Table S12

Category	Term	Number of genes	% of genes	p-value	Gene Symbols
GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	4	9.52381	0.003876	CHD7, FZD3, CELSR1, WNT9A
INTERPRO	IPR017981:GPCR, family 2-like	3	7.142857	0.006831	GPR123, FZD3, CELSR1
GOTERM_BP_FAT	GO:0042472~inner ear morphogenesis	3	7.142857	0.007764	CHD7, FZD3, CELSR1
GOTERM_BP_FAT	GO:0001736~establishment of planar polarity	2	4.761905	0.009897	FZD3, CELSR1
GOTERM_BP_FAT	GO:0042471~ear morphogenesis	3	7.142857	0.009899	CHD7, FZD3, CELSR1
GOTERM_BP_FAT	GO:0048568~embryonic organ development	4	9.52381	0.011773	CHD7, FZD3, CELSR1, WNT9A
GOTERM_BP_FAT	GO:0048839~inner ear development	3	7.142857	0.013103	CHD7, FZD3, CELSR1
GOTERM_BP_FAT	GO:0007164~establishment of tissue polarity	2	4.761905	0.01383	FZD3, CELSR1
GOTERM_BP_FAT	GO:0007423~sensory organ development	4	9.52381	0.01399	CHD7, MITF, FZD3, CELSR1
UP_SEQ_FEATURE	splice variant	17	40.47619	0.017456	SGCZ, RASEF, PIK3C2A, MITF, DQX1, ITGA3, NFIX, RICTOR, MEGF11, FLNA, PIGN, CHD7, DTNB, SLC39A8, SRGAP3, RAPGEFL1, DCAF15
GOTERM_BP_FAT	GO:0043583~ear development	3	7.142857	0.01798	CHD7, FZD3, CELSR1
GOTERM_BP_FAT	GO:0001738~morphogenesis of a polarized epithelium	2	4.761905	0.02165	FZD3, CELSR1
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	4	9.52381	0.02354	GBF1, SRGAP3, RICTOR, RAPGEFL1
GOTERM_BP_FAT	GO:0031532~actin cytoskeleton reorganization	2	4.761905	0.023595	RICTOR, FLNA
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	4	9.52381	0.024571	GBF1, SRGAP3, RICTOR, RAPGEFL1
GOTERM_MF_FAT	GO:0005085~guanyl-nucleotide exchange factor activity	3	7.142857	0.026417	GBF1, RICTOR, RAPGEFL1
KEGG_PATHWAY	mmu04916:Melanogenesis	3	7.142857	0.027241	MITF, FZD3, WNT9A
GOTERM_BP_FAT	GO:0016055~Wnt receptor signaling pathway	3	7.142857	0.027275	MITF, FZD3, WNT9A
GOTERM_BP_FAT	GO:0030318~melanocyte differentiation	2	4.761905	0.03134	MITF, HPS1
GOTERM_BP_FAT	GO:0050931~pigment cell differentiation	2	4.761905	0.033267	MITF, HPS1
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	4	9.52381	0.033472	CHD7, FZD3, CELSR1, WNT9A
SP_PIR_KEYWORDS	alternative splicing	16	38.09524	0.03582	RASEF, PIK3C2A, MITF, DQX1, ITGA3, NFIX, RICTOR, MEGF11, FLNA, PIGN, CHD7, DTNB, SLC39A8, SRGAP3, RAPGEFL1, DCAF15
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	3	7.142857	0.040355	ABCA2, CELSR1, FLNA
SP_PIR_KEYWORDS	phosphoprotein	20	47.61905	0.044746	PIK3C2A, RASEF, FILIP1, MEX3B, MITF, ABCA2, NFIX, ITGA3, CELSR1, RICTOR, FLNA, CUL5, CHD7, ELOVL5, WWP1, SLC39A8, SRGAP3, EIF3J, EIF2AK2, DCAF15
KEGG_PATHWAY	mmu05200:Pathways in cancer	4	9.52381	0.048565	MITF, FZD3, ITGA3, WNT9A
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	4	9.52381	0.049845	CHD7, FZD3, CELSR1, WNT9A