

Appendix 1. Summary of the differentially expressed genes in the three comparison groups.

Fold change range	Gene symbols		
	PN8-O/PN8N	PN12-O/PN12-N	PN13-O/PN13-N
3.00~	<i>Ccdc88b</i>		<i>Rdx</i>
2.75~3.00 ^a	<i>Syt5, Dnmt3a</i>		1700027L20Rik, <i>Edn2</i>
2.50~2.75			<i>Syt5, Mt1</i>
2.25~2.50	<i>Mtap1b</i>		<i>Vegfa, Acta2, Hsd17b2, Vim, Adm, Rmcs2</i>
2.00~2.25	<i>4833418A01Rik, Chd4</i>	<i>Jam2</i>	<i>Mt2, Anxa2, Tagln2, Pgam1, Muc2, EglN1</i>
1.90~2.00		<i>Cryge</i>	<i>Gpi1, Higd1a</i>
1.80~1.90	<i>Scaper</i>	<i>Prdx2, Zfpml</i>	<i>Ddx5, EglN1, Ero1l, Pdk1, Hmox1</i>
1.70~1.80	<i>Mdm4^b, Mllt4, Ppm1b, Ankrd11</i>		<i>Bnip3, Lgals3, Mxi1, Pdlim1, Fos, Loxl2, MGI:107378, Col2a1, Triobp, Ddx5, Rras, Neurog2, Ak3ll, Tubb6</i>
1.60~1.70	<i>Nbeal2, Ccng1, Ppm1b, Eif4b, Cryge, Spp1, 40424, Eef2, Papola, Baz2b, Papola, S100a10, Prph, Atp2c1, Herc4, Rasa1</i>	<i>Per2, Mtap1b, Usp3</i>	<i>Anp32a, Rmcs2, Gpi1, Pdlim3, Ccl4, Ccl12, Eef2, Slc14a1, P4ha2, Ppm1b, EglN1, Tpi1, Rbp1, Hist1h1c</i>

1.50~1.60	<i>Rasa1, Eif4b, Arfgef1, 40424, Mdm4^b, Dars, Dnttip2, Eef2, Ddx5, Pgk1, B2m,</i> <i>Dpysl3, Api5, Eef2, Ipmk, Ccdc87, Pop4, Cryba2, 6530401N04Rik, Ppm1b, Bhlhb2, Hk2, Ankrd37, Sat1</i> <i>Arfgef1, Tram1, Sox19, Npepps, Mtap2, Herc4</i> <i>Trim35, Sox19</i>
0.60~0.67	<i>Idi1, Anxa2, Sdhc, Ccdc39, Higd1a, Tagln2, Mylk, Anxa6, Tpbg, Helz, Egfl7, Glul, Kcne11, Ankrd11, Vcam1, P2ry14,</i> <i>Bphl, Sparc, Map2k1, Pgk1 Sebox, Alpl, Dnahc9, Rgs11, Eef1a2, Sfxn5, Slc38a5</i> <i>Ocell, Hcls1, Slc40a1, Mylk, Eltd1,</i> <i>Tube1, Pltp, Wdr78, Dlg4, Cdh5, Ptrf,</i> <i>Eng, Anxa3, Xbp1</i>
0.50~0.60	<i>Heatr5b, Igfbp7, Ak3l1, Ddx5, Nxn11, Ankrd11, Pfk1, Gnat1, Ubr3, Rcvrn, Bgn, Chd4</i> <i>Ankrd37, Slc38a5, Pdlim3, Pdk1, Rdx, Vtn, Hk2, Drd4, Col4a2, Igfbp7, Cldn5,</i> <i>Grhpr Slc25a35, Vwf, Slc38a5, Prnd, Pde6a</i>
0.40~0.50	<i>Tpi1, Pgaml Col4a1, Cd34</i>
0.30~0.40	
0.20~0.30	<i>Vegfa</i>
~0.20	

Note: ^aThe fold range covers the lower end but not the upper end. ^bSome genes have more than one probes in the microarray, and each probe gave separate fold change, thus one single gene name might fall into different subgroups based on fold change, like the case of *Mdm4*.