

Category	Term
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### Enriched GO BP terms by genes over-expressed in Subtype II eMPM

GOTERM\_BP\_DIRECT GO:0009615~response to virus

GOTERM_BP_DIRECT	GO:0060337~type I interferon signaling pathway	7	3.888889	3.35E-05	RSAD2, MX	162	64	16792	11.33719	0.027956	0.014177	0.014177
GOTERM_BP_DIRECT	GO:0051607~defense response to virus	8	4.444444	0.001071	RSAD2, MX	162	165	16792	5.025664	0.595949	0.301909	0.301909
GOTERM_BP_DIRECT	GO:0034765~regulation of ion transmembrane transport	6	3.333333	0.004316	KCNH5, KC	162	111	16792	5.602936	0.97424	0.912756	0.912756
GOTERM_BP_DIRECT	GO:0006069~ethanol oxidation	3	1.666667	0.005661	ADH1B, AD	162	12	16792	25.91358	0.991794	0.957854	0.957854
GOTERM_BP_DIRECT	GO:0006813~potassium ion transport	5	2.777778	0.007978	SLC24A3, K	162	82	16792	6.320385	0.99886	1	1
GOTERM_BP_DIRECT	GO:0016042~lipid catabolic process	5	2.777778	0.009035	LIPF, RARR	162	85	16792	6.097313	0.999537	1	1
GOTERM_BP_DIRECT	GO:0072236~metanephric loop of Henle development	2	1.111111	0.019084	WNT7B, PC	162	2	16792	103.6543	1	1	1
GOTERM_BP_DIRECT	GO:0006898~receptor-mediated endocytosis	6	3.333333	0.033625	AMN, DME	162	186	16792	3.343688	1	1	1
GOTERM_BP_DIRECT	GO:0042391~regulation of membrane potential	4	2.222222	0.035368	KCNH5, KC	162	75	16792	5.52823	1	1	1
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	7	3.888889	0.035678	CRB1, VIPR	162	254	16792	2.856615	1	1	1
GOTERM_BP_DIRECT	GO:0014066~regulation of phosphatidylinositol 3-kinase s	4	2.222222	0.039037	BTC, FGF7	162	78	16792	5.315606	1	1	1
GOTERM_BP_DIRECT	GO:0042594~response to starvation	3	1.666667	0.044221	SSTR1, IPA	162	35	16792	8.884656	1	1	1
GOTERM_BP_DIRECT	GO:0051902~negative regulation of mitochondrial depola	2	1.111111	0.047034	HS2D, HSH	162	5	16792	41.46173	1	1	1
GOTERM_BP_DIRECT	GO:0038170~somatostatin signaling pathway	2	1.111111	0.047034	SSTR1, SST	162	5	16792	41.46173	1	1	1
GOTERM_BP_DIRECT	GO:0003081~regulation of systemic arterial blood pressur	2	1.111111	0.056174	ACE2, NOX	162	6	16792	34.55144	1	1	1
GOTERM_BP_DIRECT	GO:0001895~retina homeostasis	3	1.666667	0.056211	ARMS2, AL	162	40	16792	7.774074	1	1	1
GOTERM_BP_DIRECT	GO:0007190~activation of adenylate cyclase activity	3	1.666667	0.056211	VIPR2, CRH	162	40	16792	7.774074	1	1	1
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replicati	3	1.666667	0.056211	RSAD2, MX	162	40	16792	7.774074	1	1	1
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	11	6.111111	0.059086	LIPF, C15O	162	592	16792	1.926009	1	1	1
GOTERM_BP_DIRECT	GO:0006874~cellular calcium ion homeostasis	4	2.222222	0.060117	PKHD1, SL	162	93	16792	4.45825	1	1	1
GOTERM_BP_DIRECT	GO:0046854~phosphatidylinositol phosphorylation	4	2.222222	0.061679	BTC, FGF7	162	94	16792	4.410822	1	1	1
GOTERM_BP_DIRECT	GO:0008202~steroid metabolic process	3	1.666667	0.063887	HSD17B6, I	162	43	16792	7.231697	1	1	1
GOTERM_BP_DIRECT	GO:0007187~G-protein coupled receptor signaling pathwa	3	1.666667	0.071892	NPY1R, SS	162	46	16792	6.760064	1	1	1
GOTERM_BP_DIRECT	GO:0048513~animal organ development	2	1.111111	0.074193	NRG3, NRC	162	8	16792	25.91358	1	1	1
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	9	5	0.080103	PKHD1, BT	162	466	16792	2.001907	1	1	1
GOTERM_BP_DIRECT	GO:0035457~cellular response to interferon-alpha	2	1.111111	0.083074	IFIT3, IFIT2	162	9	16792	23.03429	1	1	1
GOTERM_BP_DIRECT	GO:0010579~positive regulation of adenylate cyclase acti	2	1.111111	0.083074	CRHR1, DR	162	9	16792	23.03429	1	1	1
GOTERM_BP_DIRECT	GO:0010389~regulation of G2/M transition of mitotic cell	2	1.111111	0.083074	KCNH5, CD	162	9	16792	23.03429	1	1	1
GOTERM_BP_DIRECT	GO:0010838~positive regulation of keratinocyte proliferat	2	1.111111	0.083074	TGM1, FG	162	9	16792	23.03429	1	1	1
GOTERM_BP_DIRECT	GO:0042359~vitamin D metabolic process	2	1.111111	0.09187	CYP24A1, C	162	10	16792	20.73086	1	1	1