Table S1. Dorsal enriched genes

Unigene ID	Gene title	Dorsal bud average	Ventral bud average	Fold enrichment in dorsal bud*
Xl.23623	Insulin II	1309.2	29.5	37.91
Xl.817	Insulin I	2320.0	57.5	37.12
Xl.1272	Prohormone convertase PC2	119.4	4.0	13.20
Xl.4241	Panza	532.7	40.2	11.78
Xl.6024	Glutamate carboxypeptidase-like protein 1	964.8	87.0	10.48
Xl.22766	MGC80496	46.6	1.6	7.11
Xl.647	Paired box gene 6 (Pax6)	33.9	1.1	5.52
Xl.15	Secretogranin III	31.3	1.1	5.17
Xl.23712	MGC84798	43.1	4.2	4.68
Xl.8836	Carboxypeptidase E	47.7	5.5	4.54
Xl.21888	Similar to complement component 6	97.0	19.5	3.97
Xl.8476	Carboxypeptidase E	71.2	16.5	3.30
Xl.1105	7B2 pituitary protein	21.6	1.6	3.29
Xl.330	Neurogenic differentiation 1 (NeuroD)	53.2	11.5	3.22
Xl.212	Frzb-1	164.0	47.0	3.16
Xl.932	Deoxyribonuclease I	507.5	159.9	3.08
Xl.1929	Frzb-1	66.1	18.0	2.87
Xl.6757	DEAH (Asp-Glu-Ala-His) box polypeptide 33	27.8	5.4	2.67
Xl.3378	Endod	503.4	184.3	2.66
Xl.647	Paired box gene 6 (Pax6)	21.3	3.1	2.64
Xl.14733	Insuloma-associated 1 (Insm1)	50.5	14.6	2.58
Xl.24557	MGC84299	17.3	1.8	2.56
Xl.25952	MGC68683	58.4	17.9	2.55
Xl.3011	Transcribed locus	209.2	77.0	2.55
Xl.13620	Transcribed locus	17.8	2.1	2.53
Xl.11047	Transcribed locus	95.0	32.8	2.51
Xl.15675	Similar to stromal cell derived factor receptor 2	266.7	101.9	2.50
Xl.17296	Transcribed locus	47.4	14.0	2.50
Xl.606	Collagen, type II, alpha 1	59.1	19.1	2.46
Xl.11165	Transcribed locus	51.3	16.0	2.45
Xl.637	Early growth response protein	69.8	23.6	2.44
Xl.5831	Similar to EH-domain containing 2	26.9	6.3	2.37
Xl.15742	Transcribed locus	25.7	5.8	2.37
Xl.10636	Transcribed locus	27.5	6.8	2.33
Xl.14367	Transcribed locus	139.6	56.3	2.28
Xl.6677	Cyclin E1	25.6	6.5	2.23
Xl.15089	Transcribed locus	364.3	158.6	2.23
Xl.6353	Glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)	342.8	151.0	2.20
Xl.647	Paired box gene 6 (Pax6)	18.3	3.4	2.17
Xl.12160	Trinucleotide repeat containing 4	23.0	5.6	2.16
Xl.198	Thrombospondin 3	49.1	17.8	2.15
Xl.24221	Transcribed locus	359.5	162.6	2.15
Xl.251	Dickkopf homolog 1	25.5	6.9	2.13
Xl.647	Paired box gene 6 (Pax6)	21.6	5.1	2.13
Xl.6690	LOC495431	58.3	22.4	2.13
Xl.12180	Putative growth hormone like protein-1	41.1	14.7	2.09
Xl.21515	C-fos proto-oncogene	19.5	4.5	2.05
Xl.15593	MGC82107	123.4	55.9	2.02
Xl.17442	Procollagen C-endopeptidase enhancer 2	31.2	10.5	2.01
Xl.26111	LOC100101272	11.4	0.7	2.01
Xl.24225	Transcribed locus	17.0	3.5	1.99
Xl.22355	Transcribed locus	246.5	119.2	1.99
Xl.684	Catenin arvcf-2ABC protein	38.4	14.8	1.94
Xl.24380	MGC68923	17.2	3.9	1.92
Xl.2466	MGC82199	166.1	81.4	1.92
Xl.986	Elav-type ribonucleoprotein (etr-1)	22.1	6.6	1.91
Xl.15089	Protocadherin PCNS	554.5	288.2	1.89
Xl.12488	Transcribed locus	12.2	1.5	1.88
Xl.23706	Transcribed locus	62.4	28.3	1.87
Xl.12129	Ftz-F1-related orphan receptor B	125.8	62.4	1.87
Xl.7523	Cdc25A	22.1	6.9	1.86
Xl.15089	Protocadherin PCNS	252.9	130.9	1.86
Xl.4042	MGC80644	20.9	6.2	1.86
Xl.24847	Transcribed locus	77.2	36.7	1.85
Xl.1040	Frizzled 10A	25.0	8.7	1.82
Xl.24545	Chromogranin A	25.9	9.6	1.78
Xl.11884	Cytoplasmic FMR1 interacting protein 2	18.5	5.4	1.77
Xl.14572	Transcribed locus	11.0	1.8	1.61

*Fold enrichment is adjusted to correct for unrealistically high ratios when denominator approaches zero. The ratio used to determine fold difference was VPB/(DPB+5).