

Supplementary Table 3. Web-based PANTHER biochemical pathway analysis of the 101 genes identified in the combined data from the pilot and validation datasets.

<u>GO Molecular function complete</u>	<u>H sapiens (20972)</u>	<u>Differential splicing FECD (101)</u>	<u>FECD (expected)</u>	<u>FECD (fold Enrichment)</u>	<u>Genes</u>	<u>P-value</u>
cell adhesion molecule binding (GO:0050839)	450	15	2.0	7.4	PPFIBP1, SPTAN1, GOLGA2, FN1, ITGA6, CADM1, SCRIB, NF2, MLLT4, MYO6, ABI1, NISCH, ERC1, CD46, FGFR1	5.4E-06
cytoskeletal protein binding (GO:0008092)	836	16	3.8	4.2	MICAL3, KIFC3, SPTAN1, GOLGA2, PLEKHM2, PIFO, KIF13A, NF2, ADD3, SORBS1, SYNE1, MYO6, ABI1, NUMA1, CLASP1, INF2	2.9E-03
GTPase binding (GO:0051020)	301	10	1.4	7.3	MICAL3, EXOC1, PIFO, RAPGEF6, CSDA, MLLT4, ERC1, GOLGA4, INF2, AKAP13	3.2E-03
<u>GO cellular component complete</u>						
cell-cell adherens junction (GO:0005913)	319	12	1.5	8.3	KIFC3, PPFIBP1, SPTAN1, GOLGA2, ITGA6, CADM1, SCRIB, SORBS1, MLLT4, MYO6, ABI1, ERC1	3.3E-05
adherens junction (GO:0005912) and anchoring junction (GO:0070161)	680	16	3.1	5.2	KIFC3, PPFIBP1, SPTAN1, GOLGA2, ITGA6, CADM1, SCRIB, NF2, SORBS1, MLLT4, MYO6, ABI1, ERC1, CLASP1, CD46, DCAF6	9.1E-05
cell cortex (GO:0005938)	242	9	1.1	8.2	EXOC1, SPTAN1, NF2, ADD3, MYO6, NUMA1, CLASP1, TRIP10, AKAP13	2.2E-03
Golgi apparatus (GO:0005794)	1471	19	6.7	2.9	KIFC3, GLT8D2, GOLGA2, PIFO, ACPL2, KIF13A, SYNE1, MYO6, ERC1, NUMA1, CLASP1, PLD1, GOLGA4, AKAP9, COPZ2, CD46, PPHLN1, TRIP10, HLA-DPA1	3.7E-02

GO biological process complete						
positive regulation of GTPase activity (GO:0043547)	631	15	2.9	5.3	SPTAN1, SOS1, ARHGEF10L, ITGA6, SCRIB, RAPGEF6, DENND4C, MLLT4, ARHGAP17, AGAP3, ARHGEF40, AKAP9, TRIP10, FGFR1, AKAP13	1.4E-03