

HUGO	R	pval
ADAMTS12	0.325	6.39e-03
FRK		
<i>kinase,sign</i>	0.432	3.22e-05
<i>transd</i>		
MFN1	0.313	9.85e-03
<i>membrane</i>		
IPO9	0.430	3.49e-05
ADAM23		
<i>development,m</i>	0.313	9.82e-03
<i>embrane</i>		
CAMSAP2	0.425	4.79e-05
HECTD1	0.313	9.77e-03
PUM1	0.410	1.11e-04
PLEKHG6	0.410	1.14e-04
<i>sign transd</i>		
SUN1	0.407	1.36e-04
SH3PXD2B	0.400	2.01e-04
MAP3K4		
<i>kinase,sign</i>	0.399	2.08e-04
<i>transd</i>		
PLEKHA1	0.387	3.96e-04
<i>membrane</i>		
LRP6		
<i>development,m</i>	0.314	9.59e-03
<i>embrane</i>		
<i>,sign transd</i>		
ZNF704	0.384	4.63e-04
SHISA2	0.383	4.83e-04
FAM172A	0.314	9.40e-03
PRICKLE1	0.383	4.85e-04
<i>membrane</i>		
UBTD2	0.378	6.20e-04
SHANK1	0.378	6.39e-04
PRND	0.376	6.84e-04
<i>membrane</i>		
LRP4	0.371	8.92e-04
<i>membrane</i>		
PCLO	0.367	1.09e-03
<i>membrane</i>		
CNKSR3		
<i>membrane,sig</i>	0.315	9.20e-03
<i>n transd</i>		
LRRC17	0.315	9.20e-03
TULP3		
<i>membrane,sig</i>	0.315	9.20e-03
<i>n transd</i>		

B3GNT5		
<i>development,m</i>	0.315	9.17e-03
<i>embrane</i>		
VGLL4	0.365	1.16e-03
TOM1L1		
<i>membrane</i>	0.365	1.18e-03
TANC1	0.316	9.05e-03
ZC3HAV1L	0.316	9.05e-03
PPFIBP1		
<i>membrane</i>	0.361	1.40e-03
GALNT13		
<i>membrane</i>	0.360	1.44e-03
SERTAD4	0.360	1.47e-03
ACPP	0.360	1.48e-03
PSD3 <i>sign</i>		
<i>transd</i>	0.359	1.55e-03
MMP16		
<i>drugtarget,me</i>	0.358	1.58e-03
<i>mbrane</i>		
FZD7		
<i>development,m</i>		
<i>embrane</i>	0.358	1.59e-03
<i>,sign transd</i>		
KLHL42	0.358	1.61e-03
ACVR1		
<i>apoptosis,cell</i>		
<i>cycle</i>		
<i>,development,</i>		
<i>diff</i>	0.358	1.63e-03
<i>,drugtarget,kin</i>		
<i>ase</i>		
<i>,membrane,sig</i>		
<i>n transd</i>		
TACC2	0.356	1.73e-03
TFRC		
<i>membrane</i>	0.353	2.02e-03
ZRANB1	0.353	2.05e-03
PCYT1B		
<i>drugtarget</i>	0.350	2.26e-03
CNTN1		
<i>membrane,sig</i>	0.349	2.39e-03
<i>n transd</i>		
RASAL2 <i>sign</i>		
<i>transd</i>	0.319	8.08e-03
SHROOM4	0.349	2.40e-03
FZD6		
<i>development,m</i>		
<i>embrane</i>	0.347	2.59e-03

<i>,sign transd</i>		
DSTYK	0.319	7.96e-03
NHSL1	0.347	2.61e-03
SBF2		
<i>development,m</i>	0.319	7.84e-03
<i>embrane</i>		
RAET1L	0.345	2.91e-03
<i>membrane</i>		
IGFBP2	0.344	2.92e-03
DCUN1D1	0.342	3.20e-03
DIP2B	0.341	3.35e-03
PRICKLE2		
<i>membrane</i>	0.341	3.38e-03
CTTNBP2	0.340	3.51e-03
USP54	0.339	3.58e-03
DIRAS1		
<i>membrane,sig</i>	0.320	7.70e-03
<i>n transd</i>		
PLD1		
<i>drugtarget,me</i>		
<i>mbrane</i>	0.338	3.72e-03
<i>,sign transd</i>		
ITGAV		
<i>membrane,sig</i>	0.338	3.75e-03
<i>n transd</i>		
PCDH19	0.338	3.79e-03
<i>membrane</i>		
SERTAD4-		
AS1	0.336	4.03e-03
ATP8B1		
<i>membrane</i>	0.336	4.04e-03
CDS1		
<i>membrane,sig</i>	0.336	4.12e-03
<i>n transd</i>		
PTPRF		
<i>membrane,sig</i>	0.335	4.31e-03
<i>n transd</i>		
KIAA1715		
<i>development,m</i>	0.334	4.52e-03
<i>embrane</i>		
ULBP3	0.332	4.76e-03
<i>membrane</i>		
MTSS1L	0.321	7.28e-03
ITGB5		
<i>development,m</i>		
<i>embrane</i>	0.331	4.92e-03
<i>,sign transd</i>		

PRKG2		
<i>kinase,sign</i>	0.331	4.92e-03
<i>transd</i>		
PLEKHG1		
<i>sign transd</i>	0.331	4.92e-03
TMEM47		
<i>membrane</i>	0.331	4.94e-03
AKR1C2		
<i>drugtarget</i>	0.331	4.99e-03
CTDSPL2		
SC5D	0.330	5.11e-03
MFSD11	0.322	7.12e-03
ADGRA3	0.330	5.23e-03
FREM2	0.329	5.38e-03
<i>development,m</i>		
<i>embrane</i>	0.328	5.64e-03
APCDD1L		
<i>membrane</i>	0.328	5.67e-03
XKRX		
<i>membrane</i>	0.328	5.68e-03
GNAL		
<i>sign</i>		
<i>transd</i>	0.323	6.78e-03
ATP2B4		
<i>membrane</i>	0.327	5.91e-03
WNT5A		
<i>development,si</i>		
<i>gn transd</i>	0.323	6.76e-03
PLEKHA5		
SMO	0.327	5.99e-03
<i>apoptosis,deve</i>		
<i>lopment</i>		
<i>,diff,membran</i>		
<i>e</i>	0.324	6.60e-03
<i>,sign transd</i>		
KIAA1549L	0.326	6.04e-03
INPP5A		
<i>membrane</i>	0.326	6.22e-03
ZAK		
<i>apoptosis,cell</i>		
<i>cycle</i>	0.326	6.24e-03
<i>,diff,kinase</i>		
<i>,sign transd</i>		
LGR5		
<i>membrane,sig</i>		
<i>n transd</i>	0.324	6.48e-03

Set	R#	No of genes	P-value	Genes
<i>over-representation</i> Basal_cell_carcinoma	55	4	9.9e-10	, FZD6, FZD7,
<i>over-representation</i> Wnt_signaling_pathway	140	6	1.0e-08	, FZD6, FZD7,
<i>over-representation</i> Proteoglycans_in_cancer	200	6	6.6e-06	, FZD6, FZD7,
<i>over-representation</i> Signaling_pathways_regulating_pluripotency_of_stem_cells	141	4	9.1e-04	, ACVR1, FZD6, FZD7,
<i>over-representation</i> Glycerophospholipid_metabolism	94	3	3.3e-03	, CDS1, PCYT1B,
<i>over-representation</i> Melanogenesis	100	3	5.0e-03	, FZD6, FZD7,
<i>over-representation</i> Hedgehog_signaling_pathway	50	2	0.01	, SMO, WNT5A
<i>over-representation</i> Pathways_in_cancer	397	6	0.01	, FZD6, FZD7,
<i>over-representation</i> Cell_adhesion_molecules__CAMs__	139	3	0.03	, CNTN1, ITGAV,
<i>over-representation</i> Phagosome	150	3	0.04	, ITGAV, ITGB5,