Table S8. Pan-Ectodermal gene functions based on enrichment of Gene Ontology Biological Process Terms

Gene ontology term (gene count)	Enrichment	P.adjust
epithelial morphogenesis & development (104)		
epithelium development (36)	3.3	7.04E-07
tissue morphogenesis (32)	3.3	2.66E-06
tube development (32)	3.0	2.30E-05
gland development (26)	3.3	7.69E-05
morphogenesis of a branching structure (19)	3.8	3.26E-04
cell morphogenesis (32)	2.6	3.26E-04
regulation of cell morphogenesis (16)	4.1	7.43E-04
epithelial cell differentiation (18)	3.6	8.40E-04
morphogenesis of a polarized epithelium (6)	13.5	2.89E-03
epidermis development (17)	3.4	2.88E-03
cell morphogenesis involved in differentiation (21)	2.5	1.57E-02
regulation of morphogenesis of a branching structure (7)	7.0	1.61E-02
keratinocyte proliferation (5)	12.4	1.87E-02
morphogenesis of embryonic epithelium (11)	3.5	3.07E-02
odontogenesis (12)	6.6	1.86E-04
hair follicle development (10)	5.0	7.60E-03
neural development (66)		
regulation of nervous system development (21)	3.5	2.68E-04
neuron differentiation (36)	2.2	1.20E-03
cell projection organization (28)	2.2	1.05E-02
sensory organ development (24)	2.3	1.28E-02
other development (77)		
mesoderm development (10)	4.2	2.00E-02
embryonic morphogenesis (29)	2.0	2.22E-02
embryonic organ development (21)	2.2	4.41E-02
cell fate commitment (16)	2.7	2.62E-02
negative regulation of cell development (8)	5.0	2.85E-02
positive regulation of developmental process (20)	2.3	2.95E-02
vasculature development (22)	2.2	3.22E-02
other (76)		
sulfur metabolic process (12)	3.2	3.56E-02
phosphate metabolic process (54)	1.5	3.72E-02

Gene ontology term (gene count)	Enrichment	P.adjust
adhesion & motility (98)		
cell adhesion (65)	2.9	5.98E-11
cell-cell adhesion (32)	3.4	3.25E-06
regulation of cell adhesion (14)	3.7	5.66E-03
calcium-independent cell-cell adhesion (7)	7.6	1.09E-02
homophilic cell adhesion (15)	3.2	1.15E-02
cell motion (32)	2.2	5.17E-03
cell migration (22)	2.3	2.34E-02
extracellular structure organization (16)	2.7	2.81E-02
signaling (151)		
intracellular signaling cascade (72)	2.0	1.71E-05
regulation of kinase activity (21)	2.7	5.75E-03
enzyme linked receptor protein signaling pathway (26)	2.4	6.25E-03
cell-cell signaling (27)	2.3	6.32E-03
regulation of Ras protein signal transduction (19)	2.6	1.59E-02
negative regulation of signal transduction (18)	2.6	2.02E-02
establishment of planar polarity (4)	19.9	2.17E-02
regulation of phosphorylation (25)	2.1	2.30E-02
transmembrane receptor protein tyrosine kinase signaling pathway (19)	2.5	2.40E-02
positive regulation of catalytic activity (23)	2.2	2.64E-02
Wnt receptor signaling pathway, calcium modulating pathway (6)	7.5	2.84E-02
protein amino acid phosphorylation (43)	1.7	3.27E-02
negative regulation of cell communication (18)	2.4	3.55E-02
Wnt receptor signaling pathway (14)	2.7	5.04E-02
regulation of growth & proliferation (70)		
regulation of cell proliferation (48)	2.2	8.08E-05
negative regulation of cell differentiation (22)	3.0	1.25E-03
regulation of developmental growth (8)	5.4	2.13E-02
regulation of cell growth (12)	3.2	3.13E-02

547 of 858 pan-Ectodermal genes were associated with Biological Process GO terms. 310 were associated with enriched terms. Fold enrichment and P.adjust (P-value, with Benjamini adjustment for multiple testing) were determined using DAVID analysis. All enriched terms (p.adjust < 0.05) are reported here, after grouping by genes and eliminating redundant terms.