ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
BP	GO:000269	regulation	153/905	470/18866	1.84E-86	9.93E-83	5.22E-83	AZGP1/B2M
BP	GO:000246	adaptive in	131/905	370/18866	6.38E-79	1.73E-75	9.07E-76	AZGP1/B2M
BP	GO:000244	lymphocyte	127/905	366/18866	3.14E-75	5.67E-72	2.98E-72	AZGP1/B2M
BP	GO:000269	positive reg	132/905	406/18866	3.45E-74	4.67E-71	2.45E-71	CD4/FCER1
BP	GO:005086	positive reg	133/905	421/18866	5.51E-73	5.96E-70	3.13E-70	CD4/FCER1
BP	GO:000242	immune re	135/905	481/18866	7.13E-67	5.51E-64	2.89E-64	CD4/FCER1
BP	GO:000275	immune re	135/905	481/18866	7.13E-67	5.51E-64	2.89E-64	CD4/FCER1
BP	GO:000181	positive reg	130/905	447/18866	2.13E-66	1.44E-63	7.56E-64	B2M/CD4/
BP	GO:005125	positive reg	116/905	357/18866	5.31E-65	3.19E-62	1.68E-62	CD4/HLA-A
BP	GO:000690	phagocytos	119/905	382/18866	2.19E-64	1.19E-61	6.23E-62	CALR/FCER
BP	GO:000283	regulation	121/905	409/18866	1.22E-62	5.98E-60	3.14E-60	FCER1G/HL
BP	GO:006032	cell chemo	106/905	311/18866	1.02E-61	4.59E-59	2.41E-59	CALR/FCER
BP	GO:000695	humoral im	115/905	377/18866	4.40E-61	1.83E-58	9.61E-59	HLA-A/HLA
BP	GO:004211	T cell activa	125/905	483/18866	2.19E-57	8.47E-55	4.45E-55	B2M/CD1C
BP	GO:000223	response to	108/905	356/18866	4.70E-57	1.69E-54	8.90E-55	B2M/ICAM
BP	GO:004274	defense res	106/905	348/18866	3.49E-56	1.18E-53	6.20E-54	CD4/FCER1
BP	GO:003249	response to	103/905	334/18866	3.66E-55	1.11E-52	5.86E-53	ICAM1/LTA
BP	GO:003134	positive reg	110/905	385/18866	3.71E-55	1.11E-52	5.86E-53	FCER1G/HL
BP	GO:003059	leukocyte c	85/905	232/18866	2.00E-52	5.70E-50	2.99E-50	CALR/FCER
BP	GO:000961	response to	100/905	349/18866	3.07E-50	8.31E-48	4.37E-48	IFNG/MICA
BP	GO:005085	antigen rec	95/905	325/18866	1.44E-48	3.70E-46	1.95E-46	CD4/HLA-A
BP	GO:009752	myeloid leu	79/905	222/18866	1.23E-47	3.03E-45	1.59E-45	FCER1G/CX
BP	GO:005160	defense res	84/905	258/18866	4.28E-47	1.01E-44	5.28E-45	IFNG/MICA
BP	GO:003809	Fc receptor	81/905	241/18866	1.25E-46	2.81E-44	1.47E-44	FCER1G/HS
BP	GO:000715	leukocyte c	98/905	364/18866	1.49E-46	3.23E-44	1.70E-44	CD4/HLA-A
BP	GO:002240	regulation	106/905	439/18866	1.89E-45	3.94E-43	2.07E-43	CD4/HLA-A
BP	GO:001972	B cell medi	78/905	230/18866	2.99E-45	5.99E-43	3.15E-43	FCER1G/HL
BP	GO:190303	regulation	92/905	329/18866	3.14E-45	6.06E-43	3.18E-43	CD4/HLA-A
BP	GO:004578	positive reg	104/905	428/18866	7.31E-45	1.36E-42	7.16E-43	CALR/CD4/
BP	GO:005092	regulation	77/905	229/18866	2.28E-44	4.12E-42	2.16E-42	CALR/CXCL
BP	GO:004508	regulation	88/905	307/18866	3.10E-44	5.41E-42	2.84E-42	FCER1G/HL
BP	GO:001606	immunoglo	76/905	227/18866	1.21E-43	2.04E-41	1.07E-41	FCER1G/HL
BP	GO:007066	leukocyte p	88/905	313/18866	1.75E-43	2.88E-41	1.51E-41	CD4/HLA-A
BP	GO:007121	cellular res	78/905	246/18866	8.28E-43	1.32E-40	6.92E-41	HSPA5/ICA
BP	GO:003461	response to	88/905	320/18866	1.25E-42	1.93E-40	1.02E-40	ICAM1/LTA
BP	GO:007135	cellular res	84/905	297/18866	9.65E-42	1.45E-39	7.62E-40	ICAM1/LTA
BP	GO:190370	regulation	108/905	498/18866	1.46E-41	2.13E-39	1.12E-39	B2M/CD4/
BP	GO:000268	negative re	104/905	463/18866	1.72E-41	2.44E-39	1.28E-39	FCER1G/HL
BP	GO:005086	regulation	88/905	332/18866	3.18E-41	4.41E-39	2.32E-39	CD4/HLA-A
BP	GO:002240	positive reg	81/905	279/18866	3.32E-41	4.48E-39	2.36E-39	CD4/HLA-A
BP	GO:005072	regulation	99/905	425/18866	5.73E-41	7.56E-39	3.97E-39	FCER1G/IFI
BP	GO:004211	B cell activa	87/905	328/18866	8.74E-41	1.13E-38	5.91E-39	TGFB1/TFR
BP	GO:007122	cellular res	70/905	208/18866	2.02E-40	2.54E-38	1.33E-38	ICAM1/CXC
BP	GO:190303	positive reg	74/905	235/18866	2.08E-40	2.55E-38	1.34E-38	CD4/HLA-A
BP	GO:007121	cellular res	72/905	222/18866	2.58E-40	3.11E-38	1.63E-38	ICAM1/CXC
BP	GO:003809	Fc-gamma	59/905	142/18866	2.73E-40	3.21E-38	1.69E-38	FCER1G/HS
BP	GO:001821	peptidyl-ty	92/905	377/18866	7.41E-40	8.52E-38	4.48E-38	CD4/ICAM1
BP	GO:007066	regulation	74/905	240/18866	1.07E-39	1.20E-37	6.32E-38	CD4/HLA-A
BP	GO:000243	Fc receptor	59/905	145/18866	1.16E-39	1.28E-37	6.72E-38	FCER1G/HS

BP	GO:003809	Fc-epsilon	63/905	169/18866	1.52E-39	1.64E-37	8.61E-38	FCER1G/PS
BP	GO:001810	peptidyl-ty	91/905	374/18866	2.58E-39	2.74E-37	1.44E-37	CD4/ICAM1
BP	GO:000283	positive re	74/905	251/18866	3.34E-38	3.47E-36	1.82E-36	FCER1G/HL
BP	GO:000268	regulation	68/905	212/18866	9.09E-38	9.27E-36	4.87E-36	CALR/ICAM
BP	GO:000245	humoral in	59/905	155/18866	1.07E-37	1.07E-35	5.63E-36	HLA-DQB1,
BP	GO:007162	granulocyt	54/905	127/18866	1.34E-37	1.32E-35	6.93E-36	FCER1G/CX
BP	GO:005092	positive re	57/905	144/18866	1.47E-37	1.42E-35	7.46E-36	CALR/CXCL
BP	GO:000281	regulation	61/905	168/18866	1.54E-37	1.46E-35	7.69E-36	AZGP1/B2M
BP	GO:000243	immune re	56/905	139/18866	2.05E-37	1.88E-35	9.89E-36	HSP90AA1,
BP	GO:003809	Fc-gamma	56/905	139/18866	2.05E-37	1.88E-35	9.89E-36	HSP90AA1,
BP	GO:004665	lymphocyt	77/905	283/18866	5.30E-37	4.77E-35	2.51E-35	CD4/HLA-A
BP	GO:003294	mononucle	77/905	286/18866	1.19E-36	1.06E-34	5.55E-35	CD4/HLA-A
BP	GO:005087	positive re	67/905	214/18866	1.76E-36	1.54E-34	8.08E-35	CD4/HLA-A
BP	GO:009753	granulocyt	57/905	150/18866	2.10E-36	1.80E-34	9.47E-35	FCER1G/CX
BP	GO:003434	response t	65/905	202/18866	3.11E-36	2.62E-34	1.38E-34	B2M/HLA-A
BP	GO:000695	compleme	55/905	141/18866	7.12E-36	5.92E-34	3.11E-34	IGHE/IGHG
BP	GO:000695	compleme	61/905	178/18866	7.47E-36	6.12E-34	3.22E-34	IL1B/CD19,
BP	GO:003009	lymphocyt	86/905	368/18866	9.74E-36	7.87E-34	4.13E-34	B2M/CD4/
BP	GO:003320	tumor necr	60/905	173/18866	1.28E-35	1.01E-33	5.33E-34	LTA/PSMB8
BP	GO:005086	regulation	63/905	195/18866	2.90E-35	2.28E-33	1.20E-33	TGFB1/TFR
BP	GO:007037	ERK1 and E	80/905	325/18866	5.27E-35	4.07E-33	2.14E-33	CD4/ICAM1
BP	GO:000292	regulation	53/905	134/18866	5.65E-35	4.31E-33	2.26E-33	LTA/CXCL1
BP	GO:005067	regulation	66/905	219/18866	8.30E-35	6.24E-33	3.28E-33	CD4/HLA-A
BP	GO:007009	chemokine	44/905	88/18866	1.17E-34	8.65E-33	4.54E-33	CXCL8/CXC
BP	GO:003294	regulation	66/905	221/18866	1.55E-34	1.13E-32	5.93E-33	CD4/HLA-A
BP	GO:000244	production	77/905	306/18866	1.99E-34	1.43E-32	7.54E-33	B2M/FCER
BP	GO:007037	positive re	65/905	215/18866	2.19E-34	1.56E-32	8.20E-33	CD4/ICAM1
BP	GO:006033	type I inter	45/905	95/18866	4.39E-34	3.05E-32	1.60E-32	HLA-A/HLA
BP	GO:007135	cellular res	45/905	95/18866	4.39E-34	3.05E-32	1.60E-32	HLA-A/HLA
BP	GO:000282	regulation	55/905	153/18866	1.12E-33	7.66E-32	4.03E-32	AZGP1/B2M
BP	GO:199086	response t	45/905	97/18866	1.41E-33	9.40E-32	4.94E-32	CXCL8/CXC
BP	GO:199086	cellular res	45/905	97/18866	1.41E-33	9.40E-32	4.94E-32	CXCL8/CXC
BP	GO:007037	regulation	76/905	306/18866	1.43E-33	9.43E-32	4.95E-32	CD4/ICAM1
BP	GO:000268	positive re	53/905	142/18866	1.86E-33	1.21E-31	6.38E-32	CALR/ICAM
BP	GO:003434	response t	45/905	99/18866	4.35E-33	2.80E-31	1.47E-31	HLA-A/HLA
BP	GO:000270	regulation	63/905	211/18866	5.30E-33	3.37E-31	1.77E-31	AZGP1/B2M
BP	GO:190210	regulation	73/905	290/18866	1.09E-32	6.88E-31	3.62E-31	CD4/HLA-B
BP	GO:000181	negative re	81/905	360/18866	1.94E-32	1.21E-30	6.34E-31	HLA-F/HSP
BP	GO:007134	cellular res	58/905	182/18866	3.56E-32	2.19E-30	1.15E-30	B2M/HLA-A
BP	GO:003044	regulation	47/905	115/18866	6.48E-32	3.89E-30	2.05E-30	IL1B/CD19,
BP	GO:003260	interferon-	47/905	115/18866	6.48E-32	3.89E-30	2.05E-30	HLA-A/LTA
BP	GO:005085	B cell recep	50/905	135/18866	1.95E-31	1.16E-29	6.09E-30	CD79A/BTK
BP	GO:007055	response t	61/905	211/18866	4.15E-31	2.44E-29	1.28E-29	ICAM1/PSM
BP	GO:007167	mononucle	43/905	97/18866	4.23E-31	2.46E-29	1.29E-29	CXCL10/CX
BP	GO:003059	neutrophil	44/905	103/18866	6.01E-31	3.46E-29	1.82E-29	FCER1G/CX
BP	GO:003210	negative re	87/905	433/18866	6.71E-31	3.82E-29	2.01E-29	HLA-A/HLA
BP	GO:005073	regulation	67/905	263/18866	2.08E-30	1.17E-28	6.17E-29	CD4/ICAM1
BP	GO:000691	phagocytos	47/905	126/18866	8.80E-30	4.91E-28	2.58E-28	FCER1G/F2
BP	GO:000689	receptor-m	74/905	328/18866	8.90E-30	4.91E-28	2.58E-28	B2M/CALR,
BP	GO:000269	positive re	61/905	223/18866	1.25E-29	6.84E-28	3.59E-28	AZGP1/B2M

BP	GO:199026	neutrophil	46/905	122/18866	2.05E-29	1.10E-27	5.78E-28	FCER1G/CX
BP	GO:004209	T cell prolif	57/905	195/18866	2.05E-29	1.10E-27	5.78E-28	CD4/HLA-A
BP	GO:000270	regulation	51/905	154/18866	2.50E-29	1.33E-27	6.97E-28	AZGP1/B2M
BP	GO:000268	regulation	46/905	124/18866	4.75E-29	2.49E-27	1.31E-27	CALR/CXCL
BP	GO:004508	positive reg	59/905	213/18866	5.18E-29	2.69E-27	1.41E-27	FCER1G/HL
BP	GO:007066	positive reg	50/905	150/18866	6.30E-29	3.24E-27	1.70E-27	CD4/HLA-A
BP	GO:000269	positive reg	41/905	96/18866	6.48E-29	3.31E-27	1.74E-27	CALR/CXCL
BP	GO:000724	I-kappaB ki	68/905	286/18866	6.89E-29	3.48E-27	1.83E-27	CD4/RELB/
BP	GO:005077	negative re	51/905	159/18866	1.42E-28	7.04E-27	3.70E-27	HLA-A/HLA
BP	GO:005109	positive reg	51/905	159/18866	1.42E-28	7.04E-27	3.70E-27	ICAM1/S10
BP	GO:004212	regulation	52/905	167/18866	2.09E-28	1.03E-26	5.39E-27	CD4/HLA-A
BP	GO:009902	plasma me	47/905	135/18866	3.19E-28	1.55E-26	8.17E-27	FCER1G/F2
BP	GO:005189	positive reg	53/905	178/18866	7.31E-28	3.53E-26	1.86E-26	HSP90AA1/
BP	GO:005087	positive reg	49/905	151/18866	9.23E-28	4.42E-26	2.32E-26	TGFB1/TFR
BP	GO:003264	regulation	41/905	104/18866	2.99E-27	1.42E-25	7.44E-26	HLA-A/LTA/
BP	GO:004349	protein kin	65/905	278/18866	3.30E-27	1.55E-25	8.17E-26	HLA-G/HSP
BP	GO:009719	extrinsic ap	59/905	230/18866	4.57E-27	2.13E-25	1.12E-25	PDIA3/ICAM
BP	GO:005067	positive reg	46/905	136/18866	5.07E-27	2.35E-25	1.23E-25	CD4/HLA-A
BP	GO:001032	membrane	47/905	143/18866	5.92E-27	2.71E-25	1.43E-25	FCER1G/F2
BP	GO:005507	calcium ion	85/905	468/18866	6.04E-27	2.74E-25	1.44E-25	CALR/CD4/
BP	GO:003294	positive reg	46/905	137/18866	7.30E-27	3.29E-25	1.73E-25	CD4/HLA-A
BP	GO:000222	pattern rec	55/905	201/18866	7.95E-27	3.55E-25	1.87E-25	CTSB/CTSL/
BP	GO:004312	regulation	61/905	252/18866	1.82E-26	8.08E-25	4.24E-25	CD4/S100B
BP	GO:000687	cellular cal	83/905	456/18866	2.15E-26	9.45E-25	4.97E-25	CALR/CD4/
BP	GO:007134	cellular res	52/905	183/18866	2.79E-26	1.22E-24	6.40E-25	ICAM1/PSM
BP	GO:004340	regulation	71/905	342/18866	2.97E-26	1.28E-24	6.75E-25	TGFB1/IL1B
BP	GO:000245	T cell medi	40/905	104/18866	3.97E-26	1.70E-24	8.96E-25	AZGP1/B2M
BP	GO:007250	cellular div	86/905	492/18866	4.84E-26	2.06E-24	1.08E-24	CALR/CD4/
BP	GO:000691	phagocytos	37/905	88/18866	6.43E-26	2.72E-24	1.43E-24	IGHE/IGHG
BP	GO:000190	cell killing	50/905	172/18866	8.13E-26	3.41E-24	1.79E-24	AZGP1/B2M
BP	GO:005109	regulation	82/905	455/18866	8.79E-26	3.66E-24	1.92E-24	ICAM1/PSM
BP	GO:005073	positive reg	53/905	195/18866	9.77E-26	4.03E-24	2.12E-24	CD4/ICAM1
BP	GO:000222	toll-like rec	47/905	152/18866	1.22E-25	5.01E-24	2.63E-24	CTSB/CTSL/
BP	GO:005085	T cell recep	54/905	206/18866	2.31E-25	9.41E-24	4.95E-24	CD4/HLA-A
BP	GO:003261	interleukin	42/905	121/18866	2.73E-25	1.10E-23	5.79E-24	MR1/IFNG/
BP	GO:005067	epithelial c	81/905	453/18866	3.05E-25	1.22E-23	6.42E-24	B2M/CXCL1
BP	GO:000282	positive reg	40/905	110/18866	4.92E-25	1.96E-23	1.03E-23	AZGP1/B2M
BP	GO:000236	cytokine pr	39/905	104/18866	5.07E-25	2.00E-23	1.05E-23	B2M/FCER
BP	GO:000720	positive reg	67/905	322/18866	6.92E-25	2.71E-23	1.42E-23	CD4/CXCL1
BP	GO:003021	T cell differ	59/905	253/18866	9.98E-25	3.88E-23	2.04E-23	B2M/CD4/
BP	GO:004340	positive reg	60/905	264/18866	1.68E-24	6.51E-23	3.42E-23	TGFB1/IL1B
BP	GO:005067	regulation	74/905	395/18866	2.06E-24	7.89E-23	4.15E-23	B2M/CXCL1
BP	GO:000190	leukocyte m	39/905	108/18866	2.61E-24	9.96E-23	5.23E-23	AZGP1/B2M
BP	GO:007099	neuron dea	70/905	360/18866	3.97E-24	1.50E-22	7.90E-23	HLA-F/HSP
BP	GO:005109	positive reg	60/905	270/18866	5.88E-24	2.21E-22	1.16E-22	ICAM1/S10
BP	GO:005189	regulation	58/905	253/18866	6.36E-24	2.37E-22	1.25E-22	HLA-G/HSP
BP	GO:005072	positive reg	46/905	158/18866	7.06E-24	2.61E-22	1.37E-22	FCER1G/IF
BP	GO:000270	regulation	44/905	144/18866	7.63E-24	2.81E-22	1.48E-22	B2M/FCER
BP	GO:000282	positive reg	38/905	105/18866	9.29E-24	3.39E-22	1.78E-22	AZGP1/B2M
BP	GO:000254	monocyte c	31/905	67/18866	1.79E-23	6.49E-22	3.41E-22	CXCL10/CX

BP	GO:00421	positive re	37/905	101/18866	2.20E-23	7.93E-22	4.17E-22	CD4/HLA-
BP	GO:00300	myeloid ce	76/905	431/18866	2.41E-23	8.63E-22	4.54E-22	B2M/CD4/
BP	GO:00607	regulation	50/905	196/18866	5.42E-23	1.93E-21	1.01E-21	HSP90AB1/
BP	GO:00425	antigen pr	33/905	80/18866	6.20E-23	2.18E-21	1.15E-21	B2M/CALR
BP	GO:00514	regulation	68/905	357/18866	6.21E-23	2.18E-21	1.15E-21	CD4/CXCL1
BP	GO:00313	regulation	35/905	92/18866	7.82E-23	2.73E-21	1.43E-21	AZGP1/B2
BP	GO:00326	regulation	45/905	159/18866	7.97E-23	2.76E-21	1.45E-21	FCER1G/H
BP	GO:00027	positive re	42/905	138/18866	9.65E-23	3.32E-21	1.75E-21	AZGP1/B2
BP	GO:00024	antigen pr	36/905	99/18866	1.17E-22	4.00E-21	2.10E-21	AZGP1/B2
BP	GO:00326	interleukin	37/905	106/18866	1.58E-22	5.36E-21	2.82E-21	MR1/IFNG/
BP	GO:00326	interleukin	46/905	170/18866	2.09E-22	7.06E-21	3.71E-21	FCER1G/H
BP	GO:00025	myeloid le	51/905	210/18866	2.22E-22	7.47E-21	3.92E-21	CD4/FCER1
BP	GO:00704	response t	71/905	396/18866	2.66E-22	8.88E-21	4.67E-21	ICAM1/LT
BP	GO:00016	response t	67/905	359/18866	4.26E-22	1.41E-20	7.43E-21	ICAM1/LT
BP	GO:19012	regulation	63/905	321/18866	4.88E-22	1.61E-20	8.46E-21	HLA-F/HSP
BP	GO:00362	response t	68/905	371/18866	5.92E-22	1.94E-20	1.02E-20	ICAM1/LT
BP	GO:00603	interferon-	34/905	91/18866	6.43E-22	2.09E-20	1.10E-20	B2M/HLA-
BP	GO:00019	regulation	47/905	183/18866	8.07E-22	2.61E-20	1.37E-20	HSP90AB1/
BP	GO:00485	negative re	36/905	104/18866	8.19E-22	2.64E-20	1.39E-20	SLPI/APOB
BP	GO:00199	second-me	76/905	456/18866	8.51E-22	2.72E-20	1.43E-20	CD4/CXCL
BP	GO:00026	negative re	39/905	124/18866	8.66E-22	2.75E-20	1.45E-20	HLA-A/HLA
BP	GO:00719	positive re	65/905	345/18866	1.07E-21	3.37E-20	1.77E-20	HSP90AB1/
BP	GO:00019	regulation	31/905	75/18866	1.18E-21	3.68E-20	1.93E-20	AZGP1/B2
BP	GO:00024	antigen pr	31/905	75/18866	1.18E-21	3.68E-20	1.93E-20	B2M/CALR
BP	GO:00324	regulation	39/905	125/18866	1.20E-21	3.73E-20	1.96E-20	RELB/TLR2
BP	GO:00512	negative re	43/905	154/18866	1.30E-21	4.02E-20	2.11E-20	HLA-F/HLA
BP	GO:00506	positive re	50/905	211/18866	1.86E-21	5.70E-20	3.00E-20	CXCL12/M
BP	GO:19035	regulation	37/905	113/18866	2.02E-21	6.16E-20	3.24E-20	FCER1G/IF
BP	GO:00022	lymphocyt	47/905	187/18866	2.16E-21	6.57E-20	3.45E-20	CD1C/FCE
BP	GO:00326	type I inter	39/905	127/18866	2.29E-21	6.92E-20	3.64E-20	RELB/TLR2
BP	GO:19037	positive re	49/905	204/18866	2.51E-21	7.56E-20	3.97E-20	CD4/HLA-
BP	GO:00431	positive re	47/905	188/18866	2.75E-21	8.22E-20	4.32E-20	CD4/S100
BP	GO:00027	regulation	32/905	83/18866	3.37E-21	1.00E-19	5.27E-20	B2M/FCER
BP	GO:00439	regulation	52/905	231/18866	3.49E-21	1.03E-19	5.42E-20	CD4/SLPI/
BP	GO:00456	regulation	46/905	181/18866	3.54E-21	1.04E-19	5.46E-20	HLA-G/IFN
BP	GO:00313	negative re	56/905	269/18866	5.49E-21	1.61E-19	8.44E-20	HLA-A/HLA
BP	GO:00197	antimicrob	40/905	137/18866	5.60E-21	1.63E-19	8.55E-20	HLA-A/CXC
BP	GO:00026	negative re	46/905	184/18866	7.35E-21	2.13E-19	1.12E-19	HLA-F/HLA
BP	GO:00726	lymphocyt	37/905	117/18866	7.87E-21	2.26E-19	1.19E-19	ICAM1/CX
BP	GO:00326	regulation	36/905	111/18866	1.02E-20	2.91E-19	1.53E-19	IFNG/ORM
BP	GO:00071	negative re	59/905	301/18866	1.12E-20	3.17E-19	1.67E-19	HLA-G/CXC
BP	GO:20012	regulation	43/905	162/18866	1.13E-20	3.21E-19	1.69E-19	PDIA3/ICA
BP	GO:19039	negative re	32/905	86/18866	1.21E-20	3.42E-19	1.79E-19	SLPI/APOB
BP	GO:00321	activation	62/905	331/18866	1.31E-20	3.66E-19	1.92E-19	IL1B/TNF/
BP	GO:20012	regulation	70/905	413/18866	1.43E-20	3.99E-19	2.10E-19	PDIA3/ICA
BP	GO:00717	tumor nec	37/905	119/18866	1.52E-20	4.21E-19	2.21E-19	FCER1G/IF
BP	GO:00027	positive re	35/905	106/18866	1.80E-20	4.98E-19	2.61E-19	AZGP1/B2
BP	GO:00140	positive re	32/905	88/18866	2.75E-20	7.51E-19	3.95E-19	TNF/F2R/C
BP	GO:00327	positive re	32/905	88/18866	2.75E-20	7.51E-19	3.95E-19	FCER1G/IF
BP	GO:00508	negative re	48/905	207/18866	3.19E-20	8.66E-19	4.55E-19	HLA-F/HLA

BP	GO:003265	regulation	26/905	55/18866	3.37E-20	9.12E-19	4.79E-19	HLA-B/HLA
BP	GO:003268	regulation	35/905	110/18866	7.13E-20	1.92E-18	1.01E-18	FCER1G/TL
BP	GO:005076	regulation	33/905	97/18866	7.77E-20	2.08E-18	1.09E-18	CALR/FCER
BP	GO:000270	regulation	29/905	73/18866	9.14E-20	2.43E-18	1.28E-18	AZGP1/B2M
BP	GO:200011	regulation	51/905	239/18866	1.03E-19	2.73E-18	1.44E-18	S100A9/S1
BP	GO:003261	interleukin	26/905	57/18866	1.06E-19	2.79E-18	1.46E-18	HLA-B/HLA
BP	GO:001988	antigen pro	50/905	232/18866	1.51E-19	3.97E-18	2.09E-18	AZGP1/B2M
BP	GO:004331	neutrophil	75/905	487/18866	1.90E-19	4.96E-18	2.61E-18	B2M/CTSB/
BP	GO:009769	receptor sig	43/905	174/18866	2.25E-19	5.84E-18	3.07E-18	IFNG/IFNL1
BP	GO:000228	neutrophil	75/905	490/18866	2.73E-19	7.06E-18	3.71E-18	B2M/CTSB/
BP	GO:190210	positive reg	41/905	159/18866	2.89E-19	7.45E-18	3.91E-18	CD4/HLA-G
BP	GO:001905	viral life cy	61/905	341/18866	2.96E-19	7.58E-18	3.99E-18	CD4/CTSB/
BP	GO:003264	tumor necr	35/905	116/18866	4.94E-19	1.26E-17	6.63E-18	FCER1G/TL
BP	GO:001972	calcium-me	48/905	222/18866	7.10E-19	1.80E-17	9.47E-18	CD4/CXCL8
BP	GO:004507	negative re	26/905	61/18866	8.76E-19	2.21E-17	1.16E-17	SLPI/APOB
BP	GO:190134	regulation	70/905	444/18866	8.78E-19	2.21E-17	1.16E-17	HLA-G/ERA
BP	GO:000725	receptor sig	41/905	164/18866	9.89E-19	2.48E-17	1.30E-17	IFNG/IFNL1
BP	GO:190390	regulation	40/905	157/18866	1.27E-18	3.15E-17	1.66E-17	CD4/SLPI/C
BP	GO:190401	positive reg	49/905	235/18866	1.52E-18	3.77E-17	1.98E-17	ERAP1/CXC
BP	GO:001406	regulation	36/905	127/18866	1.53E-18	3.77E-17	1.98E-17	TNF/F2R/C
BP	GO:005079	regulation	47/905	217/18866	1.54E-18	3.77E-17	1.98E-17	CD4/SLPI/C
BP	GO:005123	maintenan	58/905	324/18866	2.22E-18	5.44E-17	2.86E-17	CALR/CD4/
BP	GO:003129	lymphocyte	25/905	58/18866	2.95E-18	7.18E-17	3.77E-17	SRC/CD40L
BP	GO:004586	positive reg	62/905	370/18866	4.36E-18	1.06E-16	5.55E-17	IFNG/PSMC
BP	GO:000166	ameboidal-	72/905	481/18866	5.18E-18	1.25E-16	6.57E-17	CALR/IFNG
BP	GO:004824	lymphocyte	26/905	65/18866	6.00E-18	1.44E-16	7.58E-17	CXCL14/CX
BP	GO:003265	regulation	31/905	97/18866	8.11E-18	1.94E-16	1.02E-16	IFNG/ORM
BP	GO:000252	acute infla	33/905	111/18866	8.38E-18	2.00E-16	1.05E-16	FCER1G/IC
BP	GO:000193	endothelia	44/905	199/18866	8.46E-18	2.01E-16	1.05E-16	CXCL12/TN
BP	GO:004860	reproducti	68/905	443/18866	1.19E-17	2.82E-16	1.48E-16	CTSB/HSPA
BP	GO:000237	immunoglo	45/905	210/18866	1.29E-17	3.03E-16	1.59E-16	HLA-DQB1/
BP	GO:003134	positive reg	25/905	61/18866	1.29E-17	3.03E-16	1.59E-16	AZGP1/B2M
BP	GO:000193	regulation	42/905	184/18866	1.38E-17	3.21E-16	1.69E-16	CXCL12/TN
BP	GO:003806	NIK/NF-kap	42/905	184/18866	1.38E-17	3.21E-16	1.69E-16	CALR/PSM
BP	GO:005091	positive ch	26/905	67/18866	1.48E-17	3.41E-16	1.79E-16	CXCL8/CXC
BP	GO:000193	positive reg	33/905	113/18866	1.53E-17	3.52E-16	1.85E-16	CXCL12/VE
BP	GO:003129	T cell costi	24/905	56/18866	1.65E-17	3.78E-16	1.98E-16	SRC/CD40L
BP	GO:004800	antigen pro	43/905	194/18866	1.82E-17	4.16E-16	2.18E-16	AZGP1/B2M
BP	GO:006145	reproducti	68/905	447/18866	1.93E-17	4.38E-16	2.30E-16	CTSB/HSPA
BP	GO:004576	regulation	64/905	403/18866	2.00E-17	4.52E-16	2.38E-16	HLA-G/ERA
BP	GO:190489	positive reg	30/905	93/18866	2.05E-17	4.62E-16	2.43E-16	IFNG/IFNL1
BP	GO:004506	regulation	31/905	100/18866	2.18E-17	4.89E-16	2.57E-16	SLPI/CXCL8
BP	GO:007188	leukocyte a	32/905	108/18866	2.95E-17	6.59E-16	3.46E-16	CTSL/FCER
BP	GO:001406	phosphatic	38/905	154/18866	3.00E-17	6.67E-16	3.51E-16	TNF/F2R/C
BP	GO:004328	regulation	45/905	215/18866	3.37E-17	7.46E-16	3.92E-16	S100A9/S1
BP	GO:003260	chemokine	27/905	75/18866	3.39E-17	7.47E-16	3.93E-16	S100A9/S1
BP	GO:004563	regulation	50/905	263/18866	3.97E-17	8.74E-16	4.59E-16	B2M/CD4/
BP	GO:004576	positive reg	44/905	208/18866	4.98E-17	1.09E-15	5.74E-16	ERAP1/CXC
BP	GO:003272	positive reg	25/905	65/18866	7.98E-17	1.74E-15	9.15E-16	HLA-A/LTA/
BP	GO:005104	positive reg	57/905	340/18866	9.89E-17	2.15E-15	1.13E-15	FCER1G/HL

BP	GO:19048	regulation	37/905	151/18866	1.01E-16	2.18E-15	1.14E-15	IFNG/IFNL
BP	GO:00028	negative re	30/905	98/18866	1.06E-16	2.29E-15	1.20E-15	HLA-A/HLA
BP	GO:00022	activation	36/905	144/18866	1.31E-16	2.82E-15	1.48E-15	FCER1G/PS
BP	GO:00487	tissue rem	40/905	178/18866	1.47E-16	3.14E-15	1.65E-15	TGFB1/NO
BP	GO:20012	negative re	46/905	233/18866	1.63E-16	3.46E-15	1.82E-15	ICAM1/PS
BP	GO:00525	regulation	68/905	466/18866	1.73E-16	3.67E-15	1.93E-15	PSMB8/PS
BP	GO:00421	macrophag	30/905	101/18866	2.70E-16	5.70E-15	2.99E-15	IFNG/TLR2
BP	GO:00507	positive re	25/905	68/18866	2.82E-16	5.94E-15	3.12E-15	CALR/FCER
BP	GO:00716	regulation	22/905	51/18866	3.10E-16	6.49E-15	3.41E-15	CXCL10/CX
BP	GO:00224	negative re	41/905	191/18866	3.42E-16	7.13E-15	3.75E-15	HLA-G/CXC
BP	GO:00109	positive re	42/905	201/18866	4.12E-16	8.56E-15	4.50E-15	PSME2/PS
BP	GO:00725	reactive ox	51/905	288/18866	4.19E-16	8.68E-15	4.56E-15	HSP90AA1
BP	GO:00019	positive re	22/905	52/18866	5.13E-16	1.06E-14	5.56E-15	AZGP1/B2
BP	GO:00464	regulation	35/905	142/18866	5.61E-16	1.15E-14	6.06E-15	IFNG/IFNL
BP	GO:00424	response t	61/905	397/18866	5.73E-16	1.17E-14	6.17E-15	B2M/CALR
BP	GO:00198	antigen pr	40/905	185/18866	6.06E-16	1.24E-14	6.50E-15	B2M/CALR
BP	GO:00464	positive re	28/905	90/18866	6.99E-16	1.42E-14	7.47E-15	IFNG/IFNL
BP	GO:00190	viral geno	33/905	127/18866	7.14E-16	1.45E-14	7.60E-15	SLPI/CXCL
BP	GO:19035	positive re	53/905	313/18866	7.87E-16	1.59E-14	8.34E-15	FCER1G/HL
BP	GO:00525	regulation	64/905	434/18866	8.29E-16	1.67E-14	8.76E-15	PSMB8/PS
BP	GO:00485	response t	56/905	346/18866	9.20E-16	1.84E-14	9.68E-15	CALR/ICAM
BP	GO:00080	cell recogn	44/905	226/18866	1.28E-15	2.55E-14	1.34E-14	PAEP/CCR
BP	GO:00109	positive re	39/905	181/18866	1.59E-15	3.16E-14	1.66E-14	PSME2/PS
BP	GO:00027	positive re	29/905	100/18866	1.72E-15	3.41E-14	1.79E-14	B2M/FCER
BP	GO:20001	regulation	27/905	86/18866	1.79E-15	3.52E-14	1.85E-14	FCER1G/C
BP	GO:00486	regulation	38/905	173/18866	1.88E-15	3.71E-14	1.95E-14	IFNG/MM
BP	GO:00019	T cell medi	20/905	44/18866	2.00E-15	3.91E-14	2.05E-14	AZGP1/B2
BP	GO:00420	T-helper 1	20/905	44/18866	2.00E-15	3.91E-14	2.05E-14	RELB/XCL1
BP	GO:00310	stress-acti	51/905	300/18866	2.37E-15	4.61E-14	2.42E-14	IL1B/TNF/
BP	GO:00022	T cell activ	30/905	109/18866	2.72E-15	5.27E-14	2.77E-14	CD1C/FCE
BP	GO:00486	smooth m	38/905	175/18866	2.81E-15	5.43E-14	2.85E-14	IFNG/MM
BP	GO:00027	positive re	21/905	50/18866	2.85E-15	5.49E-14	2.89E-14	AZGP1/B2
BP	GO:19012	negative re	42/905	212/18866	3.01E-15	5.77E-14	3.03E-14	HLA-F/HSP
BP	GO:00019	regulation	18/905	35/18866	3.22E-15	6.12E-14	3.22E-14	AZGP1/B2
BP	GO:00327	positive re	18/905	35/18866	3.22E-15	6.12E-14	3.22E-14	HLA-G/IFN
BP	GO:00326	regulation	24/905	68/18866	3.28E-15	6.23E-14	3.27E-14	TLR2/IL1B/
BP	GO:00015	ossificatio	61/905	412/18866	3.34E-15	6.32E-14	3.32E-14	PSMC2/TG
BP	GO:00455	regulation	35/905	150/18866	3.45E-15	6.51E-14	3.42E-14	HLA-G/IFN
BP	GO:00458	negative re	23/905	62/18866	3.50E-15	6.58E-14	3.46E-14	HLA-A/HLA
BP	GO:00434	response t	64/905	447/18866	3.52E-15	6.58E-14	3.46E-14	ICAM1/CX
BP	GO:20010	positive re	35/905	151/18866	4.29E-15	8.00E-14	4.21E-14	S100A9/S1
BP	GO:00027	regulation	58/905	381/18866	4.67E-15	8.68E-14	4.56E-14	IFNG/S100
BP	GO:00028	regulation	16/905	27/18866	5.48E-15	1.01E-13	5.33E-14	XCL1/IL1B/
BP	GO:00514	neuron ap	45/905	245/18866	5.80E-15	1.07E-13	5.62E-14	HSPA5/HS
BP	GO:00328	positive re	37/905	170/18866	6.05E-15	1.11E-13	5.84E-14	IL1B/TNF/
BP	GO:00514	stress-acti	49/905	286/18866	6.17E-15	1.13E-13	5.94E-14	IL1B/TNF/
BP	GO:00328	regulation	44/905	237/18866	7.80E-15	1.42E-13	7.48E-14	IL1B/TNF/
BP	GO:19030	negative re	33/905	137/18866	7.92E-15	1.44E-13	7.58E-14	HLA-G/CX
BP	GO:00480	vascular e	28/905	98/18866	8.07E-15	1.46E-13	7.69E-14	HSP90AA1
BP	GO:01500	neuroinfla	25/905	77/18866	8.19E-15	1.48E-13	7.79E-14	IFNG/MM

BP	GO:00703	positive re	37/905	172/18866	8.97E-15	1.62E-13	8.49E-14	IL1B/TNF/
BP	GO:00466	alpha-beta	34/905	146/18866	9.13E-15	1.64E-13	8.62E-14	CTSL/HLA-
BP	GO:00302	macrophag	20/905	47/18866	9.67E-15	1.73E-13	9.10E-14	CD4/IFNG/
BP	GO:00301	natural kill	26/905	85/18866	1.20E-14	2.15E-13	1.13E-13	HLA-F/MIC
BP	GO:00316	lipopolysac	22/905	59/18866	1.23E-14	2.19E-13	1.15E-13	TGFB1/TLR
BP	GO:00703	regulation	44/905	240/18866	1.25E-14	2.22E-13	1.17E-13	IL1B/TNF/
BP	GO:00480	phosphati	39/905	192/18866	1.26E-14	2.22E-13	1.17E-13	TNF/F2R/C
BP	GO:00326	regulation	20/905	48/18866	1.58E-14	2.79E-13	1.47E-13	RELB/TLR2
BP	GO:00022	natural kill	23/905	66/18866	1.70E-14	2.99E-13	1.57E-13	HLA-A/HLA
BP	GO:00027	innate imm	30/905	117/18866	2.20E-14	3.84E-13	2.02E-13	FCER1G/PS
BP	GO:00488	stem cell d	46/905	264/18866	2.22E-14	3.88E-13	2.04E-13	PSMB8/PS
BP	GO:00330	muscle cell	44/905	244/18866	2.32E-14	4.03E-13	2.12E-13	IFNG/MM
BP	GO:00024	antigen pr	37/905	177/18866	2.34E-14	4.05E-13	2.13E-13	B2M/CALR
BP	GO:00726	T cell migr	23/905	67/18866	2.48E-14	4.28E-13	2.25E-13	ICAM1/CX
BP	GO:00480	inositol lipi	39/905	196/18866	2.56E-14	4.41E-13	2.32E-13	TNF/F2R/C
BP	GO:00305	intracellula	46/905	265/18866	2.57E-14	4.41E-13	2.32E-13	CALR/DDX
BP	GO:00508	negative re	30/905	118/18866	2.81E-14	4.81E-13	2.53E-13	HLA-G/XCL
BP	GO:00027	positive re	21/905	55/18866	2.84E-14	4.84E-13	2.54E-13	B2M/FCER
BP	GO:00901	tissue migr	56/905	374/18866	2.89E-14	4.91E-13	2.58E-13	CALR/IFNG
BP	GO:00516	maintenan	41/905	216/18866	2.98E-14	5.05E-13	2.66E-13	CALR/CD4/
BP	GO:00106	epithelial c	55/905	365/18866	3.76E-14	6.36E-13	3.34E-13	CALR/IFNG
BP	GO:00716	protein loc	64/905	470/18866	3.89E-14	6.55E-13	3.44E-13	IFNG/TGFB
BP	GO:00326	interferon-	20/905	50/18866	4.07E-14	6.84E-13	3.59E-13	RELB/TLR2
BP	GO:00072	tyrosine ph	26/905	89/18866	4.10E-14	6.87E-13	3.61E-13	IFNG/IFNL1
BP	GO:00421	B cell proli	27/905	97/18866	4.95E-14	8.26E-13	4.34E-13	TFRC/CD40
BP	GO:20003	regulation	39/905	200/18866	5.11E-14	8.50E-13	4.46E-13	HSP90AA1
BP	GO:00901	epithelium	55/905	368/18866	5.34E-14	8.86E-13	4.66E-13	CALR/IFNG
BP	GO:00456	positive re	28/905	105/18866	5.53E-14	9.15E-13	4.81E-13	HLA-G/IFN
BP	GO:00093	protein sec	63/905	462/18866	5.80E-14	9.56E-13	5.02E-13	IFNG/TGFB
BP	GO:00022	stimulatory	29/905	113/18866	5.82E-14	9.56E-13	5.02E-13	FCER1G/PS
BP	GO:00715	semaphori	18/905	40/18866	6.40E-14	1.05E-12	5.51E-13	SEMA3A/S
BP	GO:00355	establishm	63/905	463/18866	6.42E-14	1.05E-12	5.51E-13	IFNG/TGFB
BP	GO:00432	positive re	47/905	284/18866	8.47E-14	1.38E-12	7.25E-13	CD4/HSPA
BP	GO:00027	regulation	30/905	123/18866	9.29E-14	1.50E-12	7.91E-13	CD4/IFNG/
BP	GO:20012	negative re	28/905	107/18866	9.29E-14	1.50E-12	7.91E-13	ICAM1/IL1
BP	GO:00506	regulation	24/905	78/18866	1.09E-13	1.76E-12	9.26E-13	MICB/MM
BP	GO:00425	superoxide	17/905	36/18866	1.18E-13	1.90E-12	1.00E-12	TGFB1/NO
BP	GO:00022	innate imm	29/905	116/18866	1.21E-13	1.94E-12	1.02E-12	FCER1G/PS
BP	GO:00003	response t	42/905	235/18866	1.25E-13	1.99E-12	1.05E-12	LCN2/MM
BP	GO:00425	regulation	25/905	86/18866	1.44E-13	2.29E-12	1.21E-12	IFNG/IFNL1
BP	GO:00331	positive re	28/905	109/18866	1.54E-13	2.45E-12	1.29E-12	HSP90AA1
BP	GO:00521	movement	35/905	169/18866	1.58E-13	2.51E-12	1.32E-12	CD4/CTSB/
BP	GO:00509	negative re	22/905	66/18866	1.82E-13	2.88E-12	1.51E-12	CXCL13/W
BP	GO:19012	positive re	24/905	80/18866	2.04E-13	3.22E-12	1.69E-12	CALR/TLR2
BP	GO:00619	glial cell ac	21/905	60/18866	2.14E-13	3.37E-12	1.77E-12	IFNG/TLR2
BP	GO:00160	cell growth	64/905	490/18866	2.72E-13	4.26E-12	2.24E-12	HSP90AA1
BP	GO:00324	positive re	23/905	74/18866	2.80E-13	4.37E-12	2.30E-12	TLR2/DDX5
BP	GO:19034	reactive ox	30/905	128/18866	2.88E-13	4.48E-12	2.36E-12	HSP90AA1
BP	GO:00019	positive re	15/905	28/18866	3.05E-13	4.74E-12	2.49E-12	AZGP1/B2
BP	GO:00620	regulation	61/905	456/18866	3.49E-13	5.41E-12	2.84E-12	IFNG/NFYA

BP	GO:005170	interaction	39/905	212/18866	3.63E-13	5.60E-12	2.94E-12	CD4/CTSB/
BP	GO:001988	antigen pro	14/905	24/18866	3.88E-13	5.97E-12	3.14E-12	AZGP1/B2M
BP	GO:004633	positive reg	31/905	138/18866	3.93E-13	6.03E-12	3.17E-12	IL1B/TNF/T
BP	GO:190210	negative re	27/905	105/18866	4.08E-13	6.25E-12	3.28E-12	HLA-G/PGL
BP	GO:004206	gliogenesis	48/905	307/18866	4.09E-13	6.26E-12	3.29E-12	IFNG/LTA/S
BP	GO:004440	entry into h	32/905	147/18866	4.12E-13	6.28E-12	3.30E-12	CD4/CTSB/
BP	GO:005070	regulation	52/905	352/18866	4.23E-13	6.40E-12	3.37E-12	IFNG/TGFB
BP	GO:000697	response to	61/905	458/18866	4.24E-13	6.40E-12	3.37E-12	MICB/LCN2
BP	GO:000725	JNK cascad	39/905	213/18866	4.24E-13	6.40E-12	3.37E-12	IL1B/TNF/T
BP	GO:004632	regulation	36/905	184/18866	4.34E-13	6.53E-12	3.43E-12	IL1B/TNF/T
BP	GO:004814	regulation	24/905	83/18866	5.03E-13	7.56E-12	3.97E-12	LTA/S100A
BP	GO:200037	positive reg	27/905	106/18866	5.23E-13	7.83E-12	4.11E-12	HSP90AA1/
BP	GO:000177	microglial c	19/905	50/18866	5.35E-13	7.97E-12	4.19E-12	IFNG/TLR2/
BP	GO:000226	leukocyte a	19/905	50/18866	5.35E-13	7.97E-12	4.19E-12	IFNG/TLR2/
BP	GO:001810	peptidyl-se	48/905	310/18866	5.92E-13	8.79E-12	4.62E-12	HSP90AA1/
BP	GO:005072	negative re	37/905	196/18866	6.46E-13	9.54E-12	5.02E-12	PGLYRP1/A
BP	GO:003261	interleukin	21/905	63/18866	6.46E-13	9.54E-12	5.02E-12	FCER1G/XC
BP	GO:006220	regulation	26/905	99/18866	6.50E-13	9.58E-12	5.03E-12	TLR2/LBP/L
BP	GO:004814	fibroblast p	24/905	84/18866	6.73E-13	9.89E-12	5.20E-12	LTA/S100A
BP	GO:000248	antigen pro	12/905	17/18866	6.85E-13	1.00E-11	5.26E-12	AZGP1/B2M
BP	GO:001988	antigen pro	12/905	17/18866	6.85E-13	1.00E-11	5.26E-12	AZGP1/B2M
BP	GO:190355	negative re	20/905	57/18866	7.59E-13	1.10E-11	5.80E-12	LBP/LTF/AD
BP	GO:002261	gland morp	29/905	124/18866	7.60E-13	1.10E-11	5.80E-12	TGFB1/TNF
BP	GO:004814	positive reg	19/905	51/18866	8.14E-13	1.18E-11	6.21E-12	S100A6/PM
BP	GO:003264	regulation	14/905	25/18866	8.42E-13	1.22E-11	6.40E-12	DDX58/IRF
BP	GO:004311	receptor m	37/905	198/18866	8.92E-13	1.29E-11	6.76E-12	FCER1G/IF
BP	GO:005093	induction o	11/905	14/18866	9.30E-13	1.34E-11	7.03E-12	CXCL8/CXC
BP	GO:004328	positive reg	30/905	134/18866	1.03E-12	1.48E-11	7.78E-12	S100A9/S1
BP	GO:001921	regulation	58/905	431/18866	1.05E-12	1.51E-11	7.91E-12	IFNG/NFYA
BP	GO:004355	regulation	20/905	58/18866	1.11E-12	1.58E-11	8.30E-12	TGFB1/SOC
BP	GO:000155	regulation	57/905	420/18866	1.16E-12	1.66E-11	8.71E-12	PSMD10/C
BP	GO:000270	negative re	19/905	52/18866	1.23E-12	1.74E-11	9.15E-12	HLA-A/HLA
BP	GO:004001	negative re	55/905	397/18866	1.27E-12	1.80E-11	9.44E-12	CALR/CXCL
BP	GO:003313	regulation	31/905	145/18866	1.60E-12	2.25E-11	1.18E-11	HSP90AA1/
BP	GO:003812	ERBB signa	31/905	145/18866	1.60E-12	2.25E-11	1.18E-11	HSP90AA1/
BP	GO:005192	regulation	42/905	253/18866	1.62E-12	2.28E-11	1.20E-11	CD4/HSPA2
BP	GO:004354	endothelia	45/905	286/18866	1.79E-12	2.51E-11	1.32E-11	CALR/CXCL
BP	GO:003248	negative re	18/905	47/18866	1.88E-12	2.61E-11	1.37E-11	RELB/DDX5
BP	GO:005091	negative ch	18/905	47/18866	1.88E-12	2.61E-11	1.37E-11	ITGAV/WN
BP	GO:000279	positive reg	36/905	193/18866	1.92E-12	2.67E-11	1.40E-11	IFNG/S100
BP	GO:000165	temperatur	34/905	174/18866	2.02E-12	2.80E-11	1.47E-11	LCN2/IL1B/
BP	GO:004352	regulation	38/905	214/18866	2.27E-12	3.14E-11	1.65E-11	HSP90AB1/
BP	GO:003273	positive reg	20/905	60/18866	2.29E-12	3.16E-11	1.66E-11	IFNG/ORM
BP	GO:001820	peptidyl-se	49/905	333/18866	2.36E-12	3.24E-11	1.71E-11	HSP90AA1/
BP	GO:007145	cellular res	40/905	235/18866	2.44E-12	3.34E-11	1.76E-11	ICAM1/PSM
BP	GO:003412	regulation	22/905	74/18866	2.53E-12	3.46E-11	1.82E-11	TLR2/LBP/L
BP	GO:003571	CD4-positiv	25/905	97/18866	2.86E-12	3.89E-11	2.04E-11	CTSL/IFNG/
BP	GO:004663	regulation	25/905	97/18866	2.86E-12	3.89E-11	2.04E-11	HLA-A/IFNG
BP	GO:000756	female pre	36/905	196/18866	3.09E-12	4.19E-11	2.20E-11	CALR/CTSB
BP	GO:004226	natural kille	20/905	61/18866	3.26E-12	4.42E-11	2.32E-11	HLA-A/HLA

BP	GO:00301	platelet ac	32/905	158/18866	3.29E-12	4.45E-11	2.34E-11	FCER1G/C
BP	GO:00488	axon exten	16/905	37/18866	3.44E-12	4.63E-11	2.43E-11	CXCL12/VE
BP	GO:19022	neuron pr	16/905	37/18866	3.44E-12	4.63E-11	2.43E-11	CXCL12/VE
BP	GO:00326	interferon-	14/905	27/18866	3.46E-12	4.65E-11	2.44E-11	DDX58/IRF
BP	GO:00621	cellular res	51/905	360/18866	3.63E-12	4.86E-11	2.55E-11	RELB/LCN2
BP	GO:00488	regulation	15/905	32/18866	3.85E-12	5.14E-11	2.70E-11	CXCL12/VE
BP	GO:00740	axonogene	61/905	482/18866	3.96E-12	5.27E-11	2.77E-11	HSP90AA1
BP	GO:00362	cellular res	38/905	218/18866	4.09E-12	5.43E-11	2.85E-11	ICAM1/PS
BP	GO:00714	cellular res	37/905	208/18866	4.19E-12	5.55E-11	2.92E-11	ICAM1/PS
BP	GO:00316	receptor in	27/905	115/18866	4.25E-12	5.63E-11	2.96E-11	FCER1G/C
BP	GO:20001	negative r	18/905	49/18866	4.33E-12	5.71E-11	3.00E-11	FCER1G/C
BP	GO:00426	ovulation	21/905	69/18866	4.80E-12	6.31E-11	3.32E-11	HSPA5/SR
BP	GO:00096	response t	37/905	209/18866	4.86E-12	6.38E-11	3.35E-11	CXCL10/CX
BP	GO:00329	positive re	12/905	19/18866	5.10E-12	6.68E-11	3.51E-11	TGFB1/MA
BP	GO:00462	nitric oxide	23/905	84/18866	5.42E-12	7.07E-11	3.72E-11	HSP90AA1
BP	GO:20004	positive re	16/905	38/18866	5.68E-12	7.40E-11	3.89E-11	CXCL14/CX
BP	GO:00512	negative r	54/905	400/18866	5.73E-12	7.44E-11	3.91E-11	CALR/CXCL
BP	GO:00512	positive re	50/905	354/18866	6.64E-12	8.61E-11	4.52E-11	HSP90AB1
BP	GO:00068	calcium io	56/905	426/18866	6.78E-12	8.78E-11	4.61E-11	CD4/HSPA
BP	GO:00510	regulation	51/905	367/18866	7.56E-12	9.76E-11	5.13E-11	B2M/HSP9
BP	GO:20000	regulation	41/905	254/18866	7.59E-12	9.77E-11	5.13E-11	PSMB8/PS
BP	GO:00425	positive re	21/905	71/18866	8.88E-12	1.14E-10	5.99E-11	IFNG/IFNL1
BP	GO:19030	regulation	34/905	183/18866	8.89E-12	1.14E-10	5.99E-11	FCER1G/PL
BP	GO:20004	regulation	20/905	64/18866	8.94E-12	1.14E-10	6.01E-11	CXCL14/CX
BP	GO:00706	negative r	23/905	86/18866	9.25E-12	1.18E-10	6.20E-11	HLA-G/XCL
BP	GO:00488	homeostas	41/905	256/18866	9.82E-12	1.25E-10	6.57E-11	B2M/FCER
BP	GO:00985	detection	13/905	24/18866	9.99E-12	1.27E-10	6.67E-11	HLA-A/HLA
BP	GO:19012	regulation	27/905	119/18866	1.01E-11	1.27E-10	6.70E-11	CALR/TMS
BP	GO:00454	fat cell diff	39/905	235/18866	1.03E-11	1.30E-10	6.84E-11	PSMB8/ER
BP	GO:00068	nitric oxide	22/905	79/18866	1.08E-11	1.36E-10	7.17E-11	HSP90AA1
BP	GO:20010	reactive ni	23/905	87/18866	1.20E-11	1.51E-10	7.94E-11	HSP90AA1
BP	GO:00001	activation	31/905	156/18866	1.21E-11	1.51E-10	7.95E-11	IL1B/TNF/
BP	GO:00704	interleukin	25/905	103/18866	1.21E-11	1.51E-10	7.95E-11	PSMB8/PS
BP	GO:00025	chronic infl	12/905	20/18866	1.22E-11	1.52E-10	8.01E-11	LTA/CXCL1
BP	GO:00603	pathway-r	20/905	65/18866	1.23E-11	1.54E-10	8.08E-11	TGFB1/BM
BP	GO:00467	protein aut	39/905	237/18866	1.35E-11	1.67E-10	8.80E-11	ADIPOQ/V
BP	GO:00106	positive re	33/905	176/18866	1.39E-11	1.72E-10	9.06E-11	CALR/IFNG
BP	GO:00716	regulation	18/905	52/18866	1.40E-11	1.72E-10	9.06E-11	CXCL8/XCL
BP	GO:20012	positive re	18/905	52/18866	1.40E-11	1.72E-10	9.06E-11	PDIA3/TNF
BP	GO:00611	morphoge	34/905	187/18866	1.66E-11	2.05E-10	1.08E-10	TNF/PML/
BP	GO:00604	calcium io	31/905	158/18866	1.71E-11	2.09E-10	1.10E-10	CD4/CXCL1
BP	GO:19037	negative r	31/905	158/18866	1.71E-11	2.09E-10	1.10E-10	HLA-G/PGL
BP	GO:00485	rhythmic p	45/905	305/18866	1.72E-11	2.10E-10	1.10E-10	HSPA5/NF
BP	GO:00226	regulation	61/905	499/18866	1.73E-11	2.11E-10	1.11E-10	CALR/ICA
BP	GO:00435	negative r	30/905	149/18866	1.83E-11	2.23E-10	1.17E-10	HSP90AB1
BP	GO:00519	positive re	27/905	122/18866	1.87E-11	2.27E-10	1.19E-10	CD4/HSPA
BP	GO:00509	positive re	13/905	25/18866	1.99E-11	2.41E-10	1.27E-10	CXCL8/CXC
BP	GO:00327	positive re	18/905	53/18866	2.02E-11	2.44E-10	1.28E-10	IFNG/ORM
BP	GO:00068	superoxide	21/905	74/18866	2.14E-11	2.59E-10	1.36E-10	TGFB1/NO
BP	GO:00075	aging	46/905	319/18866	2.28E-11	2.74E-10	1.44E-10	B2M/CALR

BP	GO:003265	regulation	19/905	60/18866	2.28E-11	2.74E-10	1.44E-10	FCER1G/XC
BP	GO:000717	epidermal	27/905	123/18866	2.29E-11	2.74E-10	1.44E-10	TGFB1/MM
BP	GO:000695	acute-phas	17/905	47/18866	2.29E-11	2.74E-10	1.44E-10	IL1B/LBP/C
BP	GO:004355	regulation	20/905	67/18866	2.30E-11	2.75E-10	1.45E-10	TGFB1/SOC
BP	GO:004339	regulation	36/905	211/18866	2.85E-11	3.40E-10	1.79E-10	B2M/HSP9
BP	GO:000696	cellular def	18/905	54/18866	2.89E-11	3.42E-10	1.80E-10	HLA-G/KIR
BP	GO:000962	response t	18/905	54/18866	2.89E-11	3.42E-10	1.80E-10	S100A9/S1
BP	GO:003262	interleukin	18/905	54/18866	2.89E-11	3.42E-10	1.80E-10	CD4/FCER1
BP	GO:003275	positive reg	18/905	54/18866	2.89E-11	3.42E-10	1.80E-10	TLR2/IL1B/
BP	GO:000176	morphogen	35/905	201/18866	2.98E-11	3.51E-10	1.84E-10	TNF/PML/S
BP	GO:003459	cellular res	45/905	310/18866	3.00E-11	3.53E-10	1.86E-10	LCN2/MMP
BP	GO:000282	negative re	17/905	48/18866	3.39E-11	3.97E-10	2.09E-10	HLA-F/HLA
BP	GO:004671	viral entry	28/905	134/18866	3.41E-11	3.99E-10	2.10E-10	CD4/CTSB/
BP	GO:190495	positive reg	50/905	370/18866	3.42E-11	3.99E-10	2.10E-10	HSP90AB1/
BP	GO:000270	negative re	16/905	42/18866	3.55E-11	4.13E-10	2.17E-10	HLA-A/HLA
BP	GO:004824	macrophag	16/905	42/18866	3.55E-11	4.13E-10	2.17E-10	CCL5/MAP
BP	GO:009730	response t	38/905	234/18866	3.70E-11	4.30E-10	2.26E-10	ICAM1/PSM
BP	GO:004884	negative re	13/905	26/18866	3.81E-11	4.40E-10	2.31E-10	WNT5A/SE
BP	GO:005092	regulation	13/905	26/18866	3.81E-11	4.40E-10	2.31E-10	CXCL8/CXC
BP	GO:001063	regulation	44/905	301/18866	3.95E-11	4.55E-10	2.39E-10	CALR/IFNG
BP	GO:003272	negative re	18/905	55/18866	4.11E-11	4.73E-10	2.49E-10	LBP/ADIPO
BP	GO:006048	mesenchym	43/905	290/18866	4.12E-11	4.73E-10	2.49E-10	TGFB1/IL1B
BP	GO:200123	positive reg	33/905	183/18866	4.16E-11	4.76E-10	2.50E-10	PDIA3/S10
BP	GO:004558	positive reg	23/905	92/18866	4.18E-11	4.78E-10	2.51E-10	HLA-G/IFN
BP	GO:006039	regulation	19/905	62/18866	4.36E-11	4.97E-10	2.61E-10	TGFB1/BM
BP	GO:005076	positive reg	59/905	485/18866	4.58E-11	5.21E-10	2.74E-10	HSPA5/IFN
BP	GO:200073	regulation	26/905	118/18866	4.90E-11	5.57E-10	2.93E-10	PSMB8/PSI
BP	GO:001401	positive reg	21/905	77/18866	4.93E-11	5.59E-10	2.94E-10	LTA/TGFB1
BP	GO:004470	multi-multi	37/905	226/18866	5.26E-11	5.95E-10	3.13E-10	CALR/CTSB
BP	GO:003267	regulation	23/905	93/18866	5.30E-11	5.99E-10	3.15E-10	TMSB4X/TI
BP	GO:000236	T cell cytok	16/905	43/18866	5.40E-11	6.07E-10	3.19E-10	B2M/HLA-
BP	GO:000282	negative re	16/905	43/18866	5.40E-11	6.07E-10	3.19E-10	HLA-F/HLA
BP	GO:003292	regulation	12/905	22/18866	5.73E-11	6.43E-10	3.38E-10	TGFB1/MA
BP	GO:000691	activation	22/905	86/18866	6.80E-11	7.61E-10	4.00E-10	S100A9/S1
BP	GO:190162	regulation	13/905	27/18866	7.02E-11	7.84E-10	4.12E-10	CXCL14/CX
BP	GO:000741	axon guida	42/905	284/18866	7.57E-11	8.44E-10	4.44E-10	CXCL12/VE
BP	GO:004876	mesenchym	37/905	229/18866	7.80E-11	8.68E-10	4.56E-10	TGFB1/IL1B
BP	GO:003268	negative re	15/905	38/18866	8.02E-11	8.91E-10	4.68E-10	XCL1/PGLY
BP	GO:006076	positive reg	18/905	57/18866	8.09E-11	8.94E-10	4.70E-10	MMP12/TL
BP	GO:190551	macrophag	18/905	57/18866	8.09E-11	8.94E-10	4.70E-10	CCL5/MAP
BP	GO:000243	inflammato	19/905	64/18866	8.11E-11	8.95E-10	4.70E-10	FCER1G/IC
BP	GO:190372	regulation	23/905	95/18866	8.46E-11	9.31E-10	4.90E-10	TGFB1/FAB
BP	GO:009748	neuron pro	42/905	285/18866	8.48E-11	9.32E-10	4.90E-10	CXCL12/VE
BP	GO:001000	glial cell dif	37/905	230/18866	8.88E-11	9.74E-10	5.12E-10	IFNG/S100
BP	GO:004873	gland deve	55/905	443/18866	9.76E-11	1.07E-09	5.61E-10	TGFB1/TNF
BP	GO:001056	regulation	33/905	189/18866	1.02E-10	1.11E-09	5.83E-10	PSMB8/PSI
BP	GO:003461	cellular res	31/905	170/18866	1.21E-10	1.31E-09	6.91E-10	LCN2/MMP
BP	GO:007083	divalent m	57/905	471/18866	1.21E-10	1.31E-09	6.91E-10	CD4/HSPA
BP	GO:190266	negative re	13/905	28/18866	1.25E-10	1.36E-09	7.15E-10	WNT5A/SE
BP	GO:001095	regulation	51/905	396/18866	1.28E-10	1.38E-09	7.27E-10	B2M/CD4/

BP	GO:006104	regulation	29/905	151/18866	1.32E-10	1.42E-09	7.49E-10	FCER1G/PL
BP	GO:000759	hemostasis	47/905	348/18866	1.37E-10	1.48E-09	7.76E-10	FCER1G/PF
BP	GO:190533	regulation	32/905	181/18866	1.40E-10	1.50E-09	7.91E-10	PSMB8/PSI
BP	GO:031666	response t	57/905	473/18866	1.42E-10	1.53E-09	8.05E-10	CD4/HSPA5
BP	GO:190355	positive re	17/905	52/18866	1.46E-10	1.57E-09	8.24E-10	FCER1G/IFI
BP	GO:005120	sequesterin	26/905	124/18866	1.58E-10	1.69E-09	8.89E-10	CALR/CXCL
BP	GO:004583	positive re	29/905	153/18866	1.83E-10	1.96E-09	1.03E-09	IFNG/TGFB
BP	GO:005069	regulation	15/905	40/18866	1.91E-10	2.03E-09	1.07E-09	MICB/MMI
BP	GO:007251	divalent in	57/905	478/18866	2.14E-10	2.28E-09	1.20E-09	CD4/HSPA2
BP	GO:006184	antimicrob	20/905	75/18866	2.22E-10	2.36E-09	1.24E-09	CXCL14/CX
BP	GO:004684	bone remo	22/905	91/18866	2.24E-10	2.37E-09	1.25E-09	TGFB1/NO
BP	GO:004580	positive re	23/905	100/18866	2.56E-10	2.71E-09	1.43E-09	B2M/VEGF
BP	GO:004542	regulation	19/905	68/18866	2.60E-10	2.74E-09	1.44E-09	HSP90AA1/
BP	GO:000759	blood coag	46/905	343/18866	2.73E-10	2.88E-09	1.51E-09	FCER1G/PF
BP	GO:003808	peptidyl-ty	15/905	41/18866	2.87E-10	3.02E-09	1.59E-09	VEGFA/MA
BP	GO:003018	B cell differ	27/905	137/18866	3.10E-10	3.26E-09	1.71E-09	CD40LG/PT
BP	GO:003263	interleukin	23/905	101/18866	3.17E-10	3.32E-09	1.74E-09	TMSB4X/TI
BP	GO:004563	positive re	23/905	101/18866	3.17E-10	3.32E-09	1.74E-09	CD4/IFNG/
BP	GO:003272	positive re	11/905	20/18866	3.29E-10	3.43E-09	1.80E-09	DDX58/IRF
BP	GO:004666	female sex	25/905	119/18866	3.40E-10	3.54E-09	1.86E-09	HSPA5/ICA
BP	GO:006109	regulation	22/905	93/18866	3.52E-10	3.66E-09	1.92E-09	NOX4/CCL5
BP	GO:001080	regulation	18/905	62/18866	3.84E-10	3.98E-09	2.09E-09	TNF/ADIPC
BP	GO:003088	regulation	18/905	62/18866	3.84E-10	3.98E-09	2.09E-09	TFRC/CD40
BP	GO:006040	cytosolic ca	31/905	178/18866	4.00E-10	4.13E-09	2.17E-09	CD4/CXCL1
BP	GO:000270	negative re	14/905	36/18866	4.37E-10	4.51E-09	2.37E-09	HLA-F/XCL1
BP	GO:000959	detection c	14/905	36/18866	4.37E-10	4.51E-09	2.37E-09	HLA-A/HLA
BP	GO:001491	regulation	21/905	86/18866	4.70E-10	4.83E-09	2.54E-09	PLAU/NOX
BP	GO:190165	response t	33/905	200/18866	4.71E-10	4.83E-09	2.54E-09	CALR/ICAM
BP	GO:004336	CD4-positiv	20/905	78/18866	4.77E-10	4.88E-09	2.57E-09	CTSL/IFNG/
BP	GO:005081	coagulation	46/905	349/18866	4.87E-10	4.98E-09	2.62E-09	FCER1G/PF
BP	GO:000301	vascular pr	32/905	190/18866	5.05E-10	5.15E-09	2.71E-09	ICAM1/TGI
BP	GO:000267	regulation	16/905	49/18866	5.20E-10	5.29E-09	2.78E-09	FCER1G/IL1
BP	GO:004687	hormone s	43/905	314/18866	5.43E-10	5.52E-09	2.90E-09	IFNG/IL1B/
BP	GO:003027	regulation	34/905	212/18866	5.60E-10	5.68E-09	2.98E-09	TGFB1/LTF/
BP	GO:000229	T cell differ	19/905	71/18866	5.86E-10	5.93E-09	3.12E-09	FCER1G/IFI
BP	GO:003235	response t	27/905	141/18866	6.11E-10	6.17E-09	3.24E-09	CALR/CD4/
BP	GO:000754	sex differen	40/905	280/18866	6.16E-10	6.22E-09	3.27E-09	HSPA5/ICA
BP	GO:014013	positive re	11/905	21/18866	6.61E-10	6.66E-09	3.50E-09	CXCL14/CX
BP	GO:001059	positive re	26/905	132/18866	6.69E-10	6.72E-09	3.53E-09	CALR/TMSI
BP	GO:009032	regulation	14/905	37/18866	6.73E-10	6.75E-09	3.55E-09	TGFB1/TNI
BP	GO:004867	axon exten	25/905	123/18866	7.12E-10	7.13E-09	3.75E-09	HSP90AA1/
BP	GO:190552	positive re	12/905	26/18866	7.16E-10	7.16E-09	3.76E-09	CCL5/MAP
BP	GO:003276	positive re	16/905	50/18866	7.30E-10	7.29E-09	3.83E-09	FCER1G/TL
BP	GO:005071	positive re	30/905	172/18866	7.37E-10	7.34E-09	3.86E-09	IFNG/TGFB
BP	GO:003164	heat gener	10/905	17/18866	8.79E-10	8.74E-09	4.59E-09	IL1B/TNF/T
BP	GO:004663	alpha-beta	23/905	106/18866	8.81E-10	8.74E-09	4.59E-09	CTSL/IFNG/
BP	GO:190266	regulation	15/905	44/18866	9.10E-10	8.99E-09	4.73E-09	CXCL12/VE
BP	GO:190552	regulation	15/905	44/18866	9.10E-10	8.99E-09	4.73E-09	CCL5/MAP
BP	GO:003196	response t	29/905	164/18866	1.01E-09	1.00E-08	5.26E-09	ICAM1/S10
BP	GO:001074	macrophag	14/905	38/18866	1.02E-09	1.00E-08	5.26E-09	TGFB1/CET

BP	GO:009007	foam cell d	14/905	38/18866	1.02E-09	1.00E-08	5.26E-09	TGFB1/CET
BP	GO:190342	regulation	23/905	107/18866	1.07E-09	1.05E-08	5.53E-09	HSP90AA1,
BP	GO:000166	fever gene	8/905	10/18866	1.12E-09	1.10E-08	5.79E-09	IL1B/TNF/T
BP	GO:001076	regulation	42/905	310/18866	1.20E-09	1.17E-08	6.17E-09	CALR/CXCL
BP	GO:005083	defense re	22/905	99/18866	1.26E-09	1.23E-08	6.48E-09	HLA-A/MR
BP	GO:000271	regulation	15/905	45/18866	1.30E-09	1.27E-08	6.68E-09	HLA-A/HLA
BP	GO:000991	hormone t	43/905	323/18866	1.32E-09	1.28E-08	6.75E-09	IFNG/IL1B/
BP	GO:000189	placenta d	28/905	156/18866	1.38E-09	1.34E-08	7.06E-09	CTSB/HSP9
BP	GO:003410	regulation	21/905	91/18866	1.44E-09	1.39E-08	7.33E-09	TGFB1/TFR
BP	GO:003302	myeloid ce	13/905	33/18866	1.53E-09	1.48E-08	7.77E-09	CTSL/FCER
BP	GO:004355	positive re	13/905	33/18866	1.53E-09	1.48E-08	7.77E-09	TGFB1/SRC
BP	GO:005120	release of	24/905	118/18866	1.53E-09	1.48E-08	7.77E-09	CXCL10/CX
BP	GO:004512	cellular ext	18/905	67/18866	1.55E-09	1.49E-08	7.83E-09	ICAM1/CX
BP	GO:004592	negative re	37/905	254/18866	1.57E-09	1.51E-08	7.93E-09	TGFB1/RB
BP	GO:004361	regulation	23/905	109/18866	1.57E-09	1.51E-08	7.94E-09	HSPA5/PS
BP	GO:007149	cellular res	43/905	326/18866	1.76E-09	1.68E-08	8.84E-09	HSPA5/ICA
BP	GO:009719	intrinsic ap	40/905	290/18866	1.76E-09	1.68E-08	8.84E-09	CXCL12/S1
BP	GO:006109	positive re	17/905	60/18866	1.79E-09	1.71E-08	8.99E-09	NOX4/CCL5
BP	GO:005128	negative re	24/905	119/18866	1.84E-09	1.75E-08	9.18E-09	CXCL10/CX
BP	GO:005079	activated T	15/905	46/18866	1.85E-09	1.76E-08	9.24E-09	AGER/EPO,
BP	GO:001057	positive re	12/905	28/18866	2.06E-09	1.95E-08	1.03E-08	TGFB1/IL1
BP	GO:001081	T cell chem	12/905	28/18866	2.06E-09	1.95E-08	1.03E-08	CXCL10/CX
BP	GO:001490	smooth mu	21/905	93/18866	2.20E-09	2.07E-08	1.09E-08	PLAU/NOX
BP	GO:003208	negative re	21/905	93/18866	2.20E-09	2.07E-08	1.09E-08	PSMD10/T
BP	GO:005105	negative re	55/905	483/18866	2.44E-09	2.30E-08	1.21E-08	HLA-F/ICA
BP	GO:011011	positive re	20/905	85/18866	2.46E-09	2.31E-08	1.21E-08	VEGFA/TN
BP	GO:009755	calcium io	26/905	140/18866	2.51E-09	2.36E-08	1.24E-08	CXCL10/CX
BP	GO:000165	urogenital	43/905	330/18866	2.57E-09	2.41E-08	1.26E-08	MMP9/RB
BP	GO:005128	regulation	24/905	121/18866	2.61E-09	2.44E-08	1.28E-08	CXCL10/CX
BP	GO:006056	developme	35/905	236/18866	2.68E-09	2.51E-08	1.32E-08	HSP90AA1,
BP	GO:000758	response t	29/905	171/18866	2.77E-09	2.58E-08	1.36E-08	CD4/LTA/C
BP	GO:004866	positive re	22/905	103/18866	2.80E-09	2.60E-08	1.37E-08	MMP9/TN
BP	GO:004226	regulation	14/905	41/18866	3.24E-09	3.01E-08	1.58E-08	HLA-A/HLA
BP	GO:005083	defense re	14/905	41/18866	3.24E-09	3.01E-08	1.58E-08	S100A9/S1
BP	GO:007162	positive re	12/905	29/18866	3.37E-09	3.11E-08	1.63E-08	CXCL8/XCL
BP	GO:001059	regulation	35/905	238/18866	3.37E-09	3.11E-08	1.63E-08	CALR/CXCL
BP	GO:003253	regulation	47/905	383/18866	3.37E-09	3.11E-08	1.63E-08	HSP90AB1,
BP	GO:004562	negative re	16/905	55/18866	3.52E-09	3.24E-08	1.70E-08	PGLYRP1/P
BP	GO:009880	regulation	13/905	35/18866	3.61E-09	3.32E-08	1.74E-08	ADIPOQ/F2
BP	GO:001086	positive re	15/905	48/18866	3.61E-09	3.32E-08	1.74E-08	TGFB1/BM
BP	GO:006108	positive re	10/905	19/18866	3.82E-09	3.50E-08	1.84E-08	FCER1G/HL
BP	GO:003574	natural kill	8/905	11/18866	3.95E-09	3.61E-08	1.90E-08	CXCL14/XC
BP	GO:000240	dendritic c	11/905	24/18866	4.09E-09	3.72E-08	1.96E-08	CALR/CCL5
BP	GO:003134	negative re	11/905	24/18866	4.09E-09	3.72E-08	1.96E-08	HLA-A/HLA
BP	GO:004663	positive re	17/905	63/18866	4.10E-09	3.72E-08	1.96E-08	HLA-A/IFN
BP	GO:200051	regulation	17/905	63/18866	4.10E-09	3.72E-08	1.96E-08	IFNG/XCL1,
BP	GO:005067	negative re	19/905	79/18866	4.15E-09	3.77E-08	1.98E-08	HLA-G/XCL
BP	GO:004362	regulation	23/905	115/18866	4.72E-09	4.27E-08	2.25E-08	HSPA5/PS
BP	GO:004864	negative re	23/905	115/18866	4.72E-09	4.27E-08	2.25E-08	RBP4/WNT
BP	GO:001481	muscle cell	22/905	106/18866	4.94E-09	4.46E-08	2.34E-08	PLAU/NOX

BP	GO:003266	regulation	15/905	49/18866	4.98E-09	4.48E-08	2.36E-08	CD4/XCL1/
BP	GO:005077	regulation	30/905	186/18866	5.02E-09	4.52E-08	2.38E-08	CXCL12/VE
BP	GO:001403	neural cres	19/905	80/18866	5.20E-09	4.67E-08	2.45E-08	MAPK3/ED
BP	GO:003294	negative re	19/905	80/18866	5.20E-09	4.67E-08	2.45E-08	HLA-G/XCL
BP	GO:001075	regulation	12/905	30/18866	5.36E-09	4.78E-08	2.51E-08	CCL5/MAP
BP	GO:003272	positive reg	12/905	30/18866	5.36E-09	4.78E-08	2.51E-08	TLR2/DDX5
BP	GO:003566	TRIF-depen	12/905	30/18866	5.36E-09	4.78E-08	2.51E-08	IRF3/TLR3/
BP	GO:006108	myeloid leu	12/905	30/18866	5.36E-09	4.78E-08	2.51E-08	FCER1G/HL
BP	GO:000275	MyD88-dep	13/905	36/18866	5.40E-09	4.80E-08	2.52E-08	TLR2/IRF1/
BP	GO:004663	alpha-beta	13/905	36/18866	5.40E-09	4.80E-08	2.52E-08	HLA-A/XCL
BP	GO:005066	cytokine se	18/905	72/18866	5.46E-09	4.84E-08	2.55E-08	IFNG/TLR2/
BP	GO:000862	extrinsic ap	20/905	89/18866	5.78E-09	5.12E-08	2.69E-08	ICAM1/TN
BP	GO:004688	regulation	37/905	267/18866	6.30E-09	5.57E-08	2.93E-08	IFNG/IL1B/
BP	GO:000196	positive reg	15/905	50/18866	6.80E-09	5.99E-08	3.15E-08	MMP12/IR
BP	GO:007022	lymphocyte	18/905	73/18866	6.93E-09	6.09E-08	3.20E-08	IDO1/CCL5
BP	GO:190203	regulation	18/905	73/18866	6.93E-09	6.09E-08	3.20E-08	PSMB8/PS
BP	GO:000209	positive reg	11/905	25/18866	7.00E-09	6.12E-08	3.22E-08	VEGFA/AR
BP	GO:004669	decidualiza	11/905	25/18866	7.00E-09	6.12E-08	3.22E-08	CTSB/MAP
BP	GO:007167	positive reg	11/905	25/18866	7.00E-09	6.12E-08	3.22E-08	CXCL10/CX
BP	GO:004232	negative re	54/905	484/18866	7.00E-09	6.12E-08	3.22E-08	IFNG/PSM
BP	GO:007054	response to	20/905	90/18866	7.11E-09	6.20E-08	3.26E-08	TLR2/FABP
BP	GO:000722	integrin-me	22/905	108/18866	7.13E-09	6.21E-08	3.26E-08	FCER1G/IS
BP	GO:000191	negative re	10/905	20/18866	7.32E-09	6.35E-08	3.34E-08	HLA-A/HLA
BP	GO:000282	positive reg	10/905	20/18866	7.32E-09	6.35E-08	3.34E-08	XCL1/IL1B/
BP	GO:009021	positive reg	13/905	37/18866	7.97E-09	6.91E-08	3.63E-08	TGFB1/SR
BP	GO:003505	cardiocyte	27/905	158/18866	8.21E-09	7.10E-08	3.73E-08	CALR/TGF
BP	GO:003030	negative re	30/905	190/18866	8.36E-09	7.21E-08	3.79E-08	TGFB1/PM
BP	GO:005104	negative re	30/905	190/18866	8.36E-09	7.21E-08	3.79E-08	HLA-F/IL1B
BP	GO:000267	positive reg	12/905	31/18866	8.37E-09	7.21E-08	3.79E-08	FCER1G/IL1
BP	GO:190289	regulation	15/905	51/18866	9.20E-09	7.91E-08	4.16E-08	TGFB1/TN
BP	GO:009702	dendritic ce	14/905	44/18866	9.25E-09	7.92E-08	4.16E-08	HLA-B/HLA
BP	GO:200040	regulation	14/905	44/18866	9.25E-09	7.92E-08	4.16E-08	CXCL10/CX
BP	GO:004870	astrocyte d	19/905	83/18866	1.00E-08	8.57E-08	4.50E-08	IFNG/S100
BP	GO:004325	regulation	51/905	449/18866	1.02E-08	8.72E-08	4.58E-08	HSPA5/HS
BP	GO:004858	developme	34/905	237/18866	1.07E-08	9.13E-08	4.80E-08	HSP90AA1/
BP	GO:004595	negative re	9/905	16/18866	1.09E-08	9.29E-08	4.88E-08	HLA-A/HLA
BP	GO:000717	transmemb	44/905	359/18866	1.11E-08	9.45E-08	4.97E-08	HSPA5/HS
BP	GO:003158	cell-substra	44/905	359/18866	1.11E-08	9.45E-08	4.97E-08	CALR/MM
BP	GO:003273	positive reg	13/905	38/18866	1.16E-08	9.80E-08	5.15E-08	FCER1G/XC
BP	GO:009002	positive reg	11/905	26/18866	1.16E-08	9.80E-08	5.15E-08	CXCL8/XCL
BP	GO:009002	regulation	11/905	26/18866	1.16E-08	9.80E-08	5.15E-08	CXCL10/CX
BP	GO:006138	regulation	22/905	111/18866	1.21E-08	1.02E-07	5.38E-08	CXCL12/VE
BP	GO:001403	mesenchym	19/905	84/18866	1.24E-08	1.04E-07	5.47E-08	MAPK3/ED
BP	GO:004886	stem cell d	19/905	84/18866	1.24E-08	1.04E-07	5.47E-08	MAPK3/ED
BP	GO:000272	regulation	12/905	32/18866	1.28E-08	1.07E-07	5.64E-08	B2M/HLA-
BP	GO:001074	regulation	12/905	32/18866	1.28E-08	1.07E-07	5.64E-08	CETP/ADIP
BP	GO:003272	positive reg	14/905	45/18866	1.28E-08	1.07E-07	5.64E-08	TLR2/IL1B/
BP	GO:004542	positive reg	14/905	45/18866	1.28E-08	1.07E-07	5.64E-08	HSP90AA1/
BP	GO:000253	production	20/905	93/18866	1.29E-08	1.08E-07	5.67E-08	FCER1G/LB
BP	GO:003545	response to	10/905	21/18866	1.34E-08	1.11E-07	5.85E-08	EIF2AK2/BS

BP	GO:00483	immunogl	10/905	21/18866	1.34E-08	1.11E-07	5.85E-08	RBP4/TNF/
BP	GO:00026	regulation	17/905	68/18866	1.45E-08	1.20E-07	6.33E-08	XCL1/TGFB
BP	GO:006161	pri-miRNA	15/905	53/18866	1.65E-08	1.37E-07	7.19E-08	TGFB1/TN
BP	GO:00420	type 2 imm	13/905	39/18866	1.66E-08	1.38E-07	7.23E-08	XCL1/IFNL
BP	GO:006141	regulation	18/905	77/18866	1.72E-08	1.42E-07	7.47E-08	PSMB8/PS
BP	GO:19044	positive re	14/905	46/18866	1.76E-08	1.46E-07	7.65E-08	HSP90AA1,
BP	GO:00486	negative re	17/905	69/18866	1.84E-08	1.52E-07	7.97E-08	IFNG/APO
BP	GO:00309	forebrain d	46/905	391/18866	1.86E-08	1.53E-07	8.04E-08	B2M/CXCL
BP	GO:19015	regulation	19/905	86/18866	1.87E-08	1.53E-07	8.06E-08	PSMB8/PS
BP	GO:00019	negative re	50/905	444/18866	1.89E-08	1.55E-07	8.14E-08	IFNG/PSM
BP	GO:00486	regulation	43/905	353/18866	1.96E-08	1.61E-07	8.44E-08	CXCL12/RB
BP	GO:00022	myeloid ce	26/905	154/18866	2.00E-08	1.64E-07	8.61E-08	B2M/FCER
BP	GO:006201	positive re	26/905	154/18866	2.00E-08	1.64E-07	8.61E-08	IFNG/TMS
BP	GO:00603	SMAD prot	18/905	78/18866	2.13E-08	1.74E-07	9.15E-08	TGFB1/FOS
BP	GO:000271	negative re	9/905	17/18866	2.22E-08	1.81E-07	9.50E-08	HLA-A/HLA
BP	GO:00069	inflammat	10/905	22/18866	2.35E-08	1.91E-07	1.00E-07	CTSL/IRF3/
BP	GO:19028	positive re	13/905	40/18866	2.35E-08	1.91E-07	1.00E-07	TGFB1/TN
BP	GO:00313	positive re	35/905	257/18866	2.53E-08	2.05E-07	1.08E-07	HSP90AA1,
BP	GO:00712	cellular res	18/905	79/18866	2.64E-08	2.14E-07	1.12E-07	IL1B/TLR3/
BP	GO:003051	regulation	20/905	97/18866	2.76E-08	2.23E-07	1.17E-07	CXCL12/VE
BP	GO:190121	positive re	20/905	97/18866	2.76E-08	2.23E-07	1.17E-07	IFNG/TNF/
BP	GO:00097	hormone-r	30/905	200/18866	2.80E-08	2.25E-07	1.18E-07	CALR/SRC/
BP	GO:00425	response t	25/905	146/18866	2.80E-08	2.25E-07	1.18E-07	LCN2/STAT
BP	GO:00316	regulation	8/905	13/18866	2.82E-08	2.27E-07	1.19E-07	IL1B/TNF/T
BP	GO:00027	MyD88-ind	12/905	34/18866	2.85E-08	2.28E-07	1.20E-07	IRF3/TLR3/
BP	GO:00702	regulation	12/905	34/18866	2.85E-08	2.28E-07	1.20E-07	IDO1/CCL5
BP	GO:190401	epithelial c	22/905	117/18866	3.32E-08	2.66E-07	1.40E-07	HLA-G/ICA
BP	GO:00140	neural cres	19/905	89/18866	3.38E-08	2.70E-07	1.42E-07	MAPK3/ED
BP	GO:00421	cellular ket	35/905	260/18866	3.41E-08	2.72E-07	1.43E-07	PSMB8/PS
BP	GO:00017	neural cres	15/905	56/18866	3.75E-08	2.97E-07	1.56E-07	EDN3/SEM
BP	GO:000271	regulation	15/905	56/18866	3.75E-08	2.97E-07	1.56E-07	FCER1G/LT
BP	GO:00028	regulation	15/905	56/18866	3.75E-08	2.97E-07	1.56E-07	FCER1G/LT
BP	GO:00702	regulation	15/905	56/18866	3.75E-08	2.97E-07	1.56E-07	IDO1/CCL5
BP	GO:00421	negative re	16/905	64/18866	3.85E-08	3.05E-07	1.60E-07	HLA-G/XCL
BP	GO:001401	regulation	23/905	128/18866	3.96E-08	3.13E-07	1.64E-07	LTA/TGFB1
BP	GO:00456	regulation	10/905	23/18866	3.97E-08	3.13E-07	1.65E-07	TGFB1/AD
BP	GO:00726	eosinophil	10/905	23/18866	3.97E-08	3.13E-07	1.65E-07	CCL13/CCL
BP	GO:00508	defense re	18/905	81/18866	4.00E-08	3.15E-07	1.66E-07	CD4/MR1/
BP	GO:00420	regulation	19/905	90/18866	4.09E-08	3.22E-07	1.69E-07	MMP9/FAS
BP	GO:00083	regulation	28/905	181/18866	4.11E-08	3.23E-07	1.70E-07	HSP90AB1,
BP	GO:00603	regulation	12/905	35/18866	4.14E-08	3.24E-07	1.70E-07	HSP90AB1,
BP	GO:00706	response t	12/905	35/18866	4.14E-08	3.24E-07	1.70E-07	HSPA5/HSP
BP	GO:00614	connective	35/905	262/18866	4.15E-08	3.24E-07	1.70E-07	TGFB1/MA
BP	GO:00140	response t	25/905	149/18866	4.25E-08	3.31E-07	1.74E-07	HSPA5/IL1
BP	GO:00510	regulation	9/905	18/18866	4.25E-08	3.31E-07	1.74E-07	RBP4/TNF/
BP	GO:00702	T cell apop	14/905	49/18866	4.34E-08	3.38E-07	1.77E-07	IDO1/CCL5
BP	GO:00017	myeloid de	11/905	29/18866	4.55E-08	3.52E-07	1.85E-07	RELB/IL10/
BP	GO:00330	regulation	11/905	29/18866	4.55E-08	3.52E-07	1.85E-07	FCER1G/AD
BP	GO:00363	dendritic c	11/905	29/18866	4.55E-08	3.52E-07	1.85E-07	CALR/CCL5
BP	GO:00430	positive re	11/905	29/18866	4.55E-08	3.52E-07	1.85E-07	LBP/WNT5

BP	GO:004600	regulation	13/905	42/18866	4.56E-08	3.53E-07	1.85E-07	AGER/EPO
BP	GO:003327	response to	19/905	91/18866	4.94E-08	3.81E-07	2.00E-07	CD4/CXCL1
BP	GO:001081	regulation	31/905	217/18866	5.23E-08	4.03E-07	2.12E-07	CALR/MMP
BP	GO:003017	positive reg	28/905	183/18866	5.24E-08	4.03E-07	2.12E-07	PSMB8/PS
BP	GO:199013	neuron pro	27/905	172/18866	5.24E-08	4.03E-07	2.12E-07	HSP90AA1
BP	GO:004513	developme	32/905	229/18866	5.43E-08	4.17E-07	2.19E-07	HSPA5/ICA
BP	GO:007067	response to	14/905	50/18866	5.76E-08	4.41E-07	2.32E-07	IFNG/PSM
BP	GO:190372	positive reg	14/905	50/18866	5.76E-08	4.41E-07	2.32E-07	TGFB1/FA
BP	GO:004574	positive reg	12/905	36/18866	5.95E-08	4.54E-07	2.39E-07	MMP9/FA
BP	GO:190520	regulation	16/905	66/18866	6.16E-08	4.70E-07	2.47E-07	TGFB1/SE
BP	GO:003051	negative re	13/905	43/18866	6.26E-08	4.77E-07	2.50E-07	WNT5A/SE
BP	GO:000247	antigen pro	8/905	14/18866	6.31E-08	4.80E-07	2.52E-07	AZGP1/B2
BP	GO:000271	negative re	10/905	24/18866	6.52E-08	4.95E-07	2.60E-07	HLA-F/XCL
BP	GO:004873	cardiac mu	32/905	231/18866	6.68E-08	5.07E-07	2.66E-07	CALR/TGF
BP	GO:001072	negative re	41/905	343/18866	7.11E-08	5.38E-07	2.83E-07	B2M/CALR
BP	GO:200011	negative re	19/905	93/18866	7.15E-08	5.41E-07	2.84E-07	MMP9/LT
BP	GO:004327	apoptotic c	14/905	51/18866	7.60E-08	5.74E-07	3.02E-07	ITGAV/CCL
BP	GO:001075	positive reg	9/905	19/18866	7.73E-08	5.80E-07	3.05E-07	CCL5/MAP
BP	GO:004824	eosinophil	9/905	19/18866	7.73E-08	5.80E-07	3.05E-07	CCL13/CCL
BP	GO:007023	negative re	9/905	19/18866	7.73E-08	5.80E-07	3.05E-07	IDO1/CCL5
BP	GO:009854	detection o	9/905	19/18866	7.73E-08	5.80E-07	3.05E-07	HLA-A/HLA
BP	GO:015014	cell junctio	9/905	19/18866	7.73E-08	5.80E-07	3.05E-07	CX3CR1/D
BP	GO:004303	regulation	15/905	59/18866	8.03E-08	6.02E-07	3.16E-07	LBP/WNT5
BP	GO:000821	regulation	28/905	187/18866	8.39E-08	6.28E-07	3.30E-07	ERAP1/CTS
BP	GO:004568	positive reg	13/905	44/18866	8.49E-08	6.34E-07	3.33E-07	TGFB1/TLR
BP	GO:003010	regulation	30/905	210/18866	8.57E-08	6.39E-07	3.36E-07	B2M/VEGF
BP	GO:190165	cellular res	45/905	398/18866	8.67E-08	6.46E-07	3.39E-07	ICAM1/IL1
BP	GO:001657	protein de	36/905	283/18866	9.41E-08	7.00E-07	3.68E-07	PSMB8/PS
BP	GO:004875	branching	25/905	155/18866	9.46E-08	7.03E-07	3.69E-07	TNF/PML/
BP	GO:000840	gonad deve	31/905	223/18866	9.87E-08	7.32E-07	3.85E-07	HSPA5/ICA
BP	GO:004826	positive reg	14/905	52/18866	9.94E-08	7.36E-07	3.87E-07	B2M/VEGF
BP	GO:000282	regulation	11/905	31/18866	1.02E-07	7.52E-07	3.95E-07	XCL1/IFNL1
BP	GO:190262	positive reg	11/905	31/18866	1.02E-07	7.52E-07	3.95E-07	CXCL8/XCL
BP	GO:200040	positive reg	11/905	31/18866	1.02E-07	7.52E-07	3.95E-07	CXCL10/CX
BP	GO:190342	positive reg	15/905	60/18866	1.02E-07	7.54E-07	3.97E-07	HSP90AA1
BP	GO:003109	regeneratio	29/905	201/18866	1.13E-07	8.30E-07	4.36E-07	CXCL12/AP
BP	GO:001400	astrocyte d	13/905	45/18866	1.14E-07	8.39E-07	4.41E-07	IFNG/S100
BP	GO:190118	positive reg	12/905	38/18866	1.18E-07	8.63E-07	4.54E-07	MMP9/FA
BP	GO:003033	negative re	41/905	350/18866	1.24E-07	9.10E-07	4.78E-07	CALR/CXCL
BP	GO:005178	positive reg	18/905	87/18866	1.29E-07	9.39E-07	4.94E-07	TGFB1/IL1
BP	GO:006021	hematopoi	18/905	87/18866	1.29E-07	9.39E-07	4.94E-07	PSMB8/PS
BP	GO:004333	response to	14/905	53/18866	1.29E-07	9.41E-07	4.95E-07	DDX58/IRF
BP	GO:004559	negative re	14/905	53/18866	1.29E-07	9.41E-07	4.95E-07	TGFB1/TN
BP	GO:002303	CD40 signa	8/905	15/18866	1.30E-07	9.43E-07	4.95E-07	CD40/TNF
BP	GO:005138	response to	24/905	147/18866	1.34E-07	9.76E-07	5.13E-07	ICAM1/S10
BP	GO:190382	positive reg	40/905	338/18866	1.34E-07	9.76E-07	5.13E-07	FCER1G/H
BP	GO:000241	immune re	9/905	20/18866	1.35E-07	9.76E-07	5.13E-07	HLA-A/MR
BP	GO:007064	protein mo	37/905	300/18866	1.39E-07	1.01E-06	5.29E-07	PSMB8/PS
BP	GO:200014	negative re	42/905	365/18866	1.44E-07	1.04E-06	5.46E-07	CALR/CXCL
BP	GO:012016	positive reg	19/905	97/18866	1.45E-07	1.04E-06	5.49E-07	LCN2/FAB

BP	GO:190118	regulation	19/905	97/18866	1.45E-07	1.04E-06	5.49E-07	MMP9/FAS
BP	GO:003267	regulation	11/905	32/18866	1.49E-07	1.07E-06	5.60E-07	FCER1G/CD
BP	GO:003812	ERBB2 sign	11/905	32/18866	1.49E-07	1.07E-06	5.60E-07	HSP90AA1/
BP	GO:004558	regulation	11/905	32/18866	1.49E-07	1.07E-06	5.60E-07	HLA-G/IFN
BP	GO:007135	cellular res	11/905	32/18866	1.49E-07	1.07E-06	5.60E-07	HSPA5/HSP
BP	GO:004333	response t	13/905	46/18866	1.52E-07	1.09E-06	5.73E-07	DDX58/IRF
BP	GO:190547	positive reg	22/905	127/18866	1.53E-07	1.09E-06	5.74E-07	IFNG/TNF/
BP	GO:005134	regulation	21/905	117/18866	1.56E-07	1.12E-06	5.86E-07	HSP90AA1/
BP	GO:003165	positive reg	7/905	11/18866	1.59E-07	1.13E-06	5.95E-07	IL1B/TNF/T
BP	GO:007075	interleukin	7/905	11/18866	1.59E-07	1.13E-06	5.95E-07	STAT1/EBI3
BP	GO:009888	synapse pr	7/905	11/18866	1.59E-07	1.13E-06	5.95E-07	CX3CR1/DK
BP	GO:003274	positive reg	10/905	26/18866	1.62E-07	1.15E-06	6.03E-07	CD4/IL1B/I
BP	GO:004210	positive reg	10/905	26/18866	1.62E-07	1.15E-06	6.03E-07	AGER/EPO/
BP	GO:000229	CD4-positiv	15/905	62/18866	1.64E-07	1.16E-06	6.10E-07	IFNG/RELB/
BP	GO:003031	osteoclast	19/905	98/18866	1.72E-07	1.22E-06	6.39E-07	FCER1G/IF
BP	GO:190595	regulation	26/905	171/18866	1.77E-07	1.25E-06	6.58E-07	IL1B/FABP3
BP	GO:004343	negative re	27/905	183/18866	1.94E-07	1.37E-06	7.18E-07	PSMD10/X
BP	GO:000224	hematopoi	26/905	172/18866	1.99E-07	1.41E-06	7.39E-07	PSMB8/PS
BP	GO:002260	ovulation c	13/905	47/18866	2.01E-07	1.42E-06	7.45E-07	HSPA5/SRC
BP	GO:000228	alpha-beta	15/905	63/18866	2.05E-07	1.44E-06	7.58E-07	IFNG/RELB/
BP	GO:000229	alpha-beta	15/905	63/18866	2.05E-07	1.44E-06	7.58E-07	IFNG/RELB/
BP	GO:007200	renal syste	36/905	292/18866	2.07E-07	1.45E-06	7.63E-07	MMP9/RB
BP	GO:004664	regulation	11/905	33/18866	2.13E-07	1.49E-06	7.84E-07	HLA-A/XCL
BP	GO:009002	regulation	11/905	33/18866	2.13E-07	1.49E-06	7.84E-07	CXCL8/XCL
BP	GO:006056	epithelial t	39/905	331/18866	2.16E-07	1.51E-06	7.94E-07	CXCL10/TG
BP	GO:014035	lipid export	12/905	40/18866	2.22E-07	1.55E-06	8.15E-07	IL1B/TNFS
BP	GO:004814	astrocyte a	10/905	27/18866	2.46E-07	1.71E-06	9.00E-07	IFNG/IL1B/
BP	GO:000252	leukocyte r	8/905	16/18866	2.48E-07	1.73E-06	9.08E-07	S100A9/S1
BP	GO:005109	positive reg	26/905	174/18866	2.52E-07	1.75E-06	9.20E-07	B2M/HSP9
BP	GO:004663	regulation	15/905	64/18866	2.57E-07	1.78E-06	9.35E-07	IFNG/SOCS
BP	GO:006013	maternal p	15/905	64/18866	2.57E-07	1.78E-06	9.35E-07	CTSB/MAP
BP	GO:001491	positive reg	13/905	48/18866	2.64E-07	1.83E-06	9.60E-07	NOX4/CCL5
BP	GO:004337	regulation	13/905	48/18866	2.64E-07	1.83E-06	9.60E-07	IFNG/SOCS
BP	GO:006068	regulation	14/905	56/18866	2.73E-07	1.88E-06	9.90E-07	TNF/VEGFA
BP	GO:001052	regulation	19/905	101/18866	2.82E-07	1.95E-06	1.02E-06	CD4/CXCL1
BP	GO:005068	negative re	26/905	175/18866	2.83E-07	1.95E-06	1.02E-06	B2M/TGFB
BP	GO:003087	mammary	23/905	142/18866	2.83E-07	1.95E-06	1.02E-06	PML/VEGFA
BP	GO:005134	negative re	36/905	296/18866	2.90E-07	1.99E-06	1.05E-06	IFNG/IL1B/
BP	GO:190204	negative re	12/905	41/18866	3.00E-07	2.06E-06	1.08E-06	ICAM1/TN
BP	GO:003281	regulation	11/905	34/18866	3.02E-07	2.07E-06	1.09E-06	HLA-F/MIC
BP	GO:003529	regulation	23/905	143/18866	3.22E-07	2.20E-06	1.16E-06	ICAM1/F2R
BP	GO:004559	regulation	23/905	143/18866	3.22E-07	2.20E-06	1.16E-06	TGFB1/TN
BP	GO:009774	regulation	23/905	143/18866	3.22E-07	2.20E-06	1.16E-06	ICAM1/F2R
BP	GO:000268	negative re	13/905	49/18866	3.44E-07	2.34E-06	1.23E-06	CXCL12/AP
BP	GO:004505	T cell selec	13/905	49/18866	3.44E-07	2.34E-06	1.23E-06	CD4/CTSL/
BP	GO:007134	cellular res	13/905	49/18866	3.44E-07	2.34E-06	1.23E-06	IFNG/PSM
BP	GO:005105	positive reg	28/905	200/18866	3.51E-07	2.39E-06	1.25E-06	HSP90AA1/
BP	GO:000255	mast cell cl	7/905	12/18866	3.66E-07	2.47E-06	1.30E-06	VEGFA/CCL
BP	GO:003249	detection c	7/905	12/18866	3.66E-07	2.47E-06	1.30E-06	TLR2/LBP/
BP	GO:003811	interleukin	7/905	12/18866	3.66E-07	2.47E-06	1.30E-06	PTK2B/IL2R

BP	GO:190353	negative re	25/905	166/18866	3.66E-07	2.47E-06	1.30E-06	HLA-F/IL1B
BP	GO:003515	regulation	23/905	144/18866	3.67E-07	2.47E-06	1.30E-06	ICAM1/F2R
BP	GO:010610	cold-induce	23/905	144/18866	3.67E-07	2.47E-06	1.30E-06	LCN2/FABP
BP	GO:012016	regulation	23/905	144/18866	3.67E-07	2.47E-06	1.30E-06	LCN2/FABP
BP	GO:000189	tissue hom	33/905	261/18866	3.69E-07	2.49E-06	1.31E-06	AZGP1/B2M
BP	GO:199084	adaptive th	24/905	155/18866	3.71E-07	2.49E-06	1.31E-06	LCN2/FABP
BP	GO:003297	regulation	44/905	405/18866	3.73E-07	2.50E-06	1.32E-06	ICAM1/CXC
BP	GO:006636	transcriptio	27/905	189/18866	3.76E-07	2.52E-06	1.32E-06	PSMC2/PSM
BP	GO:004668	response to	22/905	134/18866	4.02E-07	2.69E-06	1.41E-06	HSPA5/IL1B
BP	GO:190262	regulation	12/905	42/18866	4.02E-07	2.69E-06	1.41E-06	CXCL8/XCL
BP	GO:003110	animal orga	16/905	75/18866	4.11E-07	2.74E-06	1.44E-06	CXCL12/IL1
BP	GO:000836	regulation	24/905	156/18866	4.19E-07	2.79E-06	1.47E-06	ICAM1/CCL
BP	GO:000743	salivary gla	11/905	35/18866	4.21E-07	2.80E-06	1.47E-06	TGFB1/TNF
BP	GO:003263	interleukin	11/905	35/18866	4.21E-07	2.80E-06	1.47E-06	FCER1G/CD
BP	GO:004506	regulatory	11/905	35/18866	4.21E-07	2.80E-06	1.47E-06	HLA-G/IFNG
BP	GO:000276	positive reg	14/905	58/18866	4.36E-07	2.89E-06	1.52E-06	CD4/IFNG/
BP	GO:005159	response to	18/905	94/18866	4.38E-07	2.90E-06	1.52E-06	HSPA5/NO
BP	GO:190403	regulation	18/905	94/18866	4.38E-07	2.90E-06	1.52E-06	HLA-G/ICAM
BP	GO:004685	regulation	13/905	50/18866	4.44E-07	2.94E-06	1.54E-06	TFRC/TNFA
BP	GO:001604	detection o	8/905	17/18866	4.49E-07	2.96E-06	1.56E-06	HLA-A/HLA
BP	GO:003269	negative re	8/905	17/18866	4.49E-07	2.96E-06	1.56E-06	TLR8/CCR7
BP	GO:001077	positive reg	24/905	157/18866	4.72E-07	3.11E-06	1.64E-06	CALR/CXCL
BP	GO:004315	negative re	17/905	85/18866	4.78E-07	3.14E-06	1.65E-06	MMP9/TNF
BP	GO:004567	regulation	15/905	67/18866	4.86E-07	3.19E-06	1.68E-06	IFNG/LTF/T
BP	GO:000195	regulation	21/905	125/18866	4.95E-07	3.25E-06	1.71E-06	MMP12/PL
BP	GO:003307	T cell differ	16/905	76/18866	4.97E-07	3.26E-06	1.71E-06	B2M/MR1/
BP	GO:200010	positive reg	10/905	29/18866	5.34E-07	3.50E-06	1.84E-06	IDO1/CCL5
BP	GO:005070	regulation	14/905	59/18866	5.46E-07	3.57E-06	1.88E-06	IFNG/TLR2/
BP	GO:000276	negative re	13/905	51/18866	5.70E-07	3.72E-06	1.96E-06	LTF/TLR3/A
BP	GO:004871	positive reg	9/905	23/18866	5.75E-07	3.75E-06	1.97E-06	TLR2/HDAC
BP	GO:000189	maternal p	11/905	36/18866	5.80E-07	3.77E-06	1.98E-06	CTSB/MAP
BP	GO:003328	response to	11/905	36/18866	5.80E-07	3.77E-06	1.98E-06	CD4/CXCL1
BP	GO:003440	response to	11/905	36/18866	5.80E-07	3.77E-06	1.98E-06	SRC/PTGS2
BP	GO:000275	cytoplasmi	15/905	68/18866	5.96E-07	3.87E-06	2.03E-06	DDX58/IRF
BP	GO:007257	endothelia	15/905	68/18866	5.96E-07	3.87E-06	2.03E-06	HLA-G/ICAM
BP	GO:009009	regulation	32/905	254/18866	6.00E-07	3.89E-06	2.04E-06	HSPA5/HSP
BP	GO:003209	negative re	19/905	106/18866	6.17E-07	3.99E-06	2.10E-06	B2M/SLPI/
BP	GO:004209	T-helper ce	14/905	60/18866	6.81E-07	4.40E-06	2.31E-06	RELB/IL27/
BP	GO:003262	interleukin	12/905	44/18866	7.02E-07	4.53E-06	2.38E-06	MR1/IFNG/
BP	GO:190547	regulation	27/905	195/18866	7.08E-07	4.56E-06	2.40E-06	IFNG/TGFB
BP	GO:003295	regulation	40/905	360/18866	7.09E-07	4.57E-06	2.40E-06	ICAM1/CXC
BP	GO:004689	regulation	28/905	207/18866	7.17E-07	4.61E-06	2.42E-06	IFNG/NFYA
BP	GO:005105	positive reg	16/905	78/18866	7.21E-07	4.63E-06	2.44E-06	F2R/F2RL1/
BP	GO:003572	interleukin	7/905	13/18866	7.60E-07	4.85E-06	2.55E-06	CD4/IL15/I
BP	GO:006034	positive reg	7/905	13/18866	7.60E-07	4.85E-06	2.55E-06	MMP12/IR
BP	GO:007135	cellular res	7/905	13/18866	7.60E-07	4.85E-06	2.55E-06	CD4/IL15/I
BP	GO:007135	cellular res	7/905	13/18866	7.60E-07	4.85E-06	2.55E-06	PTK2B/IL2R
BP	GO:009753	mast cell m	7/905	13/18866	7.60E-07	4.85E-06	2.55E-06	VEGFA/CCL
BP	GO:190228	semaphorin	7/905	13/18866	7.60E-07	4.85E-06	2.55E-06	SEMA3A/P
BP	GO:009009	negative re	26/905	184/18866	7.62E-07	4.86E-06	2.55E-06	PSMB8/PSM

BP	GO:006082	regulation	35/905	295/18866	7.64E-07	4.86E-06	2.55E-06	PSMB8/PS
BP	GO:009026	positive re	23/905	150/18866	7.71E-07	4.90E-06	2.58E-06	PSMB8/PS
BP	GO:004573	respiratory	11/905	37/18866	7.90E-07	5.00E-06	2.63E-06	LBP/CYBB/
BP	GO:006220	positive re	11/905	37/18866	7.90E-07	5.00E-06	2.63E-06	TLR2/LBP/
BP	GO:007154	dopaminer	11/905	37/18866	7.90E-07	5.00E-06	2.63E-06	VEGFA/W
BP	GO:003286	response t	34/905	283/18866	8.21E-07	5.19E-06	2.73E-06	ICAM1/TL
BP	GO:000926	response t	30/905	233/18866	8.45E-07	5.34E-06	2.80E-06	HSPA2/HS
BP	GO:190204	regulation	14/905	61/18866	8.45E-07	5.34E-06	2.80E-06	ICAM1/TN
BP	GO:007155	response t	32/905	258/18866	8.51E-07	5.36E-06	2.82E-06	HSPA5/HS
BP	GO:004353	positive re	16/905	79/18866	8.65E-07	5.44E-06	2.86E-06	TMSB4X/T
BP	GO:000175	organ indu	9/905	24/18866	8.81E-07	5.52E-06	2.90E-06	WNT5A/FG
BP	GO:003275	positive re	9/905	24/18866	8.81E-07	5.52E-06	2.90E-06	FCER1G/C
BP	GO:003412	positive re	9/905	24/18866	8.81E-07	5.52E-06	2.90E-06	TLR2/LBP/
BP	GO:005077	negative re	15/905	70/18866	8.86E-07	5.55E-06	2.92E-06	WNT5A/PT
BP	GO:005237	modulatio	12/905	45/18866	9.16E-07	5.73E-06	3.01E-06	CD4/CXCL
BP	GO:003476	positive re	28/905	210/18866	9.62E-07	6.01E-06	3.16E-06	HSPA2/IFN
BP	GO:005105	regulation	40/905	365/18866	1.01E-06	6.31E-06	3.32E-06	HSP90AA1,
BP	GO:001051	positive re	14/905	62/18866	1.04E-06	6.51E-06	3.42E-06	CCL5/PDG
BP	GO:200035	regulation	14/905	62/18866	1.04E-06	6.51E-06	3.42E-06	HLA-G/ICA
BP	GO:003139	regulation	28/905	211/18866	1.06E-06	6.59E-06	3.46E-06	HSPA5/HS
BP	GO:007022	negative re	10/905	31/18866	1.08E-06	6.74E-06	3.54E-06	IDO1/CCL5
BP	GO:007030	cellular res	18/905	100/18866	1.14E-06	7.06E-06	3.71E-06	LCN2/TNF
BP	GO:001086	positive re	12/905	46/18866	1.19E-06	7.35E-06	3.86E-06	PDGFRB/C
BP	GO:003323	regulation	16/905	81/18866	1.23E-06	7.63E-06	4.01E-06	PSMB8/PS
BP	GO:000271	negative re	8/905	19/18866	1.28E-06	7.92E-06	4.16E-06	HLA-F/HLA
BP	GO:009002	positive re	8/905	19/18866	1.28E-06	7.92E-06	4.16E-06	CXCL10/CX
BP	GO:004353	blood vess	26/905	189/18866	1.28E-06	7.92E-06	4.16E-06	TMSB4X/T
BP	GO:006103	regulation	15/905	72/18866	1.30E-06	8.00E-06	4.21E-06	WNT5A/B
BP	GO:006033	regulation	9/905	25/18866	1.32E-06	8.11E-06	4.26E-06	HSP90AB1,
BP	GO:006033	regulation	9/905	25/18866	1.32E-06	8.11E-06	4.26E-06	HSP90AB1,
BP	GO:003050	BMP signal	23/905	155/18866	1.39E-06	8.52E-06	4.48E-06	TGFB1/HJV
BP	GO:000743	salivary gla	11/905	39/18866	1.42E-06	8.70E-06	4.57E-06	TGFB1/TN
BP	GO:005135	positive re	13/905	55/18866	1.45E-06	8.89E-06	4.67E-06	IFNG/S100
BP	GO:001093	regulation	7/905	14/18866	1.46E-06	8.89E-06	4.67E-06	HLA-G/TGF
BP	GO:003231	prostaglan	7/905	14/18866	1.46E-06	8.89E-06	4.67E-06	IL1B/TNFSF
BP	GO:003268	negative re	7/905	14/18866	1.46E-06	8.89E-06	4.67E-06	RELB/NLRX
BP	GO:007066	response t	7/905	14/18866	1.46E-06	8.89E-06	4.67E-06	PTK2B/IL2
BP	GO:007067	response t	7/905	14/18866	1.46E-06	8.89E-06	4.67E-06	CD4/IL15/I
BP	GO:007156	cellular res	31/905	252/18866	1.50E-06	9.14E-06	4.81E-06	HSPA5/HS
BP	GO:003469	response t	10/905	32/18866	1.51E-06	9.16E-06	4.81E-06	TNFSF4/CC
BP	GO:003545	response t	10/905	32/18866	1.51E-06	9.16E-06	4.81E-06	TLR3/STAT
BP	GO:006103	positive re	10/905	32/18866	1.51E-06	9.16E-06	4.81E-06	WNT5A/B
BP	GO:003572	interleukin	12/905	47/18866	1.52E-06	9.22E-06	4.85E-06	IFNG/PSM
BP	GO:004663	positive re	12/905	47/18866	1.52E-06	9.22E-06	4.85E-06	IFNG/SOCS
BP	GO:001051	regulation	15/905	73/18866	1.56E-06	9.45E-06	4.96E-06	CCL5/PDG
BP	GO:004545	bone resor	14/905	64/18866	1.57E-06	9.50E-06	4.99E-06	NOX4/TFR
BP	GO:005196	negative re	36/905	319/18866	1.76E-06	1.06E-05	5.59E-06	B2M/CALR,
BP	GO:004518	maintenan	17/905	93/18866	1.80E-06	1.08E-05	5.70E-06	CD4/HSPA
BP	GO:009018	regulation	13/905	56/18866	1.81E-06	1.09E-05	5.73E-06	MMP9/AD
BP	GO:190464	response t	13/905	56/18866	1.81E-06	1.09E-05	5.73E-06	ICAM1/M

BP	GO:000271	positive re	11/905	40/18866	1.87E-06	1.12E-05	5.89E-06	FCER1G/LT
BP	GO:000289	positive re	11/905	40/18866	1.87E-06	1.12E-05	5.89E-06	FCER1G/LT
BP	GO:003414	toll-like rec	11/905	40/18866	1.87E-06	1.12E-05	5.89E-06	S100A14/L
BP	GO:009018	positive re	11/905	40/18866	1.87E-06	1.12E-05	5.89E-06	ADIPOQ/V
BP	GO:190332	regulation	30/905	242/18866	1.88E-06	1.12E-05	5.91E-06	HSPA5/HS
BP	GO:003164	killing of ce	14/905	65/18866	1.92E-06	1.14E-05	6.02E-06	IFNG/CCL1
BP	GO:000234	response t	9/905	26/18866	1.93E-06	1.15E-05	6.05E-06	HLA-A/MR
BP	GO:000250	tolerance i	9/905	26/18866	1.93E-06	1.15E-05	6.05E-06	HLA-B/HLA
BP	GO:190027	regulation	12/905	48/18866	1.94E-06	1.16E-05	6.08E-06	PDGFRB/C
BP	GO:003367	negative re	32/905	268/18866	1.96E-06	1.17E-05	6.14E-06	IFNG/IL1B/
BP	GO:003011	regulation	40/905	375/18866	2.00E-06	1.19E-05	6.25E-06	PSMB8/PS
BP	GO:000272	positive re	8/905	20/18866	2.05E-06	1.21E-05	6.35E-06	B2M/HLA-
BP	GO:003413	toll-like rec	8/905	20/18866	2.05E-06	1.21E-05	6.35E-06	TLR3/TNFA
BP	GO:005176	nitric-oxide	8/905	20/18866	2.05E-06	1.21E-05	6.35E-06	IFNG/TLR2
BP	GO:005176	regulation	8/905	20/18866	2.05E-06	1.21E-05	6.35E-06	IFNG/TLR2
BP	GO:005088	endocrine	16/905	84/18866	2.05E-06	1.21E-05	6.35E-06	IL1B/CTSG
BP	GO:000720	phospholip	18/905	104/18866	2.06E-06	1.21E-05	6.38E-06	F2R/F2RL1
BP	GO:000269	regulation	10/905	33/18866	2.07E-06	1.22E-05	6.42E-06	ICAM1/CX
BP	GO:007138	cellular res	27/905	206/18866	2.09E-06	1.23E-05	6.48E-06	CALR/ICAM
BP	GO:190595	positive re	17/905	94/18866	2.10E-06	1.24E-05	6.49E-06	IL1B/FABP
BP	GO:005076	negative re	34/905	295/18866	2.12E-06	1.25E-05	6.55E-06	B2M/CALR
BP	GO:000267	regulation	6/905	10/18866	2.13E-06	1.25E-05	6.57E-06	LTA/TNF/ID
BP	GO:003230	positive re	6/905	10/18866	2.13E-06	1.25E-05	6.57E-06	IL1B/TNFS
BP	GO:000164	osteoblast	29/905	231/18866	2.15E-06	1.26E-05	6.63E-06	PSMC2/LT
BP	GO:004568	regulation	15/905	75/18866	2.24E-06	1.31E-05	6.89E-06	TGFB1/TLR
BP	GO:000154	ovarian fol	13/905	57/18866	2.24E-06	1.31E-05	6.89E-06	ICAM1/VE
BP	GO:003007	peptide ho	31/905	257/18866	2.28E-06	1.33E-05	7.01E-06	IFNG/IL1B/
BP	GO:000182	kidney dev	33/905	283/18866	2.31E-06	1.35E-05	7.08E-06	MMP9/AD
BP	GO:005500	cardiac mu	20/905	126/18866	2.31E-06	1.35E-05	7.08E-06	CALR/TGF
BP	GO:004654	developme	18/905	105/18866	2.37E-06	1.38E-05	7.26E-06	HSPA5/ICA
BP	GO:004563	negative re	17/905	95/18866	2.44E-06	1.42E-05	7.46E-06	LTF/TLR3/
BP	GO:003089	positive re	11/905	41/18866	2.45E-06	1.42E-05	7.46E-06	TFRC/CD4
BP	GO:190520	positive re	11/905	41/18866	2.45E-06	1.42E-05	7.46E-06	TGFB1/SE
BP	GO:003413	toll-like rec	7/905	15/18866	2.62E-06	1.52E-05	7.97E-06	TLR2/TNFA
BP	GO:009059	inflammato	7/905	15/18866	2.62E-06	1.52E-05	7.97E-06	TGFB1/F2R
BP	GO:000646	negative re	30/905	246/18866	2.64E-06	1.53E-05	8.03E-06	IFNG/IL1B/
BP	GO:003476	positive re	23/905	161/18866	2.70E-06	1.56E-05	8.21E-06	HSPA2/IFN
BP	GO:001003	response t	39/905	366/18866	2.75E-06	1.59E-05	8.33E-06	B2M/CALR
BP	GO:000756	embryo im	13/905	58/18866	2.77E-06	1.59E-05	8.38E-06	CALR/MM
BP	GO:006007	canonical	37/905	339/18866	2.81E-06	1.62E-05	8.52E-06	PSMB8/PS
BP	GO:005121	cartilage d	26/905	197/18866	2.82E-06	1.62E-05	8.54E-06	TGFB1/MA
BP	GO:000177	leukocyte	16/905	86/18866	2.83E-06	1.63E-05	8.55E-06	FCER1G/T
BP	GO:004308	regulation	47/905	481/18866	3.08E-06	1.77E-05	9.30E-06	ICAM1/CX
BP	GO:004564	regulation	12/905	50/18866	3.10E-06	1.78E-05	9.33E-06	B2M/STAT
BP	GO:009730	programm	12/905	50/18866	3.10E-06	1.78E-05	9.33E-06	IRF3/TNF/
BP	GO:004664	positive re	8/905	21/18866	3.16E-06	1.81E-05	9.50E-06	HLA-A/XCL
BP	GO:009028	positive re	8/905	21/18866	3.16E-06	1.81E-05	9.50E-06	CXCL12/PD
BP	GO:009027	regulation	11/905	42/18866	3.17E-06	1.81E-05	9.50E-06	CXCL12/TR
BP	GO:009876	response t	11/905	42/18866	3.17E-06	1.81E-05	9.50E-06	PDIA3/SOC
BP	GO:009876	cellular res	11/905	42/18866	3.17E-06	1.81E-05	9.50E-06	PDIA3/SOC

BP	GO:19047	regulation	16/905	87/18866	3.31E-06	1.89E-05	9.91E-06	MMP9/TN
BP	GO:19908	vascular as	16/905	87/18866	3.31E-06	1.89E-05	9.91E-06	MMP9/TN
BP	GO:00341	erythrocyt	20/905	129/18866	3.36E-06	1.91E-05	1.00E-05	B2M/STAT
BP	GO:00197	antibacteri	13/905	59/18866	3.39E-06	1.92E-05	1.01E-05	HLA-A/SLP
BP	GO:00480	platelet-de	13/905	59/18866	3.39E-06	1.92E-05	1.01E-05	APOD/ADI
BP	GO:00199	cyclic-nucl	28/905	224/18866	3.49E-06	1.98E-05	1.04E-05	CXCL10/CX
BP	GO:00071	G protein-	31/905	263/18866	3.71E-06	2.10E-05	1.10E-05	CXCL10/CX
BP	GO:00713	cellular res	36/905	330/18866	3.87E-06	2.18E-05	1.15E-05	IL1B/ADIP
BP	GO:00328	receptor bi	9/905	28/18866	3.91E-06	2.21E-05	1.16E-05	IFNG/TNF/
BP	GO:01500	regulation	11/905	43/18866	4.08E-06	2.30E-05	1.21E-05	MMP9/IL1
BP	GO:00977	positive re	13/905	60/18866	4.14E-06	2.33E-05	1.23E-05	F2RL1/NO
BP	GO:00032	cardiac ch	20/905	131/18866	4.28E-06	2.40E-05	1.26E-05	TGFB1/RB
BP	GO:00468	positive re	20/905	131/18866	4.28E-06	2.40E-05	1.26E-05	RBP4/TFR2
BP	GO:00109	macropha	7/905	16/18866	4.46E-06	2.50E-05	1.31E-05	HLA-G/TG
BP	GO:00330	negative r	7/905	16/18866	4.46E-06	2.50E-05	1.31E-05	FCER1G/C
BP	GO:00517	positive re	7/905	16/18866	4.46E-06	2.50E-05	1.31E-05	IFNG/TLR2
BP	GO:00323	regulation	6/905	11/18866	4.50E-06	2.52E-05	1.32E-05	IL1B/TNFS
BP	GO:00701	interleukin	6/905	11/18866	4.50E-06	2.52E-05	1.32E-05	STAT1/IL2
BP	GO:00435	regulation	16/905	89/18866	4.52E-06	2.52E-05	1.33E-05	TNF/WNT5
BP	GO:20012	regulation	23/905	166/18866	4.58E-06	2.56E-05	1.34E-05	CXCL12/S1
BP	GO:00901	positive re	18/905	110/18866	4.71E-06	2.63E-05	1.38E-05	HSP90AB1
BP	GO:00017	natural kill	8/905	22/18866	4.76E-06	2.65E-05	1.39E-05	PGLYRP1/P
BP	GO:00001	activation	12/905	52/18866	4.82E-06	2.68E-05	1.41E-05	F2R/EIF2A
BP	GO:003021	erythrocyt	19/905	121/18866	4.84E-06	2.69E-05	1.41E-05	B2M/STAT
BP	GO:00323	positive re	14/905	70/18866	4.85E-06	2.70E-05	1.42E-05	IL1B/FABP
BP	GO:200051	positive re	10/905	36/18866	4.99E-06	2.77E-05	1.46E-05	IFNG/XCL1
BP	GO:00023	immunogl	13/905	61/18866	5.04E-06	2.79E-05	1.47E-05	HLA-DQB1
BP	GO:00085	female go	17/905	100/18866	5.06E-06	2.80E-05	1.47E-05	HSPA5/ICA
BP	GO:00508	regulation	17/905	100/18866	5.06E-06	2.80E-05	1.47E-05	CD4/TNF/
BP	GO:00108	regulation	25/905	191/18866	5.07E-06	2.80E-05	1.47E-05	PSMD10/
BP	GO:00440	regulation	11/905	44/18866	5.20E-06	2.87E-05	1.51E-05	IL1B/F2R/F
BP	GO:000231	B cell activ	15/905	80/18866	5.21E-06	2.87E-05	1.51E-05	TGFB1/TFR
BP	GO:00022	positive re	9/905	29/18866	5.43E-06	2.98E-05	1.57E-05	APOBEC3G
BP	GO:00198	cytolysis	9/905	29/18866	5.43E-06	2.98E-05	1.57E-05	MICA/MIC
BP	GO:00455	regulation	9/905	29/18866	5.43E-06	2.98E-05	1.57E-05	BTK/CARD
BP	GO:00506	regulation	9/905	29/18866	5.43E-06	2.98E-05	1.57E-05	B2M/CD4/
BP	GO:00217	glial cell de	19/905	122/18866	5.48E-06	3.00E-05	1.58E-05	IFNG/S100
BP	GO:00454	response t	19/905	122/18866	5.48E-06	3.00E-05	1.58E-05	ICAM1/PS
BP	GO:00717	response t	23/905	168/18866	5.62E-06	3.08E-05	1.62E-05	TGFB1/HJ
BP	GO:00717	cellular res	23/905	168/18866	5.62E-06	3.08E-05	1.62E-05	TGFB1/HJ
BP	GO:00148	response t	14/905	71/18866	5.78E-06	3.15E-05	1.66E-05	ADIPOQ/C
BP	GO:00336	cell adhesi	14/905	71/18866	5.78E-06	3.15E-05	1.66E-05	ICAM1/CX
BP	GO:00356	cellular res	14/905	71/18866	5.78E-06	3.15E-05	1.66E-05	HSPA5/HS
BP	GO:00465	positive re	14/905	71/18866	5.78E-06	3.15E-05	1.66E-05	F2R/F2RL1
BP	GO:00071	cell-matrix	28/905	230/18866	5.84E-06	3.18E-05	1.67E-05	MMP12/PL
BP	GO:00431	negative r	12/905	53/18866	5.96E-06	3.24E-05	1.70E-05	ADIPOQ/S
BP	GO:00617	leukocyte	12/905	53/18866	5.96E-06	3.24E-05	1.70E-05	ICAM1/CX
BP	GO:00511	negative r	23/905	169/18866	6.22E-06	3.37E-05	1.77E-05	B2M/SLPI/
BP	GO:00972	amyloid-b	10/905	37/18866	6.55E-06	3.55E-05	1.86E-05	IFNG/TNF/
BP	GO:19049	regulation	10/905	37/18866	6.55E-06	3.55E-05	1.86E-05	ICAM1/CX

BP	GO:003412	negative re	11/905	45/18866	6.59E-06	3.56E-05	1.87E-05	BPIFB1/TLF
BP	GO:190464	cellular res	11/905	45/18866	6.59E-06	3.56E-05	1.87E-05	ICAM1/AG
BP	GO:005502	regulation	17/905	102/18866	6.67E-06	3.60E-05	1.89E-05	TGFB1/RBP
BP	GO:003017	negative re	27/905	219/18866	6.73E-06	3.63E-05	1.91E-05	PSMB8/PSI
BP	GO:003236	regulation	20/905	135/18866	6.83E-06	3.68E-05	1.93E-05	IL1B/FABP3
BP	GO:004259	glucose ho	29/905	245/18866	6.97E-06	3.75E-05	1.97E-05	ICAM1/RBP
BP	GO:003269	negative re	8/905	23/18866	7.00E-06	3.75E-05	1.97E-05	IDO1/AGEF
BP	GO:003574	CD4-positiv	8/905	23/18866	7.00E-06	3.75E-05	1.97E-05	XCL1/IL1B/
BP	GO:006044	branching i	8/905	23/18866	7.00E-06	3.75E-05	1.97E-05	TNF/FGF10
BP	GO:000264	regulation	7/905	17/18866	7.27E-06	3.88E-05	2.04E-05	HLA-B/HLA
BP	GO:001081	regulation	7/905	17/18866	7.27E-06	3.88E-05	2.04E-05	CXCL10/CX
BP	GO:001573	prostaglan	7/905	17/18866	7.27E-06	3.88E-05	2.04E-05	IL1B/TNFSF
BP	GO:003054	female gen	7/905	17/18866	7.27E-06	3.88E-05	2.04E-05	RBP4/WNT
BP	GO:004454	NLRP3 infla	7/905	17/18866	7.27E-06	3.88E-05	2.04E-05	EIF2AK2/D
BP	GO:004476	multi-orga	7/905	17/18866	7.27E-06	3.88E-05	2.04E-05	CD4/CTSL/
BP	GO:004853	lymph nod	7/905	17/18866	7.27E-06	3.88E-05	2.04E-05	LTA/TGFB1
BP	GO:001052	positive reg	12/905	54/18866	7.34E-06	3.90E-05	2.05E-05	CD4/CXCL1
BP	GO:000652	regulation	13/905	63/18866	7.35E-06	3.91E-05	2.05E-05	PSMB8/PSI
BP	GO:004337	positive reg	9/905	30/18866	7.43E-06	3.95E-05	2.07E-05	IFNG/SOCS
BP	GO:000974	response to	28/905	233/18866	7.49E-06	3.97E-05	2.09E-05	ICAM1/IL1
BP	GO:003350	carbohydra	29/905	246/18866	7.55E-06	4.00E-05	2.10E-05	ICAM1/RBP
BP	GO:000863	intrinsic ap	17/905	103/18866	7.64E-06	4.05E-05	2.13E-05	CXCL12/TN
BP	GO:000989	positive reg	44/905	454/18866	7.81E-06	4.13E-05	2.17E-05	HSP90AA1/
BP	GO:000301	renal syste	19/905	125/18866	7.88E-06	4.16E-05	2.19E-05	ADIPOQ/F2
BP	GO:000863	apoptotic r	19/905	125/18866	7.88E-06	4.16E-05	2.19E-05	PSMD10/M
BP	GO:003269	negative re	11/905	46/18866	8.29E-06	4.37E-05	2.30E-05	TNFAIP3/IL
BP	GO:004558	negative re	11/905	46/18866	8.29E-06	4.37E-05	2.30E-05	IFNL1/SOC
BP	GO:003022	monocyte	10/905	38/18866	8.51E-06	4.48E-05	2.35E-05	CD4/VEGF
BP	GO:190313	mononucle	10/905	38/18866	8.51E-06	4.48E-05	2.35E-05	CD4/VEGF
BP	GO:000286	positive reg	6/905	12/18866	8.63E-06	4.53E-05	2.38E-05	FCER1G/LT
BP	GO:007188	macrophag	6/905	12/18866	8.63E-06	4.53E-05	2.38E-05	CTSL/IRF3/
BP	GO:190228	semaphori	6/905	12/18866	8.63E-06	4.53E-05	2.38E-05	SEMA3A/P
BP	GO:007026	necrotic ce	13/905	64/18866	8.82E-06	4.62E-05	2.43E-05	IRF3/TNF/T
BP	GO:004577	positive reg	16/905	94/18866	9.38E-06	4.91E-05	2.58E-05	TGFB1/LTF/
BP	GO:004350	positive reg	14/905	74/18866	9.58E-06	5.01E-05	2.63E-05	TNF/WNT5
BP	GO:003277	positive reg	9/905	31/18866	1.00E-05	5.23E-05	2.75E-05	IFNG/S100
BP	GO:003952	cytoplasmi	9/905	31/18866	1.00E-05	5.23E-05	2.75E-05	DDX58/IRF
BP	GO:001046	regulation	23/905	174/18866	1.02E-05	5.30E-05	2.78E-05	IFNG/PLAU
BP	GO:001057	vascular en	13/905	65/18866	1.05E-05	5.49E-05	2.88E-05	TGFB1/IL1
BP	GO:009858	cellular res	13/905	65/18866	1.05E-05	5.49E-05	2.88E-05	MMP12/DI
BP	GO:004340	steroid hor	20/905	139/18866	1.07E-05	5.56E-05	2.92E-05	CALR/SRC/
BP	GO:003266	regulation	10/905	39/18866	1.10E-05	5.69E-05	2.99E-05	IFNG/TGFB
BP	GO:004566	negative re	27/905	225/18866	1.11E-05	5.77E-05	3.03E-05	B2M/CALR/
BP	GO:003803	signal trans	14/905	75/18866	1.13E-05	5.84E-05	3.07E-05	LCN2/IL1B/
BP	GO:009719	extrinsic ap	14/905	75/18866	1.13E-05	5.84E-05	3.07E-05	LCN2/IL1B/
BP	GO:001088	regulation	7/905	18/18866	1.14E-05	5.89E-05	3.10E-05	MSR1/PPA
BP	GO:004688	regulation	7/905	18/18866	1.14E-05	5.89E-05	3.10E-05	ADM/BMP
BP	GO:200118	regulation	7/905	18/18866	1.14E-05	5.89E-05	3.10E-05	HLA-A/XCL
BP	GO:003133	positive reg	39/905	390/18866	1.24E-05	6.40E-05	3.37E-05	HSP90AA1/
BP	GO:000256	somatic div	13/905	66/18866	1.26E-05	6.46E-05	3.40E-05	TGFB1/TFR

BP	GO:001644	somatic ce	13/905	66/18866	1.26E-05	6.46E-05	3.40E-05	TGFB1/TFR
BP	GO:003276	regulation	13/905	66/18866	1.26E-05	6.46E-05	3.40E-05	HSP90AA1/
BP	GO:000940	response t	11/905	48/18866	1.29E-05	6.61E-05	3.47E-05	HSPA2/HSP
BP	GO:005077	positive reg	15/905	86/18866	1.31E-05	6.71E-05	3.53E-05	CXCL12/VE
BP	GO:006019	positive reg	14/905	76/18866	1.32E-05	6.78E-05	3.56E-05	CCL5/PDGF
BP	GO:000209	regulation	12/905	57/18866	1.32E-05	6.78E-05	3.57E-05	VEGFA/ARI
BP	GO:004584	positive reg	12/905	57/18866	1.32E-05	6.78E-05	3.57E-05	IL1B/IL1A/I
BP	GO:005086	negative re	9/905	32/18866	1.34E-05	6.83E-05	3.59E-05	TNFAIP3/IL
BP	GO:190188	negative re	9/905	32/18866	1.34E-05	6.83E-05	3.59E-05	TLR2/IL1B/
BP	GO:004663	negative re	10/905	40/18866	1.40E-05	7.13E-05	3.75E-05	XCL1/SOCS
BP	GO:004871	regulation	10/905	40/18866	1.40E-05	7.13E-05	3.75E-05	TLR2/HDAC
BP	GO:006057	morphogen	8/905	25/18866	1.42E-05	7.22E-05	3.80E-05	WNT5A/FG
BP	GO:001082	positive reg	18/905	119/18866	1.45E-05	7.40E-05	3.89E-05	MMP9/TNI
BP	GO:003252	response t	17/905	108/18866	1.46E-05	7.43E-05	3.90E-05	MICB/RBP4
BP	GO:006007	Wnt signali	17/905	108/18866	1.46E-05	7.43E-05	3.90E-05	PSMB8/PSI
BP	GO:000267	respiratory	6/905	13/18866	1.54E-05	7.79E-05	4.09E-05	LBP/MPO/I
BP	GO:001074	negative re	6/905	13/18866	1.54E-05	7.79E-05	4.09E-05	CETP/ADIP
BP	GO:004324	proteasom	6/905	13/18866	1.54E-05	7.79E-05	4.09E-05	PSMD4/PS
BP	GO:190294	regulation	6/905	13/18866	1.54E-05	7.79E-05	4.09E-05	HSP90AA1/
BP	GO:000220	somatic div	14/905	77/18866	1.54E-05	7.81E-05	4.10E-05	TGFB1/TFR
BP	GO:006041	cardiac sep	14/905	77/18866	1.54E-05	7.81E-05	4.10E-05	WNT5A/SE
BP	GO:003134	positive reg	39/905	394/18866	1.57E-05	7.93E-05	4.17E-05	HSPA5/CXC
BP	GO:190379	positive reg	12/905	58/18866	1.60E-05	8.06E-05	4.24E-05	IL1B/FABP3
BP	GO:004506	T-helper 1	7/905	19/18866	1.73E-05	8.71E-05	4.58E-05	RELB/IL27/
BP	GO:006074	mammary	7/905	19/18866	1.73E-05	8.71E-05	4.58E-05	VEGFA/TNI
BP	GO:006137	mammary	7/905	19/18866	1.73E-05	8.71E-05	4.58E-05	VEGFA/TNI
BP	GO:005081	regulation	15/905	88/18866	1.74E-05	8.75E-05	4.60E-05	FCER1G/PF
BP	GO:000286	regulation	9/905	33/18866	1.76E-05	8.83E-05	4.64E-05	FCER1G/LT
BP	GO:004578	positive reg	39/905	396/18866	1.76E-05	8.84E-05	4.65E-05	CALR/HSPA
BP	GO:004231	vasoconstr	14/905	78/18866	1.80E-05	9.02E-05	4.74E-05	ICAM1/F2R
BP	GO:003139	positive reg	18/905	121/18866	1.84E-05	9.19E-05	4.83E-05	HSPA5/PSM
BP	GO:009017	regulation	17/905	110/18866	1.87E-05	9.37E-05	4.92E-05	PSMB8/PSI
BP	GO:001400	glial cell pr	11/905	50/18866	1.95E-05	9.72E-05	5.11E-05	LTA/IL1B/T
BP	GO:200072	regulation	11/905	50/18866	1.95E-05	9.72E-05	5.11E-05	TGFB1/BM
BP	GO:003166	regulation	8/905	26/18866	1.96E-05	9.78E-05	5.14E-05	LTF/TNFAIP
BP	GO:001081	positive reg	18/905	122/18866	2.06E-05	0.000103	5.39E-05	CALR/VEGF
BP	GO:200024	regulation	22/905	170/18866	2.20E-05	0.00011	5.76E-05	CALR/DEFB
BP	GO:190403	positive reg	10/905	42/18866	2.22E-05	0.000111	5.82E-05	HLA-G/CD4
BP	GO:000288	positive reg	9/905	34/18866	2.29E-05	0.000114	5.98E-05	FCER1G/DL
BP	GO:000720	activation c	9/905	34/18866	2.29E-05	0.000114	5.98E-05	CD86/C5AR
BP	GO:001922	regulation	12/905	60/18866	2.30E-05	0.000114	5.99E-05	ICAM1/F2R
BP	GO:003527	exocrine sy	11/905	51/18866	2.38E-05	0.000118	6.19E-05	TGFB1/TNF
BP	GO:006019	regulation	16/905	101/18866	2.39E-05	0.000118	6.21E-05	CCL5/PDGF
BP	GO:000204	sprouting a	24/905	196/18866	2.41E-05	0.000119	6.27E-05	S100A1/VE
BP	GO:003030	positive reg	22/905	171/18866	2.41E-05	0.000119	6.27E-05	PSMD10/C
BP	GO:000315	outflow tra	14/905	80/18866	2.43E-05	0.00012	6.30E-05	VEGFA/WN
BP	GO:000253	cytokine pr	13/905	70/18866	2.44E-05	0.00012	6.33E-05	APOD/TNF,
BP	GO:007169	anatomical	27/905	235/18866	2.45E-05	0.000121	6.35E-05	DEFB1/PAB
BP	GO:190406	positive reg	20/905	147/18866	2.47E-05	0.000122	6.40E-05	HSPA2/IFN
BP	GO:001087	cholesterol	7/905	20/18866	2.55E-05	0.000125	6.59E-05	MSR1/PPA

BP	GO:003281	positive re	7/905	20/18866	2.55E-05	0.000125	6.59E-05	HLA-F/IL15
BP	GO:200019	positive re	7/905	20/18866	2.55E-05	0.000125	6.59E-05	IL1B/FABP
BP	GO:000173	establishm	18/905	124/18866	2.58E-05	0.000126	6.64E-05	PSMB8/PS
BP	GO:007166	establishm	18/905	124/18866	2.58E-05	0.000126	6.64E-05	PSMB8/PS
BP	GO:007048	leukocyte	6/905	14/18866	2.58E-05	0.000126	6.64E-05	S100A9/S1
BP	GO:007221	positive re	6/905	14/18866	2.58E-05	0.000126	6.64E-05	ADIPOQ/P
BP	GO:000635	DNA-templ	28/905	249/18866	2.59E-05	0.000127	6.66E-05	PSMC2/PS
BP	GO:001097	positive re	31/905	290/18866	2.66E-05	0.00013	6.84E-05	HSPA5/CX
BP	GO:004567	positive re	8/905	27/18866	2.67E-05	0.00013	6.85E-05	IFNG/TNF/
BP	GO:001470	striated mu	38/905	389/18866	2.70E-05	0.000131	6.91E-05	CALR/S100
BP	GO:001057	regulation	12/905	61/18866	2.73E-05	0.000133	6.99E-05	TGFB1/IL1
BP	GO:004557	mast cell a	12/905	61/18866	2.73E-05	0.000133	6.99E-05	FCER1G/N
BP	GO:004688	negative re	12/905	61/18866	2.73E-05	0.000133	6.99E-05	IL1B/ADIP
BP	GO:004512	regulation	10/905	43/18866	2.77E-05	0.000135	7.09E-05	TFRC/TNFA
BP	GO:000196	negative re	14/905	81/18866	2.81E-05	0.000136	7.16E-05	MMP12/A
BP	GO:004269	muscle cell	38/905	390/18866	2.85E-05	0.000138	7.27E-05	CALR/CXCL
BP	GO:005178	positive re	13/905	71/18866	2.86E-05	0.000139	7.28E-05	IL1B/WNT5
BP	GO:003233	regulation	11/905	52/18866	2.88E-05	0.00014	7.34E-05	FGF18/GD
BP	GO:001993	cAMP-med	24/905	199/18866	3.10E-05	0.00015	7.88E-05	CXCL10/CX
BP	GO:004573	positive re	26/905	225/18866	3.12E-05	0.000151	7.92E-05	HSP90AA1,
BP	GO:000320	cardiac cha	22/905	174/18866	3.17E-05	0.000153	8.04E-05	TGFB1/RB
BP	GO:003019	regulation	14/905	82/18866	3.24E-05	0.000156	8.20E-05	FCER1G/PL
BP	GO:003411	heterotypi	12/905	62/18866	3.24E-05	0.000156	8.22E-05	IL1B/TNF/
BP	GO:000686	lipid transp	38/905	393/18866	3.38E-05	0.000163	8.54E-05	FABP6/IL1
BP	GO:009027	regulation	25/905	213/18866	3.39E-05	0.000163	8.57E-05	IFNG/IL1B/
BP	GO:000301	muscle sys	43/905	467/18866	3.41E-05	0.000164	8.62E-05	IL1B/IL15/
BP	GO:199077	response t	8/905	28/18866	3.58E-05	0.000172	9.04E-05	CYBB/SRC/
BP	GO:006053	muscle tiss	39/905	409/18866	3.64E-05	0.000175	9.19E-05	CALR/S100
BP	GO:007257	hepatocyte	7/905	21/18866	3.67E-05	0.000176	9.25E-05	TNFAIP3/M
BP	GO:007257	epithelial c	7/905	21/18866	3.67E-05	0.000176	9.25E-05	TNFAIP3/M
BP	GO:003114	anaphase-	14/905	83/18866	3.72E-05	0.000178	9.36E-05	PSMB8/PS
BP	GO:190004	regulation	14/905	83/18866	3.72E-05	0.000178	9.36E-05	FCER1G/PL
BP	GO:003019	extracellul	38/905	395/18866	3.77E-05	0.00018	9.43E-05	CTSL/ICAM
BP	GO:001009	specificatic	9/905	36/18866	3.77E-05	0.00018	9.43E-05	WNT5A/FG
BP	GO:003112	developme	9/905	36/18866	3.77E-05	0.00018	9.43E-05	WNT5A/FG
BP	GO:004562	regulation	9/905	36/18866	3.77E-05	0.00018	9.43E-05	IL27/TNFS
BP	GO:190533	positive re	9/905	36/18866	3.77E-05	0.00018	9.43E-05	VEGFA/AG
BP	GO:003153	actin cytos	16/905	105/18866	3.91E-05	0.000186	9.77E-05	PTK2B/HC
BP	GO:004666	male sex di	21/905	164/18866	3.94E-05	0.000187	9.83E-05	ICAM1/TLR
BP	GO:001087	lipid localiz	41/905	440/18866	3.94E-05	0.000187	9.83E-05	FABP6/IL1
BP	GO:004306	extracellul	38/905	396/18866	3.98E-05	0.000189	9.93E-05	CTSL/ICAM
BP	GO:000228	macrophag	6/905	15/18866	4.13E-05	0.000195	0.000102	IFNG/LBP/
BP	GO:003563	entry of ba	6/905	15/18866	4.13E-05	0.000195	0.000102	CXCL8/ITG
BP	GO:004297	activation	6/905	15/18866	4.13E-05	0.000195	0.000102	SOCS1/CCL
BP	GO:006009	regulation	6/905	15/18866	4.13E-05	0.000195	0.000102	F2RL1/PPA
BP	GO:009720	activation	6/905	15/18866	4.13E-05	0.000195	0.000102	IFI16/RIPK
BP	GO:190022	regulation	6/905	15/18866	4.13E-05	0.000195	0.000102	EIF2AK2/D
BP	GO:200034	regulation	6/905	15/18866	4.13E-05	0.000195	0.000102	TNFAIP3/M
BP	GO:000197	blood vess	10/905	45/18866	4.23E-05	0.000199	0.000104	TGFB1/DLL
BP	GO:000263	positive re	10/905	45/18866	4.23E-05	0.000199	0.000104	XCL1/TGFB

BP	GO:004311	regulation	10/905	45/18866	4.23E-05	0.000199	0.000104	TGFB1/VEG
BP	GO:006044	mammary	10/905	45/18866	4.23E-05	0.000199	0.000104	PML/WNT5
BP	GO:007026	necroptoti	10/905	45/18866	4.23E-05	0.000199	0.000104	TNF/TLR3/
BP	GO:003027	negative re	14/905	84/18866	4.27E-05	0.0002	0.000105	TNF/CCL3/
BP	GO:001923	sensory pe	16/905	106/18866	4.40E-05	0.000206	0.000108	CXCL12/FA
BP	GO:190303	positive reg	13/905	74/18866	4.51E-05	0.000211	0.000111	DUOX1/DU
BP	GO:003250	maintenan	12/905	64/18866	4.52E-05	0.000211	0.000111	CD4/HSPA5
BP	GO:000271	positive reg	8/905	29/18866	4.74E-05	0.000222	0.000116	HLA-F/HLA
BP	GO:200027	positive reg	9/905	37/18866	4.77E-05	0.000223	0.000117	IFNG/CCL2/
BP	GO:003209	positive reg	14/905	85/18866	4.89E-05	0.000228	0.00012	B2M/HSP9
BP	GO:000300	heart morp	28/905	258/18866	4.92E-05	0.000229	0.00012	TGFB1/RBP
BP	GO:001088	negative re	7/905	22/18866	5.17E-05	0.000238	0.000125	TNF/ITGAV
BP	GO:003612	cellular res	7/905	22/18866	5.17E-05	0.000238	0.000125	SRC/PDGF
BP	GO:004506	thymic T ce	7/905	22/18866	5.17E-05	0.000238	0.000125	CCR7/CARD
BP	GO:007115	negative re	7/905	22/18866	5.17E-05	0.000238	0.000125	CALR/HSP9
BP	GO:007257	liver morph	7/905	22/18866	5.17E-05	0.000238	0.000125	TNFAIP3/M
BP	GO:000312	heart induc	5/905	10/18866	5.17E-05	0.000238	0.000125	WNT5A/RC
BP	GO:003281	negative re	5/905	10/18866	5.17E-05	0.000238	0.000125	HLA-F/MIC
BP	GO:003497	protein fol	5/905	10/18866	5.17E-05	0.000238	0.000125	CALR/PDIA
BP	GO:004562	regulation	5/905	10/18866	5.17E-05	0.000238	0.000125	IL27/TNFSF
BP	GO:006006	vagina dev	5/905	10/18866	5.17E-05	0.000238	0.000125	RBP4/WNT
BP	GO:006060	dichotomo	5/905	10/18866	5.17E-05	0.000238	0.000125	SEMA3A/S
BP	GO:007039	response t	5/905	10/18866	5.17E-05	0.000238	0.000125	TLR2/LBP/
BP	GO:007122	cellular res	5/905	10/18866	5.17E-05	0.000238	0.000125	TLR2/LBP/
BP	GO:009003	positive reg	5/905	10/18866	5.17E-05	0.000238	0.000125	CD40/VEG
BP	GO:003230	icosanoid s	10/905	46/18866	5.18E-05	0.000238	0.000125	IL1B/PLA2G
BP	GO:003592	cellular res	13/905	75/18866	5.22E-05	0.00024	0.000126	VEGFA/DLL
BP	GO:004864	animal org	12/905	65/18866	5.30E-05	0.000244	0.000128	MAPK3/W
BP	GO:190495	negative re	20/905	155/18866	5.35E-05	0.000246	0.000129	IL1B/APOD
BP	GO:001921	regulation	18/905	131/18866	5.44E-05	0.000249	0.000131	IFNG/NFYA
BP	GO:004566	regulation	18/905	131/18866	5.44E-05	0.000249	0.000131	LTF/TNF/P
BP	GO:009775	negative re	14/905	86/18866	5.59E-05	0.000256	0.000135	ICAM1/F2R
BP	GO:000761	learning or	28/905	260/18866	5.64E-05	0.000258	0.000136	B2M/S100
BP	GO:000718	adenylate	26/905	233/18866	5.67E-05	0.000259	0.000136	CXCL10/CX
BP	GO:190165	cellular res	15/905	97/18866	5.68E-05	0.000259	0.000136	ICAM1/GN
BP	GO:001094	negative re	35/905	359/18866	5.76E-05	0.000263	0.000138	CALR/HLA-
BP	GO:003428	response t	24/905	207/18866	5.88E-05	0.000268	0.000141	ICAM1/NO
BP	GO:001644	somatic re	11/905	56/18866	5.97E-05	0.000272	0.000143	TGFB1/TFR
BP	GO:000315	regulation	9/905	38/18866	5.99E-05	0.000272	0.000143	WNT5A/FG
BP	GO:004659	regulation	9/905	38/18866	5.99E-05	0.000272	0.000143	CD4/TRIM2
BP	GO:190352	positive reg	13/905	76/18866	6.02E-05	0.000274	0.000144	ICAM1/F2R
BP	GO:000705	cell cycle a	26/905	234/18866	6.09E-05	0.000277	0.000145	CALR/HSP9
BP	GO:000717	regulation	8/905	30/18866	6.19E-05	0.000281	0.000148	AREG/BTC/
BP	GO:003271	negative re	12/905	66/18866	6.20E-05	0.000281	0.000148	TNF/NLRX1
BP	GO:200027	regulation	16/905	109/18866	6.23E-05	0.000282	0.000148	HSP90AA1/
BP	GO:009031	positive reg	22/905	182/18866	6.32E-05	0.000285	0.00015	HSP90AB1/
BP	GO:000283	positive reg	6/905	16/18866	6.34E-05	0.000285	0.00015	XCL1/IDO1
BP	GO:000283	regulation	6/905	16/18866	6.34E-05	0.000285	0.00015	MR1/IL12A
BP	GO:000283	regulation	6/905	16/18866	6.34E-05	0.000285	0.00015	MR1/IL12A
BP	GO:001082	positive reg	6/905	16/18866	6.34E-05	0.000285	0.00015	CXCL13/XC

BP	GO:003437	low-densit	6/905	16/18866	6.34E-05	0.000285	0.00015	CETP/PLA2
BP	GO:004801	hepatocyte	6/905	16/18866	6.34E-05	0.000285	0.00015	ESM1/MET
BP	GO:190515	regulation	6/905	16/18866	6.34E-05	0.000285	0.00015	F2RL1/PPA
BP	GO:006076	negative re	14/905	87/18866	6.37E-05	0.000286	0.000151	MMP12/AI
BP	GO:001077	negative re	15/905	98/18866	6.41E-05	0.000288	0.000151	WNT5A/PT
BP	GO:003050	regulation	13/905	77/18866	6.93E-05	0.000311	0.000164	TGFB1/LTF
BP	GO:003611	response t	7/905	23/18866	7.12E-05	0.000319	0.000167	SRC/PDGFI
BP	GO:007221	regulation	7/905	23/18866	7.12E-05	0.000319	0.000167	ADIPOQ/ST
BP	GO:190499	positive re	7/905	23/18866	7.12E-05	0.000319	0.000167	ICAM1/TNI
BP	GO:190001	regulation	12/905	67/18866	7.23E-05	0.000323	0.00017	APOD/TNF
BP	GO:004325	regulation	15/905	99/18866	7.23E-05	0.000323	0.00017	TGFB1/ADI
BP	GO:005130	regulation	21/905	171/18866	7.31E-05	0.000326	0.000172	TGFB1/IL1I
BP	GO:003315	regulation	28/905	264/18866	7.38E-05	0.000329	0.000173	HSP90AB1/
BP	GO:004516	cell fate co	29/905	278/18866	7.45E-05	0.000332	0.000174	CTSL/PML/
BP	GO:011005	regulation	29/905	278/18866	7.45E-05	0.000332	0.000174	ICAM1/CX(
BP	GO:003269	negative re	9/905	39/18866	7.46E-05	0.000332	0.000174	TNFAIP3/C
BP	GO:003195	regulation	10/905	48/18866	7.62E-05	0.000338	0.000178	ADIPOQ/VI
BP	GO:003362	regulation	10/905	48/18866	7.62E-05	0.000338	0.000178	CXCL13/PL
BP	GO:006024	anatomical	42/905	469/18866	7.90E-05	0.000351	0.000184	AZGP1/B2I
BP	GO:004390	regulation	13/905	78/18866	7.96E-05	0.000353	0.000186	CALR/PAEI
BP	GO:004594	positive re	8/905	31/18866	8.00E-05	0.000354	0.000186	IFNG/IL1B/
BP	GO:200051	negative re	8/905	31/18866	8.00E-05	0.000354	0.000186	XCL1/ARG2
BP	GO:000315	endotheliu	18/905	135/18866	8.11E-05	0.000359	0.000189	ICAM1/CX(
BP	GO:004566	positive re	36/905	380/18866	8.20E-05	0.000363	0.000191	HSPA5/CX(
BP	GO:000288	regulation	11/905	58/18866	8.36E-05	0.000369	0.000194	FCER1G/DI
BP	GO:005114	striated mu	30/905	295/18866	8.98E-05	0.000396	0.000208	CALR/CXCL
BP	GO:000309	regulation	5/905	11/18866	9.11E-05	0.000401	0.000211	F2R/F2RL1
BP	GO:004480	multi-orga	5/905	11/18866	9.11E-05	0.000401	0.000211	CD4/CTSL/
BP	GO:005113	NK T cell a	5/905	11/18866	9.11E-05	0.000401	0.000211	IL15/IL12A
BP	GO:005171	positive re	5/905	11/18866	9.11E-05	0.000401	0.000211	IFNG/F2RL
BP	GO:001590	fatty acid t	15/905	101/18866	9.14E-05	0.000402	0.000211	IL1B/FABP!
BP	GO:009019	regulation	10/905	49/18866	9.16E-05	0.000402	0.000212	PSMD10/M
BP	GO:000199	regulation	9/905	40/18866	9.22E-05	0.000404	0.000212	CTSG/F2R/
BP	GO:003289	positive re	9/905	40/18866	9.22E-05	0.000404	0.000212	IL1B/FABP3
BP	GO:005128	positive re	9/905	40/18866	9.22E-05	0.000404	0.000212	CXCL10/CX
BP	GO:000725	activation	6/905	17/18866	9.40E-05	0.000411	0.000216	TLR3/TNFR
BP	GO:003230	positive re	6/905	17/18866	9.40E-05	0.000411	0.000216	IL1B/TNFSI
BP	GO:003268	negative re	6/905	17/18866	9.40E-05	0.000411	0.000216	APOD/ARG
BP	GO:007136	cellular res	6/905	17/18866	9.40E-05	0.000411	0.000216	DDX58/IRF
BP	GO:000243	acute infla	7/905	24/18866	9.64E-05	0.00042	0.00022	FCER1G/IC
BP	GO:003600	positive re	7/905	24/18866	9.64E-05	0.00042	0.00022	HSPA5/VE(
BP	GO:004406	regulation	7/905	24/18866	9.64E-05	0.00042	0.00022	EDNRB/AG
BP	GO:006044	branching i	7/905	24/18866	9.64E-05	0.00042	0.00022	PML/WNT!
BP	GO:003296	collagen m	16/905	113/18866	9.67E-05	0.000421	0.000221	CTSB/CTSL
BP	GO:200057	positive re	12/905	69/18866	9.73E-05	0.000423	0.000222	HSP90AA1/
BP	GO:004230	regulation	11/905	59/18866	9.84E-05	0.000427	0.000225	HSP90AB1/
BP	GO:003527	endocrine	17/905	125/18866	9.89E-05	0.000429	0.000225	MAPK3/WI
BP	GO:004350	muscle ada	17/905	125/18866	9.89E-05	0.000429	0.000225	IL1B/IL15/
BP	GO:000020	protein pol	33/905	340/18866	0.000101	0.000438	0.00023	PSMB8/PSI
BP	GO:006060	mammary	8/905	32/18866	0.000102	0.000442	0.000233	PML/WNT!

BP	GO:003134	negative re	22/905	188/18866	0.000103	0.000444	0.000234	B2M/WNT
BP	GO:000300	regionaliza	34/905	355/18866	0.000104	0.000448	0.000236	WNT5A/DL
BP	GO:009730	cellular res	14/905	91/18866	0.000105	0.000455	0.000239	CYBB/GNA
BP	GO:000327	cardiac sep	16/905	114/18866	0.000108	0.000464	0.000244	WNT5A/LT
BP	GO:003121	biomineral	20/905	163/18866	0.000109	0.000469	0.000247	HTN3/HTN
BP	GO:011014	biomineral	20/905	163/18866	0.000109	0.000469	0.000247	HTN3/HTN
BP	GO:000304	regulation	10/905	50/18866	0.00011	0.000471	0.000248	CTSG/F2R/
BP	GO:007171	icosanoid t	10/905	50/18866	0.00011	0.000471	0.000248	IL1B/PLA2
BP	GO:190157	fatty acid d	10/905	50/18866	0.00011	0.000471	0.000248	IL1B/PLA2
BP	GO:190470	positive re	10/905	50/18866	0.00011	0.000471	0.000248	MMP9/TN
BP	GO:000974	response t	23/905	202/18866	0.00011	0.000471	0.000248	ICAM1/NO
BP	GO:005079	regulation	12/905	70/18866	0.000112	0.000482	0.000253	PTGDS/CCL
BP	GO:003357	response t	9/905	41/18866	0.000113	0.000485	0.000255	CALR/EPO/
BP	GO:005122	negative re	19/905	151/18866	0.000115	0.000491	0.000258	IL1B/APOD
BP	GO:000182	mesoneph	15/905	103/18866	0.000115	0.000491	0.000258	VEGFA/AR
BP	GO:000183	release of	11/905	60/18866	0.000115	0.000492	0.000259	PSMD10/
BP	GO:004338	positive re	11/905	60/18866	0.000115	0.000492	0.000259	IFNG/TGFB
BP	GO:004353	regulation	20/905	164/18866	0.000119	0.000506	0.000266	TMSB4X/T
BP	GO:001991	lipid storag	13/905	81/18866	0.000119	0.000506	0.000266	IL1B/TNF/
BP	GO:005127	regulation	13/905	81/18866	0.000119	0.000506	0.000266	CXCL10/CX
BP	GO:000307	renal syste	7/905	25/18866	0.000128	0.000546	0.000287	F2R/F2RL1
BP	GO:009720	renal filtrat	7/905	25/18866	0.000128	0.000546	0.000287	F2R/F2RL1
BP	GO:190580	negative re	7/905	25/18866	0.000128	0.000546	0.000287	TLR2/WNT
BP	GO:004838	retinoic aci	8/905	33/18866	0.000129	0.000549	0.000289	CALR/PML
BP	GO:006118	mammary	12/905	71/18866	0.000129	0.000549	0.000289	PML/WNT
BP	GO:000220	somatic rec	10/905	51/18866	0.000131	0.000553	0.000291	TGFB1/TFR
BP	GO:000220	somatic div	10/905	51/18866	0.000131	0.000553	0.000291	TGFB1/TFR
BP	GO:004519	isotype swi	10/905	51/18866	0.000131	0.000553	0.000291	TGFB1/TFR
BP	GO:007208	stem cell p	17/905	128/18866	0.000133	0.000563	0.000296	VEGFA/EIF
BP	GO:003114	SCF-depen	14/905	93/18866	0.000134	0.000566	0.000297	PSMB8/PS
BP	GO:190303	negative re	14/905	93/18866	0.000134	0.000566	0.000297	PLAU/TNF/
BP	GO:009030	positive re	11/905	61/18866	0.000135	0.000568	0.000299	DUOX1/DU
BP	GO:002195	central ner	13/905	82/18866	0.000135	0.000569	0.000299	HSP90AA1/
BP	GO:007023	positive re	6/905	18/18866	0.000135	0.000569	0.000299	IDO1/CCL5
BP	GO:007160	monocyte	6/905	18/18866	0.000135	0.000569	0.000299	IL1B/APOD
BP	GO:007163	regulation	6/905	18/18866	0.000135	0.000569	0.000299	IL1B/APOD
BP	GO:015007	positive re	6/905	18/18866	0.000135	0.000569	0.000299	IL1B/TNF/
BP	GO:005089	cognition	30/905	302/18866	0.000137	0.000575	0.000302	B2M/S100
BP	GO:007121	cellular res	32/905	331/18866	0.000138	0.000578	0.000304	HSPA5/REL
BP	GO:010400	cellular res	32/905	331/18866	0.000138	0.000578	0.000304	HSPA5/REL
BP	GO:004592	positive re	28/905	274/18866	0.00014	0.000587	0.000309	PSMD10/C
BP	GO:000940	response t	20/905	166/18866	0.00014	0.000587	0.000309	HSPA2/HS
BP	GO:000858	male gona	18/905	141/18866	0.000143	0.000597	0.000314	ICAM1/TL
BP	GO:190332	positive re	18/905	141/18866	0.000143	0.000597	0.000314	HSPA5/PS
BP	GO:004407	regulation	15/905	105/18866	0.000143	0.000597	0.000314	IL1B/FABP
BP	GO:004825	regulation	15/905	105/18866	0.000143	0.000597	0.000314	B2M/VEGF
BP	GO:003028	bone mine	16/905	117/18866	0.000147	0.000613	0.000322	TGFB1/LTF
BP	GO:190442	positive re	12/905	72/18866	0.000149	0.00062	0.000326	HSPA2/CX
BP	GO:001097	negative re	19/905	154/18866	0.000149	0.00062	0.000326	B2M/WNT
BP	GO:006135	neural pre	19/905	154/18866	0.000149	0.00062	0.000326	FABP7/VE

BP	GO:000251	T cell toler	5/905	12/18866	0.00015	0.000622	0.000327	HLA-B/HLA
BP	GO:000273	regulation	5/905	12/18866	0.00015	0.000622	0.000327	DDX58/TLF
BP	GO:003249	response t	5/905	12/18866	0.00015	0.000622	0.000327	IRF5/C5AR
BP	GO:006151	macrophag	5/905	12/18866	0.00015	0.000622	0.000327	MAPK3/PT
BP	GO:007049	thrombin-a	5/905	12/18866	0.00015	0.000622	0.000327	F2R/F2RL1,
BP	GO:200024	positive re	13/905	83/18866	0.000153	0.000634	0.000333	DEFB1/VEG
BP	GO:001088	regulation	10/905	52/18866	0.000155	0.000641	0.000337	TNF/ITGAV
BP	GO:005099	regulation	10/905	52/18866	0.000155	0.000641	0.000337	HSP90AA1,
BP	GO:004654	developme	18/905	142/18866	0.000156	0.000646	0.00034	ICAM1/TLF
BP	GO:190458	regulation	11/905	62/18866	0.000157	0.000647	0.00034	HSP90AB1,
BP	GO:003214	activation	8/905	34/18866	0.000162	0.000667	0.000351	WNT5A/SR
BP	GO:004564	positive re	8/905	34/18866	0.000162	0.000667	0.000351	STAT1/ISG
BP	GO:005071	positive re	8/905	34/18866	0.000162	0.000667	0.000351	IFNG/IRF3/
BP	GO:006138	heart trabe	8/905	34/18866	0.000162	0.000667	0.000351	RBP4/DLL4
BP	GO:000756	cell aging	16/905	118/18866	0.000163	0.000669	0.000352	B2M/CALR,
BP	GO:004593	positive re	20/905	168/18866	0.000165	0.000679	0.000357	HSPA2/IL1I
BP	GO:004316	proteasom	38/905	424/18866	0.000168	0.000689	0.000362	HSPA5/HSF
BP	GO:000308	regulation	7/905	26/18866	0.000168	0.00069	0.000363	CTSG/F2R/
BP	GO:003411	regulation	7/905	26/18866	0.000168	0.00069	0.000363	IL1B/TNF/
BP	GO:190073	regulation	7/905	26/18866	0.000168	0.00069	0.000363	GZMB/BID,
BP	GO:190074	positive re	7/905	26/18866	0.000168	0.00069	0.000363	GZMB/BID,
BP	GO:000307	regulation	14/905	95/18866	0.000169	0.00069	0.000363	CTSG/F2R/
BP	GO:007016	regulation	14/905	95/18866	0.000169	0.00069	0.000363	TGFB1/LTF,
BP	GO:011014	regulation	14/905	95/18866	0.000169	0.00069	0.000363	TGFB1/LTF,
BP	GO:004591	positive re	13/905	84/18866	0.000173	0.000708	0.000372	IFNG/SRC/I
BP	GO:004348	regulation	22/905	195/18866	0.000175	0.000716	0.000376	PSMB8/PSI
BP	GO:190186	regulation	19/905	156/18866	0.000177	0.000721	0.000379	S100B/TGF
BP	GO:004410	cellular am	17/905	131/18866	0.000177	0.000722	0.000379	PSMB8/PSI
BP	GO:005115	regulation	16/905	119/18866	0.00018	0.000731	0.000384	CXCL10/CX
BP	GO:005160	protein ma	29/905	293/18866	0.000187	0.000761	0.0004	CALR/CTSL,
BP	GO:001648	protein pro	24/905	223/18866	0.000188	0.000766	0.000403	CTSL/PLAU
BP	GO:001097	negative re	14/905	96/18866	0.000189	0.000768	0.000404	PSMB8/PSI
BP	GO:001074	positive re	6/905	19/18866	0.00019	0.000768	0.000404	PLA2G2A/I
BP	GO:004509	regulation	6/905	19/18866	0.00019	0.000768	0.000404	CXCL8/APC
BP	GO:004578	positive re	6/905	19/18866	0.00019	0.000768	0.000404	TFRC/TNFS
BP	GO:004685	positive re	6/905	19/18866	0.00019	0.000768	0.000404	TFRC/TNFS
BP	GO:190042	regulation	6/905	19/18866	0.00019	0.000768	0.000404	F2RL1/SPIN
BP	GO:005134	negative re	41/905	473/18866	0.000193	0.00078	0.00041	SLPI/WFDC
BP	GO:004217	regulation	36/905	397/18866	0.000196	0.000793	0.000417	HSP90AA1,
BP	GO:000610	regulation	23/905	210/18866	0.000197	0.000794	0.000417	IFNG/TGFB
BP	GO:000206	chondrocy	15/905	108/18866	0.000197	0.000794	0.000417	TGFB1/BM
BP	GO:000859	regulation	15/905	108/18866	0.000197	0.000794	0.000417	SRC/DLL4/
BP	GO:190275	negative re	15/905	108/18866	0.000197	0.000794	0.000417	PSMB8/PSI
BP	GO:003631	response t	8/905	35/18866	0.000201	0.00081	0.000426	TGFB1/CCL
BP	GO:190103	positive re	8/905	35/18866	0.000201	0.00081	0.000426	GSK3B/GZI
BP	GO:000974	response t	22/905	197/18866	0.000203	0.000817	0.000429	ICAM1/NO
BP	GO:000173	morphoger	18/905	145/18866	0.000204	0.000819	0.000431	PSMB8/PSI
BP	GO:003085	regulation	20/905	171/18866	0.00021	0.000843	0.000443	CTSL/IFNG,
BP	GO:200017	positive re	10/905	54/18866	0.000215	0.000861	0.000453	VEGFA/DLL
BP	GO:009028	regulation	30/905	310/18866	0.000216	0.000868	0.000456	HSPA5/HSF

BP	GO:003195	positive re	7/905	27/18866	0.000218	0.000871	0.000458	VEGFA/SRC
BP	GO:003289	negative re	7/905	27/18866	0.000218	0.000871	0.000458	CCL5/CCL4
BP	GO:003603	CD8-positiv	7/905	27/18866	0.000218	0.000871	0.000458	HLA-A/XCL
BP	GO:200035	positive re	7/905	27/18866	0.000218	0.000871	0.000458	HLA-G/CD4
BP	GO:000206	columnar/	16/905	121/18866	0.000218	0.000872	0.000458	WNT5A/SR
BP	GO:003166	cellular res	26/905	253/18866	0.000219	0.000873	0.000459	HSPA5/ICA
BP	GO:004544	myoblast d	13/905	86/18866	0.000221	0.00088	0.000462	CXCL14/CX
BP	GO:000237	dendritic c	5/905	13/18866	0.000234	0.000927	0.000487	DDX58/TLR
BP	GO:003065	regulation	5/905	13/18866	0.000234	0.000927	0.000487	IFNG/IL1B/
BP	GO:003272	positive re	5/905	13/18866	0.000234	0.000927	0.000487	IL1B/PAEP/
BP	GO:003282	regulation	5/905	13/18866	0.000234	0.000927	0.000487	PGLYRP1/P
BP	GO:003800	netrin-activ	5/905	13/18866	0.000234	0.000927	0.000487	PTK2/TUBB
BP	GO:004574	positive re	5/905	13/18866	0.000234	0.000927	0.000487	AREG/BTC/
BP	GO:006010	positive re	5/905	13/18866	0.000234	0.000927	0.000487	F2RL1/PPA
BP	GO:007268	T cell extra	5/905	13/18866	0.000234	0.000927	0.000487	ICAM1/CCL
BP	GO:190515	positive re	5/905	13/18866	0.000234	0.000927	0.000487	F2RL1/PPA
BP	GO:200019	regulation	5/905	13/18866	0.000234	0.000927	0.000487	SRC/AMH/
BP	GO:005081	regulation	14/905	98/18866	0.000236	0.000933	0.00049	IFNG/NFYA
BP	GO:200124	negative re	14/905	98/18866	0.000236	0.000933	0.00049	CXCL12/MI
BP	GO:003410	positive re	9/905	45/18866	0.000241	0.000952	0.0005	TFRC/IL15/
BP	GO:004348	regulation	21/905	186/18866	0.000242	0.000954	0.000501	PSMB8/PSI
BP	GO:007058	calcium ior	30/905	312/18866	0.000242	0.000954	0.000501	HSPA2/CXC
BP	GO:003007	insulin secr	23/905	213/18866	0.000242	0.000954	0.000502	IFNG/IL1B/
BP	GO:000718	adenylate c	18/905	147/18866	0.000242	0.000955	0.000502	CXCL10/CX
BP	GO:007140	cellular res	8/905	36/18866	0.000248	0.000975	0.000512	FCER1G/PF
BP	GO:190109	negative re	8/905	36/18866	0.000248	0.000975	0.000512	IL1B/TNF/I
BP	GO:200124	negative re	8/905	36/18866	0.000248	0.000975	0.000512	IL1B/TNF/I
BP	GO:000194	hair follicle	13/905	87/18866	0.000248	0.000975	0.000512	TNF/WNT5
BP	GO:000195	positive re	10/905	55/18866	0.000251	0.000986	0.000518	VEGFA/LIM
BP	GO:007074	response t	10/905	55/18866	0.000251	0.000986	0.000518	ICAM1/STA
BP	GO:003355	multicellula	12/905	76/18866	0.000252	0.000986	0.000518	IDO1/NOS1
BP	GO:005080	synapse or	38/905	433/18866	0.000256	0.001001	0.000526	TLR2/TNF/
BP	GO:000257	regulation	6/905	20/18866	0.00026	0.001013	0.000533	HLA-DOB/S
BP	GO:000725	I-kappaB pl	6/905	20/18866	0.00026	0.001013	0.000533	TLR2/TNF/T
BP	GO:003230	regulation	6/905	20/18866	0.00026	0.001013	0.000533	IL1B/TNFSF
BP	GO:003233	positive re	6/905	20/18866	0.00026	0.001013	0.000533	FGF18/GDF
BP	GO:003249	response t	6/905	20/18866	0.00026	0.001013	0.000533	TNFAIP3/IF
BP	GO:003969	single strar	6/905	20/18866	0.00026	0.001013	0.000533	CXCL8/APO
BP	GO:190593	regulation	6/905	20/18866	0.00026	0.001013	0.000533	SRC/SEMA
BP	GO:009027	positive re	14/905	99/18866	0.000263	0.001024	0.000538	RBP4/TFR2
BP	GO:009025	regulation	26/905	256/18866	0.000263	0.001025	0.000539	F2R/PTGS2
BP	GO:001067	regulation	18/905	148/18866	0.000264	0.001026	0.000539	ADIPOQ/SF
BP	GO:000701	actin filame	38/905	434/18866	0.000268	0.00104	0.000547	ICAM1/CXC
BP	GO:001644	somatic div	11/905	66/18866	0.000278	0.001079	0.000567	TGFB1/TFR
BP	GO:004390	negative re	7/905	28/18866	0.000279	0.00108	0.000567	CALR/PAEP
BP	GO:009020	positive re	7/905	28/18866	0.000279	0.00108	0.000567	MMP9/TNF
BP	GO:200019	regulation	7/905	28/18866	0.000279	0.00108	0.000567	IL1B/FABP3
BP	GO:003257	response t	9/905	46/18866	0.000287	0.001111	0.000584	TGFB1/TLR
BP	GO:005110	regulation	16/905	124/18866	0.00029	0.001123	0.00059	IFNG/TMSB
BP	GO:001033	response t	10/905	56/18866	0.000293	0.001132	0.000595	HSPA5/CXC

BP	GO:001046	negative re	27/905	272/18866	0.000293	0.001132	0.000595	SLPI/WFDC
BP	GO:004682	regulation	15/905	112/18866	0.000295	0.001141	0.000599	HSP90AB1/
BP	GO:001095	negative re	26/905	258/18866	0.000298	0.001148	0.000603	SLPI/WFDC
BP	GO:001049	proteasom	41/905	483/18866	0.000299	0.001151	0.000605	HSPA5/HSP
BP	GO:005149	positive reg	24/905	230/18866	0.0003	0.001155	0.000607	ICAM1/NO
BP	GO:004354	positive reg	36/905	406/18866	0.000302	0.001164	0.000612	ICAM1/CXC
BP	GO:004519	regulation	8/905	37/18866	0.000303	0.001166	0.000613	TGFB1/TFR
BP	GO:003227	positive reg	17/905	137/18866	0.000305	0.001171	0.000615	HSP90AA1/
BP	GO:000189	embryonic	13/905	89/18866	0.000312	0.001198	0.000629	SOCS3/IL10
BP	GO:002240	molting cyc	13/905	89/18866	0.000312	0.001198	0.000629	TNF/WNT5
BP	GO:002240	hair cycle p	13/905	89/18866	0.000312	0.001198	0.000629	TNF/WNT5
BP	GO:001050	regulation	32/905	347/18866	0.000324	0.00124	0.000652	IFNG/MAPT
BP	GO:001921	regulation	14/905	101/18866	0.000325	0.001244	0.000654	IL1B/FABP5
BP	GO:003582	modulation	15/905	113/18866	0.000326	0.001247	0.000656	CD4/SLPI/S
BP	GO:003032	lung develo	20/905	177/18866	0.000333	0.001273	0.000669	RBP4/TNF/
BP	GO:003556	non-canon	18/905	151/18866	0.000338	0.001293	0.00068	PSMB8/PSI
BP	GO:000762	circadian rh	23/905	218/18866	0.000339	0.001295	0.000681	RELB/PTGD
BP	GO:004880	genitalia de	9/905	47/18866	0.00034	0.001296	0.000681	RBP4/WNT
BP	GO:006098	endocrine	9/905	47/18866	0.00034	0.001296	0.000681	IL1B/AGT/A
BP	GO:009917	regulation	39/905	455/18866	0.000343	0.001307	0.000687	S100B/IL1B
BP	GO:009877	skin epider	13/905	90/18866	0.000349	0.001323	0.000695	TNF/WNT5
BP	GO:000269	positive reg	6/905	21/18866	0.000349	0.001323	0.000695	ICAM1/AG
BP	GO:001089	positive reg	6/905	21/18866	0.000349	0.001323	0.000695	IFNG/IL1B/
BP	GO:003581	regulation	6/905	21/18866	0.000349	0.001323	0.000695	EDNRB/AG
BP	GO:007211	cell prolifer	6/905	21/18866	0.000349	0.001323	0.000695	STAT1/PDG
BP	GO:000282	negative re	5/905	14/18866	0.00035	0.001323	0.000695	IFNL1/ARG
BP	GO:001083	positive reg	5/905	14/18866	0.00035	0.001323	0.000695	FGF10/ARE
BP	GO:003461	response to	5/905	14/18866	0.00035	0.001323	0.000695	TGFB3/ABC
BP	GO:003579	platelet-de	5/905	14/18866	0.00035	0.001323	0.000695	SRC/PDGFR
BP	GO:005170	regulation	5/905	14/18866	0.00035	0.001323	0.000695	IFNG/F2RL
BP	GO:007023	positive reg	5/905	14/18866	0.00035	0.001323	0.000695	IDO1/CCL5
BP	GO:005090	leukocyte t	7/905	29/18866	0.000352	0.00133	0.000699	CXCL12/TN
BP	GO:200072	positive reg	7/905	29/18866	0.000352	0.00133	0.000699	TGFB1/GRE
BP	GO:004244	hormone b	11/905	68/18866	0.000364	0.001372	0.000721	DUOX1/DU
BP	GO:000183	epithelial t	18/905	152/18866	0.000367	0.001384	0.000727	TGFB1/IL1B
BP	GO:004592	positive reg	8/905	38/18866	0.000368	0.001386	0.000728	IL1B/ADIPO
BP	GO:007139	cellular res	8/905	38/18866	0.000368	0.001386	0.000728	IL10/EGFR/
BP	GO:190018	regulation	16/905	127/18866	0.000382	0.001436	0.000755	HSP90AB1/
BP	GO:200017	regulation	13/905	91/18866	0.00039	0.001466	0.000771	VEGFA/WN
BP	GO:003163	zymogen a	10/905	58/18866	0.000394	0.00148	0.000778	CTSL/PLAU
BP	GO:000930	amine met	17/905	140/18866	0.000394	0.00148	0.000778	PSMB8/PSI
BP	GO:001620	regulation	18/905	153/18866	0.000398	0.001492	0.000784	S100B/TGF
BP	GO:007177	response to	18/905	153/18866	0.000398	0.001492	0.000784	CXCL8/CXC
BP	GO:004222	response to	9/905	48/18866	0.000401	0.001501	0.000789	HSPA5/HSP
BP	GO:200123	regulation	9/905	48/18866	0.000401	0.001501	0.000789	IL1B/TNF/I
BP	GO:005085	regulation	11/905	69/18866	0.000414	0.00155	0.000815	CCR7/CARD
BP	GO:000151	prostagland	7/905	30/18866	0.000441	0.001643	0.000864	PTGDS/IL1B
BP	GO:000184	protein ins	7/905	30/18866	0.000441	0.001643	0.000864	GZMB/BID/
BP	GO:003506	positive reg	7/905	30/18866	0.000441	0.001643	0.000864	IL1B/MAPK
BP	GO:004645	prostanoid	7/905	30/18866	0.000441	0.001643	0.000864	PTGDS/IL1B

BP	GO:006014	regulation	7/905	30/18866	0.000441	0.001643	0.000864	CXCL10/CX
BP	GO:004327	response t	14/905	104/18866	0.000441	0.001643	0.000864	HSPA5/HSP
BP	GO:003032	respiratory	20/905	181/18866	0.000446	0.001661	0.000873	RBP4/TNF/
BP	GO:004545	cell redox h	10/905	59/18866	0.000454	0.00169	0.000888	PDIA3/PDIA
BP	GO:000257	platelet de	16/905	129/18866	0.000455	0.001694	0.00089	FCER1G/TN
BP	GO:000721	Notch signa	21/905	195/18866	0.000459	0.001707	0.000897	STAT1/SRC
BP	GO:003580	regulation	6/905	22/18866	0.000461	0.00171	0.000899	EDNRB/AD
BP	GO:004562	positive reg	6/905	22/18866	0.000461	0.00171	0.000899	TNFSF4/CD
BP	GO:007135	cellular res	6/905	22/18866	0.000461	0.00171	0.000899	DDX58/IRF
BP	GO:007207	kidney epit	17/905	142/18866	0.000465	0.001725	0.000907	ADIPOQ/ST
BP	GO:001071	regulation	9/905	49/18866	0.00047	0.00174	0.000914	TGFB1/F2R
BP	GO:004205	negative re	9/905	49/18866	0.00047	0.00174	0.000914	AREG/BTC/
BP	GO:006138	trabecula r	9/905	49/18866	0.00047	0.00174	0.000914	RBP4/DLL4
BP	GO:009028	negative re	20/905	182/18866	0.000479	0.00177	0.00093	HSPA5/CXC
BP	GO:001076	positive reg	5/905	15/18866	0.000504	0.001856	0.000975	TGFB1/PTK
BP	GO:003264	regulation	5/905	15/18866	0.000504	0.001856	0.000975	IL1B/PAEP/
BP	GO:004440	adhesion o	5/905	15/18866	0.000504	0.001856	0.000975	HSP90AB1/
BP	GO:004484	estrous cyc	5/905	15/18866	0.000504	0.001856	0.000975	GNRH1/MI
BP	GO:004565	positive reg	5/905	15/18866	0.000504	0.001856	0.000975	TGFB1/IL34
BP	GO:190218	negative re	5/905	15/18866	0.000504	0.001856	0.000975	PML/TRIM
BP	GO:007200	nephron de	17/905	143/18866	0.000505	0.001858	0.000977	ADIPOQ/ST
BP	GO:003444	substrate a	14/905	106/18866	0.000537	0.001972	0.001036	CALR/ITGA
BP	GO:001066	regulation	13/905	94/18866	0.000537	0.001972	0.001036	IFNG/ARRE
BP	GO:000323	cardiac ver	16/905	131/18866	0.000541	0.001987	0.001044	TGFB1/WN
BP	GO:004863	regulation	18/905	157/18866	0.000544	0.001996	0.001049	S100B/TGF
BP	GO:003436	protein-lipi	7/905	31/18866	0.000546	0.001998	0.00105	CETP/PLA2
BP	GO:003436	plasma lipo	7/905	31/18866	0.000546	0.001998	0.00105	CETP/PLA2
BP	GO:007253	T-helper 17	7/905	31/18866	0.000546	0.001998	0.00105	IL23A/IL12
BP	GO:004361	keratinocyt	9/905	50/18866	0.00055	0.002011	0.001057	VDR/FGF10
BP	GO:003286	cellular res	23/905	226/18866	0.000565	0.002068	0.001087	IL1B/ADIPO
BP	GO:007132	cellular res	17/905	145/18866	0.000593	0.002168	0.00114	ICAM1/NO
BP	GO:003581	renal sodiu	6/905	23/18866	0.000599	0.002182	0.001147	EDNRB/AG
BP	GO:006054	negative re	6/905	23/18866	0.000599	0.002182	0.001147	UCN/FADD
BP	GO:007140	cellular res	6/905	23/18866	0.000599	0.002182	0.001147	FCER1G/PF
BP	GO:190001	positive reg	6/905	23/18866	0.000599	0.002182	0.001147	TNF/IL17D/
BP	GO:200082	regulation	8/905	41/18866	0.000633	0.002306	0.001212	WNT5A/SE
BP	GO:003808	vascular en	9/905	51/18866	0.000639	0.002322	0.00122	VEGFA/PD
BP	GO:006097	coronary va	9/905	51/18866	0.000639	0.002322	0.00122	VEGFA/PD
BP	GO:007135	cellular res	9/905	51/18866	0.000639	0.002322	0.00122	ICAM1/STA
BP	GO:007182	plasma lipo	9/905	51/18866	0.000639	0.002322	0.00122	CETP/PLA2
BP	GO:005080	modulation	38/905	454/18866	0.00064	0.002323	0.001221	S100B/IL1B
BP	GO:009010	negative re	16/905	133/18866	0.00064	0.002323	0.001221	HSPA5/TGF
BP	GO:003462	cellular res	17/905	146/18866	0.000642	0.002327	0.001223	CALR/HSPA
BP	GO:004434	cellular res	17/905	146/18866	0.000642	0.002327	0.001223	CXCL8/CXC
BP	GO:000600	glucose me	22/905	214/18866	0.000644	0.002331	0.001225	RBP4/FABP
BP	GO:000317	aortic valve	7/905	32/18866	0.00067	0.00242	0.001272	TGFB1/DLL
BP	GO:003235	regulation	7/905	32/18866	0.00067	0.00242	0.001272	ADM/BMP
BP	GO:003436	protein-con	7/905	32/18866	0.00067	0.00242	0.001272	CETP/PLA2
BP	GO:004340	negative re	20/905	187/18866	0.000678	0.002446	0.001286	PSMD10/IL
BP	GO:002170	developme	27/905	287/18866	0.000679	0.002446	0.001286	DEFB1/PAE

BP	GO:001061	regulation	11/905	73/18866	0.000679	0.002446	0.001286	PTK2/AGT/
BP	GO:005115	positive reg	11/905	73/18866	0.000679	0.002446	0.001286	CXCL9/TGF
BP	GO:001090	regulation	15/905	121/18866	0.000682	0.002454	0.00129	ADIPOQ/SF
BP	GO:000226	lymphocyte	10/905	62/18866	0.000682	0.002454	0.00129	TNFAIP3/M
BP	GO:000740	neuroblast	10/905	62/18866	0.000682	0.002454	0.00129	VEGFA/CX3
BP	GO:000749	mesoderm	16/905	134/18866	0.000696	0.0025	0.001314	VEGFA/WN
BP	GO:000178	neutrophil	5/905	16/18866	0.000704	0.002521	0.001325	PIK3CD/CX
BP	GO:000197	renal syste	5/905	16/18866	0.000704	0.002521	0.001325	F2R/F2RL1
BP	GO:003260	granulocyt	5/905	16/18866	0.000704	0.002521	0.001325	IL1B/PAEP/
BP	GO:003411	positive reg	5/905	16/18866	0.000704	0.002521	0.001325	IL1B/TNF/
BP	GO:004586	negative re	5/905	16/18866	0.000704	0.002521	0.001325	APOBEC3G
BP	GO:006057	morphogen	5/905	16/18866	0.000704	0.002521	0.001325	WNT5A/FG
BP	GO:004368	post-transl	32/905	363/18866	0.000706	0.002524	0.001327	PSMB8/PSI
BP	GO:000693	smooth mu	14/905	109/18866	0.000713	0.002548	0.001339	F2R/PTGS2
BP	GO:007050	calcium ion	12/905	85/18866	0.00072	0.00257	0.001351	CXCL12/TR
BP	GO:190352	regulation	28/905	303/18866	0.000721	0.002575	0.001353	ICAM1/S10
BP	GO:002153	telencepha	25/905	259/18866	0.000729	0.002601	0.001367	CXCL12/W
BP	GO:000717	transformin	21/905	202/18866	0.000732	0.002608	0.001371	HSPA5/HSI
BP	GO:199008	response to	9/905	52/18866	0.000741	0.002639	0.001387	HSPA5/MA
BP	GO:190406	regulation	31/905	349/18866	0.000749	0.002667	0.001402	HSPA2/IFN
BP	GO:000650	membrane	8/905	42/18866	0.00075	0.002668	0.001402	IFNG/ERAP
BP	GO:000309	glomerular	6/905	24/18866	0.000766	0.002715	0.001427	F2R/F2RL1
BP	GO:001064	regulation	6/905	24/18866	0.000766	0.002715	0.001427	APOD/ADII
BP	GO:001080	negative re	6/905	24/18866	0.000766	0.002715	0.001427	ADIPOQ/F2
BP	GO:001086	regulation	6/905	24/18866	0.000766	0.002715	0.001427	IFNG/ADIP
BP	GO:003469	response to	6/905	24/18866	0.000766	0.002715	0.001427	TNFSF4/CC
BP	GO:006200	secondary	6/905	24/18866	0.000766	0.002715	0.001427	WNT5A/JA
BP	GO:005500	cardiac mu	10/905	63/18866	0.000777	0.00275	0.001445	TGFB1/WN
BP	GO:007005	intrinsic ap	10/905	63/18866	0.000777	0.00275	0.001445	PML/TNFR
BP	GO:000165	ureteric bu	13/905	98/18866	0.000803	0.002839	0.001492	VEGFA/AR
BP	GO:001065	muscle cell	13/905	98/18866	0.000803	0.002839	0.001492	IFNG/ARRE
BP	GO:190437	regulation	15/905	123/18866	0.00081	0.00286	0.001503	IFNG/TGFB
BP	GO:190336	positive reg	17/905	149/18866	0.00081	0.00286	0.001503	HSP90AA1/
BP	GO:004801	neurotroph	7/905	33/18866	0.000816	0.002872	0.001509	SRC/AGT/N
BP	GO:006131	cell surface	7/905	33/18866	0.000816	0.002872	0.001509	TGFB1/WN
BP	GO:012025	olefinic com	7/905	33/18866	0.000816	0.002872	0.001509	ADM/BMP
BP	GO:200075	positive reg	7/905	33/18866	0.000816	0.002872	0.001509	IL1B/MAPK
BP	GO:000806	regulation	20/905	190/18866	0.000829	0.002916	0.001532	ICAM1/CX
BP	GO:003296	collagen bi	9/905	53/18866	0.000855	0.003005	0.001579	TGFB1/F2R
BP	GO:004230	molting cyc	14/905	111/18866	0.000856	0.003005	0.001579	TNF/WNT5
BP	GO:004263	hair cycle	14/905	111/18866	0.000856	0.003005	0.001579	TNF/WNT5
BP	GO:000252	hypersensi	4/905	10/18866	0.000875	0.003041	0.001598	FCER1G/CC
BP	GO:000266	regulation	4/905	10/18866	0.000875	0.003041	0.001598	HLA-B/HLA
BP	GO:001088	negative re	4/905	10/18866	0.000875	0.003041	0.001598	PPARG/PP
BP	GO:003308	regulation	4/905	10/18866	0.000875	0.003041	0.001598	IL1B/IL1A/
BP	GO:003413	regulation	4/905	10/18866	0.000875	0.003041	0.001598	TNFAIP3/F
BP	GO:003650	ATF6-medi	4/905	10/18866	0.000875	0.003041	0.001598	CALR/HSPA
BP	GO:003953	MDA-5 sign	4/905	10/18866	0.000875	0.003041	0.001598	IRF3/IFIH1/
BP	GO:004254	hemoglobi	4/905	10/18866	0.000875	0.003041	0.001598	EPO/INHA/
BP	GO:004275	drinking be	4/905	10/18866	0.000875	0.003041	0.001598	AGT/APLN/

BP	GO:004298	sequesteri	4/905	10/18866	0.000875	0.003041	0.001598	TMSB10/T
BP	GO:004338	regulation	4/905	10/18866	0.000875	0.003041	0.001598	IFNL1/TNF
BP	GO:006051	prostatic b	4/905	10/18866	0.000875	0.003041	0.001598	WNT5A/FG
BP	GO:007038	DNA cytosi	4/905	10/18866	0.000875	0.003041	0.001598	APOBEC3G
BP	GO:007167	smooth mu	4/905	10/18866	0.000875	0.003041	0.001598	PDGFRB/M
BP	GO:190042	positive reg	4/905	10/18866	0.000875	0.003041	0.001598	F2RL1/HAV
BP	GO:200010	regulation	4/905	10/18866	0.000875	0.003041	0.001598	CCL5/IRF7/
BP	GO:200042	regulation	4/905	10/18866	0.000875	0.003041	0.001598	CCL2/C2/C
BP	GO:000195	negative re	8/905	43/18866	0.000883	0.00306	0.001608	MMP12/A
BP	GO:005085	positive reg	8/905	43/18866	0.000883	0.00306	0.001608	CD4/TNF/C
BP	GO:005085	regulation	8/905	43/18866	0.000883	0.00306	0.001608	CCR7/CARD
BP	GO:007216	mesonephr	13/905	99/18866	0.000885	0.00306	0.001608	VEGFA/AR
BP	GO:007216	mesonephr	13/905	99/18866	0.000885	0.00306	0.001608	VEGFA/AR
BP	GO:003083	regulation	20/905	191/18866	0.000885	0.00306	0.001608	ICAM1/CX
BP	GO:003526	organ grow	20/905	191/18866	0.000885	0.00306	0.001608	RBP4/PDG
BP	GO:004586	negative re	32/905	369/18866	0.000929	0.00321	0.001687	HSP90AB1/
BP	GO:002195	central ner	20/905	192/18866	0.000944	0.003261	0.001714	B2M/HSP9
BP	GO:000312	heart field	5/905	17/18866	0.000959	0.003291	0.00173	WNT5A/R
BP	GO:001056	regulation	5/905	17/18866	0.000959	0.003291	0.00173	ADM/BMP
BP	GO:003088	negative re	5/905	17/18866	0.000959	0.003291	0.00173	IL10/BTK/T
BP	GO:004311	positive reg	5/905	17/18866	0.000959	0.003291	0.00173	TGFB1/VE
BP	GO:005066	hydrogen p	5/905	17/18866	0.000959	0.003291	0.00173	DUOX1/CY
BP	GO:006026	regulation	5/905	17/18866	0.000959	0.003291	0.00173	LBP/RAC2/
BP	GO:190494	midbrain d	5/905	17/18866	0.000959	0.003291	0.00173	WNT5A/D
BP	GO:200081	negative re	5/905	17/18866	0.000959	0.003291	0.00173	SRC/PTK2/
BP	GO:001474	regulation	11/905	76/18866	0.000959	0.003291	0.00173	PTK2/AGT/
BP	GO:006041	muscle tiss	11/905	76/18866	0.000959	0.003291	0.00173	TGFB1/WN
BP	GO:003952	RIG-I signal	6/905	25/18866	0.000968	0.003312	0.001741	DDX58/NL
BP	GO:004566	negative re	6/905	25/18866	0.000968	0.003312	0.001741	CXCL14/CX
BP	GO:004663	negative re	6/905	25/18866	0.000968	0.003312	0.001741	SOCS1/TN
BP	GO:190438	cellular res	6/905	25/18866	0.000968	0.003312	0.001741	SRC/AGT/A
BP	GO:003497	response t	27/905	294/18866	0.000977	0.003341	0.001756	CALR/PDIA
BP	GO:190118	negative re	9/905	54/18866	0.000983	0.003355	0.001763	AREG/BTC/
BP	GO:003085	granulocyt	7/905	34/18866	0.000985	0.003355	0.001763	ADIPOQ/C
BP	GO:004327	anoikis	7/905	34/18866	0.000985	0.003355	0.001763	SRC/PTK2/
BP	GO:004590	positive reg	7/905	34/18866	0.000985	0.003355	0.001763	ICAM1/F2
BP	GO:005148	positive reg	7/905	34/18866	0.000985	0.003355	0.001763	F2R/F2RL1/
BP	GO:005509	response t	7/905	34/18866	0.000985	0.003355	0.001763	FCER1G/P
BP	GO:007010	interleukin	7/905	34/18866	0.000985	0.003355	0.001763	STAT1/SO
BP	GO:000206	epithelial c	22/905	221/18866	0.000989	0.003365	0.001768	ICAM1/IL1
BP	GO:004244	hormone m	22/905	221/18866	0.000989	0.003365	0.001768	CTSB/CTSL/
BP	GO:190316	regulation	17/905	152/18866	0.001014	0.003448	0.001812	HSPA2/CX
BP	GO:003296	regulation	8/905	44/18866	0.001034	0.003514	0.001847	TGFB1/F2
BP	GO:003238	positive reg	22/905	222/18866	0.00105	0.003564	0.001873	HSP90AB1/
BP	GO:190199	negative re	24/905	251/18866	0.001051	0.003567	0.001875	PSMB8/PS
BP	GO:006101	regulation	21/905	208/18866	0.001067	0.003614	0.001899	PSMB8/PS
BP	GO:190290	positive reg	21/905	208/18866	0.001067	0.003614	0.001899	ICAM1/NO
BP	GO:003083	positive reg	13/905	101/18866	0.001069	0.00362	0.001903	ICAM1/TR
BP	GO:004657	regulation	20/905	194/18866	0.001074	0.003634	0.00191	F2R/F2RL1/
BP	GO:000167	cellular glu	17/905	153/18866	0.001091	0.003691	0.00194	ICAM1/NO

BP	GO:00432	response t	14/905	114/18866	0.001115	0.003768	0.00198	ICAM1/TN
BP	GO:00029	response t	9/905	55/18866	0.001126	0.003799	0.001997	CX3CR1/P
BP	GO:00718	protein-lip	9/905	55/18866	0.001126	0.003799	0.001997	CETP/PLA2
BP	GO:00329	circadian r	10/905	66/18866	0.001127	0.003799	0.001997	RELB/PML/
BP	GO:00343	protein loc	10/905	66/18866	0.001127	0.003799	0.001997	FCER1G/H
BP	GO:19030	positive re	15/905	127/18866	0.001129	0.003805	0.002	PSMC2/PS
BP	GO:00323	regulation	31/905	358/18866	0.001135	0.00382	0.002008	HSP90AB1/
BP	GO:00030	heart proc	27/905	297/18866	0.001136	0.003823	0.002009	S100A1/N
BP	GO:00507	regulation	19/905	181/18866	0.001142	0.003842	0.002019	IFNG/IL1B/
BP	GO:00435	regulation	13/905	102/18866	0.001173	0.003941	0.002071	PTK2/AGT/
BP	GO:00343	smooth mu	7/905	35/18866	0.001181	0.00396	0.002081	IFNG/ARR
BP	GO:00343	regulation	7/905	35/18866	0.001181	0.00396	0.002081	IFNG/ARR
BP	GO:00483	mesoderm	7/905	35/18866	0.001181	0.00396	0.002081	DKK1/INH
BP	GO:00987	bone cell d	7/905	35/18866	0.001181	0.00396	0.002081	LTF/SRC/T
BP	GO:00158	organic hy	25/905	268/18866	0.001188	0.003981	0.002092	FCER1G/C
BP	GO:00610	negative re	11/905	78/18866	0.001194	0.004	0.002102	PLAU/TNF/
BP	GO:00512	protein ins	8/905	45/18866	0.001206	0.004028	0.002117	HSP90AA1/
BP	GO:19010	regulation	8/905	45/18866	0.001206	0.004028	0.002117	GSK3B/GZ
BP	GO:00067	C21-steroi	6/905	26/18866	0.001207	0.004028	0.002117	ADM/BMP
BP	GO:00329	positive re	6/905	26/18866	0.001207	0.004028	0.002117	TGFB1/F2R
BP	GO:00428	defense re	6/905	26/18866	0.001207	0.004028	0.002117	CD40/SLC1
BP	GO:00720	glomerulus	6/905	26/18866	0.001207	0.004028	0.002117	PDGFRB/P
BP	GO:00073	pattern sp	37/905	455/18866	0.001263	0.004211	0.002213	WNT5A/DL
BP	GO:00328	regulation	10/905	67/18866	0.001269	0.004228	0.002222	IL1B/FABP
BP	GO:00327	positive re	5/905	18/18866	0.001276	0.004237	0.002227	TGFB1/IL1
BP	GO:00360	osteoclast	5/905	18/18866	0.001276	0.004237	0.002227	LTF/SRC/T
BP	GO:00430	myeloid de	5/905	18/18866	0.001276	0.004237	0.002227	RELB/CSF2
BP	GO:00900	regulation	5/905	18/18866	0.001276	0.004237	0.002227	CD40/VEG
BP	GO:00901	positive re	5/905	18/18866	0.001276	0.004237	0.002227	VEGFA/AG
BP	GO:00487	oligodendr	13/905	103/18866	0.001284	0.004264	0.002241	TLR2/EED/
BP	GO:00507	negative re	9/905	56/18866	0.001285	0.004265	0.002241	SOCS3/SO
BP	GO:00069	response t	19/905	183/18866	0.001301	0.004315	0.002268	CALR/HSP
BP	GO:00512	protein pol	27/905	300/18866	0.001317	0.004357	0.00229	HSP90AA1/
BP	GO:00017	natural kill	4/905	11/18866	0.001324	0.004357	0.00229	IL15/FLT3L
BP	GO:00327	positive re	4/905	11/18866	0.001324	0.004357	0.00229	IL33/CRLF2
BP	GO:00330	immature	4/905	11/18866	0.001324	0.004357	0.00229	IL1B/IL1A/
BP	GO:00338	regulation	4/905	11/18866	0.001324	0.004357	0.00229	AGT/AGTR
BP	GO:00433	memory T	4/905	11/18866	0.001324	0.004357	0.00229	IFNL1/TNF
BP	GO:00510	positive re	4/905	11/18866	0.001324	0.004357	0.00229	RBP4/TNFS
BP	GO:00704	uterine sm	4/905	11/18866	0.001324	0.004357	0.00229	AGT/OXT/
BP	GO:00706	response t	4/905	11/18866	0.001324	0.004357	0.00229	PDGFB/IL1
BP	GO:00721	glomerular	4/905	11/18866	0.001324	0.004357	0.00229	PDGFRB/P
BP	GO:00901	positive re	4/905	11/18866	0.001324	0.004357	0.00229	ADIPOQ/P
BP	GO:00907	immunolog	4/905	11/18866	0.001324	0.004357	0.00229	IFNL1/TNF
BP	GO:00016	metanephr	12/905	91/18866	0.001328	0.004367	0.002295	ADIPOQ/S
BP	GO:19007	regulation	8/905	46/18866	0.0014	0.004601	0.002418	IL1B/VEGF
BP	GO:00433	positive T	7/905	36/18866	0.001406	0.004617	0.002427	CTSL/IL23A
BP	GO:00716	regulation	7/905	36/18866	0.001406	0.004617	0.002427	HSP90AB1/
BP	GO:19043	positive re	10/905	68/18866	0.001425	0.004676	0.002457	IFNG/TNF/
BP	GO:00181	peptidyl-th	14/905	117/18866	0.001437	0.004709	0.002475	TGFB1/W

BP	GO:004544	endothelia	14/905	117/18866	0.001437	0.004709	0.002475	ICAM1/IL1
BP	GO:004274	hydrogen	9/905	57/18866	0.001463	0.004783	0.002513	DUOX1/CY
BP	GO:004574	positive reg	9/905	57/18866	0.001463	0.004783	0.002513	SRC/DLL4/
BP	GO:004801	inositol ph	9/905	57/18866	0.001463	0.004783	0.002513	TNF/CHP1/
BP	GO:007139	cellular res	9/905	57/18866	0.001463	0.004783	0.002513	SRC/TNFSF
BP	GO:190018	positive reg	11/905	80/18866	0.001475	0.00482	0.002533	HSP90AB1/
BP	GO:000156	response t	6/905	27/18866	0.00149	0.004852	0.00255	CD40/SLC1
BP	GO:001071	positive reg	6/905	27/18866	0.00149	0.004852	0.00255	TGFB1/F2R
BP	GO:003469	response t	6/905	27/18866	0.00149	0.004852	0.00255	ICAM1/INH
BP	GO:006054	regulation	6/905	27/18866	0.00149	0.004852	0.00255	ZBP1/FAD
BP	GO:006209	regulation	6/905	27/18866	0.00149	0.004852	0.00255	ZBP1/FAD
BP	GO:190520	negative re	6/905	27/18866	0.00149	0.004852	0.00255	BMP2/DKK
BP	GO:000763	feeding be	13/905	105/18866	0.001535	0.004991	0.002623	FOS/AGT/
BP	GO:009700	regulation	13/905	105/18866	0.001535	0.004991	0.002623	CETP/ADIP
BP	GO:001050	positive reg	15/905	131/18866	0.001548	0.005032	0.002644	IFNG/MAP
BP	GO:190188	regulation	20/905	200/18866	0.001557	0.005058	0.002658	TLR2/IL1B/
BP	GO:005114	regulation	19/905	186/18866	0.001575	0.005113	0.002687	CXCL10/CX
BP	GO:005170	interaction	12/905	93/18866	0.001606	0.005211	0.002739	LTF/CTSG/
BP	GO:004330	regulation	8/905	47/18866	0.001617	0.005242	0.002755	FCER1G/HL
BP	GO:000193	negative re	11/905	81/18866	0.001635	0.005296	0.002783	TNF/STAT1
BP	GO:000076	syncytium	9/905	58/18866	0.001659	0.005358	0.002816	CXCL10/CX
BP	GO:005105	negative re	9/905	58/18866	0.001659	0.005358	0.002816	BMP2/BMP
BP	GO:014025	cell-cell fus	9/905	58/18866	0.001659	0.005358	0.002816	CXCL10/CX
BP	GO:003267	regulation	5/905	19/18866	0.001663	0.005358	0.002816	IFNL1/IL33/
BP	GO:003318	response t	5/905	19/18866	0.001663	0.005358	0.002816	PPARG/EP
BP	GO:003439	positive reg	5/905	19/18866	0.001663	0.005358	0.002816	IFNG/ARRB
BP	GO:003953	regulation	5/905	19/18866	0.001663	0.005358	0.002816	NLRX1/DHX
BP	GO:200001	positive reg	5/905	19/18866	0.001663	0.005358	0.002816	FCER1G/HS
BP	GO:007042	nucleotide	7/905	37/18866	0.001664	0.005358	0.002816	TNFAIP3/IK
BP	GO:190531	semi-lunar	7/905	37/18866	0.001664	0.005358	0.002816	TGFB1/DLL
BP	GO:000110	response t	15/905	132/18866	0.001671	0.00538	0.002827	ICAM1/TN
BP	GO:003003	contractile	13/905	106/18866	0.001674	0.005383	0.002829	NOX4/SRC/
BP	GO:004314	stress fiber	13/905	106/18866	0.001674	0.005383	0.002829	NOX4/SRC/
BP	GO:000170	in utero en	32/905	383/18866	0.001703	0.005472	0.002876	PSMC4/SO
BP	GO:003227	regulation	22/905	231/18866	0.001753	0.005629	0.002958	HSP90AA1/
BP	GO:003083	regulation	18/905	174/18866	0.001795	0.00576	0.003027	ICAM1/TM
BP	GO:002261	extracellul	11/905	82/18866	0.001808	0.005795	0.003046	CTSL/MMP
BP	GO:190293	regulation	11/905	82/18866	0.001808	0.005795	0.003046	IFNG/NFYA
BP	GO:000318	aortic valv	6/905	28/18866	0.001821	0.005812	0.003055	TGFB1/DLL
BP	GO:004204	fluid trans	6/905	28/18866	0.001821	0.005812	0.003055	AQP9/EDN
BP	GO:004583	positive reg	6/905	28/18866	0.001821	0.005812	0.003055	TGFB1/TFR
BP	GO:006014	positive reg	6/905	28/18866	0.001821	0.005812	0.003055	CXCL9/FLT
BP	GO:006143	renal syste	6/905	28/18866	0.001821	0.005812	0.003055	PDGFRB/P
BP	GO:006144	kidney vas	6/905	28/18866	0.001821	0.005812	0.003055	PDGFRB/P
BP	GO:190293	positive reg	6/905	28/18866	0.001821	0.005812	0.003055	IFNG/IL1B/
BP	GO:007016	positive reg	8/905	48/18866	0.00186	0.005931	0.003117	TGFB1/LTF
BP	GO:011015	positive reg	8/905	48/18866	0.00186	0.005931	0.003117	TGFB1/LTF/
BP	GO:000292	regulation	4/905	12/18866	0.001911	0.006042	0.003175	LTA/TNF/
BP	GO:000621	cytidine ca	4/905	12/18866	0.001911	0.006042	0.003175	APOBEC3G
BP	GO:000997	cytidine de	4/905	12/18866	0.001911	0.006042	0.003175	APOBEC3G

BP	GO:001655	cytidine to	4/905	12/18866	0.001911	0.006042	0.003175	APOBEC3G
BP	GO:003139	regulation	4/905	12/18866	0.001911	0.006042	0.003175	IL1B/FABP5
BP	GO:003563	bone mine	4/905	12/18866	0.001911	0.006042	0.003175	LTF/BMP2/
BP	GO:003818	nerve grow	4/905	12/18866	0.001911	0.006042	0.003175	NGF/NTF3/
BP	GO:004236	vitamin D	4/905	12/18866	0.001911	0.006042	0.003175	IFNG/IL1B/
BP	GO:004608	cytidine m	4/905	12/18866	0.001911	0.006042	0.003175	APOBEC3G
BP	GO:006039	negative re	4/905	12/18866	0.001911	0.006042	0.003175	DKK1/GRE
BP	GO:007024	regulation	4/905	12/18866	0.001911	0.006042	0.003175	WNT5A/HI
BP	GO:007163	positive re	4/905	12/18866	0.001911	0.006042	0.003175	IL1B/ADIP
BP	GO:190594	positive re	4/905	12/18866	0.001911	0.006042	0.003175	SRC/SEMA
BP	GO:200120	regulation	4/905	12/18866	0.001911	0.006042	0.003175	LTF/TNFSF
BP	GO:000758	body fluid	12/905	95/18866	0.001932	0.006102	0.003207	VEGFA/VD
BP	GO:005070	negative re	12/905	95/18866	0.001932	0.006102	0.003207	IL1B/F2R/
BP	GO:007133	cellular res	15/905	134/18866	0.001942	0.00613	0.003222	ICAM1/NO
BP	GO:000238	mucosal i	7/905	38/18866	0.001956	0.00615	0.003232	XCL1/DEFB
BP	GO:001066	positive re	7/905	38/18866	0.001956	0.00615	0.003232	IFNG/ARR
BP	GO:003587	nucleotide	7/905	38/18866	0.001956	0.00615	0.003232	TNFAIP3/I
BP	GO:004800	insulin-like	7/905	38/18866	0.001956	0.00615	0.003232	PIK3R1/B
BP	GO:005193	regulation	7/905	38/18866	0.001956	0.00615	0.003232	FABP5/F2R
BP	GO:007127	cellular res	7/905	38/18866	0.001956	0.00615	0.003232	MMP9/CY
BP	GO:007160	transformi	7/905	38/18866	0.001956	0.00615	0.003232	HSP90AB1/
BP	GO:006054	respiratory	20/905	204/18866	0.001973	0.006201	0.003259	RBP4/TNF/
BP	GO:004864	muscle org	11/905	83/18866	0.001996	0.006267	0.003294	TGFB1/WN
BP	GO:004856	digestive t	15/905	135/18866	0.00209	0.00656	0.003448	CXCL8/TN
BP	GO:000694	syncytium	9/905	60/18866	0.002115	0.006628	0.003483	CXCL10/CX
BP	GO:200024	negative re	9/905	60/18866	0.002115	0.006628	0.003483	CALR/PAE
BP	GO:000268	negative re	5/905	20/18866	0.002131	0.006628	0.003483	CCL2/MIF/
BP	GO:001000	cardioblast	5/905	20/18866	0.002131	0.006628	0.003483	GREM1/N
BP	GO:003263	interleukin	5/905	20/18866	0.002131	0.006628	0.003483	IFNL1/IL33/
BP	GO:004395	positive re	5/905	20/18866	0.002131	0.006628	0.003483	NOS1/UCN
BP	GO:006054	negative re	5/905	20/18866	0.002131	0.006628	0.003483	FADD/CAS
BP	GO:006209	negative re	5/905	20/18866	0.002131	0.006628	0.003483	FADD/CAS
BP	GO:009770	connective	5/905	20/18866	0.002131	0.006628	0.003483	TGFB1/F2R
BP	GO:200077	positive re	5/905	20/18866	0.002131	0.006628	0.003483	B2M/HLA-
BP	GO:000206	glandular	8/905	49/18866	0.002131	0.006628	0.003483	WNT5A/G
BP	GO:000244	mast cell	8/905	49/18866	0.002131	0.006628	0.003483	FCER1G/BT
BP	GO:000669	prostanoid	8/905	49/18866	0.002131	0.006628	0.003483	PTGDS/IL1
BP	GO:000669	prostaglan	8/905	49/18866	0.002131	0.006628	0.003483	PTGDS/IL1
BP	GO:009015	establishm	8/905	49/18866	0.002131	0.006628	0.003483	HSP90AA1/
BP	GO:199009	cellular res	8/905	49/18866	0.002131	0.006628	0.003483	HSPA5/MA
BP	GO:001489	muscle hyp	13/905	109/18866	0.002157	0.006704	0.003523	PTK2/AGT/
BP	GO:190290	regulation	31/905	373/18866	0.002164	0.006721	0.003532	ICAM1/CX
BP	GO:006151	myeloid ce	10/905	72/18866	0.002212	0.006868	0.003609	TLR2/LTF/
BP	GO:007133	cellular res	15/905	136/18866	0.002248	0.006974	0.003665	ICAM1/NO
BP	GO:000815	actin poly	21/905	221/18866	0.002265	0.007018	0.003688	ICAM1/CX
BP	GO:003166	cellular res	21/905	221/18866	0.002265	0.007018	0.003688	HSPA5/ICA
BP	GO:001083	regulation	7/905	39/18866	0.002287	0.007067	0.003714	VDR/FGF1
BP	GO:003817	neurotrop	7/905	39/18866	0.002287	0.007067	0.003714	SRC/AGT/
BP	GO:005193	regulation	7/905	39/18866	0.002287	0.007067	0.003714	FABP5/F2R
BP	GO:190470	negative re	7/905	39/18866	0.002287	0.007067	0.003714	ADIPOQ/IL

BP	GO:200024	regulation	7/905	39/18866	0.002287	0.007067	0.003714	PTK2B/HCK
BP	GO:000660	protein imp	16/905	150/18866	0.002304	0.007117	0.00374	HSP90AB1/
BP	GO:190134	negative re	20/905	207/18866	0.002344	0.007235	0.003802	HLA-G/CXC
BP	GO:000317	heart valve	9/905	61/18866	0.002378	0.007314	0.003844	TGFB1/DLL
BP	GO:002187	forebrain g	9/905	61/18866	0.002378	0.007314	0.003844	B2M/WNT
BP	GO:003361	membrane	9/905	61/18866	0.002378	0.007314	0.003844	IFNG/ERAP
BP	GO:004584	negative re	9/905	61/18866	0.002378	0.007314	0.003844	S100B/TGF
BP	GO:009034	regulation	9/905	61/18866	0.002378	0.007314	0.003844	B2M/HLA-
BP	GO:190307	positive reg	9/905	61/18866	0.002378	0.007314	0.003844	IFNG/TNF/
BP	GO:003004	actin filame	19/905	193/18866	0.002409	0.007407	0.003892	ICAM1/TM
BP	GO:007132	cellular res	15/905	137/18866	0.002415	0.007421	0.0039	ICAM1/NO
BP	GO:004598	positive reg	8/905	50/18866	0.002433	0.007458	0.003919	IFNG/TMSB
BP	GO:010102	vascular en	8/905	50/18866	0.002433	0.007458	0.003919	CCL2/PPAR
BP	GO:190054	positive reg	8/905	50/18866	0.002433	0.007458	0.003919	IFNG/TMSB
BP	GO:190556	regulation	8/905	50/18866	0.002433	0.007458	0.003919	CCL2/PPAR
BP	GO:004846	cell matura	18/905	179/18866	0.002455	0.007516	0.00395	DEFB1/PAE
BP	GO:000320	cardiac ver	10/905	73/18866	0.002456	0.007516	0.00395	TGFB1/DLL
BP	GO:190374	regulation	10/905	73/18866	0.002456	0.007516	0.00395	MAPT/RAC
BP	GO:001633	morphogen	16/905	151/18866	0.002466	0.007543	0.003964	TGFB1/WN
BP	GO:004583	negative re	12/905	98/18866	0.002519	0.007702	0.004048	IL1B/APOD
BP	GO:000726	Ras protein	29/905	346/18866	0.002614	0.007963	0.004185	F2R/F2RL1/
BP	GO:003596	cellular res	17/905	166/18866	0.002639	0.007963	0.004185	CALR/HSPA
BP	GO:000340	axis elonga	6/905	30/18866	0.002644	0.007963	0.004185	WNT5A/FG
BP	GO:001080	positive reg	6/905	30/18866	0.002644	0.007963	0.004185	TGFB1/WN
BP	GO:003411	regulation	6/905	30/18866	0.002644	0.007963	0.004185	CCL5/TNFS
BP	GO:003811	interleukin	6/905	30/18866	0.002644	0.007963	0.004185	SOCS1/IL7R
BP	GO:006005	angiogenes	6/905	30/18866	0.002644	0.007963	0.004185	TNF/VEGFA
BP	GO:007016	negative re	6/905	30/18866	0.002644	0.007963	0.004185	TGFB1/CCL
BP	GO:007072	response to	6/905	30/18866	0.002644	0.007963	0.004185	TGFB1/CCL
BP	GO:011015	negative re	6/905	30/18866	0.002644	0.007963	0.004185	TGFB1/CCL
BP	GO:000243	complemen	4/905	13/18866	0.002656	0.007963	0.004185	C5AR1/CM
BP	GO:000283	positive reg	4/905	13/18866	0.002656	0.007963	0.004185	MR1/IL12A
BP	GO:000283	positive reg	4/905	13/18866	0.002656	0.007963	0.004185	MR1/IL12A
BP	GO:000717	activation	4/905	13/18866	0.002656	0.007963	0.004185	EGF/GREM
BP	GO:000822	opsonizatio	4/905	13/18866	0.002656	0.007963	0.004185	LBP/PTX3/
BP	GO:001062	programme	4/905	13/18866	0.002656	0.007963	0.004185	IL1B/IL1A/
BP	GO:001626	gap junctio	4/905	13/18866	0.002656	0.007963	0.004185	IL1B/AGT/
BP	GO:003235	positive reg	4/905	13/18866	0.002656	0.007963	0.004185	ADM/PPAR
BP	GO:003249	response to	4/905	13/18866	0.002656	0.007963	0.004185	TLR2/DMB
BP	GO:003312	regulation	4/905	13/18866	0.002656	0.007963	0.004185	IL1B/MAPK
BP	GO:003360	positive reg	4/905	13/18866	0.002656	0.007963	0.004185	CXCL12/GD
BP	GO:004230	negative re	4/905	13/18866	0.002656	0.007963	0.004185	APOD/CHP
BP	GO:005509	phospholip	4/905	13/18866	0.002656	0.007963	0.004185	FABP3/CET
BP	GO:006060	lateral spro	4/905	13/18866	0.002656	0.007963	0.004185	WNT5A/FG
BP	GO:006104	regulation	4/905	13/18866	0.002656	0.007963	0.004185	TNF/TNFAI
BP	GO:190027	negative re	4/905	13/18866	0.002656	0.007963	0.004185	AGER/CX3
BP	GO:190256	regulation	4/905	13/18866	0.002656	0.007963	0.004185	PLA2G2A/
BP	GO:190323	regulation	4/905	13/18866	0.002656	0.007963	0.004185	CXCL12/CC
BP	GO:190397	positive reg	4/905	13/18866	0.002656	0.007963	0.004185	CCL3/CX3C
BP	GO:190459	negative re	4/905	13/18866	0.002656	0.007963	0.004185	APOD/CHP

BP	GO:200119	regulation	4/905	13/18866	0.002656	0.007963	0.004185	HLA-B/HLA
BP	GO:001061	positive re	7/905	40/18866	0.002659	0.007963	0.004185	PTK2/AGT/
BP	GO:001093	regulation	7/905	40/18866	0.002659	0.007963	0.004185	UCN/ZBP1/
BP	GO:001657	histone ph	7/905	40/18866	0.002659	0.007963	0.004185	IL1B/MAPK
BP	GO:003050	positive re	7/905	40/18866	0.002659	0.007963	0.004185	TGFB1/LTF
BP	GO:004230	positive re	7/905	40/18866	0.002659	0.007963	0.004185	HSP90AB1/
BP	GO:007221	metanephr	7/905	40/18866	0.002659	0.007963	0.004185	ADIPOQ/ST
BP	GO:001067	positive re	9/905	62/18866	0.002665	0.007964	0.004185	SRC/IGF1/
BP	GO:004863	negative re	9/905	62/18866	0.002665	0.007964	0.004185	S100B/TGF
BP	GO:005502	positive re	9/905	62/18866	0.002665	0.007964	0.004185	TGFB1/GRE
BP	GO:200124	positive re	9/905	62/18866	0.002665	0.007964	0.004185	S100A9/S1
BP	GO:000202	desensitiza	5/905	21/18866	0.002688	0.007978	0.004193	ARRB1/ADI
BP	GO:001482	phasic smo	5/905	21/18866	0.002688	0.007978	0.004193	EDN3/EDN
BP	GO:001655	base conve	5/905	21/18866	0.002688	0.007978	0.004193	APOBEC3G
BP	GO:002240	negative a	5/905	21/18866	0.002688	0.007978	0.004193	ARRB1/ADI
BP	GO:003050	negative re	5/905	21/18866	0.002688	0.007978	0.004193	CCL3/CCR1
BP	GO:003363	positive re	5/905	21/18866	0.002688	0.007978	0.004193	CXCL13/CC
BP	GO:003649	PERK-medi	5/905	21/18866	0.002688	0.007978	0.004193	HSPA5/CX
BP	GO:004337	negative re	5/905	21/18866	0.002688	0.007978	0.004193	TNFSF4/JA
BP	GO:006021	definitive	5/905	21/18866	0.002688	0.007978	0.004193	ADAR/TEK/
BP	GO:006104	vascular w	5/905	21/18866	0.002688	0.007978	0.004193	TNF/VEGF
BP	GO:006121	positive re	5/905	21/18866	0.002688	0.007978	0.004193	VEGFA/AG
BP	GO:014046	integrated	5/905	21/18866	0.002688	0.007978	0.004193	HSPA5/CX
BP	GO:001071	regulation	12/905	99/18866	0.002745	0.008138	0.004277	TGFB1/IL1
BP	GO:005181	modulatior	12/905	99/18866	0.002745	0.008138	0.004277	CD4/LTF/C
BP	GO:000698	ER-nucleus	8/905	51/18866	0.002766	0.008197	0.004308	CALR/HSP
BP	GO:190198	negative re	24/905	270/18866	0.002792	0.008269	0.004346	PSMB8/PS
BP	GO:005080	regulation	22/905	240/18866	0.002822	0.008355	0.004391	TLR2/MX1/
BP	GO:007189	DNA biosyr	19/905	196/18866	0.002866	0.008479	0.004456	HSP90AA1/
BP	GO:001821	peptidyl-th	14/905	126/18866	0.002898	0.00857	0.004504	TGFB1/WN
BP	GO:000225	organ or ti	7/905	41/18866	0.003076	0.009081	0.004773	XCL1/DEFB
BP	GO:001474	positive re	7/905	41/18866	0.003076	0.009081	0.004773	PTK2/AGT/
BP	GO:200000	regulation	7/905	41/18866	0.003076	0.009081	0.004773	FCER1G/H
BP	GO:000317	heart valve	8/905	52/18866	0.003135	0.009238	0.004855	TGFB1/DLL
BP	GO:003051	negative re	8/905	52/18866	0.003135	0.009238	0.004855	HJV/WNT5
BP	GO:003806	p38MAPK	8/905	52/18866	0.003135	0.009238	0.004855	IL1B/VEGF
BP	GO:005085	negative re	6/905	31/18866	0.003148	0.009258	0.004865	CD22/PTPN
BP	GO:006103	negative re	6/905	31/18866	0.003148	0.009258	0.004865	GDF5/GRE
BP	GO:190074	positive re	6/905	31/18866	0.003148	0.009258	0.004865	IL1B/VEGF
BP	GO:190223	negative re	6/905	31/18866	0.003148	0.009258	0.004865	CXCL12/TP
BP	GO:006102	membrane	17/905	169/18866	0.003182	0.009352	0.004915	CALR/CD4/
BP	GO:004688	positive re	11/905	88/18866	0.003188	0.009363	0.004921	IFNG/IL1B/
BP	GO:000188	liver devel	15/905	141/18866	0.003191	0.009365	0.004922	TNFAIP3/IL
BP	GO:003001	establishm	15/905	141/18866	0.003191	0.009365	0.004922	HSP90AA1,
BP	GO:000279	negative re	12/905	101/18866	0.003245	0.009517	0.005001	IL1B/F2R/R
BP	GO:000328	ventricular	10/905	76/18866	0.003317	0.009712	0.005104	WNT5A/LT
BP	GO:007122	cellular res	10/905	76/18866	0.003317	0.009712	0.005104	TNF/CYBB/
BP	GO:007209	regulation	10/905	76/18866	0.003317	0.009712	0.005104	VEGFA/EIF
BP	GO:004668	response t	9/905	64/18866	0.003323	0.009719	0.005108	B2M/MMP
BP	GO:190186	negative re	9/905	64/18866	0.003323	0.009719	0.005108	S100B/TGF

BP	GO:002305	adaptation	5/905	22/18866	0.003343	0.009719	0.005108	ARRB1/AD
BP	GO:003206	regulation	5/905	22/18866	0.003343	0.009719	0.005108	OASL/OAS
BP	GO:003270	negative re	5/905	22/18866	0.003343	0.009719	0.005108	IFNG/TNFS
BP	GO:003953	regulation	5/905	22/18866	0.003343	0.009719	0.005108	NLRX1/DH
BP	GO:005076	negative re	5/905	22/18866	0.003343	0.009719	0.005108	TLR2/ADIP
BP	GO:005100	positive reg	5/905	22/18866	0.003343	0.009719	0.005108	S100A1/TN
BP	GO:005509	response to	5/905	22/18866	0.003343	0.009719	0.005108	PDGFRB/P
BP	GO:007137	cellular res	5/905	22/18866	0.003343	0.009719	0.005108	TNFSF4/PP
BP	GO:009018	regulation	5/905	22/18866	0.003343	0.009719	0.005108	VEGFA/AG
BP	GO:190173	regulation	5/905	22/18866	0.003343	0.009719	0.005108	CXCL10/CX
BP	GO:200031	regulation	5/905	22/18866	0.003343	0.009719	0.005108	IL23A/IL12
BP	GO:003133	negative re	15/905	142/18866	0.003415	0.009923	0.005215	HSPA5/TM
BP	GO:190307	regulation	12/905	102/18866	0.003521	0.010222	0.005372	IFNG/TGFB
BP	GO:200006	positive reg	12/905	102/18866	0.003521	0.010222	0.005372	PSMD10/P
BP	GO:004566	regulation	8/905	53/18866	0.00354	0.010253	0.005389	CXCL14/CX
BP	GO:004574	negative re	8/905	53/18866	0.00354	0.010253	0.005389	CXCL8/CCL
BP	GO:200077	regulation	8/905	53/18866	0.00354	0.010253	0.005389	B2M/HLA-
BP	GO:001090	positive reg	7/905	42/18866	0.003542	0.010253	0.005389	SRC/IGF1/
BP	GO:190459	positive reg	7/905	42/18866	0.003542	0.010253	0.005389	HSP90AB1/
BP	GO:003300	Wnt signali	4/905	14/18866	0.003578	0.010287	0.005406	WNT5A/BM
BP	GO:003021	hyaluronar	4/905	14/18866	0.003578	0.010287	0.005406	TGFB1/IL1
BP	GO:003511	genitalia m	4/905	14/18866	0.003578	0.010287	0.005406	RBP4/FGF1
BP	GO:003581	positive reg	4/905	14/18866	0.003578	0.010287	0.005406	EDNRB/AG
BP	GO:004265	regulation	4/905	14/18866	0.003578	0.010287	0.005406	WNT5A/DK
BP	GO:004392	negative re	4/905	14/18866	0.003578	0.010287	0.005406	CCL5/CCL4
BP	GO:004500	DNA deam	4/905	14/18866	0.003578	0.010287	0.005406	APOBEC3G
BP	GO:004559	positive reg	4/905	14/18866	0.003578	0.010287	0.005406	HLA-G/IFN
BP	GO:004613	pyrimidine	4/905	14/18866	0.003578	0.010287	0.005406	APOBEC3G
BP	GO:004613	pyrimidine	4/905	14/18866	0.003578	0.010287	0.005406	APOBEC3G
BP	GO:004829	isotype swi	4/905	14/18866	0.003578	0.010287	0.005406	CD40/IL27
BP	GO:009071	immunolog	4/905	14/18866	0.003578	0.010287	0.005406	IFNL1/TNF
BP	GO:200127	regulation	4/905	14/18866	0.003578	0.010287	0.005406	IL1B/FABP
BP	GO:000828	insulin rece	15/905	143/18866	0.00365	0.01049	0.005513	IL1B/SOCS
BP	GO:000758	excretion	9/905	65/18866	0.003697	0.010613	0.005577	AQP9/EDN
BP	GO:005120	protein ins	9/905	65/18866	0.003697	0.010613	0.005577	HSP90AA1/
BP	GO:003576	endothelia	6/905	32/18866	0.00372	0.010667	0.005606	CXCL13/TN
BP	GO:007052	protein kin	6/905	32/18866	0.00372	0.010667	0.005606	CD40/VEG
BP	GO:005105	regulation	27/905	323/18866	0.003734	0.0107	0.005623	F2R/F2RL1/
BP	GO:003051	intracellula	13/905	116/18866	0.003738	0.010708	0.005627	CALR/SRC/
BP	GO:005080	positive reg	17/905	172/18866	0.003814	0.010918	0.005738	S100B/TNF
BP	GO:003450	protein loc	24/905	277/18866	0.00387	0.011074	0.00582	CALR/HSP9
BP	GO:006100	hepaticobil	15/905	144/18866	0.003899	0.011152	0.005861	TNFAIP3/IL
BP	GO:003085	negative re	8/905	54/18866	0.003984	0.011389	0.005985	IFNG/MMP
BP	GO:001047	regulation	7/905	43/18866	0.004059	0.011583	0.006087	ADIPOQ/IL
BP	GO:004001	positive reg	7/905	43/18866	0.004059	0.011583	0.006087	GDNF/IGF1
BP	GO:004577	positive reg	7/905	43/18866	0.004059	0.011583	0.006087	CXCL12/VE
BP	GO:004593	negative re	28/905	341/18866	0.004082	0.011642	0.006118	PSMB8/PS
BP	GO:004566	positive reg	9/905	66/18866	0.004103	0.011648	0.006121	LTF/IFITM1
BP	GO:004662	regulation	9/905	66/18866	0.004103	0.011648	0.006121	IL1B/SOCS
BP	GO:004682	positive reg	9/905	66/18866	0.004103	0.011648	0.006121	HSP90AB1/

BP	GO:003270	negative re	5/905	23/18866	0.004105	0.011648	0.006121	XCL1/TNFA
BP	GO:003545	cellular res	5/905	23/18866	0.004105	0.011648	0.006121	TLR3/STAT
BP	GO:004202	protein ref	5/905	23/18866	0.004105	0.011648	0.006121	B2M/HSPA
BP	GO:004613	pyrimidine	5/905	23/18866	0.004105	0.011648	0.006121	APOBEC3G
BP	GO:005104	regulation	5/905	23/18866	0.004105	0.011648	0.006121	IFNG/IL1B/
BP	GO:005122	cytoplasmi	5/905	23/18866	0.004105	0.011648	0.006121	PSMD10/T
BP	GO:009034	positive re	5/905	23/18866	0.004105	0.011648	0.006121	B2M/HLA-
BP	GO:003300	cardiac mu	12/905	104/18866	0.004131	0.011714	0.006156	PTK2/AGT/
BP	GO:006664	phospholip	35/905	455/18866	0.004161	0.011795	0.006199	TGFB1/FAB
BP	GO:001571	monocarbo	17/905	174/18866	0.00429	0.012152	0.006386	IL1B/FABP5
BP	GO:002198	olfactory lo	6/905	33/18866	0.004365	0.012354	0.006492	WNT5A/SE
BP	GO:003502	positive re	6/905	33/18866	0.004365	0.012354	0.006492	F2R/F2RL1/
BP	GO:00736	gastrulatio	18/905	189/18866	0.004394	0.012414	0.006524	MMP9/AD
BP	GO:001082	regulation	10/905	79/18866	0.004403	0.012414	0.006524	IL1B/FABP5
BP	GO:003101	pancreas d	10/905	79/18866	0.004403	0.012414	0.006524	WNT5A/GS
BP	GO:004224	tissue rege	10/905	79/18866	0.004403	0.012414	0.006524	APOD/FGF
BP	GO:004340	negative re	10/905	79/18866	0.004403	0.012414	0.006524	IL1B/ADIPO
BP	GO:007037	negative re	10/905	79/18866	0.004403	0.012414	0.006524	ADIPOQ/AI
BP	GO:009039	cellular ser	10/905	79/18866	0.004403	0.012414	0.006524	B2M/CALR/
BP	GO:004247	odontogen	14/905	132/18866	0.004426	0.012474	0.006556	SRC/TNFSF
BP	GO:006034	bone devel	19/905	204/18866	0.00445	0.012534	0.006587	LTF/SRC/TN
BP	GO:003506	regulation	8/905	55/18866	0.004471	0.012574	0.006608	IL1B/MAPK
BP	GO:005081	negative re	8/905	55/18866	0.004471	0.012574	0.006608	PROCR/PLA
BP	GO:009734	mitochond	8/905	55/18866	0.004471	0.012574	0.006608	GSK3B/GZM
BP	GO:003105	positive re	11/905	92/18866	0.004505	0.012649	0.006647	IL1B/VEGFA
BP	GO:190040	regulation	11/905	92/18866	0.004505	0.012649	0.006647	TNF/IL10/M
BP	GO:190332	negative re	11/905	92/18866	0.004505	0.012649	0.006647	ISG15/TNF/
BP	GO:000602	aminoglyca	9/905	67/18866	0.004543	0.012749	0.0067	PGLYRP1/P
BP	GO:000963	response to	22/905	250/18866	0.004609	0.012929	0.006795	LCN2/S100
BP	GO:001046	mesenchym	7/905	44/18866	0.004631	0.012969	0.006816	STAT1/VEG
BP	GO:003300	regulation	7/905	44/18866	0.004631	0.012969	0.006816	FCER1G/PL
BP	GO:190198	positive re	7/905	44/18866	0.004631	0.012969	0.006816	IL1B/MAPK
BP	GO:003596	response to	19/905	205/18866	0.004691	0.013045	0.006856	CALR/HSPA
BP	GO:002246	germinal ce	4/905	15/18866	0.004696	0.013045	0.006856	CXCL13/TN
BP	GO:002886	regulation	4/905	15/18866	0.004696	0.013045	0.006856	FCER1G/CC
BP	GO:002002	hemoglobi	4/905	15/18866	0.004696	0.013045	0.006856	EPO/INHA/
BP	GO:003023	male sex de	4/905	15/18866	0.004696	0.013045	0.006856	PTGDR/GN
BP	GO:003574	T-helper 2	4/905	15/18866	0.004696	0.013045	0.006856	XCL1/RSAD
BP	GO:004236	fat-soluble	4/905	15/18866	0.004696	0.013045	0.006856	IFNG/IL1B/
BP	GO:004337	CD8-positiv	4/905	15/18866	0.004696	0.013045	0.006856	SOCS1/IRF1
BP	GO:005104	positive re	4/905	15/18866	0.004696	0.013045	0.006856	IFNG/IL1B/
BP	GO:006033	negative re	4/905	15/18866	0.004696	0.013045	0.006856	MMP12/AI
BP	GO:007180	regulation	4/905	15/18866	0.004696	0.013045	0.006856	TNF/SRC/H
BP	GO:009019	regulation	4/905	15/18866	0.004696	0.013045	0.006856	ADIPOQ/PI
BP	GO:190155	regulation	4/905	15/18866	0.004696	0.013045	0.006856	IL1B/TNF/V
BP	GO:190314	regulation	4/905	15/18866	0.004696	0.013045	0.006856	IL1B/TNF/V
BP	GO:200102	positive re	4/905	15/18866	0.004696	0.013045	0.006856	TMSB4X/V
BP	GO:000716	establishm	20/905	220/18866	0.004697	0.013045	0.006856	HSP90AA1/
BP	GO:005512	digestive sy	15/905	147/18866	0.004731	0.013133	0.006902	CXCL8/TNF
BP	GO:003139	negative re	10/905	80/18866	0.004821	0.013367	0.007025	ISG15/TNF/

BP	GO:190402	regulation	12/905	106/18866	0.004822	0.013367	0.007025	HSP90AB1/
BP	GO:190526	positive re	12/905	106/18866	0.004822	0.013367	0.007025	IL1B/VEGF
BP	GO:003051	regulation	11/905	93/18866	0.004893	0.013557	0.007125	HJV/WNT5
BP	GO:007124	cellular res	20/905	221/18866	0.004939	0.013675	0.007187	B2M/CALR
BP	GO:000693	muscle cor	29/905	362/18866	0.004962	0.013734	0.007218	F2R/DES/P
BP	GO:001052	regulation	5/905	24/18866	0.004984	0.013737	0.007219	APOBEC3G
BP	GO:001052	negative re	5/905	24/18866	0.004984	0.013737	0.007219	APOBEC3G
BP	GO:003233	negative re	5/905	24/18866	0.004984	0.013737	0.007219	GDF5/GRE
BP	GO:003414	regulation	5/905	24/18866	0.004984	0.013737	0.007219	LBP/LTF/B
BP	GO:004595	positive re	5/905	24/18866	0.004984	0.013737	0.007219	HLA-F/RAE
BP	GO:007084	inclusion b	5/905	24/18866	0.004984	0.013737	0.007219	HSPA2/MA
BP	GO:190342	regulation	5/905	24/18866	0.004984	0.013737	0.007219	PAEP/RAC
BP	GO:200020	regulation	5/905	24/18866	0.004984	0.013737	0.007219	SRC/PTK2/
BP	GO:001081	negative re	9/905	68/18866	0.005018	0.013826	0.007266	MMP12/A
BP	GO:003164	regulation	15/905	148/18866	0.005038	0.013865	0.007286	S100B/FAB
BP	GO:007190	negative re	15/905	148/18866	0.005038	0.013865	0.007286	IL1B/ADIP
BP	GO:004599	regulation	14/905	134/18866	0.005061	0.013921	0.007316	ADIPOQ/W
BP	GO:001907	viral releas	6/905	34/18866	0.00509	0.013958	0.007336	PML/PPIA/
BP	GO:003043	sleep	6/905	34/18866	0.00509	0.013958	0.007336	PTGDS/PT
BP	GO:003589	exit from h	6/905	34/18866	0.00509	0.013958	0.007336	PML/PPIA/
BP	GO:003589	exit from h	6/905	34/18866	0.00509	0.013958	0.007336	PML/PPIA/
BP	GO:190269	regulation	6/905	34/18866	0.00509	0.013958	0.007336	VEGFA/CX
BP	GO:200035	negative re	6/905	34/18866	0.00509	0.013958	0.007336	ICAM1/TN
BP	GO:001652	negative re	18/905	192/18866	0.005176	0.014188	0.007456	HLA-G/CXC
BP	GO:001489	striated mu	12/905	107/18866	0.005201	0.014241	0.007484	PTK2/AGT/
BP	GO:005501	cardiac mu	12/905	107/18866	0.005201	0.014241	0.007484	RBP4/AGT/
BP	GO:000752	myoblast f	7/905	45/18866	0.005262	0.014357	0.007545	CXCL10/CX
BP	GO:003101	endocrine	7/905	45/18866	0.005262	0.014357	0.007545	WNT5A/GS
BP	GO:003292	activin rec	7/905	45/18866	0.005262	0.014357	0.007545	HJV/FGF10
BP	GO:004277	intrinsic ap	7/905	45/18866	0.005262	0.014357	0.007545	PML/MIF/
BP	GO:004591	positive re	7/905	45/18866	0.005262	0.014357	0.007545	TGFB1/TFR
BP	GO:005502	negative re	7/905	45/18866	0.005262	0.014357	0.007545	RBP4/BMP
BP	GO:006041	ventricular	7/905	45/18866	0.005262	0.014357	0.007545	WNT5A/R
BP	GO:006099	kidney mor	11/905	94/18866	0.005308	0.014477	0.007608	STAT1/VEG
BP	GO:000761	memory	13/905	121/18866	0.005361	0.014612	0.007679	S100B/MA
BP	GO:007124	cellular res	18/905	193/18866	0.005461	0.014877	0.007819	B2M/CALR
BP	GO:007123	cellular res	9/905	69/18866	0.005532	0.015056	0.007912	TNF/CYBB/
BP	GO:190331	regulation	9/905	69/18866	0.005532	0.015056	0.007912	TFR2/SRC/
BP	GO:001931	hexose me	22/905	254/18866	0.005549	0.015095	0.007933	RBP4/FAB
BP	GO:000931	response t	34/905	447/18866	0.005562	0.015124	0.007948	HSPA5/ICA
BP	GO:004685	phosphatic	8/905	57/18866	0.00558	0.015164	0.007969	SOCS3/SO
BP	GO:004275	regulation	13/905	122/18866	0.005744	0.015602	0.0082	PTGDS/PM
BP	GO:200018	negative re	18/905	194/18866	0.005758	0.015632	0.008215	HLA-G/CXC
BP	GO:001648	peptide ho	6/905	35/18866	0.005899	0.015966	0.00839	CTSL/CTSG
BP	GO:003969	viral RNA g	6/905	35/18866	0.005899	0.015966	0.00839	CXCL8/APC
BP	GO:009700	energy hor	6/905	35/18866	0.005899	0.015966	0.00839	PIK3CA/BN
BP	GO:011011	negative re	6/905	35/18866	0.005899	0.015966	0.00839	TNF/STAT1
BP	GO:014044	signaling re	6/905	35/18866	0.005899	0.015966	0.00839	CTSL/CTSG
BP	GO:190001	negative re	6/905	35/18866	0.005899	0.015966	0.00839	APOD/NLR
BP	GO:001087	regulation	7/905	46/18866	0.005955	0.016102	0.008462	CETP/ADIP

BP	GO:004853	thymus dev	7/905	46/18866	0.005955	0.016102	0.008462	MAPK3/FG
BP	GO:000753	sex determ	5/905	25/18866	0.005988	0.016118	0.008471	PTGDR/AM
BP	GO:001073	regulation	5/905	25/18866	0.005988	0.016118	0.008471	ADIPOQ/M
BP	GO:004330	positive reg	5/905	25/18866	0.005988	0.016118	0.008471	FCER1G/HL
BP	GO:005068	negative re	5/905	25/18866	0.005988	0.016118	0.008471	MICB/NLRX
BP	GO:006025	regulation	5/905	25/18866	0.005988	0.016118	0.008471	QRFP/RETN
BP	GO:006066	embryonic	5/905	25/18866	0.005988	0.016118	0.008471	SOCS3/IL10
BP	GO:006121	regulation	5/905	25/18866	0.005988	0.016118	0.008471	VEGFA/AGT
BP	GO:190556	positive reg	5/905	25/18866	0.005988	0.016118	0.008471	AKT3/APLN
BP	GO:200102	regulation	5/905	25/18866	0.005988	0.016118	0.008471	CXCL13/TM
BP	GO:006004	heart contr	24/905	287/18866	0.006	0.016133	0.008479	S100A1/DE
BP	GO:002153	cell prolifer	4/905	16/18866	0.006026	0.016133	0.008479	C5AR1/EGF
BP	GO:004253	negative re	4/905	16/18866	0.006026	0.016133	0.008479	SOCS3/SOC
BP	GO:004299	cytoplasmi	4/905	16/18866	0.006026	0.016133	0.008479	PSMD10/T
BP	GO:004311	negative re	4/905	16/18866	0.006026	0.016133	0.008479	VEGFA/AD
BP	GO:004534	MHC class	4/905	16/18866	0.006026	0.016133	0.008479	IFNG/SLC1
BP	GO:006085	regulation	4/905	16/18866	0.006026	0.016133	0.008479	PPARG/RO
BP	GO:006145	trophoblas	4/905	16/18866	0.006026	0.016133	0.008479	CALR/VEGF
BP	GO:007210	glomerular	4/905	16/18866	0.006026	0.016133	0.008479	PDGFRB/PD
BP	GO:007222	metanephr	4/905	16/18866	0.006026	0.016133	0.008479	ADIPOQ/PD
BP	GO:190116	regulation	4/905	16/18866	0.006026	0.016133	0.008479	CALR/VEGF
BP	GO:002176	limbic syste	12/905	109/18866	0.006029	0.016134	0.008479	HDAC1/GS
BP	GO:004521	cell-cell jur	19/905	210/18866	0.006063	0.016215	0.008522	TGFB1/IL1B
BP	GO:000687	cellular iron	9/905	70/18866	0.006085	0.016266	0.008549	IFNG/LCN2
BP	GO:002188	forebrain c	8/905	58/18866	0.006207	0.016561	0.008703	CXCL12/CX
BP	GO:190040	negative re	8/905	58/18866	0.006207	0.016561	0.008703	IL10/MET/
BP	GO:190320	negative re	8/905	58/18866	0.006207	0.016561	0.008703	IL10/MET/
BP	GO:190374	positive reg	8/905	58/18866	0.006207	0.016561	0.008703	RAC2/GZM
BP	GO:000157	vasculogen	10/905	83/18866	0.006265	0.016707	0.00878	TGFB1/VEG
BP	GO:004856	embryonic	34/905	451/18866	0.006353	0.016933	0.008899	CXCL8/TGF
BP	GO:190180	positive reg	12/905	110/18866	0.006481	0.017257	0.009069	PSMC2/PSI
BP	GO:190465	glucose tra	12/905	110/18866	0.006481	0.017257	0.009069	IL1B/FABP5
BP	GO:003585	epithelial c	7/905	47/18866	0.006714	0.017843	0.009377	MMP9/AD
BP	GO:004330	mast cell d	7/905	47/18866	0.006714	0.017843	0.009377	FCER1G/BT
BP	GO:004577	negative re	7/905	47/18866	0.006714	0.017843	0.009377	ADIPOQ/N
BP	GO:004848	autonomic	7/905	47/18866	0.006714	0.017843	0.009377	SEMA3A/E
BP	GO:003647	cell death i	11/905	97/18866	0.006721	0.017853	0.009383	PML/IL10/I
BP	GO:000156	branching i	6/905	36/18866	0.006797	0.018036	0.009479	VEGFA/DLL
BP	GO:000621	pyrimidine	6/905	36/18866	0.006797	0.018036	0.009479	APOBEC3G
BP	GO:000663	unsaturate	8/905	59/18866	0.006887	0.018265	0.009599	PTGDS/IL1I
BP	GO:005114	positive reg	12/905	111/18866	0.006959	0.018447	0.009695	CXCL9/TGF
BP	GO:003096	endoplasm	13/905	125/18866	0.007028	0.018613	0.009782	CALR/HSPA
BP	GO:003460	cellular res	13/905	125/18866	0.007028	0.018613	0.009782	HSP90AA1/
BP	GO:000206	glandular e	5/905	26/18866	0.007126	0.018798	0.009879	WNT5A/GS
BP	GO:002188	forebrain n	5/905	26/18866	0.007126	0.018798	0.009879	WNT5A/SE
BP	GO:004350	skeletal mu	5/905	26/18866	0.007126	0.018798	0.009879	IL15/ACTA1
BP	GO:006074	prostate gl	5/905	26/18866	0.007126	0.018798	0.009879	WNT5A/FG
BP	GO:007220	cell differe	5/905	26/18866	0.007126	0.018798	0.009879	ADIPOQ/ST
BP	GO:014005	neuron prc	5/905	26/18866	0.007126	0.018798	0.009879	WNT5A/SE
BP	GO:190301	regulation	5/905	26/18866	0.007126	0.018798	0.009879	LTF/TNFSF1

BP	GO:190475	positive reg	5/905	26/18866	0.007126	0.018798	0.009879	AGT/PDGF
BP	GO:005080	regulation	20/905	229/18866	0.007269	0.019166	0.010072	TLR2/TNF/
BP	GO:004683	lipid phosp	9/905	72/18866	0.007318	0.019285	0.010135	SOCS3/SOC
BP	GO:003476	regulation	36/905	489/18866	0.007324	0.019294	0.01014	HSPA2/IFN
BP	GO:000697	response t	10/905	85/18866	0.0074	0.019485	0.01024	HSP90AB1/
BP	GO:007265	establishm	14/905	140/18866	0.007415	0.019515	0.010256	HSP90AA1/
BP	GO:000227	mast cell a	7/905	48/18866	0.007543	0.019821	0.010417	FCER1G/BT
BP	GO:001079	regulation	7/905	48/18866	0.007543	0.019821	0.010417	TGFB1/WN
BP	GO:190403	negative re	7/905	48/18866	0.007543	0.019821	0.010417	ICAM1/TN
BP	GO:000203	G protein-c	4/905	17/18866	0.007585	0.019865	0.01044	ARRB1/AD
BP	GO:003094	positive reg	4/905	17/18866	0.007585	0.019865	0.01044	IL1B/FGF10
BP	GO:004244	progestero	4/905	17/18866	0.007585	0.019865	0.01044	ADM/LHB/
BP	GO:004562	negative re	4/905	17/18866	0.007585	0.019865	0.01044	TNFSF4/JA
BP	GO:004853	anatomical	4/905	17/18866	0.007585	0.019865	0.01044	HSPA5/SEM
BP	GO:007024	thymocyte	4/905	17/18866	0.007585	0.019865	0.01044	WNT5A/HI
BP	GO:009706	cellular res	4/905	17/18866	0.007585	0.019865	0.01044	CTSB/CTSL/
BP	GO:190288	negative re	8/905	60/18866	0.007621	0.019948	0.010483	IL10/MET/
BP	GO:000751	muscle org	31/905	407/18866	0.00772	0.020197	0.010614	CXCL10/S1
BP	GO:003021	hyaluronar	6/905	37/18866	0.007791	0.020373	0.010707	TGFB1/IL1
BP	GO:001038	regulation	18/905	200/18866	0.007831	0.020459	0.010752	HSPA2/HSP
BP	GO:001703	protein imp	18/905	200/18866	0.007831	0.020459	0.010752	HSP90AA1/
BP	GO:000170	formation	13/905	127/18866	0.008003	0.020899	0.010983	MMP9/ITG
BP	GO:003410	homotypic	10/905	86/18866	0.008025	0.020925	0.010997	CCL5/TNFS
BP	GO:003502	regulation	10/905	86/18866	0.008025	0.020925	0.010997	F2R/F2RL1/
BP	GO:190186	positive reg	10/905	86/18866	0.008025	0.020925	0.010997	TGFB1/GR
BP	GO:005117	import into	16/905	171/18866	0.008243	0.021484	0.011291	HSP90AB1/
BP	GO:000729	female gan	14/905	142/18866	0.00837	0.021803	0.011458	SRC/PTX3/
BP	GO:000202	response t	5/905	27/18866	0.008407	0.021808	0.011461	BMP8A/VG
BP	GO:000202	regulation	5/905	27/18866	0.008407	0.021808	0.011461	NOS1/ADM
BP	GO:000314	outflow tra	5/905	27/18866	0.008407	0.021808	0.011461	SEMA3C/R
BP	GO:007253	T-helper 17	5/905	27/18866	0.008407	0.021808	0.011461	IL23A/IL12
BP	GO:190012	regulation	5/905	27/18866	0.008407	0.021808	0.011461	B2M/MMP
BP	GO:190320	regulation	5/905	27/18866	0.008407	0.021808	0.011461	IL10/NR4A
BP	GO:000602	glycosamin	8/905	61/18866	0.008412	0.021808	0.011461	PGLYRP1/P
BP	GO:190211	positive reg	8/905	61/18866	0.008412	0.021808	0.011461	GSK3B/GZM
BP	GO:190390	positive reg	8/905	61/18866	0.008412	0.021808	0.011461	CD4/PPIA/
BP	GO:200075	regulation	8/905	61/18866	0.008412	0.021808	0.011461	IL1B/MAPK
BP	GO:003085	prostate gl	7/905	49/18866	0.008445	0.021872	0.011495	WNT5A/FG
BP	GO:012017	steroid hor	7/905	49/18866	0.008445	0.021872	0.011495	ADM/BMP
BP	GO:000864	hexose tra	12/905	114/18866	0.00856	0.022161	0.011646	IL1B/FABP5
BP	GO:003051	negative re	10/905	87/18866	0.008689	0.022472	0.01181	HSPA5/TGF
BP	GO:005507	iron ion ho	10/905	87/18866	0.008689	0.022472	0.01181	B2M/IFNG/
BP	GO:004863	positive reg	17/905	187/18866	0.008708	0.022511	0.01183	CXCL12/VE
BP	GO:002153	diencephal	9/905	74/18866	0.008732	0.022563	0.011858	WNT5A/FG
BP	GO:001491	negative re	6/905	38/18866	0.008884	0.022891	0.01203	ADIPOQ/SE
BP	GO:003288	regulation	6/905	38/18866	0.008884	0.022891	0.01203	TGFB1/GSK
BP	GO:004302	T cell home	6/905	38/18866	0.008884	0.022891	0.01203	IL2RA/JAK3
BP	GO:004577	positive reg	6/905	38/18866	0.008884	0.022891	0.01203	AGT/OXT/
BP	GO:005195	positive reg	6/905	38/18866	0.008884	0.022891	0.01203	CXCL12/AG
BP	GO:190002	positive reg	6/905	38/18866	0.008884	0.022891	0.01203	CALR/LIMS

BP	GO:190288	regulation	11/905	101/18866	0.009045	0.023292	0.012241	TNF/IL10/M
BP	GO:006041	heart grow	12/905	115/18866	0.009154	0.023561	0.012382	RBP4/AGT/
BP	GO:005178	regulation	17/905	188/18866	0.00916	0.023568	0.012386	CALR/IL1B/
BP	GO:005185	modulation	8/905	62/18866	0.009263	0.02381	0.012513	LTF/CCL5/C
BP	GO:007138	cellular res	8/905	62/18866	0.009263	0.02381	0.012513	ICAM1/STC
BP	GO:003265	regulation	4/905	18/18866	0.009388	0.024073	0.012651	IFNL1/TNFS
BP	GO:004659	negative re	4/905	18/18866	0.009388	0.024073	0.012651	PTX3/IFITM
BP	GO:006003	anatomical	4/905	18/18866	0.009388	0.024073	0.012651	AMH/FLT1/
BP	GO:006097	coronary va	4/905	18/18866	0.009388	0.024073	0.012651	VEGFA/PD
BP	GO:190022	regulation	4/905	18/18866	0.009388	0.024073	0.012651	IFNG/TNF/
BP	GO:001021	response to	14/905	144/18866	0.009418	0.024073	0.012651	HSPA5/ICA
BP	GO:007058	protein loc	14/905	144/18866	0.009418	0.024073	0.012651	HSP90AA1/
BP	GO:001071	positive reg	7/905	50/18866	0.009423	0.024073	0.012651	TGFB1/IL1B
BP	GO:003019	negative re	7/905	50/18866	0.009423	0.024073	0.012651	PLAU/PRO
BP	GO:003164	protein des	7/905	50/18866	0.009423	0.024073	0.012651	SRC/BMP2/
BP	GO:004854	digestive tr	7/905	50/18866	0.009423	0.024073	0.012651	WNT5A/FG
BP	GO:005087	brown fat c	7/905	50/18866	0.009423	0.024073	0.012651	FABP3/ADI
BP	GO:190358	positive reg	7/905	50/18866	0.009423	0.024073	0.012651	IFNG/TMSB
BP	GO:000170	mesoderm	9/905	75/18866	0.009513	0.024245	0.012742	WNT5A/DK
BP	GO:004362	response to	9/905	75/18866	0.009513	0.024245	0.012742	PDGFRB/P
BP	GO:005080	negative re	9/905	75/18866	0.009513	0.024245	0.012742	IL1B/ADIPO
BP	GO:190007	regulation	9/905	75/18866	0.009513	0.024245	0.012742	IL1B/SOCS3
BP	GO:190198	regulation	9/905	75/18866	0.009513	0.024245	0.012742	IL1B/MAPK
BP	GO:000007	regulation	11/905	102/18866	0.009712	0.024729	0.012996	PSMD10/T
BP	GO:006084	artery deve	11/905	102/18866	0.009712	0.024729	0.012996	VEGFA/DLL
BP	GO:001574	monosacch	12/905	116/18866	0.009778	0.024874	0.013072	IL1B/FABP5
BP	GO:004691	cellular tra	12/905	116/18866	0.009778	0.024874	0.013072	IFNG/LCN2
BP	GO:000233	mature B c	5/905	28/18866	0.009838	0.024979	0.013128	PTK2B/CD1
BP	GO:000236	T cell lineag	5/905	28/18866	0.009838	0.024979	0.013128	CTSL/IL23A
BP	GO:006051	prostate gl	5/905	28/18866	0.009838	0.024979	0.013128	WNT5A/FG
BP	GO:008011	DNA deme	5/905	28/18866	0.009838	0.024979	0.013128	APOBEC3G
BP	GO:190199	regulation	33/905	448/18866	0.009867	0.02504	0.013159	HSPA2/HSP
BP	GO:000820	steroid me	26/905	332/18866	0.009957	0.025258	0.013274	IFNG/NFYA
BP	GO:000719	activation o	6/905	39/18866	0.010084	0.025543	0.013424	EDNRA/AD
BP	GO:001045	regulation	6/905	39/18866	0.010084	0.025543	0.013424	WNT5A/DK
BP	GO:190222	regulation	6/905	39/18866	0.010084	0.025543	0.013424	CXCL12/TP
BP	GO:190384	negative re	10/905	89/18866	0.010142	0.025651	0.013481	HSPA5/TGF
BP	GO:190268	mitochond	8/905	63/18866	0.010177	0.025651	0.013481	GSK3B/GZM
BP	GO:000155	luteinizatio	3/905	10/18866	0.010245	0.025651	0.013481	INHBA/RET
BP	GO:000229	T cell activa	3/905	10/18866	0.010245	0.025651	0.013481	HLA-DMB/
BP	GO:000330	regulation	3/905	10/18866	0.010245	0.025651	0.013481	WNT5A/BM
BP	GO:001404	regulation	3/905	10/18866	0.010245	0.025651	0.013481	RAC3/EDN
BP	GO:003281	regulation	3/905	10/18866	0.010245	0.025651	0.013481	IL15/FLT3L
BP	GO:003435	regulation	3/905	10/18866	0.010245	0.025651	0.013481	CCL2/PRKC
BP	GO:003558	sequesterin	3/905	10/18866	0.010245	0.025651	0.013481	LTBP1/GRE
BP	GO:004308	penile erec	3/905	10/18866	0.010245	0.025651	0.013481	EDNRB/OX
BP	GO:004571	low-density	3/905	10/18866	0.010245	0.025651	0.013481	ADIPOQ/IT
BP	GO:004659	positive reg	3/905	10/18866	0.010245	0.025651	0.013481	CD4/LGALS
BP	GO:004826	determinat	3/905	10/18866	0.010245	0.025651	0.013481	GREM1/GR
BP	GO:005154	elastin met	3/905	10/18866	0.010245	0.025651	0.013481	CTSL/MMP

BP	GO:00700	regulation	3/905	10/18866	0.010245	0.025651	0.013481	CCL5/HIF1
BP	GO:00704	regulation	3/905	10/18866	0.010245	0.025651	0.013481	OXT/GPER
BP	GO:00709	neutrophil	3/905	10/18866	0.010245	0.025651	0.013481	CTSG/F2RL
BP	GO:00711	response t	3/905	10/18866	0.010245	0.025651	0.013481	STAT1/IL2
BP	GO:00716	regulation	3/905	10/18866	0.010245	0.025651	0.013481	ARG2/IL10
BP	GO:00721	regulation	3/905	10/18866	0.010245	0.025651	0.013481	PDGFB/PD
BP	GO:00722	cell prolife	3/905	10/18866	0.010245	0.025651	0.013481	STAT1/PDG
BP	GO:00752	positive re	3/905	10/18866	0.010245	0.025651	0.013481	CD4/LGAL
BP	GO:19020	L-arginine	3/905	10/18866	0.010245	0.025651	0.013481	SLC11A1/A
BP	GO:19022	positive re	3/905	10/18866	0.010245	0.025651	0.013481	PMAIP1/PT
BP	GO:19043	regulation	3/905	10/18866	0.010245	0.025651	0.013481	GSK3B/DK
BP	GO:00988	cellular oxi	11/905	103/18866	0.010417	0.02607	0.013701	S100A9/DU
BP	GO:00218	forebrain n	7/905	51/18866	0.010483	0.026197	0.013767	B2M/WNT
BP	GO:004591	negative re	7/905	51/18866	0.010483	0.026197	0.013767	TGFB1/AD
BP	GO:19000	negative re	7/905	51/18866	0.010483	0.026197	0.013767	PLAU/PRO
BP	GO:00900	positive re	24/905	302/18866	0.010937	0.027319	0.014357	HSPA2/IL1
BP	GO:00000	G2/M trans	21/905	254/18866	0.010982	0.02742	0.01441	HSPA2/HS
BP	GO:001591	sterol trans	12/905	118/18866	0.011127	0.027756	0.014587	CETP/ADIP
BP	GO:003421	carbohydra	12/905	118/18866	0.011127	0.027756	0.014587	IL1B/FABP
BP	GO:00018	endothelia	8/905	64/18866	0.011156	0.027778	0.014598	ICAM1/IL1
BP	GO:00020	columnar/	8/905	64/18866	0.011156	0.027778	0.014598	WNT5A/SR
BP	GO:00328	glomerulus	8/905	64/18866	0.011156	0.027778	0.014598	ADIPOQ/P
BP	GO:00333	cholesterol	8/905	64/18866	0.011156	0.027778	0.014598	CETP/ADIP
BP	GO:00515	response t	14/905	147/18866	0.011182	0.027829	0.014625	HSPA5/S10
BP	GO:00074	peripheral	9/905	77/18866	0.011231	0.027901	0.014663	NDRG1/ED
BP	GO:00483	mesoderm	9/905	77/18866	0.011231	0.027901	0.014663	WNT5A/DK
BP	GO:00720	nephron m	9/905	77/18866	0.011231	0.027901	0.014663	STAT1/VEG
BP	GO:19032	regulation	9/905	77/18866	0.011231	0.027901	0.014663	IL10/MET/
BP	GO:00072	activation	6/905	40/18866	0.011394	0.028115	0.014776	WNT5A/D
BP	GO:00082	C21-steroi	6/905	40/18866	0.011394	0.028115	0.014776	ADM/BMP
BP	GO:19034	negative re	6/905	40/18866	0.011394	0.028115	0.014776	IL10/FYN/
BP	GO:00017	B cell hom	5/905	29/18866	0.011429	0.028115	0.014776	TNFAIP3/
BP	GO:00072	nitric oxide	5/905	29/18866	0.011429	0.028115	0.014776	VEGFA/NO
BP	GO:00321	transpositi	5/905	29/18866	0.011429	0.028115	0.014776	APOBEC3G
BP	GO:00323	positive re	5/905	29/18866	0.011429	0.028115	0.014776	CETP/ADIP
BP	GO:00323	positive re	5/905	29/18866	0.011429	0.028115	0.014776	CETP/ADIP
BP	GO:00362	response t	5/905	29/18866	0.011429	0.028115	0.014776	PDGFRB/P
BP	GO:00456	negative re	5/905	29/18866	0.011429	0.028115	0.014776	LTF/TLR3/
BP	GO:00019	regulation	4/905	19/18866	0.011448	0.028115	0.014776	CTSG/F2R/
BP	GO:00029	positive re	4/905	19/18866	0.011448	0.028115	0.014776	LTA/IL1B/T
BP	GO:00031	morphoge	4/905	19/18866	0.011448	0.028115	0.014776	CXCL10/DL
BP	GO:00359	chondrocy	4/905	19/18866	0.011448	0.028115	0.014776	LTF/STC1/
BP	GO:00433	CD4-positi	4/905	19/18866	0.011448	0.028115	0.014776	CTSL/IL23A
BP	GO:00443	cellular res	4/905	19/18866	0.011448	0.028115	0.014776	EBI3/LEPR/
BP	GO:00466	gamma-de	4/905	19/18866	0.011448	0.028115	0.014776	MICA/MIC
BP	GO:00484	parasympa	4/905	19/18866	0.011448	0.028115	0.014776	SEMA3A/P
BP	GO:00515	keratinocy	4/905	19/18866	0.011448	0.028115	0.014776	MMP9/FG
BP	GO:00602	positive re	4/905	19/18866	0.011448	0.028115	0.014776	LTA/IL1B/T
BP	GO:00606	branch elo	4/905	19/18866	0.011448	0.028115	0.014776	WNT5A/FG
BP	GO:00611	endothelia	4/905	19/18866	0.011448	0.028115	0.014776	CXCL10/DL

BP	GO:00718	podosome	4/905	19/18866	0.011448	0.028115	0.014776	TNF/SRC/H
BP	GO:19039	regulation	4/905	19/18866	0.011448	0.028115	0.014776	CCL3/CX3
BP	GO:20006	regulation	4/905	19/18866	0.011448	0.028115	0.014776	MMP9/AD
BP	GO:00550	sodium ion	7/905	52/18866	0.011626	0.028526	0.014991	EDNRB/AG
BP	GO:00721	mesenchy	7/905	52/18866	0.011626	0.028526	0.014991	WNT5A/A
BP	GO:00514	regulation	10/905	91/18866	0.011774	0.028863	0.015168	NOX4/PIK3
BP	GO:00600	roof of mo	10/905	91/18866	0.011774	0.028863	0.015168	WNT5A/G
BP	GO:00070	regulation	15/905	163/18866	0.011906	0.029173	0.015332	IL1B/IL1A/
BP	GO:00303	cholesterol	11/905	105/18866	0.011944	0.029255	0.015375	CETP/ADIP
BP	GO:00723	intrinsic ap	9/905	78/18866	0.012173	0.029801	0.015662	PML/MIF/
BP	GO:00357	positive re	8/905	65/18866	0.012203	0.029835	0.01568	GSK3B/GZ
BP	GO:00467	regulation	8/905	65/18866	0.012203	0.029835	0.01568	CCL5/CCL4
BP	GO:19059	negative re	8/905	65/18866	0.012203	0.029835	0.01568	TNF/ITGAV
BP	GO:19030	regulation	19/905	225/18866	0.012243	0.029919	0.015724	HSP90AB1
BP	GO:00711	regulation	11/905	106/18866	0.012769	0.031191	0.016392	CALR/HSP
BP	GO:00425	fear respo	6/905	41/18866	0.01282	0.031301	0.01645	MDK/UCN
BP	GO:00456	negative re	7/905	53/18866	0.012856	0.031332	0.016466	TNF/AREG
BP	GO:00517	intraspecie	7/905	53/18866	0.012856	0.031332	0.016466	LTF/BPIFA1
BP	GO:00713	cellular res	7/905	53/18866	0.012856	0.031332	0.016466	HSPA5/NO
BP	GO:19000	regulation	7/905	53/18866	0.012856	0.031332	0.016466	CALR/LIMS
BP	GO:19011	carbohydr	17/905	195/18866	0.012877	0.03137	0.016486	CTSL/MMP
BP	GO:00336	regulation	5/905	30/18866	0.013186	0.032035	0.016835	LTF/ITGAV
BP	GO:00364	neuron de	5/905	30/18866	0.013186	0.032035	0.016835	IL10/NR4A
BP	GO:00481	negative re	5/905	30/18866	0.013186	0.032035	0.016835	LTA/PPAR
BP	GO:00714	cellular res	5/905	30/18866	0.013186	0.032035	0.016835	HSPA5/NO
BP	GO:009031	positive re	5/905	30/18866	0.013186	0.032035	0.016835	CHP1/ITGB
BP	GO:19021	regulation	5/905	30/18866	0.013186	0.032035	0.016835	PML/TRIM
BP	GO:19021	regulation	8/905	66/18866	0.013321	0.032333	0.016992	GSK3B/GZ
BP	GO:20003	negative re	8/905	66/18866	0.013321	0.032333	0.016992	IL10/FYN/
BP	GO:00065	arginine ca	3/905	11/18866	0.013591	0.032421	0.017039	ARG2/NOS
BP	GO:00107	positive re	3/905	11/18866	0.013591	0.032421	0.017039	ADIPOQ/M
BP	GO:00148	muscle atr	3/905	11/18866	0.013591	0.032421	0.017039	IL15/PPAR
BP	GO:00193	cyclooxyge	3/905	11/18866	0.013591	0.032421	0.017039	PTGDS/PT
BP	GO:00215	facial nerv	3/905	11/18866	0.013591	0.032421	0.017039	SEMA3A/P
BP	GO:00216	cranial ner	3/905	11/18866	0.013591	0.032421	0.017039	SEMA3A/P
BP	GO:002161	facial nerv	3/905	11/18866	0.013591	0.032421	0.017039	SEMA3A/P
BP	GO:00322	regulation	3/905	11/18866	0.013591	0.032421	0.017039	INHA/INHB
BP	GO:00331	positive re	3/905	11/18866	0.013591	0.032421	0.017039	AR/PAK1/S
BP	GO:00334	gas homeo	3/905	11/18866	0.013591	0.032421	0.017039	HIF1A/CAV
BP	GO:003411	negative re	3/905	11/18866	0.013591	0.032421	0.017039	ADIPOQ/IL
BP	GO:00354	cellular res	3/905	11/18866	0.013591	0.032421	0.017039	IFIT3/AXL/
BP	GO:00395	negative re	3/905	11/18866	0.013591	0.032421	0.017039	NLRX1/DH
BP	GO:00450	negative t	3/905	11/18866	0.013591	0.032421	0.017039	CCR7/ZAP
BP	GO:00456	regulation	3/905	11/18866	0.013591	0.032421	0.017039	TNFSF4/CD
BP	GO:00466	negative re	3/905	11/18866	0.013591	0.032421	0.017039	XCL1/ARG
BP	GO:00613	cardiac ne	3/905	11/18866	0.013591	0.032421	0.017039	MAPK3/SE
BP	GO:00613	cardiac ne	3/905	11/18866	0.013591	0.032421	0.017039	MAPK3/SE
BP	GO:00703	response t	3/905	11/18866	0.013591	0.032421	0.017039	TLR2/TLR6
BP	GO:00705	regulation	3/905	11/18866	0.013591	0.032421	0.017039	ADIPOQ/IL
BP	GO:00712	cellular res	3/905	11/18866	0.013591	0.032421	0.017039	TLR2/TLR6

BP	GO:007122	cellular res	3/905	11/18866	0.013591	0.032421	0.017039	TLR2/TLR6/
BP	GO:007128	cellular res	3/905	11/18866	0.013591	0.032421	0.017039	B2M/NFYA
BP	GO:007160	chemokine	3/905	11/18866	0.013591	0.032421	0.017039	ARG2/IL10/
BP	GO:007180	positive reg	3/905	11/18866	0.013591	0.032421	0.017039	TNF/SRC/C
BP	GO:009704	dendritic c	3/905	11/18866	0.013591	0.032421	0.017039	CXCL12/CC
BP	GO:009739	response t	3/905	11/18866	0.013591	0.032421	0.017039	IL17C/IL17
BP	GO:009739	cellular res	3/905	11/18866	0.013591	0.032421	0.017039	IL17C/IL17
BP	GO:009740	interleukin	3/905	11/18866	0.013591	0.032421	0.017039	IL17C/IL17
BP	GO:190247	positive reg	3/905	11/18866	0.013591	0.032421	0.017039	MAPT/WN
BP	GO:190398	positive reg	3/905	11/18866	0.013591	0.032421	0.017039	CCL3/LRRK
BP	GO:190432	response t	3/905	11/18866	0.013591	0.032421	0.017039	GNAI1/CFT
BP	GO:190432	cellular res	3/905	11/18866	0.013591	0.032421	0.017039	GNAI1/CFT
BP	GO:190590	regulation	3/905	11/18866	0.013591	0.032421	0.017039	DKK1/WNT
BP	GO:199044	positive reg	3/905	11/18866	0.013591	0.032421	0.017039	HSPA5/CE
BP	GO:200004	positive reg	3/905	11/18866	0.013591	0.032421	0.017039	WNT5A/W
BP	GO:200031	positive reg	3/905	11/18866	0.013591	0.032421	0.017039	IL23A/IL12
BP	GO:200055	regulation	3/905	11/18866	0.013591	0.032421	0.017039	XCL1/RSAD
BP	GO:200066	regulation	3/905	11/18866	0.013591	0.032421	0.017039	CXCL12/CC
BP	GO:000332	type B pan	4/905	20/18866	0.013777	0.032721	0.017196	WNT5A/GS
BP	GO:001004	response t	4/905	20/18866	0.013777	0.032721	0.017196	HSPA5/PTG
BP	GO:001087	positive reg	4/905	20/18866	0.013777	0.032721	0.017196	ADIPOQ/A
BP	GO:003129	retinal gan	4/905	20/18866	0.013777	0.032721	0.017196	VEGFA/SE
BP	GO:004393	ossificatio	4/905	20/18866	0.013777	0.032721	0.017196	LTF/BMP2/
BP	GO:004501	negative re	4/905	20/18866	0.013777	0.032721	0.017196	IL10/KHSR
BP	GO:006003	pericardiu	4/905	20/18866	0.013777	0.032721	0.017196	WNT5A/DL
BP	GO:007107	regulation	4/905	20/18866	0.013777	0.032721	0.017196	FABP3/FPR
BP	GO:190174	positive reg	4/905	20/18866	0.013777	0.032721	0.017196	CXCL9/FLT3
BP	GO:190440	negative re	4/905	20/18866	0.013777	0.032721	0.017196	IL10/KHSR
BP	GO:000864	carbohydra	14/905	151/18866	0.013923	0.033054	0.017371	IL1B/FABP5
BP	GO:190336	regulation	21/905	260/18866	0.01401	0.033245	0.017471	HSP90AA1/
BP	GO:000669	steroid bio	17/905	197/18866	0.014132	0.033521	0.017616	IFNG/NFYA
BP	GO:004867	response t	9/905	80/18866	0.01423	0.033724	0.017723	APOD/TNC
BP	GO:005502	regulation	9/905	80/18866	0.01423	0.033724	0.017723	RBP4/IGF1/
BP	GO:000026	mitochond	6/905	42/18866	0.014367	0.034017	0.017877	MX1/MAP
BP	GO:004662	negative re	6/905	42/18866	0.014367	0.034017	0.017877	RBP4/PTK2
BP	GO:200125	positive reg	16/905	182/18866	0.014424	0.034138	0.017941	IL1B/PML/
BP	GO:007061	regulation	8/905	67/18866	0.014511	0.034313	0.018033	SRC/MYH9
BP	GO:190571	positive reg	8/905	67/18866	0.014511	0.034313	0.018033	GSK3B/GZ
BP	GO:004888	sensory sys	29/905	394/18866	0.015026	0.035516	0.018665	RBP4/VEG
BP	GO:000232	natural kill	5/905	31/18866	0.015116	0.035651	0.018736	HLA-F/PGL
BP	GO:002177	olfactory b	5/905	31/18866	0.015116	0.035651	0.018736	WNT5A/SE
BP	GO:004598	positive reg	5/905	31/18866	0.015116	0.035651	0.018736	F2R/PTGS2
BP	GO:006091	heart form	5/905	31/18866	0.015116	0.035651	0.018736	WNT5A/R
BP	GO:190018	negative re	5/905	31/18866	0.015116	0.035651	0.018736	APOD/CHP
BP	GO:002176	hippocamp	9/905	81/18866	0.015351	0.036188	0.019018	HDAC1/GS
BP	GO:005507	transition	13/905	138/18866	0.015412	0.036318	0.019086	B2M/IFNG/
BP	GO:004230	regulation	7/905	55/18866	0.015593	0.036727	0.019302	IL1B/FABP5
BP	GO:006132	renal tubul	10/905	95/18866	0.015621	0.036779	0.019328	STAT1/VEG
BP	GO:009031	negative re	6/905	43/18866	0.016038	0.037711	0.019818	APOD/ADI
BP	GO:190103	regulation	6/905	43/18866	0.016038	0.037711	0.019818	TNF/IL10/

BP	GO:200064	positive reg	6/905	43/18866	0.016038	0.037711	0.019818	VEGFA/CX3
BP	GO:003103	actomyosin	17/905	200/18866	0.016191	0.038054	0.019999	NOX4/SRC/
BP	GO:000236	alpha-beta	4/905	21/18866	0.016386	0.03823	0.020091	CTSL/IL23A
BP	GO:000317	pulmonary	4/905	21/18866	0.016386	0.03823	0.020091	ROBO2/JAG
BP	GO:000911	vitamin bio	4/905	21/18866	0.016386	0.03823	0.020091	IFNG/IL1B/
BP	GO:003022	platelet for	4/905	21/18866	0.016386	0.03823	0.020091	PTPN6/MY
BP	GO:003261	interleukin	4/905	21/18866	0.016386	0.03823	0.020091	IFNL1/TNFS
BP	GO:003592	steroid hor	4/905	21/18866	0.016386	0.03823	0.020091	AGT/INHBA
BP	GO:004369	reverse cho	4/905	21/18866	0.016386	0.03823	0.020091	CETP/ABCA
BP	GO:004682	negative re	4/905	21/18866	0.016386	0.03823	0.020091	APOD/CHP
BP	GO:004848	sympathet	4/905	21/18866	0.016386	0.03823	0.020091	SEMA3A/G
BP	GO:006006	uterus dev	4/905	21/18866	0.016386	0.03823	0.020091	RBP4/WNT
BP	GO:006071	labyrinthin	4/905	21/18866	0.016386	0.03823	0.020091	SOCS3/IL10
BP	GO:190320	negative re	4/905	21/18866	0.016386	0.03823	0.020091	IL10/NR4A
BP	GO:190397	regulation	4/905	21/18866	0.016386	0.03823	0.020091	CCL3/SPHK
BP	GO:190488	beta-caten	4/905	21/18866	0.016386	0.03823	0.020091	GSK3B/WN
BP	GO:200004	regulation	4/905	21/18866	0.016386	0.03823	0.020091	VEGFA/WN
BP	GO:200038	regulation	4/905	21/18866	0.016386	0.03823	0.020091	DKK1/WNT
BP	GO:200073	positive reg	4/905	21/18866	0.016386	0.03823	0.020091	SEMA3C/P
BP	GO:004648	phosphatic	16/905	185/18866	0.016617	0.038751	0.020365	SOCS3/SOC
BP	GO:190274	regulation	18/905	217/18866	0.0171	0.03986	0.020948	HSPA2/HSP
BP	GO:003003	lamellipodi	8/905	69/18866	0.01712	0.03989	0.020964	VAV3/VAV
BP	GO:000726	Rho protei	13/905	140/18866	0.017191	0.040037	0.021041	F2R/F2RL1/
BP	GO:000916	nucleoside	5/905	32/18866	0.017227	0.040069	0.021058	APOBEC3G
BP	GO:005138	response to	5/905	32/18866	0.017227	0.040069	0.021058	CYBB/SRC/
BP	GO:007129	cellular res	5/905	32/18866	0.017227	0.040069	0.021058	IL15/PPARG
BP	GO:000698	ER overloa	3/905	12/18866	0.017484	0.040236	0.021146	HSPA5/GSK
BP	GO:001023	vascular tra	3/905	12/18866	0.017484	0.040236	0.021146	FABP5/CD3
BP	GO:003273	positive reg	3/905	12/18866	0.017484	0.040236	0.021146	TNFSF4/IL3
BP	GO:003295	inositol tris	3/905	12/18866	0.017484	0.040236	0.021146	PTK2B/PLC
BP	GO:003369	positive reg	3/905	12/18866	0.017484	0.040236	0.021146	LTF/ITGAV/
BP	GO:003573	CD4-positiv	3/905	12/18866	0.017484	0.040236	0.021146	XCL1/ARG2
BP	GO:003600	response to	3/905	12/18866	0.017484	0.040236	0.021146	TLR2/PTPN
BP	GO:003600	cellular res	3/905	12/18866	0.017484	0.040236	0.021146	TLR2/PTPN
BP	GO:003646	TRAIL-activ	3/905	12/18866	0.017484	0.040236	0.021146	TNFRSF10B
BP	GO:004211	endothelia	3/905	12/18866	0.017484	0.040236	0.021146	CXCL10/TG
BP	GO:004330	negative re	3/905	12/18866	0.017484	0.040236	0.021146	HLA-F/CD3
BP	GO:004338	negative T	3/905	12/18866	0.017484	0.040236	0.021146	CCR7/ZAP7
BP	GO:004369	dedifferent	3/905	12/18866	0.017484	0.040236	0.021146	PDGFB/ESR
BP	GO:004369	cell dediffe	3/905	12/18866	0.017484	0.040236	0.021146	PDGFB/ESR
BP	GO:005154	positive reg	3/905	12/18866	0.017484	0.040236	0.021146	MMP9/FGF
BP	GO:006045	regulation	3/905	12/18866	0.017484	0.040236	0.021146	OXT/UCN/I
BP	GO:006067	branching i	3/905	12/18866	0.017484	0.040236	0.021146	SOCS3/IL10
BP	GO:007026	pyroptosis	3/905	12/18866	0.017484	0.040236	0.021146	AIM2/NLRC
BP	GO:007058	cell-cell adh	3/905	12/18866	0.017484	0.040236	0.021146	ADIPOQ/IL
BP	GO:007258	caveolin-m	3/905	12/18866	0.017484	0.040236	0.021146	MAPK3/SR
BP	GO:190011	extracellula	3/905	12/18866	0.017484	0.040236	0.021146	LTBP1/GRE
BP	GO:190011	extracellula	3/905	12/18866	0.017484	0.040236	0.021146	LTBP1/GRE
BP	GO:190396	positive reg	3/905	12/18866	0.017484	0.040236	0.021146	AGT/ITGB1
BP	GO:190495	Wnt signali	3/905	12/18866	0.017484	0.040236	0.021146	WNT5A/W

BP	GO:200056	regulation	3/905	12/18866	0.017484	0.040236	0.021146	XCL1/ARG2
BP	GO:003167	cellular res	6/905	44/18866	0.017839	0.040984	0.021538	IL15/PPAR
BP	GO:003288	regulation	6/905	44/18866	0.017839	0.040984	0.021538	TGFB1/GSK
BP	GO:004218	ketone bio	6/905	44/18866	0.017839	0.040984	0.021538	ADM/BMP
BP	GO:190305	regulation	6/905	44/18866	0.017839	0.040984	0.021538	TGFB1/AG
BP	GO:199082	response t	10/905	97/18866	0.017863	0.041003	0.021549	ICAM1/PM
BP	GO:199083	cellular res	10/905	97/18866	0.017863	0.041003	0.021549	ICAM1/PM
BP	GO:003432	cell junctio	31/905	434/18866	0.017989	0.041274	0.021691	TLR2/IL1B/
BP	GO:003090	hindbrain	14/905	156/18866	0.018046	0.041389	0.021751	HSPA5/SE
BP	GO:190198	regulation	34/905	486/18866	0.018133	0.041559	0.021841	HSPA2/HS
BP	GO:000758	digestion	13/905	141/18866	0.018136	0.041559	0.021841	RBP4/CHIT
BP	GO:000602	aminoglyca	15/905	172/18866	0.018655	0.04273	0.022456	PGLYRP1/P
BP	GO:003052	intracellula	7/905	57/18866	0.018719	0.042823	0.022505	SRC/AR/ES
BP	GO:006100	cell differe	7/905	57/18866	0.018719	0.042823	0.022505	MMP9/AD
BP	GO:007053	protein K6	7/905	57/18866	0.018719	0.042823	0.022505	TRAF3/TRI
BP	GO:005101	actin filam	14/905	157/18866	0.018972	0.043383	0.022799	NOX4/SRC/
BP	GO:001701	regulation	12/905	127/18866	0.019041	0.043522	0.022872	HSPA5/HS
BP	GO:001056	positive re	4/905	22/18866	0.019285	0.043931	0.023087	IL15/CCR7/
BP	GO:003410	negative re	4/905	22/18866	0.019285	0.043931	0.023087	TNFAIP3/A
BP	GO:003558	calcium-m	4/905	22/18866	0.019285	0.043931	0.023087	DEFB1/CCL
BP	GO:003634	platelet m	4/905	22/18866	0.019285	0.043931	0.023087	PTPN6/MY
BP	GO:004235	vitamin D	4/905	22/18866	0.019285	0.043931	0.023087	IFNG/IL1B/
BP	GO:004245	ribonucleo	4/905	22/18866	0.019285	0.043931	0.023087	APOBEC3G
BP	GO:004336	CD4-positi	4/905	22/18866	0.019285	0.043931	0.023087	CTSL/IL23A
BP	GO:004565	regulation	4/905	22/18866	0.019285	0.043931	0.023087	CD4/IRF7/
BP	GO:000333	metanephr	5/905	33/18866	0.019523	0.044343	0.023304	STAT1/PD
BP	GO:000995	proximal/d	5/905	33/18866	0.019523	0.044343	0.023304	FGF10/GR
BP	GO:001003	response t	5/905	33/18866	0.019523	0.044343	0.023304	B2M/NFYA
BP	GO:001046	regulation	5/905	33/18866	0.019523	0.044343	0.023304	STAT1/VE
BP	GO:001095	negative re	5/905	33/18866	0.019523	0.044343	0.023304	LRRK2/SER
BP	GO:004592	negative re	5/905	33/18866	0.019523	0.044343	0.023304	HLA-F/TRI
BP	GO:190331	negative re	5/905	33/18866	0.019523	0.044343	0.023304	LRRK2/SER
BP	GO:000319	endocardia	6/905	45/18866	0.019774	0.044857	0.023574	ROBO2/B
BP	GO:000677	fat-soluble	6/905	45/18866	0.019774	0.044857	0.023574	IFNG/RBP1
BP	GO:001067	negative re	6/905	45/18866	0.019774	0.044857	0.023574	ADIPOQ/G
BP	GO:003020	glycosamin	14/905	158/18866	0.019933	0.045198	0.023753	PGLYRP1/P
BP	GO:003237	regulation	8/905	71/18866	0.020051	0.045446	0.023884	CETP/ADIP
BP	GO:003530	positive re	7/905	58/18866	0.020437	0.046302	0.024333	HSP90AB1/
BP	GO:001050	negative re	9/905	85/18866	0.020485	0.046352	0.02436	IL10/PTK2/
BP	GO:004584	positive re	9/905	85/18866	0.020485	0.046352	0.02436	TGFB1/GR
BP	GO:004863	positive re	9/905	85/18866	0.020485	0.046352	0.02436	TGFB1/GR
BP	GO:005506	monovalen	14/905	159/18866	0.02093	0.047321	0.024869	MAPK3/SL
BP	GO:200005	regulation	14/905	159/18866	0.02093	0.047321	0.024869	HSP90AB1/
BP	GO:199074	cellular det	11/905	114/18866	0.021006	0.047471	0.024948	S100A9/D
BP	GO:015006	visual syst	28/905	388/18866	0.021018	0.047479	0.024952	RBP4/VEG
BP	GO:190384	regulation	12/905	129/18866	0.021261	0.048009	0.02523	HSPA5/HS
BP	GO:001076	fibroblast	6/905	46/18866	0.021847	0.049054	0.02578	TGFB1/PM
BP	GO:003164	regulation	6/905	46/18866	0.021847	0.049054	0.02578	S100B/TY
BP	GO:006102	establishm	6/905	46/18866	0.021847	0.049054	0.02578	ICAM1/IL1
BP	GO:000263	negative re	3/905	13/18866	0.021933	0.049054	0.02578	CD22/IL33/

BP	GO:000267	negative re	3/905	13/18866	0.021933	0.049054	0.02578	PPARG/IL2
BP	GO:000292	negative re	3/905	13/18866	0.021933	0.049054	0.02578	SPINK5/PT
BP	GO:000333	mesenchym	3/905	13/18866	0.021933	0.049054	0.02578	STAT1/GD
BP	GO:000749	midgut dev	3/905	13/18866	0.021933	0.049054	0.02578	WNT5A/ED
BP	GO:001064	negative re	3/905	13/18866	0.021933	0.049054	0.02578	APOD/ADI
BP	GO:001087	positive reg	3/905	13/18866	0.021933	0.049054	0.02578	IFNG/HDA
BP	GO:001580	arginine tra	3/905	13/18866	0.021933	0.049054	0.02578	SLC11A1/A
BP	GO:003166	negative re	3/905	13/18866	0.021933	0.049054	0.02578	LTF/TNFAI
BP	GO:003195	negative re	3/905	13/18866	0.021933	0.049054	0.02578	ADIPOQ/C
BP	GO:003242	regulation	3/905	13/18866	0.021933	0.049054	0.02578	AGTR1/EG
BP	GO:003308	positive reg	3/905	13/18866	0.021933	0.049054	0.02578	IL1B/IL7R/
BP	GO:003314	positive reg	3/905	13/18866	0.021933	0.049054	0.02578	AR/PAK1/S
BP	GO:004557	positive reg	3/905	13/18866	0.021933	0.049054	0.02578	BTK/CD27/
BP	GO:004830	regulation	3/905	13/18866	0.021933	0.049054	0.02578	CD40/IL27
BP	GO:004871	positive reg	3/905	13/18866	0.021933	0.049054	0.02578	BMP2/CLC
BP	GO:006031	regulation	3/905	13/18866	0.021933	0.049054	0.02578	TGFB1/FLT
BP	GO:006102	eyelid deve	3/905	13/18866	0.021933	0.049054	0.02578	HDAC1/IN
BP	GO:006146	regulation	3/905	13/18866	0.021933	0.049054	0.02578	NR4A1/NR
BP	GO:190499	negative re	3/905	13/18866	0.021933	0.049054	0.02578	CXCL12/CC
BP	GO:001076	regulation	5/905	34/18866	0.022012	0.049109	0.025808	TGFB1/PTK
BP	GO:001092	positive reg	5/905	34/18866	0.022012	0.049109	0.025808	HSP90AB1/
BP	GO:003551	DNA dealky	5/905	34/18866	0.022012	0.049109	0.025808	APOBEC3G
BP	GO:003563	maintenan	5/905	34/18866	0.022012	0.049109	0.025808	VEGFA/PTC
BP	GO:005502	negative re	5/905	34/18866	0.022012	0.049109	0.025808	RBP4/PAK1
BP	GO:006111	negative re	5/905	34/18866	0.022012	0.049109	0.025808	RBP4/PAK1
BP	GO:000165	branching i	7/905	59/18866	0.022261	0.049583	0.026057	VEGFA/AG
BP	GO:004352	positive reg	7/905	59/18866	0.022261	0.049583	0.026057	TNF/FASLG
BP	GO:004645	icosanoid b	7/905	59/18866	0.022261	0.049583	0.026057	PTGDS/IL1
BP	GO:007138	cellular res	7/905	59/18866	0.022261	0.049583	0.026057	ICAM1/STC
BP	GO:000801	regulation	20/905	256/18866	0.022356	0.049774	0.026158	S100A1/DE
BP	GO:000205	positive reg	4/905	23/18866	0.02248	0.049784	0.026164	VEGFA/CX3
BP	GO:000659	thyroid hor	4/905	23/18866	0.02248	0.049784	0.026164	CTSB/DUO
BP	GO:001022	response to	4/905	23/18866	0.02248	0.049784	0.026164	CALR/PTGS
BP	GO:003516	embryonic	4/905	23/18866	0.02248	0.049784	0.026164	VEGFA/FLT
BP	GO:005086	negative re	4/905	23/18866	0.02248	0.049784	0.026164	PTPN6/SH2
BP	GO:006014	negative re	4/905	23/18866	0.02248	0.049784	0.026164	TGFB1/TN
BP	GO:006096	negative re	4/905	23/18866	0.02248	0.049784	0.026164	TGFB1/TN
BP	GO:007097	bone matu	4/905	23/18866	0.02248	0.049784	0.026164	LTF/BMP2/
BP	GO:007130	cellular res	4/905	23/18866	0.02248	0.049784	0.026164	IL15/VDR/
BP	GO:190103	negative re	4/905	23/18866	0.02248	0.049784	0.026164	IL10/MET/
BP	GO:190152	positive reg	4/905	23/18866	0.02248	0.049784	0.026164	NFYA/VEG
BP	GO:190320	negative re	4/905	23/18866	0.02248	0.049784	0.026164	IL10/MET/
BP	GO:200072	negative re	4/905	23/18866	0.02248	0.049784	0.026164	BMP2/DKK
BP	GO:004483	cell cycle G	21/905	273/18866	0.022825	0.050527	0.026554	HSPA2/HS
BP	GO:006157	actin filame	14/905	161/18866	0.023037	0.050975	0.026789	NOX4/SRC/
BP	GO:005196	regulation	8/905	73/18866	0.023321	0.051583	0.027109	TNF/PTGS2
BP	GO:003243	positive reg	9/905	87/18866	0.02347	0.051807	0.027226	PSMD10/G
BP	GO:004801	ephrin rece	9/905	87/18866	0.02347	0.051807	0.027226	MMP9/SRC
BP	GO:006029	long-term	9/905	87/18866	0.02347	0.051807	0.027226	S100B/AGE
BP	GO:006042	regulation	9/905	87/18866	0.02347	0.051807	0.027226	RBP4/IGF1/

BP	GO:009758	lamellipodi	9/905	87/18866	0.02347	0.051807	0.027226	SRC/VAV3/
BP	GO:002241	cellular pro	27/905	375/18866	0.023729	0.052356	0.027515	HSPA2/DEF
BP	GO:003057	collagen ca	6/905	47/18866	0.024062	0.053005	0.027856	CTSB/CTSL/
BP	GO:004593	positive reg	6/905	47/18866	0.024062	0.053005	0.027856	F2R/PTGS2
BP	GO:190473	vascular as	6/905	47/18866	0.024062	0.053005	0.027856	ADIPOQ/AC
BP	GO:190475	regulation	6/905	47/18866	0.024062	0.053005	0.027856	ADIPOQ/AC
BP	GO:001082	negative re	7/905	60/18866	0.024194	0.053253	0.027987	PSMD10/T
BP	GO:003590	aorta deve	7/905	60/18866	0.024194	0.053253	0.027987	DLL4/PDGF
BP	GO:002260	digestive sy	10/905	102/18866	0.024493	0.053866	0.028308	RBP4/MUC
BP	GO:011002	regulation	10/905	102/18866	0.024493	0.053866	0.028308	NOX4/PIK3
BP	GO:200102	regulation	18/905	226/18866	0.024636	0.054159	0.028463	PSMD10/C
BP	GO:003026	apoptotic r	5/905	35/18866	0.024697	0.054162	0.028464	ACVR1C/GI
BP	GO:003094	regulation	5/905	35/18866	0.024697	0.054162	0.028464	IL1B/FGF10
BP	GO:003368	osteoblast	5/905	35/18866	0.024697	0.054162	0.028464	LTF/ITGAV/
BP	GO:006025	regulation	5/905	35/18866	0.024697	0.054162	0.028464	LTA/IL1B/T
BP	GO:007088	regulation	5/905	35/18866	0.024697	0.054162	0.028464	TNF/CHP1/
BP	GO:190403	positive reg	5/905	35/18866	0.024697	0.054162	0.028464	HSP90AB1/
BP	GO:003202	positive reg	8/905	74/18866	0.02509	0.055	0.028904	RBP4/ARRB
BP	GO:000318	atrioventri	4/905	24/18866	0.02598	0.056813	0.029857	BMP2/ZFPI
BP	GO:004432	response t	4/905	24/18866	0.02598	0.056813	0.029857	EBI3/LEPR/
BP	GO:004582	positive reg	4/905	24/18866	0.02598	0.056813	0.029857	IFNG/IGF1/
BP	GO:009874	cell aggreg	4/905	24/18866	0.02598	0.056813	0.029857	LTF/BPIFA1
BP	GO:190299	positive reg	4/905	24/18866	0.02598	0.056813	0.029857	IFNG/TNF/
BP	GO:190330	negative re	4/905	24/18866	0.02598	0.056813	0.029857	HLA-F/TRIM
BP	GO:000854	fibroblast g	11/905	118/18866	0.026349	0.057596	0.030269	MAPK3/WI
BP	GO:004560	regulation	6/905	48/18866	0.026422	0.057686	0.030316	IL1B/TNF/V
BP	GO:005197	regulation	6/905	48/18866	0.026422	0.057686	0.030316	HSP90AA1/
BP	GO:005501	ventricular	6/905	48/18866	0.026422	0.057686	0.030316	TGFB1/DLL
BP	GO:000176	neuron mig	14/905	164/18866	0.026489	0.057785	0.030368	CXCL12/VE
BP	GO:004616	alcohol bio	14/905	164/18866	0.026489	0.057785	0.030368	IFNG/NFYA
BP	GO:005500	cardiac cell	9/905	89/18866	0.026754	0.05825	0.030613	VEGFA/PDG
BP	GO:000177	immunolog	3/905	14/18866	0.026939	0.05825	0.030613	CCR7/PRF1
BP	GO:001087	regulation	3/905	14/18866	0.026939	0.05825	0.030613	AGT/AGTR
BP	GO:001487	response t	3/905	14/18866	0.026939	0.05825	0.030613	AGT/PPARG
BP	GO:001989	axonal tran	3/905	14/18866	0.026939	0.05825	0.030613	MAPT/HIF1
BP	GO:003543	maintenan	3/905	14/18866	0.026939	0.05825	0.030613	HSPA5/PDI
BP	GO:003581	positive reg	3/905	14/18866	0.026939	0.05825	0.030613	EDNRB/BTC
BP	GO:003816	angiotensin	3/905	14/18866	0.026939	0.05825	0.030613	SRC/AGTR1
BP	GO:004505	positive thy	3/905	14/18866	0.026939	0.05825	0.030613	ZAP70/CD3
BP	GO:004547	response t	3/905	14/18866	0.026939	0.05825	0.030613	OXT/CDK4/
BP	GO:004600	negative re	3/905	14/18866	0.026939	0.05825	0.030613	ARG1/CD2
BP	GO:004632	positive reg	3/905	14/18866	0.026939	0.05825	0.030613	PPARG/NR
BP	GO:005096	detection c	3/905	14/18866	0.026939	0.05825	0.030613	CXCL12/CX
BP	GO:005154	regulation	3/905	14/18866	0.026939	0.05825	0.030613	MMP9/FGF
BP	GO:007136	cellular res	3/905	14/18866	0.026939	0.05825	0.030613	CYBB/CCL7
BP	GO:009023	regulation	3/905	14/18866	0.026939	0.05825	0.030613	ARRB1/MU
BP	GO:190172	regulation	3/905	14/18866	0.026939	0.05825	0.030613	PDGFB/PDG
BP	GO:190289	negative re	3/905	14/18866	0.026939	0.05825	0.030613	PDGFB/PPA
BP	GO:200054	positive reg	3/905	14/18866	0.026939	0.05825	0.030613	WNT3A/GJ
BP	GO:001590	long-chain	8/905	75/18866	0.026949	0.05825	0.030613	FABP5/FAB

BP	GO:003241	lysosome l	8/905	75/18866	0.026949	0.05825	0.030613	FCER1G/BT
BP	GO:003314	regulation	8/905	75/18866	0.026949	0.05825	0.030613	CALR/SRC/
BP	GO:007208	nephron e	8/905	75/18866	0.026949	0.05825	0.030613	STAT1/VEG
BP	GO:003105	regulation	13/905	149/18866	0.02717	0.058703	0.030851	IL1B/VEGF
BP	GO:001054	regulation	5/905	36/18866	0.027584	0.059482	0.03126	FCER1G/PD
BP	GO:002195	central ner	5/905	36/18866	0.027584	0.059482	0.03126	HSP90AA1/
BP	GO:009031	regulation	5/905	36/18866	0.027584	0.059482	0.03126	CHP1/ITGB
BP	GO:010605	regulation	5/905	36/18866	0.027584	0.059482	0.03126	TNF/CHP1/
BP	GO:003222	regulation	10/905	104/18866	0.027585	0.059482	0.03126	NOX4/PIK3
BP	GO:000599	monosacch	22/905	296/18866	0.028353	0.061114	0.032118	RBP4/FABP
BP	GO:000611	regulation	6/905	49/18866	0.02893	0.062233	0.032706	ADIPOQ/FA
BP	GO:000759	lactation	6/905	49/18866	0.02893	0.062233	0.032706	VEGFA/VDI
BP	GO:004851	circadian b	6/905	49/18866	0.02893	0.062233	0.032706	PTGDS/CSF
BP	GO:006071	labyrinthin	6/905	49/18866	0.02893	0.062233	0.032706	SOCS3/IL10
BP	GO:009772	calcineurin	6/905	49/18866	0.02893	0.062233	0.032706	TNF/CHP1/
BP	GO:000762	locomotory	16/905	198/18866	0.029202	0.062793	0.033	CXCL12/ID
BP	GO:002154	cerebellum	10/905	105/18866	0.029232	0.062807	0.033007	HSPA5/SEN
BP	GO:006201	negative re	10/905	105/18866	0.029232	0.062807	0.033007	TGFB1/ADI
BP	GO:000205	positive re	4/905	25/18866	0.029788	0.063799	0.033529	STAT1/VEG
BP	GO:000330	type B pan	4/905	25/18866	0.029788	0.063799	0.033529	WNT5A/GS
BP	GO:001482	vascular as	4/905	25/18866	0.029788	0.063799	0.033529	EDN3/EDN
BP	GO:003416	toll-like rec	4/905	25/18866	0.029788	0.063799	0.033529	TLR8/RSAD
BP	GO:005085	positive re	4/905	25/18866	0.029788	0.063799	0.033529	CCR7/CARI
BP	GO:006057	intestinal e	4/905	25/18866	0.029788	0.063799	0.033529	SRC/IL6ST/
BP	GO:006214	detection c	4/905	25/18866	0.029788	0.063799	0.033529	CXCL12/CX
BP	GO:200067	positive re	4/905	25/18866	0.029788	0.063799	0.033529	IFNG/TGFB
BP	GO:003090	midbrain d	9/905	91/18866	0.030348	0.064876	0.034095	HSPA5/S10
BP	GO:004247	odontogen	9/905	91/18866	0.030348	0.064876	0.034095	HDAC1/FG
BP	GO:004568	regulation	9/905	91/18866	0.030348	0.064876	0.034095	CTSL/TNF/
BP	GO:004847	oogenesis	9/905	91/18866	0.030348	0.064876	0.034095	SRC/PTX3/
BP	GO:004301	camera-typ	24/905	332/18866	0.03035	0.064876	0.034095	RBP4/VEG
BP	GO:000692	cellular cor	5/905	37/18866	0.030677	0.065448	0.034396	ACVR1C/GI
BP	GO:003271	negative re	5/905	37/18866	0.030677	0.065448	0.034396	TMSB4X/A
BP	GO:004507	positive re	5/905	37/18866	0.030677	0.065448	0.034396	PPIA/CCL5/
BP	GO:005189	regulation	7/905	63/18866	0.030679	0.065448	0.034396	APOD/VEG
BP	GO:009010	regulation	7/905	63/18866	0.030679	0.065448	0.034396	APOD/VEG
BP	GO:000721	neuropepti	10/905	106/18866	0.030946	0.065907	0.034636	CYSLTR1/C
BP	GO:003241	positive re	10/905	106/18866	0.030946	0.065907	0.034636	HSPA2/IFN
BP	GO:004690	regulation	8/905	77/18866	0.030952	0.065907	0.034636	GSK3B/GZI
BP	GO:006133	renal tubul	8/905	77/18866	0.030952	0.065907	0.034636	VEGFA/AG
BP	GO:012025	olefinic cor	11/905	121/18866	0.030955	0.065907	0.034636	PTGDS/MA
BP	GO:000762	rhythmic b	6/905	50/18866	0.03159	0.067207	0.03532	PTGDS/CSF
BP	GO:004298	amyloid pr	6/905	50/18866	0.03159	0.067207	0.03532	IFNG/TNF/
BP	GO:000995	dorsal/ven	9/905	92/18866	0.032266	0.068575	0.036039	DLL4/GREN
BP	GO:001045	positive re	3/905	15/18866	0.0325	0.068575	0.036039	IL23A/IL12
BP	GO:002192	cell prolifer	3/905	15/18866	0.0325	0.068575	0.036039	EGF/RORA/
BP	GO:002193	cerebellar	3/905	15/18866	0.0325	0.068575	0.036039	EGF/RORA/
BP	GO:003085	regulation	3/905	15/18866	0.0325	0.068575	0.036039	ADIPOQ/C1
BP	GO:003227	gonadotrop	3/905	15/18866	0.0325	0.068575	0.036039	INHA/INHB
BP	GO:003315	V(D)J recor	3/905	15/18866	0.0325	0.068575	0.036039	PRKDC/RA

BP	GO:003434	glial cell ap	3/905	15/18866	0.0325	0.068575	0.036039	CCL2/PRKC
BP	GO:004506	T-helper 2	3/905	15/18866	0.0325	0.068575	0.036039	TNFSF4/CD
BP	GO:004534	regulation	3/905	15/18866	0.0325	0.068575	0.036039	IFNG/IL10/
BP	GO:004547	locomotor	3/905	15/18866	0.0325	0.068575	0.036039	USP2/MTA
BP	GO:004583	negative re	3/905	15/18866	0.0325	0.068575	0.036039	MAPT/PTN
BP	GO:004848	enteric ner	3/905	15/18866	0.0325	0.068575	0.036039	EDNRA/ED
BP	GO:005086	positive re	3/905	15/18866	0.0325	0.068575	0.036039	CCR7/CAR
BP	GO:005505	neuroblast	3/905	15/18866	0.0325	0.068575	0.036039	WNT3A/AK
BP	GO:006034	heart trabe	3/905	15/18866	0.0325	0.068575	0.036039	RBP4/TEK/
BP	GO:006039	positive re	3/905	15/18866	0.0325	0.068575	0.036039	TGFB1/TG
BP	GO:007256	chemokine	3/905	15/18866	0.0325	0.068575	0.036039	TNF/F2RL1
BP	GO:200034	regulation	3/905	15/18866	0.0325	0.068575	0.036039	TNF/F2RL1
BP	GO:200040	negative re	3/905	15/18866	0.0325	0.068575	0.036039	APOD/CCL
BP	GO:200117	positive re	3/905	15/18866	0.0325	0.068575	0.036039	TMSB4X/P
BP	GO:009723	cellular res	11/905	122/18866	0.03261	0.068781	0.036147	S100A9/DU
BP	GO:000001	regulation	10/905	107/18866	0.032731	0.068956	0.036239	TGFB1/TFR
BP	GO:004852	positive re	10/905	107/18866	0.032731	0.068956	0.036239	CD4/PPIA/
BP	GO:009917	regulation	10/905	107/18866	0.032731	0.068956	0.036239	WNT5A/PT
BP	GO:200004	regulation	15/905	185/18866	0.033099	0.069703	0.036632	PSME2/PM
BP	GO:000178	B cell apop	4/905	26/18866	0.033908	0.070938	0.03728	IL10/MIF/
BP	GO:000222	innate imm	4/905	26/18866	0.033908	0.070938	0.03728	DEFB1/LTF
BP	GO:000317	atrioventri	4/905	26/18866	0.033908	0.070938	0.03728	BMP2/ZFP
BP	GO:001943	removal of	4/905	26/18866	0.033908	0.070938	0.03728	TNF/MPO/
BP	GO:003081	positive re	4/905	26/18866	0.033908	0.070938	0.03728	TMSB4X/N
BP	GO:003631	cellular res	4/905	26/18866	0.033908	0.070938	0.03728	INHBA/RO
BP	GO:004240	thyroid hor	4/905	26/18866	0.033908	0.070938	0.03728	CTSB/DUO
BP	GO:004356	regulation	4/905	26/18866	0.033908	0.070938	0.03728	BMP2/BM
BP	GO:006034	trabecula f	4/905	26/18866	0.033908	0.070938	0.03728	RBP4/GRE
BP	GO:006039	regulation	4/905	26/18866	0.033908	0.070938	0.03728	TGFB1/GD
BP	GO:006056	apoptotic	4/905	26/18866	0.033908	0.070938	0.03728	VDR/JAG2/
BP	GO:007063	transepithe	4/905	26/18866	0.033908	0.070938	0.03728	EDNRB/CS
BP	GO:007142	hematopoi	4/905	26/18866	0.033908	0.070938	0.03728	EIF2AK2/W
BP	GO:007227	metanephr	4/905	26/18866	0.033908	0.070938	0.03728	STAT1/PD
BP	GO:009706	response t	4/905	26/18866	0.033908	0.070938	0.03728	CTSB/CTSL
BP	GO:190037	positive re	4/905	26/18866	0.033908	0.070938	0.03728	TMSB4X/N
BP	GO:190302	positive re	4/905	26/18866	0.033908	0.070938	0.03728	IL15/CCR7/
BP	GO:000329	physiologic	5/905	38/18866	0.033979	0.07095	0.037287	AGT/IGF1/
BP	GO:000330	physiologic	5/905	38/18866	0.033979	0.07095	0.037287	AGT/IGF1/
BP	GO:001943	triglyceride	5/905	38/18866	0.033979	0.07095	0.037287	FABP6/FA
BP	GO:006104	cell growth	5/905	38/18866	0.033979	0.07095	0.037287	AGT/IGF1/
BP	GO:190589	positive re	5/905	38/18866	0.033979	0.07095	0.037287	PIK3R1/PM
BP	GO:007208	nephron tu	9/905	93/18866	0.034267	0.071523	0.037588	STAT1/VEG
BP	GO:000602	glycosamin	10/905	108/18866	0.034586	0.072162	0.037924	TGFB1/IL1
BP	GO:000682	iron ion tra	8/905	79/18866	0.035343	0.073655	0.038708	B2M/IFNG
BP	GO:000749	endoderm	8/905	79/18866	0.035343	0.073655	0.038708	MMP9/ITG
BP	GO:003010	water hom	8/905	79/18866	0.035343	0.073655	0.038708	BPIFA1/CL
BP	GO:000694	regulation	7/905	65/18866	0.035596	0.074124	0.038955	F2R/PTGS2
BP	GO:006067	ureteric bu	7/905	65/18866	0.035596	0.074124	0.038955	VEGFA/AG
BP	GO:001895	phenol-cor	10/905	109/18866	0.036514	0.076008	0.039945	CTSB/DUO
BP	GO:006042	lung morph	6/905	52/18866	0.037376	0.077742	0.040856	TNF/MAPK

BP	GO:200067	regulation	6/905	52/18866	0.037376	0.077742	0.040856	IFNG/TMS
BP	GO:000166	behavioral	5/905	39/18866	0.037493	0.077806	0.04089	MDK/UCN/
BP	GO:001073	protein kin	5/905	39/18866	0.037493	0.077806	0.04089	ADIPOQ/M
BP	GO:003314	regulation	5/905	39/18866	0.037493	0.077806	0.04089	SRC/AR/PA
BP	GO:003420	amyloid-be	5/905	39/18866	0.037493	0.077806	0.04089	IFNG/TNF/
BP	GO:007252	pyrimidine	5/905	39/18866	0.037493	0.077806	0.04089	APOBEC3G
BP	GO:200027	negative re	5/905	39/18866	0.037493	0.077806	0.04089	ADIPOQ/S
BP	GO:000758	respiratory	7/905	66/18866	0.038238	0.07912	0.04158	SFTPA2/CY
BP	GO:007217	mesonephr	7/905	66/18866	0.038238	0.07912	0.04158	VEGFA/AG
BP	GO:015011	regulation	7/905	66/18866	0.038238	0.07912	0.04158	APOD/VEG
BP	GO:000965	response t	4/905	27/18866	0.038343	0.07912	0.04158	HSP90AB1/
BP	GO:001099	response t	4/905	27/18866	0.038343	0.07912	0.04158	CXCL10/M
BP	GO:003308	regulation	4/905	27/18866	0.038343	0.07912	0.04158	IL1B/IL7R/
BP	GO:004250	serine pho	4/905	27/18866	0.038343	0.07912	0.04158	IFNG/IFNE/
BP	GO:004642	negative re	4/905	27/18866	0.038343	0.07912	0.04158	SOCS3/SO
BP	GO:004879	animal org	4/905	27/18866	0.038343	0.07912	0.04158	LTF/BMP2/
BP	GO:009014	regulation	4/905	27/18866	0.038343	0.07912	0.04158	MAPT/PPA
BP	GO:190247	regulation	4/905	27/18866	0.038343	0.07912	0.04158	MAPT/WN
BP	GO:190331	positive re	4/905	27/18866	0.038343	0.07912	0.04158	TFR2/SRC/
BP	GO:007200	nephron e	10/905	110/18866	0.038515	0.07912	0.04158	ADIPOQ/S
BP	GO:009719	execution	9/905	95/18866	0.038521	0.07912	0.04158	ACVR1C/G
BP	GO:000229	T-helper ce	3/905	16/18866	0.038609	0.07912	0.04158	IL23A/IL12
BP	GO:000322	ventricular	3/905	16/18866	0.038609	0.07912	0.04158	DLL4/NRG1
BP	GO:001091	regulation	3/905	16/18866	0.038609	0.07912	0.04158	PTK2B/AD
BP	GO:001701	protein nitr	3/905	16/18866	0.038609	0.07912	0.04158	S100A9/S1
BP	GO:001811	peptidyl-cy	3/905	16/18866	0.038609	0.07912	0.04158	S100A9/S1
BP	GO:002154	dentate gy	3/905	16/18866	0.038609	0.07912	0.04158	MDK/NR2
BP	GO:003222	regulation	3/905	16/18866	0.038609	0.07912	0.04158	PTGS2/GD
BP	GO:003235	response t	3/905	16/18866	0.038609	0.07912	0.04158	INHBA/TG
BP	GO:003586	response t	3/905	16/18866	0.038609	0.07912	0.04158	GNRH1/PP
BP	GO:005096	detection	3/905	16/18866	0.038609	0.07912	0.04158	CXCL12/CX
BP	GO:005123	sequesteri	3/905	16/18866	0.038609	0.07912	0.04158	LCN2/S100
BP	GO:006057	intestinal e	3/905	16/18866	0.038609	0.07912	0.04158	SRC/IL6ST/
BP	GO:006154	ganglion de	3/905	16/18866	0.038609	0.07912	0.04158	SEMA3A/N
BP	GO:007088	positive re	3/905	16/18866	0.038609	0.07912	0.04158	TNF/IGF1/
BP	GO:007228	metanephr	3/905	16/18866	0.038609	0.07912	0.04158	STAT1/GD
BP	GO:008610	G protein-	3/905	16/18866	0.038609	0.07912	0.04158	SRC/NOS1/
BP	GO:010605	positive re	3/905	16/18866	0.038609	0.07912	0.04158	TNF/IGF1/
BP	GO:190012	negative re	3/905	16/18866	0.038609	0.07912	0.04158	B2M/ADIP
BP	GO:190372	regulation	3/905	16/18866	0.038609	0.07912	0.04158	S100A9/A
BP	GO:000989	negative re	23/905	323/18866	0.038691	0.079258	0.041653	HSP90AB1/
BP	GO:009917	postsynaps	14/905	173/18866	0.039128	0.080124	0.042108	WNT5A/N
BP	GO:004259	response t	16/905	206/18866	0.039838	0.081516	0.042839	HSPA5/EIF
BP	GO:190280	regulation	16/905	206/18866	0.039838	0.081516	0.042839	PSME2/P
BP	GO:004394	regulation	6/905	53/18866	0.040506	0.082819	0.043525	GNAI1/NO
BP	GO:009917	presynapse	6/905	53/18866	0.040506	0.082819	0.043525	WNT5A/C5
BP	GO:190367	positive re	7/905	67/18866	0.041007	0.083811	0.044046	S100A1/VE
BP	GO:000220	behavioral	5/905	40/18866	0.041222	0.08406	0.044177	MDK/UCN/
BP	GO:004390	positive re	5/905	40/18866	0.041222	0.08406	0.044177	VEGFA/ED
BP	GO:004574	positive re	5/905	40/18866	0.041222	0.08406	0.044177	CACYBP/E

BP	GO:004574	negative re	5/905	40/18866	0.041222	0.08406	0.044177	DLL4/ARRE
BP	GO:190274	apoptotic p	5/905	40/18866	0.041222	0.08406	0.044177	VDR/ROBO
BP	GO:190299	regulation	5/905	40/18866	0.041222	0.08406	0.044177	IFNG/TNF/
BP	GO:003240	regulation	21/905	291/18866	0.041396	0.084384	0.044347	HSPA2/IFN
BP	GO:004358	ear develop	17/905	224/18866	0.042005	0.085593	0.044982	CXCL14/M/
BP	GO:190161	organic hyc	19/905	258/18866	0.042673	0.086921	0.04568	IFNG/NFYA
BP	GO:002184	cell prolifer	4/905	28/18866	0.043094	0.087514	0.045992	FABP7/WN
BP	GO:003295	inositol pho	4/905	28/18866	0.043094	0.087514	0.045992	PTK2B/PLC
BP	GO:003359	mammary	4/905	28/18866	0.043094	0.087514	0.045992	WNT5A/TN
BP	GO:003588	enteroend	4/905	28/18866	0.043094	0.087514	0.045992	WNT5A/GS
BP	GO:004433	cell-cell adl	4/905	28/18866	0.043094	0.087514	0.045992	VEGFA/WN
BP	GO:004574	positive reg	4/905	28/18866	0.043094	0.087514	0.045992	NOS1/GRP/
BP	GO:007145	cellular res	4/905	28/18866	0.043094	0.087514	0.045992	TNF/MPO/
BP	GO:007145	cellular res	4/905	28/18866	0.043094	0.087514	0.045992	TNF/MPO/
BP	GO:190301	regulation	6/905	54/18866	0.043797	0.08891	0.046725	IL15/PTX3/
BP	GO:004001	regulation	7/905	68/18866	0.043902	0.089089	0.046819	PIK3CA/GD
BP	GO:002289	regulation	20/905	276/18866	0.044104	0.089465	0.047017	HSPA2/IFN
BP	GO:190351	mucopolys	10/905	113/18866	0.044967	0.091182	0.04792	TGFB1/IL1
BP	GO:000318	pulmonary	3/905	17/18866	0.045257	0.09129	0.047976	ROBO2/JA(
BP	GO:000929	mRNA tran	3/905	17/18866	0.045257	0.09129	0.047976	C5AR1/PPA
BP	GO:001071	regulation	3/905	17/18866	0.045257	0.09129	0.047976	TGFB1/FGF
BP	GO:002178	preganglio	3/905	17/18866	0.045257	0.09129	0.047976	SEMA3A/P
BP	GO:003073	sequesteri	3/905	17/18866	0.045257	0.09129	0.047976	IL1B/TNF/F
BP	GO:003363	cell-cell adl	3/905	17/18866	0.045257	0.09129	0.047976	CXCL13/CC
BP	GO:004572	positive reg	3/905	17/18866	0.045257	0.09129	0.047976	PPARGC1A
BP	GO:005158	regulation	3/905	17/18866	0.045257	0.09129	0.047976	NOS1/GDN
BP	GO:006064	mammary	3/905	17/18866	0.045257	0.09129	0.047976	HIF1A/CEB
BP	GO:006115	3'-UTR-me	3/905	17/18866	0.045257	0.09129	0.047976	MOV10/DH
BP	GO:007029	renal absor	3/905	17/18866	0.045257	0.09129	0.047976	ADIPOQ/CI
BP	GO:009018	negative re	3/905	17/18866	0.045257	0.09129	0.047976	MMP9/AD
BP	GO:190533	negative re	3/905	17/18866	0.045257	0.09129	0.047976	TNF/STAT1
BP	GO:200126	regulation	3/905	17/18866	0.045257	0.09129	0.047976	MMP9/PLA
BP	GO:006113	regulation	15/905	193/18866	0.045298	0.091332	0.047998	HSP90AB1/
BP	GO:001485	striated mu	8/905	83/18866	0.045345	0.091332	0.047998	RBP4/ANG
BP	GO:004804	focal adhes	8/905	83/18866	0.045345	0.091332	0.047998	APOD/VEG
BP	GO:200102	negative re	8/905	83/18866	0.045345	0.091332	0.047998	PSMD10/C
BP	GO:004472	DNA methy	9/905	98/18866	0.045552	0.091714	0.048199	APOBEC3G
BP	GO:000761	learning	12/905	145/18866	0.046385	0.093357	0.049062	TLR2/PTGS
BP	GO:000170	endoderm	6/905	55/18866	0.047251	0.094928	0.049888	MMP9/ITG
BP	GO:000322	ventricular	6/905	55/18866	0.047251	0.094928	0.049888	TGFB1/DLL
BP	GO:000834	glial cell mi	6/905	55/18866	0.047251	0.094928	0.049888	CCL2/CCL3
BP	GO:002202	telencepha	6/905	55/18866	0.047251	0.094928	0.049888	CXCL12/CX
BP	GO:002203	metenceph	10/905	114/18866	0.047271	0.094928	0.049888	HSPA5/SEN
BP	GO:003241	positive reg	10/905	114/18866	0.047271	0.094928	0.049888	HSPA2/IFN
CC	GO:000989	external sic	131/907	417/19559	2.88E-73	1.40E-70	1.13E-70	AZGP1/B2N
CC	GO:001981	immunoglo	53/907	163/19559	1.09E-30	2.65E-28	2.14E-28	CD79A/IGH
CC	GO:009880	plasma me	66/907	307/19559	3.46E-26	5.62E-24	4.53E-24	B2M/CD4/
CC	GO:004257	immunoglo	34/907	76/19559	1.74E-25	2.12E-23	1.71E-23	IGHE/IGHG
CC	GO:004512	membrane	52/907	329/19559	7.15E-15	6.59E-13	5.31E-13	CD4/ICAM
CC	GO:009885	membrane	52/907	330/19559	8.12E-15	6.59E-13	5.31E-13	CD4/ICAM

CC	GO:009858	membrane	52/907	343/19559	4.03E-14	2.81E-12	2.26E-12	CD4/ICAM1
CC	GO:004258	specific gra	33/907	160/19559	3.53E-13	2.12E-11	1.71E-11	B2M/SLPI/
CC	GO:003198	vesicle lum	49/907	328/19559	3.92E-13	2.12E-11	1.71E-11	B2M/HSP9
CC	GO:006020	cytoplasmi	48/907	326/19559	1.18E-12	5.74E-11	4.63E-11	B2M/HSP9
CC	GO:003066	secretory g	46/907	306/19559	1.66E-12	7.35E-11	5.93E-11	FCER1G/HL
CC	GO:003477	secretory g	47/907	322/19559	2.79E-12	1.13E-10	9.14E-11	B2M/HSP9
CC	GO:004210	T cell recep	29/907	140/19559	8.50E-12	3.18E-10	2.57E-10	CD4/PTPN6
CC	GO:007082	tertiary gra	31/907	164/19559	2.01E-11	6.98E-10	5.63E-10	B2M/FCER
CC	GO:007256	blood micr	29/907	148/19559	3.58E-11	1.16E-09	9.37E-10	HSPA2/TGF
CC	GO:003013	endocytic v	44/907	313/19559	4.98E-11	1.52E-09	1.22E-09	B2M/CALR/
CC	GO:006202	collagen-co	53/907	427/19559	6.49E-11	1.86E-09	1.50E-09	AZGP1/CAL
CC	GO:002262	proteasom	12/907	24/19559	1.49E-10	4.02E-09	3.24E-09	PSMC2/PSM
CC	GO:004533	phagocytic	27/907	140/19559	2.47E-10	6.33E-09	5.11E-09	B2M/CALR/
CC	GO:000583	proteasom	11/907	21/19559	4.62E-10	1.13E-08	9.07E-09	PSMC2/PSM
CC	GO:007082	tertiary gra	19/907	73/19559	5.61E-10	1.30E-08	1.05E-08	FCER1G/PL
CC	GO:004261	MHC prote	11/907	25/19559	4.92E-09	1.09E-07	8.79E-08	B2M/HLA-A
CC	GO:003067	phagocytic	18/907	77/19559	1.02E-08	2.17E-07	1.75E-07	B2M/CALR/
CC	GO:000576	early endos	44/907	377/19559	1.82E-08	3.70E-07	2.98E-07	B2M/CD1E
CC	GO:003066	endocytic v	26/907	164/19559	3.87E-08	7.53E-07	6.07E-07	B2M/CALR/
CC	GO:003558	specific gra	15/907	62/19559	1.06E-07	1.98E-06	1.60E-06	B2M/SLPI/
CC	GO:000177	immunolog	12/907	39/19559	1.13E-07	2.03E-06	1.64E-06	ICAM1/VAV
CC	GO:003557	specific gra	18/907	91/19559	1.60E-07	2.79E-06	2.25E-06	PLAU/CYBB
CC	GO:000050	proteasom	14/907	63/19559	8.61E-07	1.45E-05	1.17E-05	PSMB8/PSM
CC	GO:007168	endocytic v	8/907	20/19559	1.59E-06	2.58E-05	2.08E-05	CALR/HSP9
CC	GO:000592	focal adhes	42/907	415/19559	1.86E-06	2.92E-05	2.36E-05	B2M/CALR/
CC	GO:000578	endoplasm	34/907	308/19559	2.68E-06	4.06E-05	3.27E-05	B2M/CALR/
CC	GO:190536	endopeptic	14/907	69/19559	2.75E-06	4.06E-05	3.27E-05	PSMB8/PSM
CC	GO:003005	cell-substra	42/907	423/19559	3.03E-06	4.34E-05	3.50E-05	B2M/CALR/
CC	GO:000211	semaphori	6/907	11/19559	3.70E-06	5.15E-05	4.15E-05	PLXNA1/PL
CC	GO:000594	phosphatic	9/907	29/19559	4.12E-06	5.28E-05	4.26E-05	SOCS3/SOC
CC	GO:007155	integral co	9/907	29/19559	4.12E-06	5.28E-05	4.26E-05	CALR/HLA-
CC	GO:009855	lumenal sid	9/907	29/19559	4.12E-06	5.28E-05	4.26E-05	CALR/HLA-
CC	GO:006170	inflammaso	7/907	17/19559	5.82E-06	7.27E-05	5.86E-05	CASP1/DHX
CC	GO:000854	proteasom	6/907	12/19559	7.11E-06	8.65E-05	6.97E-05	PSMC2/PSM
CC	GO:003066	coated ves	23/907	183/19559	1.37E-05	0.000163	0.000131	B2M/CD4/
CC	GO:000577	vacuolar lu	22/907	173/19559	1.74E-05	0.000201	0.000162	CD1E/CTSB
CC	GO:003013	coated ves	31/907	298/19559	2.39E-05	0.00027	0.000218	B2M/CD4/
CC	GO:009857	lumenal sid	9/907	36/19559	2.89E-05	0.00032	0.000258	CALR/HLA-
CC	GO:003109	platelet alp	12/907	67/19559	5.23E-05	0.000566	0.000456	TMSB4X/TG
CC	GO:004485	plasma me	16/907	113/19559	6.52E-05	0.000691	0.000557	F2R/MAPK
CC	GO:005503	recycling e	22/907	190/19559	7.39E-05	0.000765	0.000617	B2M/PDIA3
CC	GO:003563	CD40 recep	5/907	11/19559	7.75E-05	0.000784	0.000632	CD40/TRAF
CC	GO:000579	Golgi lume	15/907	103/19559	7.89E-05	0.000784	0.000632	DEFB1/TGF
CC	GO:190536	peptidase c	14/907	92/19559	8.33E-05	0.000811	0.000654	PSMB8/PSM
CC	GO:000590	caveola	13/907	82/19559	9.64E-05	0.00092	0.000742	F2R/MAPK
CC	GO:010100	ficolin-1-ric	11/907	61/19559	9.99E-05	0.000936	0.000754	FCER1G/SL
CC	GO:000579	Golgi-assoc	21/907	181/19559	0.000104	0.000953	0.000768	B2M/HLA-A
CC	GO:003066	clathrin-co	16/907	118/19559	0.00011	0.000996	0.000803	CD4/HLA-D
CC	GO:004302	NADPH oxi	5/907	12/19559	0.000128	0.001132	0.000913	NOX4/DUO
CC	GO:003190	early endos	19/907	161/19559	0.000174	0.001515	0.001222	B2M/HLA-A

CC	GO:190472	tertiary gra	10/907	55/19559	0.000191	0.001635	0.001318	B2M/PGLY
CC	GO:009863	protein cor	8/907	36/19559	0.000197	0.001654	0.001333	ITGAV/ITG
CC	GO:001989	extrinsic cc	29/907	306/19559	0.000223	0.001842	0.001485	DEFB1/S10
CC	GO:003013	clathrin-co	21/907	194/19559	0.000275	0.002229	0.001797	CD4/HLA-D
CC	GO:003109	platelet alp	13/907	91/19559	0.000282	0.002253	0.001816	TMSB4X/T
CC	GO:004262	mast cell g	6/907	22/19559	0.000385	0.002975	0.002399	BTK/PIK3C
CC	GO:009703	perinuclea	6/907	22/19559	0.000385	0.002975	0.002399	NOX4/CYB
CC	GO:004320	lysosomal l	13/907	96/19559	0.00048	0.003654	0.002946	CD1E/CTSE
CC	GO:001250	ER to Golgi	10/907	62/19559	0.000525	0.003934	0.003171	B2M/HLA-
CC	GO:005503	recycling e	12/907	85/19559	0.000534	0.003942	0.003178	B2M/PDIA
CC	GO:003066	Golgi-asso	14/907	112/19559	0.000675	0.004905	0.003954	B2M/HLA-
CC	GO:003190	endosome	7/907	35/19559	0.000969	0.006943	0.005598	B2M/CTSB
CC	GO:003125	cell leading	34/907	421/19559	0.001257	0.008873	0.007154	S100B/S10
CC	GO:003601	endolysosc	5/907	20/19559	0.001836	0.012774	0.010299	CTSB/CTSL
CC	GO:000830	integrin co	6/907	31/19559	0.00266	0.018244	0.014709	ITGAV/ITG
CC	GO:000172	ruffle	17/907	179/19559	0.004088	0.027652	0.022294	S100B/S10
CC	GO:010100	ficolin-1-ri	13/907	124/19559	0.004992	0.03285	0.026484	CTSB/HSP9
CC	GO:190481	ficolin-1-ri	13/907	124/19559	0.004992	0.03285	0.026484	CTSB/HSP9
CC	GO:007143	invadopodi	4/907	16/19559	0.005345	0.034344	0.027689	PLAUR/PA
CC	GO:003013	transport v	31/907	410/19559	0.00536	0.034344	0.027689	B2M/HLA-
CC	GO:001632	apical plas	28/907	361/19559	0.005626	0.03558	0.028685	CTSB/CTSL
CC	GO:000566	transcriptic	31/907	413/19559	0.005943	0.037107	0.029917	NFYA/RELB
CC	GO:009856	cytoplasmi	17/907	188/19559	0.00666	0.041054	0.033099	S100A6/G
CC	GO:000577	multivesicu	8/907	62/19559	0.007628	0.045949	0.037045	CTSL/SFTP
CC	GO:001660	PML body	11/907	102/19559	0.007642	0.045949	0.037045	PML/ISG20
CC	GO:009057	RNA polym	15/907	161/19559	0.008007	0.047553	0.038338	NFYA/PPA
CC	GO:190255	serine/thre	10/907	89/19559	0.008104	0.047553	0.038338	IKBKG/ACV
CC	GO:003152	filopodium	4/907	18/19559	0.008348	0.0484	0.039021	HLA-G/ITG
CC	GO:190291	protein kin	11/907	104/19559	0.008807	0.050456	0.040679	IKBKG/ACV
CC	GO:000564	nuclear en	3/907	10/19559	0.009335	0.052739	0.042519	CACYBP/IG
CC	GO:000989	cytoplasmi	15/907	164/19559	0.009422	0.052739	0.042519	S100A6/G
CC	GO:000577	late endos	22/907	278/19559	0.010533	0.058291	0.046996	CD1E/CTSL
MF	GO:004801	receptor li	177/879	487/18352	2.42E-110	1.85E-107	1.37E-107	IFNG/LTA/
MF	GO:003054	signaling re	177/879	492/18352	1.87E-109	7.13E-107	5.29E-107	IFNG/LTA/
MF	GO:000512	cytokine re	110/879	271/18352	1.15E-73	2.94E-71	2.18E-71	IFNG/LTA/
MF	GO:000512	cytokine ac	103/879	235/18352	5.02E-73	9.59E-71	7.11E-71	IFNG/LTA/
MF	GO:000808	growth fac	68/879	162/18352	9.77E-47	1.49E-44	1.11E-44	CXCL12/TG
MF	GO:000382	antigen bir	69/879	168/18352	1.21E-46	1.54E-44	1.14E-44	CD1C/CD1
MF	GO:001995	cytokine bi	55/879	135/18352	3.98E-37	3.80E-35	2.82E-35	CD4/CCR1
MF	GO:014037	immune re	55/879	135/18352	3.98E-37	3.80E-35	2.82E-35	CD4/FCER1
MF	GO:000489	cytokine re	47/879	97/18352	3.58E-36	3.04E-34	2.25E-34	CD4/CCR1
MF	GO:007085	growth fac	48/879	141/18352	2.48E-28	1.90E-26	1.41E-26	ERAP1/IL1
MF	GO:000800	chemokine	28/879	49/18352	1.10E-24	7.65E-23	5.67E-23	CXCL14/CX
MF	GO:003498	immunoglo	34/879	80/18352	3.90E-24	2.48E-22	1.84E-22	IGHE/IGHG
MF	GO:004237	chemokine	32/879	70/18352	5.20E-24	3.06E-22	2.27E-22	CXCL14/CX
MF	GO:003281	tumor necr	26/879	48/18352	3.41E-22	1.86E-20	1.38E-20	LTA/TNF/S
MF	GO:000516	tumor necr	21/879	31/18352	4.32E-21	2.20E-19	1.63E-19	LTA/TNF/S
MF	GO:000166	G protein-c	58/879	293/18352	1.30E-20	6.21E-19	4.61E-19	CXCL14/CX
MF	GO:001983	growth fac	35/879	136/18352	1.23E-16	5.53E-15	4.10E-15	CXCL13/IT
MF	GO:000852	G protein-c	36/879	148/18352	3.17E-16	1.35E-14	9.98E-15	CCR10/F2R

MF	GO:000165	peptide rec	36/879	152/18352	7.89E-16	3.17E-14	2.35E-14	CCR10/F2R
MF	GO:004802	CCR chemc	20/879	47/18352	9.35E-15	3.57E-13	2.65E-13	CXCL13/XC
MF	GO:000517	hormone a	31/879	122/18352	1.01E-14	3.67E-13	2.72E-13	ADIPOQ/C
MF	GO:001995	C-C chemo	15/879	24/18352	1.24E-14	4.32E-13	3.20E-13	CCR10/CXC
MF	GO:001995	chemokine	17/879	33/18352	1.79E-14	5.94E-13	4.40E-13	CCR10/ITG
MF	GO:000163	G protein-c	15/879	26/18352	6.72E-14	2.05E-12	1.52E-12	CCR10/CXC
MF	GO:000495	chemokine	15/879	26/18352	6.72E-14	2.05E-12	1.52E-12	CCR10/CXC
MF	GO:000487	nuclear rec	20/879	52/18352	9.61E-14	2.72E-12	2.01E-12	PPARG/VD
MF	GO:009853	ligand-acti	20/879	52/18352	9.61E-14	2.72E-12	2.01E-12	PPARG/VD
MF	GO:001649	C-C chemo	14/879	23/18352	1.65E-13	4.50E-12	3.34E-12	CCR10/CXC
MF	GO:000471	protein tyr	30/879	135/18352	1.21E-12	3.18E-11	2.36E-11	EIF2AK2/TY
MF	GO:004205	chemoattra	16/879	37/18352	3.35E-12	8.53E-11	6.33E-11	CXCL10/VE
MF	GO:004227	peptide bir	46/879	308/18352	6.17E-12	1.52E-10	1.13E-10	CALR/CD1
MF	GO:001919	transmemb	20/879	80/18352	7.54E-10	1.80E-08	1.33E-08	HJV/PDGF
MF	GO:199078	protein tyr	22/879	98/18352	9.95E-10	2.30E-08	1.71E-08	CD4/HSP9
MF	GO:000372	double-stra	19/879	76/18352	2.00E-09	4.45E-08	3.30E-08	HSP90AB1/
MF	GO:004438	ubiquitin-li	42/879	316/18352	2.04E-09	4.45E-08	3.30E-08	CALR/HSPA
MF	GO:003321	amide bind	47/879	381/18352	2.67E-09	5.67E-08	4.20E-08	CALR/CD1
MF	GO:000517	integrin bir	26/879	144/18352	4.51E-09	9.15E-08	6.78E-08	CALR/ICAM
MF	GO:000178	phosphoty	14/879	42/18352	4.55E-09	9.15E-08	6.78E-08	SOCS3/MA
MF	GO:000514	interleukin	9/879	16/18352	1.08E-08	2.07E-07	1.53E-07	ERAP1/IL1
MF	GO:003162	ubiquitin p	39/879	297/18352	1.08E-08	2.07E-07	1.53E-07	CALR/HSPA
MF	GO:004530	protein ph	15/879	53/18352	1.61E-08	3.00E-07	2.23E-07	SOCS3/MA
MF	GO:000471	non-memb	14/879	46/18352	1.73E-08	3.14E-07	2.33E-07	EIF2AK2/TY
MF	GO:004549	chemorepe	11/879	28/18352	2.90E-08	5.15E-07	3.82E-07	SEMA3A/S
MF	GO:003021	semaphori	10/879	23/18352	3.91E-08	6.64E-07	4.92E-07	SEMA3A/S
MF	GO:003818	pattern rec	10/879	23/18352	3.91E-08	6.64E-07	4.92E-07	PGLYRP1/P
MF	GO:004523	CXCR chem	9/879	18/18352	4.19E-08	6.96E-07	5.16E-07	CXCL8/CXC
MF	GO:004260	peptide an	11/879	31/18352	1.00E-07	1.63E-06	1.21E-06	HLA-A/HLA
MF	GO:000370	steroid hor	10/879	26/18352	1.59E-07	2.53E-06	1.88E-06	ESR2/ESRR
MF	GO:001502	coreceptor	13/879	48/18352	2.59E-07	4.04E-06	2.99E-06	CD4/HJV/IT
MF	GO:000515	epidermal	11/879	34/18352	2.97E-07	4.53E-06	3.36E-06	PLSCR1/VA
MF	GO:001715	semaphori	7/879	12/18352	3.62E-07	5.42E-06	4.02E-06	PLXNA1/PL
MF	GO:004256	hormone b	17/879	84/18352	3.90E-07	5.73E-06	4.25E-06	CALR/PIK3
MF	GO:005121	phosphopr	17/879	85/18352	4.66E-07	6.72E-06	4.98E-06	SOCS3/MA
MF	GO:001920	kinase regu	29/879	216/18352	5.15E-07	7.28E-06	5.40E-06	HSP90AB1/
MF	GO:003361	receptor se	10/879	29/18352	5.26E-07	7.31E-06	5.42E-06	SRC/BMP2/
MF	GO:007070	BMP recep	7/879	13/18352	7.52E-07	1.01E-05	7.51E-06	SRC/BMP2/
MF	GO:004354	phosphatic	10/879	30/18352	7.56E-07	1.01E-05	7.51E-06	PDGFRB/PI
MF	GO:000471	transmemb	14/879	61/18352	8.29E-07	1.09E-05	8.09E-06	PDGFRB/E
MF	GO:007069	transmemb	9/879	24/18352	8.69E-07	1.12E-05	8.34E-06	SRC/BMP2/
MF	GO:000161	virus recep	15/879	74/18352	1.83E-06	2.30E-05	1.70E-05	CD4/ICAM1
MF	GO:014027	exogenous	15/879	74/18352	1.83E-06	2.30E-05	1.70E-05	CD4/ICAM1
MF	GO:000153	lipopolysac	10/879	33/18352	2.04E-06	2.52E-05	1.87E-05	TLR2/LBP/L
MF	GO:000503	tumor necr	6/879	10/18352	2.11E-06	2.56E-05	1.90E-05	TNFRSF11A
MF	GO:004693	1-phospha	7/879	16/18352	4.42E-06	5.27E-05	3.91E-05	SOCS3/SO
MF	GO:000553	glycosamin	28/879	232/18352	6.67E-06	7.80E-05	5.78E-05	CXCL10/CX
MF	GO:003097	receptor ty	14/879	72/18352	6.74E-06	7.80E-05	5.78E-05	BLNK/PIK3
MF	GO:003802	cargo rece	14/879	73/18352	7.97E-06	9.09E-05	6.74E-05	TFRC/TFR2
MF	GO:000503	death rece	6/879	12/18352	8.55E-06	9.34E-05	6.92E-05	TNFRSF11A

MF	GO:000516	neurotroph	6/879	12/18352	8.55E-06	9.34E-05	6.92E-05	PIK3R1/NG
MF	GO:003532	Toll-like re	6/879	12/18352	8.55E-06	9.34E-05	6.92E-05	S100A9/S1
MF	GO:001617	superoxide	6/879	13/18352	1.52E-05	0.000164	0.000122	NOX4/DU
MF	GO:000512	death rece	7/879	20/18352	2.53E-05	0.000264	0.000196	FASLG/NG
MF	GO:003501	phosphatic	7/879	20/18352	2.53E-05	0.000264	0.000196	SOCS3/SO
MF	GO:000517	vascular er	6/879	14/18352	2.56E-05	0.000264	0.000196	VEGFA/VE
MF	GO:001988	protein kin	23/879	185/18352	2.70E-05	0.000275	0.000204	HSP90AB1/
MF	GO:000202	protease b	19/879	137/18352	2.92E-05	0.000293	0.000217	ADRM1/LC
MF	GO:000462	phospholip	8/879	28/18352	3.54E-05	0.000351	0.00026	PDIA3/CCL
MF	GO:005142	hormone r	22/879	177/18352	4.02E-05	0.000391	0.00029	CALR/OASL
MF	GO:000495	icosanoid r	6/879	15/18352	4.09E-05	0.000391	0.00029	PPARG/PT
MF	GO:000516	platelet-de	6/879	15/18352	4.09E-05	0.000391	0.00029	VEGFA/PD
MF	GO:000549	steroid bin	16/879	106/18352	4.31E-05	0.000407	0.000302	PDIA2/CET
MF	GO:000122	transcriptio	8/879	29/18352	4.69E-05	0.000437	0.000324	AR/NR4A3/
MF	GO:004830	calcium-de	14/879	85/18352	4.81E-05	0.000442	0.000328	S100A9/S1
MF	GO:007172	lipopeptide	5/879	10/18352	5.13E-05	0.000467	0.000346	CD1C/CD1
MF	GO:000820	heparin bir	21/879	169/18352	6.00E-05	0.000539	0.0004	CXCL10/CX
MF	GO:000518	neuropepti	8/879	30/18352	6.12E-05	0.000539	0.0004	CORT/GRP/
MF	GO:000395	NAD+ nucl	6/879	16/18352	6.28E-05	0.000539	0.0004	TLR2/IL18R
MF	GO:005013	NAD(P)+ nu	6/879	16/18352	6.28E-05	0.000539	0.0004	TLR2/IL18R
MF	GO:006180	NAD+ nucl	6/879	16/18352	6.28E-05	0.000539	0.0004	TLR2/IL18R
MF	GO:000550	fatty acid b	9/879	39/18352	7.37E-05	0.000625	0.000463	S100A9/S1
MF	GO:001986	IgG binding	5/879	11/18352	9.04E-05	0.000759	0.000563	FCER1G/FC
MF	GO:000516	transformin	7/879	24/18352	9.54E-05	0.000784	0.000581	TGFB1/AM
MF	GO:001986	immunoglo	7/879	24/18352	9.54E-05	0.000784	0.000581	CD4/FCER1
MF	GO:000551	collagen bi	12/879	70/18352	0.000111	0.000899	0.000666	CTSB/CTSL/
MF	GO:002302	MHC prote	7/879	25/18352	0.000127	0.001022	0.000757	HLA-DMB/
MF	GO:001704	peptide ho	10/879	51/18352	0.000129	0.001025	0.00076	PIK3R1/ED
MF	GO:004283	peptidogly	6/879	18/18352	0.000134	0.001056	0.000783	PGLYRP1/P
MF	GO:008972	caspase bir	5/879	12/18352	0.000149	0.001161	0.00086	RIPK2/NLR
MF	GO:000443	phosphatic	7/879	26/18352	0.000167	0.001287	0.000954	CCL5/CCR5
MF	GO:000467	transmemb	6/879	19/18352	0.000188	0.001423	0.001055	HJV/LTBP1/
MF	GO:005066	oxidoreduc	6/879	19/18352	0.000188	0.001423	0.001055	NOX4/DU
MF	GO:003970	co-recepto	5/879	13/18352	0.000232	0.001741	0.00129	TFR2/BMP
MF	GO:000154	amyloid-be	12/879	77/18352	0.000281	0.002065	0.001531	TLR2/MSR
MF	GO:001990	protein pho	18/879	149/18352	0.000281	0.002065	0.001531	STAT1/MA
MF	GO:005084	extracellula	10/879	57/18352	0.000336	0.002444	0.001812	TINAGL1/V
MF	GO:005142	peptide ho	6/879	21/18352	0.000346	0.00248	0.001838	GNRH1/PT
MF	GO:004454	S100 prote	5/879	14/18352	0.000347	0.00248	0.001838	S100B/S10
MF	GO:003369	sialic acid b	6/879	22/18352	0.000457	0.003235	0.002398	ADIPOQ/C
MF	GO:006162	RNA polym	26/879	267/18352	0.000492	0.003445	0.002553	CALR/OASL
MF	GO:000184	opsonin bir	5/879	15/18352	0.0005	0.003445	0.002553	CALR/ITGA
MF	GO:003604	long-chain	5/879	15/18352	0.0005	0.003445	0.002553	S100A9/S1
MF	GO:001650	peptidase a	8/879	40/18352	0.000526	0.003589	0.00266	PSME2/PS
MF	GO:000515	insulin rece	6/879	23/18352	0.000594	0.003948	0.002926	SRC/PIK3R
MF	GO:005043	transformin	6/879	23/18352	0.000594	0.003948	0.002926	ITGAV/LTB
MF	GO:003329	monocarbo	11/879	72/18352	0.000594	0.003948	0.002926	S100A9/S1
MF	GO:004216	SH2 domai	8/879	41/18352	0.000627	0.004126	0.003059	SRC/PTK2/
MF	GO:000122	transcriptio	9/879	51/18352	0.000632	0.004126	0.003059	HDGF/AR/
MF	GO:006113	peptidase r	23/879	229/18352	0.000664	0.004298	0.003186	PSME2/PS

MF	GO:000515	insulin-like	5/879	16/18352	0.000699	0.004416	0.003273	SOCS1/ARF
MF	GO:000803	high-densit	5/879	16/18352	0.000699	0.004416	0.003273	ABCA1/SCA
MF	GO:005070	CARD dom	5/879	16/18352	0.000699	0.004416	0.003273	CARD11/CA
MF	GO:004228	MHC prote	8/879	42/18352	0.000742	0.004646	0.003444	CD4/KLRD1
MF	GO:007185	neuropepti	7/879	33/18352	0.000808	0.005018	0.00372	EDN3/APLN
MF	GO:000495	prostaglan	4/879	10/18352	0.00087	0.005362	0.003975	PPARG/PTC
MF	GO:003418	apolipopro	5/879	17/18352	0.000952	0.005819	0.004313	MAPT/ABC
MF	GO:007181	lipoprotein	7/879	34/18352	0.000976	0.005871	0.004352	MAPT/MSF
MF	GO:007181	protein-lipi	7/879	34/18352	0.000976	0.005871	0.004352	MAPT/MSF
MF	GO:001990	phosphatas	20/879	194/18352	0.001052	0.006281	0.004656	STAT1/MA
MF	GO:000203	p53 bindin	10/879	66/18352	0.001113	0.006593	0.004887	DAXX/HDA
MF	GO:000495	prostanoid	4/879	11/18352	0.001316	0.007617	0.005646	PPARG/PTC
MF	GO:003199	thioesteras	4/879	11/18352	0.001316	0.007617	0.005646	TRAF3/TRA
MF	GO:005078	RAGE recep	4/879	11/18352	0.001316	0.007617	0.005646	S100A9/S1
MF	GO:000196	fibronectin	6/879	27/18352	0.001478	0.008491	0.006294	CTSL/VEGF
MF	GO:003029	protein tyr	5/879	19/18352	0.001652	0.009418	0.006981	CCL5/EGF/
MF	GO:003503	histone ace	6/879	28/18352	0.001806	0.010221	0.007576	STAT1/NR4
MF	GO:000412	cytidine de	4/879	12/18352	0.0019	0.010593	0.007852	APOBEC3G
MF	GO:000487	complemen	4/879	12/18352	0.0019	0.010593	0.007852	C5AR1/CM
MF	GO:003024	carbohydra	24/879	267/18352	0.002363	0.01308	0.009696	CALR/KLRC
MF	GO:004317	alcohol bin	11/879	86/18352	0.002623	0.014307	0.010605	RBP1/RBP4
MF	GO:000502	transformi	4/879	13/18352	0.00264	0.014307	0.010605	LTBP1/BMI
MF	GO:003612	BMP bindir	4/879	13/18352	0.00264	0.014307	0.010605	HJV/GDF5/
MF	GO:000184	complemen	5/879	21/18352	0.00267	0.014363	0.010646	CALR/PTX3
MF	GO:004288	amide tran	8/879	51/18352	0.002739	0.014634	0.010847	AZGP1/TAF
MF	GO:190468	peptide tra	6/879	31/18352	0.003123	0.016572	0.012284	AZGP1/TAF
MF	GO:001692	nuclear rec	12/879	101/18352	0.003203	0.016875	0.012509	CALR/SRC/
MF	GO:000467	protein ser	34/879	435/18352	0.003573	0.018695	0.013857	HJV/EIF2AK
MF	GO:003525	nuclear hor	15/879	144/18352	0.003841	0.01994	0.01478	CALR/OASL
MF	GO:190168	sulfur comp	23/879	262/18352	0.003863	0.01994	0.01478	CXCL10/CX
MF	GO:004302	cysteine-ty	7/879	43/18352	0.004023	0.02063	0.015292	ARRB1/BIR
MF	GO:004633	SMAD bind	10/879	79/18352	0.004353	0.022173	0.016436	PML/FOS/E
MF	GO:003525	glucocortic	4/879	15/18352	0.004669	0.02347	0.017397	NR4A1/NR
MF	GO:009715	cysteine-ty	4/879	15/18352	0.004669	0.02347	0.017397	CASP1/PYC
MF	GO:001679	hydrolase a	6/879	34/18352	0.005051	0.025089	0.018597	TLR2/IL18R
MF	GO:014029	DNA-bindir	28/879	347/18352	0.00506	0.025089	0.018597	CALR/OASL
MF	GO:006113	endopeptic	18/879	192/18352	0.00509	0.025089	0.018597	PSME2/PSM
MF	GO:003525	steroid hor	10/879	81/18352	0.005211	0.025523	0.018919	CALR/SRC/
MF	GO:003029	protein kin	10/879	82/18352	0.005687	0.027676	0.020515	LTF/CCL5/D
MF	GO:000510	fibroblast g	5/879	25/18352	0.005948	0.028763	0.02132	FGF10/FGF
MF	GO:002302	MHC class	4/879	16/18352	0.005993	0.028796	0.021345	HLA-DMB/
MF	GO:003140	carboxylic a	19/879	212/18352	0.006583	0.031435	0.023302	S100A9/S1
MF	GO:000504	scavenger r	7/879	47/18352	0.006658	0.031593	0.023418	MSR1/DMI
MF	GO:000550	retinoid bir	6/879	36/18352	0.006746	0.031814	0.023582	PTGDS/RBF
MF	GO:003293	sterol bind	8/879	59/18352	0.006823	0.031979	0.023705	CETP/PMP2
MF	GO:003016	low-density	4/879	17/18352	0.007544	0.035143	0.02605	MSR1/SCA
MF	GO:001984	isoprenoid	6/879	37/18352	0.007733	0.035804	0.02654	PTGDS/RBF
MF	GO:000470	MAP kinase	4/879	18/18352	0.009337	0.042717	0.031664	MAPK3/PA
MF	GO:004696	retinoid X r	4/879	18/18352	0.009337	0.042717	0.031664	PPARG/VD
MF	GO:001920	kinase acti	10/879	89/18352	0.010036	0.045579	0.033786	LTF/CCL5/D

MF	GO:001712	SH3 domai	13/879	131/18352	0.010143	0.045579	0.033786	MAPT/PLS
MF	GO:003631	phosphatic	3/879	10/18352	0.010202	0.045579	0.033786	PIK3R1/CB
MF	GO:004356	insulin rece	3/879	10/18352	0.010202	0.045579	0.033786	PIK3R1/PIK
MF	GO:000814	drug bindin	11/879	104/18352	0.011037	0.049025	0.03634	HSP90AB1/
MF	GO:004323	laminin bin	5/879	29/18352	0.011357	0.050153	0.037176	TINAGL1/IT
MF	GO:004317	organic aci	19/879	224/18352	0.011531	0.050629	0.037528	S100A9/S1
MF	GO:004698	protein het	25/879	321/18352	0.011862	0.051786	0.038386	CYBB/IKBK
MF	GO:000486	protein kin	8/879	65/18352	0.012095	0.052505	0.03892	SOCS3/SO
MF	GO:004840	platelet-de	3/879	11/18352	0.013534	0.058417	0.043302	PDGFRB/P
MF	GO:003169	adrenergic	4/879	20/18352	0.013704	0.058821	0.043601	ARRB1/AD

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04060	Cytokine-c	144/643	295/8096	6.07E-83	1.54E-80	6.78E-81	CD4/IFNG/	144
hsa04061	Viral prote	58/643	100/8096	1.69E-38	2.15E-36	9.44E-37	LTA/CXCL1	58
hsa05169	Epstein-Ba	74/643	202/8096	1.51E-31	1.28E-29	5.63E-30	B2M/CALR	74
hsa04062	Chemokine	71/643	192/8096	1.39E-30	8.83E-29	3.88E-29	CXCL14/CX	71
hsa04650	Natural kill	55/643	131/8096	4.20E-27	2.14E-25	9.38E-26	FCER1G/HL	55
hsa04630	JAK-STAT s	59/643	162/8096	4.12E-25	1.74E-23	7.65E-24	IFNG/IFNL1	59
hsa05417	Lipid and a	66/643	215/8096	3.73E-23	1.35E-21	5.95E-22	HSPA2/HSP	66
hsa05323	Rheumatoi	40/643	93/8096	1.88E-20	5.96E-19	2.62E-19	CTSL/HLA-	40
hsa04620	Toll-like re	42/643	104/8096	3.75E-20	1.06E-18	4.65E-19	CXCL8/CXC	42
hsa05163	Human cyt	63/643	225/8096	8.30E-20	2.11E-18	9.26E-19	B2M/CALR	63
hsa05164	Influenza A	54/643	172/8096	1.34E-19	2.87E-18	1.26E-18	HLA-DMB/	54
hsa04668	TNF signali	43/643	112/8096	1.35E-19	2.87E-18	1.26E-18	ICAM1/LTA	43
hsa04064	NF-kappa B	41/643	104/8096	3.09E-19	6.03E-18	2.65E-18	ICAM1/LTA	41
hsa05167	Kaposi sarc	57/643	194/8096	4.31E-19	7.82E-18	3.43E-18	HLA-A/HLA	57
hsa04380	Osteoclast	45/643	128/8096	1.12E-18	1.84E-17	8.07E-18	IFNG/RELB	45
hsa05162	Measles	47/643	139/8096	1.16E-18	1.84E-17	8.07E-18	HSPA2/TLR	47
hsa04621	NOD-like re	53/643	184/8096	2.12E-17	3.16E-16	1.39E-16	CTSB/HSP9	53
hsa04659	Th17 cell d	39/643	108/8096	8.43E-17	1.19E-15	5.23E-16	CD4/HLA-D	39
hsa04660	T cell recep	38/643	104/8096	1.34E-16	1.79E-15	7.87E-16	CD4/IFNG/	38
hsa04657	IL-17 signal	36/643	94/8096	1.49E-16	1.89E-15	8.30E-16	HSP90AA1/	36
hsa05170	Human imm	56/643	212/8096	1.89E-16	2.29E-15	1.00E-15	B2M/CALR	56
hsa04010	MAPK signa	66/643	294/8096	2.48E-15	2.86E-14	1.26E-14	HSPA2/REL	66
hsa05142	Chagas dise	35/643	102/8096	2.03E-14	2.24E-13	9.84E-14	CALR/IFNG	35
hsa04625	C-type lect	35/643	104/8096	3.98E-14	4.21E-13	1.85E-13	FCER1G/RE	35
hsa04612	Antigen pro	30/643	78/8096	4.63E-14	4.71E-13	2.07E-13	B2M/CALR	30
hsa05160	Hepatitis C	43/643	157/8096	1.76E-13	1.72E-12	7.55E-13	IFNG/CXCL	43
hsa05135	Yersinia inf	39/643	137/8096	6.34E-13	5.96E-12	2.62E-12	CD4/CXCL8	39
hsa04933	AGE-RAGE	32/643	100/8096	2.41E-12	2.19E-11	9.62E-12	ICAM1/CXC	32
hsa04015	Rap1 signa	49/643	210/8096	2.62E-12	2.29E-11	1.01E-11	VEGFA/F2R	49
hsa05171	Coronaviru	52/643	232/8096	2.89E-12	2.44E-11	1.07E-11	CXCL8/CXC	52
hsa05321	Inflammato	25/643	65/8096	6.24E-12	5.11E-11	2.25E-11	HLA-DMB/	25
hsa05133	Pertussis	27/643	76/8096	8.01E-12	6.09E-11	2.68E-11	CXCL8/CXC	27
hsa04151	PI3K-Akt si	67/643	354/8096	8.15E-12	6.09E-11	2.68E-11	HSP90AA1/	67
hsa05330	Allograft re	19/643	38/8096	8.15E-12	6.09E-11	2.68E-11	HLA-A/HLA	19
hsa05140	Leishmania	27/643	77/8096	1.14E-11	8.29E-11	3.64E-11	HLA-DMB/	27
hsa04940	Type I diab	20/643	43/8096	1.26E-11	8.89E-11	3.90E-11	HLA-A/HLA	20
hsa01521	EGFR tyros	27/643	79/8096	2.28E-11	1.56E-10	6.87E-11	VEGFA/MA	27
hsa05332	Graft-versu	19/643	42/8096	7.60E-11	5.08E-10	2.23E-10	HLA-A/HLA	19

hsa05166	Human T-c	48/643	222/8096	7.96E-11	5.19E-10	2.28E-10	B2M/CALR	48
hsa05218	Melanoma	25/643	72/8096	8.56E-11	5.43E-10	2.39E-10	MAPK3/PD	25
hsa05340	Primary im	18/643	38/8096	9.30E-11	5.76E-10	2.53E-10	CD4/TAP1/	18
hsa04014	Ras signalir	49/643	232/8096	1.21E-10	7.30E-10	3.21E-10	VEGFA/MA	49
hsa04012	ErbB signal	27/643	85/8096	1.56E-10	9.19E-10	4.04E-10	MAPK3/SR	27
hsa05161	Hepatitis B	39/643	162/8096	1.79E-10	1.03E-09	4.53E-10	CXCL8/TGF	39
hsa04658	Th1 and Th	28/643	92/8096	2.19E-10	1.24E-09	5.44E-10	CD4/HLA-D	28
hsa04510	Focal adhe	44/643	201/8096	3.31E-10	1.83E-09	8.04E-10	VEGFA/ITG	44
hsa04662	B cell recep	26/643	82/8096	3.57E-10	1.93E-09	8.49E-10	MAPK3/CD	26
hsa05152	Tuberculos	41/643	180/8096	3.77E-10	1.99E-09	8.76E-10	FCER1G/HL	41
hsa05235	PD-L1 expr	27/643	89/8096	5.02E-10	2.60E-09	1.14E-09	CD4/IFNG/	27
hsa05418	Fluid shear	34/643	139/8096	1.73E-09	8.78E-09	3.86E-09	CTSL/HSP9	34
hsa04672	Intestinal i	19/643	49/8096	1.88E-09	9.35E-09	4.11E-09	HLA-DMB/	19
hsa04360	Axon guida	40/643	182/8096	1.91E-09	9.35E-09	4.11E-09	CXCL12/M	40
hsa05416	Viral myoc	21/643	60/8096	2.38E-09	1.14E-08	5.01E-09	HLA-A/HLA	21
hsa05144	Malaria	19/643	50/8096	2.82E-09	1.32E-08	5.82E-09	ICAM1/IFN	19
hsa04210	Apoptosis	33/643	136/8096	3.75E-09	1.73E-08	7.61E-09	CTSB/CTSL	33
hsa05145	Toxoplasm	29/643	112/8096	6.88E-09	3.12E-08	1.37E-08	HLA-DMB/	29
hsa05214	Glioma	23/643	75/8096	7.76E-09	3.46E-08	1.52E-08	MAPK3/PD	23
hsa05215	Prostate ca	26/643	97/8096	1.92E-08	8.42E-08	3.70E-08	HSP90AA1,	26
hsa04145	Phagosom	34/643	152/8096	2.01E-08	8.66E-08	3.81E-08	CALR/CTSL	34
hsa05205	Proteoglyc	41/643	205/8096	2.21E-08	9.34E-08	4.10E-08	CTSL/TGFB	41
hsa05224	Breast can	33/643	147/8096	2.97E-08	1.23E-07	5.39E-08	MAPK3/WI	33
hsa04640	Hematopoi	26/643	99/8096	3.05E-08	1.23E-07	5.39E-08	CD1C/CD1	26
hsa04664	Fc epsilon	21/643	68/8096	3.05E-08	1.23E-07	5.39E-08	FCER1G/TN	21
hsa04810	Regulation	42/643	218/8096	4.58E-08	1.82E-07	7.99E-08	CXCL12/TM	42
hsa04917	Prolactin si	21/643	70/8096	5.37E-08	2.10E-07	9.22E-08	STAT1/SOC	21
hsa04066	HIF-1 signa	27/643	109/8096	6.30E-08	2.42E-07	1.06E-07	IFNG/CYBB	27
hsa05223	Non-small	21/643	72/8096	9.25E-08	3.51E-07	1.54E-07	MAPK3/NR	21
hsa05134	Legionellos	18/643	57/8096	2.03E-07	7.60E-07	3.34E-07	HSPA2/CXC	18
hsa05211	Renal cell	20/643	69/8096	2.10E-07	7.73E-07	3.39E-07	TGFB1/VEG	20
hsa04217	Necroptosi	33/643	159/8096	2.17E-07	7.87E-07	3.46E-07	HSP90AA1,	33
hsa05146	Amoebiasis	25/643	102/8096	2.42E-07	8.67E-07	3.81E-07	CD1C/CD1	25
hsa05212	Pancreatic	21/643	76/8096	2.57E-07	9.05E-07	3.98E-07	TGFB1/STA	21
hsa05320	Autoimmu	17/643	53/8096	3.45E-07	1.20E-06	5.28E-07	HLA-A/HLA	17
hsa05165	Human pap	53/643	331/8096	4.89E-07	1.68E-06	7.37E-07	HLA-A/HLA	53
hsa05221	Acute mye	19/643	67/8096	6.16E-07	2.09E-06	9.16E-07	PML/MAPK	19
hsa04350	TGF-beta s	23/643	94/8096	7.58E-07	2.53E-06	1.11E-06	IFNG/TGFB	23
hsa04622	RIG-I-like r	19/643	70/8096	1.29E-06	4.25E-06	1.87E-06	CXCL8/CXC	19
hsa04072	Phospholip	30/643	148/8096	1.31E-06	4.27E-06	1.88E-06	FCER1G/CX	30
hsa01522	Endocrine	23/643	98/8096	1.66E-06	5.35E-06	2.35E-06	MMP9/MA	23
hsa04370	VEGF signa	17/643	59/8096	1.89E-06	5.99E-06	2.63E-06	VEGFA/MA	17
hsa05222	Small cell l	22/643	92/8096	2.00E-06	6.27E-06	2.75E-06	ITGAV/TRA	22
hsa04670	Leukocyte	25/643	114/8096	2.26E-06	6.99E-06	3.07E-06	ICAM1/CXC	25
hsa05203	Viral carcin	36/643	204/8096	3.75E-06	1.15E-05	5.04E-06	HLA-A/HLA	36
hsa04020	Calcium sig	40/643	240/8096	4.75E-06	1.44E-05	6.31E-06	VEGFA/F2F	40
hsa05220	Chronic my	19/643	76/8096	4.93E-06	1.47E-05	6.48E-06	TGFB1/MA	19
hsa04666	Fc gamma	22/643	97/8096	5.10E-06	1.50E-05	6.58E-06	MAPK3/HC	22
hsa04935	Growth ho	25/643	119/8096	5.13E-06	1.50E-05	6.58E-06	STAT1/SOC	25
hsa04929	GnRH secre	17/643	64/8096	6.43E-06	1.86E-05	8.15E-06	MAPK3/AR	17

hsa03050	Proteasom	14/643	46/8096	7.56E-06	2.14E-05	9.39E-06	IFNG/PSM	14
hsa04610	Compleme	20/643	85/8096	7.57E-06	2.14E-05	9.39E-06	PROCR/PL	20
hsa05210	Colorectal	20/643	86/8096	9.15E-06	2.55E-05	1.12E-05	TGFB1/MA	20
hsa04218	Cellular se	29/643	156/8096	1.18E-05	3.26E-05	1.43E-05	HLA-A/HL	29
hsa04514	Cell adhesi	28/643	149/8096	1.35E-05	3.69E-05	1.62E-05	CD4/HLA-	28
hsa05202	Transcripti	33/643	192/8096	1.69E-05	4.56E-05	2.00E-05	CXCL8/MM	33
hsa05207	Chemical c	35/643	212/8096	2.30E-05	6.16E-05	2.71E-05	HSP90AA1	35
hsa05226	Gastric can	27/643	149/8096	3.78E-05	0.0001	4.39E-05	TGFB1/MA	27
hsa05150	Staphyloco	20/643	96/8096	5.07E-05	0.000133	5.84E-05	HLA-DMB/	20
hsa05219	Bladder ca	12/643	41/8096	5.24E-05	0.000136	5.96E-05	CXCL8/MM	12
hsa04926	Relaxin sig	24/643	129/8096	6.54E-05	0.000168	7.37E-05	TGFB1/MM	24
hsa05231	Choline me	20/643	98/8096	6.91E-05	0.000175	7.70E-05	MAPK3/PD	20
hsa04613	Neutrophil	31/643	190/8096	8.44E-05	0.000212	9.33E-05	TLR2/CTSG	31
hsa04623	Cytosolic D	15/643	63/8096	8.96E-05	0.000223	9.80E-05	CXCL10/IL1	15
hsa05143	African try	11/643	37/8096	9.17E-05	0.000226	9.94E-05	ICAM1/IFN	11
hsa05225	Hepatocell	28/643	168/8096	0.000127	0.00031	0.000136	TGFB1/MA	28
hsa04722	Neurotrop	21/643	119/8096	0.000393	0.000952	0.000418	MAPK3/FA	21
hsa05310	Asthma	9/643	31/8096	0.000487	0.001168	0.000513	FCER1G/HL	9
hsa01524	Platinum d	15/643	73/8096	0.000507	0.001202	0.000528	MAPK3/FA	15
hsa05131	Shigellosis	35/643	247/8096	0.00052	0.001223	0.000537	CXCL8/IL1	35
hsa04068	FoxO signa	22/643	131/8096	0.000588	0.00137	0.000602	TGFB1/TN	22
hsa04611	Platelet ac	21/643	124/8096	0.000694	0.001603	0.000704	FCER1G/F2	21
hsa04550	Signaling p	23/643	143/8096	0.000831	0.001868	0.000821	MAPK3/W	23
hsa05017	Spinocere	23/643	143/8096	0.000831	0.001868	0.000821	NFYA/PSM	23
hsa05130	Pathogenic	29/643	197/8096	0.000831	0.001868	0.000821	CXCL8/IL1	29
hsa05020	Prion disea	37/643	273/8096	0.00086	0.001915	0.000841	HSPA2/HS	37
hsa05322	Systemic l	22/643	136/8096	0.000989	0.002184	0.000959	HLA-DMB/	22
hsa05120	Epithelial c	14/643	70/8096	0.001023	0.002241	0.000984	CXCL8/CXC	14
hsa04915	Estrogen si	22/643	138/8096	0.001205	0.002616	0.001149	HSPA2/HS	22
hsa04919	Thyroid ho	20/643	121/8096	0.00126	0.002712	0.001191	STAT1/ITG	20
hsa04540	Gap juncti	16/643	88/8096	0.001357	0.002896	0.001272	MAPK3/GN	16
hsa04080	Neuroactiv	43/643	342/8096	0.001596	0.003379	0.001484	CTSG/F2R/	43
hsa05168	Herpes sim	58/643	497/8096	0.001655	0.003468	0.001524	B2M/CALR	58
hsa04750	Inflammat	17/643	98/8096	0.001666	0.003468	0.001524	IL1B/F2RL1	17
hsa04920	Adipocyto	13/643	69/8096	0.002689	0.005552	0.002439	TNF/ADIP	13
hsa04390	Hippo sign	23/643	157/8096	0.002951	0.006046	0.002656	TGFB1/WN	23
hsa04024	cAMP sign	29/643	219/8096	0.004236	0.008608	0.003782	F2R/MAPK	29
hsa05132	Salmonella	32/643	249/8096	0.004363	0.008795	0.003863	HSP90AA1	32
hsa05010	Alzheimer	45/643	384/8096	0.004956	0.009912	0.004354	PSMC2/PS	45
hsa04071	Sphingolip	18/643	119/8096	0.005751	0.011412	0.005013	FCER1G/TN	18
hsa05100	Bacterial in	13/643	77/8096	0.00712	0.014019	0.006158	SRC/PTK2/	13
hsa04960	Aldosteron	8/643	37/8096	0.007414	0.014486	0.006363	MAPK3/PI	8
hsa05230	Central car	12/643	70/8096	0.008441	0.016367	0.00719	MAPK3/PD	12
hsa04213	Longevity r	11/643	62/8096	0.008853	0.017035	0.007483	HSPA2/HD	11
hsa04930	Type II dia	9/643	46/8096	0.009125	0.017427	0.007655	TNF/ADIP	9
hsa04211	Longevity r	14/643	89/8096	0.009993	0.018943	0.008321	ADIPOQ/P	14
hsa04932	Non-alcoh	21/643	155/8096	0.01072	0.020021	0.008795	CXCL8/TGF	21
hsa04934	Cushing sy	21/643	155/8096	0.01072	0.020021	0.008795	MAPK3/GN	21
hsa04115	p53 signal	12/643	73/8096	0.01174	0.021766	0.009561	TNFRSF10	12
hsa04923	Regulation	10/643	57/8096	0.013274	0.024432	0.010733	GNAI1/PT	10

hsa05213	Endometri	10/643	58/8096	0.014937	0.027295	0.01199	MAPK3/N	10
hsa04924	Renin secr	11/643	69/8096	0.019218	0.034868	0.015317	CTSB/GNA	11
hsa04928	Parathyroi	15/643	106/8096	0.019807	0.035681	0.015674	MAPK3/GN	15
hsa04520	Adherens j	11/643	71/8096	0.023387	0.041834	0.018377	MAPK3/SR	11
hsa04371	Apelin sign	18/643	138/8096	0.024636	0.043759	0.019223	MAPK3/GN	18
hsa04152	AMPK sign	16/643	120/8096	0.027433	0.048389	0.021257	ADIPOQ/P	16
hsa04725	Cholinergic	15/643	113/8096	0.033195	0.058149	0.025544	MAPK3/GN	15
hsa04215	Apoptosis	6/643	32/8096	0.03755	0.065141	0.028616	BIRC5/BID/	6
hsa04150	mTOR sign	19/643	155/8096	0.0377	0.065141	0.028616	TNF/MAPK	19
hsa04730	Long-term	9/643	60/8096	0.045799	0.078601	0.034529	MAPK3/GN	9

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