

**Supplementary table 1. List of P value and Log Fold Changes of ameloblastoma profile genes**

<b>Symbol</b>	<b>PValue</b>	<b>logFC</b>
OBP2A	2.36E-18	-2.9893191
LGALS4	2.92E-18	-2.9347697
NT5M	5.66E-19	-2.8690479
LILRB1	9.69E-18	-2.7996894
FLJ20343	1.03E-17	-2.7255629
DNAH9	5.93E-18	-2.7078208
EIF4ENIF1	2.62E-18	-2.6816422
IFNA8	3.41E-18	-2.6701346
FLJ10587	5.43E-18	-2.6563194
ASRGL1	3.50E-18	-2.5959203
ATP5H	1.72E-17	-2.5653845
PIGL	1.07E-17	-2.5191319
CBLC	1.27E-17	-2.489802
MX2	1.92E-17	-2.4737391
JK	1.02E-17	-2.4533314
EPN3	2.97E-18	-2.4532638
SRP14	4.86E-17	-2.4521452
HIST1H1E	1.53E-17	-2.4358077
RAI	1.42E-17	-2.4047196
FLJ20530	1.33E-17	-2.395883
RPL29	9.56E-18	-2.3938102
HLF	1.38E-16	-2.3855171
MICA	1.18E-17	-2.3849491

SUCLA2	1.91E-17	-2.3845861
PHF11	3.99E-17	-2.3675199
MRPL39	1.56E-16	-2.362284
SEC10L1	2.20E-18	-2.3483933
FLJ20045	2.40E-17	-2.3292114
PTK9	1.73E-17	-2.3249519
NRG1	6.94E-18	-2.3076019
PTPRO	8.12E-18	-2.2907231
CTSB	6.03E-17	-2.2802467
PHF3	1.45E-17	-2.2793134
FABP5	2.60E-17	-2.2790737
DUSP3	9.70E-18	-2.2738341
PSTPIP2	1.69E-17	-2.2686714
TADA2L	7.34E-17	-2.2545662
HPS5	8.56E-18	-2.2482819
RPL37	3.39E-17	-2.1453696
DNMT3A	1.73E-17	-2.1227859
TMEM14B	3.95E-18	-2.0924561
CAS1	1.83E-16	-2.0695977
SYT5	3.89E-17	-2.064543
MC4R	1.62E-17	-2.0637994
YWHAZ	2.67E-17	-2.0461605
SLC14A1	6.06E-17	-2.0459744
GLE1L	6.33E-16	-2.0364516
SUPT16H	5.62E-17	-2.0257353
BTN2A2	4.11E-16	-2.0254121
ZNF180	2.94E-16	-2.0216184

SAP18	6.04E-16	2.00329808
SFXN1	5.52E-17	2.00574822
CEPT1	1.45E-15	2.01052054
CLCN6	4.01E-17	2.01256685
ZNF195	1.54E-16	2.02032268
AK2	6.01E-17	2.02379827
MGC3169	2.61E-17	2.03019288
NTSR1	9.54E-17	2.0404398
PSMB2	1.49E-16	2.04344903
TAS2R13	1.17E-16	2.04834847
PPHLN1	5.37E-17	2.05241771
RCP	8.83E-17	2.05429376
HRPT2	8.32E-17	2.05530649
B3GAT3	1.35E-16	2.06038305
KRTHA7	6.90E-17	2.06320633
MTA2	8.55E-17	2.06546133
MYO5C	3.18E-16	2.07345118
STK25	1.02E-16	2.0753425
CTAGE1	5.51E-16	2.07634974
C7	1.98E-17	2.07707622
GTF3C2	3.43E-17	2.08051663
TAS2R1	4.54E-17	2.09188739
UPF3A	3.77E-17	2.09271133
QPCT	2.11E-17	2.09502399
DKKL1	1.57E-16	2.09879532
DRD3	5.50E-17	2.10028558
ELF4	6.78E-17	2.1070931

KCNJ4	4.50E-16	2.10780242
PDZK2	5.97E-17	2.11016307
USP36	3.03E-17	2.11017679
WDR4	4.05E-17	2.110357
PLXNC1	8.64E-17	2.11438653
COP1	2.24E-16	2.11468418
FLRT1	6.16E-17	2.12137752
HMG20B	5.31E-16	2.12140287
FGFR1	2.90E-17	2.13010528
MLLT1	3.90E-17	2.13327875
FLJ20519	3.47E-17	2.14144062
TREX2	6.52E-17	2.15015886
SF3A1	1.30E-17	2.15124917
RANBP3	1.56E-17	2.1554372
BPI	8.72E-18	2.15679823
Bit1	6.98E-16	2.16314246
DSG3	3.16E-16	2.17504474
GP1BA	1.23E-17	2.1772155
AAK1	2.15E-17	2.17968305
PLA2G5	1.06E-16	2.18216005
ARHGDIA	4.35E-16	2.18290977
FLJ10874	8.42E-18	2.18782214
GRIN2D	1.19E-16	2.19029009
HNF4G	8.54E-17	2.19412655
SF3B4	8.85E-18	2.19591995
HNRPH3	4.82E-17	2.1989628
IRAK2	5.49E-17	2.20266286

LILRB3	3.78E-16	2.21368532
CRYBB1	9.47E-18	2.22003865
SLC22A8	5.68E-17	2.22295982
RNF110	1.62E-16	2.22509986
LGALS3BP	6.50E-17	2.22524507
ITGBL1	3.17E-17	2.22706588
PLD2	4.81E-17	2.22730753
ITGB4BP	1.02E-16	2.24674944
CDY	1.90E-17	2.24775691
NBL1	7.79E-17	2.2534961
FLJ11164	4.12E-17	2.25731766
IKBKG	1.64E-16	2.26140621
ECGF1	1.22E-17	2.26372536
NKX2-8	8.30E-18	2.26810384
ADMR	8.37E-16	2.2704886
SDCBP2	8.32E-17	2.2794525
FLJ10761	6.79E-17	2.28358939
CGI-85	5.30E-17	2.2937176
FLJ20331	1.52E-16	2.29574449
MART2	1.89E-17	2.30513643
FLJ10305	2.39E-17	2.30918829
CDC20	2.08E-17	2.31728696
PBX3	7.79E-17	2.33355605
SOX8	2.64E-17	2.3335974
CCDC6	4.47E-18	2.34715435
SPIN2	1.32E-17	2.34884572
FA2H	3.46E-17	2.35256617

MAOB	1.60E-17	2.35806573
LRP5	3.96E-17	2.36246394
PIGN	9.88E-17	2.36982252
CHST6	3.69E-19	2.3712318
HSRG1	3.77E-18	2.37987054
ATP5G1	8.63E-18	2.39460089
HBD	7.94E-16	2.39876301
GABRD	2.49E-17	2.40300176
NR4A1	1.46E-17	2.40874381
FLJ20359	2.08E-17	2.42151779
PEF	4.52E-17	2.42572343
SYNGR1	2.08E-16	2.43053541
FPRL1	1.58E-17	2.43226863
SMARCA3	4.84E-16	2.44454187
TCAP	2.84E-17	2.44922815
OPTC	2.47E-17	2.46184292
GATM	2.38E-16	2.46431929
TLX3	2.72E-17	2.47027566
DKFZP566B183	1.73E-17	2.4771584
GPR44	1.44E-16	2.47725496
MYO5A	7.60E-17	2.47768658
ZNF426	9.16E-17	2.4790135
GRK6	1.84E-17	2.48850782
GYS1	2.16E-17	2.49107765
DPF2	3.85E-17	2.49343171
FBXL8	2.97E-17	2.49740084
ZCWCC2	2.50E-17	2.49991591

SYN1	8.93E-18	2.5064294
TIMM17A	9.38E-17	2.5066203
JARID1B	4.60E-17	2.50929963
WDR8	2.90E-16	2.51059502
MC1R	3.50E-17	2.5289621
MAGEB4	2.10E-17	2.55214565
MAP1A	9.06E-18	2.58212247
FEZ1	1.07E-17	2.60210037
CRHR2	9.03E-19	2.60253496
DIO3	4.84E-17	2.60619543
HS3ST3A1	1.74E-17	2.6108714
E2F4	5.65E-18	2.62300577
GORASP2	1.74E-17	2.6345349
FLJ11856	5.95E-18	2.63524616
KIAA0040	9.92E-18	2.639522
MAN2A2	1.87E-16	2.65355333
PAK1	2.20E-17	2.66211713
FOS	2.36E-17	2.66648467
KRTHA2	3.32E-17	2.67514935
XCR1	7.59E-17	2.68312598
GDF1	4.80E-18	2.68956973
TNFSF7	1.70E-17	2.69378577
GARP	3.75E-18	2.70260486
ARAP3	3.93E-18	2.71335259
GPR135	1.18E-16	2.7168394
PYCR1	4.28E-18	2.72371626
PDHA1	2.24E-17	2.72599082

KRTHA1	1.56E-16	2.73587651
FOXK2	3.40E-16	2.75202094
CTAG1B	1.12E-17	2.75339909
UBQLN3	1.03E-17	2.75681438
CDH1	4.53E-19	2.78915411
KLF8	8.94E-18	2.79814367
TOP2B	5.78E-18	2.81616414
CLDN12	7.94E-18	2.82692979
PHF1	3.53E-17	2.8290569
SOX10	2.92E-18	2.85855242
GMEB2	6.97E-17	2.86764371
ALG3	1.57E-17	2.87291486
MICAL2	9.61E-18	2.89161726
BCKDK	7.98E-17	2.90185755
MFNG	5.09E-17	2.92891435
USP1	2.68E-17	2.96199776
LIPE	7.31E-17	2.96314113
NR4A3	3.19E-17	2.96741497
DAB2	1.56E-18	2.98430045
EFNA3	1.96E-18	2.98458127
CRA	5.77E-18	2.99405993
PPY2	3.11E-18	3.00937552
DVL2	2.56E-18	3.01039684
NAG18	1.39E-18	3.01538105
EIF3S4	3.13E-18	3.04396438
pp9099	3.90E-18	3.05822593
POU5F1	6.80E-18	3.07652475

DLL3	7.53E-18	3.10711227
FLII	6.67E-17	3.13931391
RNF5	2.15E-18	3.14182047
GREM1	4.05E-18	3.15924058
IL17R	5.02E-17	3.1688108
GPR56	4.37E-17	3.18687796
ARSA	7.43E-17	3.20345866
FLJ11286	3.30E-18	3.21216492
ABHD4	1.24E-17	3.21665694
MGC3047	3.95E-18	3.23020528
STAT1	8.81E-18	3.23085491
GNRH2	5.03E-18	3.24451131
EFNA4	7.67E-18	3.26129129
MCOLN1	6.49E-17	3.26279844
ADRA1D	2.46E-18	3.26781575
SERF1A	2.03E-17	3.28629473
ZNFN1A5	1.95E-18	3.31234549
AQP5	7.30E-18	3.33982686
NDP	2.25E-18	3.3410905
HOXD4	1.28E-18	3.3584878
SIAT8E	9.65E-18	3.36930581
APOM	5.08E-18	3.3699619
OAS1	8.75E-19	3.40979339
FXD3	4.07E-18	3.45265673
KRTHA5	1.08E-17	3.46552511
PRSS8	9.11E-18	3.50206126
FLJ20249	1.83E-17	3.51299099

GPS2	9.22E-18	3.60133074
SSTR3	4.21E-18	3.6416582
TESK1	2.19E-18	3.66237453
KIF3B	2.28E-18	3.69072198
EDG5	4.31E-18	3.72560629
UTF1	7.90E-20	3.73044959
GPR3	1.35E-18	3.7426546
ARHGAP8	3.28E-18	3.74287319
ENTPD1	1.29E-18	3.90427326
SLC6A3	5.49E-19	3.94245919
DLGAP1	7.02E-18	4.09086984
AP1G2	4.17E-18	4.21903218
NKG7	9.20E-19	4.37589591

Supplementary table 2. Enrichment criteria of conventional ameloblastoma						
Enrichment FDR	n Genes	Pathway Genes	Fold Enrichment	Pathway	URL	Genes
<b>0.00132964</b>	30	1264	2.77458617	Positive regulation of transcription by RNA polymerase II	<a href="http://amigo.geneontology.org/amigo/term/GO:0045944">http://amigo.geneontology.org/amigo/term/GO:0045944</a>	DVL2 SOX8 SUPT16H SOX10 GMEB2 ELF4 HLF STAT1 NR4A3 NR4A1 MICAL2 DPF2 NKX2-8 FOXK2 MTA2 DRD3 DAB2 LRP5 HNF4G PBX3 HOXD4 FOS UTF1 CTAG1B E2F4 POU5F1 MC1R IKBKG GREM1 GPS2
<b>0.01416068</b>	3	6	58.4512821	Response to corticotropin-releasing hormone	<a href="http://amigo.geneontology.org/amigo/term/GO:0043435">http://amigo.geneontology.org/amigo/term/GO:0043435</a>	CRHR2 NR4A3 NR4A1
<b>0.01416068</b>	3	6	58.4512821	Cellular response to corticotropin-releasing hormone stimulus	<a href="http://amigo.geneontology.org/amigo/term/GO:0071376">http://amigo.geneontology.org/amigo/term/GO:0071376</a>	CRHR2 NR4A3 NR4A1
<b>0.01423179</b>	32	1716	2.1800012	Positive regulation of transcription, DNA-templated	<a href="http://amigo.geneontology.org/amigo/term/GO:0045893">http://amigo.geneontology.org/amigo/term/GO:0045893</a>	DVL2 SOX8 CDH1 SUPT16H SOX10 GMEB2 ELF4 HLF STAT1 NR4A3 NR4A1 NDP MICAL2 DPF2 NKX2-8 FOXK2 MTA2 DRD3 DAB2 LRP5 HNF4G PBX3

						HOXD4 FOS UTF1 CTAG1B E2F4 POU5F1 MC1R IKBK G REM1 GPS2
<b>0.01423179</b>	32	1717	2.17873154	Positive regulation of RNA biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:1902680">http://amigo.geneontology.org/amigo/term/GO:1902680</a>	DVL2 SOX8 CDH1 SUPT16H SOX10 GMEB2 ELF4 HLF STAT1 NR4A3 NR4A1 NDP MICAL2 DP2 NKX2- 8 FOXK2 MTA2 DRD3 DAB2 LRP5 HNF4G PBX3 HOXD4 FOS UTF1 CTAG1B E2F4 POU5F1 MC1R IKBK G REM1 GPS2
<b>0.01423179</b>	32	1716	2.1800012	Positive regulation of nucleic acid- templated transcription	<a href="http://amigo.geneontology.org/amigo/term/GO:1903508">http://amigo.geneontology.org/amigo/term/GO:1903508</a>	DVL2 SOX8 CDH1 SUPT16H SOX10 GMEB2 ELF4 HLF STAT1 NR4A3 NR4A1 NDP MICAL2 DP2 NKX2- 8 FOXK2 MTA2 DRD3 DAB2 LRP5 HNF4G PBX3 HOXD4 FOS UTF1 CTAG1B E2F4 POU5F1 MC1R IKBK G REM1 GPS2
<b>0.01429234</b>	34	1895	2.09746025	Positive regulation of RNA metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0051254">http://amigo.geneontology.org/amigo/term/GO:0051254</a>	DVL2 SOX8 CDH1 SUPT16H SOX10 GMEB2 ELF4 HLF STAT1 NR4A3 NR4A1 NDP MICAL2 DP2 NKX2- 8 FOXK2 SF3B4 MTA2 DRD3 DAB2 LRP5 HNF4G PBX3 HOXD4 FOS UTF1 CTAG1B EIF4ENIF1 E2F4 POU5F1 MC1R IKBK G REM1 GPS2
<b>0.0167191</b>	32	1757	2.12913037	Neurogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0022008">http://amigo.geneontology.org/amigo/term/GO:0022008</a>	DVL2 SOX8 SYN1 CDH1 HMG20B TOP2B FGFR1 DLL3 SOX10 FA2H STK25 CDC20 DNMT3A PLXNC1 NKX2-8 ARHGDIA EFNA3 PAK1 FEZ1 PTPRO DRD3 NRG1 NBL1 TLX3 YWHAZ MAP1A PBX3 FPR2 EIF4ENIF1 DIO3 ADGRG1 EFNA4
<b>0.02074168</b>	30	1624	2.15953013	Generation of neurons	<a href="http://amigo.geneontology.org/amigo/term/GO:0048699">http://amigo.geneontology.org/amigo/term/GO:0048699</a>	DVL2 SOX8 SYN1 CDH1 HMG20B TOP2B FGFR1 DLL3 SOX10 STK25 CDC20 DNMT3A PLXNC1 NKX2-8 ARHGDIA EFNA3 PAK1 FEZ1 PTPRO DRD3 NRG1 NBL1 TLX3 YWHAZ MAP1A PBX3 EIF4ENIF1 DIO3 ADGRG1 EFNA4
<b>0.0457034</b>	32	1885	1.98455281	Cell-cell signaling	<a href="http://amigo.geneontology.org/amigo/term/GO:0007267">http://amigo.geneontology.org/amigo/term/GO:0007267</a>	DVL2 SYN1 CDH1 MAOB SOX10 SYNGR1 NTSR1 GRIN2D CRHR2 CDC20 NDP PSMB2 SYT5 EFNA3 PTPRO DRD3 DAB2 NRG1 LRP5 FABP5 MAP1A DLGAP1 ADRA1D GABRD GRK6 ADGRG1 POU5F1 EFNA4 S1PR2 G REM1 SLC6A3 SSTR3
<b>0.0457034</b>	33	1970	1.9582663	Positive regulation of macromolecule biosynthetic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0010557">http://amigo.geneontology.org/amigo/term/GO:0010557</a>	DVL2 SOX8 CDH1 SUPT16H SOX10 GMEB2 ELF4 HLF STAT1 NR4A3 NR4A1 NDP MICAL2 DP2 NKX2- 8 FOXK2 MTA2 DRD3 DAB2 LRP5 HNF4G PBX3 UPF3A HOXD4 FOS UTF1 CTAG1B E2F4 POU5F1 MC1R IKBK G REM1 GPS2
<b>0.05149687</b>	13	460	3.30376812	Pattern specification process	<a href="http://amigo.geneontology.org/amigo/term/GO:0007389">http://amigo.geneontology.org/amigo/term/GO:0007389</a>	DVL2 DLL3 MFNG KIF3B MICAL2 NBL1 LRP5 PBX3 HOXD4 TCAP ADGRG1 POU5F1 G REM1
<b>0.05823235</b>	9	243	4.3297246	Adenylate cyclase- modulating G protein-coupled	<a href="http://amigo.geneontology.org/amigo/term/GO:0007188">http://amigo.geneontology.org/amigo/term/GO:0007188</a>	CRHR2 DRD3 MC4R FPR2 ADRA1D GPR3 ADGRG1 MC1R S1PR2

				receptor signaling pathway		
<b>0.05823235</b>	15	606	2.89362782	Regulation of system process	<a href="http://amigo.geneontology.org/amigo/term/GO:0044057">http://amigo.geneontology.org/amigo/term/GO:0044057</a>	FXYD3 SOX10 NTSR1 GRIN2D NR4A3 PAK1 PTPRO DRD3 TLX3 FABP5 PBX3 KCNJ4 DLGAP1 ADRA1D S1PR2
<b>0.05823235</b>	19	897	2.47619701	Positive regulation of cell differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0045597">http://amigo.geneontology.org/amigo/term/GO:0045597</a>	SOX8 HMG20B FGFR1 SOX10 TESK1 STAT1 STK25 PLA2G5 PLXNC1 ARHGDIA PAK1 FEZ1 DAB2 NRG1 NBL1 LRP5 FOS S1PR2 GREM1
<b>0.05823235</b>	2	3	77.9350427	Norrin signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0110135">http://amigo.geneontology.org/amigo/term/GO:0110135</a>	NDP LRP5
<b>0.05919308</b>	7	149	5.49206677	Adenylate cyclase-activating G protein-coupled receptor signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0007189">http://amigo.geneontology.org/amigo/term/GO:0007189</a>	DRD3 MC4R ADRA1D GPR3 ADGRG1 MC1R S1PR2
<b>0.05919308</b>	5	68	8.59577677	Skeletal muscle cell differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0035914">http://amigo.geneontology.org/amigo/term/GO:0035914</a>	SOX8 HMG20B HLF NR4A1 FOS
<b>0.06600716</b>	26	1473	2.06345327	Neuron differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0030182">http://amigo.geneontology.org/amigo/term/GO:0030182</a>	DVL2 SOX8 SYN1 CDH1 HMG20B TOP2B FGFR1 STK25 CDC20 DNMT3A PLXNC1 NKX2-8 ARHGDIA EFNA3 PAK1 FEZ1 PTPRO NRG1 NBL1 TLX3 YWHAZ MAP1A PBX3 EIF4ENIF1 DIO3 EFNA4
<b>0.07222863</b>	2	4	58.4512821	Compartment pattern specification	<a href="http://amigo.geneontology.org/amigo/term/GO:0007386">http://amigo.geneontology.org/amigo/term/GO:0007386</a>	DLL3 PBX3
<b>0.07222863</b>	2	4	58.4512821	Golgi reassembly	<a href="http://amigo.geneontology.org/amigo/term/GO:0090168">http://amigo.geneontology.org/amigo/term/GO:0090168</a>	STK25 YWHAZ
<b>0.11965066</b>	29	1982	1.82844576	Locomotion	<a href="http://amigo.geneontology.org/amigo/term/GO:0040011">http://amigo.geneontology.org/amigo/term/GO:0040011</a>	SOX8 CDH1 TOP2B FGFR1 SOX10 TESK1 DUSP3 NR4A3 NR4A1 PLD2 PLXNC1 EFNA3 PAK1 MTA2 FEZ1 PTPRO DRD3 PSTPIP2 DAB2 NBL1 LRP5 TLX3 FPR2 XCR1 ITGBL1 ADGRG1 EFNA4 S1PR2 GREM1
<b>0.12320477</b>	3	22	15.9412587	Postsynaptic neurotransmitter receptor internalization	<a href="http://amigo.geneontology.org/amigo/term/GO:0098884">http://amigo.geneontology.org/amigo/term/GO:0098884</a>	DRD3 NRG1 MX2
<b>0.12320477</b>	3	22	15.9412587	Postsynaptic endocytosis	<a href="http://amigo.geneontology.org/amigo/term/GO:0140239">http://amigo.geneontology.org/amigo/term/GO:0140239</a>	DRD3 NRG1 MX2
<b>0.12433392</b>	28	1738	1.88335546	Regulation of cell differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0045595">http://amigo.geneontology.org/amigo/term/GO:0045595</a>	SOX8 HMG20B FGFR1 DLL3 SOX10 TESK1 STAT1 STK25 NR4A3 PSMB2 PLA2G5 DPF2 PLXNC1 ARHGDIA PAK1 FEZ1 DRD3 DAB2 NRG1 NBL1 LRP5 TLX3 FOS EIF4ENIF1 GP1BA S1PR2 GREM1 GPS2

<b>0.12515295</b>	10	352	3.32109557	Regionalization	<a href="http://amigo.geneontology.org/amigo/term/GO:0003002">http://amigo.geneontology.org/amigo/term/GO:0003002</a>	DVL2 DLL3 NBL1 LRP5 PBX3 HOXD4 TCAP ADGRG1 POU5F1 GREM1
<b>0.12515295</b>	3	23	15.2481605	Regulation of respiratory gaseous exchange	<a href="http://amigo.geneontology.org/amigo/term/GO:0043576">http://amigo.geneontology.org/amigo/term/GO:0043576</a>	NTSR1 TLX3 PBX3
<b>0.13878656</b>	24	1590	1.91161426	Cell migration	<a href="http://amigo.geneontology.org/amigo/term/GO:0016477">http://amigo.geneontology.org/amigo/term/GO:0016477</a>	SOX8 CDH1 TOP2B FGFR1 SOX10 TESK1 DUSP3 NR4A3 NR4A1 PLXNC1 PAK1 MTA2 PTPRO PSTPIP2 DAB2 NBL1 LRP5 TLX3 FPR2 XCR1 ITGBL1 ADGRG1 S1PR2 GREM1
<b>0.15727961</b>	3	27	12.9891738	DNA methylation-dependent heterochromatin assembly	<a href="http://amigo.geneontology.org/amigo/term/GO:0006346">http://amigo.geneontology.org/amigo/term/GO:0006346</a>	DNMT3A PPHLN1 POU5F1
<b>0.15727961</b>	6	149	4.7074858	Regulation of nervous system process	<a href="http://amigo.geneontology.org/amigo/term/GO:0031644">http://amigo.geneontology.org/amigo/term/GO:0031644</a>	SOX10 NTSR1 GRIN2D FABP5 DLGAP1 S1PR2
<b>0.15727961</b>	3	26	13.4887574	Regulation of osteoblast proliferation	<a href="http://amigo.geneontology.org/amigo/term/GO:0033688">http://amigo.geneontology.org/amigo/term/GO:0033688</a>	SOX8 LRP5 GREM1
<b>0.15727961</b>	3	26	13.4887574	Cell death in response to hydrogen peroxide	<a href="http://amigo.geneontology.org/amigo/term/GO:0036474">http://amigo.geneontology.org/amigo/term/GO:0036474</a>	STK25 NR4A3 PYCR1
<b>0.15727961</b>	2	8	29.225641	D-amino acid transport	<a href="http://amigo.geneontology.org/amigo/term/GO:0042940">http://amigo.geneontology.org/amigo/term/GO:0042940</a>	NTSR1 SFXN1
<b>0.15727961</b>	7	197	4.15389822	Regulation of neuron differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0045664">http://amigo.geneontology.org/amigo/term/GO:0045664</a>	SOX8 HMG20B FGFR1 FEZ1 NBL1 TLX3 EIF4ENIF1
<b>0.15727961</b>	5	102	5.73051785	Oligodendrocyte differentiation	<a href="http://amigo.geneontology.org/amigo/term/GO:0048709">http://amigo.geneontology.org/amigo/term/GO:0048709</a>	SOX8 SOX10 FA2H DRD3 NRG1
<b>0.15727961</b>	23	1373	1.95830952	Positive regulation of developmental process	<a href="http://amigo.geneontology.org/amigo/term/GO:0051094">http://amigo.geneontology.org/amigo/term/GO:0051094</a>	DVL2 SOX8 HMG20B FGFR1 SOX10 TESK1 STAT1 STK25 CDC20 PLA2G5 PLXNC1 ARHGDIA PAK1 FEZ1 DAB2 NRG1 NBL1 LRP5 FOS DIO3 POU5F1 S1PR2 GREM1
<b>0.15727961</b>	9	324	3.24729345	Negative regulation of cellular component movement	<a href="http://amigo.geneontology.org/amigo/term/GO:0051271">http://amigo.geneontology.org/amigo/term/GO:0051271</a>	CDH1 DUSP3 ARHGDIA PTPRO NRG1 NBL1 ADGRG1 S1PR2 GREM1
<b>0.15727961</b>	2	8	29.225641	Establishment of Golgi localization	<a href="http://amigo.geneontology.org/amigo/term/GO:0051683">http://amigo.geneontology.org/amigo/term/GO:0051683</a>	STK25 YWHAZ

<b>0.15727961</b>	2	8	29.225641	Negative regulation of monocyte chemotaxis	<a href="http://amigo.geneontology.org/amigo/term/GO:0090027">http://amigo.geneontology.org/amigo/term/GO:0090027</a>	NBL1 GREM1
<b>0.15727961</b>	16	815	2.29501966	Synaptic signaling	<a href="http://amigo.geneontology.org/amigo/term/GO:0099536">http://amigo.geneontology.org/amigo/term/GO:0099536</a>	SYN1 CDH1 SYNGR1 NTSR1 GRIN2D CRHR2 CDC20 SYT5 DRD3 NRG1 FABP5 MAP1A DLGAP1 GABRD S1PR2 SLC6A3
<b>0.15727961</b>	3	29	12.0933687	Neurotransmitter receptor internalization	<a href="http://amigo.geneontology.org/amigo/term/GO:0099590">http://amigo.geneontology.org/amigo/term/GO:0099590</a>	DRD3 NRG1 MX2
<b>0.15727961</b>	2	8	29.225641	Regulation of peptidyl-tyrosine autophosphorylation	<a href="http://amigo.geneontology.org/amigo/term/GO:1900084">http://amigo.geneontology.org/amigo/term/GO:1900084</a>	NRG1 GREM1
<b>0.15727961</b>	2	7	33.4007326	Positive regulation of peptidyl-tyrosine autophosphorylation	<a href="http://amigo.geneontology.org/amigo/term/GO:1900086">http://amigo.geneontology.org/amigo/term/GO:1900086</a>	NRG1 GREM1
<b>0.15727961</b>	2	8	29.225641	Peptidyl-tyrosine dephosphorylation involved in inactivation of protein kinase activity	<a href="http://amigo.geneontology.org/amigo/term/GO:1990264">http://amigo.geneontology.org/amigo/term/GO:1990264</a>	DUSP3 PTPRO
<b>0.18125483</b>	3	31	11.3131514	Cell proliferation	<a href="http://amigo.geneontology.org/amigo/term/GO:0033687">http://amigo.geneontology.org/amigo/term/GO:0033687</a>	SOX8 LRP5 GREM1
<b>0.1819118</b>	2	9	25.9783476	Positive regulation of peroxisome proliferator activated receptor signaling pathway	<a href="http://amigo.geneontology.org/amigo/term/GO:0035360">http://amigo.geneontology.org/amigo/term/GO:0035360</a>	FABP5 GPS2
<b>0.1819118</b>	26	1776	1.77723493	Cell motility	<a href="http://amigo.geneontology.org/amigo/term/GO:0048870">http://amigo.geneontology.org/amigo/term/GO:0048870</a>	SOX8 CDH1 TOP2B FGFR1 SOX10 TESK1 DUSP3 NR4A3 NR4A1 PLD2 PLXNC1 PAK1 MTA2 PTPRO PSTPIP2 DAB2 NBL1 LRP5 TLX3 FPR2 XCR1 ITGBL1 ADGRG1 S1PR2 GREM1 SLC6A3
<b>0.1819118</b>	27	1776	1.77723493	Localization of cell	<a href="http://amigo.geneontology.org/amigo/term/GO:0051674">http://amigo.geneontology.org/amigo/term/GO:0051674</a>	SOX8 CDH1 TOP2B FGFR1 SOX10 TESK1 DUSP3 NR4A3 NR4A1 PLD2 PLXNC1 ARHGDIA PAK1 MTA2 PTPRO PSTPIP2 DAB2 NRG1 NBL1 LRP5 TLX3 FPR2 XCR1 ITGBL1 ADGRG1 S1PR2 GREM1
<b>0.1819118</b>	11	471	2.7302085	Regulation of trans-synaptic signaling	<a href="http://amigo.geneontology.org/amigo/term/GO:0099177">http://amigo.geneontology.org/amigo/term/GO:0099177</a>	SYN1 CDH1 SYNGR1 GRIN2D CRHR2 CDC20 DRD3 FABP5 MAP1A DLGAP1 S1PR2

<b>0.19293439</b>	5	114	5.12730544	Phenol-containing compound metabolic process	<a href="http://amigo.geneontology.org/amigo/term/GO:0018958">http://amigo.geneontology.org/amigo/term/GO:0018958</a>	MAOB DRD3 CTSB DIO3 MC1R
<b>0.19293439</b>	2	10	23.3805128	Sequestering of BMP from receptor via BMP binding	<a href="http://amigo.geneontology.org/amigo/term/GO:0038098">http://amigo.geneontology.org/amigo/term/GO:0038098</a>	NBL1 GREM1
<b>0.19293439</b>	5	115	5.08272018	Regulation of receptor-mediated endocytosis	<a href="http://amigo.geneontology.org/amigo/term/GO:0048259">http://amigo.geneontology.org/amigo/term/GO:0048259</a>	AAK1 DRD3 DAB2 NRG1 GREM1
<b>0.19293439</b>	2	10	23.3805128	Determination of dorsal identity	<a href="http://amigo.geneontology.org/amigo/term/GO:0048263">http://amigo.geneontology.org/amigo/term/GO:0048263</a>	NBL1 GREM1
<b>0.19293439</b>	3	34	10.3149321	Arachidonic acid secretion	<a href="http://amigo.geneontology.org/amigo/term/GO:0050482">http://amigo.geneontology.org/amigo/term/GO:0050482</a>	NTSR1 PLA2G5 DRD3
<b>0.19293439</b>	4	69	6.77696024	Negative regulation of chemotaxis	<a href="http://amigo.geneontology.org/amigo/term/GO:0050922">http://amigo.geneontology.org/amigo/term/GO:0050922</a>	DUSP3 PTPRO NBL1 GREM1
<b>0.19293439</b>	15	776	2.25971451	Trans-synaptic signaling	<a href="http://amigo.geneontology.org/amigo/term/GO:0099537">http://amigo.geneontology.org/amigo/term/GO:0099537</a>	SYN1 CDH1 SYNGR1 NTSR1 GRIN2D CRHR2 CDC20 SYT5 DRD3 FABP5 MAP1A DLGAP1 GABRD S1PR2 SLC6A3
<b>0.19293439</b>	3	34	10.3149321	Arachidonate transport	<a href="http://amigo.geneontology.org/amigo/term/GO:1903963">http://amigo.geneontology.org/amigo/term/GO:1903963</a>	NTSR1 PLA2G5 DRD3
<b>0.19304155</b>	4	71	6.58605995	Respiratory gaseous exchange by respiratory system	<a href="http://amigo.geneontology.org/amigo/term/GO:0007585">http://amigo.geneontology.org/amigo/term/GO:0007585</a>	NTSR1 TLX3 YWHAZ PBX3
<b>0.19304155</b>	9	350	3.00606593	Negative regulation of locomotion	<a href="http://amigo.geneontology.org/amigo/term/GO:0040013">http://amigo.geneontology.org/amigo/term/GO:0040013</a>	CDH1 DUSP3 ARHGDIA PTPRO NRG1 NBL1 ADGRG1 S1PR2 GREM1
<b>0.19304155</b>	3	35	10.0202198	Regulation of monocyte chemotaxis	<a href="http://amigo.geneontology.org/amigo/term/GO:0090025">http://amigo.geneontology.org/amigo/term/GO:0090025</a>	NBL1 FPR2 GREM1
<b>0.19423342</b>	13	637	2.38576661	Endocytosis	<a href="http://amigo.geneontology.org/amigo/term/GO:0006897">http://amigo.geneontology.org/amigo/term/GO:0006897</a>	EPN3 LGALS3BP AAK1 PLA2G5 SYT5 DRD3 DAB2 NRG1 LRP5 FPR2 MX2 AP1G2 GREM1
<b>0.19423342</b>	11	490	2.62434328	Axonogenesis	<a href="http://amigo.geneontology.org/amigo/term/GO:0007409">http://amigo.geneontology.org/amigo/term/GO:0007409</a>	TOP2B STK25 PLXNC1 NKX2-8 ARHGDIA EFNA3 PAK1 FEZ1 PTPRO MAP1A EFNA4