

100bp Window

GO group	Motifs	motif GC content	199 - 100	99 - TSS	-1 -- 100	-101 -- -200	-201 -- -300	-301 -- -400	-401 -- -500	-501 -- -600	-601 -- -700	-701 -- -800	-801 -- -900	-901 -- -1000	GO-classes	Unique motifs
transcription (930)	SP1.01	0.78	H	H	0	H							H	transcription GO	1	
regulation of transcription DNA dependent (1066)	SP1.01	0.78	H	H	0	H								transcription GO		
regulation of transcription (266)	SP1.01	0.78	0	0	0	0	H	0	H	M	0	0	0	transcription GO		
transcription (930)	WT1.01	0.77	H	H	H						0	H	H	transcription GO	2	
regulation of transcription DNA dependent (1066)	WT1.01	0.77			0					H	H			transcription GO		
development (530)	WT1.01	0.77	0	0	0	H		0	H	H	0	0	0	transcription GO		
regulation of transcription (266)	WT1.01	0.77	H	0	H	H		H	H	0	0	H	0	transcription GO		
regulation of transcription DNA dependent (1066)	HES1.02	0.76	0	0	0	M	H	0	H	H	0	0	H	transcription GO	3	
transcription (930)	MAZR.01	0.76	H		H	H					0	H	M	transcription GO	4	
regulation of transcription DNA dependent (1066)	MAZR.01	0.76	H	H	H	H				M	H		H	transcription GO		
development (530)	MAZR.01	0.76	0	0	0	H	H		H	M	0	H	0	transcription GO		
regulation of transcription (266)	MAZR.01	0.76	0	H	0	H	0	0	H	M	0	0	M	transcription GO		
transcription (930)	ZNF202.01	0.73	H	H	0	H		H		M	H		0	transcription GO	5	
regulation of transcription DNA dependent (1066)	ZNF202.01	0.73	H	0	0	H		H		M	H		M	transcription GO		
development (530)	ZNF202.01	0.73	0	0	H		H	0	H	0	0	0	0	transcription GO		
transcription (930)	AP2.01	0.73	H	0	0	H				H	H	H	H	transcription GO	6	
regulation of transcription DNA dependent (1066)	AP2.01	0.73	H	0	0	M				H	H	H	H	transcription GO		
development (530)	AP2.01	0.73	0	0	0	0		M	H	0	H	0	H	transcription GO		
regulation of transcription (266)	AP2.01	0.73	0	0	0					0	H	H	H	transcription GO		
transcription (930)	ZF5.01	0.72	0	0	0	H				H	H	H	H	transcription GO	7	
regulation of transcription DNA dependent (1066)	ZF5.01	0.72	H	0	0	H				H	H	H	H	transcription GO		
regulation of transcription (266)	ZF5.01	0.72	0	0	0	H		0	H	0	0	0	0	transcription GO		
transcription (930)	ZF9.01	0.72	H	H	0	0	H		H	H	H		M	transcription GO	8	
regulation of transcription DNA dependent (1066)	ZF9.01	0.72	H	H	0	0	H		H	H			H	transcription GO		
development (530)	ZF9.01	0.72	0	0	0	0	0	M	0	0	0	0	H	transcription GO		
regulation of transcription DNA dependent (1066)	EGR3.01	0.71	H	0	0	0	H		H	H	0	0	M	transcription GO	9	
regulation of transcription (266)	EGR3.01	0.71	0	0	0	0	0	0	0	0	H	0	M	transcription GO		
transcription (930)	NRF1_01	0.71	H	H	H	H				H	H	H	H	transcription GO	10	
regulation of transcription DNA dependent (1066)	NRF1_01	0.71	H	H	H					H	H	H	H	transcription GO		
transcription (930)	MYCMAX.03	0.7	0	0	0		H	H	0	H	0	H	0	transcription GO	11	
regulation of transcription DNA dependent (1066)	MYCMAX.03	0.7	0	0	0		H	0	H	H	0	H	0	transcription GO		
transcription (930)	ZBP89.01	0.7	H			0				H	M	0	0	transcription GO	12	
regulation of transcription DNA dependent (1066)	ZBP89.01	0.7	H							H	M	0	H	transcription GO		
development (530)	ZBP89.01	0.7	0	0	H		H	0	H	M	0	H	M	transcription GO		
transcription (930)	NGFIC.01	0.69	H	M	0	0	H	H	H	0	0	0	0	transcription GO	13	
regulation of transcription DNA dependent (1066)	NGFIC.01	0.69	H	M	0	0	H	H	H	0	H	0	0	transcription GO		
transcription (930)	CKROX_01	0.68	H		M	H	H		H		0	H	0	transcription GO	14	
regulation of transcription DNA dependent (1066)	CKROX_01	0.68	H		M					H	H		0	transcription GO		
development (530)	CKROX_01	0.68	0	0	0	H	H		H	0	0		0	transcription GO		
regulation of transcription (266)	CKROX_01	0.68	H	0		H	H	H	H	M	0	H	0	transcription GO		
transcription (930)	EGR1.02	0.68	H		H	H		H			H	H	H	transcription GO	15	
regulation of transcription DNA dependent (1066)	EGR1.02	0.68	H		0						H			transcription GO		
development (530)	EGR1.02	0.68	0	0	0	0	H	H	0	0	0	0	0	transcription GO		
regulation of transcription (266)	EGR1.02	0.68	H	0	0			H	H	0	0	0	0	transcription GO		
regulation of transcription DNA dependent (1066)	BKLF.01	0.68	0	0	0	0	0	0	H	0	0	0	M	transcription GO	16	
transcription (930)	GC.01	0.68	0	0	0	0	H	H		M	0	0	0	transcription GO	17	
regulation of transcription DNA dependent (1066)	GC.01	0.68	H	0	0	0	H	H	H	M	0	0	M	transcription GO		
development (530)	MZF1.01	0.68	0	0	H	H	0	H	M	0	H	0	0	transcription GO	18	
regulation of transcription DNA dependent (1066)	EGR1.01	0.67	H	0	0	H		0	H	M	0	H	H	transcription GO	19	
regulation of transcription DNA dependent (1066)	MTF-1.01	0.65	0	0	0	H	0		0	M	0	H	0	transcription GO	20	
transcription (930)	MAZ.01	0.65	H	0	0	H		H			H	H	H	transcription GO	21	

regulation of transcription DNA dependent (1066)	MAZ.01	0.65	H	H	0	H					H	H	transcription GO		
development (530)	MAZ.01	0.65	0	0	0	H	0	H	M	0	H	0	H	transcription GO	
regulation of transcription (266)	MAZ.01	0.65	0	0	0	H	H		H	M	0	H	0	transcription GO	
transcription (930)	ZIC2_01	0.65	H	0	0	0	H	M	0	0	0	M	0	transcription GO	22
regulation of transcription DNA dependent (1066)	ZIC2_01	0.65	H	0	0	0	H	0	0	0	0	M	0	transcription GO	
regulation of transcription DNA dependent (1066)	ATF6.01	0.64	0	0	0	M	0	M	0	0	H	0	H	transcription GO	23
transcription (930)	PLAG1_01	0.63	H	0	H	H	0	H		M	H	H	H	transcription GO	24
regulation of transcription DNA dependent (1066)	PLAG1_01	0.63	H	M	H	H	H				H		H	transcription GO	
development (530)	PLAG1_01	0.63	0	M	H	H	H	H	H	0	H	H	0	transcription GO	
regulation of transcription (266)	PLAG1_01	0.63	0	H	H	H	0	0	0	M	0	0	0	transcription GO	
transcription (930)	AHRARNT.02	0.62	0	0	0	0	0	H	0	0	0	0	M	transcription GO	25
regulation of transcription DNA dependent (1066)	AHRARNT.02	0.62	0	0	0	0	0	H	0	0	H	0	M	transcription GO	
regulation of transcription DNA dependent (1066)	HES1.01	0.62	0	0	0	M	H	H		0	0	H		transcription GO	26
regulation of transcription DNA dependent (1066)	MUSCLE_INI.02	0.62	0	0	0	H		H	0	H	0	0	0	transcription GO	27
regulation of transcription DNA dependent (1066)	MUSCLE_INI.01	0.61	0	0	0	H	H	M	0	H	0	0	0	transcription GO	28
regulation of transcription DNA dependent (1066)	ZNF76_143_01	0.6	0	0	0	0	0	0	M	H	H	0	0	transcription GO	29
transcription (930)	CDE.01	0.6	M	H	H	H	H	H	H	H	0	H	H	transcription GO	30
regulation of transcription DNA dependent (1066)	CDE.01	0.6	0	H	0	H		H				H	H	transcription GO	
regulation of transcription DNA dependent (1066)	ZBRK1_01	0.59	0	0	0	0	0	M	0	0	0	0	H	transcription GO	31
transcription (930)	E2F.02	0.59	0	H	H	H	0	0	H	H		0	0	transcription GO	32
regulation of transcription DNA dependent (1066)	E2F.02	0.59	0	0	0	H	0	0	H	H		0	0	transcription GO	
transcription (930)	TAXCREB.01	0.58	0	0	0	0	0	H	M	0	0	M	0	transcription GO	33
development (530)	PAX5.01	0.57	0	0	0	0	0	0	0	H	0	M	0	transcription GO	34
regulation of transcription DNA dependent (1066)	GAGA.01	0.56		0	H	0	H	H	H	M	0	0	M	transcription GO	35
development (530)	GAGA.01	0.56	0	0	H	H	H		H	0	0	0	0	transcription GO	
transcription (930)	E2F.03	0.54	0	H	H	H	0	H	0	0	M	0	0	transcription GO	36
regulation of transcription DNA dependent (1066)	E2F.03	0.54	0	H	H	H	0	H	0	0	M	0	0	transcription GO	
development (530)	GKLF.01	0.49	0		0	0	H	H	0	0	0	0	0	transcription GO	37
regulation of transcription DNA dependent (1066)	CAAT.01	0.49	0	0	H	H		0	0	0	0	0	0	transcription GO	38
development (530)	MTATA.01	0.47	0	0		0	0	0	0	0	0	0	0	transcription GO	39
protein amino acid phosphorylation (373)	SP1.01	0.78	0	0	H	0	0	H	M	H	0	H	0	general GO	
transcription RNA polyl promoter (190)	SP1.01	0.78	0	0	0	0	0	H	0	0	0	0	M	general GO	
small GTPase mediated signal transduction (124)	SP1.01	0.78	H		H	H	H	H	H	0	0	0	0	general GO	
intracellular protein transport (191)	SP1.01	0.78	H	M	H	H	0	0	0	0	0	0	0	general GO	
regulation of transcription from RNA polymerase II	SP1.01	0.78	H	0	0	0	0	0	0	0	0	0	0	general GO	
transcription RNA polyl promoter (190)	WT1.01	0.77	0	0	0	H	M	H	0	0	0	0	0	general GO	
regulation of transcription from RNA polymerase II	MAZR.01	0.76	M	0	H	H	0	H	0	M	0	0	0	general GO	
Wnt receptor signaling pathway (66)	AP2.01	0.73	H	0	0	H	H	0	0	0	M	0	0	general GO	
small GTPase mediated signal transduction (124)	ZF5.01	0.72	0	M	H	H	0	0	0	0	0	0	0	general GO	
transcription RNA polyl promoter (190)	NRF1_01	0.71	0	0	0		0	0	0	0	0	0	0	general GO	
intracellular protein transport (191)	NRF1_01	0.71	0	0		H	0	0	0	0	0	0	0	general GO	
nervous system development (225)	ZBP89.01	0.7	0	0	H	H	0	0	0	0	0	0	M	general GO	
potassium ion transport (108)	ZBP89.01	0.7	0	0	0	0	0	0	M	H	0	0	0	general GO	
regulation of transcription from RNA polymerase II	CKROX_01	0.68	M	H	0	M	0	H	0	0	0	0	0	general GO	
nervous system development (225)	CKROX_01	0.68	0	0	H	H	0	0	H	0	0	0		general GO	
small GTPase mediated signal transduction (124)	EGR1.02	0.68	H			H	H	0	H	0	0	0	0	general GO	
Wnt receptor signaling pathway (66)	EGR1.02	0.68	0	M	0	H	0	0	0	H	0	0	0	general GO	
protein amino acid phosphorylation (373)	GC.01	0.68	0	0	0	0	0	0		0	0	0	0	general GO	
intracellular protein transport (191)	GC.01	0.68	0	M	H	0	0	0	0	0	0	0	0	general GO	
intracellular protein transport (191)	EGR1.01	0.67	H	M	H	0	0	0	0	0	0	0	0	general GO	
chromatin modification (53)	HES1.01	0.62	0	0	0	0	0	0	0	M	0	H	0	general GO	
protein biosynthesis (197)	GABP.01	0.62	0	H		0	0	0	0	0	0	0	0	general GO	40
cation transport (99)	NRSF.01	0.62	0	0	M	0	0	0	0	0	0	0	H	general GO	41
inflammatory response (163)	NFKAPPAB.01	0.6	0	0		M	0	0	0	0	0	0	0	general GO	42
immune response (366)	NFKAPPAB.01	0.6	0	0			0	0	0	0	0	0	0	general GO	
intracellular protein transport (191)	ATF6.02	0.6	0	0	H	0	0	0	0	0	0	0	0	general GO	43
transcription RNA polyl promoter (190)	CDE.01	0.6	0	0	0	0	0	0	0	0	0		0	general GO	
response to DNA damage stimulus (117)	E2F.02	0.59	0		H	0	0	0	0	0	0	0	0	general GO	
nuclear mRNA splicing via spliceosome (94)	NRF2.01	0.57	0	0	H	0		0	0	0	0	0	0	general GO	44
protein biosynthesis (197)	NRF2.01	0.57	0	H		0	0	0	0	0	0	0	0	general GO	
protein targeting (37)	NRF2.01	0.57	0	0		0	0	0	0	0	0	0	0	general GO	
cation transport (99)	NRSE.01	0.57	0	0	M	0	0	0	0	0	0	0	H	general GO	45
signal transduction (1189)	NFKAPPAB.02	0.57	0	0		0	0	0	0	0	0	0	0	general GO	46
chemotaxis (98)	NFKAPPAB.02	0.57	0	0	H	M	0	0	0	0	0	0	0	general GO	

inflammatory response (163)	NFKAPPAB.02	0.57	0	0	H		0	0	0	0	0	0	0	0	general GO	
immune response (366)	NFKAPPAB.02	0.57	0	0			0	0	H	0	0	0	0	0	general GO	
chemotaxis (98)	NFKAPPAB65.01	0.55	0	0	H	M	0	0	0	0	0	0	0	0	general GO	47
inflammatory response (163)	NFKAPPAB65.01	0.55	0	0			0	0	0	0	0	0	0	0	general GO	
immune response (366)	NFKAPPAB65.01	0.55	0	0			0	0	H	0	0	0	0	0	general GO	
cell cell signaling (268)	NFKAPPAB65.01	0.55	0	0	H	M	0	0	0	0	0	0	0	0	general GO	
protein biosynthesis (197)	CETS1P54.01	0.55	0	H			0	0	0	0	0	0	0	0	general GO	48
protein biosynthesis (197)	YY1.01	0.55	0				0	0	0	0	0	0	0	0	general GO	49
chemotaxis (98)	CREL.01	0.55	0	0	H	M	0	0	0	0	0	0	0	0	general GO	50
inflammatory response (163)	CREL.01	0.55	0	0		M	0	0	0	0	0	0	0	0	general GO	
immune response (366)	CREL.01	0.55	0	0			0	0	0	H	0	0	0	0	general GO	
protein biosynthesis (197)	ELK1.02	0.55	0	H			0	0	0	0	0	0	0	0	general GO	51
signal transduction (1189)	NFKAPPAB.03	0.55	0	0			0	0	0	0	0	0	0	0	general GO	52
inflammatory response (163)	NFKAPPAB.03	0.55	0	0			0	0	0	0	0	0	0	0	general GO	
immune response (366)	NFKAPPAB.03	0.55	0	0			0	0	0	0	0	0	0	0	general GO	
response to virus (55)	NFKAPPAB.03	0.55	0	0	H	M	0	0	0	0	0	0	0	0	general GO	
inflammatory response (163)	MYCMAx.02	0.54	H	0	0	0	0	0	M	0	0	0	0	0	general GO	53
protein biosynthesis (197)	ELF2.01	0.54	0	H	M	0	0	0	0	0	0	0	0	0	general GO	54
protein biosynthesis (197)	FLI.01	0.53	0	H			0	0	0	0	0	0	0	0	general GO	55
DNA repair (148)	FLI.01	0.53	0	0	M	H	0	0	0	0	0	0	0	0	general GO	
response to DNA damage stimulus (117)	FLI.01	0.53	H	0	M	0	0	0	0	0	0	0	0	0	general GO	
protein biosynthesis (197)	STAF.01	0.53	0	0			0	0	0	0	0	0	0	0	general GO	56
protein biosynthesis (197)	STAT1.01	0.52	0	0			0	0	0	0	0	0	0	0	general GO	57
signal transduction (1189)	HIVEP1_01	0.52	0	0			0	0	0	0	0	0	0	0	general GO	58
chemotaxis (98)	HIVEP1_01	0.52	0	0	H		0	0	0	0	0	0	0	0	general GO	
inflammatory response (163)	HIVEP1_01	0.52	0	0	H		0	0	0	0	0	0	0	0	general GO	
immune response (366)	HIVEP1_01	0.52	0	0		H	0	0	0	0	0	0	0	0	general GO	
sensory perception (201)	VMAF.01	0.52	0	0	H	M	0	0	0	0	0	0	0	0	general GO	59
mRNA processing (148)	NFY.01	0.52	0	0	0	H	0	M	0	0	0	0	0	0	general GO	60
cell cycle (273)	NFY.01	0.52	0	0	H		H	0	0	0	0	0	0	0	general GO	
cell division (103)	NFY.01	0.52	0	0	H	M	H	0	0	0	0	0	0	0	general GO	
mitosis (86)	NFY.01	0.52	0	0		M	H	0	0	0	0	0	0	0	general GO	
nucleosome assembly (71)	NFY.01	0.52	0	0		H	H	0	0	0	0	0	0	0	general GO	
steroid biosynthesis (42)	NFY.01	0.52	0	0	M	H	0	0	0	0	0	0	0	0	general GO	
regulation of cyclin dependent protein kinase activity	NFY.01	0.52	0	0	0	0	H	0	M	0	0	0	0	0	general GO	
inflammatory response (163)	ETS1.01	0.52	0	0	0		0	0	0	0	0	0	0	0	general GO	61
immune response (366)	ETS1.01	0.52	0	0		H	0	0	0	0	0	0	0	0	general GO	
cellular defense response (68)	ETS1.01	0.52	H	0			0	0	0	0	0	0	0	0	general GO	
protein biosynthesis (197)	ELK1.01	0.52	0	H			0	0	0	0	0	0	0	0	general GO	62
immune response (366)	AML3.01	0.5	0	H			0	0	0	0	H	0	0	0	general GO	63
DNA metabolism (47)	E2F.01	0.5	0				0	0	0	0	0	0	0	0	general GO	64
immune response (366)	SRF.02	0.49	0	0	H	0	M	0	0	0	0	0	0	0	general GO	65
muscle development (107)	SRF.02	0.49	0	0	H		H	0	0	0	0	0	0	0	general GO	
cell cycle (273)	CAAT.01	0.49	0	0	H	M	H	0	0	0	0	0	0	0	general GO	
mitosis (86)	CAAT.01	0.49	0	0			0	0	0	0	0	0	0	0	general GO	
nucleosome assembly (71)	CAAT.01	0.49	0	0	H		H	0	0	0	0	0	0	0	general GO	
lipid biosynthesis (54)	CAAT.01	0.49	0	0	M	H	0	0	0	0	0	0	0	0	general GO	
steroid biosynthesis (42)	CAAT.01	0.49	0	0	M	H	0	0	0	0	0	0	0	0	general GO	
intracellular signaling cascade (257)	TAL1BETAE47.01	0.49	0	0	0	0	0	H	0	0	M	0	0	0	general GO	66
pregnancy (41)	AREB6.01	0.49	H	M	0	0	0	0	0	0	0	0	0	0	general GO	67
immune response (366)	PU1.01	0.48	0	0			0	0	0	0	0	0	0	0	general GO	68
inflammatory response (163)	ETS2.01	0.48	0	H	H		0	0	0	0	0	0	0	0	general GO	69
immune response (366)	ETS2.01	0.48	0	H		H	0	0	0	0	0	0	0	0	general GO	
cell cycle (273)	NFY.02	0.48	0	0	H	M	0	0	0	0	0	0	0	0	general GO	70
cell division (103)	NFY.02	0.48	0	0	H	M	H	0	0	0	0	0	0	0	general GO	
mitosis (86)	NFY.02	0.48	0	0		M	0	0	0	0	0	0	0	0	general GO	
chemotaxis (98)	NFE2L2.01	0.47	0	H	0		M	0	0	0	0	0	0	0	general GO	71
immune response (366)	NFE2L2.01	0.47	0	0		M	0	M	0	H	0	0	0	0	general GO	
cell cell signaling (268)	MTATA.01	0.47	0	0			0	0	0	0	0	0	0	0	general GO	
sensory perception of smell (40)	TAL1BETAITF2.01	0.47	H	0	0	M	0	0	0	0	0	0	0	0	general GO	72
mRNA processing (148)	NFY.03	0.47	0	0	H	0	0	M	0	0	0	0	0	0	general GO	73
cell cycle (273)	NFY.03	0.47	0	0	H	M	0	0	0	0	0	0	0	0	general GO	
cell division (103)	NFY.03	0.47	0	0	H		0	0	0	0	0	0	0	0	general GO	
mitosis (86)	NFY.03	0.47	0	0	H	M	0	0	0	0	0	0	0	0	general GO	

nucleosome assembly (71)	NFY.03	0.47	0	0	H	H	0	0	0	0	0	0	0	0	general GO
steroid biosynthesis (42)	NFY.03	0.47	0	0	M	H	0	0	0	0	0	0	0	0	general GO
immune response (366)	SRF.03	0.47	H	0	0	0	M	0	0	0	0	0	0	0	general GO
muscle development (107)	SRF.03	0.47	0	0	H	H	0	0	0	0	0	0	0	0	general GO
defense response (100)	ARE.01	0.47	0	M	H	0	0	0	0	0	0	0	0	0	general GO
sensory perception (201)	GKLF_02	0.46	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	STAT6.01	0.46	0	H	0	0	H	0	0	0	0	0	0	0	general GO
immune response (366)	MIT.01	0.46	H	0	0	H	M	0	0	0	0	0	0	0	general GO
inflammatory response (163)	CEBP.02	0.46	M	0	0	H	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	PXRCAR.01	0.45	0	M	H	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	PXRCAR.01	0.45	0	0	H	M	0	0	0	0	0	0	0	0	general GO
sensory perception (201)	PTX1.01	0.45	0	0	M	H	0	0	0	0	0	0	0	0	general GO
visual perception (142)	PTX1.01	0.45	0	0	0	0	H	0	0	0	0	0	0	0	general GO
immune response (366)	GATA1.01	0.45	M	0	H	0	0	0	0	0	0	H	0	0	general GO
immune response (366)	RTR.01	0.45	0	M	H	H	0	0	0	H	0	0	0	0	general GO
inflammatory response (163)	MYT1L.01	0.44	H	M	0	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	MYT1L.01	0.44	0	0	H	M	0	0	0	0	0	0	0	0	general GO
ubiquitin cycle (154)	VMYB.05	0.44	0	0	0	0	M	0	H	0	0	0	0	0	general GO
immune response (366)	BCL6.02	0.44	0	0	0	0	0	0	0	0	0	0	0	0	general GO
inflammatory response (163)	TCF11MAFG.01	0.43	0	0	H	0	0	0	0	0	0	0	0	0	general GO
G protein coupled receptor protein signaling pathway	TCF11MAFG.01	0.43	0	0	H	M	0	0	0	0	0	0	0	0	general GO
immune response (366)	AP1.01	0.43	0	0	0	0	H	0	0	0	0	0	0	0	general GO
inflammatory response (163)	ISRE.01	0.43	0	0	H	M	0	0	0	0	0	0	0	0	general GO
immune response (366)	ISRE.01	0.43	0	0	0	0	0	0	0	0	0	0	0	0	general GO
response to virus (55)	ISRE.01	0.43	0	H	H	0	H	0	0	0	0	0	0	0	general GO
immune response (366)	IRF2.01	0.43	0	0	0	0	0	0	0	0	0	0	0	0	general GO
response to virus (55)	IRF2.01	0.43	0	0	0	H	0	H	0	0	0	0	0	0	general GO
innate immune response (46)	IRF2.01	0.43	0	M	H	0	0	0	0	0	0	0	0	0	general GO
sensory perception (201)	GSC.01	0.43	0	0	0	H	0	0	0	0	0	0	0	0	general GO
visual perception (142)	GSC.01	0.43	0	0	0	0	0	0	0	0	0	0	0	0	general GO
inflammatory response (163)	IRF3.01	0.42	0	0	H	M	0	0	0	0	0	0	0	0	general GO
immune response (366)	IRF3.01	0.42	H	0	0	0	0	0	0	0	0	0	0	0	general GO
response to virus (55)	IRF3.01	0.42	H	0	H	0	0	0	0	0	0	0	0	0	general GO
sensory perception (201)	SRF.01	0.42	H	0	0	H	0	0	0	0	0	0	0	0	general GO
inflammatory response (163)	SRF.01	0.42	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	SRF.01	0.42	H	0	H	0	M	0	0	0	0	0	0	0	general GO
muscle development (107)	SRF.01	0.42	H	0	H	0	0	0	0	0	0	0	0	0	general GO
homophilic cell adhesion (70)	GSH1.01	0.42	0	0	0	0	0	H	0	0	M	0	0	0	general GO
immune response (366)	PRDM1.01	0.41	0	0	0	H	0	0	0	0	0	0	0	0	general GO
response to virus (55)	PRDM1.01	0.41	0	0	0	0	0	H	0	0	M	0	0	0	general GO
immune response (366)	HMG1Y.01	0.41	0	0	0	0	0	0	0	0	H	0	0	0	general GO
cell matrix adhesion (56)	HBP1_01	0.41	0	0	0	0	M	0	H	0	H	0	0	0	general GO
immune response (366)	RORA1.01	0.41	0	M	0	0	H	0	0	H	0	0	0	0	general GO
sensory perception (201)	GFI1.01	0.41	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	GFI1.01	0.41	M	0	0	H	0	H	0	0	0	0	0	0	general GO
cell cell signaling (268)	PHOX2_01	0.41	M	0	H	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	PSE_02	0.41	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell division (103)	CHR.01	0.41	0	H	0	0	0	0	0	0	0	0	0	0	general GO
mitosis (86)	CHR.01	0.41	0	H	0	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	MTBF.01	0.4	0	0	H	0	0	0	H	0	0	0	0	0	general GO
immune response (366)	IRF1.01	0.4	H	0	0	0	0	0	0	0	0	0	0	0	general GO
response to virus (55)	IRF1.01	0.4	0	H	0	H	0	H	0	0	H	0	0	0	general GO
defense response (100)	IRF1.01	0.4	0	0	0	H	0	H	0	0	0	0	0	0	general GO
inflammatory response (163)	CEBPB.01	0.4	0	0	H	0	0	H	0	0	0	0	0	0	general GO
sensory perception (201)	CRX.01	0.39	0	0	0	0	H	0	0	0	0	0	0	0	general GO
visual perception (142)	CRX.01	0.39	0	0	0	0	0	0	0	0	0	0	0	0	general GO
inflammatory response (163)	AARE.01	0.39	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune response (366)	AARE.01	0.39	0	0	0	H	H	0	0	0	0	0	0	0	general GO
proteolysis (297)	AIRE.01	0.39	0	0	0	0	M	H	0	0	0	0	H	0	general GO
cell cell signaling (268)	LTATA_01	0.39	0	0	0	0	0	0	0	0	0	0	0	0	general GO
epidermis development (59)	LTATA_01	0.39	0	0	0	0	0	0	0	0	0	0	0	0	general GO
inflammatory response (163)	BRN2.01	0.39	0	0	H	0	0	0	0	0	0	0	0	0	general GO
inflammatory response (163)	IRF4.01	0.39	0	0	0	M	H	0	0	0	0	0	0	0	general GO
immune response (366)	IRF4.01	0.39	H	0	0	H	0	0	0	0	0	0	0	0	general GO

G protein coupled receptor protein signaling pathway	IRF4.01	0.39	M	O	H	O	O	O	O	O	O	O	O	O	O	O	general GO
visual perception (142)	OTX2.01	0.39	O	O		O	O	O	O	O	O	O	O	O	O	O	general GO
protein biosynthesis (197)	OTX2.01	0.39	O	O	O	O	O	M	O	O	H	H	O	O	O	O	general GO
immune response (366)	STAT5.01	0.39	H	H	H		H	O	O	O	O	O	O	O	O	O	general GO
immune response (366)	BCL6.01	0.39	O	H	H		H	M	O	O	O	O	O	O	O	O	general GO
immune response (366)	OCT1.04	0.38				H	H	O	O	O	O	O	O	O	O	O	general GO
immune response (366)	GFI1B.01	0.38		O	O			O	O	O	O	O	O	O	O	O	general GO
RNA processing (58)	GFI1B.01	0.38	M	O	O	O	O	O	O	O	O	O	O	O	H	O	general GO
immune response (366)	AMEF2.01	0.38	O	O	H			O	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	NFAT.01	0.38	O	O	M		H	O	O	O	O	O	O	O	O	O	general GO
immune response (366)	NFAT.01	0.38	M	H			H	O	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	CDX2.01	0.38	O	O	H			O	O	O	H	O	O	O	O	O	general GO
immune response (366)	CDX2.01	0.38	M	O			H	H	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	MMEF2.01	0.37	O	O			H	O	O	O	O	O	O	O	O	O	general GO
immune response (366)	GATA1.05	0.36			H	O		O	O	O	O	O	O	O	O	O	general GO
sensory perception (201)	XFD3.01	0.36	O	H				O	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	IRF7.01	0.36	M	O	H			O	O	O	O	O	O	O	O	O	general GO
immune response (366)	IRF7.01	0.36	H	H				O	O	O	O	O	O	O	O	O	general GO
sensory perception (201)	OCT1P.01	0.36	O	O	H			H	H	H	O	O	O	O	O	O	general GO
homophilic cell adhesion (70)	OCT1P.01	0.36	O	O	O	M		O	O	O	O	H	O	O	O	O	general GO
immune response (366)	OCT.01	0.35	H					O	O	O	H	O	O	O	O	O	general GO
sensory perception (201)	SIX3.01	0.35	O	O			H	H	O	O	O	O	O	O	O	O	general GO
visual perception (142)	SIX3.01	0.35	O	O			O	H	H	O	O	O	O	O	O	H	general GO
immune response (366)	PDX1_G_SAAB3	0.35	M	O	O			H	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	CDX1.01	0.35	M	O				O	O	O	O	O	O	O	O	O	general GO
immune response (366)	CDX1.01	0.35	H	O				H	O	O	O	O	O	O	O	O	general GO
immune response (366)	NKX25.02	0.35	M	O	O			H	O	H	O	O	O	O	O	O	general GO
sensory perception (201)	FREAC2.01	0.35	O	O	O			O	M	O	O	H	O	O	O	O	general GO
immune response (366)	OCT1.02	0.34	H	M	O			O	O	O	O	H	O	O	O	O	general GO
inflammatory response (163)	XFD1.01	0.34	O	O	M			H	H	O	O	O	O	O	O	O	general GO
immune response (366)	XFD1.01	0.34	H	O	M			H	O	O	O	O	O	O	O	O	general GO
immune response (366)	GSH2_01	0.34	M	O	O			O	O	O	H	O	O	O	O	O	general GO
signal transduction (1189)	EVI1.02	0.33	O	O				O	O	O	O	O	O	O	O	O	general GO
immune response (366)	EVI1.02	0.33	O	M	H			O	H	O	O	O	O	O	O	O	general GO
G protein coupled receptor protein signaling pathway	EVI1.02	0.33	O	O				O	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	XFD2.01	0.32	O	O	M			O	O	O	O	O	H	O	O	O	general GO
immune response (366)	XFD2.01	0.32	H	O				H	H	O	O	O	H	O	O	O	general GO
innate immune response (46)	LMX1B.01	0.32	O	O	M			H	O	O	O	O	H	O	O	O	general GO
proteolysis (297)	HNF1.03	0.31	O	O				O	O	O	O	O	O	O	O	O	general GO
transport (940)	HNF1.03	0.31	O	O				H	O	O	O	O	O	O	O	O	general GO
blood coagulation (70)	HNF1.03	0.31	M	O				O	O	O	O	O	O	O	O	O	general GO
sodium ion transport (75)	HNF1.03	0.31	O	O				O	O	O	O	O	O	O	O	O	general GO
signal transduction (1189)	EVI1.01	0.31	O	O				O	O	O	O	O	O	O	O	O	general GO
G protein coupled receptor protein signaling pathway	EVI1.01	0.31	H	H				H	O	O	O	O	O	O	O	O	general GO
cell cell signaling (268)	ATATA.01	0.3	O	O				O	O	O	O	O	O	O	O	O	general GO
immune response (366)	MEF2.02	0.3	O	O				H	O	O	O	O	O	O	O	O	general GO
proteolysis (297)	HNF1.01	0.3	O	O				O	O	O	O	O	O	O	O	O	general GO
transport (940)	HNF1.01	0.3	O	O				O	O	O	O	O	O	O	O	O	general GO
immune response (366)	HNF1.01	0.3	M	O	H			H	O	O	O	O	O	O	O	O	general GO
sodium ion transport (75)	HNF1.01	0.3	O	O				O	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	MEF2.05	0.29	O	O				H	O	O	O	O	O	O	O	O	general GO
immune response (366)	MEF2.05	0.29	O	O	M			H	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	RSRFC4.02	0.29	O	O				O	O	O	O	O	O	O	O	O	general GO
immune response (366)	RSRFC4.02	0.29	O	O				H	O	O	O	O	O	O	O	O	general GO
immune response (366)	MEL1_01	0.29		O	H			H	O	O	O	O	O	O	H	H	general GO
digestion (51)	MEL1_01	0.29	M	O	O			O	H	O	O	O	O	O	O	O	general GO
G protein coupled receptor protein signaling pathway	GATA3.02	0.29	O	O	H			H	M	O	H	O	O	O	O	O	general GO
sensory perception (201)	TATA.01	0.28	O	O				H	O	O	O	O	O	H	O	O	general GO
chemotaxis (98)	TATA.01	0.28	O	O				O	O	O	O	O	O	O	O	O	general GO
inflammatory response (163)	TATA.01	0.28	O	O				H	O	O	O	O	O	O	O	O	general GO
immune response (366)	TATA.01	0.28	O	O				H	O	O	O	O	O	O	O	O	general GO
cell cell signaling (268)	TATA.01	0.28	O	H				O	O	O	O	O	O	O	O	O	general GO
nucleosome assembly (71)	TATA.01	0.28	O	O				O	H	O	O	O	O	O	O	O	general GO
chromosome organization and biogenesis (83)	TATA.01	0.28	O	O				O	H	O	O	O	O	O	O	O	general GO

development (530)	ZNF202.01	0.73	0			H	H	M		transcription GO
transcription (930)	AP2.01	0.73	0	H						transcription GO
regulation_of_transcription_DNA_dependent (1066)	AP2.01	0.73	M	0						transcription GO
regulation_of_transcription (266)	AP2.01	0.73	0	0		M	H	H		transcription GO
development (530)	AP2.01	0.73	0	0		H	H	H		transcription GO
transcription (930)	ZF5.01	0.72	0	0		H	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZF5.01	0.72		M				H		transcription GO
regulation_of_transcription (266)	ZF5.01	0.72	0	H		0	H	0		transcription GO
transcription (930)	ZF9.01	0.72	0	0			M			transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZF9.01	0.72	0	0						transcription GO
transcription (930)	EGR3.01	0.71	0	0	M		0	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR3.01	0.71	0	0	M		0			transcription GO
transcription (930)	NRF1_01	0.71	H	0						transcription GO
regulation_of_transcription_DNA_dependent (1066)	NRF1_01	0.71	H	0				H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	MYCMAX.03	0.7	0	0		H	0	0		transcription GO
transcription (930)	ZBP89.01	0.7	H			M	M	0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZBP89.01	0.7	H	M		M		M		transcription GO
regulation_of_transcription (266)	ZBP89.01	0.7	M	M			0	0		transcription GO
development (530)	ZBP89.01	0.7	0	H				H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	HELT.01	0.69	0	0	H	H		0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	NGFIC.01	0.69	0	0	M	H	H			transcription GO
transcription (930)	CKROX_01	0.68					0	0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	CKROX_01	0.68					M			transcription GO
regulation_of_transcription (266)	CKROX_01	0.68	0	M			0	0		transcription GO
development (530)	CKROX_01	0.68	0	H			H	0		transcription GO
transcription (930)	EGR1.02	0.68								transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR1.02	0.68		M						transcription GO
regulation_of_transcription_DNA_dependent (1066)	HIC1_01	0.68	0	0	0	0	H			transcription GO
transcription (930)	BKLF.01	0.68	0	0	0	0	0	0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	BKLF.01	0.68	0	0	0	0	0			transcription GO
transcription (930)	GC.01	0.68	0	0			0	0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	GC.01	0.68	0	0			0	M		transcription GO
development (530)	MZF1.01	0.68	0	H	H		H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR1.01	0.67	H	0	M	0	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	TIEG.01	0.66	0	0	H	0	0			transcription GO
transcription (930)	MAZ.01	0.65	0	0		M		H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	MAZ.01	0.65	0	0		M				transcription GO
regulation_of_transcription (266)	MAZ.01	0.65	0	0			H	0		transcription GO
development (530)	MAZ.01	0.65	0	H	H			H		transcription GO
development (530)	ZIC2_01	0.65	0	0	H	0	0			transcription GO
transcription (930)	PLAG1_01	0.63	M	H	M		H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	PLAG1_01	0.63	M	H	M					transcription GO
regulation_of_transcription (266)	PLAG1_01	0.63	M	0	H		0	0		transcription GO
development (530)	PLAG1_01	0.63	0	H		H	H	0		transcription GO
transcription (930)	HES1.01	0.62	0	M	M		H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	HES1.01	0.62	0	M			H			transcription GO
transcription (930)	MUSCLE_INI.02	0.62	0	0		H	0	0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	MUSCLE_INI.02	0.62	0	0		H	0	M		transcription GO
transcription (930)	CDE.01	0.6	H		M		M	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	CDE.01	0.6	H	M	M					transcription GO
development (530)	CDE.01	0.6	0	0	0	H	0			transcription GO
transcription (930)	E2F.02	0.59	0	H	0	0		M		transcription GO
regulation_of_transcription_DNA_dependent (1066)	E2F.02	0.59	0	H	0	0		M		transcription GO
development (530)	PAX5.01	0.57	0	0	0	0	0			transcription GO
regulation_of_transcription (266)	VDR_RXR.02	0.56	0	0	0		0	0		transcription GO
transcription (930)	GAGA.01	0.56		0	M		0	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	GAGA.01	0.56		H	H		0	H		transcription GO
regulation_of_transcription (266)	GAGA.01	0.56	H		H		0	0		transcription GO
development (530)	GAGA.01	0.56	M		H	H	H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	E2F.03	0.54	0	0	0	0	M			transcription GO
regulation_of_transcription_DNA_dependent (1066)	NFY.01	0.52	0	H			0	0	0	transcription GO
regulation_of_transcription_DNA_dependent (1066)	AG_rich_coding	0.5	M		H		0	0		transcription GO
regulation_of_transcription (266)	AG_rich_coding	0.5	M		H		H	0		transcription GO
development (530)	AG_rich_coding	0.5			H	H	0	0		transcription GO

development (530)	MTATA.01	0.47	0	0	0	0	0	0	transcription GO
regulation_of_transcription (266)	LMX1B.01	0.32	0	0	0	0	0	0	transcription GO
development (530)	TATA.01	0.28	0	0	0	0	0	0	transcription GO
small_GTPase_mediated_signal_transduction (124)	SP1.01	0.78		H	0	0	0	0	general GO
protein_transport (254)	SP1.01	0.78	H	0	0	0	0	0	general GO
intracellular_protein_transport (191)	SP1.01	0.78	H	0	0	0	0	0	general GO
Wnt_receptor_signaling_pathway (66)	WT1.01	0.77	0	0	0	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	WT1.01	0.77	H	H	0	0	0	0	general GO
cation_transport (99)	ZNF202.01	0.73	0	0	0	0	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	ZF9.01	0.72	H	0	0	0	0	0	general GO
protein_transport (254)	ZF9.01	0.72	H	0	0	0	0	0	general GO
intracellular_protein_transport (191)	ZF9.01	0.72	H	0	0	0	0	0	general GO
chromatin_modification (53)	CKROX_01	0.68	0	H	0	0	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	EGR1.02	0.68		0	0	0	0	0	general GO
protein_transport (254)	EGR1.02	0.68	H	0	0	0	0	0	general GO
intracellular_protein_transport (191)	EGR1.02	0.68	H	0	0	0	0	0	general GO
muscle_development (107)	INSM1_01	0.63	0	0	0	0	0	0	general GO
protein_biosynthesis (197)	GABP.01	0.62	H	0	0	0	0	0	general GO
protein_complex_assembly (94)	P53.01	0.61	0	0	0	0	0	0	general GO
inflammatory_response (163)	NFKAPPAB.01	0.6	0	0	0	0	0	0	general GO
immune_response (366)	NFKAPPAB.01	0.6	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB.01	0.6	0	0	0	0	0	0	general GO
transcription_RNA_polyII_promoter (190)	CDE.01	0.6	0	0	0	0	0	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.02	0.59	0	M	0	0	0	0	general GO
DNA_repair (148)	E2F.02	0.59	H	M	0	0	0	0	general GO
protein_transport (254)	WHN.01	0.59	0	0	0	0	0	0	general GO
protein_biosynthesis (197)	WHN.01	0.59	0	0	0	0	0	0	general GO
cell_division (103)	WHN.01	0.59	0	0	0	0	0	0	general GO
cell_cycle (273)	WHN.01	0.59	0	H	0	0	0	0	general GO
RNA_splicing (61)	NRF2.01	0.57	H	0	0	0	0	0	general GO
protein_transport (254)	NRF2.01	0.57	0	0	0	0	0	0	general GO
protein_biosynthesis (197)	NRF2.01	0.57		0	0	0	0	0	general GO
sensory_perception (201)	NFKAPPAB.02	0.57	0	0	0	0	0	0	general GO
inflammatory_response (163)	NFKAPPAB.02	0.57	0	0	0	0	0	0	general GO
immune_response (366)	NFKAPPAB.02	0.57	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB.02	0.57	0	0	0	0	0	0	general GO
muscle_contraction (78)	MYOD.02	0.56	0	0	0	0	0	0	general GO
inflammatory_response (163)	NFKAPPAB65.01	0.55	0	0	0	0	0	0	general GO
immune_response (366)	NFKAPPAB65.01	0.55	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB65.01	0.55	0	0	0	0	0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	NFKAPPAB65.01	0.55	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	NFKAPPAB65.01	0.55	0	0	0	0	0	0	general GO
apoptosis (258)	NFKAPPAB65.01	0.55	0	H	0	0	0	0	general GO
protein_biosynthesis (197)	CETS1P54.01	0.55	0	0	0	0	0	0	general GO
protein_biosynthesis (197)	YY1.01	0.55	0	0	0	0	0	0	general GO
inflammatory_response (163)	CREL.01	0.55	0	0	0	0	0	0	general GO
immune_response (366)	CREL.01	0.55	0	0	0	0	0	0	general GO
chemotaxis (98)	CREL.01	0.55	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	CREL.01	0.55	0	0	0	0	0	0	general GO
protein_biosynthesis (197)	ELK1.02	0.55	H	0	0	0	0	0	general GO
response_to_virus (55)	NFKAPPAB.03	0.55	0	0	0	0	0	0	general GO
inflammatory_response (163)	NFKAPPAB.03	0.55	0	0	0	0	0	0	general GO
immune_response (366)	NFKAPPAB.03	0.55	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB.03	0.55	0	0	0	0	0	0	general GO
cellular_defense_response (68)	NFKAPPAB.03	0.55	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	NFKAPPAB.03	0.55	0	0	0	H	0	0	general GO
response_to_DNA_damage_stimulus (117)	FLI.01	0.53	0	0	0	0	0	0	general GO
protein_biosynthesis (197)	FLI.01	0.53	H	0	0	0	0	0	general GO
DNA_repair (148)	FLI.01	0.53	0	0	0	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway	NF1.01	0.53	0	0	0	0	0	0	general GO
metabolism (241)	HNF4.01	0.53	0	0	0	0	0	0	general GO
electron_transport (214)	HNF4.01	0.53	0	0	0	0	0	0	general GO
inflammatory_response (163)	HIVEP1_01	0.52	M	0	0	0	0	0	general GO
immune_response (366)	HIVEP1_01	0.52	0	0	0	0	0	0	general GO

chemotaxis (98)	HIVEP1_01	0.52	0		0	0	0	0	general GO
cell_cell_signaling (268)	HIVEP1_01	0.52	0		0	0	0	0	general GO
immune_response (366)	AML1.01	0.52	0		0	0	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	ERR_01	0.52	0	0		0	0	0	general GO
steroid_biosynthesis (42)	NFY.01	0.52	0		0	0	0	0	general GO
mitosis (86)	NFY.01	0.52	0		0	0	0	0	general GO
cell_division (103)	NFY.01	0.52	0	H		0	0	0	general GO
cell_cycle (273)	NFY.01	0.52	0	H		0	0	0	general GO
immune_response (366)	ETS1.01	0.52	0		0	0	0	0	general GO
cellular_defense_response (68)	ETS1.01	0.52	0		0	0	0	0	general GO
protein_biosynthesis (197)	ELK1.01	0.52	H		0	0	0	0	general GO
immune_response (366)	AML3.01	0.5	H		0	H	0	0	general GO
immune_response (366)	RBPJK.02	0.5	H		0	0	0	0	general GO
skeletal_development (83)	AG_rich_coding	0.5	0		0	0	0	0	general GO
muscle_development (107)	TAL1ALPHA47.01	0.5	0		0	0	0	0	general GO
muscle_development (107)	SRF.02	0.49	0	H		0	0	0	general GO
immune_response (366)	TR2.01	0.49	0	H		0	0	0	general GO
steroid_biosynthesis (42)	CAAT.01	0.49	0		0	0	0	0	general GO
mitosis (86)	CAAT.01	0.49	0		0	0	0	0	general GO
chromosome_organization_and_biogenesis (83)	CAAT.01	0.49	0		0	0	0	0	general GO
cell_division (103)	CAAT.01	0.49	0		0	0	0	0	general GO
cell_cycle (273)	CAAT.01	0.49	0		0	0	0	0	general GO
immune_response (366)	TAL1BETAE47.01	0.49	M	0	M		0	0	general GO
chemotaxis (98)	IK3.01	0.49	0		0	0	0	0	general GO
sensory_perception (201)	IK2.01	0.49	0	0		0	0	0	general GO
proteolysis (297)	AREB6.02	0.48	0		0	0	0	0	general GO
immune_response (366)	PU1.01	0.48	0		0	0	0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	PU1.01	0.48	0		0	0	0	0	general GO
inflammatory_response (163)	ETS2.01	0.48	0		0	0	0	0	general GO
immune_response (366)	ETS2.01	0.48	H		0	0	0	0	general GO
chemotaxis (98)	ETS2.01	0.48	0		0	0	0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	ETS2.01	0.48	0		0	0	0	0	general GO
steroid_biosynthesis (42)	NFY.02	0.48	0		0	0	0	0	general GO
mitosis (86)	NFY.02	0.48	0		0	0	0	0	general GO
chromosome_organization_and_biogenesis (83)	NFY.02	0.48	0		0	0	0	0	general GO
cell_cycle (273)	NFY.02	0.48	0		0	0	0	0	general GO
biosynthesis (32)	NFY.02	0.48	0		0	0	0	0	general GO
immune_response (366)	PAX2.01	0.47	0		0	0	0	0	general GO
immune_response (366)	PPARA.01	0.47	H		0	0	0	0	general GO
immune_response (366)	NFE2L2.01	0.47		H		0	0	0	general GO
muscle_development (107)	MTATA.01	0.47	0		0	0	0	0	general GO
nucleosome_assembly (71)	NFY.03	0.47	0		0	0	0	0	general GO
mitosis (86)	NFY.03	0.47	0		0	0	0	0	general GO
chromosome_organization_and_biogenesis (83)	NFY.03	0.47	0		0	0	0	0	general GO
cell_division (103)	NFY.03	0.47	0		0	0	0	0	general GO
cell_cycle (273)	NFY.03	0.47	0		0	0	0	0	general GO
muscle_development (107)	SRF.03	0.47	H		H		0	0	general GO
lipid_transport (41)	SRF.03	0.47	0		0	0	0	0	general GO
immune_response (366)	BACH1.01	0.47	H			0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathwa	PLZF.01	0.47	0	0	0	0	0	0	general GO
immune_response (366)	ARE.01	0.47	H		0	0	0	0	general GO
sensory_perception (201)	MEL1_02	0.46	H		H		0	0	general GO
immune_response (366)	STAT6.01	0.46	H		H		0	0	general GO
sensory_perception_of_smell (40)	MIT.01	0.46	0		0	0	0	0	general GO
immune_response (366)	MIT.01	0.46	H	M		0	0	0	general GO
immune_response (366)	RP58.01	0.46	0		0	0	0	0	general GO
inflammatory_response (163)	COMP1.01	0.45	H		0	0	0	0	general GO
immune_response (366)	PXRCAR.01	0.45	0		0	0	0	0	general GO
inflammatory_response (163)	DBP.01	0.45	0		0	0	0	0	general GO
inflammatory_response (163)	BARBIE.01	0.45	0		0	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathwa	BRACH.01	0.45	0		0	0	0	0	general GO
visual_perception (142)	PTX1.01	0.45	0	H		0	0	0	general GO
immune_response (366)	PAX8.01	0.45	0		0	0	0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	GATA1.01	0.45	H		0	0	0	0	general GO

innate immune response (46)	STAT.01	0.44	0		0	0	0	0	general GO
immune response (366)	MYT1L.01	0.44	H		0	0	0	0	general GO
immune response (366)	STAT.01	0.44	0		0	0	0	0	general GO
immune response (366)	TCF11.01	0.44	0	H		0	0	0	general GO
inflammatory response (163)	BCL6.02	0.44	0		H	0	0	0	general GO
immune response (366)	BCL6.02	0.44	0		0	0	0	0	general GO
inflammatory response (163)	TCF11MAFG.01	0.43		H	0	H	0	0	general GO
immune response (366)	TCF11MAFG.01	0.43			0	0	0	0	general GO
G protein coupled receptor protein signaling pathway	TCF11MAFG.01	0.43	0		H	H	0	0	general GO
immune response (366)	ILF1_01	0.43	0		H	0	0	0	general GO
signal transduction (1189)	AP1.01	0.43	0		0	0	0	0	general GO
proteolysis (297)	AP1.01	0.43	0		0	0	0	0	general GO
inflammatory response (163)	AP1.01	0.43	M		0	0	0	0	general GO
immune response (366)	AP1.01	0.43	H		H	0	0	0	general GO
chemotaxis (98)	AP1.01	0.43	M		H	0	0	0	general GO
response to virus (55)	ISRE.01	0.43	0		H	0	0	0	general GO
inflammatory response (163)	ISRE.01	0.43	0		0	0	0	0	general GO
immune response (366)	ISRE.01	0.43			0	0	0	0	general GO
response to virus (55)	IRF2.01	0.43	0	H		0	0	0	general GO
immune response (366)	IRF2.01	0.43			0	0	0	0	general GO
response to virus (55)	IRF3.01	0.42	0		0	0	0	0	general GO
inflammatory response (163)	IRF3.01	0.42	0		0	0	0	0	general GO
immune response (366)	IRF3.01	0.42	H		0	0	0	0	general GO
sensory perception (201)	SRF.01	0.42	H		0	0	0	0	general GO
muscle development (107)	SRF.01	0.42	0		0	0	0	0	general GO
inflammatory response (163)	SRF.01	0.42	0		0	0	0	0	general GO
immune response (366)	SRF.01	0.42	H		M	0	0	0	general GO
chemotaxis (98)	SRF.01	0.42	0		0	0	0	0	general GO
inflammatory response (163)	PRDM1.01	0.41	M		0	0	0	0	general GO
immune response (366)	PRDM1.01	0.41	M		0	0	0	0	general GO
defense response (100)	PRDM1.01	0.41	0		0	0	0	0	general GO
inflammatory response (163)	HMG1Y.01	0.41	0		0	0	0	0	general GO
immune response (366)	HMG1Y.01	0.41	H		0	H	0	0	general GO
chemotaxis (98)	HMG1Y.01	0.41	0		H	0	0	0	general GO
pregnancy (41)	PDX1_Gabi	0.41	0		0	0	0	0	general GO
immune response (366)	HBP1_01	0.41		H	0	0	0	0	general GO
sensory perception (201)	GFI1.01	0.41	0		H	0	0	0	general GO
immune response (366)	PSE_02	0.41	0		0	0	0	0	general GO
mitosis (86)	CHR.01	0.41	H		0	0	0	0	general GO
innate immune response (46)	BRN4.01	0.4		0	0	0	0	0	general GO
immune response (366)	BRN4.01	0.4		0	H	0	0	0	general GO
immune response (366)	LEF1.02	0.4		H	H	0	0	0	general GO
cell cell signaling (268)	MTBF.01	0.4	0		0	0	0	0	general GO
response to virus (55)	IRF1.01	0.4	0		0	H	0	0	general GO
inflammatory response (163)	IRF1.01	0.4	0		0	0	0	0	general GO
immune response (366)	IRF1.01	0.4			0	0	0	0	general GO
response to virus (55)	CEBPB.01	0.4	0		0	0	0	0	general GO
proteolysis (297)	CEBPB.01	0.4	0		0	0	0	0	general GO
inflammatory response (163)	CEBPB.01	0.4	0		H	0	0	0	general GO
immune response (366)	GATA1.04	0.4		H	H	0	0	0	general GO
defense response (100)	CEBPB.01	0.4	0		0	0	0	0	general GO
visual perception (142)	CRX.01	0.39	0		0	0	0	0	general GO
sensory perception (201)	CRX.01	0.39	0		H	0	0	0	general GO
immune response (366)	OCT1.05	0.39		H	H	0	0	0	general GO
sensory perception (201)	AARE.01	0.39	0	H	0		0	0	general GO
inflammatory response (163)	AARE.01	0.39	0		0	0	0	0	general GO
immune response (366)	AARE.01	0.39	0		0	0	0	0	general GO
cell cell signaling (268)	AARE.01	0.39	0		0	0	0	0	general GO
inflammatory response (163)	LTATA_01	0.39	0		0	0	0	0	general GO
cell cell signaling (268)	LTATA_01	0.39	0		0	0	0	0	general GO
antimicrobial humoral response (87)	LTATA_01	0.39	0		0	0	0	0	general GO
inflammatory response (163)	BRN2.01	0.39	0		0	0	0	0	general GO
immune response (366)	BRN2.01	0.39	H		H	0	H	0	general GO
response to virus (55)	IRF4.01	0.39	0		0	0	0	0	general GO

inflammatory_response (163)	IRF4.01	0.39	M		0	0	0	0	general GO
immune_response (366)	IRF4.01	0.39			0	0	0	0	general GO
visual_perception (142)	OTX2.01	0.39	0		0	0	0	0	general GO
sensory_perception (201)	OTX2.01	0.39	0	H	0	0	0	0	general GO
inflammatory_response (163)	STAT5.01	0.39	0		0	0	0	0	general GO
immune_response (366)	STAT5.01	0.39	0		0	0	0	0	general GO
immune_response (366)	GATA1.03	0.39		H	H	0	0	0	general GO
chemotaxis (98)	GATA1.03	0.39	H		0	0	H	0	general GO
antimicrobial_humoral_response (87)	GATA1.03	0.39		H	H	0	0	0	general GO
immune_response (366)	BCL6.01	0.39	0			H	0	0	general GO
immune_response (366)	OCT1.04	0.38		H	H	0	0	0	general GO
immune_response (366)	GFI1B.01	0.38	0		0	0	H	0	general GO
nucleosome_assembly (71)	PDX1.01	0.38	0	H	H	0		0	general GO
muscle_development (107)	AMEF2.01	0.38	0		0	0	0	0	general GO
immune_response (366)	AMEF2.01	0.38	0		0	0	0	0	general GO
immune_response (366)	RORA2.01	0.38		H	H	H	0	0	general GO
inflammatory_response (163)	NFAT.01	0.38	M		H	0	0	0	general GO
immune_response (366)	NFAT.01	0.38			0	0	0	0	general GO
chemotaxis (98)	NFAT.01	0.38	0		0	0	0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	NFAT.01	0.38	0		0	0	0	0	general GO
cell_cell_signaling (268)	NFAT.01	0.38	0		0	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathwa	FREAC4.01	0.38	M		0	0	0	0	general GO
innate_immune_response (46)	CDX2.01	0.38		H	0	0	H	H	general GO
inflammatory_response (163)	CDX2.01	0.38	H		0	H	H	0	general GO
immune_response (366)	CDX2.01	0.38	H		H	0	0	0	general GO
chemotaxis (98)	CDX2.01	0.38	0		0	0	0	0	general GO
cell_cell_signaling (268)	CDX2.01	0.38	0		0	0	0	0	general GO
immune_response (366)	MEF2.01	0.38			0	0	0	0	general GO
inflammatory_response (163)	MMEF2.01	0.37	0		0	0	H	0	general GO
immune_response (366)	MMEF2.01	0.37	0		0	0	H	0	general GO
sensory_perception (201)	GATA2.02	0.36	0		H	H	0	0	general GO
immune_response (366)	GATA2.02	0.36	H		H	0	H	0	general GO
immune_response (366)	GATA1.05	0.36		H		0	0	0	general GO
sensory_perception (201)	XFD3.01	0.36	0		0	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathwa	XFD3.01	0.36	H		0	0	H	0	general GO
response_to_virus (55)	IRF7.01	0.36	H		0	0	0	0	general GO
inflammatory_response (163)	IRF7.01	0.36	M		0	0	0	0	general GO
immune_response (366)	IRF7.01	0.36	H		H	0	0	0	general GO
sensory_perception (201)	OCT1P.01	0.36	H		H	H	0	0	general GO
immune_response (366)	OCT1P.01	0.36		H	H	H	0	0	general GO
innate_immune_response (46)	OCT.01	0.35		H	0	0	0	0	general GO
immune_response (366)	OCT.01	0.35		H	H	0	0	0	general GO
visual_perception (142)	SIX3.01	0.35	0		H	0	0	H	general GO
sensory_perception (201)	SIX3.01	0.35	0		H	0	0	0	general GO
immune_response (366)	GATA2.01	0.35			0	M	0	0	general GO
inflammatory_response (163)	CDX1.01	0.35	M		0	0	0	0	general GO
immune_response (366)	CDX1.01	0.35	H		0	0	0	0	general GO
immune_response (366)	NKX25.02	0.35		H	H	0	0	0	general GO
immune_response (366)	OCT1.02	0.3		H	0	0	0	0	general GO
inflammatory_response (163)	DLX3.01	0.34	0		0	0	0	0	general GO
innate_immune_response (46)	HNF1.02	0.34	H		0	0	H	0	general GO
blood_coagulation (70)	HNF1.02	0.34	0		0	0	0	0	general GO
inflammatory_response (163)	XFD1.01	0.34	0		0	0	0	0	general GO
immune_response (366)	XFD1.01	0.34		H	0	0	0	0	general GO
immune_response (366)	HMEF2.01	0.34	H		0	0	0	0	general GO
sensory_perception (201)	GATA3.01	0.34	H		H	0	H	0	general GO
inflammatory_response (163)	GATA3.01	0.34	H		0	0	H	0	general GO
chemotaxis (98)	GATA3.01	0.34			0	0	H	0	general GO
inflammatory_response (163)	PAX4.01	0.33	0		0	0	0	0	general GO
inflammatory_response (163)	EVI1.04	0.33	0		0	0	0	0	general GO
immune_response (366)	EVI1.04	0.33	H		0	H	0	0	general GO
signal_transduction (1189)	EVI1.02	0.33	M		0	0	0	0	general GO
sensory_perception (201)	EVI1.02	0.33	0		H	H	0	0	general GO
immune_response (366)	EVI1.02	0.33		H	H	0	0	0	general GO

G protein coupled receptor protein signaling pathwa	EV11.02	0.33	0	H	0	0	0	0	general GO
inflammatory_response (163)	BRN3.02	0.33	0		0	0	H	0	general GO
immune_response (366)	BRN2.03	0.32	H	H	0	0	0	0	general GO
chromosome_organization_and_biogenesis (83)	BRN2.03	0.32	0	H	0	H	0	0	general GO
sensory_perception (201)	XFD2.01	0.32	0	H	0	H	0	0	general GO
immune_response (366)	XFD2.01	0.32	M	H	0	0	0	0	general GO
inflammatory_response (163)	LMX1B.01	0.32	0		0	0	H	0	general GO
immune_response (366)	LMX1B.01	0.32	0	H	0	0	0	0	general GO
proteolysis (297)	FREAC3.01	0.32	M		0	0	0	0	general GO
inflammatory_response (163)	CART1.01	0.32	0		0	0	0	0	general GO
immune_response (366)	CART1.01	0.32	H		0	0	0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	EN1.01	0.32	0		0	0	0	0	general GO
transport (940)	HNF1.03	0.31	0		0	0	0	0	general GO
sodium_ion_transport (75)	HNF1.03	0.31	0		0	0	0	0	general GO
immune_response (366)	HNF1.03	0.31	H		0	0	0	0	general GO
blood_coagulation (70)	HNF1.03	0.31	0		0	0	0	0	general GO
signal_transduction (1189)	EV11.01	0.31	M		0	0	0	0	general GO
G protein coupled receptor protein signaling pathwa	EV11.01	0.31	H		0	0	0	0	general GO
synaptic_transmission (153)	MSX.01	0.3	0		0	0	0	0	general GO
immune_response (366)	ATATA.01	0.3	0		0	0	0	0	general GO
immune_response (366)	EV11.06	0.3		H	H	H	0	0	general GO
cell_cell_signaling (268)	ATATA.01	0.3	0		0	0	0	0	general GO
muscle_development (107)	MEF2.02	0.3	0		0	0	0	0	general GO
inflammatory_response (163)	MEF2.02	0.3	0		0	0	0	0	general GO
immune_response (366)	MEF2.02	0.3	0		0	0	0	0	general GO
inflammatory_response (163)	MEF2.03	0.3	0		0	0	0	0	general GO
immune_response (366)	MEF2.03	0.3	H		0	0	0	0	general GO
transport (940)	HNF1.01	0.3	0		0	0	0	0	general GO
sodium_ion_transport (75)	HNF1.01	0.3	0		0	0	0	0	general GO
proteolysis (297)	HNF1.01	0.3	H		0	0	0	0	general GO
innate_immune_response (46)	HNF1.01	0.3		H	0	0	H	0	general GO
immune_response (366)	HNF1.01	0.3		H	0	0	0	0	general GO
blood_coagulation (70)	HNF1.01	0.3	H		0	0	0	0	general GO
immune_response (366)	MEF2.05	0.29			0	0	0	0	general GO
inflammatory_response (163)	RSRFC4.02	0.29	0		0	0	0	0	general GO
immune_response (366)	RSRFC4.02	0.29	H		0	0	0	0	general GO
immune_response (366)	MEL1_01	0.29		H		0	0	H	general GO
immune_response (366)	MEF2.04	0.29	H		0	0	0	0	general GO
immune_response (366)	EV11.05	0.29		H	H	0	0	0	general GO
G protein coupled receptor protein signaling pathwa	EV11.05	0.29	H		0	0	0	0	general GO
sensory_perception (201)	TATA.01	0.28	0		0	0	H	0	general GO
inflammatory_response (163)	TATA.01	0.28	0		0	0	0	0	general GO
immune_response (366)	TATA.01	0.28	M		0	0	0	0	general GO
epidermis_development (59)	TATA.01	0.28	0		0	0	0	0	general GO
digestion (51)	TATA.01	0.28	0		0	0	0	0	general GO
chromosome_organization_and_biogenesis (83)	TATA.01	0.28	0	H	0	0	0	0	general GO
chemotaxis (98)	TATA.01	0.28	0		0	0	0	0	general GO
cell_differentiation (192)	TATA.01	0.28	0		0	0	0	0	general GO
cell_cell_signaling (268)	TATA.01	0.28	H		0	0	0	0	general GO
calcium_ion_homeostasis (30)	TATA.01	0.28	0		0	0	0	0	general GO
immune_response (366)	RSRFC4.01	0.28	0		0	0	0	0	general GO
inflammatory_response (163)	TATA.02	0.28	0		0	0	0	0	general GO
immune_response (366)	TATA.02	0.28	0		0	0	0	0	general GO
epidermis_development (59)	TATA.02	0.28	0		0	0	0	0	general GO
cell_cell_signaling (268)	TATA.02	0.28	0		0	0	0	0	general GO
inflammatory_response (163)	MYT1.02	0.28	0		0	0	0	0	general GO
immune_response (366)	MYT1.02	0.28	H	H	0	0	0	0	general GO
inflammatory_response (163)	PIT1.01	0.27	H		0	0	0	0	general GO
immune_response (366)	PIT1.01	0.27	H		H	0	0	0	general GO
blood_coagulation (70)	SATB1.01	0.27		0	0	0	0	0	general GO
inflammatory_response (163)	HFH1.01	0.27	0		0	0	0	0	general GO
proteolysis (297)	HFH8.01	0.27	0		0	0	0	0	general GO
immune_response (366)	HFH8.01	0.27		H	0	0	0	0	general GO
inflammatory_response (163)	MYT1.01	0.27	M	H	0	0	0	0	general GO

immune_response (366)	OCT1.01	0.26	H	0	H	0	0	general GO
immune_response (366)	BRN5.01	0.26	H	0	0	0	0	general GO
steroid_metabolism (54)	HNF3B.01	0.26	0	0	0	0	0	general GO
immune_response (366)	NKX31.01	0.25	H	0	0	0	0	general GO
immune_response (366)	EVI1.03	0.24	H	H	0	0	H	general GO
G_protein_coupled_receptor_protein_signaling_pathwa	EVI1.03	0.24	H	H	0	0	0	general GO
immune_response (366)	BRIGHT.01	0.22	0	0	0	0	0	general GO
innate_immune_response (46)	OCT1.06	0.22	H	0	0	0	0	general GO
inflammatory_response (163)	OCT1.06	0.22	H	0	M	0	0	general GO
immune_response (366)	OCT1.06	0.22	0	0	0	0	0	general GO
proteolysis (297)	LHX3.01	0.14	H	0	0	0	0	general GO
immune_response (366)	LHX3.01	0.14	0	0	0	0	0	general GO

inflammatory_response (163)	poly_A	0.01	0	0	0	0	0	
immune_response (366)	poly_A	0.01	H	0	0	0	0	
transcription (930)	GC_rich	0.99	H					&H
regulation_of_transcription_DNA_dependent (1066)	GC_rich	0.99	M					&H
development (530)	GC_rich	0.99	0	0	M	0	M	
ubiquitin_cycle (154)	GC_rich	0.99	H	0	0	0	0	
intracellular_protein_transport (191)	GC_rich	0.99	H	0	0	0	0	
transcription (930)	poly_C	0.99				M		&H
regulation_of_transcription_DNA_dependent (1066)	poly_C	0.99						&H
regulation_of_transcription (266)	poly_C	0.99	M	0		0	M	
development (530)	poly_C	0.99	M	H	H		M	
Wnt_receptor_signaling_pathway (66)	poly_C	0.99	0		H	H	0	0
transcription_RNA_polyII_promoter (190)	poly_C	0.99	0	0		0	0	0
potassium_ion_transport (108)	poly_C	0.99	0	H	H		0	0

300bp Window

GO group	Motifs	motif GC	-199 - 100	101 - 400	401 - 700	701 - 1000	GO-classes
transcription (930)	GC_rich	0.99					transcription GO
transcription (930)	poly_C	0.99					transcription GO
transcription (930)	SP1.01	0.78	H				transcription GO
transcription (930)	WT1.01	0.77	H				transcription GO
transcription (930)	HES1.02	0.76	0		H		transcription GO
transcription (930)	MAZR.01	0.76					transcription GO
transcription (930)	ZNF202.01	0.73					transcription GO
transcription (930)	AP2.01	0.73	H				transcription GO
transcription (930)	ZF5.01	0.72	H		H		transcription GO
transcription (930)	ZF9.01	0.72	H				transcription GO
transcription (930)	EGR3.01	0.71	H				transcription GO
transcription (930)	NRF1_01	0.71	H				transcription GO
transcription (930)	MYCMAX.03	0.7	0	H	H		transcription GO
transcription (930)	ZBP89.01	0.7			H		transcription GO
transcription (930)	HELT.01	0.69	H	H	H		transcription GO
transcription (930)	NGFIC.01	0.69	H		H	H	transcription GO
transcription (930)	CKROX_01	0.68					transcription GO
transcription (930)	EGR1.02	0.68					transcription GO
transcription (930)	HIC1_01	0.68	0	H	0		transcription GO
transcription (930)	BKLF.01	0.68	0	0	H		transcription GO
transcription (930)	GC.01	0.68	0	H			transcription GO
transcription (930)	MZF1.01	0.68	H	M		H	transcription GO
transcription (930)	MTF-1.01	0.65	0		0	0	transcription GO
transcription (930)	MAZ.01	0.65	H				transcription GO
transcription (930)	ZIC2_01	0.65	H	H	0		transcription GO
transcription (930)	ATF6.01	0.64	0		H	0	transcription GO
transcription (930)	PLAG1_01	0.63					transcription GO
transcription (930)	EBVR.01	0.63	H	0	0		transcription GO
transcription (930)	AHRARNT.01	0.62	0	H	H		transcription GO
transcription (930)	HES1.01	0.62	H		H	H	transcription GO
transcription (930)	MUSCLE_IN	0.62	0		H	H	transcription GO
transcription (930)	GABP.01	0.62	0	M	H	H	transcription GO
transcription (930)	MUSCLE_IN	0.61	0		H	0	transcription GO
transcription (930)	CDE.01	0.6					transcription GO
transcription (930)	AHR.01	0.59	H	H	H	M	transcription GO
transcription (930)	E2F.02	0.59		H			transcription GO
transcription (930)	WHN.01	0.59	H	H	0		transcription GO
transcription (930)	PAX5.01	0.57	0	H	M	H	transcription GO
transcription (930)	GAGA.01	0.56				H	transcription GO
transcription (930)	E2F.03	0.54	H	H			transcription GO
transcription (930)	AC_rich_cod	0.5		0	0	H	transcription GO
transcription (930)	AG_rich_cod	0.5			M	0	transcription GO
transcription (930)	GKLF.01	0.49	M	H	0	0	transcription GO
transcription (930)	CAAT.01	0.49	0	H	M	0	transcription GO
transcription (930)	NFY.02	0.48	0	H	M	0	transcription GO
regulation_of_transcription_from_RNA_polymerase	CDE.01	0.6	H	H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	GC_rich	0.99					transcription GO
regulation_of_transcription_DNA_dependent (1066)	poly_C	0.99					transcription GO
regulation_of_transcription_DNA_dependent (1066)	SP1.01	0.78	H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	WT1.01	0.77					transcription GO
regulation_of_transcription_DNA_dependent (1066)	HES1.02	0.76	0			H	transcription GO

regulation_of_transcription_DNA_dependent (1066)	MAZR.01	0.76							transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZNF202.01	0.73							transcription GO
regulation_of_transcription_DNA_dependent (1066)	AP2.01	0.73							transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZF5.01	0.72						H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZF9.01	0.72	H						transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR3.01	0.71	H						transcription GO
regulation_of_transcription_DNA_dependent (1066)	NRF1_01	0.71	H						transcription GO
regulation_of_transcription_DNA_dependent (1066)	MYCMAX.03	0.7	0		H	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	NFKAPPAB5	0.7	0	M	0				transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZBP89.01	0.7							transcription GO
regulation_of_transcription_DNA_dependent (1066)	HELT.01	0.69	H					H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	NGFIC.01	0.69	H			H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	CKROX_01	0.68							transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR1.02	0.68							transcription GO
regulation_of_transcription_DNA_dependent (1066)	HIC1_01	0.68	0	0	H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	BKLF.01	0.68	0	0	H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR2.01	0.68	H	H	H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	GC.01	0.68	0						transcription GO
regulation_of_transcription_DNA_dependent (1066)	MZF1.01	0.68		M		H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR1.01	0.67	H	H	H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	MTF-1.01	0.65	0		H		0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	MAZ.01	0.65							transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZIC2_01	0.65	H		H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	ATF6.01	0.64	0		H	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	PLAG1_01	0.63							transcription GO
regulation_of_transcription_DNA_dependent (1066)	AHRARNT.01	0.62	0	H	H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	HES1.01	0.62	H					H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	MUSCLE_IN	0.62	0		H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	GABP.01	0.62	0	M	H	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	NMYC.01	0.62	0		H		0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	MUSCLE_IN	0.61	0		H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	RREB1.01	0.6	H	H	H	M			transcription GO
regulation_of_transcription_DNA_dependent (1066)	CDE.01	0.6	H						transcription GO
regulation_of_transcription_DNA_dependent (1066)	AHR.01	0.59	0	H	H	M			transcription GO
regulation_of_transcription_DNA_dependent (1066)	E2F.02	0.59		H					transcription GO
regulation_of_transcription_DNA_dependent (1066)	WHN.01	0.59	0	H	0				transcription GO
regulation_of_transcription_DNA_dependent (1066)	TAXCREB.01	0.58	0	H	M	M			transcription GO
regulation_of_transcription_DNA_dependent (1066)	PAX9.01	0.57	0		H	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	PAX5.01	0.57	0	H		H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	PAX5.03	0.56	0		0	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	VDR_RXR.02	0.56	H	0	M	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	GAGA.01	0.56				H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	TAXCREB.02	0.56	0	0	M	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	E2F.03	0.54	H	H	H				transcription GO
regulation_of_transcription_DNA_dependent (1066)	NFY.01	0.52	0				0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	AG_rich_cod	0.5					0		transcription GO
regulation_of_transcription_DNA_dependent (1066)	GKLF.01	0.49		H	0	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	CAAT.01	0.49	0		0	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	NFY.02	0.48	0		0	0			transcription GO
regulation_of_transcription (266)	GC_rich	0.99	H		H				transcription GO
regulation_of_transcription (266)	poly_C	0.99							transcription GO
regulation_of_transcription (266)	SP1.01	0.78	H		M	M			transcription GO
regulation_of_transcription (266)	WT1.01	0.77	H		H				transcription GO
regulation_of_transcription (266)	MAZR.01	0.76	H						transcription GO
regulation_of_transcription (266)	ZNF202.01	0.73					M		transcription GO
regulation_of_transcription (266)	AP2.01	0.73	0			H			transcription GO
regulation_of_transcription (266)	ZF5.01	0.72	0		H	H			transcription GO
regulation_of_transcription (266)	ZF9.01	0.72	0		H	0			transcription GO
regulation_of_transcription (266)	EGR3.01	0.71	H	M	H	M			transcription GO
regulation_of_transcription (266)	ZBP89.01	0.7				H			transcription GO
regulation_of_transcription (266)	NGFIC.01	0.69	H	M	H	M			transcription GO
regulation_of_transcription (266)	CKROX_01	0.68							transcription GO
regulation_of_transcription (266)	EGR1.02	0.68	H			H			transcription GO
regulation_of_transcription (266)	EGR2.01	0.68	H	0	0	M			transcription GO

regulation_of_transcription (266)	MTF-1.01	0.65	0	0	0	transcription GO
regulation_of_transcription (266)	MAZ.01	0.65			H	transcription GO
regulation_of_transcription (266)	PLAG1_01	0.63			H	transcription GO
regulation_of_transcription (266)	HES1.01	0.62	0	0	H	transcription GO
regulation_of_transcription (266)	CDE.01	0.6	H		H	transcription GO
regulation_of_transcription (266)	E2F.02	0.59	0	0	H	transcription GO
regulation_of_transcription (266)	TAXCREB.01	0.58	0	H	M	transcription GO
regulation_of_transcription (266)	VDR_RXR.02	0.56	H	H		transcription GO
regulation_of_transcription (266)	GAGA.01	0.56		H	M	transcription GO
regulation_of_transcription (266)	AG_rich_cod	0.5			M	transcription GO
regulation_of_transcription (266)	GKLF.01	0.49		H	0	transcription GO
regulation_of_transcription (266)	CAAT.01	0.49	0		0	transcription GO
regulation_of_transcription (266)	PBX1_MEIS1	0.44	0		0	transcription GO
development (530)	GC_rich	0.99	H			transcription GO
development (530)	poly_C	0.99			H	transcription GO
development (530)	SP1.01	0.78	0	H	M	transcription GO
development (530)	WT1.01	0.77	H			transcription GO
development (530)	HES1.02	0.76	0	0	0	transcription GO
development (530)	MAZR.01	0.76	H		H	transcription GO
development (530)	ZNF202.01	0.73				transcription GO
development (530)	AP2.01	0.73	H			transcription GO
development (530)	ZF9.01	0.72	0	0	H	transcription GO
development (530)	NFKAPPAB5	0.7	0	H	M	transcription GO
development (530)	HAND2_E12	0.7	0	M	H	transcription GO
development (530)	ZBP89.01	0.7	H			transcription GO
development (530)	NGFIC.01	0.69	0		0	transcription GO
development (530)	CKROX_01	0.68	0			transcription GO
development (530)	EGR1.02	0.68	0		H	transcription GO
development (530)	HIC1_01	0.68	0	H	H	transcription GO
development (530)	EGR2.01	0.68	0	M	0	transcription GO
development (530)	MZF1.01	0.68	H	H	H	transcription GO
development (530)	EGR1.01	0.67	0	M	H	transcription GO
development (530)	MAZ.01	0.65	H	H		transcription GO
development (530)	ZIC2_01	0.65	0	H	0	transcription GO
development (530)	PLAG1_01	0.63				transcription GO
development (530)	INSM1_01	0.63	0	0	H	transcription GO
development (530)	EBVR.01	0.63	0	H		transcription GO
development (530)	MUSCLE_IN	0.62	0		H	transcription GO
development (530)	CDE.01	0.6	0	0	H	transcription GO
development (530)	E2F.02	0.59	0	0	H	transcription GO
development (530)	PAX5.01	0.57	0	0	H	transcription GO
development (530)	GAGA.01	0.56		H	H	transcription GO
development (530)	AG_rich_cod	0.5		H	0	transcription GO
development (530)	GKLF.01	0.49	M	H	0	transcription GO
development (530)	MTATA.01	0.47		0	0	transcription GO
development (530)	AMEF2.01	0.38		0	0	transcription GO
Wnt_receptor_signaling_pathway (66)	GC_rich	0.99			H	general GO
Wnt_receptor_signaling_pathway (66)	WT1.01	0.77	0	H	M	general GO
Wnt_receptor_signaling_pathway (66)	ZNF202.01	0.73	M	H	0	general GO
Wnt_receptor_signaling_pathway (66)	ZF5.01	0.72	M	0	H	general GO
Wnt_receptor_signaling_pathway (66)	NRF1_01	0.71	H	0	M	general GO
Wnt_receptor_signaling_pathway (66)	NGFIC.01	0.69	H		0	general GO
Wnt_receptor_signaling_pathway (66)	EGR2.01	0.68	0	0	M	general GO
Wnt_receptor_signaling_pathway (66)	EGR1.01	0.67	H	M	0	general GO
Wnt_receptor_signaling_pathway (66)	CDE.01	0.6	H	M	H	general GO
Wnt_receptor_signaling_pathway (66)	PAX5.01	0.57	0		0	general GO
visual_perception (142)	HOX_PBX_0	0.48		0	0	general GO
visual_perception (142)	PTX1.01	0.45		H	0	general GO
visual_perception (142)	CRX.01	0.39		0	0	general GO
visual_perception (142)	OTX2.01	0.39		H	0	general GO
visual_perception (142)	CDX2.01	0.38	M	H	0	general GO
visual_perception (142)	SIX3.01	0.35		H	H	general GO
visual_perception (142)	EVH1.04	0.33	M	H	0	general GO
ubiquitin_dependent_protein_catabolism (72)	WHN.01	0.59		0	0	general GO

ubiquitin_cycle (154)	GC_rich	0.99		0	0	0	general GO
ubiquitin_cycle (154)	HES1.01	0.62		0	0	0	general GO
ubiquitin_cycle (154)	MUSCLE_IN	0.62		0	0	0	general GO
ubiquitin_cycle (154)	CDE.01	0.6		H	H	0	general GO
ubiquitin_cycle (154)	FLI.01	0.53		H	0	0	general GO
transport (940)	XBP1.01	0.47	H	M	0	0	general GO
transport (940)	OTX2.01	0.39	M	0	0	H	general GO
transport (940)	HNF1.03	0.31		0	0	0	general GO
transport (940)	HNF1.01	0.3		0	0	0	general GO
transmembrane_receptor_tyrosine_kinase_signaling	GAGA.01	0.56	H	M	0	0	general GO
transcription_RNA_polyll_promoter (190)	GC_rich	0.99	H		0	0	general GO
transcription_RNA_polyll_promoter (190)	poly_C	0.99	0		0	0	general GO
transcription_RNA_polyll_promoter (190)	SP1.01	0.78	0		0	0	general GO
transcription_RNA_polyll_promoter (190)	WT1.01	0.77	0		0	0	general GO
transcription_RNA_polyll_promoter (190)	ZNF202.01	0.73	0		0	0	general GO
transcription_RNA_polyll_promoter (190)	AP2.01	0.73	0	H		H	general GO
transcription_RNA_polyll_promoter (190)	EGR3.01	0.71	0	M	H	0	general GO
transcription_RNA_polyll_promoter (190)	NRF1_01	0.71	0		0	0	general GO
transcription_RNA_polyll_promoter (190)	HIC1_01	0.68	0	0	0		general GO
transcription_RNA_polyll_promoter (190)	MTF-1.01	0.65	0		0	0	general GO
transcription_RNA_polyll_promoter (190)	PLAG1_01	0.63	M	H	0	H	general GO
transcription_RNA_polyll_promoter (190)	CDE.01	0.6	0	H	M		general GO
synaptic_transmission (153)	NRSE.01	0.57	H		0	0	general GO
synaptic_transmission (153)	GAGA.01	0.56	0	0	M	H	general GO
synaptic_transmission (153)	ISL1.01	0.43	H	M	0	0	general GO
steroid_biosynthesis (42)	NFY.01	0.52	M	H	0	0	general GO
steroid_biosynthesis (42)	CAAT.01	0.49	M	H	0	0	general GO
steroid_biosynthesis (42)	NFY.03	0.47	M		0	0	general GO
sodium_ion_transport (75)	FXRE.01	0.51	0	M	H	0	general GO
sodium_ion_transport (75)	HNF1.03	0.31	H	M	0	0	general GO
sodium_ion_transport (75)	HNF1.01	0.3	H	M	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	GC_rich	0.99		H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	SP1.01	0.78		H	H	0	general GO
small_GTPase_mediated_signal_transduction (124)	WT1.01	0.77		H	H	0	general GO
small_GTPase_mediated_signal_transduction (124)	ZF5.01	0.72		H	0	H	general GO
small_GTPase_mediated_signal_transduction (124)	ZF9.01	0.72		H	H	0	general GO
small_GTPase_mediated_signal_transduction (124)	EGR3.01	0.71	H	0	H	M	general GO
small_GTPase_mediated_signal_transduction (124)	NRF1_01	0.71		H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	NGFIC.01	0.69		0	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	EGR1.02	0.68		H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	EGR2.01	0.68	H	0	0	M	general GO
small_GTPase_mediated_signal_transduction (124)	GC.01	0.68		H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	PLAG1_01	0.63		0	0	0	general GO
skeletal_development (83)	GAGA.01	0.56	H		H	0	general GO
signal_transduction (1189)	NFKAPPAB.0	0.57		0	0	0	general GO
signal_transduction (1189)	HIVEP1_01	0.52	H	M	0	0	general GO
signal_transduction (1189)	MEL1_02	0.46		0	0	0	general GO
signal_transduction (1189)	AARE.01	0.39		0	0	0	general GO
signal_transduction (1189)	EV1i.02	0.33		0	0	0	general GO
signal_transduction (1189)	EV1i.01	0.31		0	0	0	general GO
signal_transduction (1189)	poly_A	0.01		0	0	0	general GO
sensory_perception_of_smell (40)	NFE2L2.01	0.47	M	H	0	0	general GO
sensory_perception_of_smell (40)	LHX3.01	0.14	H		H	H	general GO
sensory_perception (201)	NFKAPPAB.0	0.57	H	M	0	0	general GO
sensory_perception (201)	IK2.01	0.49		0	0	0	general GO
sensory_perception (201)	SRF.03	0.47		H	0	0	general GO
sensory_perception (201)	MIT.01	0.46		H	H	0	general GO
sensory_perception (201)	MEL1_03	0.46			0	0	general GO
sensory_perception (201)	DBP.01	0.45		H	H	0	general GO
sensory_perception (201)	GATA1.01	0.45		0	0	0	general GO
sensory_perception (201)	PBX1_MEIS1	0.44	0	0	M	H	general GO
sensory_perception (201)	TGIF.01	0.44		0	0	0	general GO
sensory_perception (201)	SRF.01	0.42		H	0	0	general GO
sensory_perception (201)	RORA1.01	0.41		H	0	0	general GO

sensory_perception (201)	GF11.01	0.41	H	0	0	general GO
sensory_perception (201)	CRX.01	0.39	H	0	0	general GO
sensory_perception (201)	AARE.01	0.39	H	H	M	0 general GO
sensory_perception (201)	AIRE.01	0.39	H	H	0	general GO
sensory_perception (201)	LTATA_01	0.39	H	0	0	general GO
sensory_perception (201)	OTX2.01	0.39	H	0	0	general GO
sensory_perception (201)	GATA1.03	0.39	H	H	0	general GO
sensory_perception (201)	NFAT.01	0.38	0	0	0	general GO
sensory_perception (201)	CDX2.01	0.38	H	H	0	general GO
sensory_perception (201)	GATA2.02	0.36	H	H	0	general GO
sensory_perception (201)	XFD3.01	0.36	0	0	H	general GO
sensory_perception (201)	OCT1P.01	0.36		H	0	general GO
sensory_perception (201)	SIX3.01	0.35	H	0	0	general GO
sensory_perception (201)	PDX1_G_SA	0.35	H	H	H	general GO
sensory_perception (201)	GATA2.01	0.35	H	H	0	general GO
sensory_perception (201)	NKX25.02	0.35	H	0	0	general GO
sensory_perception (201)	FREAC2.01	0.35	0	M	H	0 general GO
sensory_perception (201)	GATA3.01	0.34	H	H	0	general GO
sensory_perception (201)	XFD2.01	0.32	H	H	H	general GO
sensory_perception (201)	HNF1.03	0.31	H	0	0	general GO
sensory_perception (201)	PBX1.01	0.31	H	H	0	general GO
sensory_perception (201)	XVENT2.01	0.3	H	0	H	general GO
sensory_perception (201)	MEF2.02	0.3	H	0	0	general GO
sensory_perception (201)	MEL1_01	0.29	H	H	0	general GO
sensory_perception (201)	GATA3.02	0.29	H	H	0	general GO
sensory_perception (201)	EV11.05	0.29	H	H	0	general GO
sensory_perception (201)	TATA.01	0.28	H	0	0	general GO
sensory_perception (201)	TATA.02	0.28	H	0	0	general GO
sensory_perception (201)	HFH8.01	0.27	H	H	0	general GO
sensory_perception (201)	OCT1.01	0.26	H	H	0	general GO
sensory_perception (201)	HNF3B.01	0.26	H	H	0	general GO
sensory_perception (201)	HFH2.01	0.25	H	H	0	general GO
sensory_perception (201)	EV11.03	0.24	H	H	0	general GO
response_to_virus (55)	ISRE.01	0.43		0	0	general GO
response_to_virus (55)	IRF2.01	0.43		0	0	general GO
response_to_virus (55)	IRF3.01	0.42		0	0	general GO
response_to_virus (55)	PRDM1.01	0.41	0		0	general GO
response_to_virus (55)	HBP1_01	0.41	M	H	0	general GO
response_to_virus (55)	IRF1.01	0.4		H	0	general GO
response_to_virus (55)	BRN2.01	0.39	0	H	H	general GO
response_to_virus (55)	STAT5.01	0.39	H	0	M	0 general GO
response_to_virus (55)	IRF7.01	0.36	H	0	0	general GO
response_to_virus (55)	TATA.01	0.28	H	H	0	general GO
response_to_unfolded_protein (40)	STAT1.01	0.52	0		0	general GO
response_to_DNA_damage_stimulus (117)	E2F.02	0.59		M	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.03	0.54	H	M	0	M general GO
response_to_DNA_damage_stimulus (117)	FLI.01	0.53		0	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.01	0.5	H	M	0	general GO
regulation_of_transcription_from_RNA_polymerase	WT1.01	0.77	H		0	general GO
regulation_of_transcription_from_RNA_polymerase	ZF5.01	0.72	H	H	0	M general GO
regulation_of_transcription_from_RNA_polymerase	MAZ.01	0.65		H	M	0 general GO
regulation_of_transcription_from_RNA_polymerase	PLAG1_01	0.63	0		0	general GO
regulation_of_transcription_from_RNA_polymerase	HES1.01	0.62	H	0	0	M general GO
regulation_of_progression_through_cell_cycle (217)	GC_rich	0.99	H	M	0	general GO
regulation_of_progression_through_cell_cycle (217)	ZF5.01	0.72	H	M	H	0 general GO
regulation_of_progression_through_cell_cycle (217)	CREB.03	0.54	H	M	0	general GO
regulation_of_cyclin_dependent_protein_kinase_acti	ZF9.01	0.72	0	0		0 general GO
regulation_of_cyclin_dependent_protein_kinase_acti	NFY.01	0.52	0	H	M	0 general GO
regulation_of_apoptosis (59)	IRF3.01	0.42	M	H	0	general GO
proteolysis (297)	NRL.01	0.51	0	0	H	M general GO
proteolysis (297)	AREB6.01	0.49		0	0	H general GO
proteolysis (297)	AREB6.02	0.48		0	0	general GO
proteolysis (297)	AP1.01	0.43		0	0	general GO
proteolysis (297)	IRF4.01	0.39	H	0	0	general GO

proteolysis (297)	GATA1.03	0.39	0	H	0	M	general GO
proteolysis (297)	HNF1.02	0.34		0	0	0	general GO
proteolysis (297)	ATBF1.01	0.34		0	0	0	general GO
proteolysis (297)	HNF1.03	0.31		0	0	0	general GO
proteolysis (297)	HNF1.01	0.3		0	0	0	general GO
proteolysis (297)	HFH1.01	0.27		0	0	0	general GO
proteolysis (297)	MYT1.01	0.27		0	0	0	general GO
protein_transport (254)	GC_rich	0.99		0	0	0	general GO
protein_transport (254)	ZF5.01	0.72		H	0	0	general GO
protein_transport (254)	EGR3.01	0.71		0	0	0	general GO
protein_transport (254)	NRF1_01	0.71		H	0	0	general GO
protein_transport (254)	EGR1.02	0.68		0	0	0	general GO
protein_transport (254)	AHRARNT.0	0.62	M	H	0	0	general GO
protein_transport (254)	MUSCLE_IN	0.62		0	0	0	general GO
protein_transport (254)	GABP.01	0.62		0	0	0	general GO
protein_transport (254)	NRF2.01	0.57		0	0	0	general GO
protein_transport (254)	CREB.02	0.56		0	0	0	general GO
protein_transport (254)	ATF.01	0.55	H	M	0	0	general GO
protein_targeting (37)	NRF2.01	0.57		0	0	0	general GO
protein_targeting (37)	FLI.01	0.53		0	0	0	general GO
protein_folding (149)	ELK1.02	0.55	H	M	0	0	general GO
protein_folding (149)	FLI.01	0.53	H		H	0	general GO
protein_complex_assembly (94)	P53.01	0.61	0	0	0		general GO
protein_biosynthesis (197)	GABP.01	0.62		0	0	0	general GO
protein_biosynthesis (197)	CDE.01	0.6		H	H	H	general GO
protein_biosynthesis (197)	WHN.01	0.59	H		H	0	general GO
protein_biosynthesis (197)	NRF2.01	0.57		M	0	0	general GO
protein_biosynthesis (197)	ATF.01	0.55	H	M	0	0	general GO
protein_biosynthesis (197)	CETS1P54.0	0.55		M	0	0	general GO
protein_biosynthesis (197)	YY1.01	0.55		H	0	0	general GO
protein_biosynthesis (197)	ELK1.02	0.55		H	0	0	general GO
protein_biosynthesis (197)	NUDR.01	0.54	H		0	0	general GO
protein_biosynthesis (197)	E2F.03	0.54	H		H	0	general GO
protein_biosynthesis (197)	FLI.01	0.53		H	0	0	general GO
protein_biosynthesis (197)	ELK1.01	0.52		0	0	0	general GO
protein_biosynthesis (197)	E2F.01	0.5		0	0	0	general GO
protein_biosynthesis (197)	ISRE.01	0.43		0	0	0	general GO
protein_amino_acid_phosphorylation (373)	SP1.01	0.78	H	H		0	general GO
protein_amino_acid_phosphorylation (373)	ZF9.01	0.72	H	H		H	general GO
protein_amino_acid_phosphorylation (373)	PAX9.01	0.57	0		0	0	general GO
protein_amino_acid_dephosphorylation (96)	MUSCLE_IN	0.61	M	0	H	0	general GO
pregnancy (41)	XVENT2.01	0.3	H	0	0	M	general GO
pregnancy (41)	CDP.02	0.29	M	0	0	H	general GO
potassium_ion_transport (108)	poly_C	0.99					general GO
potassium_ion_transport (108)	SP1.01	0.78	0	H	M	0	general GO
potassium_ion_transport (108)	NGFIC.01	0.69	0	M	0	H	general GO
potassium_ion_transport (108)	EGR2.01	0.68	0	0	0		general GO
potassium_ion_transport (108)	INSM1_01	0.63	0	M	0	H	general GO
positive_regulation_of_I_kappaB_kinase_NF_kappa	ETS1.01	0.52	H	0	0	M	general GO
positive_regulation_of_I_kappaB_kinase_NF_kappa	IRF3.01	0.42		0	0	0	general GO
positive_regulation_of_cell_proliferation (103)	HEN1.02	0.66	0	M	H	0	general GO
organ_morphogenesis (71)	GAGA.01	0.56	0	H	M	0	general GO
nucleosome_assembly (71)	NFY.02	0.48	H		H	0	general GO
nucleosome_assembly (71)	TATA.01	0.28		H	0	0	general GO
nuclear_mRNA_splicing_via_spliceosome (94)	NRF2.01	0.57		H	0	0	general GO
nervous_system_development (225)	ZNF202.01	0.73	H	H	H		general GO
nervous_system_development (225)	GAGA.01	0.56		H	H	H	general GO
nervous_system_development (225)	AG_rich_cod	0.5		H	0	0	general GO
muscle_development (107)	INSM1_01	0.63		0	0	0	general GO
muscle_development (107)	SRF.02	0.49		H	0	0	general GO
muscle_development (107)	MTATA.01	0.47		0	0	0	general GO
muscle_development (107)	SRF.03	0.47	H		0	0	general GO
muscle_development (107)	AMEF2.01	0.38	M	H	0	0	general GO
muscle_development (107)	MEF2.02	0.3	H		0	0	general GO

muscle_development (107)	RSRFC4.01	0.28		H	0	0	general GO
mRNA_processing (148)	NRF1_01	0.71	H	M	0	0	general GO
mRNA_processing (148)	E2F.02	0.59		H	0	0	general GO
morphogenesis (104)	WT1.01	0.77	0	H	H		general GO
morphogenesis (104)	AP2.01	0.73	0	H	0		general GO
morphogenesis (104)	EGR1.02	0.68	H	0	M	H	general GO
morphogenesis (104)	MUSCLE_IN	0.61	0	H	H	M	general GO
mitosis (86)	CDE.01	0.6	M	H	0	0	general GO
mitosis (86)	WHN.01	0.59	0		0	0	general GO
mitosis (86)	NFY.01	0.52			0	0	general GO
mitosis (86)	CAAT.01	0.49			0	0	general GO
mitosis (86)	NFY.02	0.48		0	0	0	general GO
mitosis (86)	CHR.01	0.41		0	0	0	general GO
metabolism (241)	NFY.02	0.48		0	0	0	general GO
metabolism (241)	E4BP4.01	0.34	M	H	0	0	general GO
metabolism (241)	GATA3.02	0.29	0	M	0	H	general GO
lipid_transport (41)	SRF.03	0.47		0	0	0	general GO
lipid_transport (41)	RORA1.01	0.41		0	0	0	general GO
lipid_catabolism (41)	RORA1.01	0.41	0	0	H	M	general GO
lipid_biosynthesis (54)	CAAT.01	0.49	M	H	0	0	general GO
lipid_biosynthesis (54)	NFY.02	0.48	M	H	0	0	general GO
lipid_biosynthesis (54)	NFY.03	0.47	M	H	0	0	general GO
ion_transport (329)	NRSE.01	0.57	M	0	0	H	general GO
intracellular_protein_transport (191)	GC_rich	0.99		H	0	0	general GO
intracellular_protein_transport (191)	NRF1_01	0.71		H	0	0	general GO
intracellular_protein_transport (191)	ATF6.02	0.6		0	0	0	general GO
intracellular_protein_transport (191)	CDE.01	0.6		H	0	0	general GO
intracellular_protein_transport (191)	AHR.01	0.59	M	H	0	0	general GO
intracellular_protein_transport (191)	ATF.01	0.55	H	M	0	0	general GO
intracellular_protein_transport (191)	XBP1.01	0.47		0	0	H	general GO
innate_immune_response (46)	PAX2.01	0.47		0	0	0	general GO
innate_immune_response (46)	TST1.01	0.43		0	0	0	general GO
innate_immune_response (46)	ISL1.01	0.43	H	M	0	0	general GO
innate_immune_response (46)	IRF2.01	0.43		0	0	0	general GO
innate_immune_response (46)	IRF3.01	0.42		0	0	0	general GO
innate_immune_response (46)	PSE_02	0.41		H	H	0	general GO
innate_immune_response (46)	BRN4.01	0.4		H	0	0	general GO
innate_immune_response (46)	CEBPB.01	0.4		H	H	0	general GO
innate_immune_response (46)	OCT1.04	0.38	M	0	H	0	general GO
innate_immune_response (46)	CDX2.01	0.38		0	0	H	general GO
innate_immune_response (46)	IRF7.01	0.36		0	0	0	general GO
innate_immune_response (46)	OCT.01	0.35		0	H	0	general GO
innate_immune_response (46)	OCT1.02	0.34		0	0	0	general GO
innate_immune_response (46)	XFD1.01	0.34		H	0	0	general GO
innate_immune_response (46)	ATBF1.01	0.34		0	0	0	general GO
innate_immune_response (46)	XFD2.01	0.32		H	H	0	general GO
innate_immune_response (46)	LMX1B.01	0.32		H	0	0	general GO
innate_immune_response (46)	EN1.01	0.32		H	0	0	general GO
innate_immune_response (46)	BRN3.01	0.3		0	0	0	general GO
innate_immune_response (46)	MEF2.03	0.3	M	H	0	0	general GO
innate_immune_response (46)	HNF1.01	0.3		0	0	0	general GO
innate_immune_response (46)	GATA3.02	0.29	0	M	H	0	general GO
innate_immune_response (46)	PIT1.01	0.27		0		0	general GO
innate_immune_response (46)	SATB1.01	0.27		0	0	H	general GO
innate_immune_response (46)	HFH8.01	0.27	M	H	0	0	general GO
innate_immune_response (46)	OCT1.01	0.26		0	0	0	general GO
innate_immune_response (46)	NKX31.01	0.25	M	0	0	H	general GO
innate_immune_response (46)	OCT1.06	0.22		0	0	0	general GO
inflammatory_response (163)	NFKAPPAB.0	0.6			0	0	general GO
inflammatory_response (163)	NFKAPPAB.0	0.57	H		0	0	general GO
inflammatory_response (163)	NFKAPPAB6	0.55		M	0	0	general GO
inflammatory_response (163)	CREL.01	0.55		M	0	0	general GO
inflammatory_response (163)	NFKAPPAB.0	0.55			0	0	general GO
inflammatory_response (163)	HIVEP1_01	0.52			0	0	general GO

inflammatory_response (163)	TH1E47.01	0.51		0	0	0	general GO
inflammatory_response (163)	ETS2.01	0.48	H		0	0	general GO
inflammatory_response (163)	GRE.01	0.47		H	0	0	general GO
inflammatory_response (163)	NFE2L2.01	0.47		0	0	0	general GO
inflammatory_response (163)	RP58.01	0.46		0	0	0	general GO
inflammatory_response (163)	CEBP.02	0.46	M		0	0	general GO
inflammatory_response (163)	COMP1.01	0.45		H	0	0	general GO
inflammatory_response (163)	BARBIE.01	0.45		0	0	0	general GO
inflammatory_response (163)	GATA1.01	0.45		M	0	0	general GO
inflammatory_response (163)	MYT1L.01	0.44		0	0	0	general GO
inflammatory_response (163)	TCF11MAFG	0.43		0	H	0	general GO
inflammatory_response (163)	AP1.01	0.43		H	0	0	general GO
inflammatory_response (163)	ISL1.01	0.43	M	H	H	0	general GO
inflammatory_response (163)	ISRE.01	0.43		0	0	0	general GO
inflammatory_response (163)	IRF3.01	0.42		0	0	0	general GO
inflammatory_response (163)	SRF.01	0.42		0	0	0	general GO
inflammatory_response (163)	PRDM1.01	0.41		H	0	0	general GO
inflammatory_response (163)	HMG1Y.01	0.41		H	H	0	general GO
inflammatory_response (163)	PDX1_Gabi	0.41	M	0	H	0	general GO
inflammatory_response (163)	GATA.01	0.41	M	H	0	0	general GO
inflammatory_response (163)	HBP1_01	0.41	H	H	0	M	general GO
inflammatory_response (163)	PSE_02	0.41	H	M	0	0	general GO
inflammatory_response (163)	BRN4.01	0.4		H	0	0	general GO
inflammatory_response (163)	IRF1.01	0.4		M	0	0	general GO
inflammatory_response (163)	CEBPB.01	0.4		H	0	0	general GO
inflammatory_response (163)	AARE.01	0.39		0	0	0	general GO
inflammatory_response (163)	AIRE.01	0.39		H	0	0	general GO
inflammatory_response (163)	LTATA_01	0.39		H	0	0	general GO
inflammatory_response (163)	BRN2.01	0.39		M	0	0	general GO
inflammatory_response (163)	IRF4.01	0.39			0	0	general GO
inflammatory_response (163)	STAT5.01	0.39		H	0	0	general GO
inflammatory_response (163)	GATA1.03	0.39	M		H	0	general GO
inflammatory_response (163)	BCL6.01	0.39		H	M	0	general GO
inflammatory_response (163)	AMEF2.01	0.38		H	0	0	general GO
inflammatory_response (163)	NFAT.01	0.38		0	0	0	general GO
inflammatory_response (163)	CDX2.01	0.38	H		H	0	general GO
inflammatory_response (163)	MMEF2.01	0.37		H	0	0	general GO
inflammatory_response (163)	SOX9.01	0.37	0	0		0	general GO
inflammatory_response (163)	XFD3.01	0.36		0	0	0	general GO
inflammatory_response (163)	IRF7.01	0.36		H	0	0	general GO
inflammatory_response (163)	OCT1P.01	0.36	H		0	0	general GO
inflammatory_response (163)	CDX1.01	0.35		H	0	0	general GO
inflammatory_response (163)	DLX3.01	0.34	0		0	0	general GO
inflammatory_response (163)	HOXC13_01	0.34	M	H	H	0	general GO
inflammatory_response (163)	HNF1.02	0.34		0	0	0	general GO
inflammatory_response (163)	XFD1.01	0.34		H	0	0	general GO
inflammatory_response (163)	ATBF1.01	0.34	M	H	H	0	general GO
inflammatory_response (163)	GATA3.01	0.34		H	H	0	general GO
inflammatory_response (163)	EV11.04	0.33		M	0	0	general GO
inflammatory_response (163)	MEIS1_HOX	0.33	H	M	H	0	general GO
inflammatory_response (163)	PBX_HOXA9	0.33	H	M	H	0	general GO
inflammatory_response (163)	BRN3.02	0.33		0	0	0	general GO
inflammatory_response (163)	BRN2.03	0.32	H		0	0	general GO
inflammatory_response (163)	XFD2.01	0.32			0	0	general GO
inflammatory_response (163)	OC2.01	0.32	0		0	0	general GO
inflammatory_response (163)	LMX1B.01	0.32		H	0	0	general GO
inflammatory_response (163)	HNF1.03	0.31		0	0	0	general GO
inflammatory_response (163)	EV11.01	0.31		0	H	0	general GO
inflammatory_response (163)	HNF6.01	0.31	M	H	H	0	general GO
inflammatory_response (163)	BRN3.01	0.3		H	0	0	general GO
inflammatory_response (163)	ATATA.01	0.3		0	0	0	general GO
inflammatory_response (163)	MEF2.02	0.3		H	H	0	general GO
inflammatory_response (163)	MEF2.03	0.3		H	H	0	general GO
inflammatory_response (163)	HNF1.01	0.3		0	0	0	general GO

inflammatory_response (163)	MEF2.05	0.29		0	H	0	general GO
inflammatory_response (163)	RSRFC4.02	0.29			M	0	general GO
inflammatory_response (163)	MEL1_01	0.29	M		H	0	general GO
inflammatory_response (163)	EVH1.05	0.29	0		0	0	general GO
inflammatory_response (163)	TATA.01	0.28		0	0	0	general GO
inflammatory_response (163)	TATA.02	0.28		0	0	0	general GO
inflammatory_response (163)	MYT1.02	0.28		H	0	0	general GO
inflammatory_response (163)	PIT1.01	0.27		H	0	0	general GO
inflammatory_response (163)	FREAC7.01	0.27		H	0	0	general GO
inflammatory_response (163)	HFH1.01	0.27		H	0	0	general GO
inflammatory_response (163)	MYT1.01	0.27		H	0	0	general GO
inflammatory_response (163)	OCT1.01	0.26		H	M	0	general GO
inflammatory_response (163)	BRN5.01	0.26		0	0	0	general GO
inflammatory_response (163)	HNF3B.01	0.26		0	0	0	general GO
inflammatory_response (163)	BRN2.02	0.25	H		0	0	general GO
inflammatory_response (163)	EVH1.03	0.24	M		H	0	general GO
inflammatory_response (163)	OCT1.06	0.22	H	H		0	general GO
induction_of_apoptosis (86)	ISRE.01	0.43	H	0	0	M	general GO
immune_response (366)	NFKAPPAB.0	0.6		H	0	0	general GO
immune_response (366)	NFKAPPAB.0	0.57		H	0	0	general GO
immune_response (366)	NFKAPPAB6	0.55			H	0	general GO
immune_response (366)	CREL.01	0.55			H	0	general GO
immune_response (366)	NFKAPPAB.0	0.55		H	0	0	general GO
immune_response (366)	HIVEP1_01	0.52		H	0	0	general GO
immune_response (366)	AML1.01	0.52		H	H	0	general GO
immune_response (366)	ERR_01	0.52		H	0	0	general GO
immune_response (366)	ETS1.01	0.52		H	0	0	general GO
immune_response (366)	AML3.01	0.5	M		0	0	general GO
immune_response (366)	AP1.02	0.49	H		0	0	general GO
immune_response (366)	TR2.01	0.49			0	0	general GO
immune_response (366)	LXRE.01	0.48		H	0	0	general GO
immune_response (366)	ETS2.01	0.48		H	0	0	general GO
immune_response (366)	GRE.01	0.47		H	0	0	general GO
immune_response (366)	PAX2.01	0.47	M	H	0	0	general GO
immune_response (366)	AP1.03	0.47		H	0	0	general GO
immune_response (366)	PPARA.01	0.47	M	H	0	0	general GO
immune_response (366)	NFE2L2.01	0.47		H	0	0	general GO
immune_response (366)	MTATA.01	0.47			0	0	general GO
immune_response (366)	SRF.03	0.47	H	H		0	general GO
immune_response (366)	BACH1.01	0.47	H		H	0	general GO
immune_response (366)	PLZF.01	0.47		0	0	0	general GO
immune_response (366)	AREB6.04	0.47		H	0	0	general GO
immune_response (366)	GKLF_02	0.46		0	0	0	general GO
immune_response (366)	TAACC.01	0.46		H	0	0	general GO
immune_response (366)	MIT.01	0.46			H	H	general GO
immune_response (366)	RP58.01	0.46		H	M	0	general GO
immune_response (366)	PXRCAR.01	0.45	H		0	0	general GO
immune_response (366)	DBP.01	0.45	M	0	H	0	general GO
immune_response (366)	BARBIE.01	0.45		H	0	0	general GO
immune_response (366)	BRACH.01	0.45	H	0	M	0	general GO
immune_response (366)	PAX8.01	0.45		M	0	0	general GO
immune_response (366)	GATA1.01	0.45		0	H	0	general GO
immune_response (366)	RTR.01	0.45		H	H	0	general GO
immune_response (366)	STAT.01	0.44		H		0	general GO
immune_response (366)	PRE.01	0.44			H	0	general GO
immune_response (366)	TCF11.01	0.44	0		0	0	general GO
immune_response (366)	BCL6.02	0.44	H		0	0	general GO
immune_response (366)	TCF11MAFG	0.43		H	H	0	general GO
immune_response (366)	ILF1_01	0.43		H	0	0	general GO
immune_response (366)	AP1.01	0.43		H	H	0	general GO
immune_response (366)	ISL1.01	0.43		H	H	0	general GO
immune_response (366)	ISRE.01	0.43			0	0	general GO
immune_response (366)	IRF2.01	0.43			0	0	general GO
immune_response (366)	IRF3.01	0.42			0	0	general GO

immune_response (366)	SRF.01	0.42		H	0	general GO	
immune_response (366)	NKX25.01	0.42		0	H	0	general GO
immune_response (366)	GATA1.02	0.41		H	0	0	general GO
immune_response (366)	PRDM1.01	0.41		H	M	0	general GO
immune_response (366)	HMG1Y.01	0.41			H	0	general GO
immune_response (366)	PDX1_Gabi	0.41	M	H	H	0	general GO
immune_response (366)	FAST1.01	0.41		H	0	0	general GO
immune_response (366)	GATA.01	0.41		H	H	0	general GO
immune_response (366)	HBP1_01	0.41		0	0	0	general GO
immune_response (366)	RORA1.01	0.41		H	H	0	general GO
immune_response (366)	PHOX2_01	0.41	M	H	H	0	general GO
immune_response (366)	PSE_02	0.41		H	0	H	general GO
immune_response (366)	BRN4.01	0.4		H	0	0	general GO
immune_response (366)	LEF1.02	0.4		H	0	0	general GO
immune_response (366)	MTBF.01	0.4	M	H	0	0	general GO
immune_response (366)	IRF1.01	0.4			0	0	general GO
immune_response (366)	CEBPB.01	0.4		H	0	0	general GO
immune_response (366)	GATA1.04	0.4		H	0	0	general GO
immune_response (366)	CRX.01	0.39	M	H	0	0	general GO
immune_response (366)	OCT1.05	0.39		H	H	0	general GO
immune_response (366)	AARE.01	0.39			0	0	general GO
immune_response (366)	AIRE.01	0.39		H	0	H	general GO
immune_response (366)	LTATA_01	0.39		H	0	0	general GO
immune_response (366)	BRN2.01	0.39		H	H	0	general GO
immune_response (366)	IRF4.01	0.39			0	0	general GO
immune_response (366)	STAT5.01	0.39	H		0	0	general GO
immune_response (366)	GATA1.03	0.39		H	0	0	general GO
immune_response (366)	BCL6.01	0.39	H		0	0	general GO
immune_response (366)	OCT1.04	0.38		H	0	0	general GO
immune_response (366)	GFI1B.01	0.38	H		0	0	general GO
immune_response (366)	AMEF2.01	0.38			0	0	general GO
immune_response (366)	RORA2.01	0.38		H	H	0	general GO
immune_response (366)	NFAT.01	0.38			0	0	general GO
immune_response (366)	FREAC4.01	0.38	M	H	0	H	general GO
immune_response (366)	CDX2.01	0.38		H	0	0	general GO
immune_response (366)	MEF2.01	0.38		H	0	0	general GO
immune_response (366)	MMEF2.01	0.37		0	0	0	general GO
immune_response (366)	GATA2.02	0.36			M	H	general GO
immune_response (366)	GATA1.05	0.36			0	H	general GO
immune_response (366)	XFD3.01	0.36		H	H	0	general GO
immune_response (366)	IRF7.01	0.36			0	0	general GO
immune_response (366)	OCT1P.01	0.36	M	H	H	0	general GO
immune_response (366)	OCT.01	0.35		H	H	0	general GO
immune_response (366)	PDX1_G_SA	0.35		H	0	0	general GO
immune_response (366)	GATA2.01	0.35			0	0	general GO
immune_response (366)	CDX1.01	0.35		H	0	0	general GO
immune_response (366)	VBP.01	0.35	M	H	0	0	general GO
immune_response (366)	NKX25.02	0.35	M	H	0	0	general GO
immune_response (366)	OCT1.02	0.34		H	H	0	general GO
immune_response (366)	DLX3.01	0.34		H	0	0	general GO
immune_response (366)	HOXC13_01	0.34		H	0	0	general GO
immune_response (366)	XFD1.01	0.34		0	H	0	general GO
immune_response (366)	GSH2_01	0.34	M	H	0	0	general GO
immune_response (366)	ATBF1.01	0.34		H	H	0	general GO
immune_response (366)	HMEF2.01	0.34		H	0	0	general GO
immune_response (366)	GATA3.01	0.34			0	0	general GO
immune_response (366)	EV11.04	0.33		H	H	0	general GO
immune_response (366)	EV11.02	0.33		H	0	0	general GO
immune_response (366)	MEIS1_HOX	0.33		H	H	H	general GO
immune_response (366)	PBX_HOXA9	0.33		H	H	H	general GO
immune_response (366)	BRN2.03	0.32	H		0	0	general GO
immune_response (366)	XFD2.01	0.32		H	0	0	general GO
immune_response (366)	OC2.01	0.32	H		0	0	general GO
immune_response (366)	LMX1B.01	0.32		H	H	0	general GO

immune_response (366)	FREAC3.01	0.32		H	0	0	general GO
immune_response (366)	CART1.01	0.32			0	0	general GO
immune_response (366)	HNF1.03	0.31		H	H	0	general GO
immune_response (366)	EV11.01	0.31		0	H	0	general GO
immune_response (366)	SOX5.01	0.31		H	0	0	general GO
immune_response (366)	MSX.01	0.3	M	H	H	0	general GO
immune_response (366)	BRN3.01	0.3		H	0	0	general GO
immune_response (366)	ATATA.01	0.3		0	0	0	general GO
immune_response (366)	EV11.06	0.3		H	H	0	general GO
immune_response (366)	MEF2.02	0.3		H	H	0	general GO
immune_response (366)	MEF2.03	0.3		H	H	0	general GO
immune_response (366)	HNF1.01	0.3		H	0	0	general GO
immune_response (366)	DLX1.01	0.29		H	0	0	general GO
immune_response (366)	MEF2.05	0.29		0	0	0	general GO
immune_response (366)	RSRFC4.02	0.29		H	H	0	general GO
immune_response (366)	MEL1_01	0.29			0	H	general GO
immune_response (366)	GATA3.02	0.29	H		H	H	general GO
immune_response (366)	MEF2.04	0.29		H	0	0	general GO
immune_response (366)	EV11.05	0.29			0	0	general GO
immune_response (366)	TATA.01	0.28		H	0	0	general GO
immune_response (366)	RSRFC4.01	0.28			H	0	general GO
immune_response (366)	TATA.02	0.28		H	0	0	general GO
immune_response (366)	PIT1.01	0.27		H	H	0	general GO
immune_response (366)	FREAC7.01	0.27		H	0	0	general GO
immune_response (366)	HFH1.01	0.27		H	0	0	general GO
immune_response (366)	HFH8.01	0.27		H	0	0	general GO
immune_response (366)	MYT1.01	0.27		H	0	0	general GO
immune_response (366)	OCT1.01	0.26		H		0	general GO
immune_response (366)	BRN5.01	0.26		0	0	0	general GO
immune_response (366)	HNF3B.01	0.26		H	M	0	general GO
immune_response (366)	HFH2.01	0.25	M	H	0	0	general GO
immune_response (366)	NKX31.01	0.25		H	0	0	general GO
immune_response (366)	EV11.03	0.24		H	0	H	general GO
immune_response (366)	S8.01	0.24	M	0	H	0	general GO
immune_response (366)	BRIGHT.01	0.22		H	H	0	general GO
immune_response (366)	OCT1.06	0.22		H	H	0	general GO
immune_response (366)	LHX3.01	0.14		H	H	0	general GO
immune_response (366)	poly_A	0.01		H	0	0	general GO
homophilic_cell_adhesion (70)	NFAT.01	0.38		0	0	0	general GO
homophilic_cell_adhesion (70)	OCT1P.01	0.36	0	M	H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	TAL1BETAIT	0.47	H	M	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	MEL1_02	0.46		0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	BRACH.01	0.45		H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	TCF11MAFG	0.43		0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	ISL1.01	0.43		0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	GATA1.04	0.4		H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	IRF4.01	0.39		0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	RORA2.01	0.38		H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	FREAC4.01	0.38		H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	GATA2.02	0.36	H		0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	XFD3.01	0.36		0	H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	GATA2.01	0.35		H	H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	GATA3.01	0.34		H	H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	EV11.02	0.33		0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	XFD2.01	0.32		0	0	H	general GO
G_protein_coupled_receptor_protein_signaling_path	OC2.01	0.32		H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	EV11.01	0.31		H	H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	MEL1_01	0.29		H	H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	GATA3.02	0.29	H		H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	EV11.05	0.29		0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	HFH1.01	0.27		0	H	0	general GO
G_protein_coupled_receptor_protein_signaling_path	EV11.03	0.24		H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	poly_A	0.01		0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_path	AT rich	0.01		H	0	0	general GO

fatty_acid_metabolism (55)	COUP.01	0.48	M	H	0	0	general GO
excretion (35)	NRL.01	0.51	H	0	M	0	general GO
ER_to_Golgi_transport (47)	ATF6.02	0.6		0	0	0	general GO
ER_to_Golgi_transport (47)	E4F.01	0.51		0	0	0	general GO
ER_to_Golgi_transport (47)	CREBP1CJU	0.44		0	0	0	general GO
epidermis_development (59)	AML3.01	0.5	M	0	H	0	general GO
epidermis_development (59)	TATA.01	0.28		0	0	0	general GO
epidermis_development (59)	TATA.02	0.28		0	0	0	general GO
electron_transport (214)	LMO2COM.0	0.48	0		0	0	general GO
electron_transport (214)	TAL1BETAIT	0.47	0	M	H	0	general GO
electron_transport (214)	PLZF.01	0.47	0		0	0	general GO
electron_transport (214)	GATA1.03	0.39	M	H	0	0	general GO
DNA_replication (91)	ELK1.02	0.55	H	M	0	0	general GO
DNA_replication (91)	E2F.03	0.54	H		0	0	general GO
DNA_repair (148)	E2F.02	0.59		M	0	0	general GO
DNA_repair (148)	E2F.03	0.54		M	0	0	general GO
DNA_repair (148)	FLI.01	0.53	H	0		0	general GO
DNA_repair (148)	NFY.01	0.52		0	0	0	general GO
DNA_repair (148)	E2F.01	0.5	H	M	0	0	general GO
DNA_metabolism (47)	E2F.02	0.59		0	0	0	general GO
DNA_metabolism (47)	E2F.03	0.54		0	0	0	general GO
DNA_metabolism (47)	E2F.01	0.5		0	0	0	general GO
digestion (51)	FREAC3.01	0.32		0	0	0	general GO
digestion (51)	MEL1_01	0.29	M	H	0	0	general GO
digestion (51)	TATA.01	0.28		0	0	0	general GO
digestion (51)	FREAC7.01	0.27		0	0	0	general GO
digestion (51)	HFH1.01	0.27		0	0	0	general GO
digestion (51)	HFH8.01	0.27		0	0	0	general GO
digestion (51)	HNF3B.01	0.26		0	0	0	general GO
digestion (51)	EV11.03	0.24	M	H	0	0	general GO
defense_response (100)	NFKAPPAB.0	0.55	M	H	0	0	general GO
defense_response (100)	PAX8.01	0.45	0	0		0	general GO
defense_response (100)	TCF11.01	0.44	H	M	0	H	general GO
defense_response (100)	MTBF.01	0.4	M	H	0	0	general GO
defense_response (100)	NKX31.01	0.25	M	H	H	0	general GO
circulation (52)	SRF.01	0.42	0	0	H	M	general GO
chromosome_organization_and_biogenesis (83)	TATA.01	0.28		H	0	0	general GO
chromatin_modification (53)	GC_rich	0.99	0	0		0	general GO
chloride_transport (38)	ER.01	0.51	0	0		0	general GO
chemotaxis (98)	NFKAPPAB.0	0.6	H	M	0	0	general GO
chemotaxis (98)	NFKAPPAB.0	0.57	H	M	0	0	general GO
chemotaxis (98)	NFKAPPAB6	0.55	H	M	0	0	general GO
chemotaxis (98)	NFKAPPAB.0	0.55	H		0	0	general GO
chemotaxis (98)	HIVEP1_01	0.52	H	M	0	0	general GO
chemotaxis (98)	AP1.03	0.47	H	M	0	0	general GO
chemotaxis (98)	NFE2L2.01	0.47		0	0	0	general GO
chemotaxis (98)	GKLF_02	0.46		0	0	0	general GO
chemotaxis (98)	BARBIE.01	0.45		0	0	0	general GO
chemotaxis (98)	GATA1.01	0.45		0	0	0	general GO
chemotaxis (98)	TCF11MAFG	0.43		0	0	0	general GO
chemotaxis (98)	AP1.01	0.43		H	0	0	general GO
chemotaxis (98)	ISL1.01	0.43	M	0	H	0	general GO
chemotaxis (98)	SRF.01	0.42		H	0	0	general GO
chemotaxis (98)	GATA.01	0.41		0	0	0	general GO
chemotaxis (98)	PSE_02	0.41	H	M	0	0	general GO
chemotaxis (98)	GATA1.04	0.4		0	0	0	general GO
chemotaxis (98)	AARE.01	0.39	M	H	0	0	general GO
chemotaxis (98)	LTATA_01	0.39		0	0	0	general GO
chemotaxis (98)	BRN2.01	0.39		0	0	0	general GO
chemotaxis (98)	GATA1.03	0.39		0	H	0	general GO
chemotaxis (98)	BCL6.01	0.39	H	0	M	0	general GO
chemotaxis (98)	NFAT.01	0.38		0	0	0	general GO
chemotaxis (98)	CDX2.01	0.38		0	H	0	general GO
chemotaxis (98)	GATA1.05	0.36		0	0	H	general GO

chemotaxis (98)	PDX1_G_SA	0.35	M	0	H	0	general GO
chemotaxis (98)	GATA2.01	0.35		0	H	0	general GO
chemotaxis (98)	CDX1.01	0.35		0	0	0	general GO
chemotaxis (98)	GATA3.01	0.34		0	H	0	general GO
chemotaxis (98)	MEF2.05	0.29		0		0	general GO
chemotaxis (98)	TATA.01	0.28		0	0	0	general GO
chemotaxis (98)	TATA.02	0.28		0	H	0	general GO
central_nervous_system_development (68)	poly_C	0.99	0		0	0	general GO
central_nervous_system_development (68)	MUSCLE_IN	0.62	0		0	0	general GO
cellular_defense_response (68)	AML3.01	0.5	H	0	M	0	general GO
cellular_defense_response (68)	ETS2.01	0.48	H	M	0	0	general GO
cellular_defense_response (68)	AP1.01	0.43		H	0	0	general GO
cell_surface_receptor_linked_signal_transduction	ETS2.01	0.48	M	H	0	0	general GO
cell_surface_receptor_linked_signal_transduction	TAL1BETAIT	0.47	0		0	0	general GO
cell_proliferation (243)	TATA.01	0.28		0	0	0	general GO
cell_motility (106)	MEL1_01	0.29	0	0	M	H	general GO
cell_division (103)	GABP.01	0.62	0	0	0	0	general GO
cell_division (103)	NFY.01	0.52	H		0	0	general GO
cell_division (103)	CAAT.01	0.49	H		0	0	general GO
cell_division (103)	NFY.02	0.48	H		0	0	general GO
cell_division (103)	NFY.03	0.47	0		0	0	general GO
cell_division (103)	CHR.01	0.41		0	0	0	general GO
cell_differentiation (192)	GC_rich	0.99	0	H	0	M	general GO
cell_differentiation (192)	ZNF202.01	0.73	0		0	0	general GO
cell_differentiation (192)	HAND2_E12	0.7	0		0	0	general GO
cell_cycle (273)	SP1.01	0.78	H		0	0	general GO
cell_cycle (273)	ZF9.01	0.72		0	0	0	general GO
cell_cycle (273)	EGR1.02	0.68	H	M	0	0	general GO
cell_cycle (273)	CDE.01	0.6			0	0	general GO
cell_cycle (273)	WHN.01	0.59	H		0	0	general GO
cell_cycle (273)	NFY.01	0.52	H		0	0	general GO
cell_cycle (273)	CAAT.01	0.49			0	0	general GO
cell_cycle (273)	NFY.02	0.48			0	0	general GO
cell_cycle (273)	NFY.03	0.47	H		0	0	general GO
cell_cycle (273)	CHR.01	0.41		0	0	0	general GO
cell_cell_signaling (268)	NFKAPPAB.0	0.57	H	M	0	0	general GO
cell_cell_signaling (268)	NFKAPPAB6	0.55	H	M	0	0	general GO
cell_cell_signaling (268)	HIVEP1_01	0.52	H	M	0	0	general GO
cell_cell_signaling (268)	MTATA.01	0.47			0	0	general GO
cell_cell_signaling (268)	IRF2.01	0.43	0		0	0	general GO
cell_cell_signaling (268)	SRF.01	0.42		0	0	0	general GO
cell_cell_signaling (268)	PDX1_Gabi	0.41		0	0	0	general GO
cell_cell_signaling (268)	LTATA_01	0.39		0	0	0	general GO
cell_cell_signaling (268)	MEF2.05	0.29		0	0	0	general GO
cell_cell_signaling (268)	TATA.01	0.28		0	0	0	general GO
cell_cell_signaling (268)	TATA.02	0.28		0	0	0	general GO
cation_transport (99)	AP2.01	0.73	0	H	H		general GO
cation_transport (99)	NRSF.01	0.62	M	H	0	0	general GO
cation_transport (99)	NRSE.01	0.57	M	0	0	H	general GO
calcium_ion_homeostasis (30)	SRF.03	0.47		0	0	0	general GO
calcium_ion_homeostasis (30)	BCL6.02	0.44	H		0	H	general GO
calcium_ion_homeostasis (30)	TATA.01	0.28		0	0	0	general GO
blood_coagulation (70)	ETS1.01	0.52		0	0	0	general GO
blood_coagulation (70)	HNF1.02	0.34		0	0	0	general GO
blood_coagulation (70)	HNF1.03	0.31		0	0	0	general GO
blood_coagulation (70)	HNF1.01	0.3		0	0	0	general GO
blood_coagulation (70)	SATB1.01	0.27		0	0	0	general GO
blood_coagulation (70)	HNF3B.01	0.26		H	0	0	general GO
biosynthesis (32)	NFY.01	0.52		0	0	0	general GO
biosynthesis (32)	CAAT.01	0.49		H	0	0	general GO
apoptosis (258)	CREL.01	0.55	M		0	0	general GO
antimicrobial_humoral_response (87)	AREB6.01	0.49	H	M	0	0	general GO
antimicrobial_humoral_response (87)	MIT.01	0.46		H	0	0	general GO
antimicrobial_humoral_response (87)	AP1.01	0.43	H	M	0	0	general GO

antimicrobial_humoral_response (87)	ISL1.01	0.43	H	H	0	general GO
antimicrobial_humoral_response (87)	GATA.01	0.41	M	H	0	general GO
antimicrobial_humoral_response (87)	MTBF.01	0.4		0	0	general GO
antimicrobial_humoral_response (87)	OCT1.05	0.39	H	0	0	general GO
antimicrobial_humoral_response (87)	LTATA_01	0.39	H	0	0	general GO
antimicrobial_humoral_response (87)	GATA1.03	0.39	H	0	0	general GO
antimicrobial_humoral_response (87)	CDX2.01	0.38		0	0	general GO
antimicrobial_humoral_response (87)	GATA1.05	0.36	H	0	0	general GO
antimicrobial_humoral_response (87)	OCT.01	0.35	H	0	H	general GO
antimicrobial_humoral_response (87)	CDX1.01	0.35	H	0	H	general GO
antimicrobial_humoral_response (87)	EVH1.04	0.33	H	M	0	general GO
antimicrobial_humoral_response (87)	EN1.01	0.32	H		0	general GO
antimicrobial_humoral_response (87)	HNF6.01	0.31	M	H	0	general GO
antimicrobial_humoral_response (87)	XVENT2.01	0.3		H	0	general GO
amino_acid_metabolism (45)	ERR_01	0.52	H	M	0	general GO

400bp Window

GO group	Motifs	motif GC	-199 - 200	201 - 600	601 - 1000	GO-classes
development (530)	GC_rich	1	H			transcription GO
development (530)	poly_C	1				transcription GO
development (530)	SP1.01	0.8	0			transcription GO
development (530)	WT1.01	0.8	H			transcription GO
development (530)	HES1.02	0.8	0	M		transcription GO
development (530)	MAZR.01	0.8				transcription GO
development (530)	ZNF202.01	0.7				transcription GO
development (530)	AP2.01	0.7	H			transcription GO
development (530)	ZF9.01	0.7	0			transcription GO
development (530)	EGR3.01	0.7	0	0		transcription GO
development (530)	MYCMAX.03	0.7	H		0	transcription GO
development (530)	NFKAPPAB5	0.7	0	H		transcription GO
development (530)	HAND2_E12.	0.7	0	H		transcription GO
development (530)	ZBP89.01	0.7				transcription GO
development (530)	NGFIC.01	0.7	0	H	M	transcription GO
development (530)	CKROX_01	0.7				transcription GO
development (530)	EGR1.02	0.7	H			transcription GO
development (530)	HIC1_01	0.7	0	H		transcription GO
development (530)	EGR2.01	0.7	0	0		transcription GO
development (530)	GC.01	0.7	0		0	transcription GO
development (530)	MZF1.01	0.7	H	H		transcription GO
development (530)	MAZ.01	0.7	H			transcription GO
development (530)	ZIC2_01	0.6	0	H		transcription GO
development (530)	PLAG1_01	0.6				transcription GO
development (530)	INSM1_01	0.6	0	H		transcription GO
development (530)	MUSCLE_INI	0.6	0	H		transcription GO
development (530)	MUSCLE_INI	0.6	0	H		transcription GO
development (530)	CDE.01	0.6	0	H		transcription GO
development (530)	AHR.01	0.6	0	0		transcription GO
development (530)	E2F.02	0.6	0	0		transcription GO
development (530)	NRSE.01	0.6	0	H		transcription GO
development (530)	PAX5.01	0.6	0	H		transcription GO
development (530)	GAGA.01	0.6				transcription GO
development (530)	AG_rich_codi	0.5		H	H	transcription GO
regulation_of_transcription (266)	GC_rich	1				transcription GO
regulation_of_transcription (266)	poly_C	1				transcription GO
regulation_of_transcription (266)	SP1.01	0.8	H	M		transcription GO
regulation_of_transcription (266)	WT1.01	0.8	H	H		transcription GO
regulation_of_transcription (266)	MAZR.01	0.8				transcription GO
regulation_of_transcription (266)	ZNF202.01	0.7				transcription GO
regulation_of_transcription (266)	AP2.01	0.7	H	H		transcription GO
regulation_of_transcription (266)	ZF5.01	0.7	H	H		transcription GO
regulation_of_transcription (266)	ZF9.01	0.7	0			transcription GO
regulation_of_transcription (266)	EGR3.01	0.7	H	0		transcription GO
regulation_of_transcription (266)	ZBP89.01	0.7			H	transcription GO
regulation_of_transcription (266)	NGFIC.01	0.7	H	0	M	transcription GO
regulation_of_transcription (266)	CKROX_01	0.7			H	transcription GO
regulation_of_transcription (266)	EGR1.02	0.7				transcription GO
regulation_of_transcription (266)	EGR2.01	0.7	H	0		transcription GO
regulation_of_transcription (266)	GC.01	0.7	0		0	transcription GO
regulation_of_transcription (266)	MZF1.01	0.7		H		transcription GO

regulation_of_transcription (266)	EGR1.01	0.7	H	0	M	transcription GO
regulation_of_transcription (266)	MAZ.01	0.7				transcription GO
regulation_of_transcription (266)	ZIC2_01	0.6	0	M	H	transcription GO
regulation_of_transcription (266)	PLAG1_01	0.6			H	transcription GO
regulation_of_transcription (266)	RREB1.01	0.6	0	H		transcription GO
regulation_of_transcription (266)	CDE.01	0.6	H			transcription GO
regulation_of_transcription (266)	E2F.02	0.6	0	H		transcription GO
regulation_of_transcription (266)	PAX5.01	0.6	0		H	transcription GO
regulation_of_transcription (266)	GAGA.01	0.6			0	transcription GO
regulation_of_transcription (266)	NFY.01	0.5	H		0	transcription GO
regulation_of_transcription (266)	AG_rich_cod	0.5			H	transcription GO
regulation_of_transcription (266)	GKLF.01	0.5		H	0	transcription GO
regulation_of_transcription (266)	CAAT.01	0.5		0	0	transcription GO
regulation_of_transcription (266)	PBX1_MEIS1	0.5	H	M	0	transcription GO
regulation_of_transcription (266)	PBX1_MEIS1	0.4	H	M	0	transcription GO
regulation_of_transcription_DNA_dependent (1066)	GC_rich	1				transcription GO
regulation_of_transcription_DNA_dependent (1066)	poly_C	1				transcription GO
regulation_of_transcription_DNA_dependent (1066)	SP1.01	0.8	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	WT1.01	0.8				transcription GO
regulation_of_transcription_DNA_dependent (1066)	HES1.02	0.8	H		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	MAZR.01	0.8				transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZNF202.01	0.7				transcription GO
regulation_of_transcription_DNA_dependent (1066)	AP2.01	0.7				transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZF5.01	0.7				transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZF9.01	0.7	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR3.01	0.7	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	NRF1_01	0.7	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	MYCMAX.03	0.7	H		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	NFKAPPAB5	0.7	0	M		transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZBP89.01	0.7				transcription GO
regulation_of_transcription_DNA_dependent (1066)	HELT.01	0.7	H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	NGFIC.01	0.7	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	CKROX_01	0.7				transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR1.02	0.7				transcription GO
regulation_of_transcription_DNA_dependent (1066)	HIC1_01	0.7	0	M		transcription GO
regulation_of_transcription_DNA_dependent (1066)	BKLF.01	0.7	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR2.01	0.7	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	GC.01	0.7	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	MZF1.01	0.7			H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	EGR1.01	0.7	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	MTF-1.01	0.7	0		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	MAZ.01	0.7				transcription GO
regulation_of_transcription_DNA_dependent (1066)	ZIC2_01	0.6	H		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	ATF6.01	0.6	M		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	PLAG1_01	0.6				transcription GO
regulation_of_transcription_DNA_dependent (1066)	EBVR.01	0.6	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	AHRARNT.02	0.6	H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	HES1.01	0.6				transcription GO
regulation_of_transcription_DNA_dependent (1066)	MUSCLE_INI	0.6	H			transcription GO
regulation_of_transcription_DNA_dependent (1066)	GABP.01	0.6	0		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	HIF1.01	0.6	0		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	MUSCLE_INI	0.6	H		H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	EKLF.01	0.6	0			transcription GO
regulation_of_transcription_DNA_dependent (1066)	RREB1.01	0.6	0	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	CDE.01	0.6				transcription GO
regulation_of_transcription_DNA_dependent (1066)	AHR.01	0.6	0	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	E2F.02	0.6	H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	WHN.01	0.6	H	H		transcription GO
regulation_of_transcription_DNA_dependent (1066)	TAXCREB.01	0.6	0		0	transcription GO
regulation_of_transcription_DNA_dependent (1066)	PAX9.01	0.6	0	M		transcription GO
regulation_of_transcription_DNA_dependent (1066)	NRSE.01	0.6	0	M	H	transcription GO
regulation_of_transcription_DNA_dependent (1066)	VDR_RXR.02	0.6	H	M	0	transcription GO
regulation_of_transcription_DNA_dependent (1066)	GAGA.01	0.6				transcription GO
regulation_of_transcription_DNA_dependent (1066)	E2F.03	0.5	H	H		transcription GO

regulation_of_transcription_DNA_dependent (1066)	NFY.01	0.5	H		0	transcription GO
regulation_of_transcription_DNA_dependent (1066)	AG_rich_codi	0.5			0	transcription GO
regulation_of_transcription_DNA_dependent (1066)	E2F.01	0.5	H	0	M	transcription GO
regulation_of_transcription_DNA_dependent (1066)	GKLF.01	0.5		M	0	transcription GO
regulation_of_transcription_DNA_dependent (1066)	CAAT.01	0.5		H	0	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	SP1.01	0.8	H		0	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	WT1.01	0.8		H	H	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	MAZR.01	0.8		H	0	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	ZF5.01	0.7	H	0	M	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	CKROX_01	0.7		H	0	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	MAZ.01	0.7			0	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	EBVR.01	0.6	H	0	M	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	HES1.01	0.6	H	0	M	transcription GO
regulation_of_transcription_from_RNA_polymerase_II_promoter (163)	CDE.01	0.6	H		0	transcription GO
transcription (930)	GC_rich	1				transcription GO
transcription (930)	poly_C	1				transcription GO
transcription (930)	SP1.01	0.8	H			transcription GO
transcription (930)	WT1.01	0.8				transcription GO
transcription (930)	HES1.02	0.8	H		H	transcription GO
transcription (930)	MAZR.01	0.8				transcription GO
transcription (930)	ZNF202.01	0.7				transcription GO
transcription (930)	AP2.01	0.7				transcription GO
transcription (930)	ZF5.01	0.7				transcription GO
transcription (930)	ZF9.01	0.7	H			transcription GO
transcription (930)	EGR3.01	0.7	H			transcription GO
transcription (930)	NRF1_01	0.7	H			transcription GO
transcription (930)	MYCMAX.03	0.7	H		H	transcription GO
transcription (930)	ZBP89.01	0.7				transcription GO
transcription (930)	HELT.01	0.7	H			transcription GO
transcription (930)	NGFIC.01	0.7	H		H	transcription GO
transcription (930)	CKROX_01	0.7				transcription GO
transcription (930)	EGR1.02	0.7				transcription GO
transcription (930)	HIC1_01	0.7	0	0		transcription GO
transcription (930)	GC.01	0.7	H			transcription GO
transcription (930)	MZF1.01	0.7		0	H	transcription GO
transcription (930)	EGR1.01	0.7	H		H	transcription GO
transcription (930)	MTF-1.01	0.7	0	M	H	transcription GO
transcription (930)	MAZ.01	0.7				transcription GO
transcription (930)	ZIC2_01	0.6	H		0	transcription GO
transcription (930)	PLAG1_01	0.6				transcription GO
transcription (930)	EBVR.01	0.6	H	H		transcription GO
transcription (930)	AHRARNT.02	0.6		H		transcription GO
transcription (930)	HES1.01	0.6			H	transcription GO
transcription (930)	MUSCLE_INI	0.6	H		H	transcription GO
transcription (930)	HIF1.01	0.6	H		H	transcription GO
transcription (930)	MUSCLE_INI	0.6	H		H	transcription GO
transcription (930)	EKLF.01	0.6	0	0		transcription GO
transcription (930)	CDE.01	0.6				transcription GO
transcription (930)	AHR.01	0.6	H	H	M	transcription GO
transcription (930)	E2F.02	0.6	H	H		transcription GO
transcription (930)	WHN.01	0.6	H	H		transcription GO
transcription (930)	TAXCREB.01	0.6	0		0	transcription GO
transcription (930)	PAX9.01	0.6	0	H		transcription GO
transcription (930)	NRSE.01	0.6	0	M	H	transcription GO
transcription (930)	PAX5.03	0.6	H	M	0	transcription GO
transcription (930)	GAGA.01	0.6			0	transcription GO
transcription (930)	E2F.03	0.5	H	H		transcription GO
transcription (930)	AG_rich_codi	0.5			0	transcription GO
transcription (930)	E2F.01	0.5	H	0	M	transcription GO
transcription_RNA_polyII_promoter (190)	GC_rich	1	H		0	general GO
transcription_RNA_polyII_promoter (190)	SP1.01	0.8	0		0	general GO
transcription_RNA_polyII_promoter (190)	WT1.01	0.8	H		0	general GO
transcription_RNA_polyII_promoter (190)	MAZR.01	0.8		H	0	general GO
transcription_RNA_polyII_promoter (190)	ZNF202.01	0.7	H		0	general GO

transcription_RNA_polyll_promoter (190)	AP2.01	0.7	H	M	H	general GO
transcription_RNA_polyll_promoter (190)	ZF9.01	0.7	0			general GO
transcription_RNA_polyll_promoter (190)	NRF1_01	0.7	0		0	general GO
transcription_RNA_polyll_promoter (190)	MYCMAX.03	0.7	H	M	0	general GO
transcription_RNA_polyll_promoter (190)	EGR1.02	0.7	H		0	general GO
transcription_RNA_polyll_promoter (190)	HIC1_01	0.7	0	0		general GO
transcription_RNA_polyll_promoter (190)	MAZ.01	0.7	H		0	general GO
transcription_RNA_polyll_promoter (190)	PLAG1_01	0.6	M	H	H	general GO
transcription_RNA_polyll_promoter (190)	MUSCLE_INI	0.6	0		0	general GO
transcription_RNA_polyll_promoter (190)	CDE.01	0.6	H			general GO
transcription_RNA_polyll_promoter (190)	WHN.01	0.6	H	0	M	general GO
actin_cytoskeleton_organization_and_biogenesis (45)	GC_rich	1			0	general GO
actin_cytoskeleton_organization_and_biogenesis (45)	NRF1_01	0.7			0	general GO
anti_apoptosis (85)	NFKAPPAB6	0.6			0	general GO
antimicrobial_humoral_response (87)	ETS1.01	0.5			0	general GO
antimicrobial_humoral_response (87)	AREB6.01	0.5			0	general GO
antimicrobial_humoral_response (87)	GATA1.01	0.4			0	general GO
antimicrobial_humoral_response (87)	ISRE.01	0.4			0	general GO
antimicrobial_humoral_response (87)	HMG1Y.01	0.4	M	H	0	general GO
antimicrobial_humoral_response (87)	GATA.01	0.4			0	general GO
antimicrobial_humoral_response (87)	MTBF.01	0.4			0	general GO
antimicrobial_humoral_response (87)	CEBPB.01	0.4			0	general GO
antimicrobial_humoral_response (87)	MEIS1B_HOX	0.4			0	general GO
antimicrobial_humoral_response (87)	OCT1.05	0.4		H	0	general GO
antimicrobial_humoral_response (87)	LTATA_01	0.4			0	general GO
antimicrobial_humoral_response (87)	IRF4.01	0.4			0	general GO
antimicrobial_humoral_response (87)	GATA1.03	0.4			0	general GO
antimicrobial_humoral_response (87)	GFI1B.01	0.4			0	general GO
antimicrobial_humoral_response (87)	CDX2.01	0.4		0	H	general GO
antimicrobial_humoral_response (87)	GATA1.05	0.4			0	general GO
antimicrobial_humoral_response (87)	OCT.01	0.4		H	0	general GO
antimicrobial_humoral_response (87)	CDX1.01	0.3		0	H	general GO
antimicrobial_humoral_response (87)	FKHRL1.01	0.3			0	general GO
antimicrobial_humoral_response (87)	HNF6.01	0.3		H	0	general GO
antimicrobial_humoral_response (87)	XVENT2.01	0.3		0	0	general GO
antimicrobial_humoral_response (87)	ATATA.01	0.3		H	0	general GO
antimicrobial_humoral_response (87)	CDP.02	0.3			0	general GO
antimicrobial_humoral_response (87)	MEF2.04	0.3			0	general GO
antimicrobial_humoral_response (87)	TATA.01	0.3		0	H	general GO
antimicrobial_humoral_response (87)	EVI1.03	0.2			0	general GO
apoptosis (258)	NFKAPPAB.0	0.6			0	general GO
apoptosis (258)	CREL.01	0.5	M	H	0	general GO
biosynthesis (32)	CAAT.01	0.5			0	general GO
biosynthesis (32)	NFY.02	0.5			0	general GO
blood_coagulation (70)	ARE.01	0.5	M	H	0	general GO
blood_coagulation (70)	BCL6.02	0.4	M	H	0	general GO
blood_coagulation (70)	AIRE.01	0.4	0	H	M	general GO
blood_coagulation (70)	FREAC4.01	0.4			0	general GO
blood_coagulation (70)	HNF1.02	0.3			0	general GO
blood_coagulation (70)	FREAC3.01	0.3	H	0	M	general GO
blood_coagulation (70)	HNF1.03	0.3			0	general GO
blood_coagulation (70)	HNF1.01	0.3			0	general GO
blood_coagulation (70)	DLX1.01	0.3	M	H	0	general GO
calcium_ion_homeostasis (30)	TATA.01	0.3			0	general GO
cation_transport (99)	SP1.01	0.8	0	H	M	general GO
cation_transport (99)	ZNF202.01	0.7		H	H	general GO
cation_transport (99)	NFKAPPAB5	0.7	H	0	M	general GO
cation_transport (99)	NRSE.01	0.6	M	0	H	general GO
cell_adhesion (378)	PDX1_Gabi	0.4	M	H	0	general GO
cell_cell_signaling (268)	NFKAPPAB6	0.6		M	0	general GO
cell_cell_signaling (268)	CREL.01	0.5	H	M	0	general GO
cell_cell_signaling (268)	NFKAPPAB.0	0.5			0	general GO
cell_cell_signaling (268)	HIVEP1_01	0.5	H	M	0	general GO
cell_cell_signaling (268)	MTATA.01	0.5			0	general GO

cell_cell_signaling (268)	AARE.01	0.4		0	0	general GO
cell_cell_signaling (268)	LTATA_01	0.4		0	0	general GO
cell_cell_signaling (268)	NFAT.01	0.4		0	0	general GO
cell_cell_signaling (268)	CDX2.01	0.4		0	0	general GO
cell_cell_signaling (268)	MEF2.05	0.3		0	0	general GO
cell_cell_signaling (268)	TATA.01	0.3		0	0	general GO
cell_cell_signaling (268)	TATA.02	0.3		0	0	general GO
cell_cell_signaling (268)	BRN2.02	0.2		0	0	general GO
cell_cycle (273)	NRF1_01	0.7		0	0	general GO
cell_cycle (273)	CDE.01	0.6		H	0	general GO
cell_cycle (273)	E2F.03	0.5	H		0	general GO
cell_cycle (273)	NFY.01	0.5			0	general GO
cell_cycle (273)	CAAT.01	0.5		H	0	general GO
cell_cycle (273)	NFY.02	0.5		H	0	general GO
cell_cycle (273)	CREB.01	0.5	H	M	0	general GO
cell_cycle (273)	NFY.03	0.5		H	0	general GO
cell_cycle (273)	CHR.01	0.4		0	0	general GO
cell_differentiation (192)	WT1.01	0.8	0		0	general GO
cell_division (103)	SP2_01	0.6	H	M	0	general GO
cell_division (103)	NFY.01	0.5		H	0	general GO
cell_division (103)	CAAT.01	0.5		H	0	general GO
cell_division (103)	NFY.02	0.5		0	0	general GO
cell_division (103)	NFY.03	0.5		0	0	general GO
cell_division (103)	CHR.01	0.4		0	0	general GO
cell_matrix_adhesion (56)	HBP1_01	0.4	0		0	general GO
cell_motility (106)	TATA.02	0.3		0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	ETS2.01	0.5		0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	AP1.01	0.4		H	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	OCT1.05	0.4		0	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	GATA1.05	0.4	H	M	0	general GO
cell_surface_receptor_linked_signal_transduction (169)	EN1.01	0.3	M	H	0	general GO
cellular_defense_response (68)	NFKAPPAB.0	0.5		0	0	general GO
cellular_defense_response (68)	GATA1.03	0.4		H	0	general GO
central_nervous_system_development (68)	MAZR.01	0.8	0		0	general GO
central_nervous_system_development (68)	MUSCLE_INI	0.6	0		0	general GO
chemotaxis (98)	NFKAPPAB.0	0.6		0	0	general GO
chemotaxis (98)	NFKAPPAB.0	0.6		0	0	general GO
chemotaxis (98)	NFKAPPAB6	0.6		0	0	general GO
chemotaxis (98)	CREL.01	0.5		0	0	general GO
chemotaxis (98)	NFKAPPAB.0	0.5		0	0	general GO
chemotaxis (98)	HIVEP1_01	0.5		0	0	general GO
chemotaxis (98)	NFE2.01	0.5		0	0	general GO
chemotaxis (98)	IK3.01	0.5		0	0	general GO
chemotaxis (98)	NFE2L2.01	0.5		0	H	general GO
chemotaxis (98)	PXRCAR.01	0.5		0	0	general GO
chemotaxis (98)	BARBIE.01	0.4		0	H	general GO
chemotaxis (98)	GATA1.01	0.4		0	0	general GO
chemotaxis (98)	MYT1L.01	0.4	H		0	general GO
chemotaxis (98)	TCF11MAFG	0.4		0	0	general GO
chemotaxis (98)	AP1.01	0.4		0	0	general GO
chemotaxis (98)	SRF.01	0.4		0	0	general GO
chemotaxis (98)	HMG1Y.01	0.4		H	0	general GO
chemotaxis (98)	GATA1.04	0.4		0	0	general GO
chemotaxis (98)	AIRE.01	0.4		H	0	general GO
chemotaxis (98)	LTATA_01	0.4		0	0	general GO
chemotaxis (98)	GATA1.03	0.4		H	0	general GO
chemotaxis (98)	NFAT.01	0.4		0	0	general GO
chemotaxis (98)	CDX2.01	0.4		H	0	general GO
chemotaxis (98)	IRF7.01	0.4		H	0	general GO
chemotaxis (98)	GATA2.01	0.4		0	H	general GO
chemotaxis (98)	CDX1.01	0.3		0	0	general GO
chemotaxis (98)	GATA3.01	0.3		0	0	general GO
chemotaxis (98)	TATA.01	0.3		0	0	general GO
chemotaxis (98)	TATA.02	0.3		H	H	general GO

chromatin_modification (53)	WT1.01	0.8	0	0	0	general GO
chromatin_modification (53)	ZNF202.01	0.7	M	0	H	general GO
chromatin_modification (53)	CKROX_01	0.7		0	0	general GO
chromosome_organization_and_biogenesis (83)	ACAAT.01	0.5		0	0	general GO
chromosome_organization_and_biogenesis (83)	CAAT.01	0.5		0	0	general GO
chromosome_organization_and_biogenesis (83)	NFY.02	0.5		H	0	general GO
chromosome_organization_and_biogenesis (83)	NFY.03	0.5		0	0	general GO
chromosome_organization_and_biogenesis (83)	BRN2.03	0.3		H	H	general GO
chromosome_organization_and_biogenesis (83)	TATA.01	0.3		H	0	general GO
circulation (52)	SRF.01	0.4	0	H	M	general GO
defense_response (100)	NFKAPPAB.0	0.5		0	0	general GO
defense_response (100)	HIVEP1_01	0.5		0	0	general GO
defense_response (100)	HOX1-3.01	0.4		0	0	general GO
defense_response (100)	PRDM1.01	0.4		0	0	general GO
defense_response (100)	CEBPB.01	0.4		0	0	general GO
defense_response (100)	HOXA9.01	0.3	0	M	H	general GO
defense_response (100)	MEF2.04	0.3	0		0	general GO
development (530)	GKLF.01	0.5	H		0	general GO
digestion (51)	NFAT.01	0.4		0	0	general GO
digestion (51)	MEL1_01	0.3		H	0	general GO
digestion (51)	TATA.01	0.3		0	0	general GO
digestion (51)	FREAC7.01	0.3		0	0	general GO
digestion (51)	HNF3B.01	0.3		0	0	general GO
digestion (51)	EVI1.03	0.2		0	0	general GO
DNA_metabolism (47)	E2F.02	0.6		0	0	general GO
DNA_metabolism (47)	E2F.03	0.5		0	0	general GO
DNA_metabolism (47)	E2F.01	0.5		0	0	general GO
DNA_recombination (38)	CAAT.01	0.5		0	0	general GO
DNA_recombination (38)	NFY.03	0.5		0	H	general GO
DNA_repair (148)	E2F.02	0.6		0	0	general GO
DNA_repair (148)	ELK1.02	0.5		0	0	general GO
DNA_repair (148)	E2F.03	0.5		0	0	general GO
DNA_repair (148)	FLI.01	0.5		0	0	general GO
DNA_repair (148)	E2F.01	0.5		0	0	general GO
DNA_replication (91)	NFY.01	0.5		0	0	general GO
electron_transport (214)	HNF4.01	0.5		0	0	general GO
electron_transport (214)	ERR_01	0.5		0	0	general GO
electron_transport (214)	SF1.01	0.5		0	0	general GO
electron_transport (214)	PPARA.01	0.5	H	M	0	general GO
electron_transport (214)	PLZF.01	0.5	0		0	general GO
electron_transport (214)	RORA1.01	0.4		0	0	general GO
elevation_of_cytosolic_calcium_ion_concentration (37)	AMEF2.01	0.4		0	0	general GO
endocytosis (65)	DEC1.01	0.6		0	0	general GO
epidermis_development (59)	HLX1.01	0.6	0	M	H	general GO
epidermis_development (59)	BRACH2.01	0.5	H	0	M	general GO
epidermis_development (59)	AIML3.01	0.5	M	0	H	general GO
epidermis_development (59)	TAL1TAL1TAL1	0.5		0	0	general GO
epidermis_development (59)	TBX5.01	0.5		0	0	general GO
epidermis_development (59)	BACH1.01	0.5	H	0	M	general GO
epidermis_development (59)	AP1.01	0.4	H	0	M	general GO
epidermis_development (59)	TATA.01	0.3		0	0	general GO
epidermis_development (59)	TATA.02	0.3		0	0	general GO
ER_to_Golgi_transport (47)	ATF6.02	0.6		0	0	general GO
ER_to_Golgi_transport (47)	CREB.02	0.6		0	0	general GO
ER_to_Golgi_transport (47)	E4F.01	0.5		0	0	general GO
ER_to_Golgi_transport (47)	ATF.02	0.5		0	0	general GO
ER_to_Golgi_transport (47)	CREBP1CJU	0.4		0	0	general GO
fatty_acid_metabolism (55)	BARX2_01	0.3	0	H	M	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	NRSF.01	0.6	0		0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	TAL1BETAIT	0.5	H		0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	MEL1_02	0.5		0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	COMP1.01	0.5		0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	BRACH.01	0.4		0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	TCF11MAFG	0.4		0	0	general GO

G_protein_coupled_receptor_protein_signaling_pathway (398)	ISL1.01	0.4	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	BRN4.01	0.4	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	GATA1.04	0.4	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	FREAC4.01	0.4	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	GATA2.02	0.4	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	XFD3.01	0.4	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	GATA2.01	0.4	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	GATA3.01	0.3	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	EVI1.02	0.3	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	FREAC3.01	0.3	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	CART1.01	0.3	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	EVI1.01	0.3	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	MEL1_01	0.3	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	EVI1.05	0.3	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	PIT1.01	0.3	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	HNF3B.01	0.3	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	NKX31.01	0.2	H	H	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	BRN2.02	0.2	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	EVI1.03	0.2	H	0	0	general GO
G_protein_coupled_receptor_protein_signaling_pathway (398)	AT_rich	0	0	0	0	general GO
generation_of_precursor_metabolites_and_energy (85)	ER.02	0.5	M	0	H	general GO
homophilic_cell_adhesion (70)	NFAT.01	0.4	0	0	0	general GO
homophilic_cell_adhesion (70)	OCT1P.01	0.4	0	H	0	general GO
immune_response (366)	NFKAPPAB.0	0.6	H	0	0	general GO
immune_response (366)	NFKAPPAB.0	0.6	H	0	0	general GO
immune_response (366)	NFKAPPAB6	0.6	H	0	0	general GO
immune_response (366)	CREL.01	0.5	H	0	0	general GO
immune_response (366)	NFKAPPAB.0	0.5	H	0	0	general GO
immune_response (366)	HIVEP1_01	0.5	H	0	0	general GO
immune_response (366)	AML1.01	0.5	0	0	0	general GO
immune_response (366)	PARAXIS_01	0.5	H	0	M	general GO
immune_response (366)	ETS1.01	0.5	H	0	0	general GO
immune_response (366)	AML3.01	0.5	H	0	0	general GO
immune_response (366)	RBPJK.02	0.5	H	0	0	general GO
immune_response (366)	TAL1ALPHA	0.5	H	0	0	general GO
immune_response (366)	NFE2.01	0.5	0	0	0	general GO
immune_response (366)	TR2.01	0.5	0	0	0	general GO
immune_response (366)	TAL1BETA4	0.5	0	0	0	general GO
immune_response (366)	AREB6.01	0.5	M	0	H	general GO
immune_response (366)	TR4.01	0.5	0	0	0	general GO
immune_response (366)	LXRE.01	0.5	0	0	0	general GO
immune_response (366)	NKX32.01	0.5	0	0	0	general GO
immune_response (366)	ETS2.01	0.5	H	0	0	general GO
immune_response (366)	GRE.01	0.5	0	0	0	general GO
immune_response (366)	PAX2.01	0.5	H	0	0	general GO
immune_response (366)	PPARA.01	0.5	H	0	0	general GO
immune_response (366)	NFE2L2.01	0.5	H	0	0	general GO
immune_response (366)	MTATA.01	0.5	0	0	0	general GO
immune_response (366)	TAL1BETAIT	0.5	0	0	0	general GO
immune_response (366)	SRF.03	0.5	H	0	0	general GO
immune_response (366)	BACH1.01	0.5	H	0	0	general GO
immune_response (366)	PLZF.01	0.5	0	0	0	general GO
immune_response (366)	AREB6.04	0.5	0	0	0	general GO
immune_response (366)	GKLF_02	0.5	0	0	0	general GO
immune_response (366)	TAACC.01	0.5	0	0	0	general GO
immune_response (366)	STAT6.01	0.5	H	0	0	general GO
immune_response (366)	MIT.01	0.5	0	H	0	general GO
immune_response (366)	MEL1_03	0.5	H	H	0	general GO
immune_response (366)	RP58.01	0.5	H	0	0	general GO
immune_response (366)	COMP1.01	0.5	0	0	0	general GO
immune_response (366)	PXRCAR.01	0.5	H	0	0	general GO
immune_response (366)	BARBIE.01	0.4	H	M	H	general GO
immune_response (366)	BRACH.01	0.4	0	0	0	general GO
immune_response (366)	PAX8.01	0.4	H	0	0	general GO

immune_response (366)	GATA1.01	0.4	0	H	general GO
immune_response (366)	RTR.01	0.4	H	H	general GO
immune_response (366)	MYT1L.01	0.4	H	0	general GO
immune_response (366)	STAT.01	0.4	H	0	general GO
immune_response (366)	PRE.01	0.4	0	0	general GO
immune_response (366)	TCF11.01	0.4	H	0	general GO
immune_response (366)	BCL6.02	0.4	0	0	general GO
immune_response (366)	TCF11MAFG	0.4	H	0	general GO
immune_response (366)	ILF1_01	0.4	H	0	general GO
immune_response (366)	AP1.01	0.4	H	0	general GO
immune_response (366)	ISRE.01	0.4	M	0	general GO
immune_response (366)	IRF2.01	0.4	0	0	general GO
immune_response (366)	IRF3.01	0.4	0	0	general GO
immune_response (366)	SRF.01	0.4	0	0	general GO
immune_response (366)	NKX25.01	0.4	0	0	general GO
immune_response (366)	PRDM1.01	0.4	0	0	general GO
immune_response (366)	HMGY.01	0.4	H	0	general GO
immune_response (366)	PDX1_Gabi	0.4	M	H	general GO
immune_response (366)	FAST1.01	0.4	H	0	general GO
immune_response (366)	GATA.01	0.4	H	0	general GO
immune_response (366)	HBP1_01	0.4	0	0	general GO
immune_response (366)	RORA1.01	0.4	H	0	general GO
immune_response (366)	GFI1.01	0.4	0	M	general GO
immune_response (366)	PHOX2_01	0.4	H	0	general GO
immune_response (366)	PSE_02	0.4	0	H	general GO
immune_response (366)	BRN4.01	0.4	H	0	general GO
immune_response (366)	LEF1.02	0.4	H	0	general GO
immune_response (366)	MTBF.01	0.4	H	0	general GO
immune_response (366)	IRF1.01	0.4	0	0	general GO
immune_response (366)	CEBPB.01	0.4	H	0	general GO
immune_response (366)	GATA1.04	0.4	H	0	general GO
immune_response (366)	OCT1.05	0.4	H	0	general GO
immune_response (366)	AARE.01	0.4	0	0	general GO
immune_response (366)	AIRE.01	0.4	H	H	general GO
immune_response (366)	LTATA_01	0.4	0	0	general GO
immune_response (366)	BRN2.01	0.4	H	0	general GO
immune_response (366)	IRF4.01	0.4	H	0	general GO
immune_response (366)	STAT5.01	0.4	0	0	general GO
immune_response (366)	GATA1.03	0.4	H	0	general GO
immune_response (366)	BCL6.01	0.4	M	0	general GO
immune_response (366)	OCT1.04	0.4	0	0	general GO
immune_response (366)	GFI1B.01	0.4	0	0	general GO
immune_response (366)	PDX1.01	0.4	0	H	general GO
immune_response (366)	AMEF2.01	0.4	0	0	general GO
immune_response (366)	RORA2.01	0.4	H	0	general GO
immune_response (366)	NFAT.01	0.4	0	0	general GO
immune_response (366)	FREAC4.01	0.4	H	0	general GO
immune_response (366)	CDX2.01	0.4	H	0	general GO
immune_response (366)	MEF2.01	0.4	H	0	general GO
immune_response (366)	MMEF2.01	0.4	0	0	general GO
immune_response (366)	GATA2.02	0.4	0	H	general GO
immune_response (366)	GATA1.05	0.4	H	H	general GO
immune_response (366)	XFD3.01	0.4	H	0	general GO
immune_response (366)	IRF7.01	0.4	0	0	general GO
immune_response (366)	OCT1P.01	0.4	H	0	general GO
immune_response (366)	OCT.01	0.4	0	0	general GO
immune_response (366)	PDX1_G_SA	0.4	H	0	general GO
immune_response (366)	GATA2.01	0.4	0	H	general GO
immune_response (366)	CDX1.01	0.3	H	0	general GO
immune_response (366)	VBP.01	0.3	H	0	general GO
immune_response (366)	NKX25.02	0.3	H	0	general GO
immune_response (366)	FREAC2.01	0.3	H	0	general GO
immune_response (366)	NMP4.01	0.3	0	0	general GO
immune_response (366)	OCT1.02	0.3	H	0	general GO

immune_response (366)	DLX3.01	0.3	H	0	general GO
immune_response (366)	HOXC13_01	0.3	H	0	general GO
immune_response (366)	HNF1.02	0.3	H	0	general GO
immune_response (366)	XFD1.01	0.3	H	0	general GO
immune_response (366)	GSH2_01	0.3	M	H	0 general GO
immune_response (366)	BARX2_01	0.3	H	0	general GO
immune_response (366)	ATBF1.01	0.3	H	0	general GO
immune_response (366)	HMEF2.01	0.3	H	0	general GO
immune_response (366)	GATA3.01	0.3	H	H	general GO
immune_response (366)	EVI1.04	0.3	H	0	general GO
immune_response (366)	EVI1.02	0.3	H	0	general GO
immune_response (366)	MEIS1_HOXA	0.3	H	H	general GO
immune_response (366)	PBX_HOXA9	0.3	H	H	general GO
immune_response (366)	BRN3.02	0.3	H	H	general GO
immune_response (366)	FKHRL1.01	0.3	H	0	general GO
immune_response (366)	BRN2.03	0.3	H	0	general GO
immune_response (366)	XFD2.01	0.3	H	0	general GO
immune_response (366)	OC2.01	0.3	H	0	general GO
immune_response (366)	LMX1B.01	0.3	H	0	general GO
immune_response (366)	FREAC3.01	0.3	0	0	general GO
immune_response (366)	CART1.01	0.3	H	0	general GO
immune_response (366)	EN1.01	0.3	H	0	general GO
immune_response (366)	CABL.01	0.3	H	0	general GO
immune_response (366)	HNF1.03	0.3	H	0	general GO
immune_response (366)	EVI1.01	0.3	H	0	general GO
immune_response (366)	HNF6.01	0.3	H	0	general GO
immune_response (366)	SOX5.01	0.3	0	0	general GO
immune_response (366)	MSX.01	0.3	M	H	0 general GO
immune_response (366)	BRN3.01	0.3	H	0	general GO
immune_response (366)	ATATA.01	0.3	0	0	general GO
immune_response (366)	EVI1.06	0.3	H	0	general GO
immune_response (366)	MEF2.02	0.3	H	0	general GO
immune_response (366)	MEF2.03	0.3	H	0	general GO
immune_response (366)	HNF1.01	0.3	H	0	general GO
immune_response (366)	DLX1.01	0.3	H	0	general GO
immune_response (366)	MEF2.05	0.3	0	0	general GO
immune_response (366)	RSRFC4.02	0.3	H	0	general GO
immune_response (366)	MEL1_01	0.3		0	general GO
immune_response (366)	GATA3.02	0.3	H	H	general GO
immune_response (366)	MEF2.04	0.3	0	0	general GO
immune_response (366)	EVI1.05	0.3	H	0	general GO
immune_response (366)	TATA.01	0.3	0	H	general GO
immune_response (366)	RSRFC4.01	0.3		0	general GO
immune_response (366)	TATA.02	0.3	0	H	general GO
immune_response (366)	MYT1.02	0.3	H	0	general GO
immune_response (366)	PIT1.01	0.3	H	0	general GO
immune_response (366)	FREAC7.01	0.3	H	H	general GO
immune_response (366)	HFH1.01	0.3	H	0	general GO
immune_response (366)	HFH8.01	0.3	H	0	general GO
immune_response (366)	MYT1.01	0.3	H	0	general GO
immune_response (366)	OCT1.01	0.3	H	0	general GO
immune_response (366)	BRN5.01	0.3	H	0	general GO
immune_response (366)	HNF3B.01	0.3	H	0	general GO
immune_response (366)	HFH2.01	0.3	H	0	general GO
immune_response (366)	NKX31.01	0.2	H	0	general GO
immune_response (366)	BRN2.02	0.2	H	0	general GO
immune_response (366)	EVI1.03	0.2	H	H	general GO
immune_response (366)	S8.01	0.2	M	H	0 general GO
immune_response (366)	BRIGHT.01	0.2	H	0	general GO
immune_response (366)	OCT1.06	0.2	H	H	general GO
immune_response (366)	LHX3.01	0.1	H	0	general GO
immune_response (366)	poly_A	0	H	0	general GO
induction_of_apoptosis (86)	GFI1.01	0.4	0	H	M general GO
induction_of_apoptosis (86)	IRF1.01	0.4		0	general GO

inflammatory_response (163)	NFKAPPAB.0	0.6		0	0	general GO
inflammatory_response (163)	NFKAPPAB.0	0.6		0	0	general GO
inflammatory_response (163)	NFKAPPAB6	0.6		0	0	general GO
inflammatory_response (163)	CREL.01	0.5	M	0	0	general GO
inflammatory_response (163)	NFKAPPAB.0	0.5		0	0	general GO
inflammatory_response (163)	HIVEP1_01	0.5		0	0	general GO
inflammatory_response (163)	AML1.01	0.5	H	0	0	general GO
inflammatory_response (163)	AP1FJ.01	0.5		0	0	general GO
inflammatory_response (163)	AP1.02	0.5		0	0	general GO
inflammatory_response (163)	LXRE.01	0.5		0	0	general GO
inflammatory_response (163)	ETS2.01	0.5		0	0	general GO
inflammatory_response (163)	GRE.01	0.5		0	0	general GO
inflammatory_response (163)	PPARA.01	0.5	M	H	0	general GO
inflammatory_response (163)	SRF.03	0.5	H	M	0	general GO
inflammatory_response (163)	ARE.01	0.5		0	0	general GO
inflammatory_response (163)	GKLF_02	0.5	M	H	0	general GO
inflammatory_response (163)	TAACC.01	0.5		H	0	general GO
inflammatory_response (163)	STAT6.01	0.5		0	0	general GO
inflammatory_response (163)	CEBP.02	0.5		0	0	general GO
inflammatory_response (163)	CDPCR3.01	0.5	0		0	general GO
inflammatory_response (163)	COMP1.01	0.5		0	H	general GO
inflammatory_response (163)	DBP.01	0.5		0	0	general GO
inflammatory_response (163)	BARBIE.01	0.4		0	H	general GO
inflammatory_response (163)	GATA1.01	0.4		M	0	general GO
inflammatory_response (163)	MYT1L.01	0.4		H	0	general GO
inflammatory_response (163)	BCL6.02	0.4		H	0	general GO
inflammatory_response (163)	TCF11MAFG	0.4		0	0	general GO
inflammatory_response (163)	AP1.01	0.4		0	0	general GO
inflammatory_response (163)	ISL1.01	0.4	M	H	0	general GO
inflammatory_response (163)	ISRE.01	0.4		0	0	general GO
inflammatory_response (163)	IRF2.01	0.4		0	0	general GO
inflammatory_response (163)	IRF3.01	0.4		0	0	general GO
inflammatory_response (163)	SRF.01	0.4		M	0	general GO
inflammatory_response (163)	PRDM1.01	0.4		H	0	general GO
inflammatory_response (163)	HMG1Y.01	0.4		H	0	general GO
inflammatory_response (163)	HBP1_01	0.4	H	0		general GO
inflammatory_response (163)	BRN4.01	0.4		0	0	general GO
inflammatory_response (163)	MTBF.01	0.4		H	0	general GO
inflammatory_response (163)	IRF1.01	0.4	M	H	0	general GO
inflammatory_response (163)	CEBPB.01	0.4		H	0	general GO
inflammatory_response (163)	AARE.01	0.4		0	0	general GO
inflammatory_response (163)	AIRE.01	0.4		H	0	general GO
inflammatory_response (163)	LTATA_01	0.4		0	0	general GO
inflammatory_response (163)	BRN2.01	0.4		0	0	general GO
inflammatory_response (163)	IRF4.01	0.4		H	0	general GO
inflammatory_response (163)	STAT5.01	0.4		0	H	general GO
inflammatory_response (163)	GATA1.03	0.4		H	0	general GO
inflammatory_response (163)	BCL6.01	0.4		H	0	general GO
inflammatory_response (163)	AMEF2.01	0.4		0	0	general GO
inflammatory_response (163)	RORA2.01	0.4		H	0	general GO
inflammatory_response (163)	NFAT.01	0.4		H	0	general GO
inflammatory_response (163)	FREAC4.01	0.4	M	H	0	general GO
inflammatory_response (163)	CDX2.01	0.4		H	0	general GO
inflammatory_response (163)	MEF2.01	0.4	H		0	general GO
inflammatory_response (163)	MMEF2.01	0.4		0	0	general GO
inflammatory_response (163)	SOX9.01	0.4	0		0	general GO
inflammatory_response (163)	GATA2.02	0.4	H	H	M	general GO
inflammatory_response (163)	XFD3.01	0.4		0	0	general GO
inflammatory_response (163)	IRF7.01	0.4		H	0	general GO
inflammatory_response (163)	OCT1P.01	0.4			0	general GO
inflammatory_response (163)	OCT.01	0.4	H		0	general GO
inflammatory_response (163)	PDX1_G_SA	0.4		0	0	general GO
inflammatory_response (163)	CDX1.01	0.3		M	0	general GO
inflammatory_response (163)	FREAC2.01	0.3		0	0	general GO

inflammatory_response (163)	OCT1.02	0.3	0	0	0	general GO
inflammatory_response (163)	DLX3.01	0.3			0	general GO
inflammatory_response (163)	HOXC13_01	0.3	H		0	general GO
inflammatory_response (163)	HNF1.02	0.3			0	general GO
inflammatory_response (163)	XFD1.01	0.3	H		0	general GO
inflammatory_response (163)	ATBF1.01	0.3	H		0	general GO
inflammatory_response (163)	GATA3.01	0.3	H		0	general GO
inflammatory_response (163)	PAX4.01	0.3			0	general GO
inflammatory_response (163)	EVI1.04	0.3			0	general GO
inflammatory_response (163)	BRN3.02	0.3			0	general GO
inflammatory_response (163)	BRN2.03	0.3			0	general GO
inflammatory_response (163)	XFD2.01	0.3			0	general GO
inflammatory_response (163)	OC2.01	0.3			0	M general GO
inflammatory_response (163)	LMX1B.01	0.3	H		0	general GO
inflammatory_response (163)	CART1.01	0.3	M		0	general GO
inflammatory_response (163)	EN1.01	0.3	H		0	general GO
inflammatory_response (163)	HNF1.03	0.3			0	general GO
inflammatory_response (163)	EVI1.01	0.3	H		0	general GO
inflammatory_response (163)	HNF6.01	0.3	H		0	general GO
inflammatory_response (163)	BRN3.01	0.3	H	H		general GO
inflammatory_response (163)	ATATA.01	0.3			0	general GO
inflammatory_response (163)	MEF2.02	0.3	H		0	general GO
inflammatory_response (163)	MEF2.03	0.3	H		0	general GO
inflammatory_response (163)	HNF1.01	0.3			0	general GO
inflammatory_response (163)	MEF2.05	0.3			0	general GO
inflammatory_response (163)	RSRFC4.02	0.3	M		0	general GO
inflammatory_response (163)	MEL1_01	0.3	H	M		general GO
inflammatory_response (163)	GATA3.02	0.3			0	general GO
inflammatory_response (163)	MEF2.04	0.3	H		0	general GO
inflammatory_response (163)	TATA.01	0.3			0	general GO
inflammatory_response (163)	RSRFC4.01	0.3	M		0	general GO
inflammatory_response (163)	TATA.02	0.3			0	general GO
inflammatory_response (163)	MYT1.02	0.3	H		0	general GO
inflammatory_response (163)	PIT1.01	0.3			0	general GO
inflammatory_response (163)	FREAC7.01	0.3	H		0	general GO
inflammatory_response (163)	SATB1.01	0.3	M		0	general GO
inflammatory_response (163)	HFH1.01	0.3	H		0	general GO
inflammatory_response (163)	HFH8.01	0.3	H		0	general GO
inflammatory_response (163)	MYT1.01	0.3	H		0	general GO
inflammatory_response (163)	OCT1.01	0.3	H		0	general GO
inflammatory_response (163)	BRN5.01	0.3			0	general GO
inflammatory_response (163)	HNF3B.01	0.3	H		0	general GO
inflammatory_response (163)	HFH2.01	0.3	M	H		general GO
inflammatory_response (163)	BRN2.02	0.2			0	general GO
inflammatory_response (163)	EVI1.03	0.2	H		0	general GO
inflammatory_response (163)	BRIGHT.01	0.2			0	general GO
inflammatory_response (163)	OCT1.06	0.2			0	general GO
inflammatory_response (163)	LHX3.01	0.1			0	general GO
inflammatory_response (163)	poly_A	0	H		0	general GO
innate_immune_response (46)	GRE.01	0.5			0	general GO
innate_immune_response (46)	STAT.01	0.4			0	H general GO
innate_immune_response (46)	ISRE.01	0.4			0	general GO
innate_immune_response (46)	IRF3.01	0.4			0	general GO
innate_immune_response (46)	PRDM1.01	0.4	M	H		general GO
innate_immune_response (46)	PSE_02	0.4	H		0	general GO
innate_immune_response (46)	BRN4.01	0.4			0	general GO
innate_immune_response (46)	CDX2.01	0.4			0	H general GO
innate_immune_response (46)	MMEF2.01	0.4			0	general GO
innate_immune_response (46)	GATA1.05	0.4	H	M		general GO
innate_immune_response (46)	GATA2.01	0.4			0	M general GO
innate_immune_response (46)	HNF1.02	0.3			0	H general GO
innate_immune_response (46)	ATBF1.01	0.3			0	general GO
innate_immune_response (46)	HMEF2.01	0.3	H	M		general GO
innate_immune_response (46)	PAX4.01	0.3			0	general GO

innate immune response (46)	XFD2.01	0.3		0	H	general GO
innate immune response (46)	LMX1B.01	0.3		0	0	general GO
innate immune response (46)	EN1.01	0.3		0	0	general GO
innate immune response (46)	HNF1.03	0.3		0	0	general GO
innate immune response (46)	SRY.01	0.3	H	M	0	general GO
innate immune response (46)	BRN3.01	0.3		0	0	general GO
innate immune response (46)	MEF2.03	0.3		0	0	general GO
innate immune response (46)	HNF1.01	0.3		0	0	general GO
innate immune response (46)	RSRFC4.01	0.3		0	0	general GO
innate immune response (46)	PIT1.01	0.3		0	H	general GO
innate immune response (46)	HFH8.01	0.3		0	0	general GO
innate immune response (46)	OCT1.01	0.3		0	0	general GO
innate immune response (46)	OCT1.06	0.2	H	M	0	general GO
intracellular protein transport (191)	GC_rich	1		0	0	general GO
intracellular protein transport (191)	SP1.01	0.8		0	0	general GO
intracellular protein transport (191)	ZF9.01	0.7		0	0	general GO
intracellular protein transport (191)	NRF1_01	0.7		H	0	general GO
intracellular protein transport (191)	EGR2.01	0.7	H	M	0	general GO
intracellular protein transport (191)	GC.01	0.7		0	0	general GO
intracellular protein transport (191)	ATF6.02	0.6		0	0	general GO
intracellular protein transport (191)	NRSE.01	0.6		0	0	general GO
intracellular protein transport (191)	ATF.01	0.6	H	M	0	general GO
intracellular protein transport (191)	XBP1.01	0.5		M	H	general GO
lipid biosynthesis (54)	CAAT.01	0.5		0	0	general GO
lipid biosynthesis (54)	NFY.02	0.5		0	0	general GO
lipid catabolism (41)	HNF6.01	0.3	M	H	0	general GO
lipid transport (41)	RORA1.01	0.4		0	0	general GO
mitosis (86)	NFY.01	0.5		H	0	general GO
mitosis (86)	CAAT.01	0.5		0	0	general GO
mitosis (86)	NFY.02	0.5		0	0	general GO
mitosis (86)	NFY.03	0.5		0	0	general GO
mitosis (86)	CHR.01	0.4		0	0	general GO
morphogenesis (104)	GC_rich	1	0	0		general GO
morphogenesis (104)	AP2.01	0.7	0	H		general GO
morphogenesis (104)	ZF5.01	0.7	0	0		general GO
morphogenesis (104)	HAND2_E12.	0.7	M	H	0	general GO
morphogenesis (104)	EGR1.02	0.7	H		H	general GO
mRNA processing (148)	E2F.02	0.6		H	0	general GO
mRNA processing (148)	NFY.01	0.5	0		0	general GO
muscle contraction (78)	MYOD.02	0.6	M	0	H	general GO
muscle development (107)	INSM1_01	0.6		0	0	general GO
muscle development (107)	HNF4.01	0.5	0		0	general GO
muscle development (107)	SRF.02	0.5		0	0	general GO
muscle development (107)	MTATA.01	0.5		0	0	general GO
muscle development (107)	SRF.03	0.5		0	0	general GO
muscle development (107)	SRF.01	0.4		0	0	general GO
muscle development (107)	AMEF2.01	0.4		0	0	general GO
muscle development (107)	MEF2.02	0.3		0	0	general GO
muscle development (107)	MEF2.03	0.3		0	0	general GO
muscle development (107)	RSRFC4.02	0.3		0	0	general GO
muscle development (107)	RSRFC4.01	0.3		0	0	general GO
negative regulation of cell proliferation (130)	PPARA.01	0.5	0		0	general GO
nervous system development (225)	GC_rich	1	H	H		general GO
nervous system development (225)	CKROX_01	0.7		H		general GO
nervous system development (225)	PLAG1_01	0.6	H		H	general GO
nervous system development (225)	GAGA.01	0.6		H	0	general GO
nuclear mRNA splicing via spliceosome (94)	NRF2.01	0.6		0	0	general GO
nuclear mRNA splicing via spliceosome (94)	ATF.02	0.5		H	H	general GO
nucleosome assembly (71)	NFY.01	0.5		H	0	general GO
nucleosome assembly (71)	NFY.02	0.5		H	0	general GO
nucleosome assembly (71)	NFY.03	0.5		0	0	general GO
nucleosome assembly (71)	TATA.01	0.3		H	0	general GO
organ morphogenesis (71)	poly_C	1	H	M	0	general GO
organ morphogenesis (71)	WT1.01	0.8	0		H	general GO

organ_morphogenesis (71)	INSM1_01	0.6	H	H	M	general GO
organ_morphogenesis (71)	GAGA.01	0.6	H	M	0	general GO
positive_regulation_of_I_kappaB_kinase_NF_kappaB_cascade (56)	ETS1.01	0.5	H	0	M	general GO
positive_regulation_of_I_kappaB_kinase_NF_kappaB_cascade (56)	IRF3.01	0.4	0	0	0	general GO
potassium_ion_transport (108)	WT1.01	0.8	0	0	0	general GO
potassium_ion_transport (108)	EGR1.01	0.7	H	M	0	general GO
potassium_ion_transport (108)	PAX9.01	0.6	0	0	0	general GO
pregnancy (41)	PDX1_Gabi	0.4	0	0	0	general GO
pregnancy (41)	XFD3.01	0.4	0	H	0	general GO
pregnancy (41)	BRN3.01	0.3	0	0	0	general GO
protein_amino_acid_dephosphorylation (96)	MUSCLE_INI	0.6	0	0	0	general GO
protein_amino_acid_phosphorylation (373)	SP1.01	0.8	H	0	0	general GO
protein_amino_acid_phosphorylation (373)	MTF-1.01	0.7	H	0	M	general GO
protein_amino_acid_phosphorylation (373)	ZNF35_01	0.5	0	0	0	general GO
protein_amino_acid_phosphorylation (373)	ATF.02	0.5	0	0	0	general GO
protein_biosynthesis (197)	GABP.01	0.6	0	0	0	general GO
protein_biosynthesis (197)	CDE.01	0.6	H	H	0	general GO
protein_biosynthesis (197)	WHN.01	0.6	0	0	0	general GO
protein_biosynthesis (197)	NRF2.01	0.6	0	H	0	general GO
protein_biosynthesis (197)	ATF.01	0.6	H	M	0	general GO
protein_biosynthesis (197)	CETS1P54.0	0.6	0	0	0	general GO
protein_biosynthesis (197)	YY1.01	0.6	0	0	0	general GO
protein_biosynthesis (197)	ELK1.02	0.5	0	0	0	general GO
protein_biosynthesis (197)	E2F.03	0.5	H	0	0	general GO
protein_biosynthesis (197)	ELF2.01	0.5	0	0	0	general GO
protein_biosynthesis (197)	FLI.01	0.5	0	0	0	general GO
protein_biosynthesis (197)	ELK1.01	0.5	0	0	0	general GO
protein_biosynthesis (197)	E2F.01	0.5	0	0	0	general GO
protein_biosynthesis (197)	ISRE.01	0.4	0	0	0	general GO
protein_biosynthesis (197)	HMG1Y.01	0.4	H	M	0	general GO
protein_biosynthesis (197)	HOXB9_01	0.4	H	M	0	general GO
protein_folding (149)	FLI.01	0.5	0	H	0	general GO
protein_folding (149)	VMYB.03	0.4	0	0	0	general GO
protein_kinase_cascade (43)	E47.01	0.6	0	0	0	general GO
protein_targeting (37)	NRF2.01	0.6	0	0	0	general GO
protein_transport (254)	GC_rich	1	0	0	0	general GO
protein_transport (254)	ZF5.01	0.7	0	0	0	general GO
protein_transport (254)	NRF1_01	0.7	0	0	0	general GO
protein_transport (254)	EGR1.02	0.7	0	0	0	general GO
protein_transport (254)	MUSCLE_INI	0.6	0	0	0	general GO
protein_transport (254)	GABP.01	0.6	0	0	0	general GO
protein_transport (254)	WHN.01	0.6	0	H	0	general GO
protein_transport (254)	NRF2.01	0.6	0	H	0	general GO
protein_transport (254)	CREB.02	0.6	0	H	0	general GO
protein_transport (254)	XPB1.01	0.5	0	H	0	general GO
protein_ubiquitination (118)	MIF1.01	0.5	H	0	M	general GO
proteolysis (297)	NRL.01	0.5	H	0	M	general GO
proteolysis (297)	TH1E47.01	0.5	H	M	0	general GO
proteolysis (297)	AREB6.01	0.5	0	H	0	general GO
proteolysis (297)	COUP.01	0.5	0	0	0	general GO
proteolysis (297)	AREB6.02	0.5	0	0	0	general GO
proteolysis (297)	AP1.01	0.4	0	0	0	general GO
proteolysis (297)	CEBPB.01	0.4	0	0	0	general GO
proteolysis (297)	AIRE.01	0.4	0	M	H	general GO
proteolysis (297)	GATA1.03	0.4	0	0	0	general GO
proteolysis (297)	XFD3.01	0.4	0	0	0	general GO
proteolysis (297)	ATBF1.01	0.3	0	0	0	general GO
proteolysis (297)	HMEF2.01	0.3	M	0	H	general GO
proteolysis (297)	XFD2.01	0.3	M	H	0	general GO
proteolysis (297)	HNF1.03	0.3	0	0	0	general GO
proteolysis (297)	HNF1.01	0.3	0	0	0	general GO
proteolysis (297)	HFH1.01	0.3	0	0	0	general GO
proteolysis (297)	HFH8.01	0.3	0	H	0	general GO
proteolysis (297)	HNF3B.01	0.3	0	H	0	general GO

proteolysis (297)	HFH2.01	0.3		0	0	general GO
regulation_of_apoptosis (59)	IRF3.01	0.4		0	0	general GO
regulation_of_cyclin_dependent_protein_kinase_activity (34)	NFY.01	0.5	0		0	general GO
regulation_of_progression_through_cell_cycle (217)	AHRARNT.02	0.6	0	M	H	general GO
regulation_of_progression_through_cell_cycle (217)	E2F.01	0.5	H		0	general GO
regulation_of_progression_through_cell_cycle (217)	HMEF2.01	0.3	M	0	H	general GO
response_to_DNA_damage_stimulus (117)	EGR1.01	0.7	H	H	M	general GO
response_to_DNA_damage_stimulus (117)	E2F.02	0.6		M	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.03	0.5		0	M	general GO
response_to_DNA_damage_stimulus (117)	FLI.01	0.5		0	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.01	0.5		M	0	general GO
response_to_virus (55)	NFKAPPAB.0	0.5		0	0	general GO
response_to_virus (55)	HIVEP1_01	0.5		0	0	general GO
response_to_virus (55)	ISRE.01	0.4		M	0	general GO
response_to_virus (55)	IRF2.01	0.4		H	0	general GO
response_to_virus (55)	IRF3.01	0.4		0	0	general GO
response_to_virus (55)	PRDM1.01	0.4	M		H	general GO
response_to_virus (55)	HBP1_01	0.4		0	0	general GO
response_to_virus (55)	IRF1.01	0.4			H	general GO
response_to_virus (55)	IRF4.01	0.4		H	0	general GO
response_to_virus (55)	GATA1.05	0.4	H		0	general GO
response_to_virus (55)	IRF7.01	0.4		0	0	general GO
response_to_virus (55)	TATA.01	0.3		H	0	general GO
RNA_splicing (61)	NRF2.01	0.6		0	0	general GO
sensory_perception (201)	NFKAPPAB.0	0.6		0	0	general GO
sensory_perception (201)	HIVEP1_01	0.5		0	0	general GO
sensory_perception (201)	NBRE.01	0.5		0	0	general GO
sensory_perception (201)	NFE2.01	0.5		0	0	general GO
sensory_perception (201)	IK2.01	0.5		0	0	general GO
sensory_perception (201)	LMO2COM.0	0.5		H	0	general GO
sensory_perception (201)	SRF.03	0.5		0	0	general GO
sensory_perception (201)	MIT.01	0.5		0	0	general GO
sensory_perception (201)	MEL1_03	0.5		H	0	general GO
sensory_perception (201)	DBP.01	0.5		H	0	general GO
sensory_perception (201)	PAX8.01	0.4		H	0	general GO
sensory_perception (201)	GATA1.01	0.4		H	0	general GO
sensory_perception (201)	AP1.01	0.4		0	0	general GO
sensory_perception (201)	SRF.01	0.4		0	0	general GO
sensory_perception (201)	RORA1.01	0.4		H	0	general GO
sensory_perception (201)	GFI1.01	0.4		H	0	general GO
sensory_perception (201)	MTBF.01	0.4		0	0	general GO
sensory_perception (201)	GATA1.04	0.4		H	0	general GO
sensory_perception (201)	CRX.01	0.4		H	0	general GO
sensory_perception (201)	AARE.01	0.4	H		0	general GO
sensory_perception (201)	LTATA_01	0.4		0	0	general GO
sensory_perception (201)	OTX2.01	0.4		H	0	general GO
sensory_perception (201)	GATA1.03	0.4		H	0	general GO
sensory_perception (201)	BCL6.01	0.4	H	M	0	general GO
sensory_perception (201)	AMEF2.01	0.4	H		M	general GO
sensory_perception (201)	CDX2.01	0.4		H	0	general GO
sensory_perception (201)	GATA2.02	0.4		H	0	general GO
sensory_perception (201)	XFD3.01	0.4		0	0	general GO
sensory_perception (201)	OCT1P.01	0.4		H	0	general GO
sensory_perception (201)	SIX3.01	0.4		H	0	general GO
sensory_perception (201)	PDX1_G_SA	0.4		H	H	general GO
sensory_perception (201)	GATA2.01	0.4		H	H	general GO
sensory_perception (201)	CDX1.01	0.3		H	0	general GO
sensory_perception (201)	NKX25.02	0.3		H	0	general GO
sensory_perception (201)	FREAC2.01	0.3	0		H	general GO
sensory_perception (201)	HMEF2.01	0.3		H	0	general GO
sensory_perception (201)	GATA3.01	0.3		H	H	general GO
sensory_perception (201)	BRN3.02	0.3		H	H	general GO
sensory_perception (201)	FKHRL1.01	0.3	H		H	general GO
sensory_perception (201)	XFD2.01	0.3			H	general GO

sensory_perception (201)	OC2.01	0.3	H	0	0	general GO
sensory_perception (201)	EN1.01	0.3	H	H		general GO
sensory_perception (201)	MEF2.02	0.3	H	0	0	general GO
sensory_perception (201)	MEF2.05	0.3	H	0	0	general GO
sensory_perception (201)	CDP.02	0.3	H	0	0	general GO
sensory_perception (201)	MEL1_01	0.3	H	0	0	general GO
sensory_perception (201)	GATA3.02	0.3	H	0	0	general GO
sensory_perception (201)	EVI1.05	0.3	H	0	0	general GO
sensory_perception (201)	TATA.01	0.3	0	0	0	general GO
sensory_perception (201)	EVI1.03	0.2	H	0	0	general GO
sensory_perception (201)	BRIGHT.01	0.2	H	0	0	general GO
sensory_perception_of_smell (40)	NFE2L2.01	0.5	0	0	0	general GO
sensory_perception_of_smell (40)	GFI1.01	0.4	M	H	0	general GO
signal_transduction (1189)	E47.01	0.6	0	H	M	general GO
signal_transduction (1189)	NFKAPPAB.0	0.5	H	M	0	general GO
signal_transduction (1189)	HNF4.01	0.5	0	0	0	general GO
signal_transduction (1189)	HIVEP1_01	0.5	M	0	0	general GO
signal_transduction (1189)	AML1.01	0.5	0	0	0	general GO
signal_transduction (1189)	MEL1_02	0.5	0	0	0	general GO
signal_transduction (1189)	AP1.01	0.4	0	0	0	general GO
signal_transduction (1189)	AARE.01	0.4	0	0	0	general GO
signal_transduction (1189)	EVI1.02	0.3	0	0	0	general GO
signal_transduction (1189)	EVI1.01	0.3	0	0	0	general GO
signal_transduction (1189)	poly_A	0	0	0	0	general GO
skeletal_development (83)	AG_rich_codi	0.5	0	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	GC_rich	1	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	SP1.01	0.8	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	ZF5.01	0.7	0	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	ZF9.01	0.7	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	EGR3.01	0.7	H	0	M	general GO
small_GTPase_mediated_signal_transduction (124)	NRF1_01	0.7	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	CKROX_01	0.7	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	EGR1.02	0.7	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	GC.01	0.7	H	0	0	general GO
small_GTPase_mediated_signal_transduction (124)	ATF6.01	0.6	H	0	M	general GO
small_GTPase_mediated_signal_transduction (124)	PLAG1_01	0.6	H	H	M	general GO
small_GTPase_mediated_signal_transduction (124)	EBVR.01	0.6	0	0	0	general GO
sodium_ion_transport (75)	FXRE.01	0.5	0	0	0	general GO
sodium_ion_transport (75)	HNF1.02	0.3	0	0	0	general GO
sodium_ion_transport (75)	HNF1.03	0.3	0	0	0	general GO
sodium_ion_transport (75)	HNF1.01	0.3	0	0	0	general GO
steroid_biosynthesis (42)	NFY.01	0.5	0	0	0	general GO
steroid_biosynthesis (42)	CAAT.01	0.5	0	0	0	general GO
steroid_biosynthesis (42)	NFY.02	0.5	0	0	0	general GO
steroid_biosynthesis (42)	NFY.03	0.5	0	0	0	general GO
steroid_biosynthesis (42)	GATA1.03	0.4	0	H	M	general GO
steroid_metabolism (54)	HNF3B.01	0.3	0	0	0	general GO
synaptic_transmission (153)	NRSF.01	0.6	M	0	H	general GO
synaptic_transmission (153)	NRSE.01	0.6	0	0	H	general GO
synaptic_transmission (153)	GAGA.01	0.6	H	M	H	general GO
transmembrane_receptor_tyrosine_kinase_signaling (65)	E47.01	0.6	0	0	0	general GO
transmembrane_receptor_tyrosine_kinase_signaling (65)	GAGA.01	0.6	0	0	M	general GO
transport (940)	ERR_01	0.5	0	H	0	general GO
transport (940)	OTX2.01	0.4	M	0	H	general GO
transport (940)	HNF1.02	0.3	0	0	0	general GO
transport (940)	HNF1.03	0.3	0	0	0	general GO
transport (940)	HNF1.01	0.3	0	0	0	general GO
ubiquitin_cycle (154)	GC_rich	1	0	0	0	general GO
ubiquitin_cycle (154)	HES1.02	0.8	0	0	0	general GO
ubiquitin_cycle (154)	ZF5.01	0.7	0	0	0	general GO
ubiquitin_cycle (154)	HES1.01	0.6	0	0	0	general GO
ubiquitin_cycle (154)	FLI.01	0.5	0	0	0	general GO
ubiquitin_cycle (154)	VMYB.05	0.4	0	0	H	general GO
ubiquitin_dependent_protein_catabolism (72)	IRF2.01	0.4	0	0	0	general GO

vesicle_mediated_transport (51)	SP1.01	0.8		0	0	general GO
visual_perception (142)	VMAF.01	0.5		0	0	general GO
visual_perception (142)	TBX5.01	0.5		0	0	general GO
visual_perception (142)	HOX_PBX_0	0.5		0	0	general GO
visual_perception (142)	GFI1.01	0.4		0	0	general GO
visual_perception (142)	CRX.01	0.4		0	0	general GO
visual_perception (142)	OTX2.01	0.4	H	0	0	general GO
visual_perception (142)	PDX1.01	0.4		0	0	general GO
visual_perception (142)	SIX3.01	0.4	H	0	0	general GO
visual_perception (142)	OC2.01	0.3	M	H	H	general GO
visual_perception (142)	GATA3.02	0.3		0	0	general GO
visual_perception (142)	HFH1.01	0.3	M	H	0	general GO
Wnt_receptor_signaling_pathway (66)	GC_rich	1	H	H		general GO
Wnt_receptor_signaling_pathway (66)	poly_C	1		H	H	general GO
Wnt_receptor_signaling_pathway (66)	SP1.01	0.8	H	0		general GO
Wnt_receptor_signaling_pathway (66)	WT1.01	0.8		0	H	general GO
Wnt_receptor_signaling_pathway (66)	MAZR.01	0.8		0	0	general GO
Wnt_receptor_signaling_pathway (66)	ZNF202.01	0.7		0	0	general GO
Wnt_receptor_signaling_pathway (66)	AP2.01	0.7	H	H		general GO
Wnt_receptor_signaling_pathway (66)	ZF5.01	0.7		H		general GO
Wnt_receptor_signaling_pathway (66)	ZF9.01	0.7	0	0		general GO
Wnt_receptor_signaling_pathway (66)	EGR1.02	0.7	H	H		general GO
Wnt_receptor_signaling_pathway (66)	EGR1.01	0.7	H		H	general GO
Wnt_receptor_signaling_pathway (66)	PLAG1_01	0.6		H	0	general GO
Wnt_receptor_signaling_pathway (66)	CDE.01	0.6	H	M	0	general GO
Wnt_receptor_signaling_pathway (66)	PAX9.01	0.6	M	0	H	general GO
Wnt_receptor_signaling_pathway (66)	NRSE.01	0.6	0	M	H	general GO
Wnt_receptor_signaling_pathway (66)	PAX5.01	0.6	0		M	general GO

700bp Window (with overlap)

[illegible]

transcription (930)	HELT.01	0.691910867	H	H	H				transcription GO
regulation_of_transcription_DNA_dependent	HELT.01	0.691910867	H	H	H				transcription GO
transcription (930)	NGFIC.01	0.685824218				H			transcription GO
regulation_of_transcription_DNA_dependent	NGFIC.01	0.685824218							transcription GO
development (530)	NGFIC.01	0.685824218	M	M		M	M	M	transcription GO
transcription (930)	CKROX_01	0.683333333							transcription GO
regulation_of_transcription_DNA_dependent	CKROX_01	0.683333333							transcription GO
regulation_of_transcription (266)	CKROX_01	0.683333333							transcription GO
development (530)	CKROX_01	0.683333333							transcription GO
transcription (930)	EGR1.02	0.683035714							transcription GO
regulation_of_transcription_DNA_dependent	EGR1.02	0.683035714							transcription GO
regulation_of_transcription (266)	EGR1.02	0.683035714				M			transcription GO
development (530)	EGR1.02	0.683035714	O	O	O				transcription GO
transcription (930)	HIC1_01	0.681615155	O	O	O	O		M	transcription GO
regulation_of_transcription_DNA_dependent	HIC1_01	0.681615155	O	O	O	M			transcription GO
regulation_of_transcription (266)	HIC1_01	0.681615155	O	O	O	O	M		transcription GO
development (530)	HIC1_01	0.681615155	M	M	M				transcription GO
regulation_of_transcription_DNA_dependent	BKLF.01	0.681578947	O	O	O	H			transcription GO
development (530)	BKLF.01	0.681578947	O	H	H	H		H	transcription GO
transcription (930)	EGR2.01	0.680134551			M	M			transcription GO
regulation_of_transcription_DNA_dependent	EGR2.01	0.680134551							transcription GO
transcription (930)	GC.01	0.679856115	H	O	O			M	transcription GO
regulation_of_transcription_DNA_dependent	GC.01	0.679856115	H	O	O			M	transcription GO
regulation_of_transcription (266)	GC.01	0.679856115	O	O	O	M	H	O	transcription GO
development (530)	GC.01	0.679856115	H	H	H	M		M	transcription GO
transcription (930)	MZF1.01	0.678571429	M		M			M	transcription GO
regulation_of_transcription_DNA_dependent	MZF1.01	0.678571429				M			transcription GO
regulation_of_transcription (266)	MZF1.01	0.678571429							transcription GO
development (530)	MZF1.01	0.678571429							transcription GO
transcription (930)	EGR1.01	0.67232125	H						transcription GO
regulation_of_transcription_DNA_dependent	EGR1.01	0.67232125							transcription GO
transcription (930)	MTF-1.01	0.653230769	O	O	O		H	O	transcription GO
regulation_of_transcription_DNA_dependent	MTF-1.01	0.653230769	M	O				M	transcription GO
development (530)	MTF-1.01	0.653230769	O	O	O	H	O	M	transcription GO
transcription (930)	MAZ.01	0.651515152							transcription GO
regulation_of_transcription_DNA_dependent	MAZ.01	0.651515152							transcription GO
regulation_of_transcription (266)	MAZ.01	0.651515152							transcription GO
development (530)	MAZ.01	0.651515152	H	H	H				transcription GO
transcription (930)	ZIC2_01	0.648148148	O	M	O	M		M	transcription GO
regulation_of_transcription_DNA_dependent	ZIC2_01	0.648148148	M	M	M	M			transcription GO
regulation_of_transcription (266)	ZIC2_01	0.648148148	M	M	O	H			transcription GO
development (530)	ZIC2_01	0.648148148	O	O	H				transcription GO
transcription (930)	ATF6.01	0.639053254	M	M			H	H	transcription GO
regulation_of_transcription_DNA_dependent	ATF6.01	0.639053254	M	M					transcription GO
transcription (930)	PLAG1_01	0.63261693							transcription GO
regulation_of_transcription_DNA_dependent	PLAG1_01	0.63261693							transcription GO
regulation_of_transcription (266)	PLAG1_01	0.63261693							transcription GO
development (530)	PLAG1_01	0.63261693							transcription GO
regulation_of_transcription_DNA_dependent	INSM1_01	0.629180602	O	O	M	M	M	H	transcription GO
development (530)	INSM1_01	0.629180602	H	H	H				transcription GO
regulation_of_transcription_DNA_dependent	EBVR.01	0.627594628	H	H	H	O		M	transcription GO
transcription (930)	AHRARNT.02	0.624493927						H	transcription GO
regulation_of_transcription_DNA_dependent	AHRARNT.02	0.624493927	O	O	H				transcription GO
transcription (930)	HES1.01	0.622222222							transcription GO
regulation_of_transcription_DNA_dependent	HES1.01	0.622222222							transcription GO
regulation_of_transcription (266)	HES1.01	0.622222222	O	H	O	O	M	O	transcription GO
transcription (930)	MUSCLE_INI	0.620813397						H	transcription GO
regulation_of_transcription_DNA_dependent	MUSCLE_INI	0.620813397	M						transcription GO
development (530)	MUSCLE_INI	0.620813397	H	H				H	transcription GO
transcription (930)	NMYC.01	0.615909091	O	O	O		O	O	transcription GO
regulation_of_transcription_DNA_dependent	NMYC.01	0.615909091	O	O	O		O	O	transcription GO
transcription (930)	HIF1.01	0.607692308	O	O	O		H	H	transcription GO
regulation_of_transcription_DNA_dependent	HIF1.01	0.607692308	O	O	O		H	H	transcription GO
transcription (930)	MUSCLE_INI	0.607655502	H		H	H		H	transcription GO

regulation_of_transcription_DNA_dependent	MUSCLE_INI	0.607655502	M							transcription GO
regulation_of_transcription_DNA_dependent	USF.03	0.6	0	0	0		0	0		transcription GO
regulation_of_transcription_DNA_dependent	ZNF76_143_0	0.6	0	H	H	H			H	transcription GO
development (530)	ZNF76_143_0	0.6	0	0	0	H			H	transcription GO
regulation_of_transcription_DNA_dependent	EKLF.01	0.595779221	0	0	0				M	transcription GO
regulation_of_transcription_DNA_dependent	RREB1.01	0.595238095	H	H	H	H			0	transcription GO
transcription (930)	CDE.01	0.595238095								transcription GO
regulation_of_transcription_DNA_dependent	CDE.01	0.595238095								transcription GO
regulation_of_transcription (266)	CDE.01	0.595238095	0	H			H		0	transcription GO
development (530)	CDE.01	0.595238095	0	0	0	0	M			transcription GO
regulation_of_transcription (266)	ZBRK1_01	0.594024416	0	M	0	0	H	H		transcription GO
regulation_of_transcription_DNA_dependent	AHR.01	0.594017094	H	H	H	H				transcription GO
regulation_of_transcription (266)	AHR.01	0.594017094	0	0	0	0	0	0		transcription GO
transcription (930)	E2F.02	0.59375	H	H	H	0	0			transcription GO
regulation_of_transcription_DNA_dependent	E2F.02	0.59375		H	H					transcription GO
regulation_of_transcription (266)	E2F.02	0.59375	0	0	0	0	0	0		transcription GO
transcription (930)	WHN.01	0.592307692	0	0	0	M	M			transcription GO
transcription (930)	PAX9.01	0.574305556	0	0				H	H	transcription GO
regulation_of_transcription_DNA_dependent	PAX9.01	0.574305556	0	0	M			H		transcription GO
development (530)	PAX9.01	0.574305556	0	0	0	0	H	M		transcription GO
transcription (930)	PAX5.01	0.568181818	H	H	H	H	H	M		transcription GO
regulation_of_transcription_DNA_dependent	PAX5.01	0.568181818	0	0	0			M		transcription GO
regulation_of_transcription (266)	PAX5.01	0.568181818	0	0	0			0	M	transcription GO
development (530)	PAX5.01	0.568181818	0	0	H	H	H			transcription GO
transcription (930)	PAX5.03	0.564251208	H	0	M	M	0	0		transcription GO
regulation_of_transcription (266)	VDR_RXR.02	0.562962963	H	H	H	H	H			transcription GO
development (530)	VDR_RXR.02	0.562962963	H	H	H			H		transcription GO
transcription (930)	GAGA.01	0.562878788					M			transcription GO
regulation_of_transcription_DNA_dependent	GAGA.01	0.562878788								transcription GO
regulation_of_transcription (266)	GAGA.01	0.562878788						H		transcription GO
development (530)	GAGA.01	0.562878788								transcription GO
development (530)	VDR_RXR.01	0.561111111	H	H	H	H				transcription GO
regulation_of_transcription_DNA_dependent	TAXCREB.02	0.555555556	0	0	M	0	H	H		transcription GO
regulation_of_transcription_DNA_dependent	E2.02	0.546195652	0	0	0	0	H			transcription GO
development (530)	ZNF35_01	0.545808967	0	0	0	0	H			transcription GO
development (530)	OLF1.01	0.545454545	0	0	0	H			H	transcription GO
regulation_of_transcription_DNA_dependent	CREB.03	0.543859649	0	0	0	0			M	transcription GO
transcription (930)	E2F.03	0.538461538	0	0	0	H				transcription GO
regulation_of_transcription_DNA_dependent	E2F.03	0.538461538	0	0	M	H				transcription GO
transcription (930)	NFY.01	0.518088822	H	H	H			H	0	transcription GO
regulation_of_transcription_DNA_dependent	NFY.01	0.518088822							M	transcription GO
regulation_of_transcription (266)	NFY.01	0.518088822						0		transcription GO
transcription (930)	AG_rich_codon	0.5						H		transcription GO
regulation_of_transcription_DNA_dependent	AG_rich_codon	0.5								transcription GO
regulation_of_transcription (266)	AG_rich_codon	0.5								transcription GO
development (530)	AG_rich_codon	0.5					H	H	H	transcription GO
regulation_of_transcription_DNA_dependent	SRF.02	0.494285714	H	H			H	H	0	transcription GO
transcription (930)	GKLF.01	0.491428571			H	H	H	0		transcription GO
regulation_of_transcription_DNA_dependent	GKLF.01	0.491428571			H	H	H	H		transcription GO
regulation_of_transcription (266)	GKLF.01	0.491428571				H				transcription GO
development (530)	GKLF.01	0.491428571	H		H			H		transcription GO
transcription (930)	CAAT.01	0.489080752				0	0	0		transcription GO
regulation_of_transcription_DNA_dependent	CAAT.01	0.489080752					M	0		transcription GO
regulation_of_transcription (266)	CAAT.01	0.489080752			M	M	0	0		transcription GO
regulation_of_transcription_DNA_dependent	NFY.02	0.477272727					M	0	0	transcription GO
regulation_of_transcription (266)	NFY.02	0.477272727		H	H			0	0	transcription GO
development (530)	MTATA.01	0.470588235			H	0	0			transcription GO
regulation_of_transcription_DNA_dependent	PBX1_MEIS1	0.462145969	H	0	0	M	M	0		transcription GO
regulation_of_transcription (266)	PBX1_MEIS1	0.462145969			M	M	M	M		transcription GO
regulation_of_transcription_DNA_dependent	PBX1_MEIS1	0.440247253	H		0	M	M	0		transcription GO
regulation_of_transcription (266)	PBX1_MEIS1	0.440247253				M	M	0		transcription GO
Wnt_receptor_signaling_pathway (66)	GC_rich	0.9915		H						general GO
ubiquitin_cycle (154)	GC_rich	0.9915	H		H	0	0	0		general GO
transcription_RNA_polyII_promoter (190)	GC_rich	0.9915		0						general GO

small_GTPase_mediated_signal_transduction	GC_rich	0.9915				H	H	0		general GO
regulation_of_transcription_from_RNA_polymera	GC_rich	0.9915		H	H	0	0	0		general GO
regulation_of_progression_through_cell_cycle	GC_rich	0.9915	0	M	0	M	H	H		general GO
protein_transport (254)	GC_rich	0.9915		H	H	0	0	0		general GO
nervous_system_development (225)	GC_rich	0.9915	0	H		H	0	H		general GO
intracellular_protein_transport (191)	GC_rich	0.9915		H	H	0	0	0		general GO
Wnt_receptor_signaling_pathway (66)	poly_C	0.989				H	H	H	H	general GO
regulation_of_transcription_from_RNA_polymera	poly_C	0.989	H	H	H	M	0	0		general GO
protein_amino_acid_phosphorylation (373)	poly_C	0.989	0	0	0	0		H		general GO
organ_morphogenesis (71)	poly_C	0.989	H	H	H	0	M	0		general GO
central_nervous_system_development (68)	poly_C	0.989	0	0	0			0		general GO
cation_transport (99)	poly_C	0.989	0	H			0	0	0	general GO
Wnt_receptor_signaling_pathway (66)	SP1.01	0.778846154	H	H	0					general GO
transcription_RNA_polyll_promoter (190)	SP1.01	0.778846154	H	H	H					general GO
small_GTPase_mediated_signal_transduction	SP1.01	0.778846154					H	H	H	general GO
regulation_of_transcription_from_RNA_polymera	SP1.01	0.778846154	H	H	0	M	0	0		general GO
protein_amino_acid_phosphorylation (373)	SP1.01	0.778846154	0	0	0	0				general GO
Wnt_receptor_signaling_pathway (66)	WT1.01	0.770561018	H	H		H				general GO
transcription_RNA_polyll_promoter (190)	WT1.01	0.770561018		H	H	H	M	M		general GO
small_GTPase_mediated_signal_transduction	WT1.01	0.770561018				H	0	0	0	general GO
regulation_of_transcription_from_RNA_polymera	WT1.01	0.770561018			0	M	H	H		general GO
Wnt_receptor_signaling_pathway (66)	HES1.02	0.763263941	H	0	H	M	M	H		general GO
ubiquitin_cycle (154)	HES1.02	0.763263941	H	M	0	0	0	0		general GO
Wnt_receptor_signaling_pathway (66)	MAZR.01	0.762075134	M	0	0	H	0	H		general GO
transcription_RNA_polyll_promoter (190)	MAZR.01	0.762075134	M	0	0	H	H	0		general GO
small_GTPase_mediated_signal_transduction	MAZR.01	0.762075134				H	H	H	H	general GO
regulation_of_transcription_from_RNA_polymera	MAZR.01	0.762075134	H	H	H	0		H		general GO
Wnt_receptor_signaling_pathway (66)	ZNF202.01	0.732919255		H	H		0	H		general GO
transcription_RNA_polyll_promoter (190)	ZNF202.01	0.732919255		H	0	H				general GO
regulation_of_transcription_from_RNA_polymera	ZNF202.01	0.732919255	H	M		M	0	0		general GO
potassium_ion_transport (108)	ZNF202.01	0.732919255	H	H	H		H	0		general GO
cation_transport (99)	ZNF202.01	0.732919255	0		M	0	0	0		general GO
Wnt_receptor_signaling_pathway (66)	AP2.01	0.725490196	H	H	H					general GO
transcription_RNA_polyll_promoter (190)	AP2.01	0.725490196	0	0	H		M			general GO
small_GTPase_mediated_signal_transduction	AP2.01	0.725490196				H	0	0		general GO
morphogenesis (104)	AP2.01	0.725490196	0	0	0	H	H			general GO
Wnt_receptor_signaling_pathway (66)	ZF5.01	0.719485294	M	0	H	H	H	H		general GO
transcription_RNA_polyll_promoter (190)	ZF5.01	0.719485294	0	H		0	H	H		general GO
small_GTPase_mediated_signal_transduction	ZF5.01	0.719485294				H	0	0	H	general GO
regulation_of_progression_through_cell_cycle	ZF5.01	0.719485294	0	0	M	M	H	0		general GO
protein_transport (254)	ZF5.01	0.719485294		H	H	0	0	0		general GO
protein_biosynthesis (197)	ZF5.01	0.719485294	0	0	0		M	0		general GO
ubiquitin_cycle (154)	ZF9.01	0.717844061	H			H	0	0	0	general GO
small_GTPase_mediated_signal_transduction	ZF9.01	0.717844061				H	H	H		general GO
protein_amino_acid_phosphorylation (373)	ZF9.01	0.717844061	H	H	H					general GO
organ_morphogenesis (71)	ZF9.01	0.717844061	0	H	0	M	0	0		general GO
Wnt_receptor_signaling_pathway (66)	EGR3.01	0.709376693	0	0	M	M	H	H		general GO
small_GTPase_mediated_signal_transduction	EGR3.01	0.709376693	H	H	0	0	M	M		general GO
Wnt_receptor_signaling_pathway (66)	NRF1_01	0.708333333	H	H	0		H	H		general GO
ubiquitin_cycle (154)	NRF1_01	0.708333333		H	H	H	H	0		general GO
transcription_RNA_polyll_promoter (190)	NRF1_01	0.708333333	0	0	M	M	M			general GO
small_GTPase_mediated_signal_transduction	NRF1_01	0.708333333				H	H	H	H	general GO
regulation_of_progression_through_cell_cycle	NRF1_01	0.708333333	0	H	0	M	0	0		general GO
regulation_of_cyclin_dependent_protein_kinase_	NRF1_01	0.708333333	H	H	0	M	M	0		general GO
protein_transport (254)	NRF1_01	0.708333333		H	H	H	0	0		general GO
cell_cycle (273)	NRF1_01	0.708333333				H	0	0	0	general GO
DNA_repair (148)	MYCMAX.03	0.701731602		H	0	0	0	0		general GO
cation_transport (99)	NFKAPPAB5	0.7	0	0	0	H	0	M		general GO
apoptosis (258)	NFKAPPAB5	0.7	H			H	0	H	0	general GO
morphogenesis (104)	HAND2_E12.	0.6957522	M	0	0	0	H	H		general GO
lipid_biosynthesis (54)	HAND2_E12.	0.6957522	0	0	0	0	H	M		general GO
transcription_RNA_polyll_promoter (190)	ZBP89.01	0.695601852	0	0	0	H	M	0		general GO
transcription_RNA_polyll_promoter (190)	HELT.01	0.691910867	0	0	0	0	H	M		general GO
DNA_repair (148)	HELT.01	0.691910867	H	H	H	0		0		general GO

Wnt_receptor_signaling_pathway (66)	NGFIC.01	0.685824218	H	H				H	general GO
small_GTPase_mediated_signal_transduction	NGFIC.01	0.685824218		H	H	0	0	M	general GO
organ_morphogenesis (71)	NGFIC.01	0.685824218	0	0	0	M	M	H	general GO
morphogenesis (104)	NGFIC.01	0.685824218	0	0	H	M	0	0	general GO
calcium_ion_transport (62)	NGFIC.01	0.685824218	H	H	0	M	M	0	general GO
Wnt_receptor_signaling_pathway (66)	CKROX_01	0.683333333	H	H	H		H	0	general GO
small_GTPase_mediated_signal_transduction	CKROX_01	0.683333333				H	0	0	H
regulation_of_transcription_from_RNA_polymera	CKROX_01	0.683333333	H		H		H	0	general GO
nervous_system_development (225)	CKROX_01	0.683333333	H		H	H	H	H	general GO
chromatin_modification (53)	CKROX_01	0.683333333			H	H	0	0	general GO
Wnt_receptor_signaling_pathway (66)	EGR1.02	0.683035714	H	H		H			general GO
transcription_RNA_polyll_promoter (190)	EGR1.02	0.683035714		H	H	M	M	M	general GO
small_GTPase_mediated_signal_transduction	EGR1.02	0.683035714					H	H	H
regulation_of_transcription_from_RNA_polymera	EGR1.02	0.683035714	H			M	M	0	0
morphogenesis (104)	EGR1.02	0.683035714	H	0	H	M	M		general GO
Wnt_receptor_signaling_pathway (66)	HIC1_01	0.681615155		H	H	H	H	0	general GO
small_GTPase_mediated_signal_transduction	HIC1_01	0.681615155	H	H	H	H		0	general GO
potassium_ion_transport (108)	HIC1_01	0.681615155	H	H	H			0	general GO
organ_morphogenesis (71)	HIC1_01	0.681615155	H		0	0	H	H	general GO
Wnt_receptor_signaling_pathway (66)	EGR2.01	0.680134551	0	0	0	M	M	H	general GO
transcription_RNA_polyll_promoter (190)	GC.01	0.679856115	H	0	M	H		M	general GO
small_GTPase_mediated_signal_transduction	GC.01	0.679856115		H	H	H	0	0	general GO
ion_transport (329)	MZF1.01	0.678571429	0	0	0	M	H	0	general GO
Wnt_receptor_signaling_pathway (66)	EGR1.01	0.67232125	H			M	M		general GO
potassium_ion_transport (108)	EGR1.01	0.67232125	H		M	M	M	0	general GO
transcription_RNA_polyll_promoter (190)	MAZ.01	0.651515152	H	H	H			M	general GO
skeletal_development (83)	MAZ.01	0.651515152	H	0	M	M	0	0	general GO
regulation_of_transcription_from_RNA_polymera	MAZ.01	0.651515152						0	0
potassium_ion_transport (108)	ZIC2_01	0.648148148	0	H	0	M	0	0	general GO
epidermis_development (59)	HEN1.01	0.644124164	0	0	M	M	M		general GO
cation_transport (99)	HEN1.01	0.644124164	H	M	0	0	0	0	general GO
transcription_RNA_polyll_promoter (190)	PLAG1_01	0.63261693	M	0	H	H	H	H	general GO
regulation_of_transcription_from_RNA_polymera	PLAG1_01	0.63261693	0	M	H	M	H	H	general GO
organ_morphogenesis (71)	PLAG1_01	0.63261693	H	H		0	0	0	general GO
nervous_system_development (225)	PLAG1_01	0.63261693	H						general GO
potassium_ion_transport (108)	INSM1_01	0.629180602	0	M	M	M	M	H	general GO
organ_morphogenesis (71)	INSM1_01	0.629180602	0	H	0	H	H	M	general GO
ion_transport (329)	INSM1_01	0.629180602	0	M			H	H	general GO
Wnt_receptor_signaling_pathway (66)	AHRARNT.02	0.624493927	H	0	0	M	0	0	general GO
regulation_of_progression_through_cell_cycle	AHRARNT.02	0.624493927	0	0	H	H		H	general GO
protein_transport (254)	AHRARNT.02	0.624493927	M	0	H	H	0	0	general GO
cell_cycle (273)	AHRARNT.01	0.623253109		M	M	M	0		general GO
ubiquitin_cycle (154)	HES1.01	0.622222222		0	0	0	0	0	general GO
protein_biosynthesis (197)	HES1.01	0.622222222	0	0		M	0	0	general GO
Wnt_receptor_signaling_pathway (66)	MUSCLE_INI	0.620813397	H	0	0		H	0	general GO
small_GTPase_mediated_signal_transduction	MUSCLE_INI	0.620813397		H	H	0	0	0	general GO
central_nervous_system_development (68)	MUSCLE_INI	0.620813397	0	M	M			M	general GO
protein_transport (254)	GABP.01	0.619791667		H	0	0	0	0	general GO
protein_biosynthesis (197)	GABP.01	0.619791667				0	0	0	general GO
ER_to_Golgi_transport (47)	GABP.01	0.619791667		M	H	0	0	0	general GO
cell_division (103)	GABP.01	0.619791667	H	M	M	0	0	0	general GO
synaptic_transmission (153)	NRSF.01	0.619047619					H	0	general GO
ion_transport (329)	NRSF.01	0.619047619		M	M	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling	NRSF.01	0.619047619	H		H	H		M	general GO
transcription_RNA_polyll_promoter (190)	MUSCLE_INI	0.607655502	0	H		H	H	H	general GO
microtubule_based_movement (38)	LMO2COM.0	0.606926407	0	0	0	M	0	H	general GO
signal_transduction (1189)	NFKAPPAB.0	0.604545455				H	0	0	general GO
inflammatory_response (163)	NFKAPPAB.0	0.604545455					0	0	general GO
immune_response (366)	NFKAPPAB.0	0.604545455					0	0	general GO
chemotaxis (98)	NFKAPPAB.0	0.604545455					0	0	general GO
cell_cell_signaling (268)	NFKAPPAB.0	0.604545455	M	M		M	0	0	general GO
apoptosis (258)	NFKAPPAB.0	0.604545455			H	0	0	0	general GO
protein_folding (149)	ZNF76_143_0	0.6	M	0	0	0	0	H	general GO
morphogenesis (104)	ZNF76_143_0	0.6	0	0	0	0		H	general GO

endocytosis (65)	USF.03	0.6	M	0	0	0	H	0	general GO
intracellular_protein_transport (191)	ATF6.02	0.596464646	M		H	0	0	0	general GO
potassium_ion_transport (108)	RREB1.01	0.595238095	0	0	H	M	0	H	general GO
ion_transport (329)	RREB1.01	0.595238095		H	H	H	M	H	general GO
Wnt_receptor_signaling_pathway (66)	CDE.01	0.595238095	H	0	0			H	general GO
ubiquitin_cycle (154)	CDE.01	0.595238095	H		H	H	0	0	general GO
transcription_RNA_polyII_promoter (190)	CDE.01	0.595238095	0	0	H		M	M	general GO
small_GTPase_mediated_signal_transduction	CDE.01	0.595238095		H	H	H		M	general GO
protein_transport (254)	CDE.01	0.595238095				H	H	0	general GO
protein_biosynthesis (197)	CDE.01	0.595238095		H	H	H	0	H	general GO
nucleosome_assembly (71)	CDE.01	0.595238095	H	M	0	0	0	0	general GO
nuclear_mRNA_splicing_via_spliceosome (94)	CDE.01	0.595238095	H		H	H	0	H	general GO
mRNA_processing (148)	CDE.01	0.595238095			H	H	H	H	general GO
cell_cycle (273)	CDE.01	0.595238095			H	H	0	0	general GO
cell_differentiation (192)	NEUROD1.0	0.594871795	0	0	0	0	0	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.02	0.59375			M	M	0	0	general GO
regulation_of_progression_through_cell_cycle	E2F.02	0.59375	0	H	0	0	0	M	general GO
DNA_replication (91)	E2F.02	0.59375	H	H			0	0	general GO
DNA_repair (148)	E2F.02	0.59375			M	M	0	0	general GO
cell_cycle (273)	E2F.02	0.59375			H	H	0	0	general GO
ubiquitin_cycle (154)	WHN.01	0.592307692	H		H	H	0	0	general GO
protein_transport (254)	WHN.01	0.592307692			H	0	0	0	general GO
protein_biosynthesis (197)	WHN.01	0.592307692	H			H	H		general GO
cell_division (103)	WHN.01	0.592307692		M			H	0	general GO
cell_cycle (273)	WHN.01	0.592307692		0	H	H	H	0	general GO
cholesterol_metabolism (38)	AREB6.03	0.588541667	0	0	H	H	0	M	general GO
intracellular_protein_transport (191)	CHREBP_ML	0.588235294	M	0	0	0	0	H	general GO
DNA_repair (148)	USF.02	0.586666667	H		H	0	0	0	general GO
protein_transport (254)	TAXCREB.01	0.584126984	H	0		M	0	0	general GO
DNA_repair (148)	MYCMAX.01	0.582417582		H	H	H	0	0	general GO
muscle_development (107)	AP4.02	0.577777778	0	M	M		0	H	general GO
Wnt_receptor_signaling_pathway (66)	PAX9.01	0.574305556			H	H	H	0	general GO
transcription_RNA_polyII_promoter (190)	PAX9.01	0.574305556	M	M	H	H	0	H	general GO
RNA_splicing (61)	NRF2.01	0.572727273	H	H			0	0	general GO
protein_transport (254)	NRF2.01	0.572727273		H	0	0	0	0	general GO
protein_biosynthesis (197)	NRF2.01	0.572727273				M	0	0	general GO
nuclear_mRNA_splicing_via_spliceosome (94)	NRF2.01	0.572727273		H	H	0	0	0	general GO
synaptic_transmission (153)	NRSE.01	0.571957672				M	H	0	general GO
ion_transport (329)	NRSE.01	0.571957672		M	M	0	H	0	general GO
G_protein_coupled_receptor_protein_signaling	NRSE.01	0.571957672	H	0	H	M		M	general GO
immune_response (366)	NF1.02	0.570065789	H	H	0	0	M	0	general GO
electron_transport (214)	NF1.02	0.570065789	M	M	0	H	0	0	general GO
signal_transduction (1189)	NFKAPPAB.0	0.56884058				0	H	H	general GO
sensory_perception (201)	NFKAPPAB.0	0.56884058							general GO
inflammatory_response (163)	NFKAPPAB.0	0.56884058							general GO
immune_response (366)	NFKAPPAB.0	0.56884058							general GO
chemotaxis (98)	NFKAPPAB.0	0.56884058							general GO
Wnt_receptor_signaling_pathway (66)	PAX5.01	0.568181818	0	H			M	0	general GO
small_GTPase_mediated_signal_transduction	PAX5.01	0.568181818	M	0			0	0	general GO
potassium_ion_transport (108)	PAX5.01	0.568181818	0	0	H		H		general GO
transmembrane_receptor_tyrosine_kinase_signa	GAGA.01	0.562878788	M	0	0	H	0	0	general GO
synaptic_transmission (153)	GAGA.01	0.562878788	H	H	0	0		0	general GO
signal_transduction (1189)	GAGA.01	0.562878788	H		0	H	H	H	general GO
potassium_ion_transport (108)	GAGA.01	0.562878788	H	H	H		0	H	general GO
nervous_system_development (225)	GAGA.01	0.562878788		H	0	0	0	0	general GO
ion_transport (329)	GAGA.01	0.562878788	H	H	H				general GO
calcium_ion_transport (62)	GAGA.01	0.562878788	H	H	H			H	general GO
ion_transport (329)	VDR_RXR.01	0.561111111	H	H	H		H	H	general GO
protein_transport (254)	CREB.02	0.56	M		H	H	H	H	general GO
protein_biosynthesis (197)	CREB.02	0.56	0		H	0	0	0	general GO
lipid_transport (41)	FTF.01	0.557291667	M	0	0	H	H	0	general GO
inflammatory_response (163)	NFKAPPAB6	0.554545455					0	0	general GO
immune_response (366)	NFKAPPAB6	0.554545455					H	0	general GO
chemotaxis (98)	NFKAPPAB6	0.554545455					0	0	general GO

cell_cell_signaling (268)	NFKAPPAB6	0.554545455				M	0	0	general GO
apoptosis (258)	NFKAPPAB6	0.554545455				H	H	0	general GO
anti_apoptosis (85)	NFKAPPAB6	0.554545455	M			H	0	0	general GO
protein_biosynthesis (197)	ATF.01	0.554187192	M	M		0	0	0	general GO
ER_to_Golgi_transport (47)	ATF.01	0.554187192				0	0	0	general GO
protein_biosynthesis (197)	CETS1P54.0	0.552631579				M	0	0	general GO
regulation_of_progression_through_cell_cycle	CREB.04	0.552083333	H	H	H	M	0	0	general GO
protein_biosynthesis (197)	CREB.04	0.552083333	H			H	H	H	general GO
protein_biosynthesis (197)	YY1.01	0.550877193				0	0	0	general GO
nuclear_mRNA_splicing_via_spliceosome (94)	YY1.01	0.550877193	M	H		0	0	H	general GO
mRNA_processing (148)	YY1.01	0.550877193	M			0	0	H	general GO
inflammatory_response (163)	CREL.01	0.547619048				M	0	M	general GO
immune_response (366)	CREL.01	0.547619048					0	0	general GO
chemotaxis (98)	CREL.01	0.547619048				M	M	0	general GO
apoptosis (258)	CREL.01	0.547619048				M	0	0	general GO
protein_biosynthesis (197)	ELK1.02	0.547619048				M	M	0	general GO
DNA_replication (91)	ELK1.02	0.547619048	H	0		M	0	0	general GO
DNA_repair (148)	ELK1.02	0.547619048				M	0	0	general GO
cell_cycle (273)	ELK1.02	0.547619048	0	0	0	0		H	general GO
signal_transduction (1189)	NFKAPPAB.0	0.546218487	M	M		0	M	M	general GO
inflammatory_response (163)	NFKAPPAB.0	0.546218487					0	0	general GO
immune_response (366)	NFKAPPAB.0	0.546218487				H	H	0	general GO
chemotaxis (98)	NFKAPPAB.0	0.546218487				H	0	0	general GO
cell_cell_signaling (268)	NFKAPPAB.0	0.546218487				M	0	0	general GO
protein_biosynthesis (197)	ZNF35_01	0.545808967	H	M		0	0	0	general GO
regulation_of_progression_through_cell_cycle	CREB.03	0.543859649	H	0	0	M	0	0	general GO
protein_folding (149)	CREB.03	0.543859649	H			H	0	0	general GO
protein_biosynthesis (197)	CREB.03	0.543859649	H				0	0	general GO
protein_folding (149)	MYCMAX.02	0.542424242	H	H	H			0	general GO
regulation_of_cyclin_dependent_protein_kinase	ACAAT.01	0.541666667	0	0	H		0	0	general GO
small_GTPase_mediated_signal_transduction	NUDR.01	0.539697282	0			0	0	0	general GO
protein_biosynthesis (197)	NUDR.01	0.539697282	0			M	M	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.03	0.538461538				M	M	0	general GO
regulation_of_progression_through_cell_cycle	E2F.03	0.538461538	0	0	0		M	M	general GO
protein_biosynthesis (197)	E2F.03	0.538461538				H	H		general GO
DNA_repair (148)	E2F.03	0.538461538				0	M	0	general GO
cell_cycle (273)	E2F.03	0.538461538	H			H	H	0	general GO
protein_biosynthesis (197)	ELF2.01	0.536217949				M	0	0	general GO
ubiquitin_cycle (154)	FLI.01	0.534588274					0	0	general GO
response_to_DNA_damage_stimulus (117)	FLI.01	0.534588274					0	0	general GO
protein_biosynthesis (197)	FLI.01	0.534588274				M	0	0	general GO
DNA_repair (148)	FLI.01	0.534588274				H	H	H	general GO
Wnt_receptor_signaling_pathway (66)	HNF4.02	0.533333333	0	0	M			0	general GO
positive_regulation_of_cell_proliferation (103)	NF1.01	0.532058119	H	0	0	0	0	0	general GO
electron_transport (214)	NF1.01	0.532058119	H	H	H		0	0	general GO
chemotaxis (98)	NF1.01	0.532058119	H	0	0	0	0	0	general GO
electron_transport (214)	HNF4.01	0.531055901					0	0	general GO
chemotaxis (98)	BACH2.01	0.525874126	0	M	H		0	0	general GO
response_to_unfolded_protein (40)	STAT1.01	0.524475687	0	0	0	M	H	0	general GO
protein_transport (254)	STAT1.01	0.524475687	H	H	H	M	0	0	general GO
signal_transduction (1189)	HIVEP1_01	0.524475524		M	M	M	0	0	general GO
inflammatory_response (163)	HIVEP1_01	0.524475524					0	0	general GO
immune_response (366)	HIVEP1_01	0.524475524				H	H	0	general GO
chemotaxis (98)	HIVEP1_01	0.524475524				H	H	0	general GO
cell_cell_signaling (268)	HIVEP1_01	0.524475524				M	M	0	general GO
signal_transduction (1189)	AML1.01	0.520833333	0			0	M	0	general GO
pregnancy (41)	AML1.01	0.520833333	M	M		0	0	H	general GO
immune_response (366)	AML1.01	0.520833333				H	H	0	general GO
chemotaxis (98)	AML1.01	0.520833333	H			0	0	0	general GO
proton_transport (41)	T3R.01	0.520634921	0	0	H	0	H		general GO
microtubule_based_movement (38)	T3R.01	0.520634921	M	0	M	M	H	0	general GO
blood_coagulation (70)	T3R.01	0.520634921	0	H	H	H	0	M	general GO
transport (940)	ERR_01	0.519924812	M	H	H	H	H	H	general GO
generation_of_precursor_metabolites_and_ener	ERR_01	0.519924812	M			M	0	0	general GO

amino_acid_metabolism (45)	ERR.01	0.519924812	H	H	M	0	0	0	general GO
immune_response (366)	PARAXIS.01	0.51879085	H	0	M	M	M	M	general GO
defense_response (100)	PARAXIS.01	0.51879085	0	H	H	H			general GO
cell_cell_signaling (268)	PARAXIS.01	0.51879085	0		M	M	0	0	general GO
visual_perception (142)	VMAF.01	0.518467852		H	0	0	0	0	general GO
steroid_biosynthesis (42)	NFY.01	0.518088822		H	H	H	0	0	general GO
regulation_of_cyclin_dependent_protein_kinase	NFY.01	0.518088822	H	H	H		M	0	general GO
mRNA_processing (148)	NFY.01	0.518088822	0	0	0	H	M	M	general GO
mitosis (86)	NFY.01	0.518088822				H	0	0	general GO
DNA_replication (91)	NFY.01	0.518088822		H	H	0	0	0	general GO
cell_division (103)	NFY.01	0.518088822					0	0	general GO
cell_cycle (273)	NFY.01	0.518088822					H	0	general GO
epidermis_development (59)	E47.02	0.517307692		0	0	H	H	0	general GO
cell_proliferation (243)	E47.02	0.517307692	0	0	M	M		M	general GO
immune_response (366)	ETS1.01	0.516363636		H	H	H	0	0	general GO
antimicrobial_humoral_response (87)	ETS1.01	0.516363636	M		H	0	0	0	general GO
protein_biosynthesis (197)	ELK1.01	0.515625					0	0	general GO
sodium_ion_transport (75)	FXRE.01	0.512820513	0	M		M	M	H	general GO
apoptosis (258)	AP1FJ.01	0.507936508	0	0		H	H	0	general GO
protein_transport (254)	E4F.01	0.505787037	M	M	0	0	0	H	general GO
visual_perception (142)	NRL.01	0.505639098	H	H	M	0	0	0	general GO
cholesterol_metabolism (38)	TEF1.01	0.505208333	H	H	0	0	0	M	general GO
proteolysis (297)	TH1E47.01	0.505050505		M	M	M	0	0	general GO
immune_response (366)	AML3.01	0.503401361				H	0	0	general GO
cellular_defense_response (68)	AML3.01	0.503401361	H	H	H		H	M	general GO
inflammatory_response (163)	RBPJK.02	0.501754386		H	H	0	0	0	general GO
skeletal_development (83)	AG_rich_codi	0.5	H		H	0	0	0	general GO
lipid_metabolism (196)	NBRE.01	0.5		H	H	H	H	0	general GO
immune_response (366)	NBRE.01	0.5		M	M	0	0	0	general GO
signal_transduction (1189)	TAL1ALPHA	0.497212739	M		M	0	0	0	general GO
muscle_development (107)	TAL1ALPHA	0.497212739	0	0	H	M	0	0	general GO
inflammatory_response (163)	TAL1ALPHA	0.497212739	M	H	M	0	0	0	general GO
epidermis_development (59)	TAL1ALPHA	0.497212739		0	0	0	0	0	general GO
cell_cell_signaling (268)	TAL1ALPHA	0.497212739	0	H	M	0	0	0	general GO
immune_response (366)	NFE2.01	0.496503497		H	H	H	H	H	general GO
chemotaxis (98)	NFE2.01	0.496503497		H	0	0	0	0	general GO
response_to_DNA_damage_stimulus (117)	E2F.01	0.496296296					M	M	general GO
DNA_repair (148)	E2F.01	0.496296296					M	0	general GO
cell_cycle (273)	E2F.01	0.496296296	H	H	H	0	0	M	general GO
protein_folding (149)	SRF.02	0.494285714	0	0	H	H	0	M	general GO
muscle_development (107)	SRF.02	0.494285714				H	0	0	general GO
immune_response (366)	AP1.02	0.49382716		H		H	H	H	general GO
chemotaxis (98)	AP1.02	0.49382716			M	0	0	0	general GO
protein_transport (254)	ATF.02	0.493506494	M	M	H	0	0	0	general GO
intracellular_protein_transport (191)	ATF.02	0.493506494	M	M	0	H	H	0	general GO
cell_cycle (273)	ATF.02	0.493506494	0	0		M	0	0	general GO
epidermis_development (59)	TBX5.01	0.492603182		H	H	M	0	0	general GO
sensory_perception (201)	TR2.01	0.490909091		H	H	H	H		general GO
excretion (35)	TR2.01	0.490909091	H		M		M	0	general GO
steroid_biosynthesis (42)	CAAT.01	0.489080752				H	0	0	general GO
regulation_of_cyclin_dependent_protein_kinase	CAAT.01	0.489080752	H	H			0	0	general GO
mitosis (86)	CAAT.01	0.489080752					0	0	general GO
chromosome_organization_and_biogenesis (83)	CAAT.01	0.489080752		H	H	H	0	0	general GO
cell_division (103)	CAAT.01	0.489080752					0	0	general GO
cell_cycle (273)	CAAT.01	0.489080752					M	0	general GO
biosynthesis (32)	CAAT.01	0.489080752		H	H	H	0	0	general GO
signal_transduction (1189)	TAL1BETAE4	0.488324176	0	H	H	M	M	0	general GO
sensory_perception (201)	TAL1BETAE4	0.488324176	H		H	H	0	H	general GO
inflammatory_response (163)	TAL1BETAE4	0.488324176	M	M	H	0	0	0	general GO
immune_response (366)	TAL1BETAE4	0.488324176					0	0	general GO
G_protein_coupled_receptor_protein_signaling	TAL1BETAE4	0.488324176	M			M	0	0	general GO
cell_cell_signaling (268)	TAL1BETAE4	0.488324176				M	0	0	general GO
ubiquitin_cycle (154)	CMYB.02	0.488290398	0	0	M	M	H	H	general GO
cell_cycle (273)	CMYB.02	0.488290398	H			0	0	H	general GO

metabolism (241)	IK3.01	0.48806366	0	0	M	0		H	general GO
elevation_of_cytosolic_calcium_ion_concentratio	AREB6.01	0.485576923	0	M	H	0	0	0	general GO
transport (940)	TR4.01	0.484188034	H	H	M		H	H	general GO
lipid_metabolism (196)	TR4.01	0.484188034	H	H	0		0	0	general GO
transport (940)	COUP.01	0.483193277	0	M	0	H	0	H	general GO
metabolism (241)	COUP.01	0.483193277	M	H	0	0	H	0	general GO
fatty_acid_metabolism (55)	COUP.01	0.483193277	H		M	0	0	0	general GO
sensory_perception (201)	LEF1.01	0.482102273	H	H	M	0	0	0	general GO
immune_response (366)	LEF1.01	0.482102273				H	H	0	general GO
protein_kinase_cascade (43)	PU1.01	0.480025183	0	M	M	M	M		general GO
inflammatory_response (163)	PU1.01	0.480025183	0	0	M			0	general GO
immune_response (366)	PU1.01	0.480025183	H	H		0	0	0	general GO
inflammatory_response (163)	ETS2.01	0.478021978				0	0	0	general GO
immune_response (366)	ETS2.01	0.478021978				0	0	0	general GO
chemotaxis (98)	ETS2.01	0.478021978	M		H	0	0	0	general GO
cellular_defense_response (68)	ETS2.01	0.478021978		M	M	0	0	0	general GO
cell_surface_receptor_linked_signal_transductio	ETS2.01	0.478021978				0	0	0	general GO
steroid_biosynthesis (42)	NFY.02	0.477272727				H	0	0	general GO
mitosis (86)	NFY.02	0.477272727				M	0	0	general GO
chromosome_organization_and_biogenesis (83)	NFY.02	0.477272727	H	H	H	0	0	0	general GO
cell_division (103)	NFY.02	0.477272727				0	0	0	general GO
cell_cycle (273)	NFY.02	0.477272727				H	0	0	general GO
biosynthesis (32)	NFY.02	0.477272727				H	0	0	general GO
intracellular_protein_transport (191)	CREB.01	0.477272727	M	M	0	0	0	H	general GO
protein_transport (254)	XBP1.01	0.473873874	M	M	0	0	0	H	general GO
intracellular_protein_transport (191)	XBP1.01	0.473873874	M	M	0	0	H	H	general GO
innate_immune_response (46)	GRE.01	0.473684211				0	0	0	general GO
immune_response (366)	GRE.01	0.473684211		H	H	0	0	0	general GO
cell_surface_receptor_linked_signal_transductio	GRE.01	0.473684211	0	M	0	H	H	0	general GO
immune_response (366)	PAX2.01	0.473429952		H	H	H	0	0	general GO
sensory_perception (201)	AP1.03	0.473251029	H	0	0	0	0	0	general GO
immune_response (366)	AP1.03	0.473251029	H	H	H	H	H		general GO
chemotaxis (98)	AP1.03	0.473251029	M		M	0	0	0	general GO
cellular_defense_response (68)	AP1.03	0.473251029	0	0	H	0	H	M	general GO
electron_transport (214)	PPARA.01	0.472727273		M	M	0	0	0	general GO
chemotaxis (98)	PPARA.01	0.472727273	0	0	0	0	M	H	general GO
immune_response (366)	NFE2L2.01	0.470833333		H	H	H	H	0	general GO
electron_transport (214)	NFE2L2.01	0.470833333				0	0	0	general GO
chemotaxis (98)	NFE2L2.01	0.470833333				H	0	0	general GO
signal_transduction (1189)	TAL1BETAIT	0.46978022	M	H		M	M	0	general GO
immune_response (366)	TAL1BETAIT	0.46978022						0	general GO
G_protein_coupled_receptor_protein_signaling_	TAL1BETAIT	0.46978022				M	0	0	general GO
cell_cell_signaling (268)	TAL1BETAIT	0.46978022		H	M	0	0	0	general GO
cell_adhesion (378)	TAL1BETAIT	0.46978022	H	0	0		H	H	general GO
mRNA_processing (148)	NFY.03	0.46875	H	H	H	0	M	M	general GO
mitosis (86)	NFY.03	0.46875				M	0	0	general GO
chromosome_organization_and_biogenesis (83)	NFY.03	0.46875		H	H	H	0	0	general GO
cell_division (103)	NFY.03	0.46875				M	0	0	general GO
cell_cycle (273)	NFY.03	0.46875				M	0	0	general GO
sensory_perception (201)	SRF.03	0.468253968				H	H	0	general GO
muscle_development (107)	SRF.03	0.468253968				H	H	0	general GO
inflammatory_response (163)	SRF.03	0.468253968				H	0	0	general GO
immune_response (366)	SRF.03	0.468253968	H					0	general GO
immune_response (366)	BACH1.01	0.467741935				H	H	H	general GO
epidermis_development (59)	BACH1.01	0.467741935	H	0	M	M	M	M	general GO
electron_transport (214)	PLZF.01	0.467532468				H	0	0	general GO
immune_response (366)	AREB6.04	0.465277778		H	0	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_	MEL1_02	0.464795009		H	H	0	0	0	general GO
defense_response (100)	TAACC.01	0.462375675	0	H	M	0	0	0	general GO
immune_response (366)	STAT6.01	0.461111111	H	H		H	0	0	general GO
signal_transduction (1189)	MIT.01	0.46076555		M	0	0	0	0	general GO
inflammatory_response (163)	MIT.01	0.46076555				H	H	H	general GO
immune_response (366)	MIT.01	0.46076555					M	H	general GO
sensory_perception (201)	MEL1_03	0.46	H	H	H	0	0	M	general GO

immune_response (366)	MEL1_03	0.46	H	H	H	H	H	general GO
cell_cell_signaling (268)	MEL1_03	0.46	0	H	0	0	0	general GO
sensory_perception (201)	RP58.01	0.457532051	H	H	M	0	0	general GO
immune_response (366)	RP58.01	0.457532051	H	H		M	M	general GO
inflammatory_response (163)	CEBP.02	0.457142857	H	H	H	0	0	general GO
sensory_perception (201)	COMP1.01	0.454545455	H		H	M		general GO
inflammatory_response (163)	COMP1.01	0.454545455			H	0	0	general GO
immune_response (366)	COMP1.01	0.454545455	H	H	0	0		general GO
chemotaxis (98)	COMP1.01	0.454545455	H	0	0	0	0	general GO
immune_response (366)	PXRCAR.01	0.452173913			M	H	0	general GO
inflammatory_response (163)	DBP.01	0.450909091		H	H	H	0	general GO
cell_proliferation (243)	DBP.01	0.450909091	0		0	0	0	general GO
inflammatory_response (163)	BARBIE.01	0.449122807	H	H		0	0	general GO
immune_response (366)	BARBIE.01	0.449122807			H	0	0	general GO
immune_response (366)	BRACH.01	0.448863636	M	H	0	0	0	general GO
G_protein_coupled_receptor_protein_signaling_	BRACH.01	0.448863636		H	H	H	0	general GO
spermatogenesis (97)	VMYB.03	0.446686196	M	H	0	0	0	general GO
inflammatory_response (163)	PAX8.01	0.446153846		H	H	0	0	general GO
immune_response (366)	PAX8.01	0.446153846		M	M	0	0	general GO
transport (940)	GATA1.01	0.446146245	0	M	M	M		general GO
proteolysis (297)	GATA1.01	0.446146245	H	H	H	0	0	general GO
inflammatory_response (163)	GATA1.01	0.446146245	M	M		0	M	general GO
cell_surface_receptor_linked_signal_transductio	GATA1.01	0.446146245		0	0	0	0	general GO
inflammatory_response (163)	MYT1L.01	0.444444444			0	H	0	general GO
immune_response (366)	MYT1L.01	0.444444444		H	H	H	0	general GO
immune_response (366)	STAT.01	0.444444444			H	0	0	general GO
ubiquitin_cycle (154)	VMYB.05	0.444012751	H	H		H	H	general GO
innate immune_response (46)	PRE.01	0.442831216			H	H	0	general GO
inflammatory_response (163)	PRE.01	0.442831216		H	H	H	H	general GO
immune_response (366)	PRE.01	0.442831216		H	0	0	0	general GO
immune_response (366)	TCF11.01	0.440816327				M	0	general GO
G_protein_coupled_receptor_protein_signaling_	TCF11.01	0.440816327	H			0	0	general GO
sensory_perception (201)	BCL6.02	0.436298077	H	0	M	M	M	general GO
inflammatory_response (163)	BCL6.02	0.436298077				M	0	general GO
immune_response (366)	BCL6.02	0.436298077				M	0	general GO
chemotaxis (98)	BCL6.02	0.436298077		M	M	M	M	general GO
cell_cell_signaling (268)	BCL6.02	0.436298077	0	0	0		0	general GO
calcium_ion_homeostasis (30)	BCL6.02	0.436298077	H	H			H	general GO
proteolysis (297)	TCF11MAFG	0.434095861			M	0	0	general GO
inflammatory_response (163)	TCF11MAFG	0.434095861		H	H	0	0	general GO
immune_response (366)	TCF11MAFG	0.434095861			H	H	0	general GO
chemotaxis (98)	TCF11MAFG	0.434095861		H	H	H	0	general GO
immune_response (366)	HOX1-3.01	0.433673469		H	M	0	M	general GO
innate immune_response (46)	TST1.01	0.433333333			M	0	0	general GO
antimicrobial_humoral_response (87)	TST1.01	0.433333333	H	0	0	0	0	general GO
immune_response (366)	ILF1_01	0.433333333				H	0	general GO
signal_transduction (1189)	AP1.01	0.432748538		M	0	0	0	general GO
innate immune_response (46)	AP1.01	0.432748538	0	0		H	0	general GO
inflammatory_response (163)	AP1.01	0.432748538			H	0	0	general GO
immune_response (366)	AP1.01	0.432748538				H	H	general GO
epidermis_development (59)	AP1.01	0.432748538	H	0	M	M	M	general GO
elevation_of_cytosolic_calcium_ion_concentratio	AP1.01	0.432748538	M	H	H	0	0	general GO
chemotaxis (98)	AP1.01	0.432748538			H	H	0	general GO
cell_surface_receptor_linked_signal_transductio	AP1.01	0.432748538	H		0	0	0	general GO
innate immune_response (46)	ISL1.01	0.430586081	H	M	0	0	M	general GO
inflammatory_response (163)	ISL1.01	0.430586081			H	H	H	general GO
response_to_virus (55)	ISRE.01	0.42745098					H	general GO
immune_response (366)	ISRE.01	0.42745098				0	0	general GO
cell_cell_signaling (268)	ISRE.01	0.42745098			H	0	0	general GO
antimicrobial_humoral_response (87)	ISRE.01	0.42745098		H	H	H	H	general GO
ubiquitin_dependent_protein_catabolism (72)	IRF2.01	0.427185044			H	H	0	general GO
response_to_virus (55)	IRF2.01	0.427185044					H	general GO
inflammatory_response (163)	IRF2.01	0.427185044		M	M	0	0	general GO
immune_response (366)	IRF2.01	0.427185044				M	0	general GO

cell_surface_receptor_linked_signal_transductio	IRF2.01	0.427185044				H	H	0	general GO				
homophilic_cell_adhesion (70)	PDX1_G_SA	0.426470588	0	0	0	M	H	H	general GO				
ubiquitin_dependent_protein_catabolism (72)	IRF3.01	0.416666667				M	0	0	0	general GO			
response_to_virus (55)	IRF3.01	0.416666667					0	0	0	general GO			
positive_regulation_of_I_kappaB_kinase_NF_kappaB	IRF3.01	0.416666667				0	0	0	0	general GO			
innate_immune_response (46)	IRF3.01	0.416666667				M	0	0	H	0	0	general GO	
inflammatory_response (163)	IRF3.01	0.416666667				H	H		H	H	0	general GO	
immune_response (366)	IRF3.01	0.416666667							0	0		general GO	
sensory_perception (201)	SRF.01	0.416534181					H	H		0		general GO	
muscle_development (107)	SRF.01	0.416534181					M	0	0			general GO	
inflammatory_response (163)	SRF.01	0.416534181						0	0	0		general GO	
immune_response (366)	SRF.01	0.416534181								M	H	general GO	
circulation (52)	SRF.01	0.416534181				0	0	H	0	0	M	general GO	
chemotaxis (98)	SRF.01	0.416534181				H			0	0	0	general GO	
response_to_virus (55)	PRDM1.01	0.412696678									H	general GO	
innate_immune_response (46)	PRDM1.01	0.412696678				M	0	H	H	H	H	general GO	
inflammatory_response (163)	PRDM1.01	0.412696678						H	0	0		general GO	
immune_response (366)	PRDM1.01	0.412696678						H	0	0		general GO	
defense_response (100)	PRDM1.01	0.412696678				0	H	0	H	0		general GO	
innate_immune_response (46)	HMG1Y.01	0.412049489					0	0	0	0		general GO	
inflammatory_response (163)	HMG1Y.01	0.412049489									M	general GO	
immune_response (366)	HMG1Y.01	0.412049489							H	H	H	general GO	
immune_response (366)	FAST1.01	0.411564626					0	0	0	0		general GO	
inflammatory_response (163)	GATA.01	0.411111111					H	H	0	M		general GO	
immune_response (366)	GATA.01	0.411111111					H	H	H	H	H	general GO	
circulation (52)	GATA.01	0.411111111					H		0	0	0	general GO	
signal_transduction (1189)	PBX1_MEIS1	0.410675303				0	0	M	M	H	0	general GO	
sensory_perception (201)	HBP1_01	0.410364146						H	H	H		general GO	
response_to_virus (55)	HBP1_01	0.410364146					H	H	0	0	0	general GO	
inflammatory_response (163)	HBP1_01	0.410364146					H	H	H	0	M	general GO	
immune_response (366)	HBP1_01	0.410364146						H	H	0	0	general GO	
cell_surface_receptor_linked_signal_transductio	HBP1_01	0.410364146						M	M	0	0	general GO	
sensory_perception (201)	GF11.01	0.408015514					H	H	H	H	0	general GO	
immune_response (366)	GF11.01	0.408015514				H	0	H	H	M	M	general GO	
immune_response (366)	PHOX2_01	0.407575758					H	H	0	H	H	general GO	
immune_response (366)	PSE_02	0.407407407						H	H	H	H	general GO	
chemotaxis (98)	PSE_02	0.407407407				H	H			0	0	general GO	
mitosis (86)	CHR.01	0.405555556						M	0	0	0	general GO	
cell_division (103)	CHR.01	0.405555556						M	0	0	0	general GO	
inflammatory_response (163)	BRN4.01	0.404761905				0	H	H	0	0		general GO	
immune_response (366)	BRN4.01	0.404761905					H	H	H	H	H	general GO	
sensory_perception (201)	MTBF.01	0.404040404					H	H	0	0	0	general GO	
inflammatory_response (163)	LEF1.02	0.404040404					H	M	H	H	H	general GO	
inflammatory_response (163)	MTBF.01	0.404040404					H	H	H	0	H	general GO	
immune_response (366)	MTBF.01	0.404040404					H	H	H	0	0	general GO	
chemotaxis (98)	MTBF.01	0.404040404					H	H	H	H	H	general GO	
cell_cell_signaling (268)	MTBF.01	0.404040404						H	0	0	0	general GO	
response_to_virus (55)	IRF1.01	0.403617536									H	general GO	
regulation_of_apoptosis (59)	IRF1.01	0.403617536				M	0	M	0	H	H	general GO	
inflammatory_response (163)	IRF1.01	0.403617536							0	0	0	general GO	
immune_response (366)	IRF1.01	0.403617536							M	0	0	general GO	
cell_surface_receptor_linked_signal_transductio	IRF1.01	0.403617536				M	H	H	H	H	H	general GO	
response_to_virus (55)	CEBPB.01	0.4					0	0	0	0	0	general GO	
proteolysis (297)	CEBPB.01	0.4								0	0	general GO	
innate_immune_response (46)	CEBPB.01	0.4					H	H	H	H	H	general GO	
inflammatory_response (163)	CEBPB.01	0.4					H	H	H	H	H	general GO	
inflammatory_response (163)	GATA1.04	0.4					H	0	0	0	0	general GO	
immune_response (366)	CEBPB.01	0.4					H	H	H	H	H	general GO	
immune_response (366)	GATA1.04	0.4					H	H	H	H	0	general GO	
defense_response (100)	GATA1.04	0.4				H	H		H	H	0	general GO	
cell_surface_receptor_linked_signal_transductio	CEBPB.01	0.4					H	H	H	0	0	general GO	
blood_coagulation (70)	CEBPB.01	0.4				M			0	0	0	general GO	
antimicrobial_humoral_response (87)	CEBPB.01	0.4					H	H	H	M	0	0	general GO
inflammatory_response (163)	MEIS1B_HOX	0.394957983				M			H	0	H	general GO	

immune_response (366)	OCT1.05	0.392857143					H	0	general GO
signal_transduction (1189)	AARE.01	0.391812865		0	0	0	0	0	general GO
sensory_perception (201)	AARE.01	0.391812865	H	H				0	general GO
inflammatory_response (163)	AARE.01	0.391812865		H	H	0	0	0	general GO
immune_response (366)	AARE.01	0.391812865		H	H	H	0	0	general GO
inflammatory_response (163)	AIRE.01	0.391419855		H	H	H	H	0	general GO
immune_response (366)	AIRE.01	0.391419855					H	H	general GO
sensory_perception (201)	LTATA_01	0.39		0	H	H	0	0	general GO
RNA_processing (58)	LTATA_01	0.39	M	M	M	0	0	H	general GO
proteolysis (297)	LTATA_01	0.39		H	0	0	0	0	general GO
nucleosome_assembly (71)	LTATA_01	0.39	H			H	H	0	general GO
inflammatory_response (163)	LTATA_01	0.39				0	0	0	general GO
cell_cell_signaling (268)	LTATA_01	0.39		0	0	0	0	0	general GO
inflammatory_response (163)	BRN2.01	0.389384921				H	0	H	general GO
antimicrobial_humoral_response (87)	BRN2.01	0.389384921	H	H		H	0	0	general GO
proteolysis (297)	IRF4.01	0.388961039		0	0	0	0	0	general GO
innate_immune_response (46)	IRF4.01	0.388961039		H	H	H	0	0	general GO
inflammatory_response (163)	IRF4.01	0.388961039		H	H	H	H	0	general GO
immune_response (366)	IRF4.01	0.388961039					M	0	general GO
inflammatory_response (163)	STAT5.01	0.388571429		H	0	H	H	H	general GO
immune_response (366)	STAT5.01	0.388571429					M	0	general GO
cell_surface_receptor_linked_signal_transductio	STAT5.01	0.388571429	H	H	H	M	0	0	general GO
inflammatory_response (163)	GATA1.03	0.387685485		H	H	H	H	H	general GO
immune_response (366)	GATA1.03	0.387685485		H	H	H	H	H	general GO
chemotaxis (98)	GATA1.03	0.387685485		H	H	H	H	H	general GO
inflammatory_response (163)	BCL6.01	0.385599694					H	M	general GO
immune_response (366)	BCL6.01	0.385599694					0	0	general GO
chemotaxis (98)	BCL6.01	0.385599694	0	0			H	0	general GO
inflammatory_response (163)	OCT1.04	0.383116883				H	H	0	general GO
immune_response (366)	OCT1.04	0.383116883				H	H	0	general GO
sensory_perception (201)	GFI1B.01	0.382387888				H	0	H	general GO
immune_response (366)	GFI1B.01	0.382387888		H	H	0	0	0	general GO
inflammatory_response (163)	PDX1_G_SA	0.380252101	0	M	M	H	0	0	general GO
sensory_perception (201)	AMEF2.01	0.379545455	H			H	H	M	general GO
inflammatory_response (163)	AMEF2.01	0.379545455		H			0	0	general GO
immune_response (366)	AMEF2.01	0.379545455		M			M	0	general GO
inflammatory_response (163)	NFAT.01	0.378787879				H	H	0	general GO
immune_response (366)	NFAT.01	0.378787879				H	0	0	general GO
homophilic_cell_adhesion (70)	NFAT.01	0.378787879		H	0	H	H	0	general GO
cell_adhesion (378)	NFAT.01	0.378787879	M			H	0	0	general GO
inflammatory_response (163)	FREAC4.01	0.377604167				0	0	0	general GO
immune_response (366)	FREAC4.01	0.377604167		M	0	0	0	0	general GO
sensory_perception (201)	CDX2.01	0.375438596	H	H	H		H	H	general GO
innate_immune_response (46)	CDX2.01	0.375438596	M		H			H	general GO
inflammatory_response (163)	CDX2.01	0.375438596			H		H	H	general GO
immune_response (366)	CDX2.01	0.375438596		H	H	H	H	0	general GO
antimicrobial_humoral_response (87)	CDX2.01	0.375438596	H	H	M	0	0	H	general GO
innate_immune_response (46)	MEF2.01	0.375		H	H	H	H	0	general GO
inflammatory_response (163)	MEF2.01	0.375	H			H	H	0	general GO
immune_response (366)	MEF2.01	0.375		H	H	0	0	0	general GO
sensory_perception (201)	MMEF2.01	0.373626374	H	H	H				general GO
proteolysis (297)	MMEF2.01	0.373626374		H	H	0	0	0	general GO
inflammatory_response (163)	MMEF2.01	0.373626374		H	H	H	0	0	general GO
immune_response (366)	MMEF2.01	0.373626374				M	0	0	general GO
inflammatory_response (163)	SOX9.01	0.370192308	0	H		H	H	H	general GO
signal_transduction (1189)	GATA2.02	0.363636364		0	H	H	0	0	general GO
sensory_perception (201)	GATA2.02	0.363636364				H	H	H	general GO
inflammatory_response (163)	GATA2.02	0.363636364		H	H	0	0	M	general GO
immune_response (366)	GATA2.02	0.363636364					H		general GO
G_protein_coupled_receptor_protein_signaling_	GATA2.02	0.363636364				H	H	H	general GO
chemotaxis (98)	GATA2.02	0.363636364		H	H	H	H	H	general GO
response_to_virus (55)	GATA1.05	0.363157895	H	H	0	0		0	general GO
innate_immune_response (46)	GATA1.05	0.363157895	H			H	H	0	general GO
inflammatory_response (163)	GATA1.05	0.363157895	H	M	H	0	0	0	general GO

immune_response (366)	GATA1.05	0.363157895		H	H	H	H	general GO
response_to_virus (55)	IRF7.01	0.356770833		H	0	0	0	general GO
inflammatory_response (163)	IRF7.01	0.356770833	H	H	H	0	0	general GO
immune_response (366)	IRF7.01	0.356770833				0	0	general GO
inflammatory_response (163)	OCT1P.01	0.356759907		H	H	H	H	general GO
immune_response (366)	OCT1P.01	0.356759907	H			0	0	general GO
antimicrobial_humoral_response (87)	OCT1P.01	0.356759907	H	H	H	H	0	general GO
sensory_perception (201)	OCT.01	0.354700855	H	H		H	0	general GO
inflammatory_response (163)	OCT.01	0.354700855		H	H	0	0	general GO
immune_response (366)	OCT.01	0.354700855		H	H	M	0	general GO
visual_perception (142)	SIX3.01	0.352962963		H	H	H	0	general GO
sensory_perception (201)	SIX3.01	0.352962963	H	H	H	H	0	general GO
immune_response (366)	PDX1_G_SA	0.352941176	H	0	0	0	0	general GO
signal_transduction (1189)	GATA2.01	0.351428571	M	0	0	0	0	general GO
sensory_perception (201)	GATA2.01	0.351428571			H	H	H	general GO
inflammatory_response (163)	GATA2.01	0.351428571		0	0	0	0	general GO
immune_response (366)	GATA2.01	0.351428571		H			H	general GO
G_protein_coupled_receptor_protein_signaling	GATA2.01	0.351428571		H	H	H	H	general GO
chemotaxis (98)	GATA2.01	0.351428571	H			0	0	general GO
cell_surface_receptor_linked_signal_transductio	GATA2.01	0.351428571	H	M	0	0	0	general GO
inflammatory_response (163)	CDX1.01	0.349621212				0	0	general GO
immune_response (366)	CDX1.01	0.349621212		H	H	H	0	general GO
antimicrobial_humoral_response (87)	CDX1.01	0.349621212	M		H	H	H	general GO
sensory_perception (201)	NKX25.02	0.347222222	H	H	H	H	H	general GO
antimicrobial_humoral_response (87)	NKX25.02	0.347222222	H	H	H	0	M	general GO
sensory_perception (201)	FREAC2.01	0.346774194	H				H	general GO
inflammatory_response (163)	DLX3.01	0.34375				0	0	general GO
immune_response (366)	DLX3.01	0.34375				0	0	general GO
antimicrobial_humoral_response (87)	DLX3.01	0.34375		H	H	0	H	general GO
proteolysis (297)	HOXC13_01	0.343589744	M	0	H	H	H	general GO
immune_response (366)	HOXC13_01	0.343589744		H	H	H	H	general GO
inflammatory_response (163)	HNF1.02	0.343382353			H	H	0	general GO
sensory_perception (201)	XFD1.01	0.342857143	H		H	H	H	general GO
inflammatory_response (163)	XFD1.01	0.342857143			M	M	0	general GO
inflammatory_response (163)	ATBF1.01	0.338562092		H	H	0	0	general GO
immune_response (366)	ATBF1.01	0.338562092	H	H	H	H	H	general GO
innate_immune_response (46)	HMEF2.01	0.3375		H	H	H	0	general GO
inflammatory_response (163)	HMEF2.01	0.3375	H		H	H	0	general GO
signal_transduction (1189)	GATA3.01	0.335555556		0	H	0	0	general GO
sensory_perception (201)	GATA3.01	0.335555556			H		H	general GO
inflammatory_response (163)	GATA3.01	0.335555556	H	H	H	H	M	general GO
immune_response (366)	GATA3.01	0.335555556			H	H		general GO
G_protein_coupled_receptor_protein_signaling	GATA3.01	0.335555556		H	H	H	0	general GO
chemotaxis (98)	GATA3.01	0.335555556	H			H	0	general GO
inflammatory_response (163)	EVI1.04	0.333333333			M	0	0	general GO
sensory_perception (201)	EVI1.02	0.333333333	H	H			H	general GO
sensory_perception (201)	MEIS1_HOXA	0.333333333	H		H	H	H	general GO
sensory_perception (201)	PBX_HOXA9	0.333333333	H		H	H	H	general GO
inflammatory_response (163)	MEIS1_HOXA	0.333333333	H		H	H	H	general GO
inflammatory_response (163)	PBX_HOXA9	0.333333333	H		H	H	H	general GO
immune_response (366)	EVI1.02	0.333333333	H	H	0	0	0	general GO
immune_response (366)	MEIS1_HOXA	0.333333333			H	H	H	general GO
immune_response (366)	PBX_HOXA9	0.333333333			H	H	H	general GO
inflammatory_response (163)	BRN3.02	0.331934732				H	H	general GO
immune_response (366)	BRN3.02	0.331934732		H	H	H	H	general GO
sensory_perception (201)	FKHRL1.01	0.327412587			0	H	0	general GO
inflammatory_response (163)	BRN2.03	0.324242424	H		0	0	0	general GO
sensory_perception (201)	XFD2.01	0.323076923			H	H	H	general GO
inflammatory_response (163)	XFD2.01	0.323076923			M	0	0	general GO
immune_response (366)	XFD2.01	0.323076923		H	H	H	0	general GO
inflammatory_response (163)	OC2.01	0.320855615	H			M	M	general GO
immune_response (366)	OC2.01	0.320855615	H	H	H	H	H	general GO
inflammatory_response (163)	LMX1B.01	0.32					H	general GO
response_to_virus (55)	FREAC3.01	0.319230769	H	H		H	H	general GO

proteolysis (297)	FREAC3.01	0.319230769		0	0	0	0	0	general GO
inflammatory_response (163)	FREAC3.01	0.319230769	M	M			H	0	general GO
immune_response (366)	FREAC3.01	0.319230769		M	H		0	H	general GO
inflammatory_response (163)	HOXA9.01	0.318627451			H	H	H		general GO
defense_response (100)	HOXA9.01	0.318627451	0	M	0	H	H	H	general GO
innate_immune_response (46)	CART1.01	0.316599389	M	M			H	0	general GO
inflammatory_response (163)	CART1.01	0.316599389		M	M		0	0	general GO
immune_response (366)	CART1.01	0.316599389					0	H	general GO
innate_immune_response (46)	EN1.01	0.315384615	H	H			H	H	general GO
antimicrobial_humoral_response (87)	EN1.01	0.315384615		H	H		0	0	general GO
transport (940)	HNF1.03	0.313664596				H	0	0	general GO
sodium_ion_transport (75)	HNF1.03	0.313664596				H	0	0	general GO
inflammatory_response (163)	HNF1.03	0.313664596		H	H		0	0	general GO
blood_coagulation (70)	HNF1.03	0.313664596					0	0	general GO
steroid_metabolism (54)	PBX1.01	0.312770468					M	0	general GO
nucleosome_assembly (71)	PBX1.01	0.312770468	H					M	general GO
inflammatory_response (163)	PBX1.01	0.312770468		H	0	H	H	0	general GO
signal_transduction (1189)	EVI1.01	0.3125		0	H		0	0	general GO
sensory_perception (201)	EVI1.01	0.3125	H	H			H	H	general GO
inflammatory_response (163)	EVI1.01	0.3125				H	0	0	general GO
inflammatory_response (163)	HNF6.01	0.311564626		H	H	H	H	0	general GO
immune_response (366)	HNF6.01	0.311564626	H	H			H	H	general GO
innate_immune_response (46)	SRY.01	0.308080808	H			H	H	0	general GO
immune_response (366)	SRY.01	0.308080808				H	H	0	general GO
inflammatory_response (163)	BRN3.01	0.301216641				H		H	general GO
immune_response (366)	BRN3.01	0.301216641		H	H	H	0	0	general GO
antimicrobial_humoral_response (87)	XVENT2.01	0.300287356		H	H	H	H	0	general GO
inflammatory_response (163)	ATATA.01	0.3		H	H	H	0	0	general GO
immune_response (366)	ATATA.01	0.3		M	M	0	0	0	general GO
sensory_perception (201)	MEF2.02	0.298701452		H	H	H	H	H	general GO
muscle_development (107)	MEF2.02	0.298701452					H	0	general GO
inflammatory_response (163)	MEF2.02	0.298701452		H	H	H	H	0	general GO
immune_response (366)	MEF2.02	0.298701452	H			H	H	0	general GO
sensory_perception (201)	MEF2.03	0.298542774		H	H	H	0	H	general GO
muscle_development (107)	MEF2.03	0.298542774		H	H	0	0	0	general GO
inflammatory_response (163)	MEF2.03	0.298542774				H	H	H	general GO
immune_response (366)	MEF2.03	0.298542774				H	H	H	general GO
transport (940)	HNF1.01	0.296715928				H	0	0	general GO
steroid_metabolism (54)	HNF1.01	0.296715928	0	0			0		general GO
inflammatory_response (163)	DLX1.01	0.292929293				H	0	0	general GO
sensory_perception (201)	MEF2.05	0.292673993	H	H	H	H	H		general GO
immune_response (366)	MEF2.05	0.292673993		M	M	M	M	M	general GO
inflammatory_response (163)	RSRFC4.02	0.292371595						H	general GO
immune_response (366)	RSRFC4.02	0.292371595	H				H	H	general GO
sensory_perception (201)	CDP.02	0.290344162				H	H	H	general GO
pregnancy (41)	CDP.02	0.290344162	0	M		0	0	0	general GO
inflammatory_response (163)	CDP.02	0.290344162		M	H	H	H	H	general GO
immune_response (366)	CDP.02	0.290344162		H	H		H	H	general GO
immune_response (366)	MEL1_01	0.288515406						H	general GO
inflammatory_response (163)	CLOX.01	0.287721893		0	0		H	H	general GO
immune_response (366)	CLOX.01	0.287721893	H	H			H	H	general GO
sensory_perception (201)	GATA3.02	0.286666667		H	H				general GO
metabolism (241)	GATA3.02	0.286666667	0	M	0		H	0	general GO
inflammatory_response (163)	GATA3.02	0.286666667		H	0		H	0	general GO
immune_response (366)	GATA3.02	0.286666667				H	H	H	general GO
chemotaxis (98)	GATA3.02	0.286666667	H	0	0			0	general GO
inflammatory_response (163)	MEF2.04	0.286298736	H	H	H			0	general GO
immune_response (366)	MEF2.04	0.286298736		H	H		0	H	general GO
sensory_perception (201)	EVI1.05	0.28620194	H			H	H	H	general GO
inflammatory_response (163)	EVI1.05	0.28620194		0	0	0	0	0	general GO
immune_response (366)	EVI1.05	0.28620194				H	H	0	general GO
sensory_perception (201)	TATA.01	0.284987277				H	H	0	general GO
nucleosome_assembly (71)	TATA.01	0.284987277				H	H	H	general GO
inflammatory_response (163)	TATA.01	0.284987277					0	0	general GO

immune_response (366)	TATA.01	0.284987277			0	0	0	general GO
epidermis_development (59)	TATA.01	0.284987277			0	0	0	general GO
chromosome_organization_and_biogenesis (83)	TATA.01	0.284987277	H		H	H	H	general GO
chemotaxis (98)	TATA.01	0.284987277			0	0	0	general GO
cell_cell_signaling (268)	TATA.01	0.284987277			0	0	0	general GO
calcium_ion_homeostasis (30)	TATA.01	0.284987277			M	0	0	general GO
antimicrobial_humoral_response (87)	TATA.01	0.284987277	H	H	0	0	0	general GO
sensory_perception (201)	RSRFC4.01	0.28125	H	H	H	H	H	general GO
muscle_development (107)	RSRFC4.01	0.28125			H	H	0	general GO
inflammatory_response (163)	RSRFC4.01	0.28125			H	H	H	general GO
immune_response (366)	RSRFC4.01	0.28125			H	H	0	general GO
chemotaxis (98)	RSRFC4.01	0.28125	0	0	0	0	0	general GO
inflammatory_response (163)	TATA.02	0.276190476			0	0	H	general GO
immune_response (366)	TATA.02	0.276190476			H	0	0	general GO
chemotaxis (98)	TATA.02	0.276190476	H	H	H	H	H	general GO
cell_cell_signaling (268)	TATA.02	0.276190476			0	0	0	general GO
inflammatory_response (163)	MYT1.02	0.275624837	M	0	0	0	0	general GO
immune_response (366)	MYT1.02	0.275624837	H	H	0	0	0	general GO
homophilic_cell_adhesion (70)	MYT1.02	0.275624837	H	H	H	H	H	general GO
sensory_perception (201)	PIT1.01	0.273333333			H	0	H	general GO
innate immune_response (46)	PIT1.01	0.273333333	H	0		H	H	general GO
inflammatory_response (163)	PIT1.01	0.273333333	H			H	H	general GO
immune_response (366)	PIT1.01	0.273333333				H	H	general GO
sensory_perception (201)	FREAC7.01	0.272727273					H	general GO
inflammatory_response (163)	FREAC7.01	0.272727273			0	M	0	general GO
immune_response (366)	FREAC7.01	0.272727273	H	H		0	0	general GO
inflammatory_response (163)	SATB1.01	0.272321429				H	H	general GO
inflammatory_response (163)	HFH1.01	0.268518519			H	H	0	general GO
sensory_perception (201)	HFH8.01	0.266025641	H	H			H	general GO
proteolysis (297)	HFH8.01	0.266025641			H	H	0	general GO
inflammatory_response (163)	HFH8.01	0.266025641	H	0	0	0	0	general GO
sensory_perception_of_smell (40)	MYT1.01	0.265925926	0	0	0	0	0	general GO
inflammatory_response (163)	MYT1.01	0.265925926	H	H	H	0	0	general GO
immune_response (366)	MYT1.01	0.265925926			H	H	0	general GO
sensory_perception (201)	OCT1.01	0.264074431	H	H			H	general GO
metabolism (241)	OCT1.01	0.264074431	M	0	0	H	0	general GO
inflammatory_response (163)	OCT1.01	0.264074431					M	general GO
sensory_perception (201)	BRN5.01	0.262032086	H		H		H	general GO
proteolysis (297)	BRN5.01	0.262032086	0	0	0	0	0	general GO
immune_response (366)	BRN5.01	0.262032086				0	0	general GO
inflammatory_response (163)	HNF3B.01	0.255731922	M	0	H	0	0	general GO
immune_response (366)	HNF3B.01	0.255731922			M	M	0	general GO
digestion (51)	HNF3B.01	0.255731922			M	0	0	general GO
innate immune_response (46)	HFH2.01	0.25	H	M	0	0	0	general GO
inflammatory_response (163)	HFH2.01	0.25			H	M	0	general GO
immune_response (366)	HFH2.01	0.25				H	0	general GO
immune_response (366)	NKX31.01	0.247412008	H	H	0	0	0	general GO
inflammatory_response (163)	BRN2.02	0.246031746					0	general GO
immune_response (366)	EVI1.03	0.24340176			H	H	H	general GO
innate immune_response (46)	BRIGHT.01	0.217287014	0	M	H	0	0	general GO
inflammatory_response (163)	BRIGHT.01	0.217287014	H				H	general GO
sensory_perception (201)	OCT1.06	0.216820628	H	H		H	0	general GO
innate immune_response (46)	OCT1.06	0.216820628	M		M	M	0	general GO
inflammatory_response (163)	OCT1.06	0.216820628				H	H	general GO
immune_response (366)	OCT1.06	0.216820628			H	H	H	general GO
inflammatory_response (163)	LHX3.01	0.138047138	H	H	H	H	H	general GO

100bp Window with overlap 50bp

GO group	Motifs	motif GC	-199 - -100	-149 - -50	-99 - 0	-49 - 50	1 - 100	51 - 150	101 - 200	151 - 250	201 - 300	251 - 350	301 - 400	351 - 450	401 - 500	451 - 550	501 - 600	551 - 650	601 - 700	651 - 750	701 - 800	751 - 850	801 - 900	851 - 950	901 - 1000	GO-classes	
transcription (930)	GC_rich	1	H	H	0	0	0	M				M						M	H								transcription GO
transcription (930)	poly_C	1	H	H	M	0	0	0	H				H			M	M	M	0	M		H	M	0	H		transcription GO
transcription (930)	SP1.01	0.8	0	0	0	0	0	0	0	0		M	M			M	M	0	0	M	M		M	0			transcription GO
transcription (930)	WT1.01	0.8	H	H	0	0	0	H	M	M	M							M	0	0	H	H	0	M			transcription GO
transcription (930)	MAZR.01	0.8	0	0		0	0	0	0			M	M				M	M	0	0	0	0	M	H	0		transcription GO
transcription (930)	ZNF202.01	0.7	H	H	0	0	0	0	H			M	0			M	M	0	0	0		0	0	0	0		transcription GO
transcription (930)	AP2.01	0.7	0	0	0	0	0	H	0	H		M	M	0			M	0	0	H	H	H	H				transcription GO
transcription (930)	ZF5.01	0.7	0	0	0	0	0	0	0	0		M	M	M			H	0	0	H	0	0	H	H	H		transcription GO
transcription (930)	NRF1_01	0.7	0	0	0	0	0	0	0	0				M	M	M	0	0	0	H	H	H	H	H			transcription GO
transcription (930)	ZBP89.01	0.7	H	H	M	0	M	M	0		M	0	M	M	H	M	M	M	0	0	0	0	0	0	0	0	transcription GO
transcription (930)	CKROX_01	0.7	H		M	0	M	H	0	0	H		M		H	M	M	0	0	0	0	0	0	0	0	0	transcription GO
transcription (930)	EGR1.02	0.7	H	H	M	0	M	H	H		M		H	H			M	M	0		H	0	H		H		transcription GO
transcription (930)	GC.01	0.7	0	0	0	0	0	0	0	0	H	M	0	0		M	M	0	0	0	0	0	0	M	0	0	transcription GO
transcription (930)	MAZ.01	0.7	0	0	0	0	0	0	0	H		M	0	M	M	M	M	0	0	0	0	H	H	0	0	0	transcription GO
transcription (930)	PLAG1_01	0.6	0	0	0	0	0	0	H		0	0	0	M	M	M	M	0	0	0	H	H	H	H	0		transcription GO
regulation_of_transcription_DNA_depe	GC_rich	1	H		0	0	0	M											H			H					transcription GO
regulation_of_transcription_DNA_depe	poly_C	1	H	H	M	M	0					0					M	M	0				M	M	H		transcription GO
regulation_of_transcription_DNA_depe	SP1.01	0.8	0	H	0	0	0	0	0							M	M	M	0	M	M						transcription GO
regulation_of_transcription_DNA_depe	WT1.01	0.8				0	0	0		M	M							M	0	0	H		M				transcription GO
regulation_of_transcription_DNA_depe	MAZR.01	0.8	H	0	H	M	0	M	0			M					M	M	M	0	0	M	M	0		0	transcription GO
regulation_of_transcription_DNA_depe	ZNF202.01	0.7	H	H	0	0	0	0	H			M	0			M	M	M	0	H		M	M	M	0		transcription GO
regulation_of_transcription_DNA_depe	AP2.01	0.7	0	0	0	0	0	H	M			M	M	H			M	H	H	H	H	H	H				transcription GO
regulation_of_transcription_DNA_depe	ZF5.01	0.7	0	0	0	0	0	0	H	M		M		M	M		H	H	H	H	H	0	H	H			transcription GO
regulation_of_transcription_DNA_depe	ZF9.01	0.7	0	0	0	0	0	0	0	H	H		M	0	H	H	H	H	M	M	M				0		transcription GO
regulation_of_transcription_DNA_depe	NRF1_01	0.7	0	0	0	0	0	0	M	0	M			M	0	0	0	H	H	H	H	H	H	H			transcription GO
regulation_of_transcription_DNA_depe	ZBP89.01	0.7	H	H	M	0	M	M	M					H			M	M	0	0	H	0	0	0	0	0	transcription GO
regulation_of_transcription_DNA_depe	CKROX_01	0.7	H			0	M	M		0							M	0	0		H	0	M	0	0	0	transcription GO
regulation_of_transcription_DNA_depe	EGR1.02	0.7	0		M	0	0	0						H			M	M	M		H	0					transcription GO
regulation_of_transcription_DNA_depe	EGR1.01	0.7	0	0	0	0	0	0	0	0		M	0	0	H	0	M	M	0	0	0	0	0	0	0	0	transcription GO
regulation_of_transcription_DNA_depe	MAZ.01	0.7	0	0	0	0	0	0	0	H		M	M	M			M	M	M	0	0	H		0	0	0	transcription GO
regulation_of_transcription_DNA_depe	PLAG1_01	0.6	0	M	M	0	0	0	H	0	0	M	M	M			M	M	0	0	M	H	H	H	0	0	transcription GO
regulation_of_transcription_DNA_depe	HES1.01	0.6	0	0	0	0	0	M	M	0	0	0	0	0	M	0	0	0	0	0	H	H	0		H	0	transcription GO
regulation_of_transcription_DNA_depe	MUSCLE_INI.0	0.6	0	0	0	0	0	0	0	0		0	0	M	0	0	H	H	0	0	0	0	M	0	0	0	transcription GO
regulation_of_transcription_DNA_depe	MUSCLE_INI.0	0.6	0	0	0	0	0	0	0	0	0	0	M		0	0	H	0	0	0	0	0	0	0	0	0	transcription GO
regulation_of_transcription_DNA_depe	CDE.01	0.6	0	0	0	0	0	0	0	M	M	0	M	0	H		M	M	M	0	M	M	0	H	H		transcription GO
regulation_of_transcription_DNA_depe	E2F.02	0.6	0	0	0	H	0	0	0	M	0	0	0	0	H	0	0	H	M		0	0	0	0	0	0	transcription GO
regulation_of_transcription_DNA_depe	GAGA.01	0.6		H	0	0	H	H	0	0	0	H	0	M	H	H	H	M	0	0	0	0	H		0	0	transcription GO
regulation_of_transcription (266)	poly_C	1	0	0	0	0	0	0	M	H			0	H	H	H	0	0	0	0	0	0	0	M	0	0	transcription GO
regulation_of_transcription (266)	WT1.01	0.8	0	0	0	0	0	0	0	H	M		0	0	H	M	0	0	0	0	0	0	0	0	0	0	transcription GO
regulation_of_transcription (266)	ZF5.01	0.7	0	0	0	0	0	0	H	M		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	transcription GO
regulation_of_transcription (266)	ZBP89.01	0.7	0	0	0	0	0	0	H		0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	transcription GO
regulation_of_transcription (266)	CKROX_01	0.7	0	0	0	0	M	M	0	0	H		0	0	H	M	M	0	0	0	0	0	0	0	0	0	transcription GO
regulation_of_transcription (266)	EGR1.02	0.7	0	0	0	0	0	0		H	M	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	transcription GO
digestion (51)	HFH8.01	0.3	H	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	transcription GO
development (530)	poly_C	1	0	0	M	0	H					H	H	H	H	H	0	0	H	0	0	0	M	0	0	M	transcription GO
development (530)	WT1.01	0.8	H	0	0	0	0	H	0	0		H	0	H	0	0	0		0	0	H	M	0	H	0		transcription GO
development (530)	MAZR.01	0.8	0	0	0	0	0	0	H			H	H	M		H	H		0	0	0	H	H	0	H	H	transcription GO
development (530)	ZNF202.01	0.7	0	0	0	0	H	H			H	H	H	0	H	H	0	0	0	0	0	0	M	0	0	0	transcription GO
development (530)	ZBP89.01	0.7	0	0	0	0	H	H			H	H	H	0	H	H	0	M	0	0	H	H	0	M	0	0	transcription GO
development (530)	CKROX_01	0.7	0	0	0	0	H	H	H			H	H	M	H	H	0	0	0	0		0	0	0	0	0	transcription GO
development (530)	MZF1.01	0.7	0	0	0	0	H	0	H	0	0	H	H		M	H	H	0	H	H	0	0	0	H	0	0	transcription GO

[illegible]

immune_response (366)	GRE.01	0.5	0	0	H		0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	PPARA.01	0.5		M	M	0	0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	NFE2L2.01	0.5	0	0	H	0			M	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	STAT6.01	0.5	0	0	H	0	H	H		0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	PXRCAR.01	0.5	0	0	0	0	H	0	M		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	RTR.01	0.4	0	0	M		H	H	0		0	0	0	0	0	0	0	H	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	MYT1L.01	0.4	0	0	0	0	H				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	STAT.01	0.4	0	0	0	0	0			H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	PRE.01	0.4	0	H	H		H	H	0		0	H	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	BCL6.02	0.4	0	0	0	0	0				H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	TCF11MAFG.0	0.4	0	0	0	0	0	0		H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	AP1.01	0.4	0	H	0	0	M			0	0	0	H	H	0	0	0	H	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	ISRE.01	0.4	0	0	M						H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	IRF2.01	0.4	0	0							0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	IRF3.01	0.4	0	0	0					M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	PRDM1.01	0.4	0	0	0					H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	HMGYI.01	0.4	0	0	0	H					0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	ROMA1.01	0.4	0	0		M	0	0	0		0	0	0	0	0	0	0	H	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	PSE_02	0.4	0	0	0	M	0				0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	MTBF.01	0.4		H	0	0	H	H	H	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	IRF1.01	0.4	0	0						M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	OCT1.05	0.4	H	0	0	0	H	H		H	H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	AARE.01	0.4	0	0	0	H		H	H	H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	LTATA_01	0.4	H	0	0		H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	IRF4.01	0.4	H	H	M					H	0	0	H	0	M	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	STAT5.01	0.4	0	0	0	H	H				H	H	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	BCL6.01	0.4	0	0	0	0	0				H	0	H	M	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	OCT1.04	0.4				H	0	H	H		0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	GFI1B.01	0.4	0	0	0	0	0	0	0		H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	AMEF2.01	0.4	H	0	0	H	H	M			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	NFAT.01	0.4	M	0	0	M				H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	GATA1.05	0.4		0	0	H	H	0	0		0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	IRF7.01	0.4	H	H	H						H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	OCT.01	0.4	H			H		H	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	CDX1.01	0.3	H	H	0	H		H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	OCT1.02	0.3	H	M		H	0	0	0	0	0	0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	HOXC13_01	0.3	0	0	0		H	0	0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	EVI1.04	0.3	0	0	0	H	H				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	EVI1.02	0.3	0	0	M	M	H	0	H	H	H	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	XFD2.01	0.3	H	0	0	M				H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	CABL.01	0.3	0	0	0	0	0	0			H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	EVI1.01	0.3	0	0	0		H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	MEF2.02	0.3	0	0	0						0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	MEF2.03	0.3	H	0	0		H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	HNF1.01	0.3		0	0	0	H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	MEF2.05	0.3	H	0	0	M				H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	RSRFC4.02	0.3	0	0	0					H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	MEL1_01	0.3			0	0	M	H	H	H	H	H	0	0	M	0	0	0	0	0	0	0	0	0	0	H	0	general GO
immune_response (366)	TATA.01	0.3	H	0	0						0	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	RSRFC4.01	0.3	0	0	0					H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	TATA.02	0.3	0	0	0					H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	PIT1.01	0.3	H	0	0					H	0	0	0	0	0	0	0	0	0	0	0	0	0	H	0	0	0	general GO
immune_response (366)	NKX31.01	0.2	H	0	0	0	0	M			H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	EVI1.03	0.2			0	0	M			0	0	H	H	0	0		0	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	OCT1.06	0.2	H	M		H	H				H	H	0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	general GO
immune_response (366)	poly_A	0	H	0	0	0	H					0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
homophilic_cell_adhesion (70)	NFAT.01	0.4	0	0	0	0	0			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
G_protein_coupled_receptor_protein_	TCF11MAFG.0	0.4	0	0	0	0	0	H			M	0	0	H	0	0	H	H	0	0	0	0	0	0	0	0	0	general GO
G_protein_coupled_receptor_protein_	EVI1.02	0.3	0	0	0	0	H				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
G_protein_coupled_receptor_protein_	EVI1.01	0.3	H	0	0	0	H				H	H	0	0	0	0	0	0	0	H	0	0	0	0	0	0	0	general GO
G_protein_coupled_receptor_protein_	EVI1.03	0.2	H	0	0	H	H				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
epidermis_development (59)	LTATA_01	0.4	0	0	0	0	H				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
epidermis_development (59)	TATA.01	0.3	0	0	0	0					0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
epidermis_development (59)	TATA.02	0.3	0	0	0	0	H				0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO

DNA_repair (148)	E2F.02	0.6	0	0		0	0	0	0	M	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
DNA_repair (148)	E2F.03	0.5	0	H	H	H	0	0	H	0	M	0	0	0	0	0	0	0	0	0	0	0	0	general GO
digestion (51)	TATA.01	0.3	0	0	0	M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
digestion (51)	TATA.02	0.3	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
defense_response (100)	ISRE.01	0.4	0	0	0	0	H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
defense_response (100)	IRF1.01	0.4	0	0	0	0	H	H	0	0	0	H	H	0	0	0	0	0	0	0	0	0	0	general GO
chromosome_organization_and_bioge	CAAT.01	0.5	0	0	0	0	0	H	H		0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chromosome_organization_and_bioge	NFY.02	0.5	0	0	0	0	H	H	H		H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chromosome_organization_and_bioge	MTATA.01	0.5	0	0	0		H	H	0	H	H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chromosome_organization_and_bioge	NFY.03	0.5	0	0	0	0	H	H	H		0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chromosome_organization_and_bioge	OCT1.04	0.4	0	0	0	0	H		H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chromosome_organization_and_bioge	TATA.01	0.3	0	0	0		H	0	H	H	H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chromatin_modification (53)	AP2.01	0.7	0	0	0	0	0	0	0	0	0	0	0	0	0		H	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB.01	0.6	0	0	0	0	0		M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB.02	0.6	0	0	0	0	0		M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB65.	0.6	0	0	0	0	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	CREL.01	0.5	0	0	0	0	H		M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	NFKAPPAB.03	0.5	0	0	0	0	H			H	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	HIVEP1_01	0.5	0	0	0	0	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	IK3.01	0.5	0	0	0	0	0		M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
chemotaxis (98)	HMGYI.01	0.4	0	0	0	0	H			0	H	0	0	0	0	H	0	0	0	0	0	0	0	general GO
chemotaxis (98)	TATA.01	0.3	0	0	0			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cellular_defense_response (68)	ETS1.01	0.5	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_divility (106)	TATA.02	0.3	0	0	H	M		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_division (103)	NFY.01	0.5	0	0	0	0	0	0			H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_division (103)	CHR.01	0.4	0	0	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_differentiation (192)	TATA.01	0.3	0	0	0	H		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cycle (273)	E2F.02	0.6	0	0	0		0	0	0	0	H	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cycle (273)	NFY.01	0.5	0	0	0	H	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cycle (273)	CAAT.01	0.5	0	0	0	H	0		M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	NFKAPPAB.02	0.6	0	0	0	H	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	CREL.01	0.5	0	0	0	0	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	HIVEP1_01	0.5	0	0	0	H	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	MTATA.01	0.5	0	0	0	H		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	LTATA_01	0.4	0	0	0	H		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	ATATA.01	0.3	0	0	0		M	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	TATA.01	0.3	0	0	H			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
cell_cell_signaling (268)	TATA.02	0.3	0	0	0			0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
calcium_ion_homeostasis (30)	TATA.01	0.3	0	0	0	H		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
blood_coagulation (70)	HNF1.03	0.3	M	0	0	0		H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
blood_coagulation (70)	SATB1.01	0.3			H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
biosynthesis (32)	NFY.02	0.5	0	0	0	0	0		H	0	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO
antimicrobial_humoral_response (87)	ISL1.01	0.4	0	0	0	0		H	0	0	0	H	0	0	0	0	H	0	0	0	0	0	0	general GO
antimicrobial_humoral_response (87)	GATA1.04	0.4	0	0	H	0	0		H	H	0	0	0	0	0	0	0	0	0	0	0	0	0	general GO