

Table S5. GO enrichment analysis of profile B by STEM (top 20)

Category ID	Category name	N _{cat}	N _{allo}	N _{exp}	N _{enr}	p-val	p-val _{Adj}	F
GO:0045177	Apical part of the cell	9	5	1.2	3.8	2.7x10 ⁻³	0.514	4.3
GO:0004872	Receptor activity	27	9	3.5	5.5	4.3x10 ⁻³	0.624	2.6
GO:0004888	Transmembrane signaling receptor activity	15	6	1.9	4.1	7.5x10 ⁻³	0.802	3.1
GO:0099600	Transmembrane receptor activity	15	6	1.9	4.1	7.5x10 ⁻³	0.802	3.1
GO:0005509	Calcium ion binding	13	5	1.7	3.3	0.02	0.956	3.0
GO:0043169	Cation binding	115	22	14.9	7.1	0.02	0.968	1.5
GO:0046872	Metal ion binding	115	22	14.9	7.1	0.02	0.968	1.5
GO:0001701	<i>In utero</i> embryonic development	19	6	2.5	3.5	0.03	0.982	2.4
GO:0098590	Plasma membrane region	19	6	2.5	3.5	0.03	0.982	2.4
GO:0031224	Intrinsic component of membrane	123	23	16	7	0.03	0.982	1.4
GO:0016021	Integral component of membrane	117	22	15.2	6.8	0.03	0.982	1.4
GO:0038023	Signaling receptor activity	21	6	2.7	3.3	0.04	0.99	2.2
GO:0043167	Ion binding	185	31	24	7	0.04	0.992	1.3
GO:0001503	Ossification	16	5	2.1	2.9	0.04	0.992	2.4
GO:0043410	Positive regulation of MAPK cascade	17	5	2.2	2.8	0.06	0.996	2.3
GO:0000165	MAPK cascade	29	7	3.8	3.2	0.07	0.998	1.9
GO:0023014	Signal transduction by protein phosphorylation	29	7	3.8	3.2	0.07	0.998	1.9
GO:0007166	Cell surface receptor signaling pathway	73	14	9.5	4.5	0.07	0.998	1.5
GO:0044425	Membrane part	152	25	19.7	5.3	0.09	1	1.3

N_{cat}, number of annotated genes to a GO category; N_{allo}, number of genes of a GO category that were allocated to Profile 42; N_{exp}, number of genes of a GO category expected to be assigned to this gene set [(Genes_In_Set)*(Genes_Category)/(Total_Unique_Genes)]; N_{enr}, difference between N_{allo} and N_{exp}; p-val, uncorrected probability of genes assigned vs expected; p-val_{Adj}, p-value corrected for multiple GO categories tested simultaneously; F, fold of enrichment (N_{allo}/N_{exp}).