	4.5E-01
SUMO1	9.00	-0.20	5.7E-01
MTMR6	8.78	-0.20	6.1E-01
CCT3	11.32	-0.20	5.1E-01
GMDS	8.54	-0.20	6.1E-01
GUSB	8.96	-0.20	5.7E-01
UBE2D1;UBE2D4	9.34	-0.20	5.4E-01
LSM12	9.26	-0.20	5.4E-01
RAD23B	10.51	-0.20	5.2E-01
SMAD4	8.77	-0.19	6.1E-01
EML2	10.01	-0.19	5.7E-01
DPYSL3	11.70	-0.19	5.2E-01
ADPRHL2	9.94	-0.19	5.7E-01
EEF1D	9.63	-0.19	4.6E-01
RAPGEF2	9.01	-0.19	5.8E-01
PHKA2	9.35	-0.19	5.5E-01
KPNA1	9.74	-0.19	4.6E-01
FAM114A2	9.52	-0.19	4.6E-01
IGF2BP3	10.15	-0.19	5.8E-01
ZC2HC1A	9.48	-0.19	5.5E-01
TSTA3	9.94	-0.19	5.8E-01
TPD52L2	10.06	-0.19	5.8E-01
SRI	10.32	-0.19	5.3E-01
APPL1	9.66	-0.19	4.7E-01
GTPBP1	9.64	-0.19	4.7E-01
DCTN5	9.53	-0.19	4.7E-01
OPTN	9.51	-0.19	5.5E-01
TUBB3	9.87	-0.19	5.9E-01
C11orf73	9.54	-0.18	4.7E-01
TCP1	11.22	-0.18	5.3E-01
SYNJ1	9.79	-0.18	4.7E-01
PYCR2	8.92	-0.18	5.9E-01
TALDO1	10.94	-0.18	5.3E-01
IGBP1	8.80	-0.18	6.2E-01
DDX19A	9.99	-0.18	5.9E-01
ABCF1	9.91	-0.18	5.9E-01
LRRC47	10.64	-0.18	5.3E-01
MESDC2	10.00	-0.18	5.9E-01
EXOC2	9.63	-0.18	4.7E-01
ATG7	8.63	-0.18	6.3E-01
TCEB2	10.78	-0.18	5.4E-01
WDR44	9.00	-0.18	5.9E-01
PAFAH1B3	10.45	-0.18	5.4E-01
CCT5	11.24	-0.18	5.4E-01
UBAP2L	9.74	-0.18	4.8E-01
MYO18B	9.78	-0.18	4.8E-01
MTHFS	8.89	-0.18	5.9E-01
CCT2	11.43	-0.18	5.4E-01
FAM177A1	8.32	-0.17	6.3E-01
DUSP3	10.52	-0.17	5.5E-01
EXOC1	9.14	-0.17	6.0E-01
PFDN4	9.68	-0.17	4.8E-01
EIF4G2	10.02	-0.17	6.0E-01
MLIP	10.31	-0.17	5.5E-01
APIP	9.27	-0.17	5.7E-01
PATL1	8.36	-0.17	6.3E-01
ANXA11	10.70	-0.17	5.5E-01
VTA1	10.07	-0.17	6.0E-01
ACAT2	10.37	-0.17	5.5E-01
UBE2M	10.17	-0.17	5.5E-01
RNF31	8.75	-0.17	6.4E-01
ARHGEF12	8.51	-0.17	6.4E-01
AP3S1	9.05	-0.17	6.0E-01
FAM96B	9.62	-0.17	4.8E-01
DBNL	10.24	-0.17	5.6E-01
ALDOA	12.38	-0.17	5.5E-01
NUDCD2	9.73	-0.17	4.9E-01
DOCK7	9.42	-0.17	5.7E-01
EPRS	10.74	-0.17	5.5E-01
HMBS	8.84	-0.17	6.4E-01
VASP	9.78	-0.17	4.9E-01
AP1M1	9.63	-0.17	4.9E-01
MAPKAPK2	9.36	-0.16	5.8E-01
EIF4E2	9.29	-0.16	5.8E-01
LAGE3	8.91	-0.16	6.1E-01
PRPS1	10.47	-0.16	5.6E-01
STRAP	10.45	-0.16	5.6E-01
NRBP2	8.92	-0.16	6.1E-01
PDAP1	9.61	-0.16	4.9E-01
HMGCS1	9.72	-0.16	4.9E-01
MAT2A	10.27	-0.16	5.6E-01
EIF2S2	9.93	-0.16	6.1E-01
SERPINB1	9.74	-0.16	4.9E-01
TBCA	10.57	-0.16	5.6E-01
ENY2	8.87	-0.16	6.1E-01
RBPMS	10.09	-0.16	6.2E-01
KPNB1	11.02	-0.16	5.6E-01
SEPHS1	9.43	-0.16	5.8E-01
DCAF8	9.09	-0.16	6.1E-01
AHCY	11.27	-0.16	5.6E-01
STRIP2;FAM40B	9.45	-0.16	5.8E-01
LAMP1	10.22	-0.16	5.7E-01
UGGT1	10.57	-0.16	5.7E-01
PDE12	8.83	-0.16	6.5E-01
NAPRT1	9.58	-0.16	5.0E-01
HEBP1	9.84	-0.16	6.2E-01
MAP7D1	9.15	-0.16	6.1E-01
UFC1	9.67	-0.16	5.0E-01
H6PD	9.51	-0.15	5.9E-01
YTHDF2	9.22	-0.15	5.9E-01
NUDCD3	9.14	-0.15	6.2E-01
MCTS1	9.90	-0.15	6.3E-01
SGTA	10.27	-0.15	5.8E-01
COL4A3BP	8.72	-0.15	6.6E-01
MAT2B	9.99	-0.15	6.3E-01
EIF4H	10.37	-0.15	5.8E-01
MSRB3	9.58	-0.15	5.0E-01
EEF1D	11.05	-0.15	5.8E-01
RHEB	9.78	-0.15	5.0E-01
ACTA2;ACTG2	12.48	-0.15	5.8E-01
SDC2	8.19	-0.15	6.6E-01
CCT7	11.18	-0.15	5.8E-01
QRICH1	8.54	-0.15	6.6E-01
VCP	11.53	-0.15	5.8E-01
GAPDH	12.70	-0.15	5.8E-01
TBC1D13	9.03	-0.15	6.2E-01
ANP32E	10.09	-0.15	6.4E-01
PPIB	11.17	-0.15	5.8E-01
OPLAH	10.08	-0.15	6.4E-01
HSP90B1	11.83	-0.15	5.8E-01
TUBAL3	9.87	-0.15	6.4E-01
WASF3	8.35	-0.14	6.6E-01
GSN	10.43	-0.14	5.9E-01
XPO1	10.73	-0.14	5.9E-01
LAMA5	9.37	-0.14	6.0E-01
CTPS2	10.04	-0.14	6.4E-01
UBQLN2	10.16	-0.14	6.4E-01
ITPA	9.14	-0.14	6.3E-01
ADK	9.61	-0.14	5.1E-01
EIF2B2	9.61	-0.14	5.1E-01
TROVE2	10.63	-0.14	5.9E-01
ADSL	10.25	-0.14	5.9E-01
TBCE	9.51	-0.14	6.0E-01
YWHAE	12.05	-0.14	5.9E-01
AGL	11.29	-0.14	5.9E-01
CLUH	9.41	-0.14	6.0E-01
HSPA8	11.92	-0.14	5.9E-01
TNNT2;HNTN1	10.84	-0.14	6.0E-01
CAMK2D	11.10	-0.14	6.0E-01
APOL2	9.56	-0.14	5.2E-01
NUP93	9.40	-0.14	6.1E-01

CRKL	9.87	-0.14	6.5E-01		TATDN1	9.45	-0.11	6.4E-01
PSMB8	9.54	-0.14	5.2E-01		PDCD5	10.22	-0.11	6.4E-01
TNPO3	9.06	-0.14	6.4E-01		PPP4C	9.38	-0.11	6.4E-01
ARHGEF11	7.86	-0.14	6.7E-01		VPS53	8.87	-0.11	6.7E-01
PGRMC2	10.31	-0.14	6.0E-01		RBBP9	9.53	-0.10	5.5E-01
PPP1CA	9.71	-0.14	5.2E-01		CCNY	8.67	-0.10	7.1E-01
PPFIA1	8.32	-0.13	6.8E-01		CDC42	10.43	-0.10	6.4E-01
FTO	8.96	-0.13	6.4E-01		CLEC16A	9.69	-0.10	5.5E-01
PPP1R7	9.93	-0.13	6.5E-01		PGAM1	11.89	-0.10	6.4E-01
PGM1	11.38	-0.13	6.0E-01		BAX	9.96	-0.10	6.9E-01
CHP1	9.74	-0.13	5.2E-01		RRAGA;RRAGB	9.46	-0.10	6.5E-01
CRADD	9.07	-0.13	6.4E-01		STRN	9.99	-0.10	7.0E-01
TUBB6	11.16	-0.13	6.0E-01		PLAA	9.68	-0.10	5.6E-01
FHOD3	8.83	-0.13	6.8E-01		PIP4K2C	8.96	-0.10	6.7E-01
DNPH1	9.96	-0.13	6.6E-01		YWHAZ	11.83	-0.10	6.5E-01
MAPRE1	10.79	-0.13	6.1E-01		OLA1	10.48	-0.10	6.5E-01
CCT4	11.39	-0.13	6.1E-01		LYPLA1	10.28	-0.10	6.5E-01
DCTN3	10.20	-0.13	6.1E-01		KLC1	10.20	-0.10	6.5E-01
FN3K	9.67	-0.13	5.3E-01		TCEB1	10.53	-0.10	6.5E-01
UBE2R2	8.53	-0.13	6.8E-01		PDCL3	9.16	-0.10	6.7E-01
GMPPA	9.67	-0.13	5.3E-01		USP11	8.64	-0.10	7.1E-01
GMFB	9.72	-0.13	5.3E-01		MYLK	9.80	-0.10	5.6E-01
CCT8	11.47	-0.13	6.1E-01		NAGK	10.29	-0.10	6.5E-01
DUSP27	9.44	-0.13	6.2E-01		RNH1	11.00	-0.10	6.5E-01
DYNC2H1	8.56	-0.13	6.8E-01		DENR	9.81	-0.10	5.6E-01
DFFA	9.24	-0.13	6.2E-01		ASAP1	8.89	-0.10	6.8E-01
EIF4G3	8.39	-0.13	6.8E-01		EZR	11.74	-0.10	6.5E-01
QKI	10.05	-0.13	6.6E-01		CAPZA2	10.73	-0.10	6.6E-01
UBE3C	9.60	-0.13	5.3E-01		IGF2BP2	10.19	-0.10	6.5E-01
MAPRE3	9.68	-0.13	5.3E-01		RAD23A	9.72	-0.10	5.6E-01
ECHDC1	8.74	-0.13	6.9E-01		GANAB	11.13	-0.09	6.6E-01
VPS51	8.94	-0.13	6.5E-01		NHLRC2	10.18	-0.09	6.6E-01
IGF2R	9.81	-0.12	5.3E-01		IGF2BP1	10.66	-0.09	6.6E-01
PCNA	10.12	-0.12	6.7E-01		CD81	9.98	-0.09	7.1E-01
EMILIN1	9.93	-0.12	6.7E-01		EDC4	9.89	-0.09	7.1E-01
RPL38	10.25	-0.12	6.2E-01		RAC1	10.52	-0.09	6.6E-01
ZZEF1	10.02	-0.12	6.7E-01		AP4S1	8.99	-0.09	6.8E-01
SHROOM3	10.02	-0.12	6.7E-01		EIF5	10.02	-0.09	7.1E-01
ADAL	8.56	-0.12	6.9E-01		EXOSC6	8.47	-0.09	7.2E-01
AP4E1	9.34	-0.12	6.2E-01		HEATR3	8.21	-0.09	7.2E-01
FAM211A	9.05	-0.12	6.5E-01		DRG2	9.47	-0.09	6.6E-01
RAB5C	9.74	-0.12	5.4E-01		PTP4A2	9.09	-0.09	6.9E-01
DIS3	8.88	-0.12	6.5E-01		ARF6	9.78	-0.09	5.7E-01
CUL3	9.96	-0.12	6.7E-01		FILIP1	9.85	-0.09	7.2E-01
NTMT1	9.13	-0.12	6.5E-01		SMS	10.61	-0.09	6.6E-01
AP1S2	9.18	-0.12	6.5E-01		EIF3A	10.63	-0.09	6.6E-01
VAC14	9.81	-0.12	5.4E-01		CAB39	10.12	-0.09	7.2E-01
VPS8	7.98	-0.12	6.9E-01		PPM1A	9.47	-0.09	6.6E-01
DVL2	8.68	-0.12	6.9E-01		YARS	10.66	-0.09	6.7E-01
WIBG	8.54	-0.12	6.9E-01		TSN	10.53	-0.09	6.7E-01
APEH	10.56	-0.12	6.2E-01		C11orf54	10.01	-0.09	7.2E-01
FN1	9.75	-0.12	5.4E-01		FRYL	9.44	-0.09	6.7E-01
TXNRD1	9.93	-0.12	6.8E-01		LZIC	9.88	-0.08	7.2E-01
ALCAM	9.42	-0.12	6.3E-01		NPLOC4	10.00	-0.08	7.2E-01
G3BP1	9.62	-0.11	5.4E-01		BTF3	10.05	-0.08	7.2E-01
AGFG1	8.98	-0.11	6.6E-01		LRBA	9.41	-0.08	6.7E-01
YWHAB	11.00	-0.11	6.3E-01		SCRN3	8.68	-0.08	7.3E-01
PPP2R4	10.15	-0.11	6.8E-01		PIN1	9.99	-0.08	7.3E-01
PPP2R5D	9.85	-0.11	6.8E-01		FRY	9.47	-0.08	6.7E-01
SCRN1	10.48	-0.11	6.3E-01		CAPZB	10.84	-0.08	6.8E-01
KPNA6	9.04	-0.11	6.6E-01		SEC16A	9.06	-0.08	7.0E-01
HSPA4	10.98	-0.11	6.3E-01		PRUNE	9.90	-0.08	7.3E-01
STAT6	8.95	-0.11	6.6E-01		C16orf62	8.89	-0.08	7.0E-01
C4orf27	8.95	-0.11	6.6E-01		PDLIM4	9.25	-0.08	6.7E-01
EIF2AK2	9.38	-0.11	6.4E-01		PCYT2	9.27	-0.08	6.8E-01
POLR2B	9.49	-0.11	6.4E-01		IMPDH2	10.58	-0.08	6.8E-01
CRYZL1	8.81	-0.11	7.0E-01		TBC1D9B	9.26	-0.08	6.8E-01
MTHFD1L	9.89	-0.11	6.9E-01		DCUN1D1	9.92	-0.08	7.4E-01
GPX4	10.02	-0.11	6.9E-01		WDR61	9.76	-0.07	5.9E-01
BABAM1	9.39	-0.11	6.4E-01		ABCE1	9.89	-0.07	7.4E-01
COL4A1	8.96	-0.11	6.6E-01		UFD1L	10.14	-0.07	7.4E-01
DNAJC10	9.25	-0.11	6.4E-01		FAM49B	10.38	-0.07	6.9E-01

PGLS	10.47	-0.07	6.9E-01		ARF5	9.83	-0.04	7.9E-01
DDT;DDTL	10.83	-0.07	6.9E-01		YY1;YY2	8.76	-0.04	7.8E-01
CSPG4	9.37	-0.07	6.8E-01		DCAF6	8.30	-0.04	7.8E-01
LDHB	12.19	-0.07	7.0E-01		NUDT4	9.83	-0.04	7.9E-01
RPL23	10.57	-0.07	6.9E-01		FAM175B	9.42	-0.04	7.2E-01
ARFGAP3	9.03	-0.07	7.1E-01		DDB1	10.72	-0.04	7.5E-01
BANF1	9.82	-0.07	7.4E-01		CHMP3	8.74	-0.04	7.9E-01
EIF2B4	9.40	-0.07	6.9E-01		AHCYL1;AHCYL2	9.82	-0.04	7.9E-01
UBE2V1;TMEM189	10.62	-0.07	6.9E-01		NUBP2	10.01	-0.04	7.9E-01
UBR1	8.91	-0.07	7.1E-01		IAH1	9.76	-0.04	6.3E-01
CCT6A	11.23	-0.07	7.0E-01		SIL1	8.89	-0.03	7.5E-01
NSDHL	10.22	-0.07	6.9E-01		ACYP1	10.12	-0.03	7.9E-01
CAPZA1	10.33	-0.07	6.9E-01		SETD3	9.21	-0.03	7.3E-01
OAT	9.13	-0.07	7.1E-01		DNPEP	10.38	-0.03	7.4E-01
HSPB1	12.37	-0.07	7.0E-01		GNPDA2	9.85	-0.03	8.0E-01
GRIPAP1	8.84	-0.07	7.5E-01		RPS27	10.26	-0.03	7.4E-01
IPO5	10.67	-0.07	7.0E-01		BAG6	9.77	-0.03	6.4E-01
HECTD4	9.32	-0.06	6.9E-01		SERPINB6	10.64	-0.03	7.6E-01
BLVRB	10.71	-0.06	7.1E-01		PARK7	11.33	-0.03	7.6E-01
LPP	10.36	-0.06	7.0E-01		CPNE1	10.44	-0.03	7.4E-01
AS3MT	9.03	-0.06	7.1E-01		VPS36	9.59	-0.03	6.4E-01
UBXN1	9.77	-0.06	6.0E-01		RABL6	9.12	-0.03	7.5E-01
MSH6	9.71	-0.06	6.0E-01		XPNPEP3	9.23	-0.03	7.3E-01
TIPRL	10.17	-0.06	7.0E-01		EIF2S1	10.47	-0.03	7.4E-01
RGL2	8.77	-0.06	7.6E-01		EIF3B	10.26	-0.03	7.4E-01
S100A16	9.18	-0.06	7.2E-01		INPPL1	9.51	-0.03	7.3E-01
DCPS	9.83	-0.06	7.6E-01		PCBD1	10.33	-0.03	7.5E-01
RPS27L	9.64	-0.06	6.1E-01		RPS11	10.81	-0.03	7.6E-01
LLGL1	9.44	-0.06	7.0E-01		TSNAX;DISC1	9.83	-0.03	8.0E-01
RPS7	10.79	-0.06	7.1E-01		STK38L	9.35	-0.03	7.3E-01
TRAFD1	8.72	-0.06	7.6E-01		VPS33A	8.97	-0.03	7.6E-01
SYNPO2L	9.31	-0.06	7.0E-01		TTC1	9.22	-0.03	7.4E-01
BLMH	10.34	-0.06	7.1E-01		TRAPPC4	9.30	-0.03	7.4E-01
PKM	12.48	-0.06	7.2E-01		MAP2K4	9.61	-0.02	6.5E-01
DNAJC13	9.57	-0.06	6.1E-01		BAG3	10.32	-0.02	7.5E-01
PEPD	9.97	-0.06	7.6E-01		DCAF7	9.49	-0.02	7.4E-01
PPIA	11.75	-0.06	7.2E-01		VPS41	8.76	-0.02	8.0E-01
CLTC	11.46	-0.06	7.2E-01		MAPK1	10.44	-0.02	7.6E-01
NAA20	8.87	-0.05	7.2E-01		PYGB	11.94	-0.02	7.7E-01
UPF1	9.94	-0.05	7.6E-01		ARMCX3	8.85	-0.02	8.0E-01
NUCB1	9.86	-0.05	7.6E-01		GCA	9.45	-0.02	7.4E-01
NEK9	9.80	-0.05	6.1E-01		EEF1G	11.33	-0.02	7.8E-01
METTL14	8.41	-0.05	7.7E-01		RQCD1	9.27	-0.02	7.4E-01
SUGT1	10.09	-0.05	7.7E-01		MTAP	10.16	-0.02	8.2E-01
LANCL1	10.41	-0.05	7.1E-01		SCYL2	9.44	-0.02	7.5E-01
SLC12A2	8.22	-0.05	7.7E-01		SLC12A7	9.52	-0.02	7.5E-01
SMYD1	10.81	-0.05	7.2E-01		YBX3	9.65	-0.02	6.6E-01
CKMT2	11.25	-0.05	7.3E-01		ENOPH1	9.78	-0.02	6.6E-01
PPIH	9.47	-0.05	7.1E-01		NSFL1C	10.42	-0.02	7.6E-01
RBM3	9.27	-0.05	7.1E-01		GLTP	9.01	-0.02	7.7E-01
SSB	10.82	-0.05	7.3E-01		USP5	10.61	-0.01	7.7E-01
CUL4B	8.68	-0.05	7.7E-01		CSTB	10.71	-0.01	7.8E-01
EIF3C;EIF3CL	10.22	-0.05	7.2E-01		CCS	9.68	-0.01	6.6E-01
LSM1	9.54	-0.05	6.2E-01		UBE2N;UBE2NL	10.88	-0.01	7.9E-01
PPP6R2	9.08	-0.05	7.3E-01		ATG5	8.76	-0.01	8.1E-01
SENP8	9.00	-0.05	7.3E-01		RPS10	10.04	-0.01	8.2E-01
FKBP9	9.90	-0.05	7.8E-01		PTPLAD1	8.56	-0.01	8.1E-01
PFDN1	10.26	-0.04	7.2E-01		USO1	10.60	-0.01	7.7E-01
RARS	10.77	-0.04	7.4E-01		PAIP1	9.91	-0.01	8.3E-01
SUMO2;SUMO4	9.82	-0.04	7.8E-01		DCTN2	10.56	-0.01	7.7E-01
EIF2S3;EIF2S3L	10.40	-0.04	7.2E-01		TTLL12	9.61	-0.01	6.6E-01
GALNS	9.13	-0.04	7.4E-01		TXNL1	10.24	-0.01	7.7E-01
NAPG	9.47	-0.04	7.2E-01		ST13;ST13P5;ST13P4	10.79	-0.01	7.9E-01
EVL	8.99	-0.04	7.4E-01		C15orf52	9.37	-0.01	7.6E-01
PAK4	8.62	-0.04	7.8E-01		RALGAPA1	10.41	-0.01	7.8E-01
GRHPR	10.95	-0.04	7.4E-01		DPYSL4	10.04	-0.01	8.3E-01
DYNLRB1;DYNLRB2	10.35	-0.04	7.3E-01		ANXA6	9.33	-0.01	7.6E-01
EPN1	8.91	-0.04	7.4E-01		DLG3	8.81	-0.01	8.2E-01
SNF8	9.41	-0.04	7.2E-01		SPG20	8.78	-0.01	8.2E-01
EHD1	10.96	-0.04	7.4E-01		ACTR1A	10.82	-0.01	7.9E-01
FAF1	9.14	-0.04	7.4E-01		UBE4B	9.25	-0.01	7.6E-01
LACTB	8.70	-0.04	7.8E-01		MOCS2	9.10	-0.01	7.8E-01

PRKAR1A	10.63	-0.01	7.9E-01		TPMT	8.69	0.00	8.2E-01
PHKB	9.69	-0.01	6.7E-01		PPP5C	10.37	0.00	7.9E-01
SH3GLB2	9.82	-0.01	8.3E-01		CSDE1	10.01	0.00	8.4E-01
UBA3	10.28	0.00	7.8E-01		HEXB	10.09	0.00	8.4E-01
PITPNB	9.89	0.00	8.4E-01		DARS	10.78	0.00	8.1E-01
PA2G4	10.86	0.00	8.0E-01		MYH7B	10.17	0.00	7.9E-01
NEDD8-MDP1;NEDD8	10.19	0.00	7.8E-01		NCALD	8.96	0.00	7.9E-01
FAM120A	9.54	0.00	6.7E-01		EEF1B2	10.81	0.00	8.1E-01
VPS18	8.92	0.00	7.8E-01		ACOX1	9.23	0.00	7.7E-01
ATP6V1C1	9.39	0.00	7.6E-01		DIS3L2	8.67	0.00	8.3E-01
MRI1	9.41	0.00	7.6E-01		PSMD10	9.84	0.00	8.5E-01

(B) 2,126 proteins with log2 fold > 0, of which 94 were significantly higher expressed in iPSC-aCMs.

Gene name	**log10 intensity**	**log2 (aCMs/ vCMs)**	**Significance B**		**Gene names**	**log10 intensity**	**log2 (aCMs/ vCMs)**	**Significance B**
PADI2	10.27	4.82	**7.2E-09**		SDHD	9.70	2.04	7.3E-02
MYH4	10.57	4.81	**8.0E-09**		MRPS30	9.02	2.04	**2.5E-02**
SMARCA4	9.61	4.31	**4.7E-05**		MT-ATP8	10.23	2.03	**2.0E-02**
GNAO1	9.97	4.02	**2.7E-05**		SMIM8	8.42	1.99	**2.1E-02**
NR2F2;NR2F1	9.05	3.84	**1.0E-05**		ATP5C1	11.23	1.98	**2.2E-02**
MYH6	12.11	3.82	**4.7E-06**		PDGFRB	10.60	1.97	**2.4E-02**
NPPA	9.31	3.78	**1.4E-04**		TMEM256	9.32	1.96	6.0E-02
METTL7B	9.44	3.74	**1.6E-04**		LYRM5	8.79	1.96	**2.3E-02**
MGARP	9.57	3.67	**6.1E-04**		SDHC	9.68	1.96	8.7E-02
DES	11.05	3.66	**1.2E-05**		BASP1	9.34	1.94	6.2E-02
VSNL1	9.89	3.58	**2.0E-04**		ATP5F1	11.24	1.93	**2.5E-02**
CASQ2	9.87	3.21	**9.0E-04**		ATP5O	11.41	1.93	**2.5E-02**
ADCY5	9.82	3.19	**9.7E-04**		TIMM10B	8.49	1.92	**2.6E-02**
MYL7	11.54	3.16	**1.7E-04**		TMEM70	9.36	1.92	6.6E-02
ATP1B2	8.72	3.13	**1.8E-04**		AIG1	8.60	1.91	**2.7E-02**
COX7A1	9.44	3.03	**2.5E-03**		MT-ATP6	10.28	1.91	**2.9E-02**
SOD3	9.42	2.96	**3.2E-03**		CES2	9.25	1.91	6.8E-02
NME4	9.63	2.81	**1.0E-02**		ATP5H	11.04	1.90	**2.8E-02**
ATP2A2	11.88	2.78	**1.0E-03**		ATP5D	10.68	1.89	**2.8E-02**
CRYM	9.45	2.72	**7.3E-03**		ATP5J2	10.63	1.89	**3.1E-02**
MYOM2	8.73	2.67	**1.5E-03**		PDHB	11.15	1.89	**2.9E-02**
MYH11	9.07	2.66	**2.8E-03**		NDUFS5	10.06	1.88	5.7E-02
PAM	9.83	2.62	**7.1E-03**		COX6C	10.35	1.88	**3.2E-02**
TMEM141	9.13	2.61	**3.3E-03**		OCIAD2	8.55	1.86	**3.2E-02**
B3GALTL	9.50	2.61	**1.0E-02**		ABAT	10.60	1.86	**3.4E-02**
CTNND2	8.20	2.55	**2.6E-03**		ATP5A1	12.13	1.85	**3.2E-02**
CMC2	8.90	2.47	**5.8E-03**		PDHA1	11.01	1.85	**3.2E-02**
NENF	9.44	2.44	**1.7E-02**		SLC25A11	10.78	1.85	**3.3E-02**
SMIM20	9.02	2.44	**6.4E-03**		PHB2	11.07	1.84	**3.3E-02**
RAB9B	9.54	2.43	**2.8E-02**		MYPN	8.59	1.84	**3.4E-02**
RAB27A	9.22	2.42	**1.8E-02**		ATP5B	12.14	1.84	**3.3E-02**
NDUFA4	10.86	2.40	**4.7E-03**		Q69YL0	8.47	1.84	**3.4E-02**
LYRM9	8.31	2.40	**4.8E-03**		NDUFB8	9.71	1.83	1.1E-01
SH3KBP1	9.10	2.37	**8.2E-03**		COX7C	9.36	1.83	8.2E-02
PTPRK	8.98	2.35	**8.8E-03**		NDUFA10	10.04	1.83	6.5E-02
DHRS7B	8.83	2.35	**5.8E-03**		TIMM21	9.16	1.83	**4.7E-02**
COA3	9.55	2.30	**3.9E-02**		NDUFB11	9.80	1.82	1.1E-01
DNAJB11	9.01	2.30	**1.1E-02**		ATP5B	9.68	1.82	1.1E-01
NRP2	8.54	2.30	**7.0E-03**		NDUFA11	9.81	1.82	1.2E-01
COX14	8.93	2.25	**1.2E-02**		MINOS1;NBL1	9.42	1.82	8.4E-02
ME3	9.43	2.20	**3.3E-02**		MRPL41	9.60	1.82	1.2E-01
C10orf35	8.95	2.17	**1.6E-02**		D2HGDH	8.80	1.81	**3.7E-02**
BDH1	9.98	2.14	**2.9E-02**		NDUFB2	8.52	1.81	**3.7E-02**
PNKD	9.19	2.11	**2.0E-02**		A2M	10.21	1.81	**3.9E-02**
ATP5E	10.53	2.11	**1.5E-02**		MGST1	8.98	1.80	5.1E-02
C11orf83	8.34	2.10	**1.4E-02**		COX5B	10.26	1.80	**4.1E-02**
ATP6V1G2;ATP6V1G2-DDX39B	9.04	2.10	**2.1E-02**		MAP1A	9.19	1.80	5.2E-02
					NDUFB5	9.63	1.79	1.2E-01
USMG5	10.36	2.09	**1.6E-02**		CMC1	9.39	1.79	8.9E-02
CISD1	10.66	2.09	**1.5E-02**		CAV1	10.71	1.79	**3.9E-02**
MP68;C14orf2	10.07	2.08	**3.4E-02**		NDUFA1	9.03	1.79	5.3E-02
ATP5L	10.98	2.08	**1.5E-02**		MT-CO2	10.62	1.79	**4.2E-02**
PLCB1	8.84	2.07	**1.6E-02**		TMEM11	9.57	1.78	1.2E-01
ATP5I	10.65	2.05	**1.7E-02**		MYBPC3	11.48	1.78	**4.0E-02**
APOO	9.90	2.05	**3.8E-02**		GNG7	8.92	1.78	5.4E-02

NDUFB4	10.13	1.78	7.3E-02		SNAP91	10.05	1.59	1.1E-01
ADCK3	9.98	1.77	7.5E-02		MRPL50	9.39	1.59	1.4E-01
ACSF2	10.75	1.77	**4.1E-02**		MRPL43	9.84	1.59	1.1E-01
CACNA2D2	9.02	1.76	5.6E-02		SLC4A7	8.57	1.58	7.2E-02
SDHB	10.58	1.76	**4.5E-02**		SAMM50	9.21	1.58	1.4E-01
COX6B1	10.24	1.76	**4.5E-02**		TMEM223	8.58	1.58	7.3E-02
AGK	9.36	1.75	9.7E-02		NDUFA6	10.12	1.58	1.2E-01
TMEM50B	8.43	1.75	**4.5E-02**		MRPL47	9.68	1.57	1.8E-01
NDUFB6	9.78	1.74	1.3E-01		MRPL30	9.30	1.57	1.4E-01
HADHB	11.24	1.74	**4.5E-02**		SLC25A5	10.57	1.57	7.8E-02
NDUFB7	9.86	1.74	8.0E-02		ATPIF1	10.36	1.57	7.8E-02
TIMM9	9.70	1.73	1.4E-01		COX5A	10.44	1.57	7.8E-02
NDUFB3	9.87	1.73	8.1E-02		TIMM10	9.11	1.57	9.5E-02
VDAC3	10.62	1.73	**4.9E-02**		MT-CO3	9.03	1.56	9.6E-02
COX7B	9.18	1.73	6.2E-02		MRPL53	9.84	1.56	1.2E-01
NDUFA3	9.33	1.72	1.0E-01		EFNB1	8.92	1.56	9.7E-02
PHB	10.99	1.72	**4.7E-02**		MRPL16	9.58	1.56	1.9E-01
MPC1;BRP44L	9.50	1.72	1.0E-01		NDUFC1	8.53	1.56	7.7E-02
OCIAD1	9.53	1.71	1.4E-01		LRRC4B	8.47	1.56	7.7E-02
ROMO1	9.01	1.71	6.5E-02		NDUFS8	10.20	1.56	8.0E-02
NPTN	10.40	1.71	5.3E-02		TPR	9.05	1.55	9.8E-02
HIBCH	10.74	1.70	5.0E-02		NLRX1	8.41	1.55	7.8E-02
NDUFA13;YJEFN3	10.22	1.70	5.4E-02		SF3B14	9.58	1.55	1.9E-01
MRPL28	9.37	1.70	1.1E-01		FAM162A	10.49	1.55	8.2E-02
NDUFS6	10.00	1.69	8.9E-02		MRPL11	9.85	1.55	1.2E-01
MRPL14	9.56	1.69	1.5E-01		TMEM126A	9.00	1.55	1.0E-01
QIL1;C19orf70	9.73	1.69	1.5E-01		NDUFS4	9.61	1.55	1.9E-01
NDUFB10	10.21	1.69	5.5E-02		CHCHD3	10.10	1.54	1.2E-01
CA13	8.50	1.69	5.3E-02		MRPS7	9.79	1.54	1.9E-01
NDUFB1	9.54	1.69	1.5E-01		MRPS18C	8.88	1.54	1.0E-01
COX4I1	10.81	1.69	5.2E-02		OGDH	10.87	1.54	7.8E-02
MED23	8.41	1.68	5.4E-02		DNAJC19	9.36	1.54	1.5E-01
NDUFA9	10.35	1.68	5.7E-02		MRPL37	9.67	1.54	2.0E-01
NDUFB9	10.00	1.68	9.2E-02		MFF	9.33	1.54	1.5E-01
DBT	10.14	1.68	9.3E-02		MRPS12	9.64	1.54	2.0E-01
ALDH4A1	10.81	1.67	5.5E-02		MTCH2	9.99	1.54	1.3E-01
MRPL33	9.17	1.67	7.3E-02		MRPL55	9.34	1.54	1.5E-01
NDRG4	9.32	1.67	1.2E-01		MRPL13	9.80	1.53	2.0E-01
MRPL3	9.34	1.66	1.2E-01		SCO2	8.63	1.53	8.2E-02
MRPL23	9.70	1.66	1.6E-01		ACOT13	10.93	1.53	8.1E-02
MRPS36	9.92	1.66	9.6E-02		MRPL45	9.62	1.53	2.0E-01
SPTB	10.55	1.66	6.1E-02		MRPL22	9.56	1.52	2.0E-01
NDUFC2;NDUFC2-KCTD14	10.05	1.67	9.4E-02		MRPL51	8.97	1.52	1.1E-01
					ALDH5A1	10.13	1.52	1.3E-01
PC	8.26	1.66	5.8E-02		AMACR	8.65	1.52	8.5E-02
NDUFA7	9.96	1.66	9.7E-02		RPP14	9.84	1.52	1.3E-01
MRP63	9.28	1.65	1.2E-01		SYNE1	9.49	1.52	1.6E-01
RABGAP1L	8.97	1.65	7.7E-02		COX7A2	9.54	1.52	2.0E-01
MRPS21	9.26	1.64	1.2E-01		MRPS24	9.49	1.52	1.6E-01
OPA3	9.72	1.64	1.6E-01		PRKCDBP	9.37	1.51	1.6E-01
MRPL17	9.69	1.64	1.6E-01		ACAD9	10.11	1.51	1.3E-01
MRPS14	9.54	1.64	1.6E-01		MRPL27	9.71	1.51	2.1E-01
C7orf55	9.08	1.64	7.9E-02		EBP	9.47	1.51	1.6E-01
MRPL9	9.75	1.64	1.6E-01		SFRP1	9.57	1.51	2.1E-01
SLC25A12	10.46	1.63	6.5E-02		HADHA	11.48	1.51	8.6E-02
NDUFA12	10.24	1.63	6.5E-02		TIMM17B	8.78	1.51	8.8E-02
MRPL35	8.80	1.63	6.3E-02		MRPS5	9.45	1.51	1.6E-01
C8orf82	9.78	1.63	1.7E-01		PHF5A	9.37	1.50	1.6E-01
DLST	10.85	1.62	6.3E-02		MRPL40	9.33	1.50	1.6E-01
ATAD3A;ATAD3B	9.75	1.62	1.7E-01		MRPL19	9.82	1.49	1.4E-01
MRPL34	8.95	1.62	8.4E-02		MRPS11	9.55	1.49	2.1E-01
MRPL18	9.38	1.62	1.3E-01		MRPL20	9.56	1.49	2.2E-01
MRPL32	9.13	1.61	8.4E-02		MRPL2	9.13	1.49	1.2E-01
TOMM22	9.06	1.61	8.5E-02		SF3B4	8.23	1.48	9.4E-02
APOOL	9.25	1.61	1.3E-01		MRPS6	9.78	1.48	2.2E-01
PRKAG2	10.41	1.61	7.0E-02		MTX2	9.15	1.48	1.2E-01
CORO7;PAM16	9.46	1.60	1.3E-01		SLC44A2	9.93	1.48	1.4E-01
NNT	10.97	1.60	6.8E-02		MRPL49	9.75	1.48	2.2E-01
SCO1	9.51	1.59	1.4E-01		MRPS33	9.51	1.48	1.7E-01
ARMCX1	8.76	1.59	7.0E-02		MRPS22	9.85	1.48	1.4E-01
NDUFA8	10.14	1.59	1.1E-01		MRPS16	9.71	1.48	2.2E-01
MPC2	9.94	1.59	1.1E-01		CCDC141	9.73	1.48	2.2E-01

EDIL3	9.48	1.48	1.7E-01		HIBADH	10.78	1.36	1.3E-01
NPTN;DKFZp566H1924	9.64	1.47	2.2E-01		UQCR11	8.64	1.36	1.3E-01
MTX1	9.59	1.47	2.2E-01		MRPS15	9.47	1.36	2.1E-01
MRPL24	9.48	1.47	1.7E-01		CLPP	9.65	1.36	2.7E-01
MRPL44	9.43	1.47	1.8E-01		IMMT	10.29	1.35	1.3E-01
MLYCD	9.66	1.46	2.2E-01		TMEM173	9.21	1.35	2.2E-01
NADK2	9.48	1.46	1.8E-01		ABCB7	8.69	1.35	1.3E-01
MRPL21	9.54	1.46	2.2E-01		DAP3	9.73	1.35	2.7E-01
NDUFA5	10.24	1.46	1.0E-01		MRPS9	9.50	1.35	2.2E-01
NDUFAB1	9.48	1.46	1.8E-01		SF3A2	9.18	1.35	1.6E-01
SF3B5	9.46	1.45	1.8E-01		FDX1L	8.67	1.34	1.3E-01
SF3A3	9.55	1.45	2.3E-01		INPP5A	8.76	1.34	1.3E-01
VDAC1	10.90	1.45	1.0E-01		FUNDC2	10.08	1.34	1.9E-01
DSC1	9.50	1.44	1.8E-01		SYNJ2BP	9.72	1.34	2.7E-01
OSGEPL1	8.34	1.44	1.0E-01		SFXN1	10.09	1.34	1.9E-01
MTCH1	8.91	1.44	1.3E-01		MRPL48	9.50	1.34	2.2E-01
MRPL38	9.31	1.43	1.9E-01		MTHFR	9.96	1.34	1.9E-01
INPP1	8.90	1.43	1.3E-01		TMPO	10.03	1.34	1.9E-01
MRPS18B	10.32	1.43	1.1E-01		NT5DC2	9.97	1.33	1.9E-01
VDAC2	10.80	1.43	1.1E-01		IGSF3	8.45	1.33	1.4E-01
MRPL1	9.74	1.43	2.4E-01		SARS2	9.75	1.33	2.8E-01
MRPL39	9.62	1.43	2.4E-01		SYNGR1	9.02	1.33	1.7E-01
MRPS17	9.61	1.43	2.4E-01		MRPS18A	9.24	1.33	2.3E-01
PDP1	9.65	1.42	2.4E-01		UQCR10	9.97	1.33	1.9E-01
ACADSB	10.44	1.42	1.1E-01		PLGRKT	8.92	1.33	1.7E-01
TSPO	9.08	1.42	1.3E-01		MNF1	9.18	1.33	1.7E-01
UQCRQ	10.17	1.42	1.1E-01		NDUFV1	10.25	1.33	1.4E-01
CD36	9.17	1.42	1.4E-01		SORT1	9.03	1.32	1.7E-01
NDUFA2	9.88	1.41	1.6E-01		SELRC1	8.73	1.32	1.4E-01
FKBP1B	8.20	1.41	1.1E-01		HSDL1	10.45	1.32	1.4E-01
MMAB	9.92	1.41	1.6E-01		SRSF7	9.23	1.32	2.3E-01
SNRNP70	9.03	1.41	1.4E-01		UQCRC2	10.93	1.32	1.4E-01
MRPS27	9.80	1.41	2.5E-01		PRPF40A	8.95	1.31	1.7E-01
RDH14	9.98	1.41	1.6E-01		MSMO1	9.08	1.31	1.7E-01
TMEM14C	9.58	1.41	2.5E-01		SLIRP	10.51	1.31	1.5E-01
SLC25A24	10.04	1.41	1.6E-01		ATP1B3	9.60	1.31	2.9E-01
HIGD2A	9.32	1.41	2.0E-01		SMIM12	9.00	1.31	1.8E-01
PDE3A	8.56	1.41	1.1E-01		MRPS25	9.80	1.31	2.9E-01
MRPS31	9.45	1.40	2.0E-01		PVR	9.16	1.31	1.8E-01
MECR	9.67	1.40	2.5E-01		SDHA	10.88	1.31	1.4E-01
CCDC167	8.63	1.40	1.2E-01		CCAR1	9.26	1.31	2.4E-01
MFN2	9.76	1.40	2.5E-01		MT-ND5	8.81	1.30	1.5E-01
ALDOC	11.86	1.40	1.1E-01		SNRPA1	9.59	1.30	2.9E-01
PTRF	10.66	1.40	1.1E-01		CYB5R3	11.29	1.30	1.4E-01
PXMP2	8.35	1.39	1.2E-01		ACSL1	10.56	1.30	1.5E-01
PGRMC1	10.11	1.39	1.7E-01		MRPS28	9.88	1.30	2.0E-01
MRPL4	9.55	1.39	2.5E-01		ATPAF2	9.48	1.30	2.4E-01
TIMM50	9.84	1.39	1.7E-01		PDHX	10.38	1.30	1.5E-01
MRPS35	9.71	1.39	2.5E-01		SF3B2	9.42	1.29	2.4E-01
C4A;C4B	9.69	1.38	2.6E-01		ETFA	11.41	1.29	1.5E-01
STOML2	9.74	1.38	2.6E-01		MRPS2	9.51	1.29	2.4E-01
PTCD3	9.74	1.38	2.6E-01		OXCT1	11.23	1.29	1.5E-01
MT-ND4	9.33	1.38	2.0E-01		OBSCN	10.35	1.28	1.6E-01
HCN4	9.66	1.38	2.6E-01		RABL3	9.38	1.28	2.4E-01
NDUFS2	10.42	1.38	1.3E-01		MRPL46	9.82	1.28	3.0E-01
MRPS34	9.85	1.38	1.7E-01		DNAJA3	8.73	1.28	1.6E-01
PLN	10.22	1.38	1.3E-01		SLC25A3	11.19	1.28	1.5E-01
HSPA12A	8.70	1.38	1.2E-01		HTATSF1	9.44	1.28	2.5E-01
MRPS10	9.52	1.38	2.6E-01		ACOT1	10.98	1.28	1.5E-01
BNIP3	8.83	1.37	1.2E-01		POPDC2	9.93	1.28	2.1E-01
MRPS23	9.75	1.37	2.6E-01		COQ6	9.84	1.28	2.1E-01
NDUFS3	10.59	1.37	1.3E-01		SMARCC2	8.92	1.28	1.9E-01
PTPLB	8.25	1.37	1.3E-01		COQ5	9.94	1.28	2.1E-01
MFN1	9.59	1.37	2.6E-01		PCCB	10.50	1.28	1.6E-01
FAM210A	9.09	1.37	1.5E-01		MT-ND2	9.04	1.27	1.9E-01
MGST3	10.40	1.37	1.3E-01		LYRM7	9.46	1.27	2.5E-01
NDUFS7	9.82	1.37	1.8E-01		PPA2	10.38	1.27	1.6E-01
RAB24	9.48	1.36	2.1E-01		PNPLA4	9.65	1.27	3.1E-01
NDUFS1	10.63	1.36	1.2E-01		COX7A2L	8.90	1.27	1.9E-01
PRDX1	11.89	1.36	1.3E-01		SEMA4B	9.03	1.27	1.9E-01
UQCRB	10.19	1.36	1.3E-01		CAV2	9.66	1.26	3.1E-01
TMEM126B	8.74	1.36	1.3E-01		SDR39U1	9.83	1.26	2.2E-01

SLC2A4	7.98	1.26	1.6E-01		TRIM33	8.11	1.15	2.1E-01
PGAM5	8.96	1.26	1.9E-01		NIPSNAP3B	10.37	1.15	2.1E-01
SF3B1	9.91	1.26	2.2E-01		TXN2	10.00	1.15	2.6E-01
HNRNPL	9.98	1.26	2.2E-01		SLMAP	10.66	1.15	2.0E-01
SLC25A10	9.76	1.25	3.1E-01		CTSA	10.00	1.15	2.6E-01
ACAT1	11.21	1.25	1.6E-01		ATP1A2	8.98	1.15	2.5E-01
ACAD8	10.07	1.25	2.2E-01		ISOC2	10.36	1.15	2.1E-01
SF3A1	9.45	1.25	2.6E-01		CDH13	8.11	1.14	2.1E-01
MARCH5	9.64	1.25	3.2E-01		IDH3A	11.17	1.14	2.1E-01
UQCC	9.43	1.25	2.6E-01		ME2	10.59	1.14	2.2E-01
SNRPE	9.75	1.25	3.2E-01		TAPBP	8.83	1.14	2.1E-01
TIMM13	9.78	1.25	3.2E-01		PCBD2	9.20	1.14	3.1E-01
RANBP2	9.47	1.25	2.6E-01		ARSB	9.80	1.13	3.8E-01
TIMM8A	10.01	1.25	2.2E-01		PIGK	9.29	1.13	3.2E-01
RALB	10.01	1.25	2.2E-01		COA6	9.10	1.13	2.5E-01
SPRYD4	10.15	1.24	2.2E-01		IDH3G;hCG_2004980	10.62	1.13	2.2E-01
SCCPDH	10.51	1.24	1.7E-01		SRSF1	10.28	1.13	2.2E-01
ICT1	9.44	1.24	2.6E-01		SF3B3	9.97	1.13	2.7E-01
MRPL15	9.52	1.24	2.6E-01		RBM25	9.24	1.13	3.2E-01
GCSH	9.35	1.24	2.6E-01		ETFB	11.26	1.13	2.1E-01
HCFC1	9.09	1.24	2.0E-01		MTFR1L	9.28	1.12	3.2E-01
WDR5	8.88	1.24	2.0E-01		DLD	11.20	1.12	2.2E-01
TMX4	9.87	1.23	2.3E-01		GDPD1	8.77	1.12	2.2E-01
MFGE8	10.57	1.23	1.8E-01		NOP10	8.43	1.12	2.2E-01
SNRPF	9.48	1.23	2.7E-01		TMEM41B	9.08	1.12	2.6E-01
TAMM41	8.77	1.23	1.8E-01		C2orf47	9.69	1.12	3.8E-01
PTP4A3	8.60	1.23	1.8E-01		HK1	11.70	1.12	2.2E-01
SLC25A6	11.47	1.22	1.7E-01		ACYP2	9.54	1.12	3.9E-01
GLB1	10.22	1.22	1.8E-01		DPM3	9.32	1.12	3.2E-01
KLHL31	8.44	1.21	1.8E-01		HDHD3	10.19	1.12	2.3E-01
LAMTOR4	9.28	1.21	2.8E-01		AGPAT2	8.26	1.12	2.2E-01
CLPTM1	8.70	1.21	1.8E-01		SMIM7	8.48	1.11	2.3E-01
NUBPL	9.88	1.21	2.4E-01		CRELD1	9.01	1.11	2.6E-01
UQCRFS1;UQCRFS1P1	10.29	1.21	1.9E-01		SNRPD2	10.19	1.11	2.3E-01
RHOT1	9.73	1.21	3.4E-01		TBL1XR1	9.55	1.11	3.9E-01
PPP1R3E	8.59	1.21	1.8E-01		MMAA	8.47	1.11	2.3E-01
NME3	9.74	1.20	3.4E-01		HMGN3	8.68	1.11	2.3E-01
RPN2	8.86	1.20	2.2E-01		HDAC2	9.72	1.11	3.9E-01
PRKAR2B	10.48	1.20	1.9E-01		CCDC47	8.95	1.11	2.6E-01
SNRPG	9.76	1.20	3.4E-01		ETFDH	10.37	1.11	2.3E-01
SNRPB2	9.69	1.20	3.4E-01		NUDT19	8.95	1.11	2.6E-01
FXN	9.58	1.20	3.4E-01		MXRA7	10.07	1.11	2.8E-01
CYC1	10.27	1.20	1.9E-01		NDUFAF2	9.54	1.11	3.9E-01
TMEM97	9.71	1.20	3.4E-01		LAMTOR1	9.90	1.10	2.8E-01
HSD17B12	10.64	1.19	1.8E-01		CDS2	8.93	1.10	2.7E-01
FUCA1	9.15	1.19	2.2E-01		CDH2	10.23	1.10	2.4E-01
COQ7	10.03	1.19	2.5E-01		GNB2	10.84	1.10	2.2E-01
CHCHD1	8.78	1.19	1.9E-01		PTRH2	9.26	1.10	3.3E-01
PDK2	9.50	1.19	2.9E-01		SLC8A1	10.64	1.10	2.3E-01
UQCRC1	10.72	1.19	1.9E-01		JUP	10.41	1.10	2.4E-01
FARP1	10.08	1.19	2.5E-01		PGM5	10.98	1.10	2.3E-01
LHPP	9.36	1.18	2.9E-01		ABHD10	10.13	1.10	2.9E-01
DPP7	9.77	1.18	3.5E-01		UQCRH	9.20	1.10	3.3E-01
BCAS2	8.60	1.18	1.9E-01		CMAS	9.47	1.10	3.3E-01
GHITM	8.19	1.18	2.0E-01		PCCA	10.56	1.09	2.4E-01
FIS1	10.32	1.18	2.0E-01		GOLGA7	8.94	1.09	2.7E-01
NDUFV2	10.14	1.18	2.5E-01		ACP6	9.00	1.09	2.7E-01
PBXIP1	9.18	1.18	2.3E-01		HYI	9.10	1.09	2.7E-01
EMC7	9.01	1.18	2.3E-01		CTNNA2	9.16	1.09	2.7E-01
PRPF19	9.96	1.18	2.5E-01		PDZD11	9.29	1.09	3.4E-01
COQ3	9.53	1.18	3.5E-01		HP1BP3	9.61	1.09	4.0E-01
MCEE	9.58	1.18	3.5E-01		ENDOG	9.49	1.09	3.4E-01
C18orf32	8.93	1.17	2.3E-01		LPCAT4	8.95	1.09	2.8E-01
TOMM70A	9.98	1.17	2.5E-01		GLRX5	9.70	1.08	4.0E-01
EPDR1	9.67	1.17	3.6E-01		PTDSS1	8.45	1.08	2.4E-01
FDXR	9.29	1.17	3.0E-01		TMLHE	9.88	1.08	3.0E-01
CHCHD7	8.59	1.17	2.0E-01		BET1;DKFZp781C0425	9.06	1.08	2.8E-01
MGST2	9.30	1.16	3.0E-01		VAPB	9.88	1.08	3.0E-01
PPOX	9.17	1.16	2.4E-01		MLEC	10.21	1.08	2.5E-01
PICK1	8.66	1.16	2.1E-01		BAG2	9.97	1.08	3.0E-01
CPNE5	9.82	1.16	2.6E-01		MCCC1	10.05	1.08	3.0E-01
COQ9	10.36	1.16	2.1E-01		VCAM1	9.26	1.08	3.4E-01

GCAT	9.95	1.08	3.0E-01	RAB23	9.12	0.98	3.4E-01
ATP2B4	11.37	1.08	2.4E-01	PAK1	8.59	0.98	3.0E-01
CISD2	10.18	1.08	2.5E-01	TIMM8B	9.30	0.98	4.0E-01
RHOT2	9.10	1.07	2.8E-01	CYB5A	10.35	0.98	3.0E-01
MTIF2	9.00	1.07	2.8E-01	HIST1H1A	8.47	0.98	3.0E-01
OGDH	9.10	1.07	2.8E-01	HIGD1A	9.50	0.98	4.0E-01
FKBP8	9.26	1.07	3.5E-01	PEX14	8.50	0.98	3.0E-01
CRMP1	10.29	1.07	2.5E-01	CLPX	9.19	0.98	3.4E-01
NIPSNAP1	10.64	1.07	2.4E-01	GPAA1	8.75	0.98	3.0E-01
SNRPD1	9.97	1.07	3.0E-01	AMT	9.85	0.98	3.5E-01
SFPQ	10.79	1.06	2.4E-01	FLOT1	10.32	0.98	3.0E-01
DHCR7	9.22	1.06	3.5E-01	HNRNPH3	8.86	0.97	3.4E-01
SRSF4	9.26	1.06	3.6E-01	CTNNB1	10.38	0.97	3.0E-01
MTFP1	8.73	1.06	2.5E-01	PRKAB2	10.09	0.97	3.5E-01
EARS2	9.38	1.05	3.6E-01	ERLIN2	10.01	0.97	3.5E-01
PRAF2;WDR45	9.69	1.05	4.2E-01	GM2A	9.72	0.97	4.7E-01
COX20	9.06	1.05	3.0E-01	MATR3	9.87	0.97	3.6E-01
PTGES2	10.40	1.05	2.6E-01	ME1	9.94	0.97	3.6E-01
LETM1	10.18	1.05	2.6E-01	ISCA2	9.58	0.97	4.7E-01
SLC25A1	9.67	1.05	4.2E-01	ALDH2	11.10	0.97	2.9E-01
ATP13A1	9.36	1.05	3.6E-01	LRPPRC	11.06	0.97	2.9E-01
STBD1	10.05	1.05	3.1E-01	SPATA20	9.53	0.97	4.7E-01
AIFM1	11.14	1.05	2.5E-01	SNRPD3	10.23	0.96	3.1E-01
MT-CYB	8.63	1.04	2.6E-01	BCL2L13	9.56	0.96	4.8E-01
NDUFAF3	9.69	1.04	4.3E-01	LAMTOR3	9.57	0.96	4.8E-01
SNRPA	9.67	1.04	4.3E-01	ECI2	10.46	0.96	3.1E-01
CBR4	10.06	1.04	3.2E-01	HNRNPA2B1	10.52	0.96	3.1E-01
EPB41L3	10.42	1.04	2.7E-01	CDK5RAP3	9.32	0.96	4.1E-01
CYB5B	10.12	1.04	3.2E-01	AK2	10.94	0.95	3.0E-01
LGALS3	10.91	1.03	2.6E-01	RYR2	10.88	0.95	3.0E-01
DARS2	10.15	1.03	3.2E-01	RCN2	9.12	0.95	3.5E-01
RRAD	9.63	1.03	4.3E-01	EMD	9.85	0.95	3.6E-01
ZADH2	9.71	1.03	4.3E-01	UBXN4	9.52	0.95	4.2E-01
OPA1	10.60	1.03	2.7E-01	SCAMP1	9.68	0.95	4.8E-01
SYPL1	9.26	1.03	3.7E-01	AKR1A1	11.14	0.95	3.0E-01
NDUFAF4	9.71	1.03	4.4E-01	HNRNPH2	9.59	0.95	4.8E-01
SSBP1	10.97	1.03	2.6E-01	HINT2	10.27	0.95	3.2E-01
TFAM	10.25	1.03	2.7E-01	TMED5	9.19	0.95	3.5E-01
GSTZ1	9.82	1.02	3.3E-01	C11orf58;SMAP	9.47	0.95	4.2E-01
GLIPR2	9.29	1.02	3.8E-01	ORMDL3	9.08	0.95	3.5E-01
CACNB2	8.36	1.02	2.7E-01	ACAA2	10.98	0.95	3.0E-01
QPRT	10.76	1.02	2.7E-01	C6orf136	8.61	0.95	3.2E-01
MRPS26	9.34	1.01	3.8E-01	EMC2	9.07	0.95	3.6E-01
SMCHD1	9.03	1.01	3.2E-01	GNB1	10.29	0.95	3.2E-01
SLC16A7	8.96	1.01	3.2E-01	HSD17B8	10.32	0.95	3.2E-01
PDPR	9.86	1.01	3.3E-01	DHRS7	9.46	0.94	4.2E-01
LAMTOR2	9.69	1.01	4.5E-01	GSK3B	8.67	0.94	3.2E-01
CHCHD2;CHCHD2P9	9.23	1.01	3.8E-01	NONO	10.77	0.94	3.1E-01
PARS2	9.00	1.01	3.2E-01	FLOT2	10.13	0.94	3.7E-01
MCCC2	10.27	1.00	2.9E-01	C14orf1	9.02	0.94	3.6E-01
CDC73	8.72	1.00	2.8E-01	CRAT	10.64	0.94	3.1E-01
BVES	9.89	1.00	3.4E-01	CPD	8.88	0.94	3.6E-01
EMC1	9.41	1.00	3.9E-01	EMC10	8.11	0.94	3.2E-01
SIRT3	9.73	1.00	4.5E-01	ITGA7	10.56	0.94	3.2E-01
TMED4	9.70	1.00	4.5E-01	DLAT	10.97	0.94	3.1E-01
C6orf203	9.16	1.00	3.3E-01	LARS2	9.39	0.94	4.2E-01
SUCLG1	10.99	1.00	2.8E-01	CIRBP	10.19	0.94	3.2E-01
HADH	11.17	1.00	2.8E-01	CLPB	9.56	0.94	4.9E-01
IDH3B	10.88	1.00	2.8E-01	TACO1	9.93	0.94	3.7E-01
CNTNAP1	8.85	0.99	2.9E-01	TOP1	8.99	0.94	3.6E-01
HTRA2	9.85	0.99	3.4E-01	EMC8	9.10	0.94	3.6E-01
CS	11.69	0.99	2.8E-01	CNRIP1	10.02	0.93	3.7E-01
CYCS	11.72	0.99	2.8E-01	CUX1	8.32	0.93	3.2E-01
ACO2	11.75	0.99	2.8E-01	CDC5L	8.46	0.93	3.2E-01
PCDHB8;PCDHB6;PCDHB7;PCDHB4;PCDHB5;PCDHB13;PCDHB10	8.44	0.99	2.9E-01	MRE11A	9.02	0.93	3.7E-01
				MANBAL	8.62	0.93	3.3E-01
				SUN2	9.17	0.93	3.7E-01
BCKDHB	9.55	0.99	4.6E-01	GAA	9.95	0.93	3.8E-01
FDX1	9.25	0.99	4.0E-01	SLC25A4	10.99	0.93	3.2E-01
HCCS	9.24	0.99	4.0E-01	ABCC1	8.40	0.93	3.3E-01
VAMP3	9.81	0.98	4.6E-01	BCKDHA	9.84	0.93	3.8E-01
B2M	9.86	0.98	3.5E-01	MYL4	12.09	0.93	3.2E-01

CAMK2A	8.95	0.93	3.7E-01		HIP1R	8.81	0.85	3.8E-01
GOT2	11.67	0.93	3.2E-01		FAM213A	10.58	0.85	3.8E-01
IRF2BP1	8.87	0.93	3.7E-01		VIM	10.79	0.85	3.7E-01
RFTN1	8.92	0.93	3.7E-01		ACOX3	9.57	0.84	5.5E-01
FITM2	9.18	0.93	3.7E-01		PNPLA6	9.16	0.84	4.3E-01
RTN4IP1	9.16	0.93	3.7E-01		KIAA0391	8.68	0.84	3.8E-01
FAM136A	10.04	0.92	3.8E-01		CLGN	9.76	0.84	5.5E-01
AK3	11.00	0.92	3.2E-01		RBP1	10.68	0.84	3.7E-01
PCYOX1L	9.51	0.92	4.3E-01		JAGN1	9.25	0.84	4.9E-01
NARS2	9.24	0.92	4.4E-01		EHD2	9.91	0.84	4.3E-01
DDRGK1	9.36	0.92	4.4E-01		DIABLO	10.58	0.84	3.9E-01
TMEM65	10.44	0.92	3.4E-01		ABCD3	9.34	0.84	4.9E-01
AK1	11.23	0.91	3.2E-01		CAMK1D	8.38	0.84	3.9E-01
KDM1A	8.87	0.91	3.8E-01		HSD17B10	11.14	0.84	3.7E-01
TMTC3	8.92	0.91	3.8E-01		SPATS2L	9.35	0.84	4.9E-01
NCAM1	11.12	0.91	3.3E-01		C1QBP	10.41	0.83	3.9E-01
TAX1BP3	9.84	0.91	3.9E-01		VMA21	9.36	0.83	4.9E-01
GNA11	10.08	0.91	3.9E-01		CYP51A1	9.76	0.83	5.6E-01
ACADVL	11.33	0.91	3.3E-01		GTF3C1	8.86	0.83	3.9E-01
CKAP4	10.98	0.91	3.3E-01		MDH2	12.19	0.83	3.8E-01
HAX1	8.95	0.91	3.8E-01		PARVB	8.11	0.83	3.9E-01
PIGT	9.63	0.91	5.1E-01		ASAH1	11.19	0.83	3.8E-01
SIRT5	9.48	0.91	4.4E-01		PTGFRN	10.65	0.83	3.8E-01
PIGS	9.63	0.91	5.1E-01		MYEF2	8.23	0.83	3.9E-01
GTF3C4	8.75	0.90	3.4E-01		TMEM245	9.80	0.83	5.6E-01
NUDT3	8.96	0.90	3.9E-01		CCBL2	9.69	0.83	5.6E-01
GABARAP;GABARAPL1	9.12	0.90	3.9E-01		PDS5A	8.99	0.83	4.4E-01
TST	10.32	0.90	3.5E-01		LYRM4	9.18	0.82	4.4E-01
CACNA2D1	9.82	0.90	5.2E-01		GBAS	9.14	0.82	4.4E-01
CAMK2G	8.61	0.90	3.5E-01		ECHS1	11.19	0.82	3.8E-01
HDGFRP2	8.95	0.90	3.9E-01		SKIV2L2	8.59	0.82	4.0E-01
FAM129A	9.93	0.90	4.0E-01		GTF3C3	7.94	0.82	4.0E-01
NFIA	9.30	0.89	4.5E-01		HIST1H1D	9.46	0.82	5.0E-01
SUCLA2	11.07	0.89	3.4E-01		SLC35A4	10.14	0.82	4.4E-01
SPR	9.71	0.89	5.2E-01		AFG3L2	10.42	0.82	4.0E-01
LSS	10.31	0.89	3.6E-01		C7orf50	8.74	0.82	4.0E-01
GPD2	9.62	0.89	5.2E-01		PLEKHA5	9.50	0.82	5.0E-01
VAPA	10.56	0.89	3.6E-01		MRC2	9.67	0.82	5.7E-01
FAM3C	9.24	0.89	4.6E-01		CANX	11.18	0.81	3.9E-01
TUFM	11.60	0.88	3.4E-01		ZMPSTE24	8.36	0.81	4.0E-01
CNN1	10.68	0.88	3.4E-01		HSPD1	12.00	0.81	3.9E-01
SNRPN;SNRPB	9.79	0.88	5.3E-01		ARVCF	9.51	0.81	5.1E-01
SLC2A14;SLC2A3	8.94	0.88	4.0E-01		RDH13	9.66	0.81	5.7E-01
STX7	9.95	0.88	4.1E-01		ISCA1	8.48	0.81	4.1E-01
GCDH	9.80	0.88	5.3E-01		MAGED1	8.45	0.81	4.1E-01
SPHKAP	9.46	0.87	4.7E-01		GUF1	8.46	0.81	4.1E-01
LNP	9.89	0.87	4.1E-01		EPN3	8.42	0.81	4.1E-01
TSTD1	9.62	0.87	5.3E-01		PEX11B	9.31	0.81	5.1E-01
DHRS4	9.64	0.87	5.3E-01		HNRNPA3	9.65	0.81	5.8E-01
MCM5	9.59	0.87	5.3E-01		UFL1	9.75	0.80	5.8E-01
CDIPT	9.67	0.87	5.3E-01		STXBP3	9.18	0.80	4.5E-01
NEXN	9.85	0.87	4.1E-01		PREB	8.81	0.80	4.1E-01
RFC5	8.70	0.87	3.7E-01		IDH2	12.04	0.80	4.0E-01
CTNNA1	10.50	0.87	3.7E-01		SUCLG2	10.70	0.80	4.0E-01
SUPV3L1	8.94	0.87	4.1E-01		GNG12	9.95	0.80	4.6E-01
SRSF6	8.95	0.87	4.1E-01		AQP1	9.77	0.80	5.8E-01
RBM26	8.80	0.86	3.7E-01		DMD	10.07	0.80	4.6E-01
BCS1L	9.07	0.86	4.1E-01		ATP6AP1	8.89	0.80	4.6E-01
MT-ND1	8.24	0.86	3.7E-01		ERGIC3	9.37	0.80	5.2E-01
ZFP62	9.17	0.86	4.2E-01		MACROD1	10.12	0.80	4.6E-01
PRR14L	8.91	0.86	4.2E-01		AARS2	9.45	0.79	5.2E-01
HNRNPA0	10.06	0.86	4.2E-01		GNB4	9.01	0.79	4.6E-01
ARMC1	9.75	0.86	5.4E-01		ERBB2	9.37	0.79	5.2E-01
MTIF3	9.03	0.85	4.2E-01		ALDH6A1	10.81	0.79	4.1E-01
NDUFAF7	9.09	0.85	4.2E-01		STX4	9.25	0.79	5.2E-01
MAP1LC3A	9.73	0.85	5.5E-01		NCLN	9.56	0.79	5.9E-01
CHD4	9.37	0.85	4.8E-01		ATP6V0C	9.61	0.79	5.9E-01
NAT14	8.68	0.85	3.8E-01		DCAKD	9.57	0.79	5.9E-01
MVK	9.11	0.85	4.2E-01		FECH	10.03	0.79	4.7E-01
SPG7	8.90	0.85	4.2E-01		MSRB2	9.56	0.78	5.9E-01
ATP13A3	8.14	0.85	3.8E-01		HSPA9	11.52	0.78	4.1E-01
RPN1	11.04	0.85	3.7E-01		SRSF3	10.04	0.78	4.7E-01

GNAS	10.09	0.78	4.7E-01		TMEM33	9.51	0.71	5.8E-01
HNRNPH1	10.47	0.78	4.3E-01		IBA57	9.64	0.71	6.5E-01
C14orf159	10.41	0.78	4.3E-01		GLS	9.76	0.70	6.5E-01
GBAS	11.05	0.78	4.2E-01		MCAT	8.87	0.70	5.3E-01
FAHD1	10.51	0.77	4.3E-01		VSTM2L	9.11	0.70	5.3E-01
IRF2BPL	9.59	0.77	6.0E-01		GOLT1B	8.97	0.62	6.0E-01
ATP6V0D1	9.59	0.77	6.0E-01		STX12	9.37	0.62	6.5E-01
HIST1H1B	10.45	0.77	4.4E-01		DHTKD1	9.63	0.62	7.1E-01
CDKN2AIP	9.40	0.77	5.4E-01		CAMK2D	8.99	0.62	6.0E-01
FMR1	8.73	0.77	4.3E-01		TJP2	9.68	0.62	7.1E-01
NES	10.14	0.77	4.8E-01		ARL6IP5	10.79	0.62	5.4E-01
ARL5A	8.54	0.77	4.4E-01		C16orf58	8.82	0.61	5.6E-01
HNRNPU	10.43	0.77	4.4E-01		LIN7A	9.17	0.61	6.0E-01
KHDRBS1	10.41	0.77	4.4E-01		COX17	9.97	0.61	5.9E-01
CLPTM1L	8.62	0.77	4.4E-01		CPSF7	9.50	0.61	6.5E-01
WARS2	8.93	0.76	4.8E-01		MARC2	9.41	0.61	6.5E-01
PDE4D	10.25	0.76	4.4E-01		HRSP12	9.86	0.61	5.9E-01
TSFM	10.12	0.76	4.8E-01		DAAM1	8.46	0.61	5.6E-01
PMVK	10.44	0.76	4.4E-01		FUS	9.64	0.61	7.2E-01
ATPAF1	9.57	0.76	6.1E-01		RALA	9.75	0.61	7.2E-01
GATM	10.17	0.76	4.4E-01		ILF2	10.47	0.61	5.6E-01
ACOT9	10.91	0.76	4.3E-01		DNAJC5	9.12	0.61	6.1E-01
CTNNA3	10.36	0.76	4.5E-01		RBBP4	10.07	0.61	5.9E-01
RAP2A;RAP2B	8.75	0.76	4.4E-01		DDX5	10.28	0.61	5.6E-01
NIPSNAP3A	10.77	0.76	4.3E-01		RMDN1	10.54	0.61	5.6E-01
SEC61G	8.84	0.76	4.4E-01		ANO6	8.85	0.61	5.6E-01
PRDX3	11.42	0.76	4.3E-01		ACSS3	9.21	0.61	6.5E-01
ELOVL5	8.28	0.75	4.5E-01		LGALS3BP	10.13	0.61	5.9E-01
ERBB2IP	8.41	0.75	4.5E-01		ADPRHL1	10.63	0.61	5.7E-01
ARL8B	10.02	0.75	4.9E-01		FBXO30	8.36	0.61	5.7E-01
CRNKL1	9.18	0.75	4.9E-01		NDUFV3	9.05	0.60	6.1E-01
PRKAA1	10.19	0.75	4.5E-01		SRSF5	9.18	0.60	6.1E-01
NKX2-5	8.41	0.75	4.5E-01		CLTB	9.89	0.60	5.9E-01
CHMP6	9.40	0.75	5.5E-01		RPA2	9.98	0.60	5.9E-01
BCAT2	10.37	0.74	4.6E-01		NUDT21	10.30	0.60	5.7E-01
QRSL1	8.48	0.74	4.5E-01		PSPC1	10.07	0.60	5.9E-01
THYN1	9.78	0.74	6.2E-01		H1F0	10.71	0.60	5.5E-01
ABHD11	10.02	0.74	5.0E-01		KDELC1	8.57	0.60	5.7E-01
PLXNB2	9.41	0.74	5.6E-01		TMED7	10.17	0.60	5.7E-01
TMCO1	9.11	0.74	5.0E-01		RRAS	10.22	0.60	5.7E-01
PABPN1	9.32	0.74	5.6E-01		KBTBD11	8.75	0.60	5.7E-01
U2AF2	9.98	0.74	5.0E-01		PRKACB	9.99	0.60	6.0E-01
CXADR	9.18	0.74	5.0E-01		STX8	9.07	0.60	6.2E-01
ADCY6	8.25	0.74	4.6E-01		PPIF	10.26	0.59	5.8E-01
IVD	10.81	0.73	4.5E-01		METAP2	9.08	0.59	6.2E-01
ABHD12	9.22	0.73	5.6E-01		DDOST	10.55	0.59	5.8E-01
RAB4A	9.45	0.73	5.6E-01		SEL1L	9.27	0.59	6.7E-01
ELMOD2	9.50	0.73	5.6E-01		LMAN2L	9.76	0.59	7.3E-01
KIF1A	8.67	0.73	4.6E-01		RPA1	10.48	0.59	5.8E-01
DAD1	10.06	0.73	5.0E-01		MTUS2	9.01	0.59	6.3E-01
SEC11A	9.78	0.73	6.3E-01		RPA3	9.68	0.59	7.4E-01
DSP	10.65	0.73	4.5E-01		EMC3	8.96	0.59	6.3E-01
KIAA1967	10.02	0.73	5.1E-01		CCDC58	10.19	0.58	5.8E-01
WDR82	9.18	0.73	5.1E-01		SRRT	9.74	0.58	7.4E-01
ECHDC3	9.70	0.72	6.3E-01		ITPRIP	9.09	0.58	6.3E-01
ETHE1	9.95	0.72	5.1E-01		OXSM	9.08	0.58	6.3E-01
KDSR	9.11	0.72	5.1E-01		PDLIM3	11.00	0.58	5.7E-01
GLUD1	10.94	0.72	4.5E-01		POR	9.47	0.58	6.8E-01
PTPN1	8.65	0.72	4.7E-01		RAB35	9.65	0.58	7.4E-01
GGH	9.59	0.72	6.4E-01		RAD50	9.53	0.58	7.4E-01
PURA	10.25	0.72	4.7E-01		NCSTN	9.40	0.58	6.8E-01
APP	8.74	0.72	4.7E-01		PDS5B	9.12	0.58	6.3E-01
EHD4	10.90	0.72	4.6E-01		FAHD2A;FAHD2B	10.55	0.58	5.9E-01
LYRM2	8.88	0.71	5.2E-01		ALYREF	9.36	0.58	6.8E-01
ERLEC1	8.78	0.71	4.8E-01		NAGA	9.65	0.57	7.5E-01
PTBP2	9.60	0.71	6.4E-01		PTN	9.27	0.57	6.8E-01
FH	11.59	0.71	4.6E-01		POLR2J;POLR2J3;POLR2J2	8.69	0.58	6.0E-01
ATP6V0A1	8.58	0.71	4.8E-01					
TRMT61A	8.72	0.71	4.8E-01		SART3	9.95	0.57	6.2E-01
ADD3	9.87	0.71	5.2E-01		TARDBP	10.14	0.57	6.2E-01
DPM1	9.69	0.71	6.5E-01		RAB3D;RAB3A	8.26	0.57	6.0E-01
LAMTOR5	9.27	0.71	5.8E-01		TOLLIP	10.13	0.57	6.2E-01

CRIP1	9.75	0.57	7.5E-01		ACSF3	9.01	0.52	6.8E-01
ACAA1	9.73	0.57	7.5E-01		SPCS3	9.48	0.52	7.2E-01
TMED2	10.17	0.57	6.0E-01		TMED10	10.54	0.52	6.4E-01
SRR	9.69	0.57	7.5E-01		FUBP3	8.99	0.52	6.9E-01
OSTC	9.35	0.57	6.9E-01		KRAS	9.79	0.52	7.9E-01
MYH1	11.32	0.56	5.8E-01		PRPF31	9.08	0.52	6.9E-01
DDX46	9.69	0.56	7.5E-01		SAT2	9.54	0.52	7.9E-01
UBXN6	8.86	0.56	6.0E-01		RAB18	10.19	0.52	6.4E-01
MSRA	9.21	0.56	6.9E-01		SLC25A13	9.68	0.52	7.9E-01
PDK3	9.60	0.56	7.5E-01		TRMT10C	9.75	0.51	7.9E-01
NUDT2	9.86	0.56	6.2E-01		DHX9	10.37	0.51	6.5E-01
PPT1	9.98	0.56	6.3E-01		LRPAP1	9.89	0.51	6.6E-01
SLC12A4	8.32	0.56	6.0E-01		CTNNBL1	9.20	0.51	7.3E-01
CPSF6	9.67	0.56	7.6E-01		FLJ00186;RASSF5	8.37	0.51	6.5E-01
IMPAD1	9.57	0.56	7.6E-01		PPP1CC	9.38	0.51	7.3E-01
GSTM1	9.98	0.56	6.3E-01		ACTL6A	8.93	0.51	6.9E-01
SYVN1	8.66	0.56	6.1E-01		DAZAP1	9.55	0.51	8.0E-01
ATE1	9.64	0.56	7.6E-01		PROS1	10.33	0.51	6.5E-01
FAM171A1	8.12	0.56	6.1E-01		TBL2	9.26	0.51	7.3E-01
CTSB	10.98	0.56	5.9E-01		BOLA1	8.33	0.51	6.5E-01
ACADM	10.83	0.55	5.9E-01		KDM3B	8.73	0.51	6.5E-01
GNAI2	10.78	0.55	5.9E-01		DEK	10.04	0.51	6.7E-01
SPTAN1	11.52	0.55	5.9E-01		CYB5R1	10.57	0.51	6.5E-01
GLRX	9.69	0.55	7.6E-01		LAP3	9.94	0.50	6.7E-01
PIGU	8.23	0.55	6.1E-01		RAB7A	10.66	0.50	6.3E-01
ROR2	9.11	0.55	6.6E-01		C17orf62	8.49	0.50	6.5E-01
POLG	9.39	0.55	7.0E-01		RAP1A	10.53	0.50	6.6E-01
SMC3	9.36	0.55	7.0E-01		C21orf33	11.07	0.50	6.3E-01
ELAC2	9.12	0.55	6.6E-01		HNRNPUL1	10.00	0.50	6.7E-01
PNKP	8.79	0.55	6.2E-01		PGAM2	11.01	0.50	6.4E-01
SELH;C11orf31	9.46	0.55	7.0E-01		USE1	8.34	0.50	6.6E-01
GOLGA2	8.84	0.54	6.2E-01		TPP1	10.48	0.50	6.6E-01
ARL8A	10.27	0.54	6.2E-01		WRNIP1	8.73	0.50	6.6E-01
CNPY3	9.54	0.54	7.7E-01		NMNAT3	8.32	0.50	6.6E-01
COG3	8.69	0.54	6.2E-01		PPP1R21	9.09	0.49	7.1E-01
GNA13	8.57	0.54	6.2E-01		SLC20A2	8.59	0.49	6.7E-01
MCM6	9.93	0.54	6.4E-01		VTI1B	9.55	0.49	8.1E-01
PRKDC	11.13	0.54	6.0E-01		EPS15L1	9.37	0.49	7.5E-01
DNAJB2	8.73	0.54	6.2E-01		ALDH18A1	9.90	0.49	6.8E-01
MTDH	9.59	0.54	7.7E-01		NELFCD;TH1L	9.00	0.49	7.1E-01
GSTM2	10.71	0.54	6.0E-01		RANBP3	9.80	0.49	8.1E-01
CMBL	9.85	0.54	6.4E-01		TOM1	10.01	0.49	6.8E-01
ANK2	10.39	0.54	6.2E-01		HNRNPM	10.91	0.49	6.5E-01
BAD	8.43	0.54	6.2E-01		CPT2	10.49	0.49	6.7E-01
SACM1L	9.64	0.54	7.7E-01		NPM1	10.73	0.49	6.5E-01
CBR1	10.32	0.54	6.3E-01		VKORC1L1	9.02	0.49	7.2E-01
TGM2	11.78	0.54	6.0E-01		HMOX2	9.87	0.49	6.8E-01
MCM4	9.74	0.54	7.7E-01		ILVBL	10.21	0.48	6.7E-01
SNCA	9.70	0.54	7.7E-01		VAMP7	8.41	0.48	6.7E-01
WFS1	8.50	0.53	6.3E-01		TIMM44	10.29	0.48	6.7E-01
HSPB8	9.90	0.53	6.5E-01		MCM7	9.93	0.48	6.9E-01
YPEL5	8.64	0.53	6.3E-01		CNP	10.18	0.48	6.7E-01
XRN2	9.21	0.53	7.1E-01		NTPCR	9.84	0.48	6.9E-01
MAP1LC3B;MAP1LC3B2	9.51	0.53	7.1E-01		TRIM55	10.08	0.48	6.9E-01
SIRPA;SIRPB1	9.25	0.53	7.1E-01		EPM2AIP1	10.02	0.48	6.9E-01
SCFD2	8.73	0.53	6.3E-01		RBM39	9.37	0.48	7.6E-01
SCARB2	10.45	0.53	6.3E-01		DUT	9.91	0.48	6.9E-01
EWSR1	9.78	0.53	7.8E-01		BPHL	9.41	0.48	7.6E-01
LARP7	8.93	0.53	6.8E-01		SMEK1	8.91	0.48	7.2E-01
PRCP	10.08	0.53	6.5E-01		MLTK	10.14	0.47	6.9E-01
LIN7C	9.53	0.53	7.8E-01		TARS2	9.87	0.47	6.9E-01
TMED9	10.18	0.53	6.3E-01		ANKMY2	8.96	0.47	7.3E-01
MCM3	9.92	0.53	6.5E-01		IER3IP1	9.66	0.47	8.2E-01
STT3B	9.31	0.53	7.2E-01		TXLNB	9.80	0.47	8.2E-01
GNAI1	9.32	0.53	7.2E-01		CADM1	9.45	0.47	7.6E-01
ATP6V1F	9.07	0.52	6.8E-01		NBAS	8.84	0.47	6.8E-01
GRSF1	8.99	0.52	6.8E-01		HLA-A	9.62	0.47	8.3E-01
DCXR	10.47	0.52	6.4E-01		NUPL1	8.72	0.47	6.9E-01
PPP1R12B	9.47	0.52	7.2E-01		SRPR	9.74	0.47	8.3E-01
PVRL2	9.10	0.52	6.8E-01		NSF	9.71	0.47	8.3E-01
RAB13	9.49	0.52	7.2E-01		STRN3	9.16	0.47	7.3E-01
PTPMT1	8.95	0.52	6.8E-01		HSPA13	8.54	0.47	6.9E-01

NUDT14	9.39	0.47	7.7E-01		AKAP8L	8.35	0.41	7.4E-01
ACTN2	9.72	0.46	8.3E-01		DAG1	10.13	0.41	7.4E-01
JMJD7	9.60	0.46	8.3E-01		RNF20	8.87	0.41	7.9E-01
TMEM199	8.77	0.46	6.9E-01		ALDH9A1	10.88	0.41	7.2E-01
NPC2	10.03	0.46	7.0E-01		NRP1	9.28	0.41	8.1E-01
HDHD2	10.00	0.46	7.0E-01		ATM	8.65	0.41	7.5E-01
VWA8	9.53	0.46	8.3E-01		RTN4	11.36	0.41	7.2E-01
MPDU1;HBEBP2BPA	9.20	0.46	7.4E-01		CISD3	8.88	0.41	7.9E-01
PITRM1	10.10	0.46	7.1E-01		IARS2	10.94	0.41	7.2E-01
GOSR2	9.32	0.46	7.8E-01		RPL36AL	9.54	0.40	8.8E-01
TMX3	9.99	0.45	7.1E-01		PDDC1	9.59	0.40	8.8E-01
STXBP1	9.11	0.45	7.4E-01		API5	9.93	0.40	7.5E-01
RAB11A	9.33	0.45	7.8E-01		DDX39B	10.40	0.40	7.5E-01
RARS2	8.42	0.45	7.0E-01		LMAN2	10.06	0.40	7.5E-01
BRI3BP	9.49	0.45	7.8E-01		LGMN	9.69	0.40	8.8E-01
SDF2	9.27	0.45	7.8E-01		RRAS2	9.12	0.40	7.9E-01
LNPEP	9.70	0.45	8.4E-01		FER	9.14	0.40	7.9E-01
SSR1	9.50	0.45	7.8E-01		ALDH3A2	10.58	0.40	7.5E-01
GTF2I	9.66	0.45	8.4E-01		SRP9	10.22	0.40	7.5E-01
HEXA	9.76	0.45	8.4E-01		FSTL1	9.57	0.40	8.8E-01
EPHX1	9.74	0.45	8.4E-01		NMNAT1	9.02	0.40	8.0E-01
ATP6V1B2	9.98	0.45	7.1E-01		SDHAF2	8.83	0.40	7.5E-01
LRRC20	9.08	0.45	7.5E-01		HDGFRP3	9.15	0.40	8.0E-01
MVB12A	9.13	0.45	7.5E-01		DDAH1	10.50	0.40	7.5E-01
VPS37A	9.11	0.45	7.5E-01		ATP6V1D	9.74	0.40	8.8E-01
MCM2	9.89	0.45	7.1E-01		PPP1R2;PPP1R2P3	9.24	0.40	8.2E-01
SMC1A	9.99	0.44	7.2E-01		SSR3	9.21	0.39	8.3E-01
KTN1	10.74	0.44	6.9E-01		SMAD2	9.35	0.39	8.3E-01
HNMT	9.06	0.44	7.5E-01		MANBA	9.18	0.39	8.0E-01
BCAP29	9.48	0.44	7.9E-01		APMAP	10.18	0.39	7.6E-01
DPAGT1	8.33	0.44	7.1E-01		GBA	9.75	0.39	8.9E-01
RAP2C	8.99	0.44	7.6E-01		SMPD1	8.91	0.39	8.0E-01
ASPH	10.28	0.44	7.1E-01		PALM	8.69	0.39	7.6E-01
MTMR9	8.81	0.44	7.1E-01		TCEAL3;TCEAL6;TCEAL5	8.92	0.39	8.0E-01
TOMM34	8.99	0.44	7.6E-01		PHPT1	10.66	0.39	7.4E-01
TECR	9.43	0.44	7.9E-01		CSNK2A1;CSNK2A3	9.93	0.39	7.6E-01
SNRNP200	9.90	0.44	7.2E-01		CSNK1A1	9.68	0.39	8.9E-01
DLG1	9.92	0.44	7.2E-01		TBC1D24	9.20	0.39	8.3E-01
GPR89A;GPR89B;GPR89C	7.97	0.44	7.1E-01		ACP2	9.38	0.39	8.3E-01
					ITGB1	10.65	0.39	7.4E-01
SEC63	9.12	0.44	7.6E-01		GFM1	10.08	0.39	7.6E-01
PKM	11.13	0.44	6.9E-01		VAMP5	8.64	0.39	7.6E-01
COPS7A	9.98	0.44	7.2E-01		IRF2BP2	8.90	0.38	8.1E-01
KDELC2	9.26	0.44	7.9E-01		RAB11B	10.99	0.38	7.4E-01
PFKM	11.50	0.44	6.9E-01		MSI2	8.78	0.38	7.7E-01
HSDL2	10.61	0.44	7.2E-01		SSR4	10.19	0.38	7.7E-01
CD99	10.15	0.44	7.2E-01		PUF60	9.97	0.38	7.7E-01
UACA	9.50	0.44	7.9E-01		ATP1A1	11.31	0.38	7.4E-01
MYOM1	10.58	0.43	7.2E-01		GLG1	9.49	0.38	8.4E-01
RAB1B	10.16	0.43	7.2E-01		CTBP2	8.85	0.38	7.7E-01
HLA-B	9.04	0.43	7.6E-01		SMIM1	8.62	0.38	7.7E-01
GFM2	9.49	0.43	8.0E-01		NELFB	9.05	0.38	8.1E-01
CECR5	10.39	0.43	7.2E-01		PRKACA;KIN27	11.06	0.38	7.5E-01
SRSF2	10.27	0.43	7.3E-01		REEP5	10.72	0.38	7.5E-01
DDX17	10.24	0.43	7.3E-01		HNRNPF	9.99	0.38	7.7E-01
C12orf23	9.57	0.43	8.6E-01		NUCB2;Nucb2	9.78	0.38	9.0E-01
RAB1A	10.96	0.42	7.1E-01		UAP1L1	9.46	0.38	8.4E-01
ECI1;DCI	11.15	0.42	7.1E-01		STARD9	9.76	0.38	9.0E-01
TF	10.45	0.42	7.3E-01		CARS2	9.83	0.38	7.7E-01
TBCEL	8.73	0.42	7.3E-01		TRIM32	8.46	0.38	7.7E-01
ARFIP1	8.89	0.42	7.8E-01		C9orf142	9.14	0.37	8.2E-01
RNF5	9.01	0.42	7.8E-01		HOMER1	8.66	0.37	7.8E-01
RBBP7	9.25	0.42	8.1E-01		BLOC1S1	8.82	0.37	7.8E-01
FKBP2	10.21	0.42	7.3E-01		TMEM43	9.54	0.37	9.0E-01
PNPT1	9.71	0.42	8.7E-01		PCYOX1	10.63	0.37	7.8E-01
PSMB6	10.57	0.41	7.4E-01		AP2S1	9.87	0.37	7.7E-01
VPS13A	9.55	0.41	8.7E-01		EXOSC2	8.61	0.37	7.8E-01
LMAN1	10.00	0.41	7.4E-01		OVCA2	8.80	0.37	7.8E-01
BCAM	10.39	0.41	7.4E-01		POFUT1	9.73	0.37	9.0E-01
PLBD2	9.09	0.41	7.9E-01		HNRNPK	11.18	0.37	7.5E-01
HNRNPLL;HNRPLL	9.75	0.41	8.7E-01		HNRNPD	9.24	0.37	8.5E-01
MYH8	9.17	0.41	7.9E-01		PPCS	10.09	0.37	7.8E-01

RPRD1B	9.23	0.37	8.5E-01
LYPLAL1	10.30	0.37	7.8E-01
IDH1	10.95	0.37	7.6E-01
TMEM192	8.86	0.37	7.8E-01
SDC3	8.04	0.36	7.9E-01
AP2M1	10.25	0.36	7.8E-01
MRAS	9.14	0.36	8.3E-01
NELFA	8.43	0.36	7.9E-01
FUCA2	9.14	0.36	8.3E-01
SAR1B;DKFZp434B2017	9.89	0.36	7.8E-01
RAB5B	10.52	0.36	7.9E-01
TNFAIP8	9.42	0.36	8.5E-01
EIF4EBP2	8.34	0.36	7.9E-01
STK3	9.08	0.36	8.3E-01
PDIA5	9.13	0.36	8.3E-01
TBC1D1	8.53	0.36	7.9E-01
ATP2B1	8.83	0.36	7.9E-01
PURB	10.03	0.36	7.9E-01
SMAP1	9.13	0.36	8.3E-01
PACSIN2	10.14	0.36	7.9E-01
CD59	10.15	0.35	7.9E-01
RBM24;RBM38	9.81	0.35	9.2E-01
MIPEP	9.17	0.35	8.4E-01
GTF2F2	9.35	0.35	8.6E-01
HEBP2	10.06	0.35	7.9E-01
NLN	9.16	0.35	8.4E-01
GSR	10.94	0.35	7.8E-01
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	9.71	0.35	9.2E-01
CDC42	8.34	0.35	8.0E-01
CTBP1	9.95	0.35	7.9E-01
USP10	9.10	0.35	8.4E-01
RDH11	10.04	0.35	8.0E-01
ITGA7	8.78	0.35	8.0E-01
AKAP9	8.63	0.34	8.1E-01
LMF2	8.72	0.34	8.1E-01
ATP6V1E1	9.93	0.34	8.0E-01
CCDC134	8.77	0.34	8.1E-01
PMPCA	9.87	0.34	8.0E-01
UBL4A	9.72	0.34	9.3E-01
PSMC3	10.56	0.34	8.1E-01
DTNA	8.85	0.34	8.1E-01
NAA38	9.67	0.34	9.3E-01
STARD10	8.93	0.34	8.5E-01
ALG2	9.35	0.34	8.7E-01
RAB14	10.25	0.34	8.1E-01
PSAP	10.55	0.34	8.1E-01
STAT5B;STAT5A	9.23	0.34	8.7E-01
SVIL	8.69	0.34	8.1E-01
ASNA1	10.18	0.34	8.1E-01
NT5C	9.78	0.34	9.3E-01
YIF1A	9.07	0.34	8.5E-01
CBX3	9.40	0.34	8.7E-01
ITGB6	9.81	0.34	9.3E-01
TBC1D4	9.93	0.34	8.0E-01
SRPRB	9.84	0.34	8.0E-01
PSMD3	10.77	0.33	7.9E-01
TMEM41A	8.93	0.33	8.6E-01
CKM	11.46	0.33	7.9E-01
ECH1	11.09	0.33	7.9E-01
LRRC59	10.59	0.33	8.1E-01
ATP6V1H	9.31	0.33	8.8E-01
UGP2	11.79	0.33	7.9E-01
STT3A	9.69	0.33	9.4E-01
NHP2L1	9.55	0.33	9.4E-01
PPP1CB	10.88	0.33	8.0E-01
NCL	11.11	0.33	8.0E-01
RTN3	10.26	0.33	8.2E-01
TBC1D17	9.14	0.33	8.6E-01
GIGYF2	8.81	0.33	8.2E-01
SHMT2	10.67	0.33	8.0E-01
COPS6	10.31	0.32	8.2E-01
DYRK1A;DYRK1B	8.87	0.32	8.7E-01
MAPK8IP3	8.80	0.32	8.2E-01
SEC61A1	9.63	0.32	9.4E-01
SPTBN1	11.37	0.32	8.0E-01
NIF3L1	9.98	0.32	8.2E-01
CFDP1	8.31	0.32	8.3E-01
TTC7B	8.90	0.32	8.7E-01
PDK1	10.97	0.32	8.0E-01
DTYMK	10.14	0.32	8.2E-01
HNRNPAB	9.40	0.32	8.9E-01
WDR37	9.53	0.32	9.5E-01
PDIA3	10.22	0.32	8.3E-01
LSM7	9.22	0.32	8.9E-01
AKR7A2	10.53	0.32	8.3E-01
RPS29	9.94	0.32	8.2E-01
HNRNPD	10.79	0.31	8.1E-01
MANF	10.32	0.31	8.3E-01
CD151	9.83	0.31	8.2E-01
DDX42	9.01	0.31	8.8E-01
MOCS2	9.01	0.31	8.8E-01
LONP1	10.58	0.31	8.3E-01
CAPRIN1	9.56	0.31	9.5E-01
SLC27A1	9.01	0.31	8.8E-01
HSPA2	9.39	0.31	9.0E-01
RPLP1	10.42	0.31	8.3E-01
CBS	8.97	0.31	8.8E-01
CTSZ	9.67	0.31	9.5E-01
SRPK2	9.30	0.31	9.0E-01
NASP	10.73	0.31	8.1E-01
ERAP1	9.53	0.31	9.5E-01
USP7	9.67	0.31	9.5E-01
TPP2	10.46	0.31	8.4E-01
LSM5	9.30	0.31	9.0E-01
TRAP1	10.38	0.31	8.4E-01
PSMD14	10.27	0.31	8.4E-01
JPH2	9.98	0.31	8.3E-01
KHSRP	10.42	0.30	8.4E-01
PSMC2	10.73	0.30	8.2E-01
PSMC6	10.52	0.30	8.4E-01
TMEM167A	9.54	0.30	9.6E-01
PSMD4	10.22	0.30	8.5E-01
CLYBL	9.67	0.30	9.6E-01
RNF7	9.04	0.30	8.9E-01
SLC16A3	9.30	0.30	9.1E-01
VPS37B	9.27	0.30	9.1E-01
TTN	12.67	0.30	8.2E-01
PMPCB	9.88	0.30	8.4E-01
PREP	10.80	0.30	8.3E-01
GNS	9.39	0.30	9.1E-01
CORO6	9.32	0.30	9.1E-01
PEBP1	11.27	0.29	8.3E-01
COPG2	9.68	0.29	9.7E-01
WBP11	8.36	0.29	8.5E-01
RFC4	8.58	0.29	8.6E-01
XRCC5	10.98	0.29	8.3E-01
BDH2	10.40	0.29	8.5E-01
GPS1	10.29	0.29	8.5E-01
TCERG1	9.70	0.29	9.7E-01
SH3BGRL	10.55	0.29	8.6E-01
CDK5	9.26	0.29	9.1E-01
GORASP2	9.43	0.29	9.1E-01
PSMD11	10.73	0.29	8.3E-01
NEDD4	8.57	0.29	8.6E-01
RBM20	8.39	0.29	8.6E-01
NCBP2	8.83	0.29	8.6E-01
DDX1	10.57	0.29	8.6E-01
RPL30	10.87	0.29	8.4E-01
HSPA1A	11.77	0.28	8.4E-01
PSMC5	10.64	0.28	8.4E-01
PCID2	8.88	0.28	9.1E-01
PSMB5	10.98	0.28	8.4E-01

RRM1	9.56	0.28	9.8E-01
CNOT7	9.18	0.28	9.1E-01
PSMC4	10.53	0.28	8.7E-01
COPS5	10.39	0.28	8.7E-01
TRIP12	8.02	0.28	8.7E-01
UCHL5	9.63	0.28	9.8E-01
CCT6B	9.61	0.28	9.8E-01
RPL4	11.04	0.28	8.4E-01
HECTD3	8.49	0.28	8.7E-01
PRDX4	10.80	0.28	8.5E-01
CALR	11.65	0.28	8.5E-01
PRDX6	11.66	0.28	8.5E-01
COG4	9.06	0.28	9.1E-01
XRCC6	11.17	0.28	8.5E-01
LAMB2	10.15	0.28	8.6E-01
RANGAP1	9.09	0.27	9.1E-01
PTRHD1	9.95	0.27	8.6E-01
NAPA	10.23	0.27	8.7E-01
NKIRAS2	8.66	0.27	8.7E-01
PSMC1	10.61	0.27	8.7E-01
UBE4A	9.45	0.27	9.3E-01
RPS28	10.33	0.27	8.7E-01
FNBP1L	8.48	0.27	8.8E-01
NIT1	10.28	0.27	8.7E-01
PRKRA	9.90	0.27	8.6E-01
EDC3	8.73	0.27	8.8E-01
DNAJB11	9.77	0.27	9.8E-01
GPC1	9.66	0.27	9.9E-01
MZT2B;MZT2A	8.48	0.27	8.8E-01
EEF1E1;hCG_2043275	10.23	0.26	8.8E-01
PSMB7	10.54	0.26	8.8E-01
SNAPIN	9.05	0.26	9.2E-01
KPNA3	9.98	0.26	8.7E-01
C22orf28	10.55	0.26	8.8E-01
RPL37A	10.41	0.26	8.8E-01
LSM6	10.03	0.26	8.7E-01
DHX30	9.26	0.26	9.4E-01
PSMD12	10.53	0.26	8.8E-01
ZNF207	9.61	0.26	9.9E-01
POLR2I	8.29	0.26	8.9E-01
PI4K2A	8.57	0.26	8.9E-01
ARHGAP1	10.72	0.26	8.6E-01
STRN4	8.97	0.26	9.3E-01
RPLP2	9.98	0.26	8.7E-01
PTGR2	9.89	0.26	8.7E-01
PSMD8	10.46	0.26	8.9E-01
GPX7	9.74	0.26	1.0E+00
DNAJC8	9.37	0.26	9.4E-01
FUK	8.76	0.25	8.9E-01
TP53I11	9.20	0.25	9.4E-01
SMARCA1;SMARCA5	8.34	0.25	8.9E-01
GUK1	9.92	0.25	8.7E-01
SRRM1	8.88	0.25	9.3E-01
MSH2	9.67	0.25	1.0E+00
LMOD1	9.47	0.25	9.5E-01
IDE	9.67	0.25	1.0E+00
TFCP2	8.86	0.25	9.4E-01
CPOX	10.19	0.25	8.9E-01
RPL35A	10.84	0.25	8.7E-01
CUTA	10.19	0.25	8.9E-01
KIF2A	8.84	0.25	9.0E-01
MTPN	10.40	0.25	9.0E-01
SH3BGRL2	9.30	0.25	9.5E-01
UROD	9.54	0.25	1.0E+00
TAB1	9.34	0.25	9.5E-01
PSMD13	10.68	0.25	8.7E-01
VPS45	9.22	0.25	9.5E-01
PSMD2	10.90	0.25	8.8E-01
IFT27	9.41	0.24	9.5E-01
AIMP2	10.03	0.24	8.8E-01
ZW10	8.76	0.24	9.0E-01
XRCC1	8.55	0.24	9.0E-01
BCAP31	10.46	0.24	9.0E-01
SEPT15	9.52	0.24	9.9E-01
AAMDC	10.44	0.24	9.0E-01
POLR2E	8.82	0.24	9.0E-01
DDX6	10.11	0.24	8.8E-01
SF1	9.75	0.24	9.9E-01
ADRM1	10.00	0.24	8.8E-01
EHD3	10.58	0.24	9.0E-01
EIF3L	10.50	0.24	9.0E-01
BZW2	10.65	0.24	8.8E-01
C14orf166	10.44	0.24	9.1E-01
CD276	8.57	0.24	9.1E-01
MIEN1	9.30	0.24	9.6E-01
BPNT1	10.40	0.24	9.1E-01
BUB3	10.06	0.24	8.9E-01
HSPA4L	9.25	0.24	9.6E-01
CUL5	9.91	0.24	8.9E-01
RRAGC;RRAGD	9.44	0.24	9.6E-01
CLINT1	9.30	0.23	9.6E-01
MYH2	9.68	0.23	9.8E-01
RAB6A	10.76	0.23	8.9E-01
PPP1R1B	8.62	0.23	9.2E-01
TACC2	9.48	0.23	9.6E-01
TFRC	10.67	0.23	8.9E-01
HMGB3	9.68	0.23	9.7E-01
ITGA3	9.23	0.23	9.6E-01
THAP4	9.73	0.23	9.7E-01
COPS2	10.38	0.23	9.2E-01
RHOG	9.96	0.23	8.9E-01
NCDN	9.30	0.23	9.7E-01
RNMT	9.45	0.23	9.7E-01
SSH3	8.87	0.23	9.6E-01
TOR1A	8.66	0.23	9.2E-01
ATP6V1A	10.29	0.23	9.2E-01
PABPC4	10.29	0.22	9.2E-01
TUBA1C	9.47	0.22	9.7E-01
ARL3	10.28	0.22	9.2E-01
COPS8	10.03	0.22	9.0E-01
ITCH;WWP1	8.24	0.22	9.3E-01
RABEP2	9.07	0.22	9.6E-01
ALDH16A1	9.29	0.22	9.7E-01
MDH1	12.08	0.22	9.0E-01
EFHD2	9.07	0.22	9.6E-01
DNMT1	9.22	0.22	9.7E-01
PCYT1A	9.49	0.22	9.7E-01
EXOSC4	8.72	0.22	9.3E-01
RPL29	10.17	0.22	9.0E-01
SGPL1	9.48	0.22	9.7E-01
HSPA5	11.88	0.22	9.0E-01
RTN2	9.88	0.22	9.0E-01
MYO18A	10.14	0.22	9.1E-01
SLC4A4	8.01	0.22	9.3E-01
PRRC2C	8.81	0.22	9.3E-01
RPL31	10.72	0.21	9.1E-01
SPEG	8.97	0.21	9.7E-01
CNN3	10.51	0.21	9.3E-01
PTK7	9.90	0.21	9.1E-01
SUPT5H	8.93	0.21	9.7E-01
CLASP2	9.20	0.21	9.8E-01
EP300	8.91	0.21	9.7E-01
ALAD	10.14	0.21	9.1E-01
GABARAPL2	9.80	0.21	9.5E-01
PIP4K2B	9.28	0.21	9.8E-01
TUBG1;TUBG2	9.73	0.21	9.4E-01
TNPO2	9.46	0.21	9.8E-01
SARNP	10.02	0.21	9.1E-01
GOLGB1	9.93	0.21	9.1E-01
INPP4B	9.81	0.21	9.4E-01
ABLIM1	9.13	0.21	9.8E-01
RPL8	10.87	0.21	9.1E-01
AGPAT1	8.74	0.21	9.4E-01
PSMG3	8.95	0.21	9.8E-01

DSTN	11.01	0.20	9.1E-01		PSMD7	10.42	0.18	9.6E-01
USP47	9.68	0.20	9.4E-01		SNX5	9.39	0.18	9.9E-01
MGME1	8.25	0.20	9.4E-01		RPL6	11.00	0.18	9.4E-01
PAPOLA	8.75	0.20	9.4E-01		PRKAR2A	10.85	0.18	9.4E-01
SCFD1	10.18	0.20	9.4E-01		RPL7	11.11	0.18	9.4E-01
APEX1	10.68	0.20	9.2E-01		DCTN4	9.83	0.18	9.4E-01
TUBB2A	9.60	0.20	9.4E-01		UBQLN4	8.81	0.17	9.7E-01
FUBP1	10.41	0.20	9.4E-01		LSM4	9.88	0.17	9.4E-01
RPLP0;RPLP0P6	11.08	0.20	9.2E-01		PSMA3	10.96	0.17	9.4E-01
FLAD1	8.81	0.20	9.5E-01		PANK4	10.34	0.17	9.7E-01
ITSN1	9.33	0.20	9.9E-01		GLOD4	10.61	0.17	9.7E-01
GAS6	8.55	0.20	9.5E-01		EIF1B	9.26	0.17	9.8E-01
ARPC1A	10.44	0.20	9.4E-01		DNAJC3	9.12	0.17	9.9E-01
POFUT2	9.31	0.20	9.9E-01		COG2	8.93	0.17	9.9E-01
PSMB1	10.94	0.20	9.2E-01		GDI1	10.62	0.17	9.7E-01
RPS21	10.38	0.20	9.4E-01		DHX38	8.44	0.17	9.8E-01
PDXK	10.29	0.20	9.4E-01		RPL7A	11.02	0.17	9.5E-01
LSM3	9.47	0.20	9.9E-01		DNAJA2	10.41	0.17	9.7E-01
ESD	10.88	0.20	9.2E-01		CTNND1	10.20	0.17	9.7E-01
AP2A1	10.35	0.20	9.4E-01		C19orf53	8.76	0.17	9.8E-01
CUL7	8.51	0.20	9.5E-01		RAP1B	9.18	0.17	9.8E-01
RPL32	10.60	0.20	9.5E-01		FXR1	9.66	0.17	8.9E-01
LPCAT1	8.27	0.20	9.5E-01		FYCO1	9.70	0.17	8.9E-01
PSMA1	11.04	0.20	9.2E-01		RAB8A	9.62	0.17	8.9E-01
PDIA3	11.63	0.20	9.2E-01		RPL10A	10.86	0.17	9.5E-01
SULT1A1;SULT1A2	9.59	0.19	9.3E-01		KIAA0907	8.36	0.17	9.8E-01
CAMK2B	9.86	0.19	9.2E-01		PSMD1	10.67	0.17	9.5E-01
NAA30	8.58	0.19	9.5E-01		NUDT16	9.38	0.17	9.7E-01
LAMA2	9.57	0.19	9.2E-01		PPA1	10.15	0.17	9.5E-01
MOGS	9.87	0.19	9.2E-01		RER1	8.82	0.17	9.8E-01
RPL5	10.83	0.19	9.3E-01		EIF3E	10.28	0.17	9.8E-01
LTA4H	10.66	0.19	9.3E-01		MAP3K7;DKFZp586F0420	8.90	0.17	9.8E-01
PSMB4	10.71	0.19	9.3E-01		NUP54	8.92	0.16	9.8E-01
PSMA6	11.01	0.19	9.3E-01		NPC1	8.56	0.16	9.8E-01
COG8	8.84	0.19	9.6E-01		RPL36A	10.24	0.16	9.8E-01
TPRKB	8.76	0.19	9.6E-01		PRKAB1	9.28	0.16	9.7E-01
PSMD6	10.57	0.19	9.5E-01		NAP1L4	10.74	0.16	9.5E-01
ADI1	9.74	0.19	9.2E-01		SELK	8.35	0.16	9.8E-01
ATXN2L	9.19	0.19	9.9E-01		BSG	10.80	0.16	9.6E-01
GOLPH3	9.14	0.19	1.0E+00		DNM2	10.59	0.16	9.8E-01
HMGA1;C2orf81	8.56	0.19	9.6E-01		RPL34	10.63	0.16	9.8E-01
CGGBP1	9.34	0.19	1.0E+00		GET4	9.30	0.16	9.7E-01
C6orf211	10.07	0.19	9.3E-01		PSMA5	10.89	0.16	9.6E-01
ARSA	9.35	0.19	1.0E+00		EIF3I	10.32	0.16	9.8E-01
PSMA4	10,82	0,19	9.3E-01		CRYZ	10.75	0.16	9.6E-01
Nbla03646;DHCR24	8.84	0.19	9.6E-01		HMGCL	9.60	0.16	8.8E-01
RPS12	10.82	0.19	9.3E-01		RPL12	10.92	0.16	9.6E-01
ACBD3	9.75	0.19	9.1E-01		OSGEP	9.15	0.16	9.7E-01
GCHFR	8.90	0.19	1.0E+00		EFNB3	9.27	0.16	9.7E-01
ACOX2	8.57	0.19	9.6E-01		COPS4	10.47	0.16	9.8E-01
AARSD1;PTGES3L-AARSD1	9.39	0.19	1.0E+00		GIPC1	8.88	0.16	9.7E-01
					RPL21	10.59	0.16	9.9E-01
POLR2L	8.55	0.18	9.6E-01		RPL13	10.95	0.16	9.6E-01
PCMT1	10.51	0.18	9.6E-01		GPX1	10.24	0.16	9.9E-01
HLA-C	8.92	0.18	1.0E+00		PSMB3	10.70	0.16	9.6E-01
SND1	10.54	0.18	9.6E-01		SURF4	9.80	0.16	8.7E-01
PFN2	9.55	0.18	9.1E-01		RPL14	10.65	0.16	9.6E-01
PRDX2	11.82	0.18	9.4E-01		GALK1	9.94	0.16	9.6E-01
EIF3F	10.06	0.18	9.3E-01		OXSR1	10.06	0.15	9.6E-01
CASK	8.86	0.18	1.0E+00		NUDT9	9.16	0.15	9.6E-01
TMOD1	10.17	0.18	9.6E-01		RPL28	10.72	0.15	9.7E-01
SEPT5	10.54	0.18	9.6E-01		ITGAV	10.17	0.15	9.9E-01
UBE2O	9.64	0.18	9.1E-01		FDPS	10.60	0.15	9.9E-01
NPEPPS	11.22	0.18	9.4E-01		RUVBL1	10.49	0.15	9.9E-01
CNPY2	10.04	0.18	9.3E-01		SOD2	11.21	0.15	9.7E-01
AP2B1	10.59	0.18	9.6E-01		RPL27A	10.51	0.15	9.9E-01
PLSCR1	8.40	0.18	9.7E-01		DYNLL2	10.50	0.15	9.9E-01
PSMB2	10.75	0.18	9.4E-01		MSH3	7.97	0.15	1.0E+00
ERP44	10.18	0.18	9.6E-01		SRP14	10.55	0.15	9.9E-01
MAN2B1	9.85	0.18	9.4E-01		MAP1B	10.79	0.15	9.7E-01
PSMA2	10.83	0.18	9.4E-01		COG7	8.91	0.15	9.6E-01
RPL18A	10.61	0.18	9.6E-01		RPL18	10.93	0.15	9.7E-01

AASS	10.11	0.15	9.6E-01		TMEM47	8.96	0.12	9.3E-01
PLEC	11.31	0.15	9.7E-01		SYNE2	9.54	0.12	8.3E-01
MGEA5	9.66	0.15	8.6E-01		RPL27	10.84	0.12	1.0E+00
HLA-B	8.75	0.15	1.0E+00		NIT2	10.36	0.12	9.7E-01
CNPY4	9.59	0.15	8.6E-01		RPL24	10.65	0.12	1.0E+00
RBX1	9.74	0.15	8.6E-01		EIF3H;EIF3S3	10.24	0.12	9.7E-01
SAMHD1	8.94	0.15	9.6E-01		RPL26;KRBA2	10.66	0.12	1.0E+00
SNTA1	10.08	0.15	9.6E-01		NUP133	8.46	0.12	9.7E-01
DYNC1LI2	9.77	0.15	8.6E-01		RPSA;RPSAP58	10.99	0.12	1.0E+00
FBLN2	8.49	0.15	1.0E+00		STAM2	8.43	0.12	9.7E-01
MYH7	13.17	0.15	9.7E-01		XRN1	8.11	0.12	9.7E-01
MEF2D	9.24	0.15	9.5E-01		AMPD2	9.31	0.12	9.1E-01
GNB2L1	11.14	0.14	9.7E-01		HSPA6;HSPA7	11.06	0.12	1.0E+00
SNAP23	9.11	0.14	9.5E-01		KARS	10.34	0.12	9.6E-01
SERBP1	10.61	0.14	1.0E+00		BRE	9.47	0.12	9.1E-01
MYCBP	9.49	0.14	9.4E-01		CCBL1	9.20	0.11	9.1E-01
COPS3	10.25	0.14	1.0E+00		RPS20	10.87	0.11	9.9E-01
PPFIA4	8.77	0.14	9.9E-01		KPNA4	9.69	0.11	8.2E-01
GALM	9.82	0.14	9.7E-01		UCHL3	9.98	0.11	9.9E-01
SNX4	8.63	0.14	9.9E-01		RPL15	10.73	0.11	9.9E-01
RPS17L;RPS17	10.75	0.14	9.8E-01		TRAPPC2P1;TRAPPC2	8.61	0.11	9.6E-01
ERP29	10.48	0.14	1.0E+00		KDELR1;KDELR2	9.35	0.11	9.1E-01
AK4	10.95	0.14	9.8E-01		DYNLL1	9.64	0.11	8.2E-01
LACTB2	9.32	0.14	9.4E-01		UBE2G2	8.38	0.11	9.6E-01
GOT1	11.78	0.14	9.8E-01		GNAQ	9.70	0.11	8.1E-01
GOPC	8.30	0.14	9.9E-01		RPS25	10.74	0.11	9.8E-01
RPL35	10.68	0.14	9.8E-01		TRAPPC6B	9.51	0.11	9.0E-01
HRC	10.67	0.14	9.8E-01		AIMP1	10.25	0.11	9.5E-01
SELM	8.46	0.14	9.9E-01		CORO1C	9.64	0.11	8.1E-01
BPGM	9.02	0.14	9.5E-01		NACA	11.17	0.11	9.8E-01
THUMPD1	9.55	0.14	8.5E-01		DYNLT1	10.32	0.11	9.5E-01
SLC39A7	9.40	0.14	9.4E-01		RAB3IP	8.45	0.11	9.5E-01
STUB1	9.08	0.14	9.5E-01		EIF4A3	9.53	0.11	8.1E-01
AP1G1	9.80	0.14	8.5E-01		MARCKSL1	9.59	0.11	8.1E-01
FARSA	10.33	0.14	9.9E-01		AP1B1	9.78	0.10	8.1E-01
S4R3N1	9.96	0.14	9.7E-01		EIF3K	10.19	0.10	9.4E-01
ATIC	10.69	0.14	9.8E-01		RPS15	10.16	0.10	1.0E+00
FARSB	10.50	0.14	9.9E-01		GRB2	11.25	0.10	9.8E-01
PPP2R5E	8.98	0.14	9.4E-01		RPS3	11.16	0.10	9.8E-01
CHKB	9.07	0.14	9.4E-01		MARS	10.31	0.10	9.4E-01
ADSS	8.68	0.13	9.8E-01		OSBP	9.73	0.10	8.1E-01
PRMT1	10.14	0.13	9.8E-01		CLIC5	9.83	0.10	1.0E+00
TXNDC12	9.92	0.13	9.8E-01		RBPMS2	9.68	0.10	8.0E-01
FUT11	8.64	0.13	9.8E-01		RPL19	10.58	0.10	9.4E-01
ROR1	8.61	0.13	9.8E-01		CSNK2A2	9.32	0.10	8.9E-01
RDX	10.63	0.13	9.9E-01		TUBGCP2	9.48	0.10	8.9E-01
EIF3D	10.20	0.13	9.8E-01		RPS19	10.98	0.10	9.7E-01
ARF1;ARF3	11.11	0.13	9.9E-01		AGA	9.06	0.10	9.0E-01
RPL9	10.66	0.13	9.9E-01		OGT	8.89	0.10	9.0E-01
RUVBL2	10.52	0.13	9.8E-01		APOA1BP	10.45	0.10	9.3E-01
MIA3	9.78	0.13	8.4E-01		ATL2	9.36	0.10	8.9E-01
RAB5A	9.97	0.13	9.8E-01		TPM1	10.19	0.10	9.3E-01
GSTO1	10.74	0.13	9.9E-01		GSTM3	10.94	0.10	9.6E-01
ANXA7	10.45	0.13	9.8E-01		TRAPPC3	9.68	0.09	8.0E-01
RPL22	10.56	0.13	9.8E-01		RPS3A	11.28	0.09	9.6E-01
TSG101	10.16	0.13	9.8E-01		ARMC8	8.76	0.09	9.4E-01
CDC42BPB	9.38	0.13	9.2E-01		RPS24	10.29	0.09	9.3E-01
SIK2	9.50	0.13	9.2E-01		HDGF	10.43	0.09	9.3E-01
PRPF38B	8.44	0.13	9.8E-01		LUC7L3	8.93	0.09	8.9E-01
SAR1A	10.57	0.13	9.8E-01		YBX1	10.64	0.09	9.6E-01
RAB21	10.53	0.13	9.7E-01		LDB3	10.60	0.09	9.3E-01
ACY1;ABHD14A-ACY1	9.17	0.13	9.3E-01		RPL3	10.89	0.09	9.6E-01
PSMA7	10.99	0.13	9.8E-01		PTGR1	10.38	0.09	9.2E-01
ARFGAP2	9.53	0.13	8.5E-01		QDPR	10.55	0.09	9.2E-01
FAM98B	9.71	0.13	8.5E-01		COG1	8.81	0.09	9.3E-01
ARL1	9.89	0.13	9.7E-01		AP2A2	9.98	0.09	9.8E-01
RPL11	10.74	0.13	9.9E-01		RPS18	10.99	0.09	9.5E-01
SEPW1	10.19	0.12	9.7E-01		CEP97	9.30	0.09	8.8E-01
NRAS	9.26	0.12	9.2E-01		KRT18	11.24	0.09	9.5E-01
PKP2	10.18	0.12	9.7E-01		MYADM	9.53	0.09	7.9E-01
FAT1	8.45	0.12	9.7E-01		PI4KA	9.32	0.09	8.7E-01
RPL36	10.41	0.12	9.7E-01		LDB3	11.58	0.09	9.5E-01

FAM213B	9.06	0.08	8.8E-01
TMED3	8.92	0.08	8.8E-01
GLO1	10.90	0.08	9.4E-01
MAVS	9.77	0.08	7.8E-01
TRAPPC1	9.26	0.08	8.7E-01
DTD1	9.19	0.08	8.8E-01
RPS16	11.00	0.08	9.4E-01
DCAF11	8.51	0.08	9.2E-01
HSPB11	9.44	0.08	8.7E-01
DERA	9.54	0.08	7.8E-01
CRIP2	11.32	0.08	9.4E-01
GPX8	9.43	0.08	8.7E-01
PPP2R1A	11.20	0.08	9.4E-01
RPS5	10.88	0.08	9.4E-01
LCMT1	9.34	0.08	8.7E-01
DHX16	8.18	0.08	9.2E-01
TUBGCP3	9.11	0.08	8.8E-01
BRCC3	9.45	0.08	8.6E-01
ATG9A	7.97	0.08	9.2E-01
QARS	10.52	0.08	9.0E-01
EIF4A2	11.00	0.08	9.3E-01
GNPAT	8.83	0.08	9.2E-01
GRPEL1	10.10	0.08	9.6E-01
HYOU1	10.85	0.08	9.3E-01
ABCA8	8.23	0.07	9.1E-01
RPL13A;RPL13a	10.73	0.07	9.2E-01
RPS4X	11.05	0.07	9.2E-01
DHX29	8.89	0.07	8.7E-01
RPS14	10.75	0.07	9.2E-01
SH3GL1	9.85	0.07	9.5E-01
CNOT10	8.74	0.07	9.1E-01
EEF1A2	11.28	0.07	9.2E-01
RPL17	10.72	0.07	9.2E-01
LSM2	10.02	0.07	9.5E-01
USP14	10.61	0.07	8.9E-01
TNPO1	10.09	0.07	9.5E-01
DNM1L	10.62	0.07	8.9E-01
PPP1R12A	10.22	0.07	8.9E-01
HARS	10.08	0.07	9.5E-01
RPS15A	10.82	0.07	9.2E-01
PPP1R14C	9.27	0.07	8.5E-01
HAGH	10.33	0.07	8.9E-01
PGP	10.08	0.07	9.4E-01
NEBL	10.97	0.07	9.1E-01
TRMT112	9.80	0.07	7.6E-01
RPS2	11.02	0.07	9.2E-01
GNPDA1	10.35	0.07	8.9E-01
RPS13	10.86	0.06	9.1E-01
PPIL3	9.73	0.06	7.6E-01
TP53RK	9.37	0.06	8.5E-01
PHKG2	9.02	0.06	8.6E-01
DHX15	10.15	0.06	9.4E-01
HIST1H4A	10.70	0.06	9.1E-01
PPIL1	10.24	0.06	8.8E-01
CAPG	9.13	0.06	8.5E-01
AGO2	9.49	0.06	8.4E-01
EIF3G	9.86	0.06	9.3E-01
DERL1	9.08	0.06	8.5E-01
CLTCL1	9.08	0.06	8.5E-01
CAT	10.30	0.06	8.8E-01
ARFGEF2	9.39	0.06	8.4E-01
RPS8	10.96	0.06	9.0E-01
C19orf43	8.79	0.06	9.0E-01
FERMT2	9.52	0.06	7.5E-01
MPI	10.09	0.06	9.3E-01
ARL15	8.99	0.06	8.5E-01
POLR2H	9.28	0.06	8.4E-01
MAPK9;MAPK10	8.85	0.06	8.9E-01
ABR	9.45	0.06	8.4E-01
TUBB2B	10.88	0.06	9.0E-01
CUL1	9.71	0.06	7.4E-01
SNAP29	9.33	0.06	8.3E-01
KLHL41	10.04	0.05	9.3E-01
HDHD1	9.46	0.05	8.3E-01
CALM1;CALM2	10.50	0.05	8.7E-01
SHROOM1	8.54	0.05	8.9E-01
WDR1	11.23	0.05	8.9E-01
SAMD4B	8.45	0.05	8.9E-01
VPS11	9.72	0.05	7.4E-01
LRSAM1	8.99	0.05	8.4E-01
PCBP2	10.88	0.05	8.9E-01
TRNT1	9.24	0.05	8.3E-01
YTHDF3	9.60	0.05	7.4E-01
GOLGA3	8.91	0.05	8.4E-01
SPAG7	9.44	0.05	8.3E-01
CALU	10.89	0.05	8.8E-01
MAN2C1	10.64	0.05	8.8E-01
ANK3	10.23	0.05	8.6E-01
PLCD1	9.95	0.04	9.1E-01
SET	10.59	0.04	8.5E-01
BUD31	8.79	0.04	8.8E-01
PPP2R2A	9.97	0.04	9.1E-01
EIF4B	9.87	0.04	9.1E-01
FN3KRP	9.77	0.04	7.3E-01
RAB34	8.87	0.04	8.3E-01
ACAD10	8.82	0.04	8.8E-01
ATP1B1	10.52	0.04	8.5E-01
RPL23A	10.77	0.04	8.7E-01
RBM12	9.56	0.04	7.3E-01
EIF3J	9.81	0.04	7.2E-01
POGLUT1	8.86	0.04	8.3E-01
MGLL	8.98	0.04	8.3E-01
SEC24B	9.38	0.04	8.1E-01
IGFBP5	8.40	0.04	8.7E-01
FAU	9.93	0.04	9.0E-01
RPL10	10.64	0.04	8.7E-01
HSPBP1	9.33	0.04	8.1E-01
SACS	8.77	0.04	8.7E-01
RPS6	10.75	0.04	8.6E-01
AGPS	9.74	0.04	7.2E-01
GMPPB	10.07	0.03	9.0E-01
NULP1;TCF25	8.66	0.03	8.7E-01
SLC1A4	8.53	0.03	8.7E-01
CC2D1A	8.91	0.03	8.2E-01
ARPC5L	9.94	0.03	8.9E-01
VPS28	10.07	0.03	8.9E-01
SPTLC2	8.75	0.03	8.6E-01
ACSL4	9.07	0.03	8.2E-01
ZCCHC3	8.53	0.03	8.6E-01
TBCB	10.10	0.03	8.9E-01
RPS27A	11.50	0.03	8.6E-01
ARL2	9.72	0.03	7.1E-01
RPS26;RPS26P11	10.57	0.03	8.3E-01
SIPA1L2	8.72	0.03	8.6E-01
TPM1	10.25	0.03	8.3E-01
CHMP2B	8.94	0.03	8.2E-01
SYNGR2	9.81	0.03	7.1E-01
PPIL4	8.68	0.03	8.6E-01
RHOA;RHOC	10.77	0.03	8.5E-01
PPP1R12C	8.94	0.03	8.1E-01
IMPA1	10.61	0.03	8.3E-01
RPS10	10.74	0.03	8.5E-01
ATG16L1	8.82	0.03	8.6E-01
ESYT2	9.21	0.03	8.0E-01
RPS23	10.50	0.03	8.2E-01
PDIA4	11.14	0.02	8.5E-01
VPS16	9.21	0.02	8.0E-01
SHOC2	8.64	0.02	8.6E-01
PPP2CA	10.70	0.02	8.5E-01
HEATR2	8.76	0.02	8.5E-01
BICD2	9.18	0.02	8.1E-01
DNM2	8.68	0.02	8.5E-01
COG5	9.16	0.02	8.1E-01
H3F3B;H3F3A;H3F3C	10.23	0.02	8.2E-01

RPL39P5;RPL39	9.72	0.02	7.0E-01		MPST	10.31	0.01	8.1E-01
UBE2V2	9.62	0.02	7.0E-01		CUTC	8.81	0.01	8.4E-01
DR1	8.58	0.02	8.5E-01		CEP170	8.81	0.01	8.4E-01
NEMF	8.96	0.02	8.1E-01		EEFSEC	9.70	0.01	6.9E-01
YWHAQ	11.27	0.02	8.4E-01		USP28	9.55	0.01	6.9E-01
PDIA6	11.21	0.02	8.4E-01		EIF3M	10.14	0.01	8.6E-01
WNK1	9.94	0.02	8.7E-01		GOLGA4	9.12	0.01	8.0E-01
NAE1	10.54	0.02	8.1E-01		DCTN6	9.49	0.01	7.8E-01
TXNDC17	10.30	0.02	8.1E-01		C7orf55	9.86	0.01	8.6E-01
VPS25	9.93	0.02	8.7E-01		ERI3	9.26	0.01	7.8E-01
CUL4A	9.72	0.02	7.0E-01		SKP1	10.13	0.01	8.6E-01
ACTR10	9.48	0.02	7.9E-01		FAM96A	8.67	0.01	8.4E-01
PSME3	9.44	0.02	7.9E-01		HINT1	10.98	0.01	8.2E-01
RALGAPB	8.72	0.02	8.5E-01		USP13	8.98	0.01	7.9E-01
ACO1	10.66	0.02	8.3E-01		UBFD1	9.22	0.01	7.8E-01
ANXA6	12.20	0.01	8.3E-01		KATNAL2	10.27	0.01	8.0E-01
OTUB1	10.79	0.01	8.3E-01		RPS9	11.05	0.01	8.2E-01
MAPK14	10.06	0.01	8.6E-01		CDK14;CDK16	7.62	0.01	8.3E-01
LMOD2	9.89	0.01	8.6E-01		NUDT4	10.29	0.01	8.0E-01
POLR2C	8.63	0.01	8.4E-01		NUBP1	9.58	0.01	6.8E-01
PTMS	9.28	0.01	7.8E-01		IFIT5	9.07	0.01	7.9E-01

Supplemental Table 6: Correlation of the SILAC data with the RNA sequencing data of iPSC-derived atrial and ventricular cardiomyocytes (aCMs and vCMs) and with the published proteomic data sets obtained from human fetal and adult atrial (A) and ventricular (V) tissues. SILAC: n = 4 vCM and n = 4 aCM independent differentiation experiments at day 68 from iPSC line isWT1.Bld2; RNA sequencing: n = 4 iPSC-vCM and n = 4 iPSC-aCM independent differentiation experiments at day 90 from 3 iPSC lines. Proteomics: 17-23-week-old fetal heart tissues (3), 21-47-year-old adult healthy heart tissues (4).

(A) List of candidates that are significantly lower expressed in iPSC-aCMs in both proteomic data (178 differential proteins vs. iPSC-vCMs) and RNA sequencing data (1.560 differential genes vs. iPSC-vCMs; log2 fold < -0.5; *P*< 0.05), in published proteomic data of human fetal atria (81 differential proteins vs. fetal ventricles) (3), or in human adult atrial tissues (409 differential proteins vs. ventricular tissues) (4), of which 67 candidates show the overlap between proteomic and transcriptomic data of iPSC-CMs, whereas 14 and 19 proteins revealed an overlap between proteomic data of iPSC-CMs and published proteomic data from human fetal and adult heart tissues, respectively.

	Proteomics	**RNAseq**	**Lu *et al.***	**Doll *et al.***
Gene name	**log2 (aCMs/ vCMs)**	**log2 (aCMs/ vCMs)**	**log2 (A/V)**	**log2 (A/V)**
KCTD12	-3.58	-0.97		* 0.72
MYL3	-3.50	n.s.	-4.94	-4.56
S100A4	-3.36	-1.12		* 1.15
MYL2	-3.22	-3.20	-11.05	-1.79
COL12A1	-3.22	-5.19		* 1.77
MYL5	-3.01	* 1.18	-30.04	-2.23
AIF1L	-3.00	-2.04		
NNMT	-2.72	-1.79		* 2.54
MDK	-2.68	-1.87		
RAB8B	-2.50	-1.31		* 0.95
CLDN6	-2.41	-1.34		
COL15A1	-2.30	-2.75	-1.31	
MST4	-2.29	-1.66		
NAV1	-2.23	-4.03	-1.13	-2.30
SLC1A3	-2.20	n.s.		-1.26
ARPC1B	-2.15	-1.15		
MYLK3	-2.07	-2.09		
PYGL	-2.06	-1.79	-1.63	* 1.47
PHLDB2	-1.97	-3.18	-22.67	-2.83
FGF12; FGF14	-1.95	-2.54; -3.38		* 0.93; -
HSPB3	-1.87	-0.93		* 0.68
FBN2	-1.87	-2.18		
NRAP	-1.84	-3.25		
CDH3	-1.83	-3.31		
COL6A6	-1.81	-2.47		* 2.24
EPB41L2	-1.78	n.s.		-2.20
PDE1C	-1.73	-1.68		-1.42
PSMB9	-1.72	-2.86		
CSRP1	-1.71	-1.51		* 1.18
SERPINE2	-1.70	-1.90		
FAM84B	-1.68	-2.34		
CAB39L	-1.68	-1.48		* 2.06
PRKCA	-1.65	-0.97		
AHNAK	-1.64	-1.86		
SNX18	-1.61	-1.94		
MAOB	-1.56	-2.89	-3.12	-0.48
HEPH	-1.56	-1.17		
COL5A1	-1.55	-1.90		* 1.99
IKBIP	-1.51	-0.69		
CGNL1	-1.50	-2.54		
ANKRD50	-1.49	-1.58		
GUCY1A3	-1.47	-2.39		
KIF21A	-1.43	-1.05		
ABRACL	-1.42	-1.46		
LTBP1	-1.41	-1.40		* 2.85
RCSD1	-1.37	-1.42		
LAMA4	-1.35	-2.17		
PLCXD3	-1.30	-3.27		-0.98
FGF1	-1.29	-1.80		
SORBS2	-1.27	-1.30	-1.26	-1.12
XIRP1	-1.24	-1.17	-1.11	
RAI14	-1.22	-2.22		
TLN2	-1.19	-1.41		
ANXA2; ANXA2P2	-1.18	-0.74		* 0.54
TNS1	-1.17	-2.55	-2.26	
PRKAG1	-1.15	n.s.		-1.27
UBE2E2; UBE2E1	-1.15	-1.03; -0.84		
METAP1	-1.15	-1.25		
ANXA3	-1.15	-0.91		-0.67
GUCY1B3	-1.14	-1.72		
SDCBP	-1.10	-1.02		
RPS6KA3	-1.07	-1.70		
GPD1L	-1.06	-1.37	-1.36	
HSPB6	-1.05	-1.37		-1.10
WARS	-1.05	n.s.		-0.73
PPFIBP1	-1.01	-1.66		-0.85
CAST	-1.01	-0.50		
PDLIM1	-1.01	-1.11	-1.13	-0.97
SEPT9	-0.94	-0.86		
MAP4	-0.90	-0.82		
FHL1	-0.88	-1.80		
ADH5	-0.88	-1.22		-0.65
SORBS2	-0.84	-1.30	-1.26	-1.12

*reverse expression, n.s. not significant

(B) List of candidates that are significantly higher expressed in iPSC-aCMs in both proteomic data (94 differential proteins vs. iPSC-vCMs) and RNA sequencing data (1,629 differential genes vs. iPSC-vCMs; log2 fold > 0.5; $P < 0.05$), in published proteomic data of human fetal atrium (134 differential proteins vs. fetal ventricle) (3), or in human adult atrial tissues (1,220 differential proteins vs. ventricular tissues) (4), of which 24 candidates show the overlap between proteomic and transcriptomic data of iPSC-CMs, whereas 7 and 17 proteins revealed an overlap between proteomic data of iPSC-CMs and published proteomic data from human fetal and adult heart tissues, respectively.

	Proteomics	**RNAseq**	**Lu *et al.***	**Doll *et al.***			**Proteomics**	**RNAseq**	**Lu *et al.***	**Doll *et al.***
Gene name	**log2 (aCMs/ vCMs)**	**log2 (aCMs/ vCMs)**	**log2 (A/V)**	**log2 (A/V)**		**Gene name**	**log2 (aCMs/ vCMs)**	**log2 (aCMs/ vCMs)**	**log2 (A/V)**	**log2 (A/V)**
PADI2	4.82	2.40				MYH11	2.66	n.s.		1.28
MYH4	4.81	n.s.		3.67		PAM	2.62	n.s.	7.57	3.86
GNAO1	4.02	1.77		2.14		TMEM141	2.61	0.98		
NR2F2; NR2F1	3.84	1.83; 2.71		1.04		RAB27A	2.42	1.25		
MYH6	3.82	2.01	7.77	3.57		SH3KBP1	2.37	1.39		
NPPA	3.78	n.s.	5.34	8.08		DHRS7B	2.35	n.s.		0.73
METTL7B	3.74	2.76		3.90		DNAJB11	2.30	n.s.		0.95
MGARP	3.67	2.73		3.42		C10orf35	2.17	0.70		
VSNL1	3.58	1.20		2.30		PNKD	2.11	0.83		
ADCY5	3.19	0.77				ATP6V1G2; ATP6V1G2-DDX39B	2.10	0.85		1.16
MYL7	3.16	-	2.74	6.10		PLCB1	2.07	n.s.	23.65	2.63
ATP1B2	3.13	1.00				TIMM10B	1.92	n.s.		1.67
SOD3	2.96	1.81		1.99		D2HGDH	1.81	0.77		
NME4	2.81	0.51				A2M	1.81	0.93		
ATP2A2	2.78	1.12	1.66			CAV1	1.79	0.93		
MYOM2	2.67	1.27				ACSF2	1.77	1.15	1.64	

n.s. not significant

Supplemental Table 7: Antibodies and dilutions used for immunofluorescence (IF), flow cytometry (FC) and western blot (WB) analyses.

Primary antibody	**Dilution**	**Supplier**
α-actinin, monoconal mouse IgG1	IF 1:1,000 FC 1:4,000	Sigma-Aldrich, clone EA-53
CX43, polyclonal rabbit IgG	IF 1:1,000	Abcam, catalog ab11370
cTNT, monoclonal mouse IgG1	FC 1:200 WB 1:10,000	Thermo Fisher Scientific, clone 13-11
GAPDH, monoclonal mouse IgG1	WB 1:5,000	Merck Millipore, clone 6C5
LIN28, polyclonal goat IgG	IF 1:300	R&D Systems, catalog AF3757
MLC2A, monoclonal mouse IgG2a	IF 1:200 WB 1:2,000	Synaptic Systems, clone 56F5
MLC2V, polyclonal rabbit IgG	IF 1:200 WB 1:2,000	Proteintech, catalog 10906-1-AP
NANOG, polyclonal rabbit IgG	IF 1:100	Thermo Fisher Scientific, catalog PA1-097
OCT3/4, polyclonal goat IgG	IF 1:40	R&D Systems, catalog AF1759
Phalloidin conjugate Alexa Fluor 555	IF 1: 200	Thermo Fisher Scientific, catalog A34055
Phalloidin conjugate Alexa Fluor 633	IF 1: 200	Thermo Fisher Scientific, catalog A22284
RYR2, polyclonal rabbit IgG	IF 1:500	Sigma-Aldrich, catalog HPA020028
SOX2, monoclonal mouse IgG1	IF 1:200	Thermo Fisher Scientific, clone 20G5
SSEA4, monoclonal mouse IgG3	IF 1:100	Thermo Fisher Scientific, clone MC-813-70
TRA-1-60, monoclonal mouse IgM	IF 1:200	Abcam, clone TRA-1-60
Secondary antibody	**Dilution**	**Supplier**
Alexa Fluor 488, polyclonal donkey α-mouse IgG	IF 1:1,000 FC 1:1,000	Thermo Fisher Scientific, catalog A21202
Alexa Fluor 555, polyclonal donkey α-goat IgG	IF 1:1,000	Thermo Fisher Scientific, catalog A21432
Alexa Fluor 555, polyclonal donkey α-mouse IgG	IF 1:1,000	Thermo Fisher Scientific, catalog A31570
Alexa Fluor 555, polyclonal donkey α-rabbit IgG	IF 1:1,000	Thermo Fisher Scientific, catalog A31572
FITC, polyclonal goat α-mouse IgM	FC 1:200	Jackson Immuno, catalog 115-097-020
HRP, polyclonal donkey anti-mouse IgG	WB 1:10,000	Thermo Fisher Scientific, catalog A16017
HRP, polyclonal donkey anti-rabbit IgG	WB 1:10,000	Thermo Fisher Scientific, catalog A16035

Supplemental Table 8: Primer sequences, annealing temperatures and cycles used for RT-PCR and real time-PCR analyses.

Gene	**Primer for / rev**	**Length**	**Temp / cycles**
FOXD3	GTGAAGCCGCCTTACTCGTAC / CGAAGCTCTGCATCATGAG	353 bps	58°C / 38
GAPDH	AGAGGCAGGGATGATGTTCT / TCTGCTGATGCCCCCATGTT	258 bps	60°C / 30
GDF3	TTCGCTTTCTCCCAGACCAAGGTTTC / TACATCCAGCAGGTTGAAGTGAACAGCACC	311 bps	58°C / 32
GJA1	GGGTTAAGGGAAAGAGCGACC / CCCCATTCGATTTTGTTCTGC	248 bps	60°C / 30
GJA5	CCACAGAGAAGAATGTCTTCA / TGCTGCTGGCCTTACTAAGA	447 bps	56°C / 30
HEY2	ATGAGCATAGGATTCCGAGAGTG / GGCAGGAGGCACTTCTGAAG	300 bps	58°C / 30
HOXA1	GGGAAAGTTGGAGAGTACGGC / CCTCAGTGGGAGGTAGTCAG	359 bps	58°C / 30
IRX4	TTCCGTTCTGAAGCGTGGTC / TGAAGCAGGCAATTATTGGTGT	188 bps	56°C / 30
LEF1	CCAGCTATTGTAACACCTCA / TTCAGATGTAGGCAGCTGTC	421 bps	56°C / 30
LIN28	AGTAAGCTGCACATGGAAGG / ATTGTGGCTCAATTCTGTGC	410 bps	58°C / 36
MYL2	GGCGAGTGAACGTGAAAAAT / CAGCATTTCCCGAACGTAAT	200 bps	56°C / 30
MYL7	GAAGGTGAGTGTCCCAGAGG / CTTGTAGTCGATGTTCCCCG	289 bps	58°C / 22
NANOG	AGTCCCAAAGGCAAACAACCCACTTC / ATCTGCTGGAGGCTGAGGTATTTCTGTCTC	164 bps	64°C / 36
NKX2-5	GGCCTCAATCCCTACGGTTA / CACGAGAGTCAGGGAGCTGT	308 bps	58°C / 30
NKX2-5 real time	ACCTCAACAGCTCCCTGACTCT / TAATCGCCGCCACAAACTCTCC	155 bps	
NPPA	ACAGACGTAGGCCAAGAGAG / GTCTGACCTAGGAGCTGGAA	158 bps	60°C / 26
NR2F2	CCGACCGGGTGGTCGCCTTTATGGA / CGGCTGGTTGGGGTACTGGCTCCTA	227 bps	60°C / 30
RARB	AGAGTTTGATGGAGTTGGGTGGAC / GGAAGACGGACTCGCAGTGTAG	168 bps	58°C / 30
SOX2	ATGCACCGCTACGACGTGA / CTTTTGCACCCCTCCCATTT	437 bps	60°C / 30
TNNT2	GACAGAGCGGAAAAGTGGGA / TGAAGGAGGCCAGGCTCTAT	305 bps	56°C / 26
WNT3A	GCCCCACTCGGATACTTCT / GGCATGATCTCCACGTAGT	188 bps	58°C / 30
WNT8A	ACAGGTCCCAAGGCCTATCT / ATCCTTTCCCCAAATTCCAC	335 bps	58°C / 30

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