



Grouping and classifying electrophysiologically-defined classes of neocortical neurons by single cell, whole-genome expression profiling

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Table S1 | Electrophysiological properties of 18 mouse layer II/III cortical neurons.

Cell	Input resistance (Mohm)	Decrement Rate (mv/s)	First spike amplitude (mV)	Steady spike amplitude	Max frequency (s-1)	Frequency ratio (Max/min)	Spike width (ms)	Spike ratio (Max/Min)	AHP (mV)	Age, days after birth	Comments	Firing
18	444	105.2	46.1	N/A	N/A	N/A	N/A	N/A	N/A	5	Very immature FS cell	FS
4	1245	216	15.4	11	39.4	1.51	6.95	4.77	N/A	6	Immature FS cell	FS
12	206	70.9	80	73.9	23.9	4.54	3.55	1.79	1745	10	Depolarisation blocked	FS
17	383	102.7	55.7	50.3	N/A	N/A	3.2	1.37	173	10	Immature FS, bursting	FS
3	836	166.2	48.1	275	7.9	1.51	40	17.5	N/A	6	Immature RS cell	RS
2	762	110.5	60	49.4	14.3	1.53	6.46	2.21	15.47	9	Immature RS cell	RS
1	506	82.4	64.3	50.3	10.4	2.01	7	1.2	17.7	10	Depolarisation blocked	RS
9	600	92.9	59	578	18.2	2.12	8	1.25	15.6	10	Typical RS	RS
14	382	64.7	86.9	80.8	59.8	1.71	2.65	1.7	22.77	13	Typical FS	FS
20	741	149.3	74.4	62.9	18.1	1.67	1.81	1.45	23.1	13	Depolarisation blocked	FS
10	406	74.3	82.2	73	54.4	2.11	2.05	1.63	21.33	22	Depolarisation blocked	FS
16	283	47	68.8	68.6	51.1	3.5	2.55	1.67	1785	22	Typical FS	FS
15	163	32.8	81.7	73.5	51.1	3.51	1.75	1.9	1745	22	Typical FS	FS
19	212	42.9	83.4	73.2	23.9	4.54	5.05	1.67	1755	22	FS-like, some RS features	FS
13	278	66.6	60.6	48.4	179	3.8	10.4	4.15	18.6	13	Regular spiking neuron	RS
11	219	42.9	83.4	75	23.9	4.54	5.03	1.64	1755	22	RS, depolarisation blocked	RS
7	125	24.5	88.1	74.6	15.4	2.96	3.7	1.45	1785	22	RS, depolarisation blocked	RS
8	157	34.3	92.2	88.7	32	5	3.15	1.85	16.15	22	Typical RS	RS

Electrophysiological parameters were measured as described in Tateno et al., (2004). RS, regular spiking pattern; FS, fast spiking pattern.

Table S2 | RS-enriched gene transcripts.

RS cells	FS cells	Accession	UniGene	Name	Symbol
3.067	-0.399	BC004813	Mm.193041	Mitogen-activated protein kinase kinase kinase 7 interacting protein 2	Map3k7ip2
2.506	-1.01	AK010596	Mm.280013	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	Psmc1
2.506	-1.521	AK007678	Mm.29019	DTW domain containing 1	Dtwd1
2.271	-1.675	BC003286	Mm.275554	Ankyrin repeat domain 13a	Ankrd13a
2.205	0.043	AK016004	Mm.206631	Exonuclease 3'-5' domain containing 2	Exd2
2.139	0.032	NM_015780	Mm.220362	Complement factor H-related 1	Cfhr1
2.131	-0.576	NM_015749	Mm.20948	Transcobalamin 2	Tcn2
2.126	-0.446	AK015548	Mm.108061	Transcribed locus, weakly similar to XP_978670.1 PREDICTED: similar to pORF1 [Mus musculus]	
1.833	-0.11	AK012160	Mm.348422	Transcribed locus	
1.792	-1.019	AK007217	Mm.59300	Transcribed locus	
1.773	-0.119	AK006954	Mm.417843	Transcribed locus	
1.763	0.211	AK011823	Data not found		
1.76	-2.295	NM_009837	Mm.296985	Chaperonin containing Tcp1, subunit 4 (delta)	Cct4
1.698	-2.074	NM_025437	Mm.294623	Eukaryotic translation initiation factor 1A, Y-linked	Eif1ay
1.649	-0.181	U66888	Mm.2254	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	Emr1
1.641	-0.995	AK005047	Mm.288742	RNA (guanine-9-) methyltransferase domain containing 1	Rg9mtd1
1.624	-0.248	NM_018856	Data not found		CCn12
1.596	-0.501	NM_019674	Mm.41998	Protein phosphatase 4, catalytic subunit	PPP4c
1.594	-1.323	NM_008344	Mm.358609	Insulin-like growth factor binding protein 6	Igfbp6
1.568	0.167	AK002294	Mm.281019	Coenzyme Q10 homolog B (S. cerevisiae)	Coq10b
1.535	-0.29	NM_009034	Mm.12825	Retinol binding protein 2, cellular	Rbp2
1.521	-0.234	S49542	Data not found		Htr2a?
1.51	0.043	AK006619	Data not found	RIKEN clone	
1.476	0.005	AK019394	Mm.399211	Transcribed locus	
1.468	-1.037	BC007161	Mm.293175	Jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)	Jhdm1d
1.435	-0.115	AK006668	Mm.425204	Coiled-coil domain containing 30	Ccdc30?RIKEN
1.433	-0.001	NM_013683	Mm.14814	Transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	Tap1
1.429	-0.32	NM_011796	Mm.294315	Calpain 10	Capn10
1.41	-0.224	NM_010110	Mm.3374	Ephrin B1	Efnb1
1.409	-0.168	AK003491	Mm.151018	Transcribed locus	
1.395	0.006	BC004738	Data not found		
1.392	-0.334	Y13989	Mm.303767	Immunoglobulin heavy chain 2 (serum IgA)	Igh-2
1.347	-0.065	NM_007376	Mm.260144	Pregnancy zone protein	Pzp
1.335	-0.627	AK020183	Mm.394930	Glycogen synthase kinase 3 beta	Gsk3b
1.306	-0.15	NM_008852	Mm.6255	Paired-like homeodomain transcription factor 3	Pitx3
1.306	-0.288	NM_007930	Mm.241073	Ectodermal-neural cortex 1	Enc1
1.305	-0.128	NM_009008	Mm.1972	RAS-related C3 botulinum substrate 2	Rac2
1.279	-0.305	AI840604	Mm.1155	Tubulin, alpha 4A	Tuba4a
1.249	-0.249	AK020271	Mm.231441	Transcribed locus	
1.236	-0.241	NM_009523	Mm.20355	Wingless-related MMTV integration site 4	Wnt4
1.235	0.162	AK016917	Mm.85000	Na ⁺ /H ⁺ exchanger domain containing 1	Nhedc1
1.225	-0.147	AK003103	Mm.427742	Transcribed locus	
1.225	0.052	AB044560	Mm.477072	C1q-like 3	C1ql3
1.209	-0.934	NM_025562	Mm.25849	Fission 1 (mitochondrial outer membrane) homolog (yeast)	Fis1
1.203	0.087	NM_009534	Mm.221992	Yes-associated protein 1	Yap1
1.19	-0.184	AB010310	Mm.38948	Zinc finger protein 7	Zfp7
1.17	-0.312	AK016974	Mm.158634	RIKEN cDNA 4933428M09 gene	4933428M09Rik
1.158	-0.222	L08075	Mm.440883	Phosducin	Pdc

(Continued)

Table S2 | (Continued)

RS cells	FS cells	Accession	UniGene	Name	Symbol
1.154	0.107	NM_026341	Mm.317636	Nudix (nucleoside diphosphate linked moiety X)-type motif 13	Nudt13
1.142	-0.12	AF373847	Mm.240047	Tumor necrosis factor receptor superfamily, member 13c	Tnfrsf13c
1.141	-0.509	AK014905	Mm.187793	Tubulin tyrosine ligase-like family, member 7	Ttl7
1.121	0.051	AK013527	Mm.323322	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4	Galnt4
1.118	-0.182	NM_010916	Mm.2474	Nescient helix loop helix 1	Nhlh1
1.118	0.029	L08652	Data not found		
1.117	-0.494	NM_019560	Data not found		
1.114	-0.201	BC006701	Mm.27839	UBX domain protein 1	Ubxn1
1.082	-0.28	AK007043	Mm.48791	RIKEN cDNA 1700092M07 gene	1700092M07Rik
1.066	-0.112	AK015030	Mm.449994	Transcribed locus, moderately similar to NP_001003861.1 ribosomal protein L9 [Danio rerio]	
1.064	-0.131	NM_009863	Mm.20842	Cell division cycle 7 (S. cerevisiae)	Cdc7
1.049	-0.303	NM_007688	Mm.276826	Cofilin 2, muscle	Cfl2
1.046	-0.266	AF283667	Mm.476732	Phosphoglycerate mutase 1	Pgam1
1.043	-0.487	AK006417	Mm.396202	Transcribed locus	
1.04	-0.352	AK006359	Mm.271215	RIKEN cDNA 1700025M24 gene	1700025M24Rik
1.028	-0.817	AK018556	Mm.387335	Transcribed locus	
1.019	0.157	U55616	Mm.389775	Clone SEAM 12 immunoglobulin light chain variable region	
1.014	-0.242	AK006931	Mm.17757	Leucine rich repeat containing 27	Lrrc27
1.008	-0.039	AK008020	Mm.30021	OMA1 homolog, zinc metalloproteinase (S. cerevisiae)	Oma1
1.004	0.042	AF402611	Mm.256131	FYVE, RhoGEF and PH domain containing 4	Fgd4
0.998	0.025	AB045718	Data not found		
0.99	-0.273	AK002668	Mm.73608	Transmembrane protein 93	Tmem93
0.986	0.01	X89678	Mm.246535	Olfactory receptor 32	Olf32
0.986	-0.274	AK020983	Mm.153204	Transcribed locus	
0.985	-0.281	NM_016970	Mm.20434	Killer cell lectin-like receptor subfamily G, member 1	Klrg1
0.964	-0.582	AF156890	Data not found		
0.961	-0.421	AK016024	Mm.156095	Transcribed locus	
0.96	-0.124	AK021008	Mm.28449	RIKEN cDNA B230219D22 gene	B230219D22Rik
0.953	0.158	D29940	Data not found		
0.949	-0.239	D12731	Data not found		
0.945	-0.477	AK015013	Mm.772	Rotatin	Rttm
0.944	0.043	BF166296	Mm.21002	Solute carrier family 2 (facilitated glucose transporter), member 1	Slc2a1
0.944	-0.31	AK014715	Data not found		
0.941	-0.217	NM_028889	Mm.247951	EF hand domain containing 1	Efh1
0.934	-0.293	BC011331	Mm.20313	Coiled-coil-helix-coiled-coil-helix domain containing 6	Chchd6
0.931	0.114	AF272146	Mm.150813	Frizzled homolog 5 (Drosophila)	Fzd5
0.928	-0.027	AK008832	Mm.253147	RIKEN cDNA 2210404O07 gene	2210404O07Rik
0.925	0.092	NM_018746	Mm.34819	Inter alpha-trypsin inhibitor, heavy chain 4	Itih4
0.923	-0.082	NM_010691	Mm.116815	Ladybird homeobox homolog 1 (Drosophila)	Lbx1
0.921	-0.035	NM_013684	Mm.244820	TATA box binding protein	Tbp
0.913	0.067	AB049967	Mm.426557	Immunoglobulin kappa chain variable 19 (V19)-14	Igk-V19-14
0.913	-0.149	U30240	Mm.389775	Clone SEAM 12 immunoglobulin light chain variable region	
0.911	-0.219	NM_018863	Mm.6239	Prodynorphin	Pdyn
0.907	0.022	AK002717	Mm.220984	Snurportin 1	Snupn
0.905	-0.092	D32210	Mm.254017	Notch gene homolog 2 (Drosophila)	Notch2
0.892	0	AK008031	Mm.230169	Glutamate oxaloacetate transaminase 2, mitochondrial	Got2
0.89	-0.19	AK019414	Mm.157212	Centrosomal protein 57	Cep57
0.884	-0.98	NM_008110	Mm.9714	Growth differentiation factor 9	Gdf9
0.882	-0.39	AK010974	Mm.394279	Transcribed locus	
0.878	-0.469	U55663	Mm.333130	Clone anti-MS613II-2-19 immunoglobulin kappa light chain variable region	

(Continued)

Table S2 | (Continued)

RS cells	FS cells	Accession	UniGene	Name	Symbol
0.864	-0.076	AL136158	Data not found		
0.861	-0.158	NM_009413	Mm.439966	Tumor protein D52-like 1	Tpd52l1
0.853	-0.243	NM_008700	Mm.41974	NK2 transcription factor related, locus 5 (Drosophila)	Nkx2-5
0.849	0.039	AF226663	Mm.271932	EST AA881470	AA881470
0.846	-0.964	AK010545	Mm.28626	TM2 domain containing 2	Tm2d2
0.844	-0.076	NM_031391	Mm.275728	General transcription factor II A, 1	Gtf2a1
0.838	-0.12	AF178619	Mm.305352	Gene model 1499, (NCBI)	Gm1499
0.835	-0.061	AK020873	Data not found		
0.834	-0.113	AK019660	Mm.427734	Transcribed locus	
0.833	-1.008	AB049355	Mm.157700	Family with sequence similarity 129, member A	Fam129a
0.829	-0.55	AK013050	Mm.474523	Ribosomal protein S19 pseudogene	Gm13143
0.826	-0.983	NM_021356	Mm.277409	Growth factor receptor bound protein 2-associated protein 1	Gab1
0.823	-0.145	NM_011100	Mm.16766	Protein kinase, cAMP dependent, catalytic, beta	Prkacb
0.813	-0.138	AK017198	Data not found		
0.812	-0.072	BC004845	Mm.254336	Oligophrenin 1	Ophn1
0.811	-0.011	M30387	Mm.184441	Immunoglobulin lambda-like polypeptide 1	Igl1
0.809	-0.423	AK018519	Mm.439331	Transcribed locus	
0.808	-0.253	AK003524	Mm.300178	Arylsulfatase B	Arsb
0.806	0.167	AK009063	Mm.305318	Trafficking protein, kinesin binding 1	Trak1
0.804	-0.059	NM_013752	Mm.20866	Nibrin	Nbn
0.801	-0.754	AF092039	Mm.29058	Steroid receptor RNA activator 1	Sra1
0.789	-0.079	NM_008131	Mm.210745	Glutamate-ammonia ligase (glutamine synthetase)	Glul
0.773	0.209	X14620	Mm.457994	Immunoglobulin kappa light chain variable region mRNA, clone MRL1-46	
0.771	0.014	NM_013634	Mm.12926	Mediator complex subunit 1	Med1
0.771	0.032	AK015725	Mm.126220	Maestro	Mro
0.769	-0.181	AB010353	Mm.296071	Zinc finger with KRAB and SCAN domains 3	Zkscan3
0.769	-0.194	AK009282	Mm.41381	LY6/PLAUR domain containing 6B	Lypd6b
0.758	-0.32	AK011730	Mm.45367	Zinc finger protein 715	Zfp715
0.756	-0.013	AF274590	Mm.241276	Intraflagellar transport 57 homolog (Chlamydomonas)	Ift57
0.756	-0.507	AK012120	Mm.238279	Solute carrier family 39 (zinc transporter), member 9	Slc39a9
0.752	0.079	AK014057	Mm.45533	BEN domain containing 5	Bend5
0.748	-0.904	BC005559	Mm.170023	Ring finger protein 181	Rnf181
0.743	-0.158	AK015638	Mm.401979	Transcribed locus	
0.732	-0.288	NM_020596	Mm.44137	Early growth response 4	Egr4
0.732	-0.25	AK016512	Data not found		
0.73	-0.18	AK012292	Mm.275524	Ectonucleoside triphosphate diphosphohydrolase 6	Entpd6
0.726	-0.178	NM_029231	Mm.340601	Proline, glutamic acid and leucine rich protein 1	Pelp1
0.723	-0.128	Z12508	Data not found		
0.718	0.095	AK012979	Mm.391716	Transcribed locus	
0.713	-0.099	AK016921	Mm.440937	Zinc finger, RAN-binding domain containing 3	Zranb3
0.712	-0.078	AK003121	Mm.30724	Collectin sub-family member 11	Colec11
0.711	-0.254	AK004884	Mm.29342	R3H domain containing 2	R3hdm2
0.702	-0.276	NM_010865	Mm.10694	Myocilin	Myoc
0.698	-0.192	NM_009349	Mm.299	Indolethylamine N-methyltransferase	Inmt
0.693	-0.361	AK015444	Mm.107775	Transcribed locus	
0.689	-0.025	AK020792	Data not found		
0.685	-0.476	AK013928	Data not found		
0.684	-0.091	AK013578	Data not found		
0.683	-0.4	BC002107	Mm.30204	Quinoid dihydropteridine reductase	Qdpr
0.678	-0.015	AK014420	Mm.221269	Family with sequence similarity 175, member A	Fam175a
0.669	-0.033	AK020410	Mm.28326	Heparan-alpha-glucosaminide N-acetyltransferase	Hgsnat
0.668	-0.099	X89682	Data not found		

(Continued)

Table S2 | (Continued)

RS cells	FS cells	Accession	UniGene	Name	Symbol
0.664	-0.935	AK015217	Mm.458438	DNA segment, Chr 19, ERATO Doi 652, expressed	D19Erttd652e
0.661	-0.041	AE000664	Data not found		
0.659	-0.169	NM_007911	Mm.249637	Ephrin B3	Efnb3
0.657	-0.252	AY033650	Mm.290450	Lethal giant larvae homolog 2 (Drosophila)	Lgl2
0.656	0.114	AF050426	Data not found		
0.656	-0.176	NM_025679	Mm.208619	RIKEN cDNA 5730470L24 gene	5730470L24Rik
0.656	-0.088	AK004025	Mm.69020	Transcribed locus, strongly similar to XP_930163.1 PREDICTED: hypothetical protein LOC68740 [Mus musculus]	
0.654	-0.897	NM_019412	Mm.10119	Periaxin	Prx
0.643	-0.092	AJ002433	Data not found		
0.637	-0.09	NM_011361	Mm.28405	Serum/glucocorticoid regulated kinase 1	Sgk1
0.635	-0.475	AF073956	Data not found		
0.634	0.02	AK018068	Data not found		
0.63	-2.79	NM_007496	Mm.416972	Zinc finger homeobox 3	Zfhx3
0.623	-0.099	AK005492	Mm.326858	Pregnancy-specific glycoprotein 21	Psg21
0.623	-0.014	X90779	Data not found		
0.617	-0.053	NM_025827	Mm.324550	Lon peptidase 2, peroxisomal	Lonp2
0.605	-0.085	NM_008599	Mm.766	Chemokine (C-X-C motif) ligand 9	Cxcl9
0.6	-1.052	NM_012031	Mm.475669	Phosphorylase kinase alpha 1	Phka1
0.592	-0.232	AK015830	Mm.72666	Transcribed locus	
0.591	-0.001	NM_009381	Mm.28585	Thyroid hormone responsive SPOT14 homolog (Rattus)	Thrsp
0.587	-0.573	NM_007425	Mm.3383	Advanced glycosylation end product-specific receptor	Ager
0.584	-0.142	AK013081	Mm.154087	Microtubule-associated protein 6	Mtap6
0.577	-0.043	AK019180	Mm.330507	Phospholipase A2, group IVD	Pla2g4d
0.577	-0.057	AK018115	Mm.36544	BTB (POZ) domain containing 11	Btbd11
0.575	0.028	NM_007637	Mm.282158	Chaperonin containing Tcp1, subunit 5 (epsilon)	Cct5
0.566	-0.003	AJ243933	Mm.214224	Cyclic nucleotide gated channel alpha 3	Cnga3
0.566	-0.38	BC004810	Mm.279898	Polymerase (RNA) II (DNA directed) polypeptide D	Polr2d
0.564	-0.027	NM_016682	Mm.27560	Ubiquitin-like modifier activating enzyme 2	Uba2
0.563	-0.132	AK018356	Data not found		
0.56	-0.304	NM_008003	Mm.3904	Fibroblast growth factor 15	Fgf15
0.559	-0.988	NM_019437	Mm.7013	Riboflavin kinase	Rfk
0.555	-0.193	U92070	Mm.360305	DNA segment, Chr 6, Massachusetts Institute of Technology 97	D6Mit97
0.554	0.03	NM_025419	Mm.268307	RIKEN cDNA 1110059G10 gene	1110059G10Rik
0.553	0.014	NM_007417	Mm.235195	Adrenergic receptor, alpha 2a	Adra2a
0.551	-0.069	Z37502	Mm.342177	Immunoglobulin heavy chain 6 (heavy chain of IgM)	Igh-6
0.548	0.053	AF158133	Data not found		
0.544	0.047	AK020308	Mm.24176	Euchromatic histone methyltransferase 1	Ehmt1
0.542	-0.418	AK015080	Mm.159067	RIKEN cDNA 4930404H21 gene	4930404H21Rik
0.533	-0.36	AK019148	Mm.28520	Ski sarcoma viral oncogene homolog (avian)	Ski
0.533	-0.218	NM_028982	Mm.34182	RIKEN cDNA 8430419L09 gene	8430419L09Rik
0.53	-0.125	AK007533	Mm.476015	Motile sperm domain containing 1	Mospd1
0.529	-0.045	AK008415	Mm.32615	Transmembrane protein 167B	Tmem167b
0.521	-0.121	AK010559	Mm.233879	Castor homolog 1, zinc finger (Drosophila)	Casz1
0.52	-1.135	U57327	Mm.295194	T-box 1	Tbx1
0.519	-0.184	AK019600	Mm.379264	Armadillo repeat containing 9	Armc9
0.514	-0.237	AK016488	Mm.159169	RIKEN cDNA 4931429L15 gene	4931429L15Rik
0.512	-0.007	BC004087	Mm.218350	F-box and leucine-rich repeat protein 20	Fbxl20
0.509	-0.063	U51463	Mm.359198	Immunoglobulin heavy chain (S107 family)	Igh-VS107
0.506	-0.274	AF212998	Mm.293574	Aspartoacylase	Aspa
0.5	-0.074	AJ278999	Mm.153429	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	Spock2
0.498	-0.296	NM_023268	Mm.27035	Quiescin Q6 sulfhydryl oxidase 1	Qsox1
0.496	-0.128	AK016606	Mm.158545	Transcribed locus	

(Continued)

Table S2 | (Continued)

RS cells	FS cells	Accession	UniGene	Name	Symbol
0.493	-0.158	NM_011069	Mm.20901	Peroxisomal biogenesis factor 11 beta	Pex11b
0.48	0.001	AF291485	Data not found		
0.475	-2.142	AK011515	Mm.44201	Phosphatidylinositol glycan anchor biosynthesis, class Y	Pigy
0.475	-0.044	NM_026297	Data not found		
0.464	-0.766	AK011506	Data not found		
0.462	0.058	NM_008164	Mm.57052	Rhopilin, Rho GTPase binding protein 1	Rhpn1
0.461	-0.022	NM_023137	Mm.140210	Ubiquitin D	Ubd
0.461	-0.113	NM_026253	Mm.46115	Leucine rich repeat containing 18	Lrrc18
0.447	-0.175	AK016437	Mm.440524	Phosphoglucomutase 2-like 1	Pgm2l1
0.433	-0.986	NM_024273	Mm.132231	RIKEN cDNA 4930455C21 gene	4930455C21Rik
0.428	-0.121	U86728	Data not found		
0.427	0.05	NM_007627	Mm.44513	Cholecystokinin B receptor	Cckbr
0.425	-0.157	NM_011707	Mm.3667	Vitronectin	Vtn
0.424	-0.271	BC002235	Mm.132006	Tetratricopeptide repeat domain 15	Ttc15
0.421	-0.236	Z12269	Mm.333026	T-cell receptor beta, joining region	Tcrb-J
0.421	-0.02	M16073	Mm.305352	Gene model 1499, (NCBI)	Gm1499
0.419	-1.648	AK020957	Mm.25874	NUAK family, SNF1-like kinase, 1	Nuak1
0.412	-0.094	AK020819	Mm.387130	Transcribed locus	
0.412	-0.271	AK011565	Mm.158306	Transcribed locus	
0.412	-0.343	AK018940	Mm.245981	Transcribed locus	
0.404	-0.334	BC005527	Mm.338425	Ectonucleotide pyrophosphatase/phosphodiesterase 3	Enpp3
0.4	-0.472	X96700	Mm.2534	Proline-serine-threonine phosphatase-interacting protein 1	Pstpip1
0.399	-0.269	NM_027149	Mm.435546	WD repeat domain 20A	Wdr20a
0.398	-0.245	AF279479	Mm.423397	Trans-acting transcription factor 5	Sp5
0.397	-0.303	AF139193	Mm.256414	Solute carrier family 9 (sodium/hydrogen exchanger), member 2	Slc9a2
0.396	-1.065	NM_017390	Mm.99395	Semenogelin I	Semg1
0.393	-0.103	AF357465	Data not found		
0.39	-0.179	AK016395	Mm.402098	Transcribed locus	
0.381	-0.451	AK019796	Mm.243881	Transcribed locus	
0.378	-1.058	NM_008162	Mm.359573	Glutathione peroxidase 4	Gpx4
0.375	-0.565	AK010512	Mm.260627	DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40
0.365	-0.145	NM_013517	Mm.1233	Fc receptor, IgE, low affinity II, alpha polypeptide	Fcer2a
0.357	-0.146	AK018075	Mm.248820	Prickle-like 2 (Drosophila)	Prickle2
0.356	-0.04	AK016157	Data not found		
0.345	-0.204	AK020883	Mm.423205	PDZ domain containing 2	Pdzd2
0.341	-0.071	NM_013779	Data not found		
0.33	-0.463	AK009519	Mm.87417	Dishevelled associated activator of morphogenesis 1	Daam1
0.329	-0.274	AK005818	Mm.44186	Zinc finger and BTB domain containing 43	Zbtb43
0.322	-0.277	NM_023146	Mm.440985	RAN binding protein 17	Ranbp17
0.319	-0.482	NM_013645	Mm.2766	Parvalbumin	Pvalb
0.317	-0.11	AK007413	Mm.478042	Family with sequence similarity 58, member B	Fam58b
0.312	-1.049	NM_016957	Mm.319660	High mobility group nucleosomal binding domain 2	Hmgn2
0.309	-0.76	M81747	Mm.282093	1400 base pair ubiquitin mRNA, 5' end	
0.298	-0.453	AF222802	Mm.275901	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor q	Taf8
0.294	-0.643	NM_019482	Mm.142253	Pannexin 1	Panx1
0.286	-0.305	NM_020519	Mm.27630	Secreted Ly6/Plaur domain containing 1	Slurp1
0.274	-0.314	AF022078	Mm.439763	Distal-less homeobox 6	Dlx6
0.266	-0.162	AK020551	Data not found		
0.264	-0.097	AK016264	Mm.74704	Zinc finger CCCH type containing 13	Zc3h13
0.259	-0.386	AF037437	Data not found		
0.258	-0.225	AK013280	Mm.38529	PRP18 pre-mRNA processing factor 18 homolog (yeast)	Prpf18
0.256	-0.379	NM_008090	Mm.476843	GATA binding protein 2	Gata2

(Continued)

Table S2 | (Continued)

RS cells	FS cells	Accession	UniGene	Name	Symbol
0.255	-0.247	AF012181	Mm.425913	T-cell receptor alpha-chain precursor	
0.254	-0.149	NM_026533	Mm.14798	Ribosomal protein S13	Rps13
0.251	-1.577	NM_021538	Mm.28668	Coatomer protein complex, subunit epsilon	Cope
0.242	-0.311	NM_030262	Mm.203556	Protein O-fucosyltransferase 2	Pofut2
0.241	-0.408	NM_023852	Mm.151600	RAB3C, member RAS oncogene family	Rab3c
0.229	-0.149	NM_025586	Mm.2050	Ribosomal protein L15	Rpl15
0.221	-0.303	U54563	Mm.289992	Eukaryotic translation initiation factor 3, subunit E	Eif3e
0.217	-0.494	NM_009359	Mm.14485	Testis expressed gene 9	Tex9
0.216	-0.161	BF580261	Mm.10353	CAMP responsive element binding protein 3-like 1	Creb3l1
0.215	-0.356	BC008150	Mm.385009	SPRY domain containing 3	Spryd3
0.202	-0.469	AK017856	Mm.289653	Dehydrogenase/reductase (SDR family) member 7	Dhrs7
0.2	-0.384	AK011425	Mm.33574	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	Slc25a24
0.187	-0.461	NM_010437	Mm.42157	Human immunodeficiency virus type I enhancer binding protein 2	Hivep2
0.182	-2.156	NM_008594	Mm.1451	Milk fat globule-EGF factor 8 protein	Mfge8
0.173	-0.259	NM_009438	Mm.180458	Ribosomal protein L13A	Rpl13a
0.173	-0.158	AK021318	Mm.244075	Transcribed locus	
0.151	-0.773	NM_009028	Mm.322186	RAS-like, family 2, locus 9	Rasl2-9
0.125	-0.193	AK015465	Mm.410820	Transcribed locus	
0.111	-0.302	NM_025779	Mm.31056	Coiled-coil domain containing 109B	Ccdc109b
0.099	-0.509	AK009590	Mm.65906	Pre-B-cell leukemia transcription factor interacting protein 1	Pbxip1
0.097	-0.619	AB037685	Mm.218657	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	Anp32e
0.042	-0.742	AY029532	Mm.478288	LAG1 homolog, ceramide synthase 2	Lass2
0.029	-0.316	AK007851	Mm.25479	Leucine rich repeat containing 8 family, member E	Lrrc8e
0.026	-0.57	AK012833	Mm.297698	Zinc finger, CCHC domain containing 12	Zcchc12
-0.158	-1.639	L35549	Data not found		

Gene expression ratios are log2-transformed values, averaged across all mature cells within that class, relative to the reference of all pooled single cells in the sample.

REFERENCE

Tateno, T., Harsch, A., and Robinson, H. P. (2004). Threshold firing frequency-current relationships of neurons in rat somatosensory cortex: type 1 and type 2 dynamics. *J. Neurophysiol.* 92, 2283–2294.