TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
1	TLR1	Ambion_Plate 1	C3	TLR1	7096	siRNA1	s14191	GGCAUACAACUGUAUGGUAtt	UACCAUACAGUUGUAUGCCaa	
1	TLR1	Ambion_Plate 1	G8	TLR1	7096	siRNA2	s14192	CCAGUAUCUUGAUAUCAGUtt	ACUGAUAUCAAGAUACUGGat	
1	TLR1	Ambion_Plate 1	K16	TLR1	7096	siRNA3	s14193	CAUCCAAAAUUAGCCCGUUtt	AACGGGCUAAUUUUGGAUGgg	
1	TLR1	Qiagen_Plate 1	C3	TLR1	7096	siRNA4	SI03098088			CTGGCGAAACTTCAAACAAAT
1	TLR1	Qiagen_Plate 1	G8	TLR1	7096	siRNA5	SI03093545			CTGAGGGCCTTCAAGACTTTA
1	TLR1	Qiagen_Plate 1	K16	TLR1	7096	siRNA6	SI03027360			AACAATCTTAAATATATCGCA
2	TLR2	Ambion_Plate 1	D3	TLR2	7097	siRNA1	s168	GCCUUGACCUGUCCAACAAtt	UUGUUGGACAGGUCAAGGCtt	
2	TLR2	Ambion_Plate 1	H8	TLR2	7097	siRNA2	s169	GACUUAUCCUAUAAUUACUtt	AGUAAUUAUAGGAUAAGUCta	
2	TLR2	Ambion_Plate 1	L16	TLR2	7097	siRNA3	s170	GGAUCACCUACAUUAGCAAtt	UUGCUAAUGUAGGUGAUCCtg	
2	TLR2	Qiagen_Plate 1	D3	TLR2	7097	siRNA4	SI00050036			CCGCAACTCAAAGAACTTTAT
2	TLR2	Qiagen_Plate 1	H8	TLR2	7097	siRNA5	SI00050029			AACATTTAGACTTATCCTATA
2	TLR2	Qiagen_Plate 1	L16	TLR2	7097	siRNA6	SI00050022			CAGGTAAAGTGGAAACGTTAA
3	TLR3	Ambion_Plate 1	E3	TLR3	7098	siRNA1	s235	GGAUAGGUGCCUUUCGUCAtt	UGACGAAAGGCACCUAUCCgt	
3	TLR3	Ambion_Plate 1	I8	TLR3	7098	siRNA2	s236	CCGAUGAUCUACCCACAAAtt	UUUGUGGGUAGAUCAUCGGgt	
3	TLR3	Ambion_Plate 1	M16	TLR3	7098	siRNA3	s234	CAACGACUGAUGCUCCGAAtt	UUCGGAGCAUCAGUCGUUGaa	
3	TLR3	Qiagen_Plate 1	E3	TLR3	7098	siRNA4	SI02655156			AAGAACTGGATATCTTTGCCA
3	TLR3	Qiagen_Plate 1	I8	TLR3	7098	siRNA5	SI02630782			CACATTAGATCTGTCTCATAA
3	TLR3	Qiagen_Plate 1	M16	TLR3	7098	siRNA6	SI02630775			CAGCACAATGAGCTATCTCAA
4	TLR4	Ambion_Plate 1	F3	TLR4	7099	siRNA1	s14194	GAGCCGCUGGUGUAUCUUUtt	AAAGAUACACCAGCGGCUCtg	
4	TLR4	Ambion_Plate 1	J8	TLR4	7099	siRNA2	s14195	CAUUGAAGAAUUCCGAUUAtt	UAAUCGGAAUUCUUCAAUGgt	
4	TLR4	Ambion_Plate 1	N16	TLR4	7099	siRNA3	s14196	CUAGAGCACUUGGACCUUUtt	AAAGGUCCAAGUGCUCUAGat	
4	TLR4	Qiagen_Plate 1	F3	TLR4	7099	siRNA4	SI04951149			ACCATTGAAGAATTCCGATTA
4	TLR4	Qiagen_Plate 1	J8	TLR4	7099	siRNA5	SI04951142			AAGAGGGTACCTCTCATGTTA
4	TLR4	Qiagen_Plate 1	N16	TLR4	7099	siRNA6	SI04951135			AACCCGGAGGCCATTATGCTA
5	TLR5	Ambion_Plate 1	G3	TLR5	7100	siRNA1	s14197	GAAUAGCCUUUUAUCGUUUtt	AAACGAUAAAAGGCUAUUCgg	
5	TLR5	Ambion_Plate 1	K8	TLR5	7100	siRNA2	s14198	CACGGAAGGUUGUGAUGAAtt	UUCAUCACAACCUUCCGUGga	
5	TLR5	Ambion_Plate 1	C17	TLR5	7100	siRNA3	s14199	CCAUCUGUUUGAACUUAGAtt	UCUAAGUUCAAACAGAUGGaa	
5	TLR5	Qiagen_Plate 1	G3	TLR5	7100	siRNA4	SI02655163			AATAGCTTGTATAGCAGAGTC
5	TLR5	Qiagen_Plate 1	K8	TLR5	7100	siRNA5	SI03026534			AAAGATCAACCTTACAGCGAA
5	TLR5	Qiagen_Plate 1	C17	TLR5	7100	siRNA6	SI02630810			GAGGGACTTTCTCATCTTCAA
6	TLR6	Ambion_Plate 1	H3	TLR6	10333	siRNA1	s20215	CCAGAAUCCAGUUCUCCGAtt	UCGGAGAACUGGAUUCUGGtt	
6	TLR6	Ambion_Plate 1	L8	TLR6	10333	siRNA2	s20216	GCAACUUAUCACAACUGAAtt	UUCAGUUGUGAUAAGUUGCca	
6	TLR6	Ambion_Plate 1	D17	TLR6	10333	siRNA3	s20217	GGUGCUUACAACUGACUAAtt	UUAGUCAGUUGUAAGCACCct	
6	TLR6	Qiagen_Plate 1	H3	TLR6	10333	siRNA4	SI03112011			TAGGGTGCTTACAACTGACTA
6	TLR6	Qiagen_Plate 1	L8	TLR6	10333	siRNA5	SI03052658			CAAAGTAGGTCTCATGACGAA
6	TLR6	Qiagen_Plate 1	D17	TLR6	10333	siRNA6	SI02636592			CTCACTTGCATCTAAGTTATA
7	TLR7	Ambion_Plate 1	I3	TLR7	51284	siRNA1	s27842	GGAAUUACUCAUAUGCUAAtt	UUAGCAUAUGAGUAAUUCCtt	
7	TLR7	Ambion_Plate 1	M8	TLR7	51284	siRNA2	s27843	CCAUUAACCACAUACCAGAtt	UCUGGUAUGUGGUUAAUGGtg	
7	TLR7	Ambion_Plate 1	E17	TLR7	51284	siRNA3	s27844	GAGCAUACAGCUUAGCAAAtt	UUUGCUAAGCUGUAUGCUCtg	
7	TLR7	Qiagen_Plate 1	I3	TLR7	51284	siRNA4	SI03107447			TAACCTCTCGCCATTACATAA
7	TLR7	Qiagen_Plate 1	M8	TLR7	51284	siRNA5	SI03097283			CTGGAGGTATTCCCACGAACA
7	TLR7	Qiagen_Plate 1	E17	TLR7	51284	siRNA6	SI02642416			ATGGTATGCCTCCAAATCTAA
8	TLR8	Ambion_Plate 1	J3	TLR8	51311	siRNA1	s27920	GACCCAACUUCGAUACCUAtt	UAGGUAUCGAAGUUGGGUCaa	
8	TLR8	Ambion_Plate 1	N8	TLR8	51311	siRNA2	s27921	GGAUCUUGAAUUCAACUAUtt	AUAGUUGAAUUCAAGAUCCag	
8	TLR8	Ambion_Plate 1	F17	TLR8	51311	siRNA3	s27922	GGCUGCAAAAUCUCACUAAtt	UUAGUGAGAUUUUGCAGCCct	
8	TLR8	Qiagen_Plate 1	J3	TLR8	51311	siRNA4	SI03062864			CAGAACGGAAATCCCGGTATA
8	TLR8	Qiagen_Plate 1	N8	TLR8	51311	siRNA5	SI02642458			CAAGTGTTAAGTGGAACTGAA
8	TLR8	Qiagen_Plate 1	F17	TLR8	51311	siRNA6	SI02642451			TCGCGCCATAATAAAGATGCA
9	TLR9	Ambion_Plate 1	K3	TLR9	54106	siRNA1	s28872	CUGGAAGAGCUAAACCUGAtt	UCAGGUUUAGCUCUUCCAGgg	
9	TLR9	Ambion_Plate 1	C9	TLR9	54106	siRNA2	s28873	ACAAUAAGCUGGACCUCUAtt	UAGAGGUCCAGCUUAUUGUgg	
9	TLR9	Ambion_Plate 1	G17	TLR9	54106	siRNA3	s28874	CUGUCCUUCAAUUACCAAAtt	UUUGGUAAUUGAAGGACAGgt	
9	TLR9	Qiagen_Plate 1	K3	TLR9	54106	siRNA4	SI03118612			TGCCTTCGTGGTCTTCGACAA
9	TLR9	Qiagen_Plate 1	C9	TLR9	54106	siRNA5	SI03108504			TACCAACATCCTGATGCTAGA
9	TLR9	Qiagen_Plate 1	G17	TLR9	54106	siRNA6	SI02642612			CACTCAATAAATGCTACCGAA
10	LBP	Ambion_Plate 1	L3	LBP	3929	siRNA1	s8097	CGACAUUGAUUAUAGCUUAtt	UAAGCUAUAAUCAAUGUCGgc	
10	LBP	Ambion_Plate 1	D9	LBP	3929	siRNA2	s8098	GGUAAAAGUGGAACUGAAAtt	UUUCAGUUCCACUUUUACCtt	
10	LBP	Ambion_Plate 1	H17	LBP	3929	siRNA3	s8099	GCCUGACUCUAAUAUCCGAtt	UCGGAUAUUAGAGUCAGGCgg	
10	LBP	Qiagen_Plate 1	L3	LBP	3929	siRNA4	SI03058160			CACCGACAAGGGACTGCAGTA
10	LBP	Qiagen_Plate 1	D9	LBP	3929	siRNA5	SI00060200			CAAGATCACTGGGTTCCTGAA
10	LBP	Qiagen_Plate 1	H17	LBP	3929	siRNA6	SI00060186			CCGCCTGACTCTAATATCCGA
11	MD2	Ambion_Plate 1	M3	LY96	23643	siRNA1	s24262	GAAUCUUCCAAAGCGCAAAtt	UUUGCGCUUUGGAAGAUUCat	
11	MD2	Ambion_Plate 1	E9	LY96	23643	siRNA2	s24263	AGAAGUUAUUUGCCGAGGAtt	UCCUCGGCAAAUAACUUCUtt	
11	MD2	Ambion_Plate 1	I17	LY96	23643	siRNA3	s24264	CUACUGUGAUAAAAUGCAAtt	UUGCAUUUUAUACACAGUAGgt	
11	MD2	Qiagen_Plate 1	M3	LY96	23643	siRNA4	SI03246446			AACAATATCATTCTCCTTCAA
11	MD2	Qiagen_Plate 1	E9	LY96	23643	siRNA5	SI04322556			TGCTTGGAGTTTGTCATCCTA
11	MD2	Qiagen_Plate 1	I17	LY96	23643	siRNA6	SI04219684			TTGGAGATATTGAATCATGTT
12	CD14	Ambion_Plate 1	N3	CD14	929	siRNA1	s2600	ACCUGACACUGGACGGGAAtt	UUCCCGUCCAGUGUCAGGUta	
12	CD14	Ambion_Plate 1	F9	CD14	929	siRNA2	s2601	CGUCUGCAACUUCUCCGAAtt	UUCGGAGAAGUUGCAGACGca	
12	CD14	Ambion_Plate 1	J17	CD14	929	siRNA3	s2602	ACCUAGAGCCGUUUCUAAAtt	UUUAGAAACGGCUCUAGGUtg	
12	CD14	Qiagen_Plate 1	N3	CD14	929	siRNA4	SI02623852			CTCAGAGGTTCGGAAGACTTA
12	CD14	Qiagen_Plate 1	F9	CD14	929	siRNA5	SI02623845			CAGCCTAGACCTGTCTGACAA
12	CD14	Qiagen_Plate 1	J17	CD14	929	siRNA6	SI00012404			CCCGAGGTGGATAACCTGACA
13	CD11b	Ambion_Plate 1	C4	ITGAM	3684	siRNA1	s7565	GGGUCAUGCAGCAUCAAUAtt	UAUUGAUGCUGCAUGACCCga	
13	CD11b	Ambion_Plate 1	G9	ITGAM	3684	siRNA2	s7566	GAACAACCCUAACCCAAGAtt	UCUUGGGUUAGGGUUGUUCtg	
13	CD11b	Ambion_Plate 1	K17	ITGAM	3684	siRNA3	s7567	CUUGGACACUGAAAACGCAtt	UGCGUUUUCAGUGUCCAAGtt	
13	CD11b	Qiagen_Plate 1	C4	ITGAM	3684	siRNA4	SI03118430			TGCCGCCATCATCTTACGGAA
13	CD11b	Qiagen_Plate 1	G9	ITGAM	3684	siRNA5	SI00013223			TCAGACATCGGTTCATATTAA
13	CD11b	Qiagen_Plate 1	K17	ITGAM	3684	siRNA6	SI00013216			TCGGGTCATGCAGCATCAATA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
14	CD11c	Ambion_Plate 1	D4	ITGAX	3687	siRNA1	s7571	UCAUCACAGCGGUACUGUAtt	UACAGUACCGCUGUGAUGAgt	
14	CD11c	Ambion_Plate 1	H9	ITGAX	3687	siRNA2	s7572	AGUCCAACAUCUGCCUUUAtt	UAAAGGCAGAUGUUGGACUgt	
14	CD11c	Ambion_Plate 1	L17	ITGAX	3687	siRNA3	s7573	ACAGAUACCAGGUCAAUAAtt	UUAUUGACCUGGUAUCUGUgc	
14	CD11c	Qiagen_Plate 1	D4	ITGAX	3687	siRNA4	SI03110058			TACGTGGCAGAGGGCCAGAAA
14	CD11c	Qiagen_Plate 1	H9	ITGAX	3687	siRNA5	SI03084053			CGCAGAAGTGATGGTGTGGAA
14	CD11c	Qiagen_Plate 1	L17	ITGAX	3687	siRNA6	SI03066126			CAGCCACGAACAATTCACCAA
15	ARF6	Ambion_Plate 1	E4	ARF6	382	siRNA1	s1565	GUCUCAUCUUCGUAGUGGAtt	UCCACUACGAAGAUGAGACct	
15	ARF6	Ambion_Plate 1	I9	ARF6	382	siRNA2	s1566	AGACGGUGACUUACAAAAAtt	UUUUUGUAAGUCACCGUCUcc	
15	ARF6	Ambion_Plate 1	M17	ARF6	382	siRNA3	s1567	CCAAGGUCUCAUCUUCGUAtt	UACGAAGAUGAGACCUUGGgt	
15	ARF6	Qiagen_Plate 1	E4	ARF6	382	siRNA4	SI02757286			CAACGTGGAGACGGTGACTTA
15	ARF6	Qiagen_Plate 1	I9	ARF6	382	siRNA5	SI04335793			TTGGACAGTATTGGTCCTTCA
15	ARF6	Qiagen_Plate 1	M17	ARF6	382	siRNA6	SI04308619			CTGGTGATATCCAGATCCTAA
16	MyD88	Ambion_Plate 1	F4	MYD88	4615	siRNA1	s9136	CUAGUGAGCUCAUCGAAAAtt	UUUUCGAUGAGCUCACUAGca	
16	MyD88	Ambion_Plate 1	J9	MYD88	4615	siRNA2	s9137	CGGCAACUGGAACAGACAAtt	UUGUCUGUUCCAGUUGCCGga	
16	MyD88	Ambion_Plate 1	N17	MYD88	4615	siRNA3	s9138	CAGACAAACUAUCGACUGAtt	UCAGUCGAUAGUUUGUCUGtt	
16	MyD88	Qiagen_Plate 1	F4	MYD88	4615	siRNA4	SI05426057			CAGGACCAGCTGAGACTAAGA
16	MyD88	Qiagen_Plate 1	J9	MYD88	4615	siRNA5	SI03100902			CTTGATTGCCTTACAAAGTTA
16	MyD88	Qiagen_Plate 1	N17	MYD88	4615	siRNA6	SI02628661			CTCTGGCATATTCATCAAGTA
17	Mal	Ambion_Plate 1	G4	TIRAP	114609	siRNA1	s41563	GCUUUCGUCAAGUCAAAGAtt	UCUUUGACUUGACGAAAGCca	
17	Mal	Ambion_Plate 1	K9	TIRAP	114609	siRNA2	s195607	CCUCCAGCGAUGCUUCACAtt	UGUGAAGCAUCGCUGGAGGtg	
17	Mal	Ambion_Plate 1	C18	TIRAP	114609	siRNA3	s195608	GCGCUAUAGUGUCCGAGCUtt	AGCUCGGACACUAUAGCGCcg	
17	Mal	Qiagen_Plate 1	G4	TIRAP	114609	siRNA4	SI03108308			TACATAGGAAGTCCTTCTAAA
17	Mal	Qiagen_Plate 1	K9	TIRAP	114609	siRNA5	SI03075135			CCAGCGATGCTTCACAGCCTA
17	Mal	Qiagen_Plate 1	C18	TIRAP	114609	siRNA6	SI03037062			AAGTGTCACTAGAATACTACA
18	IRAK1	Ambion_Plate 1	H4	IRAK1	3654	siRNA1	s322	GGUUGUCCUUGAGUAAUAAtt	UUAUUACUCAAGGACAACCtg	
18	IRAK1	Ambion_Plate 1	L9	IRAK1	3654	siRNA2	s323	CAAGUCAGGUUUCAUGUAAtt	UUACAUGAAACCUGACUUGct	
18	IRAK1	Ambion_Plate 1	D18	IRAK1	3654	siRNA3	s324	GGAAAAGACAUGUAUCACAtt	UGUGAUACAUGUCUUUUCCct	
18	IRAK1	Qiagen_Plate 1	H4	IRAK1	3654	siRNA4	SI00605262			CCGGGCAATTCAGTTTCTACA
18	IRAK1	Qiagen_Plate 1	L9	IRAK1	3654	siRNA5	SI03649429			CCAGGTTGTCCTTGAGTAATA
18	IRAK1	Qiagen_Plate 1	D18	IRAK1	3654	siRNA6	SI03099166			CTGGGTCATGTGCCGCTTCTA
19	IRAK2	Ambion_Plate 1	I4	IRAK2	3656	siRNA1	s7495	CAGGAUCAAUCGAAAGAUUtt	AAUCUUUCGAUUGAUCCUGga	
19	IRAK2	Ambion_Plate 1	M9	IRAK2	3656	siRNA2	s7497	AGUCCAGGAUCAAUCGAAAtt	UUUCGAUUGAUCCUGGACUtg	
19	IRAK2	Ambion_Plate 1	E18	IRAK2	3656	siRNA3	s7496	CCUCCUACGUGAUCACAGAtt	UCUGUGAUCACGUAGGAGGcg	
19	IRAK2	Qiagen_Plate 1	I4	IRAK2	3656	siRNA4	SI00605283			CCAGATCATCCTGAACTGGAA
19	IRAK2	Qiagen_Plate 1	M9	IRAK2	3656	siRNA5	SI00605276			CAGCAACGTCAAGAGCTCTAA
19	IRAK2	Qiagen_Plate 1	E18	IRAK2	3656	siRNA6	SI04435522			CACGGGCATCCCTGCAATGGA
20	IRAK4	Ambion_Plate 1	J4	IRAK4	51135	siRNA1	s27527	GGUUGACAUUACUACUGAAtt	UUCAGUAGUAAUGUCAACCat	
20	IRAK4	Ambion_Plate 1	N9	IRAK4	51135	siRNA2	s27528	GCCUAAUGGUUCAUUGCUAtt	UAGCAAUGAACCAUUAGGCat	
20	IRAK4	Ambion_Plate 1	F18	IRAK4	51135	siRNA3	s27529	GGUGUGGUUUUACUAGAAAtt	UUUCUAGUAAAACCACACCaa	
20	IRAK4	Qiagen_Plate 1	J4	IRAK4	51135	siRNA4	SI02224705			TTGCAGGACAGTGGTTATTAA
20	IRAK4	Qiagen_Plate 1	N9	IRAK4	51135	siRNA5	SI02224698			ATCCTATTAGTCATATATTTA
20	IRAK4	Qiagen_Plate 1	F18	IRAK4	51135	siRNA6	SI00300566			AACACCGTGAACCTCAGTTAT
21	Pellino	Ambion_Plate 1	K4	PELI1	57162	siRNA1	s32811	GGAUUUAUGCUGCAGGAUUtt	AAUCCUGCAGCAUAAAUCCgt	
21	Pellino	Ambion_Plate 1	C10	PELI1	57162	siRNA2	s32812	CAAAGACCAGCAUAGCAUAtt	UAUGCUAUGCUGGUCUUUGtt	
21	Pellino	Ambion_Plate 1	G18	PELI1	57162	siRNA3	s32813	GCAUUUCCUAGUAUGAAGAtt	UCUUCAUACUAGGAAAUGCta	
21	Pellino	Qiagen_Plate 1	K4	PELI1	57162	siRNA4	SI04908953			CAGAATCATATGTGAACGGAA
21	Pellino	Qiagen_Plate 1	C10	PELI1	57162	siRNA5	SI04297573			CTGGTGAACAAGGCTACATCA
21	Pellino	Qiagen_Plate 1	G18	PELI1	57162	siRNA6	SI04284665			CAGTTACAAGATGGCTCGTTA
22	Uev1a	Ambion_Plate 1	L4	UBE2V1	7335	siRNA1	s14598	AGUAAAUAGUUCUAAUGGAtt	UCCAUUAGAACUAUUUACUcc	
22	Uev1a	Ambion_Plate 1	D10	UBE2V1	7335	siRNA2	s14599	GAAUUCAUAUAGCAUCAAAtt	UUUGAUGCUAUAUGAAUUCtg	
22	Uev1a	Ambion_Plate 1	H18	UBE2V1	7335	siRNA3	s14600	UGGAGUAAAUAGUUCUAAUtt	AUUAGAACUAUUUACUCCAtt	
22	Uev1a	Qiagen_Plate 1	L4	UBE2V1	7335	siRNA4	SI04951254			CAGCAACTATCAAGTCTGAAA
22	Uev1a	Qiagen_Plate 1	D10	UBE2V1	7335	siRNA5	SI04951247			ACCACTGTCCACGTAGTTGAA
22	Uev1a	Qiagen_Plate 1	H18	UBE2V1	7335	siRNA6	SI04951240			TGGCCGAAGCATAGATTGTAA
23	Ubc13	Ambion_Plate 1	M4	UBE2N	7334	siRNA1	s14595	GCAUCAGUAUCUGACCUUUtt	AAAGGUCAGAUACUGAUGCtt	
23	Ubc13	Ambion_Plate 1	E10	UBE2N	7334	siRNA2	s14596	CUUGAUUGUUGGAACCAAAtt	UUUGGUUCCAACAAUCAAGct	
23	Ubc13	Ambion_Plate 1	I18	UBE2N	7334	siRNA3	s14597	GGAAGAAUAUGUUUAGAUAtt	UAUCUAAACAUAUUCUUCCca	
23	Ubc13	Qiagen_Plate 1	M4	UBE2N	7334	siRNA4	SI03114027			TCCCAATTTGACAATCGTATT
23	Ubc13	Qiagen_Plate 1	E10	UBE2N	7334	siRNA5	SI03097983			CTGGCCCTGAGCATGCATAAA
23	Ubc13	Qiagen_Plate 1	I18	UBE2N	7334	siRNA6	SI03032176			AAGATAGTACTGAATGGAGTA
24	TRAF6	Ambion_Plate 1	N4	TRAF6	7189	siRNA1	s14389	GCCUAAUCAUUAUGAUCUAtt	UAGAUCAUAAUGAUUAGGCat	
24	TRAF6	Ambion_Plate 1	F10	TRAF6	7189	siRNA2	s14388	GAAGGUUGUUUGCACAAGAtt	UCUUGUGCAAACAACCUUCat	
24	TRAF6	Ambion_Plate 1	J18	TRAF6	7189	siRNA3	s14390	GGAAACUAUUCACCAGUUAtt	UAACUGGUGAAUAGUUUCCtg	
24	TRAF6	Qiagen_Plate 1	N4	TRAF6	7189	siRNA4	SI03050145			ATGCGCTTGCACCTTCAGTTA
24	TRAF6	Qiagen_Plate 1	F10	TRAF6	7189	siRNA5	SI03046043			AGGGTACAATACGCCTTACAA
24	TRAF6	Qiagen_Plate 1	J18	TRAF6	7189	siRNA6	SI00066122			CAGCGCTGTGCAAACTATATA
25	TRAF3	Ambion_Plate 1	C5	TRAF3	7187	siRNA1	s14382	CGCUAAAGCUGCACACUGAtt	UCAGUGUGCAGCUUUAGCGgc	
25	TRAF3	Ambion_Plate 1	G10	TRAF3	7187	siRNA2	s14383	GGAUAAUUGCUGCAAGAGAtt	UCUCUUGCAGCAAUUAUCCtt	
25	TRAF3	Ambion_Plate 1	K18	TRAF3	7187	siRNA3	s14384	GAGAGCAUCGUUAAAGAUAtt	UAUCUUUAACGAUGCUCUCtt	
25	TRAF3	Qiagen_Plate 1	C5	TRAF3	7187	siRNA4	SI02225629			TCCGATGATCGCGCTGCAGAA
25	TRAF3	Qiagen_Plate 1	G10	TRAF3	7187	siRNA5	SI02225622			AGAGAGCATCGTTAAAGATAA
25	TRAF3	Qiagen_Plate 1	K18	TRAF3	7187	siRNA6	SI03035508			AAGGCGTGTAAATACCGGGAA
26	TAK1	Ambion_Plate 1	D5	MAP3K7	6885	siRNA1	s13766	CGUGUGAACCAUCCUAAUAtt	UAUUAGGAUGGUUCACACGgg	
26	TAK1	Ambion_Plate 1	H10	MAP3K7	6885	siRNA2	s13767	AGAUACCAAUGGAUCAGAUtt	AUCUGAUCCAUUGGUAUCUgt	
26	TAK1	Ambion_Plate 1	L18	MAP3K7	6885	siRNA3	s13768	GACUCGUUGUUGGUCUAAAtt	UUUAGACCAACAACGAGUCat	
26	TAK1	Qiagen_Plate 1	D5	MAP3K7	6885	siRNA4	SI02758763			AAGATGGTATATACCAAGTTA
26	TAK1	Qiagen_Plate 1	H10	MAP3K7	6885	siRNA5	SI02758756			AACGGACAGCCAAGACGTAGA
26	TAK1	Qiagen_Plate 1	L18	MAP3K7	6885	siRNA6	SI02758749			AAGACTTGACTGTAACTGGAA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
27	TAB1	Ambion_Plate 1	E5	TAB1	10454	siRNA1	s20451	CGUGCACUUUUAUGCAAAUtt	AUUUGCAUAAAAGUGCACGgt	
27	TAB1	Ambion_Plate 1	I10	TAB1	10454	siRNA2	s20452	CUGCGAUGAUUGACACUGAtt	UCAGUGUCAAUCAUCGCAGca	
27	TAB1	Ambion_Plate 1	M18	TAB1	10454	siRNA3	s20453	CGGUCCUUCUCAACAACAAtt	UUGUUGUUGAGAAGGACCGcc	
27	TAB1	Qiagen_Plate 1	E5	TAB1	10454	siRNA4	SI02758903			AACGGCTATGATGGCAACCGA
27	TAB1	Qiagen_Plate 1	I10	TAB1	10454	siRNA5	SI02660329			ACGCCTTGGCTGAGAAGGCAA
27	TAB1	Qiagen_Plate 1	M18	TAB1	10454	siRNA6	SI04952325			CAGCTACTCTGCTGATGGCAA
28	TAB2	Ambion_Plate 1	F5	TAB2	23118	siRNA1	s23073	GAAUAAGUGAAACACGGAAtt	UUCCGUGUUUCACUUAUUCta	
28	TAB2	Ambion_Plate 1	J10	TAB2	23118	siRNA2	s23075	GUCGAGCAAUAGGCAAUAAtt	UUAUUGCCUAUUGCUCGACtt	
28	TAB2	Ambion_Plate 1	N18	TAB2	23118	siRNA3	s23074	GGUUUUACAUGACCUGCGAtt	UCGCAGGUCAUGUAAAACCtg	
28	TAB2	Qiagen_Plate 1	F5	TAB2	23118	siRNA4	SI02224642			TGGCTGGGTATCTCAGTTTAA
28	TAB2	Qiagen_Plate 1	J10	TAB2	23118	siRNA5	SI02224635			CAGTCAATAGCCAGACCTTAA
28	TAB2	Qiagen_Plate 1	N18	TAB2	23118	siRNA6	SI03107685			TAAGGTCTATATTTCAGCGAA
29	TAB3	Ambion_Plate 1	G5	TAB3	257397	siRNA1	s48890	GACAAUAGGAUGAAUAGAAtt	UUCUAUUCAUCCUAUUGUCat	
29	TAB3	Ambion_Plate 1	K10	TAB3	257397	siRNA2	s48891	GCUGAUAUGUUUAGUUCAAtt	UUGAACUAAACAUAUCAGCtg	
29	TAB3	Ambion_Plate 1	C19	TAB3	257397	siRNA3	s48892	GGAAUACCAUAGUCCAGAUtt	AUCUGGACUAUGGUAUUCCat	
29	TAB3	Qiagen_Plate 1	G5	TAB3	257397	siRNA4	SI02779504			CTCGGTATAGTACAAATCCAA
29	TAB3	Qiagen_Plate 1	K10	TAB3	257397	siRNA5	SI03111248			TAGCGTGACCTCCAAAGTACA
29	TAB3	Qiagen_Plate 1	C19	TAB3	257397	siRNA6	SI00738332			CCGGTTAACATCCATTTCCTA
30	NEMO	Ambion_Plate 1	H5	IKBKG	8517	siRNA1	s16186	AAACAGGAGGUGAUCGAUAtt	UAUCGAUCACCUCCUGUUUgg	
30	NEMO	Ambion_Plate 1	L10	IKBKG	8517	siRNA2	s16187	GGAUCGAGGACAUGAGGAAtt	UUCCUCAUGUCCUCGAUCCtg	
30	NEMO	Ambion_Plate 1	D19	IKBKG	8517	siRNA3	s16188	GAUUGUGAUGGAGACCGUUtt	AACGGUCUCCAUCACAAUCtt	
30	NEMO	Qiagen_Plate 1	H5	IKBKG	8517	siRNA4	SI04899174			CAGGATCGAGGACATGAGGAA
30	NEMO	Qiagen_Plate 1	L10	IKBKG	8517	siRNA5	SI04437692			CTGCAGAGGGAGTACAGCAAA
30	NEMO	Qiagen_Plate 1	D19	IKBKG	8517	siRNA6	SI04437685			TCGCTTGGAGGCTGCCACTAA
31	IKKa	Ambion_Plate 1	I5	CHUK	1147	siRNA1	s3076	GGACUAAAAGAAGACUAUAtt	UAUAGUCUUCUUUUAGUCCag	
31	IKKa	Ambion_Plate 1	M10	CHUK	1147	siRNA2	s3077	GAAGGAUCCAAAGUGUAUAtt	UAUACACUUUGGAUCCUUCtt	
31	IKKa	Ambion_Plate 1	E19	CHUK	1147	siRNA3	s3078	GCCUAGAGCUAAGUACCAAtt	UUGGUACUUAGCUCUAGGCga	
31	IKKa	Qiagen_Plate 1	I5	CHUK	1147	siRNA4	SI02654659			AAGCAGAAGATTATTGATCTA
31	IKKa	Qiagen_Plate 1	M10	CHUK	1147	siRNA5	SI00605122			TTCCATAAGCTTGGTGACAAA
31	IKKa	Qiagen_Plate 1	E19	CHUK	1147	siRNA6	SI00605115			CAGGAGAAGTTCGGTTTAGTA
32	IKKb	Ambion_Plate 1	J5	IKBKB	3551	siRNA1	s7263	GGGCAGUCUUUGCACAUCAtt	UGAUGUGCAAAGACUGCCCtg	
32	IKKb	Ambion_Plate 1	N10	IKBKB	3551	siRNA2	s7264	GGACAUUGUUGUUAGCGAAtt	UUCGCUAACAACAAUGUCCac	
32	IKKb	Ambion_Plate 1	F19	IKBKB	3551	siRNA3	s7265	GACUUGAAUGGAACGGUGAtt	UCACCGUUCCAUUCAAGUCtt	
32	IKKb	Qiagen_Plate 1	J5	IKBKB	3551	siRNA4	SI05460700			GTGGACATTGTTGTTAGCGAA
32	IKKb	Qiagen_Plate 1	N10	IKBKB	3551	siRNA5	SI05460686			AAAGCTGGTTCATATCTTGAA
32	IKKb	Qiagen_Plate 1	F19	IKBKB	3551	siRNA6	SI02622725			CTGGATGACATCTTAAACTTA
33	IkBa	Ambion_Plate 1	K5	NFKBIA	4792	siRNA1	s9510	GCACUGACCAUGGAAGUGAtt	UCACUUCCAUGGUCAGUGCct	
33	IkBa	Ambion_Plate 1	C14	NFKBIA	4792	siRNA2	s9511	CAAGCACCCGGAUACAGCAtt	UGCUGUAUCCGGGUGCUUGgg	
33	IkBa	Ambion_Plate 1	G19	NFKBIA	4792	siRNA3	s9512	AGUUCACGGAGUUCACAGAtt	UCUGUGAACUCCGUGAACUct	
33	IkBa	Qiagen_Plate 1	K5	NFKBIA	4792	siRNA4	SI03114930			TCCGAGACTTTCGAGGAAATA
33	IkBa	Qiagen_Plate 1	C14	NFKBIA	4792	siRNA5	SI00126826			CAGCCAGAAATTGCTGAGGCA
33	IkBa	Qiagen_Plate 1	G19	NFKBIA	4792	siRNA6	SI00126819			CTGGGCCAGCTGACACTAGAA
34	IkBb	Ambion_Plate 1	L5	NFKBIB	4793	siRNA1	s9513	ACGACGACAUUGUGGUUCAtt	UGAACCACAAUGUCGUCGUat	
34	IkBb	Ambion_Plate 1	D14	NFKBIB	4793	siRNA2	s194651	UGAUUUGUUUCAUUGUUAAtt	UUAACAAUGAAACAAAUCAca	
34	IkBb	Ambion_Plate 1	H19	NFKBIB	4793	siRNA3	s194652	ACGUGGCCGUUAUCCACAAtt	UUGUGGAUAACGGCCACGUgg	
34	IkBb	Qiagen_Plate 1	L5	NFKBIB	4793	siRNA4	SI04252241			CAGAATGACCTAGGCCAGACA
34	IkBb	Qiagen_Plate 1	D14	NFKBIB	4793	siRNA5	SI03140718			ACGCAGATGAATGGTGCGACA
34	IkBb	Qiagen_Plate 1	H19	NFKBIB	4793	siRNA6	SI00658098			CCCGAGGGCGAGGACGAGAAA
35	IkBe	Ambion_Plate 1	M5	NFKBIE	4794	siRNA1	s9514	AGGAAUCCCUUGUCCUUUUtt	AAAAGGACAAGGGAUUCCUca	
35	IkBe	Ambion_Plate 1	E14	NFKBIE	4794	siRNA2	s9515	GGCUGUACAUCUGGACCAAtt	UUGGUCCAGAUGUACAGCCag	
35	IkBe	Ambion_Plate 1	I19	NFKBIE	4794	siRNA3	s9516	GGGCACCAGUGGUAAGACAtt	UGUCUUACCACUGGUGCCCtc	
35	IkBe	Qiagen_Plate 1	M5	NFKBIE	4794	siRNA4	SI03085663			CGGAATGGAGCTGACATTGAT
35	IkBe	Qiagen_Plate 1	E14	NFKBIE	4794	siRNA5	SI03058839			CACCGTTGTTTAAAGACTTCA
35	IkBe	Qiagen_Plate 1	I19	NFKBIE	4794	siRNA6	SI00065149			CACCTGGCTGTGGAAACCCAA
36	Nfkb1	Ambion_Plate 1	N5	NFKB1	4790	siRNA1	s9504	GGCUCAUGUUUACAGCUUUtt	AAAGCUGUAAACAUGAGCCgc	
36	Nfkb1	Ambion_Plate 1	F14	NFKB1	4790	siRNA2	s9505	CCACCUUCAUUCUCAACUUtt	AAGUUGAGAAUGAAGGUGGat	
36	Nfkb1	Ambion_Plate 1	J19	NFKB1	4790	siRNA3	s9506	GCAGCUGUAUAAGUUACUAtt	UAGUAACUUAUACAGCUGCag	
36	Nfkb1	Qiagen_Plate 1	N5	NFKB1	4790	siRNA4	SI02662618			GACGCCATCTATGACAGTAAA
36	Nfkb1	Qiagen_Plate 1	F14	NFKB1	4790	siRNA5	SI02662093			CTGGGTATACTTCATGTGACA
36	Nfkb1	Qiagen_Plate 1	J19	NFKB1	4790	siRNA6	SI02654939			TCAGTTGGTCACAAATGGAAA
37	NFkb2	Ambion_Plate 1	C6	NFKB2	4791	siRNA1	s9507	GGUUCUAUGAGGAUGAUGAtt	UCAUCAUCCUCAUAGAACCga	
37	NFkb2	Ambion_Plate 1	G14	NFKB2	4791	siRNA2	s9508	CCACAGAUGUGCAUAAACAtt	UGUUUAUGCACAUCUGUGGga	
37	NFkb2	Ambion_Plate 1	K19	NFKB2	4791	siRNA3	s9509	GCACCAAGGUGAAGACCUUtt	AAGGUCUUCACCUUGGUGCtg	
37	NFkb2	Qiagen_Plate 1	C6	NFKB2	4791	siRNA4	SI00300965			AACCCAGGTCTGGATGGTATT
37	NFkb2	Qiagen_Plate 1	G14	NFKB2	4791	siRNA5	SI04245318			CGGCGTTGTCAACCTCACCAA
37	NFkb2	Qiagen_Plate 1	K19	NFKB2	4791	siRNA6	SI04224290			AAGGACATGACTGCCCAATTT
38	RelA	Ambion_Plate 1	D6	RELA	5970	siRNA1	s11914	CCCUUUACGUCAUCCCUGAtt	UCAGGGAUGACGUAAAGGGat	
38	RelA	Ambion_Plate 1	H14	RELA	5970	siRNA2	s11915	GGAGUACCCUGAGGCUAUAtt	UAUAGCCUCAGGGUACUCCat	
38	RelA	Ambion_Plate 1	L19	RELA	5970	siRNA3	s11916	GCCCUAUCCCUUUACGUCAtt	UGACGUAAAGGGAUAGGGCtg	
38	RelA	Qiagen_Plate 1	D6	RELA	5970	siRNA4	SI02663101			ATGGAGTACCCTGAGGCTATA
38	RelA	Qiagen_Plate 1	H14	RELA	5970	siRNA5	SI02663094			CCGGATTGAGGAGAAACGTAA
38	RelA	Qiagen_Plate 1	L19	RELA	5970	siRNA6	SI00301672			AAGATCAATGGCTACACAGGA
39	RelB	Ambion_Plate 1	E6	RELB	5971	siRNA1	s11917	GCUACGGCGUGGACAAGAAtt	UUCUUGUCCACGCCGUAGCtg	
39	RelB	Ambion_Plate 1	I14	RELB	5971	siRNA2	s11918	GGAUUUGCCGAAUUAACAAtt	UUGUUAAUUCGGCAAAUCCgc	
39	RelB	Ambion_Plate 1	M19	RELB	5971	siRNA3	s11919	GCCCGUCUAUGACAAGAAAtt	UUUCUUGUCAUAGACGGGCtc	
39	RelB	Qiagen_Plate 1	E6	RELB	5971	siRNA4	SI03038483			ACCACTGACACTGGACTCGTA
39	RelB	Qiagen_Plate 1	I14	RELB	5971	siRNA5	SI00089138			CAGCTACGGCGTGGACAAGAA
39	RelB	Qiagen_Plate 1	M19	RELB	5971	siRNA6	SI00089131			CACAGATGAATTGGAGATCAT

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
40	cRel	Ambion_Plate 1	F6	REL	5966	siRNA1	s11905	CCUUCUAAUUCGCAAGGUAtt	UACCUUGCGAAUUAGAAGGaa	
40	cRel	Ambion_Plate 1	J14	REL	5966	siRNA2	s11906	GAAGCUAUUAUUACAAGAAtt	UUCUUGUAAUAAUAGCUUCtt	
40	cRel	Ambion_Plate 1	N19	REL	5966	siRNA3	s11907	CCCAAUUUAUGACAACCGUtt	ACGGUUGUCAUAAAUUGGGtt	
40	cRel	Qiagen_Plate 1	F6	REL	5966	siRNA4	SI03070599			CAGGCGCCAATTCCAATACTA
40	cRel	Qiagen_Plate 1	J14	REL	5966	siRNA5	SI02629949			CCCGTATATAGAGATAATTGA
40	cRel	Qiagen_Plate 1	N19	REL	5966	siRNA6	SI00045591			CACAGAACCCGTAACAGTAAA
41	Tpl2	Ambion_Plate 1	G6	MAP3K8	1326	siRNA1	s3383	CCGCAGACCUACUAAAACAtt	UGUUUUAGUAGGUCUGCGGct	
41	Tpl2	Ambion_Plate 1	K14	MAP3K8	1326	siRNA2	s3384	CCCUCCUACCUGUACAUAAtt	UUAUGUACAGGUAGGAGGGat	
41	Tpl2	Ambion_Plate 1	C20	MAP3K8	1326	siRNA3	s3385	GGAACUUCCUGAGAACAUUtt	AAUGUUCUCAGGAAGUUCCag	
41	Tpl2	Qiagen_Plate 1	G6	MAP3K8	1326	siRNA4	SI02777362			AAGGATAATAGAGTAGCCTAA
41	Tpl2	Qiagen_Plate 1	K14	MAP3K8	1326	siRNA5	SI02634674			AAGAAAGTGATCCATCATGAT
41	Tpl2	Qiagen_Plate 1	C20	MAP3K8	1326	siRNA6	SI00073773			AAGAGCAACAGTAATGGAGTA
42	Mekk1	Ambion_Plate 1	H6	MAP3K1	4214	siRNA1	s8667	GCGUAGCUCAAGGAUCAAAtt	UUUGAUCCUUGAGCUACGCct	
42	Mekk1	Ambion_Plate 1	L14	MAP3K1	4214	siRNA2	s8668	GGCUCUUCGUUGUUUAGAAtt	UUCUAAACAACGAAGAGCCac	
42	Mekk1	Ambion_Plate 1	D20	MAP3K1	4214	siRNA3	s8669	GAAUCUCCAGGAGUAAGGAtt	UCCUUACUCCUGGAGAUUCtg	
42	Mekk1	Qiagen_Plate 1	H6	MAP3K1	4214	siRNA4	SI02659965			CTCCGGGTGTTTCAACTAGAA
42	Mekk1	Qiagen_Plate 1	L14	MAP3K1	4214	siRNA5	SI02659958			CACGCATGTCAAATTCTCATA
42	Mekk1	Qiagen_Plate 1	D20	MAP3K1	4214	siRNA6	SI00300727			AAACAAACCGCCGTGTTAACA
43	Mkk1	Ambion_Plate 1	I6	MAP2K1	5604	siRNA1	s11167	GGAACCAGAUCAUAAGGGAtt	UCCCUUAUGAUCUGGUUCCgg	
43	Mkk1	Ambion_Plate 1	M14	MAP2K1	5604	siRNA2	s11168	UGUUCAGUCUGGAAUUUCAtt	UGAAAUUCCAGACUGAACAct	
43	Mkk1	Ambion_Plate 1	E20	MAP2K1	5604	siRNA3	s11169	AGGCCUUUCUUACCCAGAAtt	UUCUGGGUAAGAAAGGCCUca	
43	Mkk1	Qiagen_Plate 1	I6	MAP2K1	5604	siRNA4	SI02222962			CTGGATCAAGTCCTGAAGAAA
43	Mkk1	Qiagen_Plate 1	M14	MAP2K1	5604	siRNA5	SI02222955			CTGGAAGAATTCCTGAACAAA
43	Mkk1	Qiagen_Plate 1	E20	MAP2K1	5604	siRNA6	SI00300699			TTGTGAATAAATGCTTAATAA
44	Mkk2	Ambion_Plate 1	J6	MAP2K2	5605	siRNA1	s11170	GAUCAGCAUUUGCAUGGAAtt	UUCCAUGCAAAUGCUGAUCtc	
44	Mkk2	Ambion_Plate 1	N14	MAP2K2	5605	siRNA2	s11171	GAACUUGACGAGCAGCAGAtt	UCUGCUGCUCGUCAAGUUCca	
44	Mkk2	Ambion_Plate 1	F20	MAP2K2	5605	siRNA3	s11172	CAAAGACGAUGACUUCGAAtt	UUCGAAGUCAUCGUCUUUGag	
44	Mkk2	Qiagen_Plate 1	J6	MAP2K2	5605	siRNA4	SI02225097			CCGGCCTGCCATGGCCATCTT
44	Mkk2	Qiagen_Plate 1	N14	MAP2K2	5605	siRNA5	SI02225090			CAGCATTTGCATGGAACACAT
44	Mkk2	Qiagen_Plate 1	F20	MAP2K2	5605	siRNA6	SI04436733			CTCAAAGACGATGACTTCGAA
45	Erk1	Ambion_Plate 1	K6	MAPK3	5595	siRNA1	s11141	GGACCGGAUGUUAACCUUUtt	AAAGGUUAACAUCCGGUCCag	
45	Erk1	Ambion_Plate 1	C15	MAPK3	5595	siRNA2	s230179	UGAUGGAGACUGACCUGUAtt	UACAGGUCAGUCUCCAUCAgg	
45	Erk1	Ambion_Plate 1	G20	MAPK3	5595	siRNA3	s230180	CAGCUGAGCAAUGACCAUAtt	UAUGGUCAUUGCUCAGCUGct	
45	Erk1	Qiagen_Plate 1	K6	MAPK3	5595	siRNA4	SI00606004			CTCCCTGACCCGTCTAATATA
45	Erk1	Qiagen_Plate 1	C15	MAPK3	5595	siRNA5	SI00605997			CCCGTCTAATATATAAATATA
45	Erk1	Qiagen_Plate 1	G20	MAPK3	5595	siRNA6	SI04379445			CAAGACTCGCGTGGCCATCAA
46	Erk2	Ambion_Plate 1	L6	MAPK1	5594	siRNA1	s11137	CAGGGUUCCUGACAGAAUAtt	UAUUCUGUCAGGAACCCUGtg	
46	Erk2	Ambion_Plate 1	D15	MAPK1	5594	siRNA2	s11138	CAACCAUCGAGCAAAUGAAtt	UUCAUUUGCUCGAUGGUUGgt	
46	Erk2	Ambion_Plate 1	H20	MAPK1	5594	siRNA3	s11139	GCAGAAAUGCUUUCUAACAtt	UGUUAGAAAGCAUUUCUGCca	
46	Erk2	Qiagen_Plate 1	L6	MAPK1	5594	siRNA4	SI00300762			AATGACATTATTCGAGCACCA
46	Erk2	Qiagen_Plate 1	D15	MAPK1	5594	siRNA5	SI00300755			AAGTTCGAGTAGCTATCAAGA
46	Erk2	Qiagen_Plate 1	H20	MAPK1	5594	siRNA6	SI00300748			AACAAAGTTCGAGTAGCTATC
47	Mkk3	Ambion_Plate 1	M6	MAP2K3	5606	siRNA1	s11173	GGUCGACUGUUUCUACACUtt	AGUGUAGAAACAGUCGACCgt	
47	Mkk3	Ambion_Plate 1	E15	MAP2K3	5606	siRNA2	s11175	CCCGGACCUUCAUCACCAUtt	AUGGUGAUGAAGGUCCGGGag	
47	Mkk3	Ambion_Plate 1	I20	MAP2K3	5606	siRNA3	s11174	ACAGAAACUUUGAGGUGGAtt	UCCACCUCAAAGUUUCUGUct	
47	Mkk3	Qiagen_Plate 1	M6	MAP2K3	5606	siRNA4	SI02222976			CCGGGCCACCGTGAACTCACA
47	Mkk3	Qiagen_Plate 1	E15	MAP2K3	5606	siRNA5	SI02222969			ACGGATATCCTGCATGTCCAA
47	Mkk3	Qiagen_Plate 1	I20	MAP2K3	5606	siRNA6	SI03649604			TCGACTGTTTCTACACTGTCA
48	Mkk6	Ambion_Plate 1	N6	MAP2K6	5608	siRNA1	s11180	GGAUACAUCACUAGAUAAAtt	UUUAUCUAGUGAUGUAUCCat	
48	Mkk6	Ambion_Plate 1	F15	MAP2K6	5608	siRNA2	s11181	GGUGGACUCUGUUGCUAAAtt	UUUAGCAACAGAGUCCACCaa	
48	Mkk6	Ambion_Plate 1	J20	MAP2K6	5608	siRNA3	s11179	GCAUCACGAUGAUUGAGUUtt	AACUCAAUCAUCGUGAUGCcc	
48	Mkk6	Qiagen_Plate 1	N6	MAP2K6	5608	siRNA4	SI02222997			AAGGCTTGCATTTCTATTGGA
48	Mkk6	Qiagen_Plate 1	F15	MAP2K6	5608	siRNA5	SI03089072			CTCATCAATGCTCTCGGTCAA
48	Mkk6	Qiagen_Plate 1	J20	MAP2K6	5608	siRNA6	SI00042805			TACGGTAGTGATGAAATTATA
49	p38a	Ambion_Plate 1	C7	MAPK14	1432	siRNA1	s3585	CCUAAAACCUAGUAAUCUAtt	UAGAUUACUAGGUUUUAGGtc	
49	p38a	Ambion_Plate 1	G15	MAPK14	1432	siRNA2	s3586	GAAGCUCUCCAGACCAUUUtt	AAAUGGUCUGGAGAGCUUCtt	
49	p38a	Ambion_Plate 1	K20	MAPK14	1432	siRNA3	s3587	CUGCGGUUACUUAAACAUAtt	UAUGUUUAAGUAACCGCAGtt	
49	p38a	Qiagen_Plate 1	C7	MAPK14	1432	siRNA4	SI00605157			CAGAGAACTGCGGTTACTTAA
49	p38a	Qiagen_Plate 1	G15	MAPK14	1432	siRNA5	SI00300769			AACTGCGGTTACTTAAACATA
49	p38a	Qiagen_Plate 1	K20	MAPK14	1432	siRNA6	SI03098683			CTGGGAGGTGCCCGAGCGTTA
50	p38b	Ambion_Plate 1	D7	MAPK11	5600	siRNA1	s11155	GCGACUACAUUGACCAGCUtt	AGCUGGUCAAUGUAGUCGCtt	
50	p38b	Ambion_Plate 1	H15	MAPK11	5600	siRNA2	s11156	GAACACGCCCGGACAUAUAtt	UAUAUGUCCGGGCGUGUUCtg	
50	p38b	Ambion_Plate 1	L20	MAPK11	5600	siRNA3	s11157	GGAGCUCACUUACCAGGAAtt	UUCCUGGUAAGUGAGCUCCtt	
50	p38b	Qiagen_Plate 1	D7	MAPK11	5600	siRNA4	SI00606060			CTGAGCGACGAGCACGTTCAA
50	p38b	Qiagen_Plate 1	H15	MAPK11	5600	siRNA5	SI00606053			CAGGATGGAGCTGATCCAGTA
50	p38b	Qiagen_Plate 1	L20	MAPK11	5600	siRNA6	SI03649597			TCCATCGAGGACTTCAGCGAA
51	MK2	Ambion_Plate 1	E7	MAPKAPK2	9261	siRNA1	s569	GGAUCAUGCAAUCAACAAAtt	UUUGUUGAUUGCAUGAUCCaa	
51	MK2	Ambion_Plate 1	I15	MAPKAPK2	9261	siRNA2	s570	CAGUAUCUGCAUUCAAUCAtt	UGAUUGAAUGCAGAUACUGga	
51	MK2	Ambion_Plate 1	M20	MAPKAPK2	9261	siRNA3	s571	GGACGGUGGAGAACUCUUUtt	AAAGAGUUCUCCACCGUCCaa	
51	MK2	Qiagen_Plate 1	E7	MAPKAPK2	9261	siRNA4	SI02223697			CTACGAGCAGATCAAGATAAA
51	MK2	Qiagen_Plate 1	I15	MAPKAPK2	9261	siRNA5	SI00288246			CGCCATCATCGATGACTACAA
51	MK2	Qiagen_Plate 1	M20	MAPKAPK2	9261	siRNA6	SI04438182			CCCGGGCACCATGCTGTCCAA
52	Mkk4	Ambion_Plate 1	F7	MAP2K4	6416	siRNA1	s12703	GCAACUGUGAAAGCACUAAtt	UUAGUGCUUUCACAGUUGCta	
52	Mkk4	Ambion_Plate 1	J15	MAP2K4	6416	siRNA2	s12701	GGUAAACGCAAAGCACUGAtt	UCAGUGCUUUGCGUUUACCct	
52	Mkk4	Ambion_Plate 1	N20	MAP2K4	6416	siRNA3	s12702	GCAUGCAGGGUAAACGCAAtt	UUGCGUUUACCCUGCAUGCtg	
52	Mkk4	Qiagen_Plate 1	F7	MAP2K4	6416	siRNA4	SI02655079			TTGGACGAGGAGCTTATGGTT
52	Mkk4	Qiagen_Plate 1	J15	MAP2K4	6416	siRNA5	SI02223102			AGGGTGTATAGTGTTCACAAA
52	Mkk4	Qiagen_Plate 1	N20	MAP2K4	6416	siRNA6	SI02223095			AGGGAGAATGGTGCTGTTTAA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
53	Mkk7	Ambion_Plate 1	G7	MAP2K7	5609	siRNA1	s11182	CGUCAUUGCCGUUAAGCAAtt	UUGCUUAACGGCAAUGACGtg	
53	Mkk7	Ambion_Plate 1	K15	MAP2K7	5609	siRNA2	s11183	GACAGUUUCCCUACAAGAAtt	UUCUUGUAGGGAAACUGUCct	
53	Mkk7	Ambion_Plate 1	C21	MAP2K7	5609	siRNA3	s11184	GCAUUGAGAUUGACCAGAAtt	UUCUGGUCAAUCUCAAUGCtc	
53	Mkk7	Qiagen_Plate 1	G7	MAP2K7	5609	siRNA4	SI02660588			CAGGAAGAGACCAAAGTATAA
53	Mkk7	Qiagen_Plate 1	K15	MAP2K7	5609	siRNA5	SI00300720			AAAGATGACAGTGGCGATTGT
53	Mkk7	Qiagen_Plate 1	C21	MAP2K7	5609	siRNA6	SI04380831			CTGCGCTGAGAAGCTCAAGAA
54	Jnk1	Ambion_Plate 1	H7	MAPK8	5599	siRNA1	s11152	GUUGCAAUCAAGAAGCUAAtt	UUAGCUUCUUGAUUGCAACat	
54	Jnk1	Ambion_Plate 1	L15	MAPK8	5599	siRNA2	s11153	CAAAGAUCCCUGACAAGCAtt	UGCUUGUCAGGGAUCUUUGgt	
54	Jnk1	Ambion_Plate 1	D21	MAPK8	5599	siRNA3	s11154	CCAGUAAUAUAGUAGUAAAtt	UUUACUACUAUAUUACUGGgc	
54	Jnk1	Qiagen_Plate 1	H7	MAPK8	5599	siRNA4	SI02758651			ATGATGTGTCTTCAATGTCAA
54	Jnk1	Qiagen_Plate 1	L15	MAPK8	5599	siRNA5	SI02758644			ATGAAATGTGTTAATCACAAA
54	Jnk1	Qiagen_Plate 1	D21	MAPK8	5599	siRNA6	SI02758637			GCCCAGTAATATAGTAGTAAA
55	Jnk2	Ambion_Plate 1	I7	MAPK9	5601	siRNA1	s229708	GCAUUCAGCUGGUAUAAUUtt	AAUUAUACCAGCUGAAUGCag	
55	Jnk2	Ambion_Plate 1	M15	MAPK9	5601	siRNA2	s229709	GGAAAGAGCUAAUUUACAAtt	UUGUAAAUUAGCUCUUUCCat	
55	Jnk2	Ambion_Plate 1	E21	MAPK9	5601	siRNA3	s229710	GAAUUAUGUCGAAAACAGAtt	UCUGUUUUCGACAUAAUUCct	
55	Jnk2	Qiagen_Plate 1	I7	MAPK9	5601	siRNA4	SI02222920			ATCGTGAACTTGTCCTCTTAA
55	Jnk2	Qiagen_Plate 1	M15	MAPK9	5601	siRNA5	SI00300797			AAGAGAGCTTATCGTGAACTT
55	Jnk2	Qiagen_Plate 1	E21	MAPK9	5601	siRNA6	SI04950344			ATCCTGGGTATGGGCTACAAA
56	Jnk3	Ambion_Plate 1	J7	MAPK10	5602	siRNA1	s11161	GGAAUAAGGUAAUUGAACAtt	UGUUCAAUUACCUUAUUCCac	
56	Jnk3	Ambion_Plate 1	N15	MAPK10	5602	siRNA2	s11162	CAAGUAACAUUGUAGUCAAtt	UUGACUACAAUGUUACUUGgt	
56	Jnk3	Ambion_Plate 1	F21	MAPK10	5602	siRNA3	s11163	CCAUAUGUGGUGACACGUUtt	AACGUGUCACCACAUAUGGag	
56	Jnk3	Qiagen_Plate 1	J7	MAPK10	5602	siRNA4	SI02222934			TCCGAGCACAATAAACTCAAA
56	Jnk3	Qiagen_Plate 1	N15	MAPK10	5602	siRNA5	SI02222927			CCGCATGTGTCTGTATTCATA
56	Jnk3	Qiagen_Plate 1	F21	MAPK10	5602	siRNA6	SI04436719			ACCAAGTAACATTGTAGTCAA
57	Erk3	Ambion_Plate 1	K7	MAPK12	6300	siRNA1	s12467	CAGUUCCUCGUGUACCAGAtt	UCUGGUACACGAGGAACUGga	
57	Erk3	Ambion_Plate 1	C16	MAPK12	6300	siRNA2	s12468	GAAGUAUGAUGACUCCUUUtt	AAAGGAGUCAUCAUACUUCtg	
57	Erk3	Ambion_Plate 1	G21	MAPK12	6300	siRNA3	s12469	GCAAGCUCAUGAAACAUGAtt	UCAUGUUUCAUGAGCUUGCcc	
57	Erk3	Qiagen_Plate 1	K7	MAPK12	6300	siRNA4	SI02223088			TGGAAGCGTGTTACTTACAAA
57	Erk3	Qiagen_Plate 1	C16	MAPK12	6300	siRNA5	SI02223081			CTGGACGTATTCACTCCTGAT
57	Erk3	Qiagen_Plate 1	G21	MAPK12	6300	siRNA6	SI03649625			CTGGGAGGTGCGCGCCGTGTA
58	p38d	Ambion_Plate 1	L7	MAPK13	5603	siRNA1	s11164	AAUGAGGACUGUGAACUGAtt	UCAGUUCACAGUCCUCAUUca	
58	p38d	Ambion_Plate 1	D16	MAPK13	5603	siRNA2	s11165	GGUGUAUCAGAUGCUCAAAtt	UUUGAGCAUCUGAUACACCag	
58	p38d	Ambion_Plate 1	H21	MAPK13	5603	siRNA3	s11166	GCACAUCUACAAGGAGAUUtt	AAUCUCCUUGUAGAUGUGCtg	
58	p38d	Qiagen_Plate 1	L7	MAPK13	5603	siRNA4	SI02222948			CGGGATGAGCCTCATCCGGAA
58	p38d	Qiagen_Plate 1	D16	MAPK13	5603	siRNA5	SI02222941			CCGGAGTGGCATGAAGCTGTA
58	p38d	Qiagen_Plate 1	H21	MAPK13	5603	siRNA6	SI04379459			CAGCCGTTTGATGATTCCTTA
59	TRIF	Ambion_Plate 1	M7	TICAM1	148022	siRNA1	s45113	GACAAGCUCUUGUAUCUGAtt	UCAGAUACAAGAGCUUGUCct	
59	TRIF	Ambion_Plate 1	E16	TICAM1	148022	siRNA2	s45114	GAAUCAUCAUCGGAACAGAtt	UCUGUUCCGAUGAUGAUUCca	
59	TRIF	Ambion_Plate 1	I21	TICAM1	148022	siRNA3	s45115	CCAACUUUCUGUAGAAGAUtt	AUCUUCUACAGAAAGUUGGag	
59	TRIF	Qiagen_Plate 1	M7	TICAM1	148022	siRNA4	SI03074946			CCAGAGCTACTTGTCCTACCA
59	TRIF	Qiagen_Plate 1	E16	TICAM1	148022	siRNA5	SI03069332			CAGGACGCCATAGACCACTCA
59	TRIF	Qiagen_Plate 1	I21	TICAM1	148022	siRNA6	SI03032127			AAGATACCACCTCTCCAAATA
60	TRAM	Ambion_Plate 1	N7	TICAM2	353376	siRNA1	s51476	GAAAGUCGUGGAUUUCCUAtt	UAGGAAAUCCACGACUUUCtt	
60	TRAM	Ambion_Plate 1	F16	TICAM2	353376	siRNA2	s51477	GGAAUAAUCUUUGCUGAGAtt	UCUCAGCAAAGAUUAUUCCgg	
60	TRAM	Ambion_Plate 1	J21	TICAM2	353376	siRNA3	s51478	CGUUAACAGGCAGCAUAAAtt	UUUAUGCUGCCUGUUAACGga	
60	TRAM	Qiagen_Plate 1	N7	TICAM2	353376	siRNA4	SI03113845			TCCAGTTCTATACGTCCCTAA
60	TRAM	Qiagen_Plate 1	F16	TICAM2	353376	siRNA5	SI02644880			TTGCCTGAGATGAAACATATA
60	TRAM	Qiagen_Plate 1	J21	TICAM2	353376	siRNA6	SI00130893			CTCCGTTAACAGGCAGCATAA
61	RIP1	Ambion_Plate 1	C8	RIPK1	8737	siRNA1	s16651	CCACUAGUCUGACGGAUAAtt	UUAUCCGUCAGACUAGUGGta	
61	RIP1	Ambion_Plate 1	G16	RIPK1	8737	siRNA2	s16653	GCAAAGACCUUACGAGAAUtt	AUUCUCGUAAGGUCUUUGCtg	
61	RIP1	Ambion_Plate 1	K21	RIPK1	8737	siRNA3	s16652	GUGUAGAAGAGGACGUGAAtt	UUCACGUCCUCUUCUACACtt	
61	RIP1	Qiagen_Plate 1	C8	RIPK1	8737	siRNA4	SI02621983			CCGACATTTCCTGGCATTGAA
61	RIP1	Qiagen_Plate 1	G16	RIPK1	8737	siRNA5	SI00288092			TACCACTAGTCTGACGGATAA
61	RIP1	Qiagen_Plate 1	K21	RIPK1	8737	siRNA6	SI04437860			TCCGTTAACGTTAATACCCAA
62	FADD	Ambion_Plate 1	D8	FADD	8772	siRNA1	s16705	GCAGUCCUCUUAUUCCUAAtt	UUAGGAAUAAGAGGACUGCtt	
62	FADD	Ambion_Plate 1	H16	FADD	8772	siRNA2	s16706	ACAGCAUCGAGGACAGAUAtt	UAUCUGUCCUCGAUGCUGUcg	
62	FADD	Ambion_Plate 1	L21	FADD	8772	siRNA3	s16707	AGAUCGACAGCAUCGAGGAtt	UCCUCGAUGCUGUCGAUCUtg	
62	FADD	Qiagen_Plate 1	D8	FADD	8772	siRNA4	SI03649016			CAGCGGGATCTCGTATCTTTA
62	FADD	Qiagen_Plate 1	H16	FADD	8772	siRNA5	SI03648911			AGCGGGATCTCGTATCTTTAA
62	FADD	Qiagen_Plate 1	L21	FADD	8772	siRNA6	SI00300223			AAGAAGACCTGTGTGCAGCAT
63	Caspase 8	Ambion_Plate 1	E8	CASP8	841	siRNA1	s2427	GAUACUGUCUGAUCAUCAAtt	UUGAUGAUCAGACAGUAUCcc	
63	Caspase 8	Ambion_Plate 1	I16	CASP8	841	siRNA2	s2425	GAUAAUCAACGACUAUGAAtt	UUCAUAGUCGUUGAUUAUCtt	
63	Caspase 8	Ambion_Plate 1	M21	CASP8	841	siRNA3	s2426	GAUCAGAAUUGAGGUCUUUtt	AAAGACCUCAAUUCUGAUCtg	
63	Caspase 8	Qiagen_Plate 1	E8	CASP8	841	siRNA4	SI02662457			GACAAAGTTTACCAAATGAAA
63	Caspase 8	Qiagen_Plate 1	I16	CASP8	841	siRNA5	SI02661946			AAGAGTCTGTGCCCAAATCAA
63	Caspase 8	Qiagen_Plate 1	M21	CASP8	841	siRNA6	SI00299593			AAGTTCCTGAGCCTGGACTAC
64	TBK1	Ambion_Plate 1	F8	TBK1	29110	siRNA1	s761	GAACGUAGAUUAGCUUAUAtt	UAUAAGCUAAUCUACGUUCtg	
64	TBK1	Ambion_Plate 1	J16	TBK1	29110	siRNA2	s763	GGCACAACAUUUCCCUAAAtt	UUUAGGGAAAUGUUGUGCCag	
64	TBK1	Ambion_Plate 1	N21	TBK1	29110	siRNA3	s762	GGAACCUCUGAAUACCAUAtt	UAUGGUAUUCAGAGGUUCCcg	
64	TBK1	Qiagen_Plate 1	F8	TBK1	29110	siRNA4	SI02224418			CTGACTTGACACGTTTGTAAA
64	TBK1	Qiagen_Plate 1	J16	TBK1	29110	siRNA5	SI02224411			CAGAACGTAGATTAGCTTATA
64	TBK1	Qiagen_Plate 1	N21	TBK1	29110	siRNA6	SI00301889			AAAGCGGCAGAGTTAGGTGAA
65	IKKe	Ambion_Plate 2	C3	IKBKE	9641	siRNA1	s18536	CGACACCAGGAGUACCUCUtt	AGAGGUACUCCUGGUGUCGgg	
65	IKKe	Ambion_Plate 2	G8	IKBKE	9641	siRNA2	s18537	CAGUGCUGUUUGGACAAGAtt	UCUUGUCCAAACAGCACUGaa	
65	IKKe	Ambion_Plate 2	K16	IKBKE	9641	siRNA3	s18538	AGCUGGAUAAGGUGAAUUUtt	AAAUUCACCUUAUCCAGCUtg	
65	IKKe	Qiagen_Plate 2	C3	IKBKE	9641	siRNA4	SI02655324			CAAGATGAACTTCATCTACAA
65	IKKe	Qiagen_Plate 2	G8	IKBKE	9641	siRNA5	SI02655317			AAGAAGCATCCAGCAGATTCA
65	IKKe	Qiagen_Plate 2	K16	IKBKE	9641	siRNA6	SI02622326			CCGCATCATCGAACGGCTAAA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
66	IRF3	Ambion_Plate 2	D3	IRF3	3661	siRNA1	s7507	ACACCUCUCCGGACACCAAtt	UUGGUGUCCGGAGAGGUGUct	
66	IRF3	Ambion_Plate 2	H8	IRF3	3661	siRNA2	s7508	GCAGUACUUCUGAUACCCAtt	UGGGUAUCAGAAGUACUGCct	
66	IRF3	Ambion_Plate 2	L16	IRF3	3661	siRNA3	s7509	ACAUAAAAUCUACGAGUUUtt	AAACUCGUAGAUUUUAUGUgg	
66	IRF3	Qiagen_Plate 2	D3	IRF3	3661	siRNA4	SI05587617			TTGGGTCTGTTACCCAAAGAA
66	IRF3	Qiagen_Plate 2	H8	IRF3	3661	siRNA5	SI03117359			TCTGGATGAGTTACTGGGTAA
66	IRF3	Qiagen_Plate 2	L16	IRF3	3661	siRNA6	SI02626526			CAGCCTCGAGTTTGAGAGCTA
67	Duba	Ambion_Plate 2	E3	OTUD5	55593	siRNA1	s31035	GAAUAUCCACUAUAAUUCAtt	UGAAUUAUAGUGGAUAUUCcg	
67	Duba	Ambion_Plate 2	I8	OTUD5	55593	siRNA2	s31036	CCACCUACAUUAACAGGAAtt	UUCCUGUUAAUGUAGGUGGta	
67	Duba	Ambion_Plate 2	M16	OTUD5	55593	siRNA3	s31037	CCAUCGGAAUAUCCACUAUtt	AUAGUGGAUAUUCCGAUGGta	
67	Duba	Qiagen_Plate 2	E3	OTUD5	55593	siRNA4	SI04303754			CCCATTCGTGTTAGCTACCAT
67	Duba	Qiagen_Plate 2	I8	OTUD5	55593	siRNA5	SI04245283			TGCCGACTACTTCTCCAACTA
67	Duba	Qiagen_Plate 2	M16	OTUD5	55593	siRNA6	SI04153982			TACCACCTACATTAACAGGAA
68	TRADD	Ambion_Plate 2	F3	TRADD	8717	siRNA1	s16606	CUGUUUGAGUUGCAUCCUAtt	UAGGAUGCAACUCAAACAGcg	
68	TRADD	Ambion_Plate 2	J8	TRADD	8717	siRNA2	s16607	GCGCAUACCUGUUUGUGGAtt	UCCACAAACAGGUAUGCGCtg	
68	TRADD	Ambion_Plate 2	N16	TRADD	8717	siRNA3	s16608	GAUGCGCUGCGAAAUCUGAtt	UCAGAUUUCGCAGCGCAUCct	
68	TRADD	Qiagen_Plate 2	F3	TRADD	8717	siRNA4	SI02655240			CAGGGTCAGCCTGTAGTGAAT
68	TRADD	Qiagen_Plate 2	J8	TRADD	8717	siRNA5	SI03098942			CTGGGCCTGACCGATCCCAAT
68	TRADD	Qiagen_Plate 2	N16	TRADD	8717	siRNA6	SI03085026			CGCGCGCTCTGTGGGTCTCAA
69	TANK	Ambion_Plate 2	G3	TANK	10010	siRNA1	s19453	CACUCAAGAUAACAAUUAUtt	AUAAUUGUUAUCUUGAGUGga	
69	TANK	Ambion_Plate 2	K8	TANK	10010	siRNA2	s19454	GAACUAUGAGCAGAGAAUAtt	UAUUCUCUGCUCAUAGUUCtc	
69	TANK	Ambion_Plate 2	C17	TANK	10010	siRNA3	s19455	GAGAUUCUGCAGUAAAAGAtt	UCUUUUACUGCAGAAUCUCta	
69	TANK	Qiagen_Plate 2	G3	TANK	10010	siRNA4	SI03115322			TCCGGCAGGCATGCATGGATA
69	TANK	Qiagen_Plate 2	K8	TANK	10010	siRNA5	SI03023608			TTGACTCTTGATCAGCCACAA
69	TANK	Qiagen_Plate 2	C17	TANK	10010	siRNA6	SI02632665			ATCCTTTATAGTGATGCTACA
70	SINTBAD	Ambion_Plate 2	H3	TBKBP1	9755	siRNA1	s18828	GCCUCAAAGUCUACGAGAUtt	AUCUCGUAGACUUUGAGGCgg	
70	SINTBAD	Ambion_Plate 2	L8	TBKBP1	9755	siRNA2	s18829	GGAUGAUGCCCUCAUCAAAtt	UUUGAUGAGGGCAUCAUCCgg	
70	SINTBAD	Ambion_Plate 2	D17	TBKBP1	9755	siRNA3	s18830	CAGCAUGAGUUACAGAAGAtt	UCUUCUGUAACUCAUGCUGga	
70	SINTBAD	Qiagen_Plate 2	H3	TBKBP1	9755	siRNA4	SI04227629			CACCATGGAGTCCATGTTCGA
70	SINTBAD	Qiagen_Plate 2	L8	TBKBP1	9755	siRNA5	SI04201575			CCGACGCCGCCTCAAAGTCTA
70	SINTBAD	Qiagen_Plate 2	D17	TBKBP1	9755	siRNA6	SI04177579			CACTGCTTACGGAGACATCAA
71	BTK	Ambion_Plate 2	I3	BTK	695	siRNA1	s2124	GAAACUGUUUGGUAAACGAtt	UCGUUUACCAAACAGUUUCga	
71	BTK	Ambion_Plate 2	M8	BTK	695	siRNA2	s2125	CACCAGCUCAAAAACGUAAtt	UUACGUUUUUGAGCUGGUGaa	
71	BTK	Ambion_Plate 2	E17	BTK	695	siRNA3	s2126	CAGUAAGAAGGGUUCAAUAtt	UAUUGAACCCUUCUUACUGcc	
71	BTK	Qiagen_Plate 2	I3	BTK	695	siRNA4	SI03058468			CACCGGAAGTCCTGATGTATA
71	BTK	Qiagen_Plate 2	M8	BTK	695	siRNA5	SI00001043			CCCTTTATGATTACATGCCAA
71	BTK	Qiagen_Plate 2	E17	BTK	695	siRNA6	SI00001036			ACAGACTGAATTTGCGATGAA
72	NIK	Ambion_Plate 2	J3	MAP3K14	9020	siRNA1	s17186	GUCCAAAUACAGUCUCUUAtt	UAAGAGACUGUAUUUGGACtt	
72	NIK	Ambion_Plate 2	N8	MAP3K14	9020	siRNA2	s17187	GGAUUGACCUCACCCAGAAtt	UUCUGGGUGAGGUCAAUCCtg	
72	NIK	Ambion_Plate 2	F17	MAP3K14	9020	siRNA3	s17188	GGAUUAUGAGUACCGAGAAtt	UUCUCGGUACUCAUAAUCCac	
72	NIK	Qiagen_Plate 2	J3	MAP3K14	9020	siRNA4	SI02632343			TACCTAGTGCATGCTCTGCAA
72	NIK	Qiagen_Plate 2	N8	MAP3K14	9020	siRNA5	SI02632336			CACATGCATGTGACTCCTCAA
72	NIK	Qiagen_Plate 2	F17	MAP3K14	9020	siRNA6	SI00058324			CCCGCTTGGATCAGTGACCAT
73	AKT1	Ambion_Plate 2	K3	AKT1	207	siRNA1	s659	GCGUGACCAUGAACGAGUUtt	AACUCGUUCAUGGUCACGCgg	
73	AKT1	Ambion_Plate 2	C9	AKT1	207	siRNA2	s660	GAACAAUCCGAUUCACGUAtt	UACGUGAAUCGGAUUGUUCtg	
73	AKT1	Ambion_Plate 2	G17	AKT1	207	siRNA3	s661	CGGUAGCACUUGACCUUUUtt	AAAAGGUCAAGUGCUACCGtg	
73	AKT1	Qiagen_Plate 2	K3	AKT1	207	siRNA4	SI02758406			CACCATGAGCGACGTGGCTAT
73	AKT1	Qiagen_Plate 2	C9	AKT1	207	siRNA5	SI02757244			CACGCTTGGTCCCGAGGCCAA
73	AKT1	Qiagen_Plate 2	G17	AKT1	207	siRNA6	SI00299159			AAGTACTCTTTCCAGACCCAC
74	AKT2	Ambion_Plate 2	L3	AKT2	208	siRNA1	s1215	CAACUUCUCCGUAGCAGAAtt	UUCUGCUACGGAGAAGUUGtt	
74	AKT2	Ambion_Plate 2	D9	AKT2	208	siRNA2	s1216	CGGGCUAAAGUGACCAUGAtt	UCAUGGUCACUUUAGCCCGtg	
74	AKT2	Ambion_Plate 2	H17	AKT2	208	siRNA3	s1217	UGACUUCGACUAUCUCAAAtt	UUUGAGAUAGUCGAAGUCAtt	
74	AKT2	Qiagen_Plate 2	L3	AKT2	208	siRNA4	SI00299173			AAGGTACTTCGATGATGAATT
74	AKT2	Qiagen_Plate 2	D9	AKT2	208	siRNA5	SI00299166			AACAACTTCTCCGTAGCAGAA
74	AKT2	Qiagen_Plate 2	H17	AKT2	208	siRNA6	SI00287679			CAAGCGTGGTGAATACATCAA
75	AKT3	Ambion_Plate 2	M3	AKT3	10000	siRNA1	s19427	GUAACAUCUGAGACAGAUAtt	UAUCUGUCUCAGAUGUUACtt	
75	AKT3	Ambion_Plate 2	E9	AKT3	10000	siRNA2	s19428	GGACUAUCUACAUUCCGGAtt	UCCGGAAUGUAGAUAGUCCaa	
75	AKT3	Ambion_Plate 2	I17	AKT3	10000	siRNA3	s19429	GCUCAUUCAUAGGAUAUAAtt	UUAUAUCCUAUGAAUGAGCca	
75	AKT3	Qiagen_Plate 2	M3	AKT3	10000	siRNA4	SI02757762			ACCAGAGGTGTTAGAAGATAA
75	AKT3	Qiagen_Plate 2	E9	AKT3	10000	siRNA5	SI04899874			ATGAAGTGGCACACACTCTAA
75	AKT3	Qiagen_Plate 2	I17	AKT3	10000	siRNA6	SI04899867			ATGGCTCATTCATAGGATATA
76	PIK3CA	Ambion_Plate 2	N3	PIK3CA	5290	siRNA1	s10520	GACUAGCUAGAGACAAUGAtt	UCAUUGUCUCUAGCUAGUCtg	
76	PIK3CA	Ambion_Plate 2	F9	PIK3CA	5290	siRNA2	s10521	GUAAUUACCCAGAUCCUAUtt	AUAGGAUCUGGGUAAUUACag	
76	PIK3CA	Ambion_Plate 2	J17	PIK3CA	5290	siRNA3	s10522	GGUGCACUGCAGUUCAACAtt	UGUUGAACUGCAGUGCACCtt	
76	PIK3CA	Qiagen_Plate 2	N3	PIK3CA	5290	siRNA4	SI02665369			CTCCGTGAGGCTACATTAATA
76	PIK3CA	Qiagen_Plate 2	F9	PIK3CA	5290	siRNA5	SI02622207			CTGAGTCAGTATAAGTATATA
76	PIK3CA	Qiagen_Plate 2	J17	PIK3CA	5290	siRNA6	SI04380635			AAGCTTTAGAATAATGCGCAA
77	PIK3CB	Ambion_Plate 2	C4	PIK3CB	5291	siRNA1	s10524	CUCCAAAUGUUGCGCUUGAtt	UCAAGCGCAACAUUUGGAGtg	
77	PIK3CB	Ambion_Plate 2	G9	PIK3CB	5291	siRNA2	s10525	GGGAAAGCUGGACUACUAAtt	UUAGUAGUCCAGCUUUCCCtg	
77	PIK3CB	Ambion_Plate 2	K17	PIK3CB	5291	siRNA3	s10523	GUAAAUGAAUUUCGAAGAAtt	UUCUUCGAAAUUCAUUUACtt	
77	PIK3CB	Qiagen_Plate 2	C4	PIK3CB	5291	siRNA4	SI02622221			TCGGGAAGCTACCATTTCTTA
77	PIK3CB	Qiagen_Plate 2	G9	PIK3CB	5291	siRNA5	SI02622214			CCCTTCGATAAGATTATTGAA
77	PIK3CB	Qiagen_Plate 2	K17	PIK3CB	5291	siRNA6	SI04436327			TACGTTCGAGAATATGCTGTA
78	PIK3CD	Ambion_Plate 2	D4	PIK3CD	5293	siRNA1	s10529	GUGAGAAAUUUGAACGGUUtt	AACCGUUCAAAUUUCUCACta	
78	PIK3CD	Ambion_Plate 2	H9	PIK3CD	5293	siRNA2	s10530	GACUAAUAAUAGUGAGAAAtt	UUUCUCACUAUUAUUAGUCtt	
78	PIK3CD	Ambion_Plate 2	L17	PIK3CD	5293	siRNA3	s10531	GCACUUCCGAGUGAAGUUUtt	AAACUUCACUCGGAAGUGCtt	
78	PIK3CD	Qiagen_Plate 2	D4	PIK3CD	5293	siRNA4	SI02223816			CGCCGTGATCGAGAAAGCCAA
78	PIK3CD	Qiagen_Plate 2	H9	PIK3CD	5293	siRNA5	SI02223809			CCGGTCACGCATGAAGGCAAA
78	PIK3CD	Qiagen_Plate 2	L17	PIK3CD	5293	siRNA6	SI04436334			CACGGGCACTGTGCGCAGTAA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
79	PIK3CG	Ambion_Plate 2	E4	PIK3CG	5294	siRNA1	s10532	GCUUUAGAGUUCCAUAUGAtt	UCAUAUGGAACUCUAAAGCtt	
79	PIK3CG	Ambion_Plate 2	I9	PIK3CG	5294	siRNA2	s10533	GCUGCACGACUUUACCCAAtt	UUGGGUAAAGUCGUGCAGCat	
79	PIK3CG	Ambion_Plate 2	M17	PIK3CG	5294	siRNA3	s10534	GUAAUCGAGAUGUUACAAAtt	UUUGUAACAUCUCGAUUACtt	
79	PIK3CG	Qiagen_Plate 2	E4	PIK3CG	5294	siRNA4	SI00605843			CACCTTTACTCTATAACTCAA
79	PIK3CG	Qiagen_Plate 2	I9	PIK3CG	5294	siRNA5	SI00605836			ATCGAAGTTTGCAGAGACAAA
79	PIK3CG	Qiagen_Plate 2	M17	PIK3CG	5294	siRNA6	SI04436341			CAAACTCACGTCTGCAACTAA
80	PIK3R1	Ambion_Plate 2	F4	PIK3R1	5295	siRNA1	s10535	CUACCGGAAUGAAUCUCUAtt	UAGAGAUUCAUUCCGGUAGtg	
80	PIK3R1	Ambion_Plate 2	J9	PIK3R1	5295	siRNA2	s10536	CAACGGUAUGAAUAACAAUtt	AUUGUUAUUCAUACCGUUGtt	
80	PIK3R1	Ambion_Plate 2	N17	PIK3R1	5295	siRNA3	s10537	GCAGCUGAGUAUCGAGAAAtt	UUUCUCGAUACUCAGCUGCct	
80	PIK3R1	Qiagen_Plate 2	F4	PIK3R1	5295	siRNA4	SI02225412			TAGCTGGTTATGAACTAGTAA
80	PIK3R1	Qiagen_Plate 2	J9	PIK3R1	5295	siRNA5	SI02225405			CAGCATTAAACCAGACCTTAT
80	PIK3R1	Qiagen_Plate 2	N17	PIK3R1	5295	siRNA6	SI04379417			CACTACCGGAATGAATCTCTA
81	PIK3R2	Ambion_Plate 2	G4	PIK3R2	5296	siRNA1	s10538	GCAUUGCCGAGAUCCAUGAtt	UCAUGGAUCUCGGCAAUGCgg	
81	PIK3R2	Ambion_Plate 2	K9	PIK3R2	5296	siRNA2	s10539	GCAAGAUCCGAGACCAGUAtt	UACUGGUCUCGGAUCUUGCgc	
81	PIK3R2	Ambion_Plate 2	C18	PIK3R2	5296	siRNA3	s10540	GGAAAGGCGGGAACAAUAAtt	UUAUUGUUCCCGCCUUUCCtg	
81	PIK3R2	Qiagen_Plate 2	G4	PIK3R2	5296	siRNA4	SI00287539			TTGGTACGTGGGCAAGATCAA
81	PIK3R2	Qiagen_Plate 2	K9	PIK3R2	5296	siRNA5	SI00287532			CCGCGAGTATGACCAGCTTTA
81	PIK3R2	Qiagen_Plate 2	C18	PIK3R2	5296	siRNA6	SI04378990			AAGGATCCTGCTGAACTCCGA
82	PIK3R3	Ambion_Plate 2	H4	PIK3R3	8503	siRNA1	s16151	GGAUAUCAAUCGAGUACAAtt	UUGUACUCGAUUGAUAUCCtc	
82	PIK3R3	Ambion_Plate 2	L9	PIK3R3	8503	siRNA2	s229780	GGACUGCAAUAGAAGCUUUtt	AAAGCUUCUAUUGCAGUCCtc	
82	PIK3R3	Ambion_Plate 2	D18	PIK3R3	8503	siRNA3	s229781	CCCUAUUCGACAGAACUGAtt	UCAGUUCUGUCGAAUAGGGca	
82	PIK3R3	Qiagen_Plate 2	H4	PIK3R3	8503	siRNA4	SI02777446			ATGAATTATGATAAATTGAAA
82	PIK3R3	Qiagen_Plate 2	L9	PIK3R3	8503	siRNA5	SI02777439			CAGGGCTGTAGTATTCAGTAA
82	PIK3R3	Qiagen_Plate 2	D18	PIK3R3	8503	siRNA6	SI02777432			AAGGGAGGCAATAATAAGTTA
83	PIK3R5	Ambion_Plate 2	I4	PIK3R5	23533	siRNA1	s24027	GGGCAGAAGUUCAUCAGGAtt	UCCUGAUGAACUUCUGCCCag	
83	PIK3R5	Ambion_Plate 2	M9	PIK3R5	23533	siRNA2	s24028	GCACAUCGCAGAUCAAAGUtt	ACUUUGAUCUGCGAUGUGCta	
83	PIK3R5	Ambion_Plate 2	E18	PIK3R5	23533	siRNA3	s24029	GGCUGUUCCUCUAACACUAtt	UAGUGUUAGAGGAACAGCCtc	
83	PIK3R5	Qiagen_Plate 2	I4	PIK3R5	23533	siRNA4	SI04954110			TAGCAGCTCAGTTCTAGCTAA
83	PIK3R5	Qiagen_Plate 2	M9	PIK3R5	23533	siRNA5	SI00104636			CAGGATCTATAAACTCTTCAA
83	PIK3R5	Qiagen_Plate 2	E18	PIK3R5	23533	siRNA6	SI00104629			TAGGATCCTTTCTAGAAGGAA
84	RAC1	Ambion_Plate 2	J4	RAC1	5879	siRNA1	s11711	CUACUGUCUUUGACAAUUAtt	UAAUUGUCAAAGACAGUAGgg	
84	RAC1	Ambion_Plate 2	N9	RAC1	5879	siRNA2	s11712	ACAGAUUAAUUUUUCCAUAtt	UAUGGAAAAAUUAAUCUGUaa	
84	RAC1	Ambion_Plate 2	F18	RAC1	5879	siRNA3	s11713	GGAACUAAACUUGAUCUUAtt	UAAGAUCAAGUUUAGUUCCca	
84	RAC1	Qiagen_Plate 2	J4	RAC1	5879	siRNA4	SI02655051			ATGCATTTCCTGGAGAATATA
84	RAC1	Qiagen_Plate 2	N9	RAC1	5879	siRNA5	SI03065531			CAGCACGTGTTCCCGACATAA
84	RAC1	Qiagen_Plate 2	F18	RAC1	5879	siRNA6	SI03040884			ACGAAGTGGAGATTTACACTA
85	IRF5	Ambion_Plate 2	K4	IRF5	3663	siRNA1	s7513	AGCUGAUAGUAUCCGGCUAtt	UAGCCGGAUACUAUCAGCUga	
85	IRF5	Ambion_Plate 2	C10	IRF5	3663	siRNA2	s7514	CCACCCUUCGAGAUCUUCUtt	AGAAGAUCUCGAAGGGUGGtg	
85	IRF5	Ambion_Plate 2	G18	IRF5	3663	siRNA3	s7515	GGAUUACUCUUUUGGUGCAtt	UGCACCAAAAGAGUAAUCCtc	
85	IRF5	Qiagen_Plate 2	K4	IRF5	3663	siRNA4	SI04311762			TCAGCTGATAGTATCCGGCTA
85	IRF5	Qiagen_Plate 2	C10	IRF5	3663	siRNA5	SI04276615			AGGGCAGTGCATGTAAATCAT
85	IRF5	Qiagen_Plate 2	G18	IRF5	3663	siRNA6	SI04253949			CTCCCTGTCCTCTGAGATAAT
86	IRF7	Ambion_Plate 2	L4	IRF7	3665	siRNA1	s7519	CGAGCUGCACGUUCCUAUAtt	UAUAGGAACGUGCAGCUCGgg	
86	IRF7	Ambion_Plate 2	D10	IRF7	3665	siRNA2	s194563	GUCUAAUGAGAACUCCAGAtt	UCUGGAGUUCUCAUUAGACtg	
86	IRF7	Ambion_Plate 2	H18	IRF7	3665	siRNA3	s194564	GCCUAGAACCCAGUCUAAUtt	AUUAGACUGGGUUCUAGGCgg	
86	IRF7	Qiagen_Plate 2	L4	IRF7	3665	siRNA4	SI04137623			CCGCGGCCGCCCAGTCTAATA
86	IRF7	Qiagen_Plate 2	D10	IRF7	3665	siRNA5	SI03171763			CAGCGCCAACAGCCTCTATGA
86	IRF7	Qiagen_Plate 2	H18	IRF7	3665	siRNA6	SI00448693			CTGGAAGCACTTCGCGCGCAA
87	STAT1	Ambion_Plate 2	M4	STAT1	6772	siRNA1	s277	CCUACGAACAUGACCCUAUtt	AUAGGGUCAUGUUCGUAGGtg	
87	STAT1	Ambion_Plate 2	E10	STAT1	6772	siRNA2	s278	CGGUUGAACCCUACACGAAtt	UUCGUGUAGGGUUCAACCGca	
87	STAT1	Ambion_Plate 2	I18	STAT1	6772	siRNA3	s279	GGUUCACUAUAGUUGCGGAtt	UCCGCAACUAUAGUGAACCag	
87	STAT1	Qiagen_Plate 2	M4	STAT1	6772	siRNA4	SI02662884			CCAGATGTCTATGATCATTTA
87	STAT1	Qiagen_Plate 2	E10	STAT1	6772	siRNA5	SI02662324			CAGAAAGAGCTTGACAGTAAA
87	STAT1	Qiagen_Plate 2	I18	STAT1	6772	siRNA6	SI04950960			CTGCAGAACTGGTTCACTATA
88	Fos	Ambion_Plate 2	N4	FOS	2353	siRNA1	s5339	CACUCCAAGCGGAGACAGAtt	UCUGUCUCCGCUUGGAGUGta	
88	Fos	Ambion_Plate 2	F10	FOS	2353	siRNA2	s5340	CUUCCUUCGUCUUCACCUAtt	UAGGUGAAGACGAAGGAAGac	
88	Fos	Ambion_Plate 2	J18	FOS	2353	siRNA3	s5341	GAAUCCGAAGGGAAAGGAAtt	UUCCUUUCCCUUCGGAUUCtc	
88	Fos	Qiagen_Plate 2	N4	FOS	2353	siRNA4	SI02781464			TGGGTTCATTATTGGAATTAA
88	Fos	Qiagen_Plate 2	F10	FOS	2353	siRNA5	SI02781429			GACCAATATTATACTAAGAAA
88	Fos	Qiagen_Plate 2	J18	FOS	2353	siRNA6	SI03091844			CTCGGGCTTCAACGCAGACTA
89	Jun	Ambion_Plate 2	C5	JUN	3725	siRNA1	s7658	GGCACAGCUUAAACAGAAAtt	UUUCUGUUUAAGCUGUGCCac	
89	Jun	Ambion_Plate 2	G10	JUN	3725	siRNA2	s7659	CCAAGUGCCGAAAAAGGAAtt	UUCCUUUUUCGGCACUUGGag	
89	Jun	Ambion_Plate 2	K18	JUN	3725	siRNA3	s7660	GGAUCAAGGCGGAGAGGAAtt	UUCCUCUCCGCCUUGAUCCgc	
89	Jun	Qiagen_Plate 2	C5	JUN	3725	siRNA4	SI00300580			AAGAACGTGACAGATGAGCAG
89	Jun	Qiagen_Plate 2	G10	JUN	3725	siRNA5	SI03077599			CCCGAGCTGGAGCGCCTGATA
89	Jun	Qiagen_Plate 2	K18	JUN	3725	siRNA6	SI00034678			CGCGCGCGAGTCGACAAGTAA
90	PYK2	Ambion_Plate 2	D5	PTK2B	2185	siRNA1	s5007	GAUGUGGUCCUGAAUCGUAtt	UACGAUUCAGGACCACAUCtt	
90	PYK2	Ambion_Plate 2	H10	PTK2B	2185	siRNA2	s5006	GUGAAGAUGUGGUCCUGAAtt	UUCAGGACCACAUCUUCACgg	
90	PYK2	Ambion_Plate 2	L18	PTK2B	2185	siRNA3	s5008	GGAUCAUCAUGGAAUUGUAtt	UACAAUUCCAUGAUGAUCCag	
90	PYK2	Qiagen_Plate 2	D5	PTK2B	2185	siRNA4	SI02225328			CAGGAGAACTTAAAGCCCAAA
90	PYK2	Qiagen_Plate 2	H10	PTK2B	2185	siRNA5	SI02225321			AAGCTGATCGGCATCATTGAA
90	PYK2	Qiagen_Plate 2	L18	PTK2B	2185	siRNA6	SI02649031			CTGGCATTCTTGTACAGTGTA
91	ETS1	Ambion_Plate 2	F5	ETS1	2113	siRNA1	s4847	GGACUCUUUUGAAAGCAUAtt	UAUGCUUUCAAAAGAGUCCtg	
91	ETS1	Ambion_Plate 2	J10	ETS1	2113	siRNA2	s4848	GCAUUAAAAGCUACUUUCAtt	UGAAAGUAGCUUUUAAUGCtt	
91	ETS1	Ambion_Plate 2	N18	ETS1	2113	siRNA3	s4849	GCCUGAAAGGUGUAGACUUtt	AAGUCUACACCUUUCAGGCtg	
91	ETS1	Qiagen_Plate 2	F5	ETS1	2113	siRNA4	SI05181603			TCCACCGTTCCTATTAAATTT
91	ETS1	Qiagen_Plate 2	J10	ETS1	2113	siRNA5	SI05147842			CACGACCTAAGTTGAAGAGTT
91	ETS1	Qiagen_Plate 2	N18	ETS1	2113	siRNA6	SI03068632			CAGCTTCGACTCAGAGGACTA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
92	ELK1	Ambion_Plate 2	G5	ELK1	2002	siRNA1	s4632	GGCCUUGCGGUACUACUAUtt	AUAGUAGUACCGCAAGGCCcg	
92	ELK1	Ambion_Plate 2	K10	ELK1	2002	siRNA2	s4633	GAAACAUAGUUCAACUGAAtt	UUCAGUUGAACUAUGUUUCtc	
92	ELK1	Ambion_Plate 2	C19	ELK1	2002	siRNA3	s4634	CAUCAUCUCCUGGACUUCAtt	UGAAGUCCAGGAGAUGAUGtg	
92	ELK1	Qiagen_Plate 2	G5	ELK1	2002	siRNA4	SI02662506			AGGGAGTCATCTCTTCCTATA
92	ELK1	Qiagen_Plate 2	K10	ELK1	2002	siRNA5	SI00300146			CTGCTGAGAGAGCAAGGCAAT
92	ELK1	Qiagen_Plate 2	C19	ELK1	2002	siRNA6	SI00074081			GAGAAACATAGTTCAACTGAA
93	ELK4	Ambion_Plate 2	H5	ELK4	2005	siRNA1	s4638	CUCAGAUACUAUUAUGUAAtt	UUACAUAAUAGUAUCUGAGgg	
93	ELK4	Ambion_Plate 2	L10	ELK4	2005	siRNA2	s4639	CUAACGUAAUGACUGCUUUtt	AAAGCAGUCAUUACGUUAGag	
93	ELK4	Ambion_Plate 2	D19	ELK4	2005	siRNA3	s4640	GGACAAAGUAAAUAAUUCAtt	UGAAUUAUUUACUUUGUCCtt	
93	ELK4	Qiagen_Plate 2	H5	ELK4	2005	siRNA4	SI03104101			GAGGGTGACTGTGAAAGTTTA
93	ELK4	Qiagen_Plate 2	L10	ELK4	2005	siRNA5	SI03079328			CCCTCAGATACTATTATGTAA
93	ELK4	Qiagen_Plate 2	D19	ELK4	2005	siRNA6	SI03073861			CATGATCTGTTGGACCTCTAA
94	SP1	Ambion_Plate 2	I5	SP1	6667	siRNA1	s13318	GCAACAUGGGAAUUAUGAAtt	UUCAUAAUUCCCAUGUUGCtg	
94	SP1	Ambion_Plate 2	M10	SP1	6667	siRNA2	s13319	GGCAGACCUUUACAACUCAtt	UGAGUUGUAAAGGUCUGCCct	
94	SP1	Ambion_Plate 2	E19	SP1	6667	siRNA3	s13320	CCACAAGCCCAAACAAUCAtt	UGAUUGUUUGGGCUUGUGGgt	
94	SP1	Qiagen_Plate 2	I5	SP1	6667	siRNA4	SI02648072			CTAGGACGCAATAAATTTATA
94	SP1	Qiagen_Plate 2	M10	SP1	6667	siRNA5	SI02648065			CAGCAAGTTCTGACAGGACTA
94	SP1	Qiagen_Plate 2	E19	SP1	6667	siRNA6	SI00150990			TCCCAGAAAGTATATACTGAA
95	EGR1	Ambion_Plate 2	J5	EGR1	1958	siRNA1	s4538	CAACGACAGCAGUCCCAUUtt	AAUGGGACUGCUGUCGUUGga	
95	EGR1	Ambion_Plate 2	N10	EGR1	1958	siRNA2	s4537	GGACAUGACAGCAACCUUUtt	AAAGGUUGCUGUCAUGUCCga	
95	EGR1	Ambion_Plate 2	F19	EGR1	1958	siRNA3	s4539	CCAUGGACAACUACCCUAAtt	UUAGGGUAGUUGUCCAUGGtg	
95	EGR1	Qiagen_Plate 2	J5	EGR1	1958	siRNA4	SI03078950			CCCGTCGGTGGCCACCACGTA
95	EGR1	Qiagen_Plate 2	N10	EGR1	1958	siRNA5	SI03069108			CAGGACAATTGAAATTTGCTA
95	EGR1	Qiagen_Plate 2	F19	EGR1	1958	siRNA6	SI03052511			CAAACCAATGGTGATCCTCTA
96	EGR2	Ambion_Plate 2	K5	EGR2	1959	siRNA1	s4540	GAUCCACCUGAGACAGAAAtt	UUUCUGUCUCAGGUGGAUCtt	
96	EGR2	Ambion_Plate 2	C14	EGR2	1959	siRNA2	s4541	CACUCUCUACAAUCCGUAAtt	UUACGGAUUGUAGAGAGUGga	
96	EGR2	Ambion_Plate 2	G19	EGR2	1959	siRNA3	s4542	CAUCUUUCCCAAUGCCGAAtt	UUCGGCAUUGGGAAAGAUGgt	
96	EGR2	Qiagen_Plate 2	K5	EGR2	1959	siRNA4	SI04948762			CACCTAGAAACCAGACCTTCA
96	EGR2	Qiagen_Plate 2	C14	EGR2	1959	siRNA5	SI04948755			CTGGATGTCAGAGTTGATCTA
96	EGR2	Qiagen_Plate 2	G19	EGR2	1959	siRNA6	SI00008785			TCCACTCTCTACAATCCGTAA
97	ATF2	Ambion_Plate 2	L5	ATF2	1386	siRNA1	s3492	GUGAUACUGUCAAAGGUCAtt	UGACCUUUGACAGUAUCACca	
97	ATF2	Ambion_Plate 2	D14	ATF2	1386	siRNA2	s3493	CAAGUACUGUAAUCACCCAtt	UGGGUGAUUACAGUACUUGag	
97	ATF2	Ambion_Plate 2	H19	ATF2	1386	siRNA3	s3494	GACAUUUCAGUGCCGAGUAtt	UACUCGGCACUGAAAUGUCtt	
97	ATF2	Qiagen_Plate 2	L5	ATF2	1386	siRNA4	SI02780309			CGCGGGTGACCGAAAGGATCA
97	ATF2	Qiagen_Plate 2	D14	ATF2	1386	siRNA5	SI03095946			CTGCTCTTTCACAGATCGTTA
97	ATF2	Qiagen_Plate 2	H19	ATF2	1386	siRNA6	SI00305886			TGCGAAATCTGTGGTTGTAAA
98	ATF7	Ambion_Plate 2	M5	ATF7	11016	siRNA1	s21693	CCGAUACAAUCGCAUGUAAtt	UUACAUGCGAUUGUAUCGGca	
98	ATF7	Ambion_Plate 2	E14	ATF7	11016	siRNA2	s21694	CAGUCACUGCACUACAGAAtt	UUCUGUAGUGCAGUGACUGgg	
98	ATF7	Ambion_Plate 2	I19	ATF7	11016	siRNA3	s21695	CACCAGACAUCAAAAUCAAtt	UUGAUUUUGAUGUCUGGUGtg	
98	ATF7	Qiagen_Plate 2	M5	ATF7	11016	siRNA4	SI04952584			CAGTAGCAGCCTTGCCCTAAA
98	ATF7	Qiagen_Plate 2	E14	ATF7	11016	siRNA5	SI04374909			AACAGCTACTGTTAGCTCATA
98	ATF7	Qiagen_Plate 2	I19	ATF7	11016	siRNA6	SI04247264			CAGCCCGAACTGACTCAGTCA
99	CBP	Ambion_Plate 2	N5	CREBBP	1387	siRNA1	s3495	GAAUCUUUCCCAUAUCGAAtt	UUCGAUAUGGGAAAGAUUCag	
99	CBP	Ambion_Plate 2	F14	CREBBP	1387	siRNA2	s3497	CAGCUAUCAGAAUAGGUAUtt	AUACCUAUUCUGAUAGCUGta	
99	CBP	Ambion_Plate 2	J19	CREBBP	1387	siRNA3	s3496	GGAUAUUGCUGUGGACGCAtt	UGCGUCCACAGCAAUAUCCaa	
99	CBP	Qiagen_Plate 2	N5	CREBBP	1387	siRNA4	SI02633099			CTGCCAGTGAATCGCATGCAA
99	CBP	Qiagen_Plate 2	F14	CREBBP	1387	siRNA5	SI02633092			CCCGATCCTGGTGAATCCAAA
99	CBP	Qiagen_Plate 2	J19	CREBBP	1387	siRNA6	SI02633085			AACGGAGGTCGCGTTTACATA
100	p300	Ambion_Plate 2	C6	EP300	2033	siRNA1	s4695	GGACUACCCUAUCAAGUAAtt	UUACUUGAUAGGGUAGUCCaa	
100	p300	Ambion_Plate 2	G14	EP300	2033	siRNA2	s4696	CCACUACUGGAAUUCGGAAtt	UUCCGAAUUCCAGUAGUGGat	
100	p300	Ambion_Plate 2	K19	EP300	2033	siRNA3	s4697	GCCUGGUUAUAUAACCGGAtt	UCCGGUUAUAUAACCAGGCat	
100	p300	Qiagen_Plate 2	C6	EP300	2033	siRNA4	SI03078761			CCCGGTGAACTCTCCTATAAT
100	p300	Qiagen_Plate 2	G14	EP300	2033	siRNA5	SI03038259			ACCAAGGGTTGCAAACGGAAA
100	p300	Qiagen_Plate 2	K19	EP300	2033	siRNA6	SI02626267			TTGGACTACCCTATCAAGTAA
101	ISGF3G	Ambion_Plate 2	D6	IRF9	10379	siRNA1	s20290	CACAGAAUCUUAUCACAGUtt	ACUGUGAUAAGAUUCUGUGga	
101	ISGF3G	Ambion_Plate 2	H14	IRF9	10379	siRNA2	s20291	CAAUAUUUAAGGGAAAGUAtt	UACUUUCCCUUAAAUAUUGcc	
101	ISGF3G	Ambion_Plate 2	L19	IRF9	10379	siRNA3	s20292	GCUAAGACCAUGUUCCGGAtt	UCCGGAACAUGGUCUUAGCtg	
101	ISGF3G	Qiagen_Plate 2	D6	IRF9	10379	siRNA4	SI03037650			ACAGAATCTTATCACAGTGAA
101	ISGF3G	Qiagen_Plate 2	H14	IRF9	10379	siRNA5	SI00084378			CAAGGCCTGGGCAATATTTAA
101	ISGF3G	Qiagen_Plate 2	L19	IRF9	10379	siRNA6	SI00084371			CAACAAGAGTTCTGAATTTAA
102	ELF4	Ambion_Plate 2	E6	ELF4	2000	siRNA1	s4626	GCGGAAGUCUUACUCAAUAtt	UAUUGAGUAAGACUUCCGCgg	
102	ELF4	Ambion_Plate 2	I14	ELF4	2000	siRNA2	s4627	CCAUCUAUCUGUGGGAGUUtt	AACUCCCACAGAUAGAUGGtg	
102	ELF4	Ambion_Plate 2	M19	ELF4	2000	siRNA3	s4628	GCGAUAUCCUGGAUGAGAAtt	UUCUCAUCCAGGAUAUCGCtg	
102	ELF4	Qiagen_Plate 2	E6	ELF4	2000	siRNA4	SI04339076			CAGACGGGACCTTGTGCATGA
102	ELF4	Qiagen_Plate 2	I14	ELF4	2000	siRNA5	SI04327946			AACCGCGGAAGTCTTACTCAA
102	ELF4	Qiagen_Plate 2	M19	ELF4	2000	siRNA6	SI00378490			AAGGACCTGGTGGTCATTGAA
103	IFNAR1	Ambion_Plate 2	F6	IFNAR1	3454	siRNA1	s783	CUAUAUCGGUGCUCCAAAAtt	UUUUGGAGCACCGAUAUAGat	
103	IFNAR1	Ambion_Plate 2	J14	IFNAR1	3454	siRNA2	s784	CCAUUUCGCAAAGCUCAGAtt	UCUGAGCUUUGCGAAAUGGtg	
103	IFNAR1	Ambion_Plate 2	N19	IFNAR1	3454	siRNA3	s782	GGUAUGAGGUUGACUCAUUtt	AAUGAGUCAACCUCAUACCat	
103	IFNAR1	Qiagen_Plate 2	F6	IFNAR1	3454	siRNA4	SI03065104			CAGATTGGTCCTCCAGAAGTA
103	IFNAR1	Qiagen_Plate 2	J14	IFNAR1	3454	siRNA5	SI00013195			TGCCAGAAAGATGATCCCTAA
103	IFNAR1	Qiagen_Plate 2	N19	IFNAR1	3454	siRNA6	SI00013181			CAGGGACCTTATTATTCATTA
104	IFNAR2	Ambion_Plate 2	G6	IFNAR2	3455	siRNA1	s7184	GAGUGGAAAUUUCACCUAUtt	AUAGGUGAAAUUUCCACUCat	
104	IFNAR2	Ambion_Plate 2	K14	IFNAR2	3455	siRNA2	s7185	GAACUGUGCAAAUACCACAtt	UGUGGUAUUUGCACAGUUCtt	
104	IFNAR2	Ambion_Plate 2	C20	IFNAR2	3455	siRNA3	s7186	CCUAUAUCAUUGACAAGUUtt	AACUUGUCAAUGAUAUAGGtg	
104	IFNAR2	Qiagen_Plate 2	G6	IFNAR2	3455	siRNA4	SI02780575			CACAGTGATGAGCAAGCAGTA
104	IFNAR2	Qiagen_Plate 2	K14	IFNAR2	3455	siRNA5	SI04949385			CCGGTCCATCTTATCATGGGA
104	IFNAR2	Qiagen_Plate 2	C20	IFNAR2	3455	siRNA6	SI03031035			AAGAAGCATAAACCCGAAATA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
105	IFNB1	Ambion_Plate 2	H6	IFNB1	3456	siRNA1	s7187	GCAUUGACCAUCUAUGAGAtt	UCUCAUAGAUGGUCAAUGCgg	
105	IFNB1	Ambion_Plate 2	L14	IFNB1	3456	siRNA2	s7188	CUAAGGAACUUUUACUUCAtt	UGAAGUAAAAGUUCCUUAGga	
105	IFNB1	Ambion_Plate 2	D20	IFNB1	3456	siRNA3	s7189	GGACCAUAGUCAGAGUGGAtt	UCCACUCUGACUAUGGUCCag	
105	IFNB1	Qiagen_Plate 2	H6	IFNB1	3456	siRNA4	SI00033642			CAAGGACAGGATGAACTTTGA
105	IFNB1	Qiagen_Plate 2	L14	IFNB1	3456	siRNA5	SI00033635			CAGAGTGGAAATCCTAAGGAA
105	IFNB1	Qiagen_Plate 2	D20	IFNB1	3456	siRNA6	SI00033628			CAGGTAGTAGGCGACACTGTT
106	IL12A	Ambion_Plate 2	I6	IL12A	3592	siRNA1	s7356	GGCCCUGAAUUUCAACAGUtt	ACUGUUGAAAUUCAGGGCCtg	
106	IL12A	Ambion_Plate 2	M14	IL12A	3592	siRNA2	s7357	GAAUGAGAGUUGCCUAAAUtt	AUUUAGGCAACUCUCAUUCtt	
106	IL12A	Ambion_Plate 2	E20	IL12A	3592	siRNA3	s7358	CAUUGGAAUUAACCAAGAAtt	UUCUUGGUUAAUUCCAAUGgt	
106	IL12A	Qiagen_Plate 2	I6	IL12A	3592	siRNA4	SI00017710			AAGGCCAGACAAACTCTAGAA
106	IL12A	Qiagen_Plate 2	M14	IL12A	3592	siRNA5	SI00017703			CCGCGCCTCGGGACAATTATA
106	IL12A	Qiagen_Plate 2	E20	IL12A	3592	siRNA6	SI00017696			ACCATTGGAATTAACCAAGAA
107	IL12B	Ambion_Plate 2	J6	IL12B	3593	siRNA1	s7359	AUAUUUUAAAGGACCAGAAtt	UUCUGGUCCUUUAAAAUAUca	
107	IL12B	Ambion_Plate 2	N14	IL12B	3593	siRNA2	s7360	CAAGGAGUAUGAGUACUCAtt	UGAGUACUCAUACUCCUUGtt	
107	IL12B	Ambion_Plate 2	F20	IL12B	3593	siRNA3	s7361	GGACCGCUACUAUAGCUCAtt	UGAGCUAUAGUAGCGGUCCtg	
107	IL12B	Qiagen_Plate 2	J6	IL12B	3593	siRNA4	SI03069227			CAGGACCGCTACTATAGCTCA
107	IL12B	Qiagen_Plate 2	N14	IL12B	3593	siRNA5	SI03032393			AAGATGCGAGGCCAAGAATTA
107	IL12B	Qiagen_Plate 2	F20	IL12B	3593	siRNA6	SI03028599			AACCCTGACCATCCAAGTCAA
108	IL1B	Ambion_Plate 2	K6	IL1B	3553	siRNA1	s7269	GCACCUGUACGAUCACUGAtt	UCAGUGAUCGUACAGGUGCat	
108	IL1B	Ambion_Plate 2	C15	IL1B	3553	siRNA2	s7270	GCACCUCUCAAGCAGAAAAtt	UUUUCUGCUUGAGAGGUGCtg	
108	IL1B	Ambion_Plate 2	G20	IL1B	3553	siRNA3	s7271	CGAUGCACCUGUACGAUCAtt	UGAUCGUACAGGUGCAUCGtg	
108	IL1B	Qiagen_Plate 2	K6	IL1B	3553	siRNA4	SI03095701			CTGCGTGTTGAAAGATGATAA
108	IL1B	Qiagen_Plate 2	C15	IL1B	3553	siRNA5	SI03059966			CACGATGCACCTGTACGATCA
108	IL1B	Qiagen_Plate 2	G20	IL1B	3553	siRNA6	SI00012166			CAGCCAATCTTCATTGCTCAA
109	IL6	Ambion_Plate 2	L6	IL6	3569	siRNA1	s7311	GAACGAAUUGACAAACAAAtt	UUUGUUUGUCAAUUCGUUCtg	
109	IL6	Ambion_Plate 2	D15	IL6	3569	siRNA2	s7312	CUUCCAAUCUGGAUUCAAUtt	AUUGAAUCCAGAUUGGAAGca	
109	IL6	Ambion_Plate 2	H20	IL6	3569	siRNA3	s7313	GGAGUUUGAGGUAUACCUAtt	UAGGUAUACCUCAAACUCCaa	
109	IL6	Qiagen_Plate 2	L6	IL6	3569	siRNA4	SI03094371			CTGCAGGACATGACAACTCAT
109	IL6	Qiagen_Plate 2	D15	IL6	3569	siRNA5	SI03040660			ACCTCAGATTGTTGTTGTTAA
109	IL6	Qiagen_Plate 2	H20	IL6	3569	siRNA6	SI00012579			CAGAACTTATGTTGTTCTCTA
110	TNF	Ambion_Plate 2	N6	TNF	7124	siRNA1	s14247	AGGCGGUGCUUGUUCCUCAtt	UGAGGAACAAGCACCGCCUgg	
110	TNF	Ambion_Plate 2	F15	TNF	7124	siRNA2	s14248	GACCUCACCUAGAAAUUGAtt	UCAAUUUCUAGGUGAGGUCtt	
110	TNF	Ambion_Plate 2	J20	TNF	7124	siRNA3	s14249	GCGUGGAGCUGAGAGAUAAtt	UUAUCUCUCAGCUCCACGCca	
110	TNF	Qiagen_Plate 2	N6	TNF	7124	siRNA4	SI03066399			CAGCCGCATCGCCGTCTCCTA
110	TNF	Qiagen_Plate 2	F15	TNF	7124	siRNA5	SI00012453			TAGGGTCGGAACCCAAGCTTA
110	TNF	Qiagen_Plate 2	J20	TNF	7124	siRNA6	SI00012446			CCGACTCAGCGCTGAGATCAA
111	CCL3	Ambion_Plate 2	C7	CCL3	6348	siRNA1	s12568	CUGCAUCACUUGCUGCUGAtt	UCAGCAGCAAGUGAUGCAGag	
111	CCL3	Ambion_Plate 2	G15	CCL3	6348	siRNA2	s12569	CCACAGCUACCUCUUCUAUtt	AUAGAAGAGGUAGCUGUGGag	
111	CCL3	Ambion_Plate 2	K20	CCL3	6348	siRNA3	s12570	GGACUCUUCUUAACUUAAAtt	UUUAAGUUAAGAAGAGUCCca	
111	CCL3	Qiagen_Plate 2	C7	CCL3	6348	siRNA4	SI03107111			GTGGGACTCTTCTTAACTTAA
111	CCL3	Qiagen_Plate 2	G15	CCL3	6348	siRNA5	SI03078439			CCCGGCAGATTCCACAGAATT
111	CCL3	Qiagen_Plate 2	K20	CCL3	6348	siRNA6	SI03073028			CAGTGAGGAGTGGGTCCAGAA
112	CXCL11	Ambion_Plate 2	D7	CXCL11	6373	siRNA1	s12620	AAGUGAUUAUUACCCUGAAtt	UUCAGGGUAAUAAUCACUUct	
112	CXCL11	Ambion_Plate 2	H15	CXCL11	6373	siRNA2	s12621	GCCUAAAUCCCAAAUCGAAtt	UUCGAUUUGGGAUUUAGGCat	
112	CXCL11	Ambion_Plate 2	L20	CXCL11	6373	siRNA3	s12622	GUACCCAAGUAACAACUGUtt	ACAGUUGUUACUUGGGUACat	
112	CXCL11	Qiagen_Plate 2	D7	CXCL11	6373	siRNA4	SI03050047			ATGCCTAAATCCCAAATCGAA
112	CXCL11	Qiagen_Plate 2	H15	CXCL11	6373	siRNA5	SI03033317			AAGCCTCCATAATGTACCCAA
112	CXCL11	Qiagen_Plate 2	L20	CXCL11	6373	siRNA6	SI00076720			AAGACTAGTTTAAAGAATCAA
113	CXCL9	Ambion_Plate 2	E7	CXCL9	4283	siRNA1	s8781	AAAUCAUUGCUACACUGAAtt	UUCAGUGUAGCAAUGAUUUca	
113	CXCL9	Ambion_Plate 2	I15	CXCL9	4283	siRNA2	s8782	CCAAGGGACUAUCCACCUAtt	UAGGUGGAUAGUCCCUUGGtt	
113	CXCL9	Ambion_Plate 2	M20	CXCL9	4283	siRNA3	s8783	GAAAGACCUUAAACAAUUUtt	AAAUUGUUUAAGGUCUUUCaa	
113	CXCL9	Qiagen_Plate 2	E7	CXCL9	4283	siRNA4	SI03054618			CAAGGGACTATCCACCTACAA
113	CXCL9	Qiagen_Plate 2	I15	CXCL9	4283	siRNA5	SI00037387			CCACCCGAACGTCTTATCTAA
113	CXCL9	Qiagen_Plate 2	M20	CXCL9	4283	siRNA6	SI00037380			CCGGTGGAGATCCCACCCGAA
114	RP105	Ambion_Plate 2	F7	CD180	4064	siRNA1	s8347	GCCUACAAUUCACAAUAGAtt	UCUAUUGUGAAUUGUAGGCaa	
114	RP105	Ambion_Plate 2	J15	CD180	4064	siRNA2	s8348	GUGUAAAUCAUUUCGAUCAtt	UGAUCGAAAUGAUUUACACtg	
114	RP105	Ambion_Plate 2	N20	CD180	4064	siRNA3	s8349	GGAUACAUGAAGACACUUUtt	AAAGUGUCUUCAUGUAUCCag	
114	RP105	Qiagen_Plate 2	F7	CD180	4064	siRNA4	SI04750340			CTGCTGCAGTCTGCAACTCAA
114	RP105	Qiagen_Plate 2	J15	CD180	4064	siRNA5	SI04383008			CTGGAGCAGGCCATCAACCTA
114	RP105	Qiagen_Plate 2	N20	CD180	4064	siRNA6	SI02635514			AAGCCTGAACTTCAATGGCAA
115	MD1	Ambion_Plate 2	G7	LY86	9450	siRNA1	s18098	CAAUAAUCCUGAAUUUACUtt	AGUAAAUUCAGGAUUAUUGac	
115	MD1	Ambion_Plate 2	K15	LY86	9450	siRNA2	s18099	GGAAAGGAGAGCAGAUUUAtt	UAAAUCUGCUCUCCUUUCCtt	
115	MD1	Ambion_Plate 2	C21	LY86	9450	siRNA3	s18100	CCAGAGUUGCGAUCCAUUAtt	UAAUGGAUCGCAACUCUGGta	
115	MD1	Qiagen_Plate 2	G7	LY86	9450	siRNA4	SI04353769			CTGACTGTGGCCTGTAGCAAA
115	MD1	Qiagen_Plate 2	K15	LY86	9450	siRNA5	SI04287899			AAAGTGTTCCAAGCAATTAAA
115	MD1	Qiagen_Plate 2	C21	LY86	9450	siRNA6	SI04281781			CAGCGGCTTGGAAGTGCTCTA
116	TIR8	Ambion_Plate 2	H7	SIGIRR	59307	siRNA1	s33985	UCAUCGUGGUGCUUUCGGAtt	UCCGAAAGCACCACGAUGAgg	
116	TIR8	Ambion_Plate 2	L15	SIGIRR	59307	siRNA2	s195333	GGAUGAUAUGUAGCUCCCAtt	UGGGAGCUACAUAUCAUCCtt	
116	TIR8	Ambion_Plate 2	D21	SIGIRR	59307	siRNA3	s195334	GCUGAUUCUUCGAGGCCGAtt	UCGGCCUCGAAGAAUCAGCat	
116	TIR8	Qiagen_Plate 2	H7	SIGIRR	59307	siRNA4	SI03204600			CTCGGATCTCGGCTCGCGAAA
116	TIR8	Qiagen_Plate 2	L15	SIGIRR	59307	siRNA5	SI03152828			ATGCTGATTCTTCGAGGCCGA
116	TIR8	Qiagen_Plate 2	D21	SIGIRR	59307	siRNA6	SI00718788			CTCCGCCGACCTCTTGGTGAA
117	ST2	Ambion_Plate 2	I7	IL1RL1	9173	siRNA1	s17530	CCGUAAGACUAAGUAGGAAtt	UUCCUACUUAGUCUUACGGtg	
117	ST2	Ambion_Plate 2	M15	IL1RL1	9173	siRNA2	s17531	GGUAUUACUCACAAACAAAtt	UUUGUUUGUGAGUAAUACCaa	
117	ST2	Ambion_Plate 2	E21	IL1RL1	9173	siRNA3	s17532	GUUACACCGUGGAUUGGUAtt	UACCAAUCCACGGUGUAACta	
117	ST2	Qiagen_Plate 2	I7	IL1RL1	9173	siRNA4	SI03046757			ATCAAGGTACAGGGCGCACAA
117	ST2	Qiagen_Plate 2	M15	IL1RL1	9173	siRNA5	SI00114618			TGGATTGGTATTACTCACAAA
117	ST2	Qiagen_Plate 2	E21	IL1RL1	9173	siRNA6	SI00114611			CAGACTTTGGTGAACCAAGAA

TABLE S1 (HUMAN siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
118	IRAK3	Ambion_Plate 2	J7	IRAK3	11213	siRNA1	s22133	GAGAGAUUUUUGAGGUAUAtt	UAUACCUCAAAAAUCUCUCct	
118	IRAK3	Ambion_Plate 2	N15	IRAK3	11213	siRNA2	s22134	GUAGAGUAGUGUUAGAUGAtt	UCAUCUAACACUACUCUACat	
118	IRAK3	Ambion_Plate 2	F21	IRAK3	11213	siRNA3	s22135	GGAUGUUCGUCAUAUUGAAtt	UUCAAUAUGACGAACAUCCag	
118	IRAK3	Qiagen_Plate 2	J7	IRAK3	11213	siRNA4	SI02224278			CACATTCGAATCGGTATATTA
118	IRAK3	Qiagen_Plate 2	N15	IRAK3	11213	siRNA5	SI04952724			TGGGTGTATTAATAAGCGTTA
118	IRAK3	Qiagen_Plate 2	F21	IRAK3	11213	siRNA6	SI04438875			CTGCGGGATCTCCTTAGAGAA
119	SHP1	Ambion_Plate 2	K7	PTPN6	5777	siRNA1	s662	CCCAUAUUCGGAUCCAGAAtt	UUCUGGAUCCGAAUAUGGGtc	
119	SHP1	Ambion_Plate 2	C16	PTPN6	5777	siRNA2	s663	GAACCGCUACAAGAACAUUtt	AAUGUUCUUGUAGCGGUUCtt	
119	SHP1	Ambion_Plate 2	G21	PTPN6	5777	siRNA3	s664	ACCUCUCCCUGACCCUGUAtt	UACAGGGUCAGGGAGAGGUgg	
119	SHP1	Qiagen_Plate 2	K7	PTPN6	5777	siRNA4	SI02658733			TAGGCCCTGATGAGAACGCTA
119	SHP1	Qiagen_Plate 2	C16	PTPN6	5777	siRNA5	SI02658726			CCGGAACAAATGCGTCCCATA
119	SHP1	Qiagen_Plate 2	G21	PTPN6	5777	siRNA6	SI04950407			CAAGGAGGATGTGTATGAGAA
120	Cyld	Ambion_Plate 2	L7	CYLD	1540	siRNA1	s590	GAAUGGUCUUUUAUCAACAtt	UGUUGAUAAAAGACCAUUCta	
120	Cyld	Ambion_Plate 2	D16	CYLD	1540	siRNA2	s591	GCUUUGUAGUUUUGCGUGUtt	ACACGCAAAACUACAAAGCtg	
120	Cyld	Ambion_Plate 2	H21	CYLD	1540	siRNA3	s592	GAUUGUUACUUCUAUCAAAtt	UUUGAUAGAAGUAACAAUCtt	
120	Cyld	Qiagen_Plate 2	L7	CYLD	1540	siRNA4	SI03056949			CACCAAGATGCCCAATACCAA
120	Cyld	Qiagen_Plate 2	D16	CYLD	1540	siRNA5	SI00110096			AAGGTTCATCCAGTCATAATA
120	Cyld	Qiagen_Plate 2	H21	CYLD	1540	siRNA6	SI00110089			AAAGAACGATGTAGAATATTA
121	A20	Ambion_Plate 2	M7	TNFAIP3	7128	siRNA1	s14259	CAAAGUUGGAUGAAGCUAAtt	UUAGCUUCAUCCAACUUUGcg	
121	A20	Ambion_Plate 2	E16	TNFAIP3	7128	siRNA2	s14260	GGAUGUUACCAGGACAUUUtt	AAAUGUCCUGGUAACAUCCtg	
121	A20	Ambion_Plate 2	I21	TNFAIP3	7128	siRNA3	s14261	CAACGGCUACUGCAACGAAtt	UUCGUUGCAGUAGCCGUUGca	
121	A20	Qiagen_Plate 2	M7	TNFAIP3	7128	siRNA4	SI02637166			CAGCCTTTACTCATACTATTA
121	A20	Qiagen_Plate 2	E16	TNFAIP3	7128	siRNA5	SI00087010			CTCGGCTATGACAGCCATCAT
121	A20	Qiagen_Plate 2	I21	TNFAIP3	7128	siRNA6	SI00087003			CAGATGTATGGCTAACCGGAA
122	DUSP2	Ambion_Plate 2	N7	DUSP2	1844	siRNA1	s4366	GUCCCGAUCUGUGCUCUGAtt	UCAGAGCACAGAUCGGGACag	
122	DUSP2	Ambion_Plate 2	F16	DUSP2	1844	siRNA2	s4367	ACUUAGCACUUUAUAUUUAtt	UAAAUAUAAAGUGCUAAGUtt	
122	DUSP2	Ambion_Plate 2	J21	DUSP2	1844	siRNA3	s4368	GGCCUUUUCCGCUACAAGAtt	UCUUGUAGCGGAAAAGGCCct	
122	DUSP2	Qiagen_Plate 2	N7	DUSP2	1844	siRNA4	SI04892692			AACATTCAGGATATGTCAATA
122	DUSP2	Qiagen_Plate 2	F16	DUSP2	1844	siRNA5	SI03083829			CGAGGCCTTTGACTTCGTTAA
122	DUSP2	Qiagen_Plate 2	J21	DUSP2	1844	siRNA6	SI03025848			TTGTGCTCAGCTGACATTTAA
123	AIP1	Ambion_Plate 2	C8	DAB2IP	153090	siRNA1	s237	CGAUCUUUCCGGUCUGAUAtt	UAUCAGACCGGAAAGAUCGtt	
123	AIP1	Ambion_Plate 2	G16	DAB2IP	153090	siRNA2	s238	GCUGUGGACUCCAAACAGAtt	UCUGUUUGGAGUCCACAGCcg	
123	AIP1	Ambion_Plate 2	K21	DAB2IP	153090	siRNA3	s239	GAGCAUGAGUGGACCAACAtt	UGUUGGUCCACUCAUGCUCta	
123	AIP1	Qiagen_Plate 2	C8	DAB2IP	153090	siRNA4	SI00359198			CACGGTCACTGTCCACCTGTA
123	AIP1	Qiagen_Plate 2	G16	DAB2IP	153090	siRNA5	SI00359191			AACGATCTTTCCGGTCTGATA
123	AIP1	Qiagen_Plate 2	K21	DAB2IP	153090	siRNA6	SI00359184			CTCGAGTTACTCGGAAGCCAA
124	Tollip	Ambion_Plate 2	D8	TOLLIP	54472	siRNA1	s29037	GCUGUUGAUUUAAGGCACAtt	UGUGCCUUAAAUCAACAGCtc	
124	Tollip	Ambion_Plate 2	H16	TOLLIP	54472	siRNA2	s29038	GACUCUUUCUAUCUCGAGAtt	UCUCGAGAUAGAAAGAGUCca	
124	Tollip	Ambion_Plate 2	L21	TOLLIP	54472	siRNA3	s29039	GCACUGUGCAUGAUUCCGAtt	UCGGAAUCAUGCACAGUGCtg	
124	Tollip	Qiagen_Plate 2	D8	TOLLIP	54472	siRNA4	SI03091032			CTCGAGATCTTCGATGAGAGA
124	Tollip	Qiagen_Plate 2	H16	TOLLIP	54472	siRNA5	SI03081470			CCGCTGGAATAAGGTCATCCA
124	Tollip	Qiagen_Plate 2	L21	TOLLIP	54472	siRNA6	SI03061310			CACGGTGGTACAGGCAAAGTT
125	MKP1	Ambion_Plate 2	E8	DUSP1	1843	siRNA1	s4363	CCACCACCGUGUUCAACUUtt	AAGUUGAACACGGUGGUGGtg	
125	MKP1	Ambion_Plate 2	I16	DUSP1	1843	siRNA2	s4364	GGACUAAUCGAGUCAAGCUtt	AGCUUGACUCGAUUAGUCCtc	
125	MKP1	Ambion_Plate 2	M21	DUSP1	1843	siRNA3	s4365	AGGCCUUUGAGUUUGUGAAtt	UUCACAAACUCAAAGGCCUcg	
125	MKP1	Qiagen_Plate 2	E8	DUSP1	1843	siRNA4	SI03100048			CTGGTTCAACGAGGCCATTGA
125	MKP1	Qiagen_Plate 2	I16	DUSP1	1843	siRNA5	SI00374822			CAGTTGTATGTTTGCTGATTA
125	MKP1	Qiagen_Plate 2	M21	DUSP1	1843	siRNA6	SI00374815			CACGAACAGTGCGCTGAGCTA
126	RIP3	Ambion_Plate 2	F8	RIPK3	11035	siRNA1	s21740	GGCAAGUCUGGAUAACGAAtt	UUCGUUAUCCAGACUUGCCat	
126	RIP3	Ambion_Plate 2	J16	RIPK3	11035	siRNA2	s21741	GAACUGUUUGUUAACGUAAtt	UUACGUUAACAAACAGUUCtg	
126	RIP3	Ambion_Plate 2	N21	RIPK3	11035	siRNA3	s21742	GGAGAACCAUAGAAAACCAtt	UGGUUUUCUAUGGUUCUCCta	
126	RIP3	Qiagen_Plate 2	F8	RIPK3	11035	siRNA4	SI00092813			ATGGCAAGTCTGGATAACGAA
126	RIP3	Qiagen_Plate 2	J16	RIPK3	11035	siRNA5	SI00092806			CAGCCTGATGTCGTGCGTCAA
126	RIP3	Qiagen_Plate 2	N21	RIPK3	11035	siRNA6	SI00092799			CACAGGGTTGGTATAATCATA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
1	TLR1	Ambion_Plate 1	C3	Tlr1	21897	siRNA1	84606	GGAAUGUGAGCUUAUCAUAtt	UAUGAUAAGCUCACAUUCCtc	
1	TLR1	Ambion_Plate 1	G8	Tlr1	21897	siRNA2	188923	GGGUCCUGAUAAUGUCCUAtt	UAGGACAUUAUCAGGACCCtc	
1	TLR1	Ambion_Plate 1	K16	Tlr1	21897	siRNA3	188924	CCUUUUAACAGACAUGGUUtt	AACCAUGUCUGUUAAAAGGtt	
1	TLR1	Qiagen_Plate 1	C3	Tlr1	21897	siRNA4	SI02744966			AACGTGTTACACACAGCAATA
1	TLR1	Qiagen_Plate 1	G8	Tlr1	21897	siRNA5	SI02719829			CAGGGCTGCTCTTATTTCTTA
1	TLR1	Qiagen_Plate 1	K16	Tlr1	21897	siRNA6	SI02696463			AAGGCTTTGTCGATACATCAA
2	TLR2	Ambion_Plate 1	D3	Tlr2	24088	siRNA1	70425	GGAGUCUCUGUCAUGUGAUtt	AUCACAUGACAGAGACUCCtg	
2	TLR2	Ambion_Plate 1	H8	Tlr2	24088	siRNA2	70614	GGAUAUUAACUAUGGGUUUtt	AAACCCAUAGUUAAUAUCCtc	
2	TLR2	Ambion_Plate 1	L16	Tlr2	24088	siRNA3	187990	GCCUUGACCUGUCUUUCAAtt	UUGAAAGACAGGUCAAGGCtt	
2	TLR2	Qiagen_Plate 1	D3	Tlr2	24088	siRNA4	SI00204330			CTCGTTCTCCCAGCATTTAAA
2	TLR2	Qiagen_Plate 1	H8	Tlr2	24088	siRNA5	SI00204323			CCCAATCTCACAAATTTACAA
2	TLR2	Qiagen_Plate 1	L16	Tlr2	24088	siRNA6	SI00204316			AAGCCTTGACCTGTCTTTCAA
3	TLR3	Ambion_Plate 1	E3	Tlr3	142980	siRNA1	86292	GGAUUUAACUCCAUUUCAAtt	UUGAAAUGGAGUUAAAUCCtg	
3	TLR3	Ambion_Plate 1	I8	Tlr3	142980	siRNA2	172524	CCUACCAACUUUACAAGAUtt	AUCUUGUAAAGUUGGUAGGtg	
3	TLR3	Ambion_Plate 1	M16	Tlr3	142980	siRNA3	172526	CCAUUCAUUUUUGAUGACCtt	GGUCAUCAAAAAUGAAUGGtt	
3	TLR3	Qiagen_Plate 1	E3	Tlr3	142980	siRNA4	SI00231931			CTCGGAATTCAGCACATTAAA
3	TLR3	Qiagen_Plate 1	I8	Tlr3	142980	siRNA5	SI00231924			AAGGGTGTTCCTCTTATCTAA
3	TLR3	Qiagen_Plate 1	M16	Tlr3	142980	siRNA6	SI00231917			CAAGAACTTATTCGAACTAAA
4	TLR4	Ambion_Plate 1	F3	Tlr4	21898	siRNA1	75594	GGCCCAUAUUUGACUAUAAtt	UUAUAGUCAAAUAUGGGCCtt	
4	TLR4	Ambion_Plate 1	J8	Tlr4	21898	siRNA2	188776	GGUAGUUCCUAAUAUUACCtt	GGUAAUAUUAGGAACUACCtc	
4	TLR4	Ambion_Plate 1	N16	Tlr4	21898	siRNA3	188777	GCAUCUAUGAUGCAUUUGUtt	ACAAAUGCAUCAUAGAUGCtt	
4	TLR4	Qiagen_Plate 1	F3	Tlr4	21898	siRNA4	SI02742453			ATCCAGAATCTTTACCTTTAA
4	TLR4	Qiagen_Plate 1	J8	Tlr4	21898	siRNA5	SI02717589			CTGAATGTCATTCTTAAGTTA
4	TLR4	Qiagen_Plate 1	N16	Tlr4	21898	siRNA6	SI01449560			CTGGATCTTTCTAAATGTCAA
5	TLR5	Ambion_Plate 1	G3	Tlr5	53791	siRNA1	73023	GGGCAAAACACUGUCUUUCtt	GAAAGACAGUGUUUUGCCCtg	
5	TLR5	Ambion_Plate 1	K8	Tlr5	53791	siRNA2	184717	GCGACGUAAAUUUUGCUUUtt	AAAGCAAAAUUUACGUCGCtt	
5	TLR5	Ambion_Plate 1	C17	Tlr5	53791	siRNA3	184718	CGGUUACUUCAGAAAUCUAtt	UAGAUUUCUGAAGUAACCGtc	
5	TLR5	Qiagen_Plate 1	G3	Tlr5	53791	siRNA4	SI02741032			TGCCTTCAACAAGATAAACAA
5	TLR5	Qiagen_Plate 1	K8	Tlr5	53791	siRNA5	SI02693502			GACGGTTACTTCAGAAATCTA
5	TLR5	Qiagen_Plate 1	C17	Tlr5	53791	siRNA6	SI02673153			ACCAAACATTCAGATTATTAA
6	TLR6	Ambion_Plate 1	H3	Tlr6	21899	siRNA1	69628	GGAACCUUACUCAUGUCCCtt	GGGACAUGAGUAAGGUUCCtg	
6	TLR6	Ambion_Plate 1	L8	Tlr6	21899	siRNA2	69814	GGAAUGGUUUGAAGAACUUtt	AAGUUCUUCAAACCAUUCCtt	
6	TLR6	Ambion_Plate 1	D17	Tlr6	21899	siRNA3	187345	GGUCCAACCUUAUUGAAUGtt	CAUUCAAUAAGGUUGGACCtc	
6	TLR6	Qiagen_Plate 1	H3	Tlr6	21899	siRNA4	SI02714383			CTCGGTGTTTGCTGAGATGAA
6	TLR6	Qiagen_Plate 1	L8	Tlr6	21899	siRNA5	SI02691787			TTGGGTTTCTAACTTAATAAA
6	TLR6	Qiagen_Plate 1	D17	Tlr6	21899	siRNA6	SI02671599			TACCTCAATATTTACAACTTA
7	TLR7	Ambion_Plate 1	I3	Tlr7	170743	siRNA1	86644	GGCUAACAACAUCUUCUCCtt	GGAGAAGAUGUUGUUAGCCtc	
7	TLR7	Ambion_Plate 1	M8	Tlr7	170743	siRNA2	86736	GGAAUUACUCACAUGCUAAtt	UUAGCAUGUGAGUAAUUCCtt	
7	TLR7	Ambion_Plate 1	E17	Tlr7	170743	siRNA3	172656	CCUCAACAUAUUCAAACAUtt	AUGUUUGAAUAUGUUGAGGtc	
7	TLR7	Qiagen_Plate 1	I3	Tlr7	170743	siRNA4	SI02720487			TACCATGCATCTATAACTTTA
7	TLR7	Qiagen_Plate 1	M8	Tlr7	170743	siRNA5	SI02697023			ACCAGAGTTCAATGAAATAAA
7	TLR7	Qiagen_Plate 1	E17	Tlr7	170743	siRNA6	SI02676380			CTGATTCTTAAGCATAATCAA
8	TLR8	Ambion_Plate 1	J3	Tlr8	170744	siRNA1	86550	GGCACAACUCCCUUGUGAUtt	AUCACAAGGGAGUUGUGCCtt	
8	TLR8	Ambion_Plate 1	N8	Tlr8	170744	siRNA2	86737	GGUACUCUCAUUAUCUUUCtt	GAAAGAUAAUGAGAGUACCtt	
8	TLR8	Ambion_Plate 1	F17	Tlr8	170744	siRNA3	172658	GCCAAUUUGAAGGUUUUCAtt	UGAAAACCUUCAAAUUGGCtt	
8	TLR8	Qiagen_Plate 1	J3	Tlr8	170744	siRNA4	SI01449588			ACGCCTGGACTTATCATACAA
8	TLR8	Qiagen_Plate 1	N8	Tlr8	170744	siRNA5	SI01449581			AACCATCAACTTGGGCATTAA
8	TLR8	Qiagen_Plate 1	F17	Tlr8	170744	siRNA6	SI01449574			TAGGATTTATCCAGAACTTAA
9	TLR9	Ambion_Plate 1	K3	Tlr9	81897	siRNA1	84869	GGAGCUGAACCUGAGCUAUtt	AUAGCUCAGGUUCAGCUCCtc	
9	TLR9	Ambion_Plate 1	C9	Tlr9	81897	siRNA2	84965	GGACAGCUCUCUCCAUACAtt	UGUAUGGAGAGAGCUGUCCtt	
9	TLR9	Ambion_Plate 1	G17	Tlr9	81897	siRNA3	85055	GGUGUAAGAACUUCAAGUUtt	AACUUGAAGUUCUUACACCtg	
9	TLR9	Qiagen_Plate 1	K3	Tlr9	81897	siRNA4	SI01449616			CTGGCACACAATGACATTCAT
9	TLR9	Qiagen_Plate 1	C9	Tlr9	81897	siRNA5	SI01449609			AGCGAGAACTTTCTCTATGAA
9	TLR9	Qiagen_Plate 1	G17	Tlr9	81897	siRNA6	SI01449602			CAAGCTCAACCTGTCCTTCAA
10	LBP	Ambion_Plate 1	L3	Lbp	16803	siRNA1	62784	GGUGUCACCAUUUCAGUGGtt	CCACUGAAAUGGUGACACCtt	
10	LBP	Ambion_Plate 1	D9	Lbp	16803	siRNA2	62867	GGGUGAAAUUUUUAAUCGGtt	CCGAUUAAAAAUUUCACCCtt	
10	LBP	Ambion_Plate 1	H17	Lbp	16803	siRNA3	155124	GGCAUUCCUUAACUACUACtt	GUAGUAGUUAAGGAAUGCCtg	
10	LBP	Qiagen_Plate 1	L3	Lbp	16803	siRNA4	SI04449228			CAGCCTCTACCCTGATGTCAA
10	LBP	Qiagen_Plate 1	D9	Lbp	16803	siRNA5	SI04405772			CCGGCTTGGCGTGGTCACTAA
10	LBP	Qiagen_Plate 1	H17	Lbp	16803	siRNA6	SI02687482			CCAGAAAGTACTGGAGAATAA
11	MD2	Ambion_Plate 1	M3	Ly96	17087	siRNA1	72828	GGAGAGACUGUGAAUACAUtt	AUGUAUUCACAGUCUCUCCtt	
11	MD2	Ambion_Plate 1	E9	Ly96	17087	siRNA2	156956	GCGUAAGGAAGUUCUGUGCtt	GCACAGAACUUCCUUACGCtt	
11	MD2	Ambion_Plate 1	I17	Ly96	17087	siRNA3	156957	GGGCCAUUACAGAUGUGUUtt	AACACAUCUGUAAUGGCCCtt	
11	MD2	Qiagen_Plate 1	M3	Ly96	17087	siRNA4	SI01297604			TCCCATATTGACTGAATCTGA
11	MD2	Qiagen_Plate 1	E9	Ly96	17087	siRNA5	SI01297597			CGAGGGAATACTATTTCCTAA
11	MD2	Qiagen_Plate 1	I17	Ly96	17087	siRNA6	SI01297590			CCGCCGTGATGTCAATTAGAA
12	CD14	Ambion_Plate 1	N3	Cd14	12475	siRNA1	66006	GGAACUGACUCUUGAAAAUtt	AUUUUCAAGAGUCAGUUCCtg	
12	CD14	Ambion_Plate 1	F9	Cd14	12475	siRNA2	161078	GCUAAACUCGCUCAAUCUGtt	CAGAUUGAGCGAGUUUAGCtg	
12	CD14	Ambion_Plate 1	J17	Cd14	12475	siRNA3	161079	CGAUGUAAGGAAAGAAAGGtt	CCUUUCUUUCCUUACAUCGtg	
12	CD14	Qiagen_Plate 1	N3	Cd14	12475	siRNA4	SI00944552			CTCTGCTTTAAATTTATTAAA
12	CD14	Qiagen_Plate 1	F9	Cd14	12475	siRNA5	SI00944545			AAGGTACTGAGTATTGCCCAA
12	CD14	Qiagen_Plate 1	J17	Cd14	12475	siRNA6	SI00944538			CTCCAGGAACTGACTCTTGAA
13	CD11b	Ambion_Plate 1	C4	Itgam	16409	siRNA1	62429	GGCUUUGGACAGAAUGUGGtt	CCACAUUCUGUCCAAAGCCtt	
13	CD11b	Ambion_Plate 1	G9	Itgam	16409	siRNA2	62614	GGAUAAAGUCACCUUCAUCtt	GAUGAAGGUGACUUUAUCCtt	
13	CD11b	Ambion_Plate 1	K17	Itgam	16409	siRNA3	154928	GGUCACAUUUAAUGUCACAtt	UGUGACAUUAAAUGUGACCtc	
13	CD11b	Qiagen_Plate 1	C4	Itgam	16409	siRNA4	SI02733304			AAGGAGAATACTTATGTGAAT
13	CD11b	Qiagen_Plate 1	G9	Itgam	16409	siRNA5	SI02687300			CACATTTAATGTCACATTTGA
13	CD11b	Qiagen_Plate 1	K17	Itgam	16409	siRNA6	SI02667630			CAGAGTGGATTCAGACATGAA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
14	CD11c	Ambion_Plate 1	D4	Itgax	16411	siRNA1	75628	GGCCUUUUACAAUGAACAUtt	AUGUUCAUUGUAAAAGGCCtt	
14	CD11c	Ambion_Plate 1	H9	Itgax	16411	siRNA2	157064	GCUGACACAUUUUCACAUGtt	CAUGUGAAAAUGUGUCAGCtt	
14	CD11c	Ambion_Plate 1	L17	Itgax	16411	siRNA3	157066	GCAUCAUUCGUUAUGCAAUtt	AUUGCAUAACGAAUGAUGCtt	
14	CD11c	Qiagen_Plate 1	D4	Itgax	16411	siRNA4	SI02742502			TACAATGAACATTCCAAGCAA
14	CD11c	Qiagen_Plate 1	H9	Itgax	16411	siRNA5	SI02717610			CAGAGTGGGAAGTGAGAATAA
14	CD11c	Qiagen_Plate 1	L17	Itgax	16411	siRNA6	SI02694622			ATCCTCATTTCTAATAAAGTA
15	ARF6	Ambion_Plate 1	E4	Arf6	11845	siRNA1	60284	GGAGAGAAAUCCAAAACCCtt	GGGUUUUGGAUUUCUCUCCtt	
15	ARF6	Ambion_Plate 1	I9	Arf6	11845	siRNA2	60378	GGUUCUUAUCACUUGCUGUtt	ACAGCAAGUGAUAAGAACCtg	
15	ARF6	Ambion_Plate 1	M17	Arf6	11845	siRNA3	159719	CCCAUUCCUAGGAUUAUCGtt	CGAUAAUCCUAGGAAUGGGtt	
15	ARF6	Qiagen_Plate 1	E4	Arf6	11845	siRNA4	SI02731554			AACGATCCTGTACAAGTTGAA
15	ARF6	Qiagen_Plate 1	I9	Arf6	11845	siRNA5	SI00166600			ATGGTTAACCTCTAACTACAA
15	ARF6	Qiagen_Plate 1	M17	Arf6	11845	siRNA6	SI00166593			CAAGTCTGTTTCATCTAGTAA
16	MyD88	Ambion_Plate 1	F4	Myd88	17874	siRNA1	68300	GGAGGACUGCCAGAAAUACtt	GUAUUUCUGGCAGUCCUCCtc	
16	MyD88	Ambion_Plate 1	J9	Myd88	17874	siRNA2	68394	GGUUUGCAUCUUCUUAUUCtt	GAAUAAGAAGAUGCAAACCtc	
16	MyD88	Ambion_Plate 1	N17	Myd88	17874	siRNA3	156409	GCGACUGAUUCCUAUUAAAtt	UUUAAUAGGAAUCAGUCGCtt	
16	MyD88	Qiagen_Plate 1	F4	Myd88	17874	siRNA4	SI02713277			AAGCAGTGTCCCACAAACAAA
16	MyD88	Qiagen_Plate 1	J9	Myd88	17874	siRNA5	SI00196196			CCGCCTATCGCTGTTCTTGAA
16	MyD88	Qiagen_Plate 1	N17	Myd88	17874	siRNA6	SI00196182			AGGGCTCGTGTTTGTACTTAA
17	Mal	Ambion_Plate 1	G4	Tirap	117149	siRNA1	172379	CGGAGGCUUUUACCAAGUCtt	GACUUGGUAAAAGCCUCCGtc	
17	Mal	Ambion_Plate 1	K9	Tirap	117149	siRNA2	172380	GGCUGUUAUACACUAUCUGtt	CAGAUAGUGUAUAACAGCCtc	
17	Mal	Ambion_Plate 1	C18	Tirap	117149	siRNA3	172381	CCUUAUCUAUAACUCUGCUtt	AGCAGAGUUAUAGAUAAGGtt	
17	Mal	Qiagen_Plate 1	G4	Tirap	117149	siRNA4	SI05459300			ACAGCAGTCATTAATCCAGTA
17	Mal	Qiagen_Plate 1	K9	Tirap	117149	siRNA5	SI05459293			CAAGTCAAGGAGGCTGTTATA
17	Mal	Qiagen_Plate 1	C18	Tirap	117149	siRNA6	SI01448965			CAGGCAGGCTCTGTTGAAGAA
18	IRAK1	Ambion_Plate 1	H4	Irak1	16179	siRNA1	62585	GGAAUUGGGUAGUACAAAAtt	UUUUGUACUACCCAAUUCCtt	
18	IRAK1	Ambion_Plate 1	L9	Irak1	16179	siRNA2	240525	GCAGUCAUGAGAAAUACUAtt	UAGUAUUUCUCAUGACUGCtc	
18	IRAK1	Ambion_Plate 1	D18	Irak1	16179	siRNA3	240526	GGAGAACUCCUACAUGUCUtt	AGACAUGUAGGAGUUCUCCtg	
18	IRAK1	Qiagen_Plate 1	H4	Irak1	16179	siRNA4	SI01077496			ACCGAGCAGTCATGAGAAATA
18	IRAK1	Qiagen_Plate 1	L9	Irak1	16179	siRNA5	SI01077489			CAGAGGTGGAACAGCTATCAA
18	IRAK1	Qiagen_Plate 1	D18	Irak1	16179	siRNA6	SI01077482			CAGGGAGGCACTACCAGAGAA
19	IRAK2	Ambion_Plate 1	I4	Irak2	108960	siRNA1	93641	GGAUGAACAGGAGAAAGUCtt	GACUUUCUCCUGUUCAUCCtt	
19	IRAK2	Ambion_Plate 1	M9	Irak2	108960	siRNA2	93735	GGUUGUGUGUUAUUUAUAGtt	CUAUAAAUAACACACAACCtc	
19	IRAK2	Ambion_Plate 1	E18	Irak2	108960	siRNA3	173516	CCGGUAUUUAGGAACUGCCtt	GGCAGUUCCUAAAUACCGGtg	
19	IRAK2	Qiagen_Plate 1	I4	Irak2	108960	siRNA4	SI01077552			CAGAGGTTGTGTGTTATTTAT
19	IRAK2	Qiagen_Plate 1	M9	Irak2	108960	siRNA5	SI01077545			CCCAGTCTAAGTATTGCAGTA
19	IRAK2	Qiagen_Plate 1	E18	Irak2	108960	siRNA6	SI01077538			CTCAGTATCCTTGTAAGATAA
20	IRAK4	Ambion_Plate 1	J4	Irak4	266632	siRNA1	84197	GGAGAUUCGAAGCCUUACUtt	AGUAAGGCUUCGAAUCUCCtt	
20	IRAK4	Ambion_Plate 1	N9	Irak4	266632	siRNA2	84288	GGUUUCUGCAUGAAAAUCAtt	UGAUUUUCAUGCAGAAACCtg	
20	IRAK4	Ambion_Plate 1	F18	Irak4	266632	siRNA3	152515	CCAAACUAUAGUGAACUUAtt	UAAGUUCACUAUAGUUUGGtg	
20	IRAK4	Qiagen_Plate 1	J4	Irak4	266632	siRNA4	SI01077608			CACCGCTTTCCTGGCACACAA
20	IRAK4	Qiagen_Plate 1	N9	Irak4	266632	siRNA5	SI01077601			CAGCAACATCACCAAACTATA
20	IRAK4	Qiagen_Plate 1	F18	Irak4	266632	siRNA6	SI01077594			CAGTTTGATCAAGAAATTAAA
21	Pellino	Ambion_Plate 1	K4	Peli1	67245	siRNA1	76839	GGAAGGAGGAAAAGUAGGUtt	ACCUACUUUUCCUCCUUCCtc	
21	Pellino	Ambion_Plate 1	C10	Peli1	67245	siRNA2	76934	GGAGGAAAAGUAGGUUUGCtt	GCAAACCUACUUUUCCUCCtt	
21	Pellino	Ambion_Plate 1	G18	Peli1	67245	siRNA3	77024	GGGUUUGAUUCAUCAAAAAtt	UUUUUGAUGAAUCAAACCCtg	
21	Pellino	Qiagen_Plate 1	K4	Peli1	67245	siRNA4	SI01374912			AGGAAGGATGTTGTAGATGAA
21	Pellino	Qiagen_Plate 1	C10	Peli1	67245	siRNA5	SI01374905			CTGCAGGGTTTGATTCATCAA
21	Pellino	Qiagen_Plate 1	G18	Peli1	67245	siRNA6	SI01374898			AACCTGGAATATGGAGAGAAA
22	Uev1a	Ambion_Plate 1	L4	Ube2v1	66589	siRNA1	164855	GCAGUUCGAAUGGAGUGGUtt	ACCACUCCAUUCGAACUGCtc	
22	Uev1a	Ambion_Plate 1	D10	Ube2v1	66589	siRNA2	164856	GCAAUUAGUCACCAAGGCCtt	GGCCUUGGUGACUAAUUGCtg	
22	Uev1a	Ambion_Plate 1	H18	Ube2v1	66589	siRNA3	164857	GGUGUUGAAAUCGGUUUCCtt	GGAAACCGAUUUCAACACCtt	
22	Uev1a	Qiagen_Plate 1	L4	Ube2v1	66589	siRNA4	SI01460816			CACTCTGTTCAGGACCACTAA
22	Uev1a	Qiagen_Plate 1	D10	Ube2v1	66589	siRNA5	SI01460809			TCGTCCGAGTCTACTATAATA
22	Uev1a	Qiagen_Plate 1	H18	Ube2v1	66589	siRNA6	SI01460802			AAGCAGCAGCTATGAGGTCTA
23	Ubc13	Ambion_Plate 1	M4	Ube2n	93765	siRNA1	86252	GGGAGGGACUUUUAAACUUtt	AAGUUUAAAAGUCCCUCCCtc	
23	Ubc13	Ambion_Plate 1	E10	Ube2n	93765	siRNA2	86348	GGGACUUUUAAACUUGAACtt	GUUCAAGUUUAAAAGUCCCtc	
23	Ubc13	Ambion_Plate 1	I18	Ube2n	93765	siRNA3	175627	GCACCUAAAGUACGUUUCAtt	UGAAACGUACUUUAGGUGCtg	
23	Ubc13	Qiagen_Plate 1	M4	Ube2n	93765	siRNA4	SI02745624			TTGGTTTGTGCTATTAGGAAA
23	Ubc13	Qiagen_Plate 1	E10	Ube2n	93765	siRNA5	SI02720382			ATGGATTTCTTCATAACTTAA
23	Ubc13	Qiagen_Plate 1	I18	Ube2n	93765	siRNA6	SI02696974			CAGGAATGTACTTGTAAGATA
24	TRAF6	Ambion_Plate 1	N4	Traf6	22034	siRNA1	64942	GGGCUACGAUGUGGAGUUUtt	AAACUCCACAUCGUAGCCCtg	
24	TRAF6	Ambion_Plate 1	F10	Traf6	22034	siRNA2	186840	GCAAGUAUGAGUGUCCCAUtt	AUGGGACACUCAUACUUGCtc	
24	TRAF6	Ambion_Plate 1	J18	Traf6	22034	siRNA3	186841	GCGAGAGAUUCUUUCCCUGtt	CAGGGAAAGAAUCUCUCGCtt	
24	TRAF6	Qiagen_Plate 1	N4	Traf6	22034	siRNA4	SI00184884			CTGAGTGTTACTGCCATGGAA
24	TRAF6	Qiagen_Plate 1	F10	Traf6	22034	siRNA5	SI00184877			AACGAGTGATTTAGCTCACTA
24	TRAF6	Qiagen_Plate 1	J18	Traf6	22034	siRNA6	SI00184870			TAGCTTATAAGGTTAATTGAA
25	TRAF3	Ambion_Plate 1	C5	Traf3	22031	siRNA1	69745	GGCUACAAGGAGAAGUUUGtt	CAAACUUCUCCUUGUAGCCtc	
25	TRAF3	Ambion_Plate 1	G10	Traf3	22031	siRNA2	187406	GCACCUGUAGUUUUAAGCGtt	CGCUUAAAACUACAGGUGCtg	
25	TRAF3	Ambion_Plate 1	K18	Traf3	22031	siRNA3	187408	GGUUAUUUUGGCUAUAAGAtt	UCUUAUAGCCAAAAUAACCtg	
25	TRAF3	Qiagen_Plate 1	C5	Traf3	22031	siRNA4	SI01454572			AACTTTGGAGTTCTAAACAAA
25	TRAF3	Qiagen_Plate 1	G10	Traf3	22031	siRNA5	SI01454565			CAGCGGGTAATCGACAGCCAA
25	TRAF3	Qiagen_Plate 1	K18	Traf3	22031	siRNA6	SI01454558			AAGGTTTCATTTGGTATTTAT
26	TAK1	Ambion_Plate 1	D5	Map3k7	26409	siRNA1	94455	GUGUUCGAACAACAUUGUAtt	UACAAUGUUGUUCGAACACtg	
26	TAK1	Ambion_Plate 1	H10	Map3k7	26409	siRNA2	94549	GCAUCGUCUGUGAAAUAUGtt	CAUAUUUCACAGACGAUGCtc	
26	TAK1	Ambion_Plate 1	L18	Map3k7	26409	siRNA3	189006	GCCUUUCUACUUAUUACCAtt	UGGUAAUAAGUAGAAAGGCtt	
26	TAK1	Qiagen_Plate 1	D5	Map3k7	26409	siRNA4	SI01300152			AAGAGAATATTTATATTGTTA
26	TAK1	Qiagen_Plate 1	H10	Map3k7	26409	siRNA5	SI01300145			TAACTTAAAGGTAATAATAAA
26	TAK1	Qiagen_Plate 1	L18	Map3k7	26409	siRNA6	SI01300138			AAAGATGATGATGTAGCTTAA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
27	TAB1	Ambion_Plate 1	E5	Tab1	66513	siRNA1	183116	CCGCGUGACCAACUUUGUGtt	CACAAAGUUGGUCACGCGGtt	
27	TAB1	Ambion_Plate 1	I10	Tab1	66513	siRNA2	183117	GGUAGCUUACAAACCAUCAtt	UGAUGGUUUGUAAGCUACCtg	
27	TAB1	Ambion_Plate 1	M18	Tab1	66513	siRNA3	183118	CGUUUAAAGACUAGCAAGAtt	UCUUGCUAGUCUUUAAACGtg	
27	TAB1	Qiagen_Plate 1	E5	Tab1	66513	siRNA4	SI04923051			CAGGTAGCTTACAAACCATCA
27	TAB1	Qiagen_Plate 1	I10	Tab1	66513	siRNA5	SI04923044			GAGCGTGATGACGGCACCTTA
27	TAB1	Qiagen_Plate 1	M18	Tab1	66513	siRNA6	SI01300180			ATGCCTTAGCTGAGAAAGCAA
28	TAB2	Ambion_Plate 1	F5	Tab2	68652	siRNA1	88251	GGAGAGUACAAGGUAUCUUtt	AAGAUACCUUGUACUCUCCtg	
28	TAB2	Ambion_Plate 1	J10	Tab2	68652	siRNA2	181213	GGAGACCUGAAUUUUUCAGtt	CUGAAAAAUUCAGGUCUCCtt	
28	TAB2	Ambion_Plate 1	N18	Tab2	68652	siRNA3	181215	CCACAUCUAAAGUUCAAGAtt	UCUUGAACUUUAGAUGUGGtt	
28	TAB2	Qiagen_Plate 1	F5	Tab2	68652	siRNA4	SI01300208			CAGCCAGACCTTAAATAGAAA
28	TAB2	Qiagen_Plate 1	J10	Tab2	68652	siRNA5	SI01300201			CACAGTCATGTGTATTTATAA
28	TAB2	Qiagen_Plate 1	N18	Tab2	68652	siRNA6	SI01300194			CAGATAGAAATCAAACTTGAA
29	TAB3	Ambion_Plate 1	G5	Tab3	66724	siRNA1	78868	GGUGGUUUUGUUUCUUUUUtt	AAAAAGAAACAAAACCACCtg	
29	TAB3	Ambion_Plate 1	K10	Tab3	66724	siRNA2	78961	GGGAAAUGACAAUUGAAAGtt	CUUUCAAUUGUCAUUUCCCtt	
29	TAB3	Ambion_Plate 1	C19	Tab3	66724	siRNA3	183321	CCUGACUCUACAUUUUACAtt	UGUAAAAUGUAGAGUCAGGtc	
29	TAB3	Qiagen_Plate 1	G5	Tab3	66724	siRNA4	SI00838292			CCAGTGCATGTTACAGAATAA
29	TAB3	Qiagen_Plate 1	K10	Tab3	66724	siRNA5	SI00838285			AAGATAGAAATTACAGTTGAA
29	TAB3	Qiagen_Plate 1	C19	Tab3	66724	siRNA6	SI00838278			CAGCTGCAGATGAACATTTAA
30	NEMO	Ambion_Plate 1	H5	Ikbkg	16151	siRNA1	67420	GGACAUGCUGGGUGAAGAAtt	UUCUUCACCCAGCAUGUCCtg	
30	NEMO	Ambion_Plate 1	L10	Ikbkg	16151	siRNA2	67511	GGAGAAGGAGUUCCUUAUGtt	CAUAAGGAACUCCUUCUCCtc	
30	NEMO	Ambion_Plate 1	D19	Ikbkg	16151	siRNA3	261066	GGAUUCGAGCAGUUAGUGAtt	UCACUAACUGCUCGAAUCCtt	
30	NEMO	Qiagen_Plate 1	H5	Ikbkg	16151	siRNA4	SI01075312			CAAACAGGAATTGATTGATAA
30	NEMO	Qiagen_Plate 1	L10	Ikbkg	16151	siRNA5	SI01075305			TTGGGTCTATAACATGTGTTA
30	NEMO	Qiagen_Plate 1	D19	Ikbkg	16151	siRNA6	SI01075298			CAGGATTGAGGATATGAGGAA
31	IKKa	Ambion_Plate 1	I5	Chuk	12675	siRNA1	60754	GGAAGUCUCUGUACAUCUUtt	AAGAUGUACAGAGACUUCCtt	
31	IKKa	Ambion_Plate 1	M10	Chuk	12675	siRNA2	60850	GGAAUAAAUACAGGUUCUCtt	GAGAACCUGUAUUUAUUCCtg	
31	IKKa	Ambion_Plate 1	E19	Chuk	12675	siRNA3	60939	GGAUCAAAUUAUGUCUUUGtt	CAAAGACAUAAUUUGAUCCtc	
31	IKKa	Qiagen_Plate 1	I5	Chuk	12675	siRNA4	SI04025854			CACCGGGAACTTGATCTCAAA
31	IKKa	Qiagen_Plate 1	M10	Chuk	12675	siRNA5	SI00951328			AAGATGCCTGTTAATTTATAA
31	IKKa	Qiagen_Plate 1	E19	Chuk	12675	siRNA6	SI00951321			ATGGGTTACTTGTTTAAACAA
32	IKKb	Ambion_Plate 1	J5	Ikbkb	16150	siRNA1	159138	GGUGAACAGAUCGCCAUCAtt	UGAUGGCGAUCUGUUCACCtg	
32	IKKb	Ambion_Plate 1	N10	Ikbkb	16150	siRNA2	159139	GCGAAGUGGACAUCGUUGUtt	ACAACGAUGUCCACUUCGCtc	
32	IKKb	Ambion_Plate 1	F19	Ikbkb	16150	siRNA3	159140	GGUGCAUUCAUUAUCUUAAtt	UUAAGAUAAUGAAUGCACCtg	
32	IKKb	Qiagen_Plate 1	J5	Ikbkb	16150	siRNA4	SI05165475			CTGAAGATCGCCTGTAGCAAA
32	IKKb	Qiagen_Plate 1	N10	Ikbkb	16150	siRNA5	SI05163242			CAGGTTATCATAGGCAGGTAT
32	IKKb	Qiagen_Plate 1	F19	Ikbkb	16150	siRNA6	SI01075249			CCAGCTCTCTTAGACAGTTAA
33	IkBa	Ambion_Plate 1	K5	Nfkbia	18035	siRNA1	68242	GGACGAGGAGUACGAGCAAtt	UUGCUCGUACUCCUCGUCCtt	
33	IkBa	Ambion_Plate 1	C14	Nfkbia	18035	siRNA2	68337	GGAGUACGAGCAAAUGGUGtt	CACCAUUUGCUCGUACUCCtc	
33	IkBa	Ambion_Plate 1	G19	Nfkbia	18035	siRNA3	68428	GGAAUUGCUGAGGCACUUCtt	GAAGUGCCUCAGCAAUUCCtg	
33	IkBa	Qiagen_Plate 1	K5	Nfkbia	18035	siRNA4	SI01327060			CCCGCGGGATGGCCTCAAGAA
33	IkBa	Qiagen_Plate 1	C14	Nfkbia	18035	siRNA5	SI01327053			TCCGAGACTTTCGAGGAAATA
33	IkBa	Qiagen_Plate 1	G19	Nfkbia	18035	siRNA6	SI01327046			AAGGACGAGGAGTACGAGCAA
34	IkBb	Ambion_Plate 1	L5	Nfkbib	18036	siRNA1	156514	GCUGAAAACUAUGAUGGCCtt	GGCCAUCAUAGUUUUCAGCtt	
34	IkBb	Ambion_Plate 1	D14	Nfkbib	18036	siRNA2	156515	GGACGAUAAGCUUAGCCCUtt	AGGGCUAAGCUUAUCGUCCtc	
34	IkBb	Ambion_Plate 1	H19	Nfkbib	18036	siRNA3	156516	GCGAUGGCUAUUUUGAUUGtt	CAAUCAAAAUAGCCAUCGCtt	
34	IkBb	Qiagen_Plate 1	L5	Nfkbib	18036	siRNA4	SI02713347			AACAGAGATGAGGGCGATGAA
34	IkBb	Qiagen_Plate 1	D14	Nfkbib	18036	siRNA5	SI00196721			CCAGTTGGAAGTGGAGCAGAA
34	IkBb	Qiagen_Plate 1	H19	Nfkbib	18036	siRNA6	SI00196714			CAGCTGGTTTATGTAGCAACA
35	IkBe	Ambion_Plate 1	M5	Nfkbie	18037	siRNA1	63220	GGAACCAGAGAAAGAAGAUtt	AUCUUCUUUCUCUGGUUCCtt	
35	IkBe	Ambion_Plate 1	E14	Nfkbie	18037	siRNA2	63316	GGAAGUCCUGGACAUUCAGtt	CUGAAUGUCCAGGACUUCCtg	
35	IkBe	Ambion_Plate 1	I19	Nfkbie	18037	siRNA3	155571	CCUAAAAUACCUUUGUGAGtt	CUCACAAAGGUAUUUUAGGtg	
35	IkBe	Qiagen_Plate 1	M5	Nfkbie	18037	siRNA4	SI02733997			CACCGCAAAGTTATCTAAAGA
35	IkBe	Qiagen_Plate 1	E14	Nfkbie	18037	siRNA5	SI02709812			CTGGGTATGGTAGGAGACCTA
35	IkBe	Qiagen_Plate 1	I19	Nfkbie	18037	siRNA6	SI02687832			CAGAATGGAGCTGACATTGAT
36	Nfkb1	Ambion_Plate 1	N5	Nfkb1	18033	siRNA1	63219	GGUUAUCGUUCAGUUGGUCtt	GACCAACUGAACGAUAACCtt	
36	Nfkb1	Ambion_Plate 1	F14	Nfkb1	18033	siRNA2	155567	GCCAGCUUCCGUGUUUGUUtt	AACAAACACGGAAGCUGGCtt	
36	Nfkb1	Ambion_Plate 1	J19	Nfkb1	18033	siRNA3	155568	GGACCUAUUGAAGGCAAAAtt	UUUUGCCUUCAAUAGGUCCtt	
36	Nfkb1	Qiagen_Plate 1	N5	Nfkb1	18033	siRNA4	SI02733990			TAAGTTGTGCATTCAAATTAA
36	Nfkb1	Qiagen_Plate 1	F14	Nfkb1	18033	siRNA5	SI02709805			TACCCTGAAATCAAAGACAAA
36	Nfkb1	Qiagen_Plate 1	J19	Nfkb1	18033	siRNA6	SI01326997			CACCATAAACACCAAATTTAA
37	NFkb2	Ambion_Plate 1	C6	Nfkb2	18034	siRNA1	73524	GGCUUCAGAUUUCGAUAUGtt	CAUAUCGAAAUCUGAAGCCtc	
37	NFkb2	Ambion_Plate 1	G14	Nfkb2	18034	siRNA2	156991	GCAGAUAGCCCACGUCAUUtt	AAUGACGUGGGCUAUCUGCtc	
37	NFkb2	Ambion_Plate 1	K19	Nfkb2	18034	siRNA3	156992	CCUAUCCUACUGUCAAGAUtt	AUCUUGACAGUAGGAUAGGtc	
37	NFkb2	Qiagen_Plate 1	C6	Nfkb2	18034	siRNA4	SI01327032			CGCGGTGGAGACGAAGTTTAT
37	NFkb2	Qiagen_Plate 1	G14	Nfkb2	18034	siRNA5	SI01327025			CCCAAGGACATGACTGCTCAA
37	NFkb2	Qiagen_Plate 1	K19	Nfkb2	18034	siRNA6	SI01327018			CTCCAAACAGTTCACATATTA
38	RelA	Ambion_Plate 1	D6	Rela	19697	siRNA1	64078	GGACCAGGAACAGUUCGAAtt	UUCGAACUGUUCCUGGUCCtg	
38	RelA	Ambion_Plate 1	H14	Rela	19697	siRNA2	150535	GGUGUAUUUCACGGGACCAtt	UGGUCCCGUGAAAUACACCtc	
38	RelA	Ambion_Plate 1	L19	Rela	19697	siRNA3	150536	GCGCAAAAGGACCUAUGAGtt	CUCAUAGGUCCUUUUGCGCtt	
38	RelA	Qiagen_Plate 1	D6	Rela	19697	siRNA4	SI01399636			AAGGACCTATGAGACCTTCAA
38	RelA	Qiagen_Plate 1	H14	Rela	19697	siRNA5	SI01399629			CACCATCAAGATCAATGGCTA
38	RelA	Qiagen_Plate 1	L19	Rela	19697	siRNA6	SI01399622			ATGGAGTACCCTGAAGCTATA
39	RelB	Ambion_Plate 1	E6	Relb	19698	siRNA1	64079	GGACCACAGAUGAAUUGGAtt	UCCAAUUCAUCUGUGGUCCtg	
39	RelB	Ambion_Plate 1	I14	Relb	19698	siRNA2	64256	GGAAAAAGAAACCAGUGUUtt	AACACUGGUUUCUUUUUCCtt	
39	RelB	Ambion_Plate 1	M19	Relb	19698	siRNA3	150537	CGAAUACAUUAAGGAGAACtt	GUUCUCCUUAAUGUAUUCGtc	
39	RelB	Qiagen_Plate 1	E6	Relb	19698	siRNA4	SI02734697			CACGCTCTTCACTATGTTGGA
39	RelB	Qiagen_Plate 1	I14	Relb	19698	siRNA5	SI02710358			CAGCTACGGTGTGGACAAGAA
39	RelB	Qiagen_Plate 1	M19	Relb	19698	siRNA6	SI02688441			CACAGATGAATTGGAAATCAT

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
40	cRel	Ambion_Plate 1	F6	Rel	19696	siRNA1	64169	GGAUUAGUGCAGGAAUCAAtt	UUGAUUCCUGCACUAAUCCtt	
40	cRel	Ambion_Plate 1	J14	Rel	19696	siRNA2	64254	GGUGUGUUUUCAUGUUUUUtt	AAAAACAUGAAAACACACCtc	
40	cRel	Ambion_Plate 1	N19	Rel	19696	siRNA3	150531	GGAAGUUAGUGAGUCUAUGtt	CAUAGACUCACUAACUUCCtg	
40	cRel	Qiagen_Plate 1	F6	Rel	19696	siRNA4	SI01399608			AAGGATTAGTGCAGGAATCAA
40	cRel	Qiagen_Plate 1	J14	Rel	19696	siRNA5	SI01399601			TAGGACTTAAATAAGTATATA
40	cRel	Qiagen_Plate 1	N19	Rel	19696	siRNA6	SI01399594			CAGATGCATTTGATAGATCAA
41	Tpl2	Ambion_Plate 1	G6	Map3k8	26410	siRNA1	60792	GGAUCUGCUUGCAUUUGCAtt	UGCAAAUGCAAGCAGAUCCtc	
41	Tpl2	Ambion_Plate 1	K14	Map3k8	26410	siRNA2	60976	GGAUCAUUUCUGGUGAUAAtt	UUAUCACCAGAAAUGAUCCtt	
41	Tpl2	Ambion_Plate 1	C20	Map3k8	26410	siRNA3	186561	GCUGUUUUGGUAGAUUUUGtt	CAAAAUCUACCAAAACAGCtt	
41	Tpl2	Qiagen_Plate 1	G6	Map3k8	26410	siRNA4	SI02732023			AAGGATCATTTCTGGTGATAA
41	Tpl2	Qiagen_Plate 1	K14	Map3k8	26410	siRNA5	SI02707971			CTGTTCTTGGTTCTTATTTAA
41	Tpl2	Qiagen_Plate 1	C20	Map3k8	26410	siRNA6	SI01300236			TCCAATGTGACTAGTCAAATA
42	Mekk1	Ambion_Plate 1	H6	Map3k1	26401	siRNA1	188082	GCUCAAGGCGACCUGUAUGtt	CAUACAGGUCGCCUUGAGCtt	
42	Mekk1	Ambion_Plate 1	L14	Map3k1	26401	siRNA2	188083	GGAGUAAGACGGAAACGAGtt	CUCGUUUCCGUCUUACUCCtg	
42	Mekk1	Ambion_Plate 1	D20	Map3k1	26401	siRNA3	188084	CGUGGUAGUUAAUUGUUCAtt	UGAACAAUUAACUACCACGtg	
42	Mekk1	Qiagen_Plate 1	H6	Map3k1	26401	siRNA4	SI01299844			CACTCTCAGAATGAAATTCTA
42	Mekk1	Qiagen_Plate 1	L14	Map3k1	26401	siRNA5	SI01299837			AAGAACAGAAGCATAAATTTA
42	Mekk1	Qiagen_Plate 1	D20	Map3k1	26401	siRNA6	SI01299830			GACGACGTCAATCATAATCAA
43	Mkk1	Ambion_Plate 1	I6	Map2k1	26395	siRNA1	63788	GGAUGAUGACUUUGAGAAGtt	CUUCUCAAAGUCAUCAUCCtt	
43	Mkk1	Ambion_Plate 1	M14	Map2k1	26395	siRNA2	63974	GGAUUUUGUGAAUAAAUGCtt	GCAUUUAUUCACAAAAUCCtg	
43	Mkk1	Ambion_Plate 1	E20	Map2k1	26395	siRNA3	186575	CGUGUACGUCAUGGUAUUUtt	AAAUACCAUGACGUACACGtt	
43	Mkk1	Qiagen_Plate 1	I6	Map2k1	26395	siRNA4	SI02710120			TACCAATGCTATTGTAAACAA
43	Mkk1	Qiagen_Plate 1	M14	Map2k1	26395	siRNA5	SI02688196			CTGGTTGTATTTCTATATTTA
43	Mkk1	Qiagen_Plate 1	E20	Map2k1	26395	siRNA6	SI02668379			CAAGATGTTTATCAAATCTAA
44	Mkk2	Ambion_Plate 1	J6	Map2k2	26396	siRNA1	76592	GGACGACGACUUUGAGAGGtt	CCUCUCAAAGUCGUCGUCCtt	
44	Mkk2	Ambion_Plate 1	N14	Map2k2	26396	siRNA2	76770	GGAGUUUGUGAAUAAAUGUtt	ACAUUUAUUCACAAACUCCtg	
44	Mkk2	Ambion_Plate 1	F20	Map2k2	26396	siRNA3	188842	GCAUAGCUAACUCAGCAUAtt	UAUGCUGAGUUAGCUAUGCtc	
44	Mkk2	Qiagen_Plate 1	J6	Map2k2	26396	siRNA4	SI01299676			CTCAGCCACAGTGGCCTGTAA
44	Mkk2	Qiagen_Plate 1	N14	Map2k2	26396	siRNA5	SI01299669			CTCACTGGACCAGGTACTGAA
44	Mkk2	Qiagen_Plate 1	F20	Map2k2	26396	siRNA6	SI01299662			CTGGACCTGGATGAGCAGCAA
45	Erk1	Ambion_Plate 1	K6	Mapk3	26417	siRNA1	70654	GGACCUUAAUUGCAUCAUUtt	AAUGAUGCAAUUAAGGUCCtc	
45	Erk1	Ambion_Plate 1	C15	Mapk3	26417	siRNA2	188103	GCUCAGCUUAUGACCACGUtt	ACGUGGUCAUAAGCUGAGCtg	
45	Erk1	Ambion_Plate 1	G20	Mapk3	26417	siRNA3	188105	CCACAUUCUAGGUAUCUUGtt	CAAGAUACCUAGAAUGUGGtt	
45	Erk1	Qiagen_Plate 1	K6	Mapk3	26417	siRNA4	SI02714894			TTCCGCCATGAGAATGTTATA
45	Erk1	Qiagen_Plate 1	C15	Mapk3	26417	siRNA5	SI01300600			CTGCAGATTGTTAGAAAGTGA
45	Erk1	Qiagen_Plate 1	G20	Mapk3	26417	siRNA6	SI01300593			GTGCCTGTATCTAATATATAA
46	Erk2	Ambion_Plate 1	L6	Mapk1	26413	siRNA1	70462	GGGCUAAAGUAUAUCCAUUtt	AAUGGAUAUACUUUAGCCCtc	
46	Erk2	Ambion_Plate 1	D15	Mapk1	26413	siRNA2	188094	GGGUUAUACCAAGUCCAUUtt	AAUGGACUUGGUAUAACCCtt	
46	Erk2	Ambion_Plate 1	H20	Mapk1	26413	siRNA3	188095	GGCCUAUCUUCCCAGGAAAtt	UUUCCUGGGAAGAUAGGCCtg	
46	Erk2	Qiagen_Plate 1	L6	Mapk1	26413	siRNA4	SI05165916			CTGGAGCAGTATTATGACCCA
46	Erk2	Qiagen_Plate 1	D15	Mapk1	26413	siRNA5	SI02714880			CACAGGGTTCTTGACAGAGTA
46	Erk2	Qiagen_Plate 1	H20	Mapk1	26413	siRNA6	SI02692326			CACAAGAGGATTGAAGTTGAA
47	Mkk3	Ambion_Plate 1	M6	Map2k3	26397	siRNA1	63883	GGUGCUGGAGAAGAACAUGtt	CAUGUUCUUCUCCAGCACCtt	
47	Mkk3	Ambion_Plate 1	E15	Map2k3	26397	siRNA2	63975	GGAACCUAUUGCUGUUUUAtt	UAAAACAGCAAUAGGUUCCtg	
47	Mkk3	Ambion_Plate 1	I20	Map2k3	26397	siRNA3	186576	GGGCAUGUGAAGAUGUGCGtt	CGCACAUCUUCACAUGCCCtt	
47	Mkk3	Qiagen_Plate 1	M6	Map2k3	26397	siRNA4	SI01299704			CCCATTCTTCACCTTGCACAA
47	Mkk3	Qiagen_Plate 1	E15	Map2k3	26397	siRNA5	SI01299697			CAGCACTTACCTACAGCCATA
47	Mkk3	Qiagen_Plate 1	I20	Map2k3	26397	siRNA6	SI01299690			CCTGGGCATTTGAGAAATTAA
48	Mkk6	Ambion_Plate 1	N6	Map2k6	26399	siRNA1	188076	GGCUUGCAUAUCUAUUGGAtt	UCCAAUAGAUAUGCAAGCCtt	
48	Mkk6	Ambion_Plate 1	F15	Map2k6	26399	siRNA2	188077	GCUCAUGGAUACGUCACUAtt	UAGUGACGUAUCCAUGAGCtc	
48	Mkk6	Ambion_Plate 1	J20	Map2k6	26399	siRNA3	188078	CCAUGAAAGUCACUUGUAUtt	AUACAAGUGACUUUCAUGGtt	
48	Mkk6	Qiagen_Plate 1	N6	Map2k6	26399	siRNA4	SI01299788			CTGGTCGACTCTGTTGCTAAA
48	Mkk6	Qiagen_Plate 1	F15	Map2k6	26399	siRNA5	SI01299781			AGGACTTGAAATGGTGATTAA
48	Mkk6	Qiagen_Plate 1	J20	Map2k6	26399	siRNA6	SI01299774			CAGGGTGAAGAAAGTTCACTA
49	p38a	Ambion_Plate 1	C7	Mapk14	26416	siRNA1	70559	GGAAUUCAAUGACGUGUACtt	GUACACGUCAUUGAAUUCCtc	
49	p38a	Ambion_Plate 1	G15	Mapk14	26416	siRNA2	240555	CCAUAUUGAUCAGUUGAAGtt	CUUCAACUGAUCAAUAUGGtc	
49	p38a	Ambion_Plate 1	K20	Mapk14	26416	siRNA3	240556	GCACUUUGUGCUAUAUAAGtt	CUUAUAUAGCACAAAGUGCtc	
49	p38a	Qiagen_Plate 1	C7	Mapk14	26416	siRNA4	SI02714887			CTCCTTTACTATCTTTCTCAA
49	p38a	Qiagen_Plate 1	G15	Mapk14	26416	siRNA5	SI01300544			CAGGTCTTGTGTTTAGGTCAA
49	p38a	Qiagen_Plate 1	K20	Mapk14	26416	siRNA6	SI01300537			CTCCAGCTACTTTGTGTTGAA
50	p38b	Ambion_Plate 1	D7	Mapk11	19094	siRNA1	68856	GGAUUUCAGCGAAGUGUACtt	GUACACUUCGCUGAAAUCCtc	
50	p38b	Ambion_Plate 1	H15	Mapk11	19094	siRNA2	151242	CCUCUUUGGAAGAAUGCUGtt	CAGCAUUCUUCCAAAGAGGtc	
50	p38b	Ambion_Plate 1	L20	Mapk11	19094	siRNA3	151244	CCAUCAGAUUAUCUAUCUAtt	UAGAUAGAUAAUCUGAUGGtg	
50	p38b	Qiagen_Plate 1	D7	Mapk11	19094	siRNA4	SI02738267			CTGGATTGGGAGGAAGGCTAA
50	p38b	Qiagen_Plate 1	H15	Mapk11	19094	siRNA5	SI01300460			CTGAGCGATGAGCATGTTCAA
50	p38b	Qiagen_Plate 1	L20	Mapk11	19094	siRNA6	SI01300446			CACCAAGAGTGTGCACAATAA
51	MK2	Ambion_Plate 1	E7	Mapkapk2	17164	siRNA1	164702	CCCGGAGUGGUCAGAAGUAtt	UACUUCUGACCACUCCGGGtt	
51	MK2	Ambion_Plate 1	I15	Mapkapk2	17164	siRNA2	164703	GGACAAGCAAUAACUCUACtt	GUAGAGUUAUUGCUUGUCCtc	
51	MK2	Ambion_Plate 1	M20	Mapkapk2	17164	siRNA3	164704	CGAUUAACCCACUCUUGUCtt	GACAAGAGUGGGUUAAUCGtg	
51	MK2	Qiagen_Plate 1	E7	Mapkapk2	17164	siRNA4	SI01300880			TCCGTGTTATACACCATACTA
51	MK2	Qiagen_Plate 1	I15	Mapkapk2	17164	siRNA5	SI01300873			AACCTCTTATATACTTCCAAA
51	MK2	Qiagen_Plate 1	M20	Mapkapk2	17164	siRNA6	SI01300866			CAGGTCCTTTCCCATCTACAA
52	Mkk4	Ambion_Plate 1	F7	Map2k4	26398	siRNA1	64447	GGACUUGAAAGACCUUGGAtt	UCCAAGGUCUUUCAAGUCCtc	
52	Mkk4	Ambion_Plate 1	J15	Map2k4	26398	siRNA2	64539	GGUCAACAUUAAAAUACUGtt	CAGUAUUUUAAUGUUGACCtc	
52	Mkk4	Ambion_Plate 1	N20	Map2k4	26398	siRNA3	186583	GGGCAAGGAAUUUAUUACAtt	UGUAAUAAAUUCCUUGCCCtt	
52	Mkk4	Qiagen_Plate 1	F7	Map2k4	26398	siRNA4	SI01299732			CTGCAGGTCAGTTGTAATAAA
52	Mkk4	Qiagen_Plate 1	J15	Map2k4	26398	siRNA5	SI01299725			CTGGACAGAAGTGGAAATATA
52	Mkk4	Qiagen_Plate 1	N20	Map2k4	26398	siRNA6	SI01299718			ATAGATTATTATAAACTATAA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
53	Mkk7	Ambion_Plate 1	G7	Map2k7	26400	siRNA1	70554	GGCAGAAAUCAAUGACUUGtt	CAAGUCAUUGAUUUCUGCCtg	
53	Mkk7	Ambion_Plate 1	K15	Map2k7	26400	siRNA2	70648	GGAAGAGACCAAAGUAUAAtt	UUAUACUUUGGUCUCUUCCtg	
53	Mkk7	Ambion_Plate 1	C21	Map2k7	26400	siRNA3	188081	GCUGAAACAAAGGGUAUAUtt	AUAUACCCUUUGUUUCAGCtg	
53	Mkk7	Qiagen_Plate 1	G7	Map2k7	26400	siRNA4	SI04404701			CTCCAACATCCTGCTAGATGA
53	Mkk7	Qiagen_Plate 1	K15	Map2k7	26400	siRNA5	SI04404694			AAGCCTGACTATGACATCCGA
53	Mkk7	Qiagen_Plate 1	C21	Map2k7	26400	siRNA6	SI04404687			CCGCAGGAGGATCGACCTCAA
54	Jnk1	Ambion_Plate 1	H7	Mapk8	26419	siRNA1	72374	GGAGCUCAAGGAAUAGUGUtt	ACACUAUUCCUUGAGCUCCtg	
54	Jnk1	Ambion_Plate 1	L15	Mapk8	26419	siRNA2	72566	GGACUUAUGUUGAAAACAGtt	CUGUUUUCAACAUAAGUCCtt	
54	Jnk1	Ambion_Plate 1	D21	Mapk8	26419	siRNA3	188653	GGAACGAACUAAGAAUGGAtt	UCCAUUCUUAGUUCGUUCCtc	
54	Jnk1	Qiagen_Plate 1	H7	Mapk8	26419	siRNA4	SI02672936			ATGAAGTGTGTTAATCACAAA
54	Jnk1	Qiagen_Plate 1	L15	Mapk8	26419	siRNA5	SI01300712			GCCTAGTAATATAGTAGTCAA
54	Jnk1	Qiagen_Plate 1	D21	Mapk8	26419	siRNA6	SI01300705			CTCAGAGCATAACAAACTTAA
55	Jnk2	Ambion_Plate 1	I7	Mapk9	26420	siRNA1	72933	GGAAUUGUUUGUGCUGCUUtt	AAGCAGCACAAACAAUUCCtt	
55	Jnk2	Ambion_Plate 1	M15	Mapk9	26420	siRNA2	73029	GGUUAUUCAUAUGGAACUGtt	CAGUUCCAUAUGAAUAACCtg	
55	Jnk2	Ambion_Plate 1	E21	Mapk9	26420	siRNA3	73119	GGAAUUAUGUGGAAAACAGtt	CUGUUUUCCACAUAAUUCCtt	
55	Jnk2	Qiagen_Plate 1	I7	Mapk9	26420	siRNA4	SI02749117			ACCGTCATATATCATATCTTA
55	Jnk2	Qiagen_Plate 1	M15	Mapk9	26420	siRNA5	SI02723588			AAGGAATATAATTAAATTTAT
55	Jnk2	Qiagen_Plate 1	E21	Mapk9	26420	siRNA6	SI01300810			ACCTTTAATGGACAACATTAA
56	Jnk3	Ambion_Plate 1	J7	Mapk10	26414	siRNA1	64448	GGUGGACAACCAGUUCUACtt	GUAGAACUGGUUGUCCACCtt	
56	Jnk3	Ambion_Plate 1	N15	Mapk10	26414	siRNA2	64540	GGGAUUUGUUGUCUAAGAUtt	AUCUUAGACAACAAAUCCCtg	
56	Jnk3	Ambion_Plate 1	F21	Mapk10	26414	siRNA3	186584	CGUGGAUGUGUCAUCUAUUtt	AAUAGAUGACACAUCCACGtg	
56	Jnk3	Qiagen_Plate 1	J7	Mapk10	26414	siRNA4	SI05348238			CGGAATGGCGGATGTGCTTAA
56	Jnk3	Qiagen_Plate 1	N15	Mapk10	26414	siRNA5	SI05348231			TCCGTATGTGGTGACGCGATA
56	Jnk3	Qiagen_Plate 1	F21	Mapk10	26414	siRNA6	SI02734886			ATGGAAAGAACTTATCTACAA
57	Erk3	Ambion_Plate 1	K7	Mapk12	29857	siRNA1	71824	GGCAGACAGUGAGAUGACAtt	UGUCAUCUCACUGUCUGCCtg	
57	Erk3	Ambion_Plate 1	C16	Mapk12	29857	siRNA2	72014	GGAGAUCAUGAAGAUCACAtt	UGUGAUCUUCAUGAUCUCCtt	
57	Erk3	Ambion_Plate 1	G21	Mapk12	29857	siRNA3	184105	GCGUGUGACUUACAAGGAAtt	UUCCUUGUAAGUCACACGCtt	
57	Erk3	Qiagen_Plate 1	K7	Mapk12	29857	siRNA4	SI01300488			TACTGGGAAGATCCTGTTCAA
57	Erk3	Qiagen_Plate 1	C16	Mapk12	29857	siRNA5	SI01300481			CAGGCTGTGAATCTCCTGGAA
57	Erk3	Qiagen_Plate 1	G21	Mapk12	29857	siRNA6	SI01300474			CAGCCATTTGGTGTTGCCTAA
58	p38d	Ambion_Plate 1	L7	Mapk13	26415	siRNA1	70463	GGAUAAGGUCCAGUACUUGtt	CAAGUACUGGACCUUAUCCtc	
58	p38d	Ambion_Plate 1	D16	Mapk13	26415	siRNA2	70652	GGUCUAAAGUACAUCCACUtt	AGUGGAUGUACUUUAGACCtt	
58	p38d	Ambion_Plate 1	H21	Mapk13	26415	siRNA3	188098	GCGUGGACGAAUGGAAACAtt	UGUUUCCAUUCGUCCACGCtg	
58	p38d	Qiagen_Plate 1	L7	Mapk13	26415	siRNA4	SI01300516			CCGCGAGCTTCTGCTCTTGAA
58	p38d	Qiagen_Plate 1	D16	Mapk13	26415	siRNA5	SI01300509			CTGGCTAGACCTGCAACTCAA
58	p38d	Qiagen_Plate 1	H21	Mapk13	26415	siRNA6	SI01300502			CAGCGAGGATAAGGTCCAGTA
59	TRIF	Ambion_Plate 1	M7	Ticam1	106759	siRNA1	173696	GCUAUGUAACACACCGCUGtt	CAGCGGUGUGUUACAUAGCtt	
59	TRIF	Ambion_Plate 1	E16	Ticam1	106759	siRNA2	173697	GCCCAGAUACAACCAGACUtt	AGUCUGGUUGUAUCUGGGCtg	
59	TRIF	Ambion_Plate 1	I21	Ticam1	106759	siRNA3	288153	GGGUCCUGUUUUUAUAAUAtt	UAUUAUAAAAACAGGACCCtc	
59	TRIF	Qiagen_Plate 1	M7	Ticam1	106759	siRNA4	SI00909328			CAGCCTATGTCCATAGCTATA
59	TRIF	Qiagen_Plate 1	E16	Ticam1	106759	siRNA5	SI00909321			CAGGGAAGACCACACCTATAA
59	TRIF	Qiagen_Plate 1	I21	Ticam1	106759	siRNA6	SI00909314			TAGGGTTACCACACGAAATTA
60	TRAM	Ambion_Plate 1	N7	Ticam2	225471	siRNA1	95553	GGAGCAAGAUGAAGAAGAGtt	CUCUUCUUCAUCUUGCUCCtc	
60	TRAM	Ambion_Plate 1	F16	Ticam2	225471	siRNA2	95742	GGUACUCAUAAAACAUGAAtt	UUCAUGUUUUAUGAGUACCtg	
60	TRAM	Ambion_Plate 1	J21	Ticam2	225471	siRNA3	167481	GGGCUUUAAUUCACAGAGCtt	GCUCUGUGAAUUAAAGCCCtg	
60	TRAM	Qiagen_Plate 1	N7	Ticam2	225471	siRNA4	SI01448300			CTGGTGTAACTTCCAGTTCTA
60	TRAM	Qiagen_Plate 1	F16	Ticam2	225471	siRNA5	SI01448293			TTGCATCATCATCGATATTTA
60	TRAM	Qiagen_Plate 1	J21	Ticam2	225471	siRNA6	SI01448286			CTCCTTTGTCTGCGAAATAAA
61	RIP1	Ambion_Plate 1	C8	Ripk1	19766	siRNA1	150580	CCUGAUGCACGUGCUAAAGtt	CUUUAGCACGUGCAUCAGGtt	
61	RIP1	Ambion_Plate 1	G16	Ripk1	19766	siRNA2	150581	GGCAUGUGCUACUUACAUGtt	CAUGUAAGUAGCACAUGCCtt	
61	RIP1	Ambion_Plate 1	K21	Ripk1	19766	siRNA3	150582	GCAAACUAUUUGUCUGGUGtt	CACCAGACAAAUAGUUUGCtt	
61	RIP1	Qiagen_Plate 1	C8	Ripk1	19766	siRNA4	SI01402296			CACAGGCTAGGCCATCATTAA
61	RIP1	Qiagen_Plate 1	G16	Ripk1	19766	siRNA5	SI01402289			TTGGAGATTCTGAGCAATCAA
61	RIP1	Qiagen_Plate 1	K21	Ripk1	19766	siRNA6	SI01402282			CAGCATGGATTTGGAACTACA
62	FADD	Ambion_Plate 1	D8	Fadd	14082	siRNA1	158473	GCAAGAGUGAGAAUAUGUCtt	GACAUAUUCUCACUCUUGCtc	
62	FADD	Ambion_Plate 1	H16	Fadd	14082	siRNA2	158474	GCCUCAAGCCUACCAUGUUtt	AACAUGGUAGGCUUGAGGCtg	
62	FADD	Ambion_Plate 1	L21	Fadd	14082	siRNA3	158475	GCUCAGAUAUGAGCAAGCUtt	AGCUUGCUCAUAUCUGAGCtg	
62	FADD	Qiagen_Plate 1	D8	Fadd	14082	siRNA4	SI00998872			AACCATTGTCTCAGCTTTCTA
62	FADD	Qiagen_Plate 1	H16	Fadd	14082	siRNA5	SI00998865			GACCATATCTCAAATAAATAA
62	FADD	Qiagen_Plate 1	L21	Fadd	14082	siRNA6	SI00998858			CAAGAATTTCTATTATATTAA
63	Caspase 8	Ambion_Plate 1	E8	Casp8	12370	siRNA1	161006	GCGAGUUGGAAUUGAGAUCtt	GAUCUCAAUUCCAACUCGCtc	
63	Caspase 8	Ambion_Plate 1	I16	Casp8	12370	siRNA2	161007	GCCUCAAAAUGGCGGAACUtt	AGUUCCGCCAUUUUGAGGCtc	
63	Caspase 8	Ambion_Plate 1	M21	Casp8	12370	siRNA3	161008	CCUGUAUACUAUCACUUGUtt	ACAAGUGAUAGUAUACAGGtt	
63	Caspase 8	Qiagen_Plate 1	E8	Casp8	12370	siRNA4	SI00941864			TTGGATGAGATGAGCCTCAAA
63	Caspase 8	Qiagen_Plate 1	I16	Casp8	12370	siRNA5	SI00941857			AACTATGACGTGAGCAATAAA
63	Caspase 8	Qiagen_Plate 1	M21	Casp8	12370	siRNA6	SI00941850			ATCGAGGATTATGAAAGATCA
64	TBK1	Ambion_Plate 1	F8	Tbk1	56480	siRNA1	74349	GGAAGGCAUAAGAAAACUGtt	CAGUUUUCUUAUGCCUUCCtc	
64	TBK1	Ambion_Plate 1	J16	Tbk1	56480	siRNA2	74444	GGAGACAACAACAAGACAUtt	AUGUCUUGUUGUUGUCUCCtc	
64	TBK1	Ambion_Plate 1	N21	Tbk1	56480	siRNA3	74536	GGAACAAAGAAGUAAUGUAtt	UACAUUACUUCUUUGUUCCtc	
64	TBK1	Qiagen_Plate 1	F8	Tbk1	56480	siRNA4	SI01443008			TAGAAAGGTTTGGGTCTTTAA
64	TBK1	Qiagen_Plate 1	J16	Tbk1	56480	siRNA5	SI01443001			AAGATTGTTTCCTCAAATCAA
64	TBK1	Qiagen_Plate 1	N21	Tbk1	56480	siRNA6	SI01442994			CTGGGTGAGATTTCAGACATA
65	IKKe	Ambion_Plate 2	C3	Ikbke	56489	siRNA1	74342	GGCCCGAAACAAGAAAUCCtt	GGAUUUCUUGUUUCGGGCCtt	
65	IKKe	Ambion_Plate 2	G8	Ikbke	56489	siRNA2	74437	GGCUGAAUCACCAGAACAUtt	AUGUUCUGGUGAUUCAGCCtc	
65	IKKe	Ambion_Plate 2	K16	Ikbke	56489	siRNA3	74529	GGAUAACAAAAGUAUCCAGtt	CUGGAUACUUUUGUUAUCCtc	
65	IKKe	Qiagen_Plate 2	C3	Ikbke	56489	siRNA4	SI02717078			CAGAAGCAATAGAAACATTCA
65	IKKe	Qiagen_Plate 2	G8	Ikbke	56489	siRNA5	SI01075284			AAGGTAAATTTCAGTCATCTA
65	IKKe	Qiagen_Plate 2	K16	Ikbke	56489	siRNA6	SI01075277			CAGATTCATGAGGATAACAAA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
66	IRF3	Ambion_Plate 2	D3	Irf3	54131	siRNA1	72761	GGACCCUUAUGACCCUCAUtt	AUGAGGGUCAUAAGGGUCCtt	
66	IRF3	Ambion_Plate 2	H8	Irf3	54131	siRNA2	72855	GGUUGUUCCUACAUGUCUUtt	AAGACAUGUAGGAACAACCtt	
66	IRF3	Ambion_Plate 2	L16	Irf3	54131	siRNA3	184586	GGAAAACCUACCGAAGUUAtt	UAACUUCGGUAGGUUUUCCtg	
66	IRF3	Qiagen_Plate 2	D3	Irf3	54131	siRNA4	SI02740920			CTCGGAGGCTTAGCTGACAAA
66	IRF3	Qiagen_Plate 2	H8	Irf3	54131	siRNA5	SI00210791			CCGGTCAGCCCTGAACCGGAA
66	IRF3	Qiagen_Plate 2	L16	Irf3	54131	siRNA6	SI00210784			GACCCTTATGACCCTCATAAA
67	Duba	Ambion_Plate 2	E3	Otud5	54644	siRNA1	186380	GCAGGAACACUGGUUUGAAtt	UUCAAACCAGUGUUCCUGCtg	
67	Duba	Ambion_Plate 2	I8	Otud5	54644	siRNA2	186381	GCGGAAAAACAACUGCCAUtt	AUGGCAGUUGUUUUUCCGCtt	
67	Duba	Ambion_Plate 2	M16	Otud5	54644	siRNA3	186382	CCGGAAUAUCCACUAUAAUtt	AUUAUAGUGGAUAUUCCGGtg	
67	Duba	Qiagen_Plate 2	E3	Otud5	54644	siRNA4	SI00985096			CACCACCTATATCAACCGGAA
67	Duba	Qiagen_Plate 2	I8	Otud5	54644	siRNA5	SI00985089			CAAGAAAGGCTTCATCATCAA
67	Duba	Qiagen_Plate 2	M16	Otud5	54644	siRNA6	SI00985082			CCGAAGAATCTGAGCCTTCAA
68	TRADD	Ambion_Plate 2	F3	Tradd	71609	siRNA1	284462	GCCAUACAGGUAGCUUCUGtt	CAGAAGCUACCUGUAUGGCtc	
68	TRADD	Ambion_Plate 2	J8	Tradd	71609	siRNA2	284463	GCUGCUGGAGUGCAACUAAtt	UUAGUUGCACUCCAGCAGCtc	
68	TRADD	Ambion_Plate 2	N16	Tradd	71609	siRNA3	284464	CCUUCUGAAACCUAGCUCAtt	UGAGCUAGGUUUCAGAAGGtc	
68	TRADD	Qiagen_Plate 2	F3	Tradd	71609	siRNA4	SI01454516			CTGGAGGATGAGCTCTGCAAA
68	TRADD	Qiagen_Plate 2	J8	Tradd	71609	siRNA5	SI01454509			AACCAGCAGTTCAGTGTTTGA
68	TRADD	Qiagen_Plate 2	N16	Tradd	71609	siRNA6	SI01454502			CAGGGTGGAGCCATACAGGTA
69	TANK	Ambion_Plate 2	G3	Tank	21353	siRNA1	69577	GGACAAAGAGGAAUGGAUAtt	UAUCCAUUCCUCUUUGUCCtg	
69	TANK	Ambion_Plate 2	K8	Tank	21353	siRNA2	69767	GGAAUGGAUAAAAACAUUGtt	CAAUGUUUUUAUCCAUUCCtc	
69	TANK	Ambion_Plate 2	C17	Tank	21353	siRNA3	187204	GGAAACUUUGUUAAAACAGtt	CUGUUUUAACAAAGUUUCCtg	
69	TANK	Qiagen_Plate 2	G3	Tank	21353	siRNA4	SI01441384			CAGAAGAAACTTTATTTGAAA
69	TANK	Qiagen_Plate 2	K8	Tank	21353	siRNA5	SI01441377			CAGGCTAAAGATGATATAAAT
69	TANK	Qiagen_Plate 2	C17	Tank	21353	siRNA6	SI01441370			CCCAGGGAAATTTAAACATTA
70	SINTBAD	Ambion_Plate 2	H3	Tbkbp1	73174	siRNA1	179203	GCAACGACUCAACCAAUUCtt	GAAUUGGUUGAGUCGUUGCtg	
70	SINTBAD	Ambion_Plate 2	L8	Tbkbp1	73174	siRNA2	179204	GGAAAGACCUCUUGAUAGGtt	CCUAUCAAGAGGUCUUUCCtg	
70	SINTBAD	Ambion_Plate 2	D17	Tbkbp1	73174	siRNA3	179205	GGCAUCUUAUUUCUUGUUAtt	UAACAAGAAAUAAGAUGCCtc	
70	SINTBAD	Qiagen_Plate 2	H3	Tbkbp1	73174	siRNA4	SI00831124			CCAGGGTGCTGTGGAGATTAA
70	SINTBAD	Qiagen_Plate 2	L8	Tbkbp1	73174	siRNA5	SI00831117			CTCCAGAGACATGTCATTGTA
70	SINTBAD	Qiagen_Plate 2	D17	Tbkbp1	73174	siRNA6	SI00831110			CCAGATGATGCTCTCATCAAA
71	BTK	Ambion_Plate 2	I3	Btk	12229	siRNA1	70766	GGCAGUAAGAAAGGUUCAAtt	UUGAACCUUUCUUACUGCCtc	
71	BTK	Ambion_Plate 2	M8	Btk	12229	siRNA2	70952	GGAUGAAUUCAUUGAAGAAtt	UUCUUCAAUGAAUUCAUCCtc	
71	BTK	Ambion_Plate 2	E17	Btk	12229	siRNA3	161642	CCUUUAAACUUCAAGAAGCtt	GCUUCUUGAAGUUUAAAGGtg	
71	BTK	Qiagen_Plate 2	I3	Btk	12229	siRNA4	SI00931784			CAGAACTGAGTACACAAACAA
71	BTK	Qiagen_Plate 2	M8	Btk	12229	siRNA5	SI00931777			CAGCTCGAAACTGTTTGGTAA
71	BTK	Qiagen_Plate 2	E17	Btk	12229	siRNA6	SI00931770			GAGGATGAATTCATTGAAGAA
72	NIK	Ambion_Plate 2	J3	Map3k14	53859	siRNA1	72803	GGCUGAAUGUGAGAAUAGCtt	GCUAUUCUCACAUUCAGCCtg	
72	NIK	Ambion_Plate 2	N8	Map3k14	53859	siRNA2	184656	CGACGUGAUCACCAAAGGCtt	GCCUUUGGUGAUCACGUCGtt	
72	NIK	Ambion_Plate 2	F17	Map3k14	53859	siRNA3	184657	GCCCGAAAAAAACGUAGGAtt	UCCUACGUUUUUUUCGGGCtt	
72	NIK	Qiagen_Plate 2	J3	Map3k14	53859	siRNA4	SI01299984			CAGGAAGATGAGTCTCCACTA
72	NIK	Qiagen_Plate 2	N8	Map3k14	53859	siRNA5	SI01299977			TAGCATTAAGTTCACTGTGAA
72	NIK	Qiagen_Plate 2	F17	Map3k14	53859	siRNA6	SI01299970			CCCTTGGAAAGGAGAATATAA
73	AKT1	Ambion_Plate 2	K3	Akt1	11651	siRNA1	65496	GGCCCAACACCUUUAUCAUtt	AUGAUAAAGGUGUUGGGCCtt	
73	AKT1	Ambion_Plate 2	C9	Akt1	11651	siRNA2	162426	GCACCGUGUGACCAUGAACtt	GUUCAUGGUCACACGGUGCtt	
73	AKT1	Ambion_Plate 2	G17	Akt1	11651	siRNA3	162428	CGAGUUUGAGUACCUGAAAtt	UUUCAGGUACUCAAACUCGtt	
73	AKT1	Qiagen_Plate 2	K3	Akt1	11651	siRNA4	SI04715235			AACGGACTTCGGGCTGTGCAA
73	AKT1	Qiagen_Plate 2	C9	Akt1	11651	siRNA5	SI02652433			CATGCTGTTCAGAGACATTTA
73	AKT1	Qiagen_Plate 2	G17	Akt1	11651	siRNA6	SI02652426			AACAATTAGATTCATGTAGAA
74	AKT2	Ambion_Plate 2	L3	Akt2	11652	siRNA1	60063	GGUAGCUGUCAACAAGGCAtt	UGCCUUGUUGACAGCUACCtc	
74	AKT2	Ambion_Plate 2	D9	Akt2	11652	siRNA2	60152	GGUACUUUGAUGACGAGUUtt	AACUCGUCAUCAAAGUACCtt	
74	AKT2	Ambion_Plate 2	H17	Akt2	11652	siRNA3	162215	GCAGUAAUGUCCAGGGACAtt	UGUCCCUGGACAUUACUGCtt	
74	AKT2	Qiagen_Plate 2	L3	Akt2	11652	siRNA4	SI04446638			AAGGAGGTCATGGAGCATAGA
74	AKT2	Qiagen_Plate 2	D9	Akt2	11652	siRNA5	SI00895944			TACTCTCTTGATTCTCAATAA
74	AKT2	Qiagen_Plate 2	H17	Akt2	11652	siRNA6	SI00895930			CTGGCAGGACGTGGTACAGAA
75	AKT3	Ambion_Plate 2	M3	Akt3	23797	siRNA1	70322	GGUAUUAGAAGAUAAUGACtt	GUCAUUAUCUUCUAAUACCtc	
75	AKT3	Ambion_Plate 2	E9	Akt3	23797	siRNA2	187720	GCCUCACAGAUUGAUAAUAtt	UAUUAUCAAUCUGUGAGGCtg	
75	AKT3	Ambion_Plate 2	I17	Akt3	23797	siRNA3	187721	GGAAGUAGAUUAGAUGGUAtt	UACCAUCUAAUCUACUUCCtt	
75	AKT3	Qiagen_Plate 2	M3	Akt3	23797	siRNA4	SI00895972			AAGAATTGTGTTGTCATGTTA
75	AKT3	Qiagen_Plate 2	E9	Akt3	23797	siRNA5	SI00895965			TAGGAGATAAATCAAGAACTA
75	AKT3	Qiagen_Plate 2	I17	Akt3	23797	siRNA6	SI00895958			CAGATTGATAATATAGGAGAA
76	PIK3CA	Ambion_Plate 2	N3	Pik3ca	18706	siRNA1	150105	GCUGCCGAUUGAUAGCUUCtt	GAAGCUAUCAAUCGGCAGCtg	
76	PIK3CA	Ambion_Plate 2	F9	Pik3ca	18706	siRNA2	150106	GGAGAACCCUUAUGUGACAtt	UGUCACAUAAGGGUUCUCCtc	
76	PIK3CA	Ambion_Plate 2	J17	Pik3ca	18706	siRNA3	150107	CCUUUAUCUUGGGAAUUGGtt	CCAAUUCCCAAGAUAAAGGtt	
76	PIK3CA	Qiagen_Plate 2	N3	Pik3ca	18706	siRNA4	SI01378496			CAGCTGAAACTCTGTGTCTTA
76	PIK3CA	Qiagen_Plate 2	F9	Pik3ca	18706	siRNA5	SI01378489			ATGGCTGAATTATGATATATA
76	PIK3CA	Qiagen_Plate 2	J17	Pik3ca	18706	siRNA6	SI01378482			TTGGAATATTTCACAAAGCAA
77	PIK3CB	Ambion_Plate 2	C4	Pik3cb	74769	siRNA1	83595	GGUGGAAGCACUCAAUAAGtt	CUUAUUGAGUGCUUCCACCtg	
77	PIK3CB	Ambion_Plate 2	G9	Pik3cb	74769	siRNA2	178213	GGAAAGAACGACCAUAUUUtt	AAAUAUGGUCGUUCUUUCCtg	
77	PIK3CB	Ambion_Plate 2	K17	Pik3cb	74769	siRNA3	178214	CGCGAGUUAUUUCUCAUAUtt	AUAUGAGAAAUAACUCGCGtt	
77	PIK3CB	Qiagen_Plate 2	C4	Pik3cb	74769	siRNA4	SI01378524			AACGACCATATTTGGAATGAA
77	PIK3CB	Qiagen_Plate 2	G9	Pik3cb	74769	siRNA5	SI01378517			CTGGAGAACTTGGAAGATAAA
77	PIK3CB	Qiagen_Plate 2	K17	Pik3cb	74769	siRNA6	SI01378510			CTCGGTTGGAGTGATCTTTAA
78	PIK3CD	Ambion_Plate 2	D4	Pik3cd	18707	siRNA1	63625	GGUCUCCAUGAGUUUGAUUtt	AAUCAAACUCAUGGAGACCtt	
78	PIK3CD	Ambion_Plate 2	H9	Pik3cd	18707	siRNA2	63716	GGCACUGAAUGACUUUGUGtt	CACAAAGUCAUUCAGUGCCtt	
78	PIK3CD	Ambion_Plate 2	L17	Pik3cd	18707	siRNA3	150109	GCCAUUCUCCAUUGAGCUGtt	CAGCUCAAUGGAGAAUGGCtg	
78	PIK3CD	Qiagen_Plate 2	D4	Pik3cd	18707	siRNA4	SI01378552			CTCCACAAAGAAGAAGTCTAA
78	PIK3CD	Qiagen_Plate 2	H9	Pik3cd	18707	siRNA5	SI01378545			CAACGTGGGCATCATCTTTAA
78	PIK3CD	Qiagen_Plate 2	L17	Pik3cd	18707	siRNA6	SI01378538			CCGCGTGAAGAAGCTCATTAA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
79	PIK3CG	Ambion_Plate 2	E4	Pik3cg	30955	siRNA1	75098	GGAAACCUAUUUCAUAUAGtt	CUAUAUGAAAUAGGUUUCCtg	
79	PIK3CG	Ambion_Plate 2	I9	Pik3cg	30955	siRNA2	185960	GCAAUGUGCACGAUGAUGAtt	UCAUCAUCGUGCACAUUGCtg	
79	PIK3CG	Ambion_Plate 2	M17	Pik3cg	30955	siRNA3	185961	CCAUUGAUAUUAAAUCGCUtt	AGCGAUUUAAUAUCAAUGGtg	
79	PIK3CG	Qiagen_Plate 2	E4	Pik3cg	30955	siRNA4	SI01378580			CCCAAGTTATTTCACAGCTTA
79	PIK3CG	Qiagen_Plate 2	I9	Pik3cg	30955	siRNA5	SI01378573			CTCCATGATGTTGAAGAATAT
79	PIK3CG	Qiagen_Plate 2	M17	Pik3cg	30955	siRNA6	SI01378566			CCCAATCAGCTTCGAAAGCAA
80	PIK3R1	Ambion_Plate 2	F4	Pik3r1	18708	siRNA1	151107	CCUUUUUGGUACGAGACGCtt	GCGUCUCGUACCAAAAAGGtc	
80	PIK3R1	Ambion_Plate 2	J9	Pik3r1	18708	siRNA2	151108	GGAUUAUGCAUAACCAUGAtt	UCAUGGUUAUGCAUAAUCCtt	
80	PIK3R1	Ambion_Plate 2	N17	Pik3r1	18708	siRNA3	151109	GCGAAUGAUAUGUAUCAGAtt	UCUGAUACAUAUCAUUCGCtc	
80	PIK3R1	Qiagen_Plate 2	F4	Pik3r1	18708	siRNA4	SI04953431			AACCAATCGCTTTGTCGTATA
80	PIK3R1	Qiagen_Plate 2	J9	Pik3r1	18708	siRNA5	SI04953424			ATAGAGAAGTTTAAACGCGAA
80	PIK3R1	Qiagen_Plate 2	N17	Pik3r1	18708	siRNA6	SI01378601			AAGCATTTAATGAAACCATAA
81	PIK3R2	Ambion_Plate 2	G4	Pik3r2	18709	siRNA1	150111	CCUAAGCCCUCUAAGGCAAtt	UUGCCUUAGAGGGCUUAGGtg	
81	PIK3R2	Ambion_Plate 2	K9	Pik3r2	18709	siRNA2	150112	GCACAAUGACGCACUUACCtt	GGUAAGUGCGUCAUUGUGCtg	
81	PIK3R2	Ambion_Plate 2	C18	Pik3r2	18709	siRNA3	150113	GGUCGAAGUGAAACCAGUCtt	GACUGGUUUCACUUCGACCtt	
81	PIK3R2	Qiagen_Plate 2	G4	Pik3r2	18709	siRNA4	SI05170844			AAGCGCATGAACAGCCTCAAA
81	PIK3R2	Qiagen_Plate 2	K9	Pik3r2	18709	siRNA5	SI01378629			ATGGGTGACACAAGCCAAATA
81	PIK3R2	Qiagen_Plate 2	C18	Pik3r2	18709	siRNA6	SI01378622			CAGGAGCATGTGGAGGAGCAA
82	PIK3R3	Ambion_Plate 2	H4	Pik3r3	18710	siRNA1	152412	GCUUAUUAACCACUACCACtt	GUGGUAGUGGUUAAUAAGCtc	
82	PIK3R3	Ambion_Plate 2	L9	Pik3r3	18710	siRNA2	152413	GCUGACGUACCCAGUAUCCtt	GGAUACUGGGUACGUCAGCtt	
82	PIK3R3	Ambion_Plate 2	D18	Pik3r3	18710	siRNA3	152414	GCAGUUAUAUGCUCAAGAUtt	AUCUUGAGCAUAUAACUGCtt	
82	PIK3R3	Qiagen_Plate 2	H4	Pik3r3	18710	siRNA4	SI03650227			ATCCGGGATCAGCACCTTGTA
82	PIK3R3	Qiagen_Plate 2	L9	Pik3r3	18710	siRNA5	SI03650206			GAGGATATCAACCGAGTACAA
82	PIK3R3	Qiagen_Plate 2	D18	Pik3r3	18710	siRNA6	SI01378664			CTGCCGCATTATGATGAGAAA
83	PIK3R5	Ambion_Plate 2	I4	Pik3r5	320207	siRNA1	168079	CGCAAUGUGUUGGGCCUCAtt	UGAGGCCCAACACAUUGCGtt	
83	PIK3R5	Ambion_Plate 2	M9	Pik3r5	320207	siRNA2	168080	CCCUGACAGAAGUGGUGAAtt	UUCACCACUUCUGUCAGGGtt	
83	PIK3R5	Ambion_Plate 2	E18	Pik3r5	320207	siRNA3	168081	CCCUAAAUCCAAAAAGGGCtt	GCCCUUUUUGGAUUUAGGGtt	
83	PIK3R5	Qiagen_Plate 2	I4	Pik3r5	320207	siRNA4	SI01378720			ACCCAAGAGGTCCAAGAGAAA
83	PIK3R5	Qiagen_Plate 2	M9	Pik3r5	320207	siRNA5	SI01378713			CAGGAAGTCCTTCTCAAGGAA
83	PIK3R5	Qiagen_Plate 2	E18	Pik3r5	320207	siRNA6	SI01378706			CAGGACAGCTTTGACATCCTA
84	RAC1	Ambion_Plate 2	J4	Rac1	19353	siRNA1	164725	CGUGUUCUUAAUUUGCUUUtt	AAAGCAAAUUAAGAACACGtc	
84	RAC1	Ambion_Plate 2	N9	Rac1	19353	siRNA2	240531	CGGAGCUGUUGGUAAAACCtt	GGUUUUACCAACAGCUCCGtc	
84	RAC1	Ambion_Plate 2	F18	Rac1	19353	siRNA3	240532	CGCACCUGUAACUUAUCAGtt	CUGAUAAGUUACAGGUGCGtt	
84	RAC1	Qiagen_Plate 2	J4	Rac1	19353	siRNA4	SI02734620			ATGGAGTAATTCAACTGAATA
84	RAC1	Qiagen_Plate 2	N9	Rac1	19353	siRNA5	SI00181377			AAGCTTGATCTTAGGGATGAT
84	RAC1	Qiagen_Plate 2	F18	Rac1	19353	siRNA6	SI00181370			GGGCGTTGAGTCCATATTTAA
85	IRF5	Ambion_Plate 2	K4	Irf5	27056	siRNA1	188320	CCCACUGAUGAUUACGUUCtt	GAACGUAAUCAUCAGUGGGtt	
85	IRF5	Ambion_Plate 2	C10	Irf5	27056	siRNA2	188321	GCCACGUAGACUGAUAUAGtt	CUAUAUCAGUCUACGUGGCtg	
85	IRF5	Ambion_Plate 2	G18	Irf5	27056	siRNA3	188322	CGUAGACUGAUAUAGCAAUtt	AUUGCUAUAUCAGUCUACGtg	
85	IRF5	Qiagen_Plate 2	K4	Irf5	27056	siRNA4	SI01077748			CACCCAGTTGGCATGCAATAA
85	IRF5	Qiagen_Plate 2	C10	Irf5	27056	siRNA5	SI01077741			CAGGAGCAAGTGGAACTCTTT
85	IRF5	Qiagen_Plate 2	G18	Irf5	27056	siRNA6	SI01077734			CACCTTCTGGTGATTTCTCTA
86	IRF7	Ambion_Plate 2	L4	Irf7	54123	siRNA1	72667	GGUGUACGAACUUAGCCGGtt	CCGGCUAAGUUCGUACACCtt	
86	IRF7	Ambion_Plate 2	D10	Irf7	54123	siRNA2	72762	GGAUCAUUUCUGGCAAGAGtt	CUCUUGCCAGAAAUGAUCCtg	
86	IRF7	Ambion_Plate 2	H18	Irf7	54123	siRNA3	184589	GCCACGGAAAAUAGGGAAGtt	CUUCCCUAUUUUCCGUGGCtg	
86	IRF7	Qiagen_Plate 2	L4	Irf7	54123	siRNA4	SI02740927			CAAGACCGTGTTTACGAGGAA
86	IRF7	Qiagen_Plate 2	D10	Irf7	54123	siRNA5	SI01077797			CCCGAGGGAGGTGGCCACCTA
86	IRF7	Qiagen_Plate 2	H18	Irf7	54123	siRNA6	SI01077790			CAGCCACATACTGGAATCCGA
87	STAT1	Ambion_Plate 2	M4	Stat1	20846	siRNA1	64816	GGACUUCAUGCAUCUUACUtt	AGUAAGAUGCAUGAAGUCCtt	
87	STAT1	Ambion_Plate 2	E10	Stat1	20846	siRNA2	151009	GCUGAACUAUAACUUGAAAtt	UUUCAAGUUAUAGUUCAGCtc	
87	STAT1	Ambion_Plate 2	I18	Stat1	20846	siRNA3	240534	CCUAACCAUUGCUUAUAUAtt	UAUAUAAGCAAUGGUUAGGtc	
87	STAT1	Qiagen_Plate 2	M4	Stat1	20846	siRNA4	SI02735054			ATGAGTTGGTTTAATATATAT
87	STAT1	Qiagen_Plate 2	E10	Stat1	20846	siRNA5	SI02710729			ATGCATCTTACTGAAGGTGAA
87	STAT1	Qiagen_Plate 2	I18	Stat1	20846	siRNA6	SI02668862			TCCTATTATTATTTAATATAA
88	Fos	Ambion_Plate 2	N4	Fos	14281	siRNA1	67034	GGCAGAACCCUUUGAUGACtt	GUCAUCAAAGGGUUCUGCCtt	
88	Fos	Ambion_Plate 2	F10	Fos	14281	siRNA2	240543	GCUGAUUUUAACAAUACCUtt	AGGUAUUGUUAAAAUCAGCtg	
88	Fos	Ambion_Plate 2	J18	Fos	14281	siRNA3	240544	CCUCUUCCAGAGAUGUAGCtt	GCUACAUCUCUGGAAGAGGtg	
88	Fos	Qiagen_Plate 2	N4	Fos	14281	siRNA4	SI02736825			TAGATAGAAATCAATAGCTAT
88	Fos	Qiagen_Plate 2	F10	Fos	14281	siRNA5	SI00191184			GACCAATATTAAACTAAGAAA
88	Fos	Qiagen_Plate 2	J18	Fos	14281	siRNA6	SI00191170			TTCCAAGACATTGTCAATAAA
89	Jun	Ambion_Plate 2	C5	Jun	16476	siRNA1	67634	GGAAAAAGUGAAAACCUUGtt	CAAGGUUUUCACUUUUUCCtc	
89	Jun	Ambion_Plate 2	G10	Jun	16476	siRNA2	67730	GGGUACACAAGAUGGACUGtt	CAGUCCAUCUUGUGUACCCtt	
89	Jun	Ambion_Plate 2	K18	Jun	16476	siRNA3	155944	CGAUGGACUUUUCGUUAACtt	GUUAACGAAAAGUCCAUCGtt	
89	Jun	Qiagen_Plate 2	C5	Jun	16476	siRNA4	SI01079876			ATCATTTATAATCATAGGAAA
89	Jun	Qiagen_Plate 2	G10	Jun	16476	siRNA5	SI01079869			CTGCCCAGTGTTTGTAAATAA
89	Jun	Qiagen_Plate 2	K18	Jun	16476	siRNA6	SI01079862			AAGCTGATTACTGTCAATAAA
90	PYK2	Ambion_Plate 2	D5	Ptk2b	19229	siRNA1	94190	GGGAAGAACUUCAAGCUUGtt	CAAGCUUGAAGUUCUUCCCtg	
90	PYK2	Ambion_Plate 2	H10	Ptk2b	19229	siRNA2	94285	GGACAAGUAUGAAUGUCUAtt	UAGACAUUCAUACUUGUCCtg	
90	PYK2	Ambion_Plate 2	L18	Ptk2b	19229	siRNA3	152396	CCCUAUGGUUUAUAUGAAUtt	AUUCAUAUAAACCAUAGGGtc	
90	PYK2	Qiagen_Plate 2	D5	Ptk2b	19229	siRNA4	SI01392468			TACAGTGTACATTGGAATTTA
90	PYK2	Qiagen_Plate 2	H10	Ptk2b	19229	siRNA5	SI01392461			CAGCATAGAGTCAGACATCTA
90	PYK2	Qiagen_Plate 2	L18	Ptk2b	19229	siRNA6	SI01392454			CAGGACAAGTATGAATGTCTA
91	ETS1	Ambion_Plate 2	E5	Ets1	23871	siRNA1	70153	GGAAAAACAAACCUAGCAUtt	AUGCUAGGUUUGUUUUUCCtc	
91	ETS1	Ambion_Plate 2	I10	Ets1	23871	siRNA2	101968	GCUACUUUAGUGGUUUCACtt	GUGAAACCACUAAAGUAGCtt	
91	ETS1	Ambion_Plate 2	M18	Ets1	23871	siRNA3	187765	GCUUUGACUACGAGGAUUAtt	UAAUCCUCGUAGUCAAAGCtg	
91	ETS1	Qiagen_Plate 2	E5	Ets1	23871	siRNA4	SI04447926			TAGGTGGGATCATTTGGATTA
91	ETS1	Qiagen_Plate 2	I10	Ets1	23871	siRNA5	SI04403336			CTGAGGTAGCTTAGAGATGTA
91	ETS1	Qiagen_Plate 2	M18	Ets1	23871	siRNA6	SI04403329			CACTGTATAGCTGCCTAGTTA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
92	ELK1	Ambion_Plate 2	F5	Elk1	13712	siRNA1	61298	GGUGAGCGGCCAGAAGUUUtt	AAACUUCUGGCCGCUCACCtt	
92	ELK1	Ambion_Plate 2	J10	Elk1	13712	siRNA2	61394	GGUGGCUUAGCACGAAGCAtt	UGCUUCGUGCUAAGCCACCtt	
92	ELK1	Ambion_Plate 2	N18	Elk1	13712	siRNA3	261017	GCCGGAAUGAAUACAUGCGtt	CGCAUGUAUUCAUUCCGGCtg	
92	ELK1	Qiagen_Plate 2	F5	Elk1	13712	siRNA4	SI02732401			CTGCAGCTTCTGAGAGAACAA
92	ELK1	Qiagen_Plate 2	J10	Elk1	13712	siRNA5	SI02708321			CCCAGCCATCCTAACAGAGAA
92	ELK1	Qiagen_Plate 2	N18	Elk1	13712	siRNA6	SI00992789			ATGGCTTGAGAGGAACCTTTA
93	ELK4	Ambion_Plate 2	G5	Elk4	13714	siRNA1	61395	GGGAGACUGUGAAGCUUUAtt	UAAAGCUUCACAGUCUCCCtc	
93	ELK4	Ambion_Plate 2	K10	Elk4	13714	siRNA2	102751	GUGAAUGGUCAGAAGUUUGtt	CAAACUUCUGACCAUUCACtt	
93	ELK4	Ambion_Plate 2	C19	Elk4	13714	siRNA3	157305	GGGUUAGAACUGACACCCGtt	CGGGUGUCAGUUCUAACCCtt	
93	ELK4	Qiagen_Plate 2	G5	Elk4	13714	siRNA4	SI02732408			CAAGTCAATAAAGATAGAGAA
93	ELK4	Qiagen_Plate 2	K10	Elk4	13714	siRNA5	SI02666783			CTGGTTTGTATTCTTCATTTA
93	ELK4	Qiagen_Plate 2	C19	Elk4	13714	siRNA6	SI00170464			TACGTAAAGAACATCATTAAA
94	SP1	Ambion_Plate 2	H5	Sp1	20683	siRNA1	71295	GGUGAACUUGACCUCACAGtt	CUGUGAGGUCAAGUUCACCtg	
94	SP1	Ambion_Plate 2	L10	Sp1	20683	siRNA2	152025	GCAGAAUUGAGUCACCCAAtt	UUGGGUGACUCAAUUCUGCtg	
94	SP1	Ambion_Plate 2	D19	Sp1	20683	siRNA3	152026	GGUCUACCUGGAGUAAUGCtt	GCAUUACUCCAGGUAGACCtg	
94	SP1	Qiagen_Plate 2	H5	Sp1	20683	siRNA4	SI02740171			CAGCACATTTGTCACATCCAA
94	SP1	Qiagen_Plate 2	L10	Sp1	20683	siRNA5	SI02715440			CAGATTCTATATTATATATAT
94	SP1	Qiagen_Plate 2	D19	Sp1	20683	siRNA6	SI01429876			CCAGGTGATCATGGAACTCAA
95	EGR1	Ambion_Plate 2	I5	Egr1	13653	siRNA1	157281	CCUUUCCUACUCCCAACACtt	GUGUUGGGAGUAGGAAAGGtg	
95	EGR1	Ambion_Plate 2	M10	Egr1	13653	siRNA2	157282	GGCUCUUAAUACCACCUACtt	GUAGGUGGUAUUAAGAGCCtt	
95	EGR1	Ambion_Plate 2	E19	Egr1	13653	siRNA3	157283	GGCAUACCAAAAUCCAUUUtt	AAAUGGAUUUUGGUAUGCCtc	
95	EGR1	Qiagen_Plate 2	I5	Egr1	13653	siRNA4	SI00990920			CAGGACTTAAAGGCTCTTAAT
95	EGR1	Qiagen_Plate 2	M10	Egr1	13653	siRNA5	SI00990913			AAATGTAAATTTATACATCTA
95	EGR1	Qiagen_Plate 2	E19	Egr1	13653	siRNA6	SI00990906			TTGGCTTATAAACACATTGAA
96	EGR2	Ambion_Plate 2	J5	Egr2	13654	siRNA1	66675	GGAUCCUUCAGCAUUCUUAtt	UAAGAAUGCUGAAGGAUCCtg	
96	EGR2	Ambion_Plate 2	N10	Egr2	13654	siRNA2	158361	GCUGCUAUCCAGAAGGUAUtt	AUACCUUCUGGAUAGCAGCtg	
96	EGR2	Ambion_Plate 2	F19	Egr2	13654	siRNA3	240541	GGUGAGAAUGUGCUUCAAUtt	AUUGAAGCACAUUCUCACCtg	
96	EGR2	Qiagen_Plate 2	J5	Egr2	13654	siRNA4	SI02712171			TTGAAATGAGTCAAAGGTTAA
96	EGR2	Qiagen_Plate 2	N10	Egr2	13654	siRNA5	SI02689974			CTGACTGTTATAATAACACTA
96	EGR2	Qiagen_Plate 2	F19	Egr2	13654	siRNA6	SI02669961			AACAATCTATTCTAACATAAA
97	ATF2	Ambion_Plate 2	K5	Atf2	11909	siRNA1	160772	GCCCACAUCAGCUAUCGUUtt	AACGAUAGCUGAUGUGGGCtg	
97	ATF2	Ambion_Plate 2	C14	Atf2	11909	siRNA2	160773	GCUAUCGUUCGUCCAGCAUtt	AUGCUGGACGAACGAUAGCtg	
97	ATF2	Ambion_Plate 2	G19	Atf2	11909	siRNA3	160774	CCUCAAGUACUGUAAUCACtt	GUGAUUACAGUACUUGAGGtt	
97	ATF2	Qiagen_Plate 2	K5	Atf2	11909	siRNA4	SI02735803			AAGCAGGATTCCATTCTGTAA
97	ATF2	Qiagen_Plate 2	C14	Atf2	11909	siRNA5	SI02711478			CAGCTTCAAGATGCCGACAAA
97	ATF2	Qiagen_Plate 2	G19	Atf2	11909	siRNA6	SI02652545			CAGTCTGTACTCAGCAAATAA
98	ATF7	Ambion_Plate 2	L5	Atf7	223922	siRNA1	90648	GGUAUUGAGUAUCUUAGGUtt	ACCUAAGAUACUCAAUACCtg	
98	ATF7	Ambion_Plate 2	D14	Atf7	223922	siRNA2	163712	CGGACUCAGUCAUCAUUGCtt	GCAAUGAUGACUGAGUCCGtt	
98	ATF7	Ambion_Plate 2	H19	Atf7	223922	siRNA3	163714	GCGAAAUCAGUUGGUAAAUtt	AUUUACCAACUGAUUUCGCtt	
98	ATF7	Qiagen_Plate 2	L5	Atf7	223922	siRNA4	SI00905996			CAGTAATAACATAACTAGAAA
98	ATF7	Qiagen_Plate 2	D14	Atf7	223922	siRNA5	SI00905989			CAGCTACTGTTAGCTCATAAA
98	ATF7	Qiagen_Plate 2	H19	Atf7	223922	siRNA6	SI00905982			TCCAGGTGTGTTATTTGTTAA
99	CBP	Ambion_Plate 2	M5	Crebbp	12914	siRNA1	283827	CCAAGGAGACUCAUCAACAtt	UGUUGAUGAGUCUCCUUGGtt	
99	CBP	Ambion_Plate 2	E14	Crebbp	12914	siRNA2	283828	GCGGAGGUCACGUUUACAUtt	AUGUAAACGUGACCUCCGCtt	
99	CBP	Ambion_Plate 2	I19	Crebbp	12914	siRNA3	283829	CCUAUACCGAGCAAACAUCtt	GAUGUUUGCUCGGUAUAGGtg	
99	CBP	Qiagen_Plate 2	M5	Crebbp	12914	siRNA4	SI00959252			CAGGTGCTGAACATCCTTAAA
99	CBP	Qiagen_Plate 2	E14	Crebbp	12914	siRNA5	SI00959245			CAGAGCATGGTCAATAGTTTA
99	CBP	Qiagen_Plate 2	I19	Crebbp	12914	siRNA6	SI00959238			CTGCCTCAACATCAAACATAA
100	p300	Ambion_Plate 2	N5	Ep300	328572	siRNA1	99177	GGCUUGACUUCUCCAAACAtt	UGUUUGGAGAAGUCAAGCCtg	
100	p300	Ambion_Plate 2	F14	Ep300	328572	siRNA2	99273	GGUAUGAUGAACAGUCCAGtt	CUGGACUGUUCAUCAUACCtg	
100	p300	Ambion_Plate 2	J19	Ep300	328572	siRNA3	261617	GCGAAAUCAACAGUCAAUUtt	AAUUGACUGUUGAUUUCGCtt	
100	p300	Qiagen_Plate 2	N5	Ep300	328572	siRNA4	SI00994280			ATCACTTGTTATAACACTAAA
100	p300	Qiagen_Plate 2	F14	Ep300	328572	siRNA5	SI00994273			CTGAGGGATAATAGATTACAA
100	p300	Qiagen_Plate 2	J19	Ep300	328572	siRNA6	SI00994266			AAGGTTGATTACTTATAAATA
101	ISGF3G	Ambion_Plate 2	C6	Irf9	16391	siRNA1	62609	GGGAAGAAAAUAUGGAAAAtt	UUUUCCAUAUUUUCUUCCCtc	
101	ISGF3G	Ambion_Plate 2	G14	Irf9	16391	siRNA2	154911	CCCUACAAAGUAUAUCGAAtt	UUCGAUAUACUUUGUAGGGtt	
101	ISGF3G	Ambion_Plate 2	K19	Irf9	16391	siRNA3	154913	GCUCCAAAUUAAAUUUUGCtt	GCAAAAUUUAAUUUGGAGCtc	
101	ISGF3G	Qiagen_Plate 2	C6	Irf9	16391	siRNA4	SI01078112			ATGCTTATAAGTCAGATGTAA
101	ISGF3G	Qiagen_Plate 2	G14	Irf9	16391	siRNA5	SI01078105			AAGGAACTGGAAAGTTCCAAA
101	ISGF3G	Qiagen_Plate 2	K19	Irf9	16391	siRNA6	SI01078098			CAGTCCCAAACTCTAAATCTA
102	ELF4	Ambion_Plate 2	D6	Elf4	56501	siRNA1	74071	GGUCCACAAUGGCAUCAUAtt	UAUGAUGCCAUUGUGGACCtc	
102	ELF4	Ambion_Plate 2	H14	Elf4	56501	siRNA2	74259	GGAAAAUCUUAGGAAGAUGtt	CAUCUUCCUAAGAUUUUCCtc	
102	ELF4	Ambion_Plate 2	L19	Elf4	56501	siRNA3	185441	GGUCUAGGUAGGAGAACUUtt	AAGUUCUCCUACCUAGACCtt	
102	ELF4	Qiagen_Plate 2	D6	Elf4	56501	siRNA4	SI04956462			AGGCCTGGTCATACTTCGTTA
102	ELF4	Qiagen_Plate 2	H14	Elf4	56501	siRNA5	SI00992740			CAGCCCTATGCTTGACAATAA
102	ELF4	Qiagen_Plate 2	L19	Elf4	56501	siRNA6	SI00992733			CACAGGGAATTTACCATCCAA
103	IFNAR1	Ambion_Plate 2	E6	Ifnar1	15975	siRNA1	67499	GGCGAAGUGGUUAAAAGUGtt	CACUUUUAACCACUUCGCCtc	
103	IFNAR1	Ambion_Plate 2	I14	Ifnar1	15975	siRNA2	67586	GGCAUGAACCAUUCAGUAAtt	UUACUGAAUGGUUCAUGCCtg	
103	IFNAR1	Ambion_Plate 2	M19	Ifnar1	15975	siRNA3	159104	CCUUUUCAGCAGAAUAUCGtt	CGAUAUUCUGCUGAAAAGGtc	
103	IFNAR1	Qiagen_Plate 2	E6	Ifnar1	15975	siRNA4	SI02737224			CTGAATGTCAACATACTACAA
103	IFNAR1	Qiagen_Plate 2	I14	Ifnar1	15975	siRNA5	SI02690408			CAGGCACATGTTCTTAAGGAA
103	IFNAR1	Qiagen_Plate 2	M19	Ifnar1	15975	siRNA6	SI02670339			CACGGTCGCTGTAGAAGTAAA
104	IFNAR2	Ambion_Plate 2	F6	Ifnar2	15976	siRNA1	67408	GGUUAAGAACUGUUCAGAUtt	AUCUGAACAGUUCUUAACCtt	
104	IFNAR2	Ambion_Plate 2	J14	Ifnar2	15976	siRNA2	67500	GGAAAAGAUGAAGACUACAtt	UGUAGUCUUCAUCUUUUCCtg	
104	IFNAR2	Ambion_Plate 2	N19	Ifnar2	15976	siRNA3	67587	GGUGGUUUGUGUUACAUUUtt	AAAUGUAACACAAACCACCtt	
104	IFNAR2	Qiagen_Plate 2	F6	Ifnar2	15976	siRNA4	SI04947866			TACCACGAAGTCATCATGTGA
104	IFNAR2	Qiagen_Plate 2	J14	Ifnar2	15976	siRNA5	SI04947859			CACAGTCATGAGCAAAGACGA
104	IFNAR2	Qiagen_Plate 2	N19	Ifnar2	15976	siRNA6	SI02712745			ATCCTGGGAATTAGAGAACAA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
105	IFNB1	Ambion_Plate 2	G6	Ifnb1	15977	siRNA1	67501	GGAAAAGCAAGAGGAAAGAtt	UCUUUCCUCUUGCUUUUCCtc	
105	IFNB1	Ambion_Plate 2	K14	Ifnb1	15977	siRNA2	67588	GGUACCUUAAACUCAUGAAtt	UUCAUGAGUUUAAGGUACCtt	
105	IFNB1	Ambion_Plate 2	C20	Ifnb1	15977	siRNA3	159108	CGAACAUUCGGAAAUGUCAtt	UGACAUUUCCGAAUGUUCGtc	
105	IFNB1	Qiagen_Plate 2	G6	Ifnb1	15977	siRNA4	SI01073884			CCGAGCAGAGATCTTCAGGAA
105	IFNB1	Qiagen_Plate 2	K14	Ifnb1	15977	siRNA5	SI01073877			AGCCCTCTCCATCAACTATAA
105	IFNB1	Qiagen_Plate 2	C20	Ifnb1	15977	siRNA6	SI01073870			TGGAATGAGACTATTGTTGTA
106	IL12A	Ambion_Plate 2	H6	Il12a	16159	siRNA1	62385	GGACUUGAAGAUGUACCAGtt	CUGGUACAUCUUCAAGUCCtc	
106	IL12A	Ambion_Plate 2	L14	Il12a	16159	siRNA2	102773	GACCACAGAUGACAUGGUGtt	CACCAUGUCAUCUGUGGUCtt	
106	IL12A	Ambion_Plate 2	D20	Il12a	16159	siRNA3	158261	CCAAACCAGCACAUUGAAGtt	CUUCAAUGUGCUGGUUUGGtc	
106	IL12A	Qiagen_Plate 2	H6	Il12a	16159	siRNA4	SI02733150			ACCACTGGAACTACACAAGAA
106	IL12A	Qiagen_Plate 2	L14	Il12a	16159	siRNA5	SI02709049			AACCATCAGCAGATCATTCTA
106	IL12A	Qiagen_Plate 2	D20	Il12a	16159	siRNA6	SI00174594			CACCCGCGTCGTGACCATCAA
107	IL12B	Ambion_Plate 2	I6	Il12b	16160	siRNA1	62386	GGAAAAUGGAAUUUGGUCCtt	GGACCAAAUUCCAUUUUCCtt	
107	IL12B	Ambion_Plate 2	M14	Il12b	16160	siRNA2	158263	GCUCAGGAUCGCUAUUACAtt	UGUAAUAGCGAUCCUGAGCtt	
107	IL12B	Ambion_Plate 2	E20	Il12b	16160	siRNA3	158264	CGGCAGCAGAAUAAAUAUGtt	CAUAUUUAUUCUGCUGCCGtg	
107	IL12B	Qiagen_Plate 2	I6	Il12b	16160	siRNA4	SI02733157			AGAAGTGATATTGATAAGAAA
107	IL12B	Qiagen_Plate 2	M14	Il12b	16160	siRNA5	SI02667483			TTGAAATATTTAAGTAATTTA
107	IL12B	Qiagen_Plate 2	E20	Il12b	16160	siRNA6	SI00174615			AGGCTGGGTATCGGTGGTATA
108	IL1B	Ambion_Plate 2	J6	Il1b	16176	siRNA1	158282	CCCAUAUGAGCUGAAAGCUtt	AGCUUUCAGCUCAUAUGGGtc	
108	IL1B	Ambion_Plate 2	N14	Il1b	16176	siRNA2	158283	GCGGUUUGUCUUCAACAAGtt	CUUGUUGAAGACAAACCGCtt	
108	IL1B	Ambion_Plate 2	F20	Il1b	16176	siRNA3	158284	GGUCUUUCAUUGAAGCUGAtt	UCAGCUUCAAUGAAAGACCtc	
108	IL1B	Qiagen_Plate 2	J6	Il1b	16176	siRNA4	SI02709091			TTGATTGGTTGATCTATTTAA
108	IL1B	Qiagen_Plate 2	N14	Il1b	16176	siRNA5	SI02687181			AAGATAGAAGTCAAGAGCAAA
108	IL1B	Qiagen_Plate 2	F20	Il1b	16176	siRNA6	SI02667532			TTCATTGAAGCTGAGAATAAA
109	IL6	Ambion_Plate 2	K6	Il6	16193	siRNA1	84958	GGCUUAAUUACACAUGUUCtt	GAACAUGUGUAAUUAAGCCtc	
109	IL6	Ambion_Plate 2	C15	Il6	16193	siRNA2	85048	GGAAAUUUGCCUAUUGAAAtt	UUUCAAUAGGCAAAUUUCCtg	
109	IL6	Ambion_Plate 2	G20	Il6	16193	siRNA3	159540	CCAAGACCAUCCAAUUCAUtt	AUGAAUUGGAUGGUCUUGGtc	
109	IL6	Qiagen_Plate 2	K6	Il6	16193	siRNA4	SI02719934			CACTTGAAATGTTATATGTTA
109	IL6	Qiagen_Plate 2	C15	Il6	16193	siRNA5	SI02696547			TAGACTGTCTTCAAACAAATA
109	IL6	Qiagen_Plate 2	G20	Il6	16193	siRNA6	SI00229334			TACGAAGAACTGACAATATGA
110	TNF	Ambion_Plate 2	L6	Tnf	21926	siRNA1	188363	CGUCGUAGCAAACCACCAAtt	UUGGUGGUUUGCUACGACGtg	
110	TNF	Ambion_Plate 2	D15	Tnf	21926	siRNA2	188364	GCCGAUUUGCUAUCUCAUAtt	UAUGAGAUAGCAAAUCGGCtg	
110	TNF	Ambion_Plate 2	H20	Tnf	21926	siRNA3	240560	GGGAAUGGGUGUUCAUCCAtt	UGGAUGAACACCCAUUCCCtt	
110	TNF	Qiagen_Plate 2	L6	Tnf	21926	siRNA4	SI00207697			CACGCTCTTCTGTCTACTGAA
110	TNF	Qiagen_Plate 2	D15	Tnf	21926	siRNA5	SI00207690			ACCCTGGTATGAGCCCATATA
110	TNF	Qiagen_Plate 2	H20	Tnf	21926	siRNA6	SI00207683			AAGGGAATGGGTGTTCATCCA
111	CCL3	Ambion_Plate 2	M6	Ccl3	20302	siRNA1	69171	GGGACUCUUCACUUGAAAUtt	AUUUCAAGUGAAGAGUCCCtc	
111	CCL3	Ambion_Plate 2	E15	Ccl3	20302	siRNA2	102821	GAUUCCACGCCAAUUCAUCtt	GAUGAAUUGGCGUGGAAUCtt	
111	CCL3	Ambion_Plate 2	I20	Ccl3	20302	siRNA3	151589	CGCCAAUUCAUCGUUGACUtt	AGUCAACGAUGAAUUGGCGtg	
111	CCL3	Qiagen_Plate 2	M6	Ccl3	20302	siRNA4	SI00943376			CACACTGTTTGGTGACAGCTA
111	CCL3	Qiagen_Plate 2	E15	Ccl3	20302	siRNA5	SI00943369			TCGAGGGACTCTTCACTTGAA
111	CCL3	Qiagen_Plate 2	I20	Ccl3	20302	siRNA6	SI00943362			TTGTGACTATTTATTCTGAAA
112	CXCL11	Ambion_Plate 2	N6	Cxcl11	56066	siRNA1	73784	GGCUCAUAAACGACAAAGGtt	CCUUUGUCGUUUAUGAGCCtt	
112	CXCL11	Ambion_Plate 2	F15	Cxcl11	56066	siRNA2	73878	GGUCCGAUACAUCUAAACUtt	AGUUUAGAUGUAUCGGACCtt	
112	CXCL11	Ambion_Plate 2	J20	Cxcl11	56066	siRNA3	73966	GGGCUACACAAAAUUUUAAtt	UUAAAAUUUUGUGUAGCCCtg	
112	CXCL11	Qiagen_Plate 2	N6	Cxcl11	56066	siRNA4	SI03975419			CCCGGGATGAAAGCCGTCAAA
112	CXCL11	Qiagen_Plate 2	F15	Cxcl11	56066	siRNA5	SI02741529			AAGAATTGTGTTTCTCTAGTA
112	CXCL11	Qiagen_Plate 2	J20	Cxcl11	56066	siRNA6	SI02716728			CACCTTAATTTCAGCACTTGA
113	CXCL9	Ambion_Plate 2	C7	Cxcl9	17329	siRNA1	63140	GGAAGACUACAUAAGAGACtt	GUCUCUUAUGUAGUCUUCCtt	
113	CXCL9	Ambion_Plate 2	G15	Cxcl9	17329	siRNA2	155360	CCCUAGUGAUAAGGAAUGCtt	GCAUUCCUUAUCACUAGGGtt	
113	CXCL9	Ambion_Plate 2	K20	Cxcl9	17329	siRNA3	155362	GCCUUUAAUACAUAGGCUUtt	AAGCCUAUGUAUUAAAGGCtg	
113	CXCL9	Qiagen_Plate 2	C7	Cxcl9	17329	siRNA4	SI02733787			CAGAGCAGCCTTTAATACATA
113	CXCL9	Qiagen_Plate 2	G15	Cxcl9	17329	siRNA5	SI02687678			AACAAGCACCCTGAATCTTAA
113	CXCL9	Qiagen_Plate 2	K20	Cxcl9	17329	siRNA6	SI02667945			AAGTGTTAATTTGAAATTATA
114	RP105	Ambion_Plate 2	D7	Cd180	17079	siRNA1	62821	GGCAUUGAAGCAUCUGUUCtt	GAACAGAUGCUUCAAUGCCtt	
114	RP105	Ambion_Plate 2	H15	Cd180	17079	siRNA2	62903	GGAAUAUCCAGUAUUGAUUtt	AAUCAAUACUGGAUAUUCCtg	
114	RP105	Ambion_Plate 2	L20	Cd180	17079	siRNA3	155218	GCAGAGGACCAUUAAUUUAtt	UAAAUUAAUGGUCCUCUGCtg	
114	RP105	Qiagen_Plate 2	D7	Cd180	17079	siRNA4	SI02733626			CTGCACTTGCTCAAACATTTA
114	RP105	Qiagen_Plate 2	H15	Cd180	17079	siRNA5	SI02709497			CTGGCACTTTACCAAACTCAA
114	RP105	Qiagen_Plate 2	L20	Cd180	17079	siRNA6	SI02687531			CTCAGCCATGATGACATTGAA
115	MD1	Ambion_Plate 2	E7	Ly86	17084	siRNA1	67927	GGAUUUUGGCCUUUCCAUUtt	AAUGGAAAGGCCAAAAUCCtg	
115	MD1	Ambion_Plate 2	I15	Ly86	17084	siRNA2	68022	GGCUCUUCUAUUCUGAACUtt	AGUUCAGAAUAGAAGAGCCtt	
115	MD1	Ambion_Plate 2	M20	Ly86	17084	siRNA3	156191	GCAGAUCCAAUCAAAUCUCtt	GAGAUUUGAUUGGAUCUGCtt	
115	MD1	Qiagen_Plate 2	E7	Ly86	17084	siRNA4	SI05392660			AGCAGTGACCATGGCAGCGAA
115	MD1	Qiagen_Plate 2	I15	Ly86	17084	siRNA5	SI01297548			CTGAGTAGTCTTGAAGCCCTA
115	MD1	Qiagen_Plate 2	M20	Ly86	17084	siRNA6	SI01297541			TCCAATCAAATCTCAACATTA
116	TIR8	Ambion_Plate 2	F7	Sigirr	24058	siRNA1	76562	GGACUAUGGAACCUUCACCtt	GGUGAAGGUUCCAUAGUCCtc	
116	TIR8	Ambion_Plate 2	J15	Sigirr	24058	siRNA2	76747	GGGUGUCACAAAAUAAAAUtt	AUUUUAUUUUGUGACACCCtg	
116	TIR8	Ambion_Plate 2	N20	Sigirr	24058	siRNA3	188836	CCCGACUUCAGGAUGACAAtt	UUGUCAUCCUGAAGUCGGGtt	
116	TIR8	Qiagen_Plate 2	F7	Sigirr	24058	siRNA4	SI00892192			CAGCGTTTGGCCTGCCGTGAA
116	TIR8	Qiagen_Plate 2	J15	Sigirr	24058	siRNA5	SI00892185			CACCAACTCCACTGCAGGAAA
116	TIR8	Qiagen_Plate 2	N20	Sigirr	24058	siRNA6	SI00892178			CCGGTGGAGGGAGACCCTCAA
117	ST2	Ambion_Plate 2	G7	Il1rl1	17082	siRNA1	67926	GGCUUUAAUUGUGAGAUGCtt	GCAUCUCACAAUUAAAGCCtc	
117	ST2	Ambion_Plate 2	K15	Il1rl1	17082	siRNA2	68021	GGUCCUACUUGUUCAUUGAtt	UCAAUGAACAAGUAGGACCtg	
117	ST2	Ambion_Plate 2	C21	Il1rl1	17082	siRNA3	156184	CCAUACAUAAAAAGCCGCCtt	GGCGGCUUUUUAUGUAUGGtg	
117	ST2	Qiagen_Plate 2	G7	Il1rl1	17082	siRNA4	SI02737616			AACGTGACTCATGATGATGAA
117	ST2	Qiagen_Plate 2	K15	Il1rl1	17082	siRNA5	SI02713067			CAGCACCTGTTCAGTGGTTTA
117	ST2	Qiagen_Plate 2	C21	Il1rl1	17082	siRNA6	SI02690744			AAGAGGAAGGTCGAAATGAAA

TABLE S1 (MOUSE siRNA)										
Gene#	Name	Plate Name	Location	Gene Symbol	Gene ID	siRNA#	siRNA ID	Ambion Sense siRNA Sequence	Ambion Antisense siRNA Sequence	Qiagen siRNA target sequence
118	IRAK3	Ambion_Plate 2	H7	Irak3	73914	siRNA1	82960	GGUAAAAGUGGAACAAGAGtt	CUCUUGUUCCACUUUUACCtt	
118	IRAK3	Ambion_Plate 2	L15	Irak3	73914	siRNA2	177805	CGAUCGGCGACCUUUUAGAtt	UCUAAAAGGUCGCCGAUCGtc	
118	IRAK3	Ambion_Plate 2	D21	Irak3	73914	siRNA3	177807	CGAGCUAUCCACUUAAUCAtt	UGAUUAAGUGGAUAGCUCGtt	
118	IRAK3	Qiagen_Plate 2	H7	Irak3	73914	siRNA4	SI04451363			ATCAACGAGCTATCCACTTAA
118	IRAK3	Qiagen_Plate 2	L15	Irak3	73914	siRNA5	SI04405457			AGCAGCAGAGTTCTACCATAA
118	IRAK3	Qiagen_Plate 2	D21	Irak3	73914	siRNA6	SI01077580			AGGGAAGTTGCTCAAATGCAA
119	SHP1	Ambion_Plate 2	I7	Ptpn6	15170	siRNA1	71010	GGUGACUCAUAUUCGGAUCtt	GAUCCGAAUAUGAGUCACCtg	
119	SHP1	Ambion_Plate 2	M15	Ptpn6	15170	siRNA2	71198	GGAAGAGAAAGUAAAGAAGtt	CUUCUUUACUUUCUCUUCCtt	
119	SHP1	Ambion_Plate 2	E21	Ptpn6	15170	siRNA3	159276	GCUGACAUUGAGAAUCGGGtt	CCCGAUUCUCAAUGUCAGCtg	
119	SHP1	Qiagen_Plate 2	I7	Ptpn6	15170	siRNA4	SI04919369			CTGGATCAGATCAACCAGCGA
119	SHP1	Qiagen_Plate 2	M15	Ptpn6	15170	siRNA5	SI04919362			CTGGACATTTCTTGTGCGTGA
119	SHP1	Qiagen_Plate 2	E21	Ptpn6	15170	siRNA6	SI02739961			TCGGGTCTTGGAACTGAACAA
120	Cyld	Ambion_Plate 2	J7	Cyld	74256	siRNA1	95627	GGCAAGAAAAAUCAGAUUGtt	CAAUCUGAUUUUUCUUGCCtt	
120	Cyld	Ambion_Plate 2	N15	Cyld	74256	siRNA2	95721	GGGAUAUGAAAUCAUUUUCtt	GAAAAUGAUUUCAUAUCCCtg	
120	Cyld	Ambion_Plate 2	F21	Cyld	74256	siRNA3	178797	GGGUUGAACCAUUGUUAAAtt	UUUAACAAUGGUUCAACCCtt	
120	Cyld	Qiagen_Plate 2	J7	Cyld	74256	siRNA4	SI00963396			AAGGTTCATCTAGTCATAATA
120	Cyld	Qiagen_Plate 2	N15	Cyld	74256	siRNA5	SI00963389			AAGGGTTGAACCATTGTTAAA
120	Cyld	Qiagen_Plate 2	F21	Cyld	74256	siRNA6	SI00963382			TCCATTGAGGATGTAAATAAA
121	A20	Ambion_Plate 2	K7	Tnfaip3	21929	siRNA1	65012	GGAAUUUGUGGAAACAGGAtt	UCCUGUUUCCACAAAUUCCtg	
121	A20	Ambion_Plate 2	C16	Tnfaip3	21929	siRNA2	65107	GGAAAAGCUUCUAAAGGAGtt	CUCCUUUAGAAGCUUUUCCtt	
121	A20	Ambion_Plate 2	G21	Tnfaip3	21929	siRNA3	186779	GCUAACUUACCCAAAGAAAtt	UUUCUUUGGGUAAGUUAGCtt	
121	A20	Qiagen_Plate 2	K7	Tnfaip3	21929	siRNA4	SI02668995			TTCAAAGTTAATAGTCTATTA
121	A20	Qiagen_Plate 2	C16	Tnfaip3	21929	siRNA5	SI00184443			CCGAAGTGGACTTCAGTACAA
121	A20	Qiagen_Plate 2	G21	Tnfaip3	21929	siRNA6	SI00184436			ACAGTTGTCTTTCAAAGGATA
122	DUSP2	Ambion_Plate 2	L7	Dusp2	13537	siRNA1	66563	GGCGGUUUCAAAAGCUUCCtt	GGAAGCUUUUGAAACCGCCtc	
122	DUSP2	Ambion_Plate 2	D16	Dusp2	13537	siRNA2	161578	GGUUGUGUCAAUAAAAACAtt	UGUUUUUAUUGACACAACCtc	
122	DUSP2	Ambion_Plate 2	H21	Dusp2	13537	siRNA3	161579	CGUGUGUGUCAUGUUACGGtt	CCGUAACAUGACACACACGtc	
122	DUSP2	Qiagen_Plate 2	L7	Dusp2	13537	siRNA4	SI04918480			AACATTGAGGTTGTGTCAATA
122	DUSP2	Qiagen_Plate 2	D16	Dusp2	13537	siRNA5	SI04918473			CCCGAGGGTTCCGATCTATGA
122	DUSP2	Qiagen_Plate 2	H21	Dusp2	13537	siRNA6	SI04918466			CAGCTTCATAGACTCGGTGAA
123	AIP1	Ambion_Plate 2	M7	Dab2ip	69601	siRNA1	223185	CGGCGAGUUCAGAAACAGCtt	GCUGUUUCUGAACUCGCCGtt	
123	AIP1	Ambion_Plate 2	E16	Dab2ip	69601	siRNA2	223186	CGCACUAGGUGAGUUCAUCtt	GAUGAACUCACCUAGUGCGtc	
123	AIP1	Ambion_Plate 2	I21	Dab2ip	69601	siRNA3	223187	GGUUGAUGUCAGUGGAAGAtt	UCUUCCACUGACAUCAACCtg	
123	AIP1	Qiagen_Plate 2	M7	Dab2ip	69601	siRNA4	SI00974148			CTGGAGGAGTATGAGACCCTA
123	AIP1	Qiagen_Plate 2	E16	Dab2ip	69601	siRNA5	SI00974141			CAGGGATAGGCTAAGGAGTAA
123	AIP1	Qiagen_Plate 2	I21	Dab2ip	69601	siRNA6	SI00974134			CAGGTTGATGTCAGTGGAAGA
124	Tollip	Ambion_Plate 2	N7	Tollip	54473	siRNA1	77146	GGCAAAAUUGGCAAAGAAUtt	AUUCUUUGCCAAUUUUGCCtg	
124	Tollip	Ambion_Plate 2	F16	Tollip	54473	siRNA2	77331	GGAAGAGUGAUGGUUUUAAtt	UUAAAACCAUCACUCUUCCtc	
124	Tollip	Ambion_Plate 2	J21	Tollip	54473	siRNA3	186071	GCAUCCUUCUGAGUUGAUGtt	CAUCAACUCAGAAGGAUGCtg	
124	Tollip	Qiagen_Plate 2	N7	Tollip	54473	siRNA4	SI01453452			CTGGGCTATGCTGTTTATGAA
124	Tollip	Qiagen_Plate 2	F16	Tollip	54473	siRNA5	SI01453445			AAGACCAATGTTTATTAAATA
124	Tollip	Qiagen_Plate 2	J21	Tollip	54473	siRNA6	SI01453438			CACTATGTGCTTACTACTAAA
125	MKP1	Ambion_Plate 2	C8	Dusp1	19252	siRNA1	71364	GGCUAUUGACUUCAUAGACtt	GUCUAUGAAGUCAAUAGCCtc	
125	MKP1	Ambion_Plate 2	G16	Dusp1	19252	siRNA2	71455	GGGAGAGUGUUUGUUCAUUtt	AAUGAACAAACACUCUCCCtc	
125	MKP1	Ambion_Plate 2	K21	Dusp1	19252	siRNA3	151971	CGAGGCUAUUGACUUCAUAtt	UAUGAAGUCAAUAGCCUCGtt	
125	MKP1	Qiagen_Plate 2	C8	Dusp1	19252	siRNA4	SI04921063			AAGCGCGGTGAAGCCAGATTA
125	MKP1	Qiagen_Plate 2	G16	Dusp1	19252	siRNA5	SI04921056			ATCACGCTTCTCGGAAGGATA
125	MKP1	Qiagen_Plate 2	K21	Dusp1	19252	siRNA6	SI04921049			CCCGATGACATGCGCGTATGA
126	RIP3	Ambion_Plate 2	D8	Ripk3	56532	siRNA1	74827	GGAGUUAAUGAUUCAUUGCtt	GCAAUGAAUCAUUAACUCCtt	
126	RIP3	Ambion_Plate 2	H16	Ripk3	56532	siRNA2	185795	CCCAGAGCUGUUAUUUAAAtt	UUUAAAUAACAGCUCUGGGtc	
126	RIP3	Ambion_Plate 2	L21	Ripk3	56532	siRNA3	185797	CCCAUCUCCUUAAAGUCAAtt	UUGACUUUAAGGAGAUGGGtc	
126	RIP3	Qiagen_Plate 2	D8	Ripk3	56532	siRNA4	SI05183514			ACCGGCTCTCGTCTTCAACAA
126	RIP3	Qiagen_Plate 2	H16	Ripk3	56532	siRNA5	SI01402352			GAGGGAAACCATGGTTTCTAA
126	RIP3	Qiagen_Plate 2	L21	Ripk3	56532	siRNA6	SI01402345			CTCCTTAAAGTCAATAAACAT

TABLE S2 (HUMAN SCREEN SCORES)

Gene#	Name	Gene Symbol	Gene ID	LPS-hTNF_Median	P3C-hTNF_Median	R848-hTNF_Median	P2C-hTNF_Median	PGN-hTNF_Median	FLG-hTNF_Median	LPS-hTNF_siRNA1	LPS-hTNF_siRNA2	LPS-hTNF_siRNA3	LPS-hTNF_siRNA4	LPS-hTNF_siRNA5	LPS-hTNF_siRNA6	P3C-hTNF_siRNA1	P3C-hTNF_siRNA2	P3C-hTNF_siRNA3	P3C-hTNF_siRNA4	P3C-hTNF_siRNA5	P3C-hTNF_siRNA6	R848-hTNF_siRNA1	R848-hTNF_siRNA2	R848-hTNF_siRNA3	R848-hTNF_siRNA4	R848-hTNF_siRNA5	R848-hTNF_siRNA6	P2C-hTNF_siRNA1	P2C-hTNF_siRNA2	P2C-hTNF_siRNA3	P2C-hTNF_siRNA4	P2C-hTNF_siRNA5	P2C-hTNF_siRNA6	PGN-hTNF_siRNA1	PGN-hTNF_siRNA2	PGN-hTNF_siRNA3	PGN-hTNF_siRNA4	PGN-hTNF_siRNA5	PGN-hTNF_siRNA6	FLG-hTNF_siRNA1	FLG-hTNF_siRNA2	FLG-hTNF_siRNA3	FLG-hTNF_siRNA4	FLG-hTNF_siRNA5	FLG-hTNF_siRNA6
1	TLR1	TLR1	7096	-0.092	-0.600	-0.338	-0.265	-0.370	-0.425	-0.076	-0.173	0.720	0.957	-0.108	-0.180	1.951	-1.091	-1.754	1.070	-0.999	-0.201	2.209	-0.279	-2.952	1.472	-0.396	-0.435	2.390	-0.323	-0.510	0.934	-1.184	-0.207	-0.080	-1.193	-1.423	0.807	-0.429	-0.311	0.660	-0.652	-1.535	2.375	-0.799	-0.199
2	TLR2	TLR2	7097	-0.143	-0.748	0.367	-0.720	-2.648	-0.170	1.177	0.674	-0.621	0.151	-0.629	-0.437	1.515	-1.142	-1.512	0.680	-0.878	-0.618	1.344	0.415	-1.624	1.279	-0.676	0.319	-0.315	-1.353	-1.875	-0.040	-0.124	-1.126	-3.947	-2.684	-3.194	-2.215	-0.845	-2.611	0.649	-0.510	-1.664	1.558	-0.516	0.170
3	TLR3	TLR3	7098	-0.543	-0.180	-0.015	-0.448	-0.259	-0.397	-0.384	-0.887	-0.701	-2.506	0.050	0.171	1.861	-1.754	0.007	-0.171	-0.189	-0.451	0.891	-0.203	-0.302	-0.853	0.619	0.173	-0.044	-0.400	-0.371	-1.136	-0.497	-0.510	0.272	-0.557	-0.567	-1.529	0.039	0.217	0.439	-0.746	-0.438	-0.327	-0.357	-1.255
4	TLR4	TLR4	7099	-4.482	-0.182	-0.168	-0.413	-0.309	-0.301	-4.465	-5.757	-4.763	-4.498	-1.196	-3.405	1.451	-0.661	0.297	0.957	-1.130	-0.969	1.764	-0.184	-0.805	0.413	-0.152	-0.900	-0.634	-0.339	0.440	0.231	-1.158	-0.488	0.816	-0.292	-0.393	0.574	-0.327	-1.588	-0.197	-0.809	0.164	0.612	-0.404	-0.610
5	TLR5	TLR5	7100	-1.076	-0.201	-0.278	-0.196	-0.614	-3.659	-3.644	-1.085	0.068	-1.066	-2.688	0.429	0.309	1.674	-1.213	-0.712	0.374	-1.534	-0.011	-0.318	0.146	-0.238	-0.666	-0.729	-0.246	0.116	-0.716	-0.147	0.255	-1.796	-0.431	0.681	-0.700	-0.527	-0.872	-1.026	-5.331	-2.155	-3.688	-3.630	-2.282	-4.281
6	TLR6	TLR6	10333	-0.447	-0.178	0.139	0.117	-1.549	-0.757	-0.099	1.327	-0.315	-0.579	-2.129	-1.602	-0.137	1.413	-1.558	-0.219	0.569	-0.555	-0.923	0.473	0.823	0.405	-0.127	-0.510	0.220	0.521	-0.447	0.650	0.015	-0.355	-1.535	0.059	-1.752	-1.564	-1.832	-1.393	0.245	-1.875	-0.573	-1.386	0.209	-0.942
7	TLR7	TLR7	51284	-0.305	-0.014	-0.201	-0.316	-0.271	-0.271	-0.296	-0.322	-0.244	-0.427	-0.314	0.520	0.085	0.014	-0.515	-0.422	0.124	-0.041	-0.785	1.614	-0.311	-0.234	0.284	-0.168	0.056	0.598	-0.060	-0.747	-0.801	-0.573	-0.525	1.560	-1.245	-0.858	-0.017	0.174	-0.547	0.885	-0.294	-0.438	0.048	-0.247
8	TLR8	TLR8	51311	-0.378	0.006	-2.731	-0.149	-0.089	-0.324	-0.467	1.026	-0.289	-0.929	-0.702	-0.106	0.416	1.150	-0.776	-1.678	0.672	-0.403	-2.308	-2.776	-3.745	-2.978	-2.622	-2.686	-0.162	0.456	-0.136	-1.286	-0.102	-0.295	-0.204	1.483	-0.237	-1.759	0.026	0.134	-0.412	0.547	-0.838	-1.385	0.236	-0.235
9	TLR9	TLR9	54106	-0.034	0.957	-0.138	0.497	0.134	0.119	-0.985	0.026	-3.320	0.940	-0.095	0.056	-2.013	0.727	2.152	1.187	-0.425	1.497	-0.887	-0.070	-0.207	0.664	-0.548	0.804	-1.192	-0.004	0.762	1.339	0.232	1.016	-1.272	0.517	-0.688	0.202	0.065	0.968	-1.418	0.389	-1.602	0.316	-0.079	0.945
10	LBP	LBP	3929	-0.330	-0.138	-0.545	-0.156	0.022	-0.072	-0.499	-0.516	0.152	-0.160	0.511	-2.316	-0.676	-0.321	1.316	-1.632	0.045	0.485	-0.529	-0.688	0.230	-0.562	0.986	-1.510	-0.170	-0.859	0.615	-1.275	-0.142	0.395	-0.631	-0.111	1.794	-0.583	0.170	0.156	-0.338	0.194	0.683	-1.239	0.446	-1.110
11	MD2	LY96	23643	-1.344	0.160	-0.097	-0.211	-0.094	-0.183	-0.023	-1.246	-1.442	-1.529	-0.253	-1.836	-0.764	-0.186	1.993	-0.580	0.713	0.507	-0.541	-1.501	1.463	-0.589	0.846	0.346	-0.174	-0.086	0.451	-1.387	-0.491	-0.248	-0.076	0.643	1.383	-0.873	-0.279	-0.111	-0.392	-0.223	0.503	-0.840	0.409	-0.143
12	CD14	CD14	929	-0.450	0.265	-0.142	0.025	0.113	0.235	-0.223	-1.720	-0.131	-0.677	0.872	-3.292	0.432	0.007	1.754	-0.361	0.257	0.272	-0.325	-0.446	1.851	-2.073	1.496	0.040	0.517	0.156	0.558	-0.608	-1.448	-0.106	0.492	-0.181	1.168	-0.494	-0.981	0.407	0.670	-0.223	0.869	0.134	0.337	-0.488
13	CD11b	ITGAM	3684	-0.333	-0.495	-0.363	-0.493	-0.273	-0.573	-1.219	-0.927	0.098	-0.758	0.316	0.093	1.403	-1.467	-0.975	-0.446	-0.545	0.369	0.804	-1.269	-0.033	-0.585	-0.288	-0.437	0.898	-1.645	-0.460	-0.782	-0.526	1.709	0.927	-1.389	-0.323	-0.756	-0.223	0.506	2.094	-0.931	-1.164	-0.903	-0.242	0.958
14	CD11c	ITGAX	3687	-0.885	-0.707	-0.679	-1.042	-0.864	-0.592	-1.125	0.037	-0.423	-2.563	-1.246	-0.645	-0.873	-1.173	0.898	-0.466	-0.998	-0.541	0.917	-1.715	-0.088	-1.224	-1.624	-0.133	-0.957	0.147	-0.070	-1.643	-1.417	-1.127	-0.871	0.549	-0.474	-1.454	-0.857	-1.632	-0.626	-0.753	0.247	-1.594	-0.308	-0.559
15	ARF6	ARF6	382	0.202	-0.056	0.157	0.380	-0.009	0.260	-0.585	0.032	0.372	-0.916	1.227	0.685	0.657	-0.129	0.675	-1.508	-0.618	0.017	0.989	0.056	0.040	-1.361	0.573	0.258	0.349	0.552	0.552	-1.852	-0.271	0.410	0.211	-0.942	0.503	-0.811	-0.229	0.281	0.857	-0.213	0.008	-1.075	0.523	0.512
16	MyD88	MYD88	4615	-1.949	-0.246	-3.301	-0.236	-1.583	-3.569	-5.076	-1.659	-2.928	-2.239	0.564	-1.069	-1.868	-0.725	-2.501	0.232	0.949	0.975	-4.482	-5.002	-4.543	-2.120	0.471	0.591	-0.877	0.038	-2.157	-0.510	1.230	1.581	-4.184	-1.843	-3.573	-1.021	1.825	-1.322	-6.286	-3.295	-7.020	-3.843	0.374	-1.023
17	Mal	TIRAP	114609	-2.870	-1.188	-0.441	-3.240	-5.061	-0.292	-3.691	-3.200	-3.906	-0.520	-0.503	-2.541	-1.691	-0.685	-3.299	0.551	1.222	-3.554	-0.586	0.460	-0.760	-0.296	0.178	-1.057	-3.951	-2.529	-4.348	0.602	-0.541	-4.117	-4.892	-5.421	-5.825	-0.022	-0.933	-5.231	0.141	-2.924	-0.878	-0.235	0.548	-0.348
18	IRAK1	IRAK1	3654	-1.568	-2.780	-2.413	-2.685	-3.026	-2.119	-0.606	-3.255	-1.716	-0.964	-1.420	-2.117	-0.960	-2.994	-4.312	-1.419	-2.567	-3.309	-1.103	-2.819	-3.375	-1.150	-2.161	-2.665	-1.705	-2.355	-3.015	-0.458	-3.719	-4.032	-0.887	-3.368	-3.777	-1.339	-2.799	-3.253	-1.104	-1.944	-5.227	-1.378	-3.114	-2.295
19	IRAK2	IRAK2	3656	0.096	-0.298	-0.019	-0.128	0.295	0.127	-0.418	1.969	-0.073	0.265	-0.206	1.336	0.338	1.296	-0.295	-0.300	-0.374	-0.527	-0.807	1.818	-0.491	-0.480	0.442	0.850	-0.260	0.004	0.541	0.085	-2.004	-0.854	-0.633	1.094	0.549	0.042	-2.448	0.956	0.589	-1.367	0.119	0.135	-1.913	1.071
20	IRAK4	IRAK4	51135	-0.019	0.148	-0.436	-0.326	-0.345	-0.462	-0.082	1.020	0.622	-0.553	-0.370	0.045	-0.844	0.507	0.466	-0.020	0.316	-0.527	-0.331	1.148	-0.532	-0.532	-0.341	-0.672	-0.711	0.228	0.371	-0.560	-0.445	-0.208	-0.599	-0.424	0.035	-1.559	-0.266	0.061	-0.773	0.405	-0.698	-0.977	-0.226	-0.124
21	Pellino	PELI1	57162	-0.335	0.010	-0.573	-0.058	-0.478	-0.236	-0.361	-0.544	1.998	-0.909	-0.140	-0.309	-0.536	-0.070	0.704	-1.860	0.091	0.547	-0.779	-0.734	0.891	-1.891	-0.413	-0.088	0.369	-0.259	0.504	-0.873	0.143	-0.425	-0.774	0.127	0.022	-1.665	-0.183	-0.972	-0.160	-0.359	1.761	-1.627	-0.134	-0.312
22	Uev1a	UBE2V1	7335	-0.024	0.153	-0.425	0.003	-0.085	-0.174	0.062	-0.557	1.229	-0.073	-1.093	0.024	0.803	-0.170	0.476	-1.027	-0.309	0.591	-0.169	-1.213	0.426	-1.045	-0.680	0.095	0.927	0.027	0.007	-1.201	-0.001	-0.550	-0.337	0.226	0.751	-0.745	-0.512	0.168	0.006	-0.259	-0.088	-0.872	-0.454	0.745
23	Ubc13	UBE2N	7334	0.144	-0.609	-0.133	-0.126	0.094	-0.107	0.447	-1.490	1.285	-0.783	-0.159	1.001	-0.795	-1.630	0.451	-0.422	-0.889	1.281	-0.234	-1.294	0.426	-0.031	-1.523	0.900	0.337	-1.491	0.869	-0.521	-0.630	0.269	0.267	-0.599	0.677	-1.211	-0.078	0.789	0.142	-0.786	1.507	-1.896	-0.357	0.515
24	TRAF6	TRAF6	7189	-1.858	-3.617	-1.993	-3.883	-3.292	-2.956	-1.793	-3.156	-2.107	-1.337	-1.897	-1.819	-4.622	-4.220	-4.516	-2.615	-3.014	-2.006	-3.019	-3.445	-2.064	-1.923	-0.729	-1.577	-3.747	-4.193	-6.119	-2.383	-4.019	-3.256	-3.810	-3.547	-4.743	-2.154	-3.036	-2.279	-4.873	-2.826	-5.069	-2.409	-2.667	-3.085
25	TRAF3	TRAF3	7187	-0.779	-0.432	-0.529	0.010	-1.027	-0.831	-0.903	-0.726	-1.191	-0.832	-0.485	0.159	0.283	-0.738	-0.443	-0.421	-1.348	0.098	1.558	-1.132	-0.173	-0.884	-1.292	0.089	0.242	0.199	-0.108	-0.388	-0.753	0.127	-1.062	-0.992	-0.658	-1.063	-1.414	0.507	-1.210	-2.792	0.182	-0.883	-0.780	1.041
26	TAK1	MAP3K7	6885	-1.795	-3.448	-2.469	-3.498	-3.075	-2.760	-1.575	-2.988	-2.845	-1.533	-2.015	-1.304	-2.870	-5.115	-5.171	-0.927	-4.027	-2.134	-2.185	-4.226	-4.543	-2.022	-2.754	-1.679	-2.337	-3.472	-5.103	-2.370	-4.926	-3.525	-2.184	-3.072	-4.162	-2.265	-3.655	-3.079	-2.798	-2.648	-5.659	-2.285	-2.722	-2.985
27	TAB1	TAB1	10454	-0.915	-1.415	-1.094	-0.946	-1.046	-1.221	-0.789	-1.066	-0.041	-1.041	-0.361	-1.703	-1.074	-1.973	-0.204	-1.312	-1.518	-2.108	-0.173	-2.214	0.370	-1.993	-1.523	-0.666	-0.379	-0.692	-0.609	-1.855	-1.201	-2.237	-1.176	-0.538	0.005	-1.507	-0.916	-1.272	-1.031	-2.632	-1.239	-1.202	-0.266	-1.331
28	TAB2	TAB2	23118	-1.138	-2.074	-1.992	-2.049	-2.102	-1.929	-0.956	-1.036	-1.241	-1.573	-2.231	-1.030	0.032	-1.973	-2.382	-2.065	-5.378	-2.084	2.213	-1.159	-1.992	-2.083	-2.896	-1.993	0.798	-0.381	-2.402	-3.117	-5.032	-1.695	0.639	-1.200	-2.587	-2.145	-4.061	-2.058	0.958	-1.197	-2.330	-2.269	-3.120	-1.589
29	TAB3	TAB3	257397	-0.089	-0.297	-0.366	0.123	-0.250	-0.290	-0.700	-0.613	-0.391	0.591	0.574	0.214	-0.312	-0.404	-0.281	-0.087	1.464	-0.534	-0.616	-0.455	-0.760	0.540	0.889	-0.276	-0.310	0.726	-0.043	0.339	0.289	-0.989	-0.425	0.106	-0.626	-0.024	-0.075	-0.932	-0.147	-1.218	-0.432	-0.619	0.220	0.177
30	NEMO	IKBKG	8517	-0.556	-0.902	-0.228	-0.905	-0.747	-1.056	-1.905	-2.948	0.140	-0.832	0.517	-0.280	-2.365	-0.994	-0.811	-1.518	1.832	-0.136	-2.486	-0.145	-0.311	-1.127	2.168	0.095	-1.969	-0.625	-0.538	-1.766	-0.077	-1.184	-1.983	-0.401	-0.320	-1.093	0.694	-2.129	-1.527	-1.080	-0.631	-1.439	0.575	-1.031
31	IKKa	CHUK	1147	-0.099	-0.639	-0.493	-0.364	-0.540	-0.749	0.036	-2.076	0.026	-0.224	-1.072	0.441	-0.652	-0.766	-0.849	-0.625	-0.557	0.363	-0.314	-0.008	-1.140	-0.672	-1.405	0.077	-1.105	-0.269	-0.160	-0.460	-0.767	0.003	-1.097	-0.201	-0.825	-0.370	-0.710	0.589	-0.231	-1.253	-1.128	-0.436	-1.062	0.118
32	IKKb	IKBKB	3551	0.426	0.081	-0.639	0.078	0.102	0.138	0.081	0.997	0.612	-0.307	0.523	0.328	0.798	-0.578	-0.242	-0.122	0.352	0.285	-0.693	1.073	-0.841	-0.626	-0.188	-0.653	0.361	-0.903	0.532	0.219	-0.062	-0.247	0.075	0.130	0.063	-0.227	0.298	0.580	0.403	-0.783	0.111	0.164	-0.104	0.901
33	IkBa	NFKBIA	4792	-0.235	-0.348	-0.508	-0.497	-0.564	-0.438	0.025	-0.163	0.758	-1.905	-1.577	-0.306	-1.380	0.236	0.248	-0.936	-0.625	-0.071	-0.505	-0.510	2.117	-1.722	-1.722	-0.364	-1.522	-0.051	-0.051	-1.029	-0.314	-0.680	-1.166	0.161	1.434	-0.808	-0.320	-0.997	0.013	0.322	-0.192	-1.925	-2.348	-0.683
34	IkBb	NFKBIB	4793	-0.467	-0.253	-0.586	-0.431	-0.366	-0.644	-1.037	-0.310	0.034	-1.662	-0.327	-0.607	-0.805	-0.304	-0.202	-0.749	0.605	0.081	-1.561	-0.529	0.022	-1.564	1.104	-0.643	-0.619	-0.794	-1.191	-0.244	0.391	-0.162	-1.291	-0.399	-0.334	-0.861	0.104	-0.187	-0.969	0.358	-0.812	-1.112	-0.152	-0.477
35	IkBe	NFKBIE	4794	-1.630	-1.275	-1.633	-1.199	-1.795	-1.799	-0.833	-1.330	-1.366	-2.104	-2.112	-1.893	-0.720	-1.296	-1.255	-1.214	-1.549	-2.059	-1.441	-1.849	-0.575	-0.821	-1.825	-1.980	-1.098	-1.299	-0.769	-0.353	-1.474	-1.961	-1.934	-1.656	-0.889	-2.953	-1.335	-3.430	-1.831	-0.952	-1.766	-1.989	-0.597	-2.493
36	Nfkb1	NFKB1	4790	-0.266	-0.572	0.200	-0.649	-0.365	-1.066	-0.828	1.079	-0.370	-0.820	1.319	-0.162	-1.160	-0.338	-0.924	-0.806	1.540	0.811	-0.931	1.373	0.297	-1.243	1.426	0.102	-1.745	-0.788	-1.184	-0.510	0.636	-0.505	-0.943	-0.155	-0.574	-1.017	0.763	0.043	-1.674	-0.833	-1.682	-1.299	0.899	-0.617
37	NFkb2	NFKB2	4791	-0.501	-0.025	-0.191	-0.079	-0.021	-0.702	-0.654	-0.320	1.712	-0.348	-2.603	-1.331	-0.001	-0.425	1.774	-0.050	-1.445	0.471	-0.061	-0.322	0.048	-0.506	-1.601	0.348	-0.103	-0.480	1.492	0.094	-2.522	-0.056	-0.190	-0.985	2.155	0.148	-4.703	0.206	-1.388	-0.624	1.504	-0.253	-2.159	-0.780
38	RelA	RELA	5970	-1.204	-1.540	-0.604	-1.848	-1.225	-1.266	-1.776	-0.873	-1.098	-1.310	-0.454	-2.598	-2.178	-1.380	-1.152	-1.700	-0.582	-2.263	-0.178	-0.642	-0.566	-1.329	0.284	-1.243	-1.858	-1.526	-1.838	-2.518	-1.621	-2.829	-1.345	-1.106	-1.359	-0.824	-0.820	-3.415	-3.541	-0.826	-1.419	-1.112	-0.035	-2.610
39	RelB	RELB	5971	-0.471	-0.318	-0.316	0.207	0.746	0.365	-1.102	0.144	0.215	-1.184	-0.374	-0.568	-0.425	-0.368	1.109	-0.268	-0.370	-0.188	-0.154	-0.322	-0.311	-1.210	-0.700	0.449	0.277	-0.166	0.429	0.137	0.096	0.711	0.952	1.041	1.100	-0.341	0.423	0.540	1.487	-0.159	0.757	-1.349	1.044	-0.026
40	cRel	REL	5966	-0.573	-0.649	-0.610	-0.397	-0.393	-0.119	-1.057	-0.790	0.130	-0.492	-0.197	-0.654	-0.835	-1.093	0.046	-1.540	-0.463	0.172	1.445	-0.952	-0.760	-1.168	-0.460	-0.449	-0.592	-0.344	-0.396	-1.356	-0.398	0.390	0.256	-0.494	-0.174	-0.526	-0.450	-0.336	-0.058	-0.005	-0.019	-2.017	-0.181	-0.284
41	Tpl2	MAP3K8	1326	-1.110	-2.191	-1.507	-1.961	-1.711	-1.832	-0.947	-1.952	-0.487	-1.273	-2.394	-0.934	-1.907	-2.721	-2.887	-1.018	-2.474	-0.736	-1.865	-1.276	-1.588	-1.427	-2.709	-0.044	-1.936	-1.987	-2.789	-1.397	-2.251	-1.514	-2.008	-2.497	-1.387	-1.451	-1.970	-1.284	-2.018	-1.536	-2.381	-1.646	-2.141	-0.630
42	Mekk1	MAP3K1	4214	-0.913	-0.647	-0.933	-0.439	-0.675	-0.819	-1.256	-1.141	-0.292	-1.464	-0.685	-0.193	-0.417	-0.593	-0.693	-2.923	-0.601	-0.936	-1.389	-0.404	-0.924	-1.722	-0.942	-0.025	-0.431	-0.446	-0.069	-2.941	-0.408	-1.005	-0.936	-0.451	0.252	-3.345	-0.289	-0.898	-0.621	-1.631	-0.505	-2.346	-0.885	-0.752
43	Mkk1	MAP2K1	5604	0.007	-0.456	0.114	-0.843	-0.368	-0.342	-0.661	-0.079	-1.423	0.093	0.261	0.544	-0.662	-0.662	-1.487	-0.250	-0.141	0.182	-0.797	1.316	-1.471	-0.318	0.547	1.389	-0.866	-0.913	-0.820	-0.447	-1.494	0.121	-0.494	0.026	-1.856	-0.113	-0.384	-0.351	0.575	-0.530	-0.753	-0.155	-0.738	0.757
44	Mkk2	MAP2K2	5605	-0.033	-0.524	0.409	-0.764	-0.012	-0.035	-0.225	0.749	-0.119	0.145	-0.087	0.022	-0.835	-0.334	-1.678	0.425	0.563	-0.715	-0.504	1.073	-1.441	0.895	0.677	0.141	-1.167	-0.090	-0.964	0.102	-0.858	-0.671	0.060	-0.085	-1.303	-0.106	0.232	0.382	-0.235	-0.268	-0.861	0.818	0.164	0.446
45	Erk1	MAPK3	5595	-0.731	-0.980	-1.089	-1.277	-0.544	-0.763	-0.419	-1.284	-1.044	0.137	0.161	-1.999	-1.089	-0.174	-1.643	0.274	-0.872	-1.944	-0.852	-1.688	-1.325	-0.437	0.095	-1.336	-0.460	-1.314	-1.240	0.503	-1.910	-1.327	-1.101	-0.096	-0.674	0.389	-0.413	-2.777	-1.002	-0.524	-1.944	-0.058	-0.412	-2.023
46	Erk2	MAPK1	5594	-0.185	-0.236	-0.243	-0.589	-0.060	0.171	-0.282	-0.167	0.503	1.044	-0.802	-0.204	-0.072	-0.399	-0.944	0.091	-1.017	0.018	-0.231	-0.529	1.396	0.242	-0.643	-0.256	-0.072	-1.322	-0.839	-0.192	-1.073	-0.340	-0.134	0.135	-0.172	0.525	-0.975	0.013	1.009	-0.375	0.225	0.618	0.118	-0.548
47	Mkk3	MAP2K3	5606	-1.066	-0.725	-0.522	-1.013	-1.327	-1.241	0.451	-0.853	-1.392	-1.278	-0.444	-3.326	0.062	-0.954	-0.497	-2.370	0.068	-3.039	-0.533	-0.276	-0.510	-1.697	0.095	-3.345	-0.738	-1.289	-0.688	-2.947	-0.331	-3.672	-0.697	-1.190	-1.463	-2.724	-0.158	-3.593	-0.373	-0.672	-1.714	-2.076	-0.768	-3.802
48	Mkk6	MAP2K6	5608	0.015	0.214	-0.633	0.246	0.198	-0.178	-0.060	0.261	-0.626	-0.144	0.091	0.090	-0.321	0.191	-0.137	0.622	0.237	0.897	-1.221	-0.566	0.024	-0.853	0.533	-0.700	-0.313	-0.525	0.454	0.464	0.038	0.697	-0.590	0.138	0.258	-0.008	0.284	0.505	0.026	-0.810	-0.030	-0.326	0.035	-0.923
49	p38a	MAPK14	1432	-0.805	-1.949	-1.112	-1.775	-1.608	-1.261	-1.915	-0.779	-0.832	-1.699	-0.243	-0.512	-2.657	-2.227	-1.973	-1.321	-1.286	-1.924	-0.112	-1.957	-1.131	-1.220	-0.192	-1.094	-1.868	-1.683	-1.891	-1.199	-1.121	-2.278	-1.316	-1.901	-0.906	-2.244	-1.162	-1.959	-1.531	-1.283	-1.184	-1.857	-0.740	-1.239
50	p38b	MAPK11	5600	-0.339	-0.042	-0.443	-0.395	-0.275	-0.525	-0.781	0.221	-0.258	-0.420	-1.007	-0.125	-0.126	-0.662	-0.096	0.038	1.280	0.013	-0.431	-0.734	-1.297	-0.364	-0.455	-0.126	-0.310	-1.187	-1.167	-0.247	1.528	-0.479	-0.414	-0.628	-0.136	0.030	0.083	-0.747	-0.888	-1.484	-0.091	-0.783	0.185	-0.267
51	MK2	MAPKAPK2	9261	-0.448	-0.560	-0.205	-0.323	-0.137	-0.279	-0.367	-0.330	-0.706	-1.129	0.488	-0.529	-1.026	-0.506	-0.615	-0.473	0.737	-0.957	0.497	-0.222	-1.028	-0.759	0.179	-0.188	0.169	-0.431	-0.853	-0.215	0.650	-1.310	-0.201	0.612	-0.072	-0.677	0.494	-0.764	-0.008	-0.550	-1.317	0.072	0.558	-1.243
52	Mkk4	MAP2K4	6416	-0.065	-0.472	-0.279	-0.236	-0.031	-0.544	-0.467	-0.808	0.219	0.459	0.203	-0.334	-1.667	-1.766	-0.718	-0.225	0.158	0.127	-0.551	-1.753	0.087	0.615	-0.562	-0.006	-1.333	-1.568	-0.270	-0.077	-0.202	0.093	-1.027	-1.388	0.280	0.211	0.057	-0.120	-1.348	-1.220	0.159	0.634	-0.075	-1.013
53	Mkk7	MAP2K7	5609	-1.127	-1.269	-0.782	-0.722	-1.271	-1.059	-1.298	-1.893	-0.751	-0.957	-2.443	-0.427	-0.400	-1.817	-1.206	-0.609	-3.107	-1.333	-0.432	-1.269	-0.711	1.233	-3.111	-0.852	-1.001	-0.444	-0.226	-0.183	-2.254	-1.160	-1.193	-1.112	-1.109	-1.826	-1.776	-1.350	-0.395	-1.877	-0.906	-1.140	-1.900	-0.977
54	Jnk1	MAPK8	5599	-0.200	-0.001	-0.218	-0.176	0.087	0.018	-0.249	-1.101	0.674	-0.151	-1.185	0.430	0.880	-1.590	0.002	-0.005	-0.771	0.439	-0.469	1.407	-0.140	-0.296	-1.361	0.532	-0.045	-0.307	-0.569	0.952	-0.433	0.642	0.106	-0.479	0.409	0.211	0.068	-0.200	0.326	-1.301	0.027	0.073	-0.379	0.008
55	Jnk2	MAPK9	5601	-0.098	-0.236	-0.652	-0.471	-0.190	-0.180	-0.701	-1.818	0.651	0.505	-0.751	0.702	0.494	-1.294	-0.227	0.655	-1.364	-0.246	-0.665	-1.186	-0.051	-0.639	-1.210	0.591	-0.458	-0.537	-0.349	1.570	-0.688	-0.483	-0.733	-0.204	-0.315	0.311	-0.176	0.067	-0.195	-1.212	-0.259	1.147	-0.165	0.051
56	Jnk3	MAPK10	5602	-0.180	-0.389	-0.336	-0.016	0.155	-0.133	0.123	-0.904	-0.133	-0.438	0.424	-0.228	0.399	-0.541	-0.515	-0.349	0.194	-0.429	-1.928	1.123	-0.282	-0.455	0.603	-0.390	-0.883	0.006	-0.441	-0.027	0.388	-0.005	-0.954	0.285	-0.565	0.135	0.671	0.174	-0.200	-1.039	-0.287	0.117	0.288	-0.067
57	Erk3	MAPK12	6300	-0.195	-0.410	-0.543	-0.281	-0.208	-0.512	-0.268	-0.089	-0.123	-0.268	0.614	-1.699	-0.137	0.094	-0.892	-0.679	-0.141	-0.904	-0.675	-1.132	0.922	0.628	-0.764	-0.411	0.318	-0.826	-0.244	-1.045	0.164	-0.318	-0.226	-0.191	-0.081	-1.464	0.387	-1.274	0.164	-0.588	-0.436	-1.648	1.166	-1.040
58	p38d	MAPK13	5603	-0.745	-0.555	-0.529	-1.645	-1.281	-0.963	-1.267	-0.650	-0.840	-2.050	-0.527	0.018	-1.706	-0.634	-2.359	-0.201	-0.446	-0.475	-2.052	-1.883	0.378	-0.387	-0.672	0.348	-1.963	-1.660	-2.106	0.447	-0.959	-1.630	-2.093	-1.258	-1.303	-1.823	-0.627	0.309	-2.514	-0.877	-1.963	-1.049	-0.499	-0.688
59	TRIF	TICAM1	148022	-1.775	-0.538	0.236	-0.572	-0.360	-0.853	-1.730	-1.821	-1.978	-2.707	-1.434	-1.005	-0.479	0.710	-0.166	-2.905	-1.191	-0.597	-1.458	0.119	1.229	-1.474	0.442	0.354	-0.206	0.062	0.275	-2.750	-1.165	-0.939	-1.066	0.225	-0.178	-1.885	-0.384	-0.336	-0.763	-1.007	-0.376	-1.593	-0.944	-0.629
60	TRAM	TICAM2	353376	-1.371	-0.441	-0.375	-0.171	0.002	-0.318	-1.418	-1.412	-1.329	0.943	-1.694	-0.919	-0.309	0.537	-0.573	0.647	-1.689	-1.035	-0.016	-0.734	1.207	1.263	-1.045	-0.790	-0.202	-0.140	-0.020	0.491	-0.879	-1.056	-0.817	0.740	0.255	0.169	-0.164	-0.167	-0.202	0.415	-0.435	0.545	-1.175	-1.047
61	RIP1	RIPK1	8737	-0.059	-0.704	-0.833	-0.360	-0.338	-0.233	0.384	1.196	0.558	-1.167	-0.501	-1.563	-1.099	0.141	1.095	-0.940	-1.035	-0.467	-0.972	0.076	0.534	-0.979	-0.694	-1.132	-0.225	-0.423	-0.555	-0.452	-0.297	-0.032	-0.559	0.009	0.446	-1.088	-0.287	-0.389	-0.330	0.276	0.123	-1.499	-0.494	-0.135
62	FADD	FADD	8772	-0.631	-0.411	-0.795	-0.583	0.069	-0.161	0.237	-0.550	-0.042	-1.073	-0.712	-2.133	-0.287	-0.536	0.191	-1.093	0.077	-2.174	0.168	-1.471	-0.145	-1.127	-0.463	-2.178	0.993	-0.368	-0.814	-0.798	0.311	-1.560	0.645	0.201	1.108	-1.188	-0.063	-0.726	1.141	-0.209	-0.113	-0.747	-0.057	-1.832
63	Caspase 8	CASP8	841	-0.298	-0.351	-0.583	-0.227	-0.136	-0.272	-0.498	-0.274	-0.149	-0.322	0.246	-1.391	-0.392	-0.304	0.655	-0.600	-0.310	-0.904	-0.337	-1.269	-0.553	-0.510	-0.613	-0.672	0.150	-0.508	0.054	-0.513	0.259	-0.550	-0.107	-0.164	0.483	-0.343	0.540	-0.593	0.404	-0.644	-0.121	-0.424	-0.002	-1.237
64	TBK1	TBK1	29110	0.076	-0.577	0.189	-0.880	-0.142	-0.564	-1.109	0.220	0.151	0.923	0.000	-0.320	-1.413	-0.533	1.402	0.613	-0.621	-1.027	-0.811	-0.805	0.093	1.255	0.485	0.284	-0.972	-1.319	0.576	0.283	-0.966	-0.794	-0.862	-0.199	0.607	0.675	-1.061	-0.085	-1.677	-1.304	1.298	0.389	-0.600	-0.528
65	IKKe	IKBKE	9641	-0.397	-0.238	-1.145	-0.123	-0.302	0.465	0.721	-1.192	0.397	1.167	-2.630	-2.617	2.801	0.225	-1.265	2.514	-0.700	-0.846	-2.425	-0.325	1.295	-1.071	-1.220	-2.445	-1.026	-0.128	-0.985	0.999	-0.061	-0.119	1.509	-1.428	0.199	2.526	-0.855	-0.804	0.465	-1.225	0.554	0.642	-1.401	0.465
66	IRF3	IRF3	3661	-1.254	-0.397	-1.228	-0.798	-0.681	-0.536	0.816	-1.403	-1.379	1.959	-2.977	-1.130	-0.480	-0.314	-1.078	1.130	-1.451	-0.272	-2.494	-0.779	-1.113	0.374	-1.343	-1.389	-0.935	-0.051	-1.030	-1.710	-0.662	-0.510	-0.509	-0.853	-1.215	0.387	-0.245	-1.210	0.618	-0.402	-1.832	-0.404	-0.669	-1.015
67	Duba	OTUD5	55593	-1.021	-0.865	-0.566	-1.849	-0.917	-0.692	0.384	-1.921	-1.200	-0.842	-1.811	-0.817	1.218	-2.602	-0.682	1.413	-1.646	-1.049	-1.804	-0.126	-1.233	-0.316	-0.817	1.627	-1.463	-1.926	-0.878	-2.033	-1.902	-1.796	0.831	-1.751	-1.132	1.431	-0.701	-1.611	-0.525	-0.289	-1.374	-0.567	-1.635	-0.817
68	TRADD	TRADD	8717	-0.032	-0.706	-0.569	-1.432	-0.351	-0.709	-1.721	-0.189	0.488	0.124	1.339	-1.155	1.526	-0.698	-0.714	-1.151	0.993	-5.010	-3.438	-0.934	0.785	-0.205	1.017	-3.107	-1.474	-1.391	0.122	-2.151	0.339	-3.613	-0.146	-0.259	-0.443	-1.595	1.194	-3.350	-0.865	-0.553	0.410	-2.929	1.106	-2.879
69	TANK	TANK	10010	-0.471	0.909	0.061	-0.323	-0.220	-0.264	-0.421	0.200	-0.846	0.359	-1.103	-0.520	0.877	3.049	-0.052	0.941	1.290	0.774	0.795	-0.117	0.063	0.059	-1.387	1.035	0.957	-0.695	0.049	1.151	-0.827	-1.275	-0.163	1.004	-0.379	0.717	-1.901	-0.277	0.342	0.039	-0.567	1.390	-2.137	-2.364
70	SINTBAD	TBKBP1	9755	0.782	0.613	-0.136	-0.400	0.190	-0.026	0.246	0.935	1.137	1.277	0.629	-0.112	0.920	0.949	-0.173	0.307	1.073	-0.266	-0.170	-1.777	-0.486	0.860	0.027	-0.103	1.261	-1.803	-0.272	0.436	-0.969	-0.528	0.311	0.069	-0.465	0.822	0.322	-0.823	-0.017	-0.035	0.690	0.473	-0.161	-0.829
71	BTK	BTK	695	0.261	-0.537	-0.524	-0.201	-0.754	-0.025	-0.262	0.099	0.424	-0.699	1.169	0.451	-0.321	1.652	-1.632	-0.752	1.456	-0.868	-0.073	-0.682	-0.365	-0.455	-0.592	-0.660	0.300	-0.891	-0.901	0.121	-0.022	-0.381	-0.177	-1.127	-1.268	-1.073	0.960	-0.436	0.276	0.304	-0.973	-0.958	-0.278	0.228
72	NIK	MAP3K14	9020	0.377	0.069	-0.224	-0.112	0.576	0.475	0.599	0.809	-2.591	-1.114	0.977	0.156	0.354	2.250	-0.564	-0.216	1.630	-1.479	0.184	0.962	-1.149	0.836	-0.633	-1.416	1.287	-0.087	0.693	-0.204	-0.137	-1.467	0.484	1.684	-1.213	0.669	1.290	-1.160	1.032	0.998	1.028	-0.249	-0.049	-0.698
73	AKT1	AKT1	207	-0.776	-0.137	-0.446	0.159	-0.257	0.087	0.287	-0.684	-1.141	-0.931	0.141	-0.868	0.812	-0.127	0.678	-0.298	-0.146	-0.660	0.778	-0.325	-1.431	-0.566	0.256	-2.205	0.843	0.842	-2.567	-0.019	0.337	-0.981	-0.360	0.988	-1.258	-0.626	1.182	-0.153	0.278	0.742	-2.197	-0.015	0.189	-0.706
74	AKT2	AKT2	208	-0.863	0.236	-0.433	0.288	-0.433	-0.307	-2.529	-0.453	-1.273	-1.431	-0.143	1.610	-0.361	-0.557	1.276	-0.176	0.648	1.797	-1.729	-0.285	-0.582	-1.623	1.019	1.567	-0.466	0.416	-0.957	0.197	0.832	0.379	-1.313	-0.085	-0.861	-0.780	0.923	-0.050	-2.443	-0.529	-0.150	-0.140	1.134	-0.464
75	AKT3	AKT3	10000	0.166	0.131	-0.309	-0.201	0.014	-0.618	-0.111	-1.621	0.443	0.523	-0.668	0.537	0.238	0.249	2.339	-1.465	-0.958	0.024	0.111	-1.326	-1.566	-0.047	0.192	-0.571	0.432	-0.139	-0.263	-1.741	-0.628	-0.100	-0.259	0.117	0.576	-0.089	-0.328	0.698	0.033	-0.981	1.484	-0.444	-0.792	-1.590

TABLE S2 (HUMAN SCREEN SCORES)

Gene#	Name	Gene Symbol	Gene ID	LPS-hTNF_Median	P3C-hTNF_Median	R848-hTNF_Median	P2C-hTNF_Median	PGN-hTNF_Median	FLG-hTNF_Median	LPS-hTNF_siRNA1	LPS-hTNF_siRNA2	LPS-hTNF_siRNA3	LPS-hTNF_siRNA4	LPS-hTNF_siRNA5	LPS-hTNF_siRNA6	P3C-hTNF_siRNA1	P3C-hTNF_siRNA2	P3C-hTNF_siRNA3	P3C-hTNF_siRNA4	P3C-hTNF_siRNA5	P3C-hTNF_siRNA6	R848-hTNF_siRNA1	R848-hTNF_siRNA2	R848-hTNF_siRNA3	R848-hTNF_siRNA4	R848-hTNF_siRNA5	R848-hTNF_siRNA6	P2C-hTNF_siRNA1	P2C-hTNF_siRNA2	P2C-hTNF_siRNA3	P2C-hTNF_siRNA4	P2C-hTNF_siRNA5	P2C-hTNF_siRNA6	PGN-hTNF_siRNA1	PGN-hTNF_siRNA2	PGN-hTNF_siRNA3	PGN-hTNF_siRNA4	PGN-hTNF_siRNA5	PGN-hTNF_siRNA6	FLG-hTNF_siRNA1	FLG-hTNF_siRNA2	FLG-hTNF_siRNA3	FLG-hTNF_siRNA4	FLG-hTNF_siRNA5	FLG-hTNF_siRNA6
76	PIK3CA	PIK3CA	5290	0.097	-0.238	-0.302	-0.284	-0.226	-0.373	0.405	-0.212	1.436	-0.217	-0.985	0.440	-0.067	-0.982	1.732	-0.409	-1.159	1.283	0.164	0.645	-0.908	-0.232	-0.371	-0.411	0.285	-0.510	-1.142	-0.058	-0.717	0.464	0.061	-0.512	-1.996	0.390	-1.047	0.936	0.011	-0.842	-0.333	0.078	-0.840	-0.412
77	PIK3CB	PIK3CB	5291	-0.084	-0.094	-0.227	-0.514	-0.618	-0.339	-0.753	-0.262	-1.037	0.463	0.834	0.094	-0.121	-1.558	-0.921	0.346	0.763	-0.068	-1.075	-0.474	-0.440	-0.014	1.587	0.161	-1.531	-0.769	-0.566	-0.088	0.571	-0.462	-2.219	-0.795	-0.726	-0.510	0.374	-0.055	-1.834	-0.785	-0.861	0.107	0.707	0.393
78	PIK3CD	PIK3CD	5293	-0.717	0.230	-0.711	0.550	-0.199	-1.043	-1.218	-0.056	-0.216	-2.729	0.017	-1.708	-0.435	-0.651	0.228	0.417	0.761	0.232	-1.511	-0.325	0.421	-1.098	0.704	-1.328	-1.250	-0.438	0.806	0.320	0.780	0.839	-1.609	-0.318	0.389	-1.395	0.967	-0.079	-1.399	-0.687	0.651	-1.731	0.952	-1.407
79	PIK3CG	PIK3CG	5294	-0.451	-0.578	-0.451	-0.763	-0.577	-1.256	-2.297	-0.447	-0.156	-0.368	-0.454	-1.178	-1.132	-0.426	-0.731	-0.346	0.151	-1.763	-0.510	-0.790	-0.126	-0.392	0.330	-1.156	-2.165	-0.331	-0.058	-0.791	-0.734	-1.533	-2.325	-0.034	-0.713	-0.493	0.539	-0.662	-3.360	-0.209	-1.336	-2.264	-0.203	-1.177
80	PIK3R1	PIK3R1	5295	0.253	-0.028	-0.106	0.183	0.164	-0.062	0.573	-0.067	0.778	-0.611	-1.904	1.212	-0.086	-0.933	0.030	0.307	-2.212	0.037	1.392	-0.510	0.298	-0.660	-2.364	1.177	-0.817	0.003	0.594	0.651	-1.697	0.362	-0.793	0.157	0.171	0.874	-2.300	0.376	0.725	-0.027	-0.097	-1.474	-1.626	0.164
81	PIK3R2	PIK3R2	5296	-0.537	0.143	0.116	-0.735	-0.716	-0.333	-0.645	-1.320	0.223	-1.252	-0.309	-0.430	0.330	-1.278	0.418	-0.645	0.125	0.162	0.039	-1.375	0.327	-0.854	1.093	0.194	0.928	-1.291	0.050	-0.534	-0.936	-1.008	-0.460	-2.276	-0.031	-2.251	-0.132	-0.972	0.837	-0.227	0.321	-0.438	-1.787	-1.042
82	PIK3R3	PIK3R3	8503	-0.325	-0.226	-0.945	-0.681	-0.481	-0.877	-0.805	0.324	0.155	-1.488	0.217	-2.544	0.755	0.225	-0.706	-0.677	1.574	-1.259	-1.002	-0.888	0.647	-1.112	0.309	-2.030	1.237	-0.780	-0.582	-0.399	-0.969	-1.939	-0.142	-0.442	-0.496	-2.008	-0.466	-3.143	0.451	-0.253	-0.961	-1.155	-0.794	-3.937
83	PIK3R5	PIK3R5	23533	-0.250	-0.802	-0.045	-0.279	-0.824	-0.947	-0.189	-0.544	0.052	-0.311	1.181	-2.154	-0.862	-0.751	0.894	-0.853	0.571	-1.062	-0.427	-0.041	0.737	-0.048	-0.194	0.406	0.409	-1.143	0.012	0.171	-0.569	-0.965	0.069	-1.319	-0.657	-0.330	-0.992	-1.118	-1.210	-1.407	-0.077	0.183	-0.685	-2.639
84	RAC1	RAC1	5879	-0.351	-0.133	-0.515	-0.086	-0.030	-0.341	-0.374	0.589	-0.461	-0.327	1.152	-0.841	-0.334	0.580	0.068	-1.106	1.327	-0.925	-0.235	-1.134	0.547	-0.720	-0.310	-1.551	0.110	-0.359	0.154	-0.282	0.123	-1.738	0.011	-0.765	0.140	-0.072	0.120	-2.724	-0.053	-1.768	0.073	-0.448	-0.234	-1.415
85	IRF5	IRF5	3663	-0.212	-0.810	-0.955	-1.260	-1.260	-0.353	-4.092	-0.413	0.549	-0.011	-0.978	0.549	-3.719	-0.741	-0.880	-0.251	-2.145	1.611	-2.926	-1.094	-0.816	-0.260	-1.171	0.573	-3.879	0.473	-1.675	0.016	-1.086	-1.433	-3.765	-0.630	-1.544	-0.298	-1.420	-1.100	-3.806	-0.862	0.290	0.071	-0.776	0.809
86	IRF7	IRF7	3665	-0.640	-0.832	-1.301	-1.125	-1.014	-0.883	-0.644	-1.400	1.031	-0.637	-1.078	0.124	-0.854	-1.499	1.942	-0.811	-1.528	0.286	0.164	-1.326	-0.531	-1.581	-1.277	-1.391	-1.035	-1.568	-0.843	-0.615	-1.766	-1.214	-0.544	-1.134	-0.424	-0.895	-1.169	-1.376	-1.075	-0.535	-0.691	-0.105	-1.765	-1.594
87	STAT1	STAT1	6772	-0.413	0.245	-0.026	0.050	-0.460	-0.567	-0.507	-0.570	0.469	-0.319	0.846	-2.664	0.017	-0.721	0.412	0.180	0.311	0.928	-0.166	-0.726	-1.484	0.494	1.271	0.115	0.284	-0.604	-2.996	-0.184	0.586	0.437	-0.312	0.217	-2.093	-0.607	1.063	-1.891	-0.580	-0.366	-0.604	-0.553	1.265	-0.773
88	Fos	FOS	2353	0.659	-0.516	0.237	-0.366	0.085	-0.016	0.251	-0.259	1.220	-0.220	1.068	2.211	-0.605	-0.792	1.118	-0.635	-0.427	1.505	0.510	0.283	0.022	-0.345	0.192	1.494	-0.056	0.151	-2.579	-0.675	0.497	-0.988	0.327	0.164	-0.431	0.005	0.810	-0.066	-0.003	-0.170	1.639	-0.029	0.815	-0.135
89	Jun	JUN	3725	-1.237	-0.784	-0.413	-0.955	-1.058	-0.885	-3.285	-1.389	-0.697	-1.084	-0.415	-1.546	-0.906	-3.066	-0.663	-0.495	-1.791	0.294	-0.754	-1.002	0.341	-0.073	0.595	-2.329	-1.798	-3.327	-0.750	-0.219	-1.160	0.709	-3.230	-2.098	-0.525	-1.447	-0.669	0.735	-1.844	-0.978	-0.664	-1.028	0.002	-0.791
90	PYK2	PTK2B	2185	-0.982	-0.752	-0.845	-0.935	-0.690	-0.893	-0.994	-0.862	0.829	-0.970	-1.386	-1.454	0.386	-1.427	0.701	-1.316	-1.086	-0.418	-1.198	-0.771	0.964	-0.919	-1.358	1.094	0.002	-1.232	-0.858	-1.988	-1.012	-0.514	0.067	-0.663	0.251	-2.873	-0.718	-0.952	-0.861	-1.918	-0.837	-1.565	-0.820	-0.926
91	ETS1	ETS1	2113	-0.480	-0.661	-0.370	-0.418	-0.712	-0.792	-0.124	-1.737	-0.415	-0.544	0.946	-1.319	-0.009	-1.682	-0.951	-0.372	0.883	-2.255	-1.511	-0.406	-0.334	-0.278	1.895	-1.120	-0.220	-1.346	-0.617	-0.011	0.885	-1.544	-0.571	-0.842	-0.639	-0.786	1.490	-2.373	0.103	-1.007	-1.673	-0.577	0.965	-1.828
92	ELK1	ELK1	2002	-0.861	-1.304	-0.871	-0.379	-1.131	-0.706	-2.441	-1.957	-1.303	-0.419	0.192	-0.337	-1.627	-2.682	-2.014	-0.980	-0.644	0.203	-0.793	-2.260	-1.262	-0.566	-0.948	0.351	-0.334	-2.574	-1.416	-0.418	-0.340	0.135	-2.397	-2.179	-1.708	-0.531	-0.555	0.441	-1.412	-0.966	-1.141	0.291	-0.446	0.767
93	ELK4	ELK4	2005	-0.582	-0.798	-0.536	-0.556	-0.502	-0.754	-0.961	-0.532	0.361	0.404	-0.631	-1.155	-0.588	-1.003	-0.890	-1.361	-0.706	-0.070	-0.216	-1.649	-0.856	-0.103	-0.927	0.154	-0.535	-1.216	-0.430	-0.618	-0.313	-0.577	-1.083	-0.583	-0.180	0.554	-0.676	-0.420	-0.717	-0.874	0.222	-0.112	-0.792	-1.298
94	SP1	SP1	6667	0.243	-0.476	0.294	-0.810	-0.818	-0.303	-3.902	-1.609	0.877	1.707	0.973	-0.392	-3.234	-1.569	0.344	1.501	0.407	-1.296	-2.224	-1.148	2.288	2.260	1.672	-1.084	-3.178	-1.814	1.044	1.699	-0.023	-1.597	-3.469	-2.834	0.041	1.575	-0.329	-1.307	-2.207	-1.224	0.671	2.690	-0.125	-0.480
95	EGR1	EGR1	1958	-1.183	-1.706	-1.263	-1.077	-1.669	-1.483	-1.623	-2.617	-3.130	-0.743	0.538	-0.674	-2.724	-2.355	-2.182	-1.229	-0.505	0.719	-1.607	-2.192	-2.843	-0.915	-0.919	1.543	-2.800	-2.415	-1.184	-0.970	-0.509	-0.883	-2.244	-1.956	-2.077	-0.735	-1.126	-1.381	-1.969	-2.324	-3.005	-0.997	-0.374	-0.734
96	EGR2	EGR2	1959	-1.204	-1.424	-0.872	-1.085	-0.773	-0.741	-1.248	-1.060	0.047	-1.306	-1.160	-1.504	-1.441	-1.246	-1.693	-1.406	-0.823	-3.506	-1.489	-0.928	-0.816	-1.153	0.446	-0.633	-0.095	-1.092	-2.345	-1.077	-0.656	-2.202	-0.953	0.218	-0.783	-0.763	-0.264	-1.607	-0.693	-0.913	-0.294	0.002	-0.789	-1.325
97	ATF2	ATF2	1386	-0.562	-0.227	-0.163	-0.836	-0.686	-0.364	-2.173	0.039	-0.321	-0.272	-0.802	-1.571	-2.344	-0.538	0.085	0.309	0.241	-1.969	-2.009	-0.305	-0.020	0.879	0.917	-1.762	-1.457	-0.651	-1.010	-0.295	-0.663	-1.212	-1.534	-0.169	-0.654	-0.269	-0.718	-2.320	-1.798	0.090	-0.485	0.179	-0.243	-2.175
98	ATF7	ATF7	11016	-0.704	-1.070	-1.326	-0.699	-0.625	-1.071	-2.377	-0.151	-1.624	-1.052	-0.356	0.485	-1.861	-0.784	-1.105	-1.034	-2.249	-0.847	-2.494	-0.187	-2.391	-1.465	-0.297	-1.188	-0.954	0.028	-0.445	0.130	-2.584	-1.285	-2.010	-0.429	-0.780	-0.330	-2.061	-0.469	-2.411	-0.046	-0.768	-1.221	-0.945	-1.197
99	CBP	CREBBP	1387	0.437	0.573	-0.195	0.057	0.682	0.094	1.815	0.728	0.685	-0.014	-0.216	0.189	0.290	0.877	1.292	0.761	0.385	-0.221	0.224	-0.073	-0.317	1.522	-1.124	-1.298	-0.358	0.047	-0.277	0.546	0.600	0.068	1.608	0.164	1.158	0.614	0.475	0.751	2.225	0.057	0.130	0.238	0.027	-0.694
100	p300	EP300	2033	0.146	0.286	-0.608	0.302	0.540	0.633	-0.695	0.005	0.609	-0.273	0.404	0.287	1.054	0.135	0.371	0.200	-0.424	1.327	-2.558	-1.881	-0.092	-1.125	0.595	0.498	1.689	0.062	0.200	0.405	-0.531	1.982	0.349	0.508	0.572	1.124	0.115	0.814	0.976	0.568	0.752	0.309	0.440	0.698
101	ISGF3G	IRF9	10379	-0.986	-1.158	-1.227	-0.674	-0.459	-0.785	-1.175	-1.252	-0.209	-1.631	-0.789	-0.798	-1.299	-0.701	-0.818	-2.565	-1.021	-1.296	-1.092	-1.122	0.022	-2.020	-1.356	-1.332	-0.596	-0.240	-0.705	-2.234	-0.643	-0.822	0.264	-0.668	-0.797	-2.615	0.205	-0.250	0.439	0.195	-0.993	-1.995	-0.712	-0.858
102	ELF4	ELF4	2000	-1.505	-1.334	-1.329	-1.413	-1.417	-0.964	-2.275	-3.401	-0.965	0.703	-1.292	-1.718	-2.464	-2.239	-0.271	-1.216	-1.451	-0.834	-2.841	-2.519	-1.326	-0.613	-1.332	-0.927	-1.905	-1.612	-0.496	-1.468	-1.359	-0.444	-2.891	-1.838	-0.792	-1.515	-0.756	-1.319	-3.685	-0.989	-0.247	-0.631	-1.871	-0.939
103	IFNAR1	IFNAR1	3454	-1.054	-0.565	-0.539	-0.368	-0.303	-1.170	-1.911	-1.755	0.047	-2.127	-0.353	-0.340	-0.715	-0.643	0.690	-0.486	-1.289	-0.087	-0.510	-1.822	0.601	-1.328	0.288	-0.568	-1.262	-0.884	0.148	0.177	-1.236	0.181	-0.061	-1.198	-0.315	-0.632	-0.292	-0.091	-1.910	-1.449	-0.442	-1.352	-0.988	0.046
104	IFNAR2	IFNAR2	3455	-1.179	-1.005	-0.801	-0.545	-0.932	-0.640	-2.742	-1.293	-1.666	-1.065	-0.501	-0.794	-1.075	-1.807	-2.103	-0.935	-0.043	-0.907	-2.558	-1.352	0.011	-1.287	0.075	-0.316	-0.063	-1.053	-2.656	-0.338	0.717	-0.751	-1.184	-0.863	-1.728	-1.000	1.321	-0.738	-0.317	-1.414	-1.809	-0.090	-0.507	-0.773
105	IFNB1	IFNB1	3456	-0.885	-1.358	-1.109	-0.544	-0.667	-1.094	-1.154	-1.537	-0.571	-0.557	-0.615	-2.087	-1.208	0.015	-1.509	-0.744	-1.690	-1.986	-1.050	-1.656	0.286	-0.655	-1.167	-2.020	-0.950	-0.052	-0.138	0.104	-1.712	-1.770	-1.606	-0.152	-0.212	-0.747	-0.587	-1.903	-0.859	-1.312	0.205	-0.876	-1.935	-1.835
106	IL12A	IL12A	3592	-0.368	-0.297	-0.493	-0.147	-0.252	-0.050	0.179	0.104	-3.368	-0.376	-1.330	-0.360	0.118	-0.924	0.323	0.062	-0.655	-0.686	-0.085	-0.170	-2.977	-0.477	-1.063	-0.510	0.340	-1.047	0.620	0.449	-0.970	-0.635	0.011	-0.542	0.028	0.224	-1.381	-0.516	0.709	-0.995	-0.115	0.578	-1.121	0.014
107	IL12B	IL12B	3593	-0.799	-1.132	-0.702	-1.083	-1.011	-1.259	-0.033	-0.664	-1.250	-1.900	-0.137	-0.935	-1.300	-0.219	-1.133	-0.676	-1.854	-1.132	-0.456	0.164	-0.207	-0.948	-1.253	-1.287	-1.984	-0.887	-1.279	-0.197	-2.154	-0.801	-1.216	-0.875	0.742	-1.146	-1.368	-0.799	-1.695	-0.351	-1.111	-1.022	-2.697	-1.407
108	IL1B	IL1B	3553	-1.128	-0.485	-0.075	-0.859	-0.752	-1.263	0.123	-1.185	-0.815	-1.363	-1.072	-1.259	-0.289	-0.432	-1.303	-0.537	-1.568	-0.325	0.129	0.536	-0.948	-0.278	0.474	-0.434	0.418	-0.801	-1.414	-0.570	-1.661	-0.916	-0.721	-0.592	0.103	-1.095	-2.027	-0.783	-1.097	-0.653	-0.963	-1.476	-1.429	-1.626
109	IL6	IL6	3569	-0.309	-0.619	-0.659	-0.341	-0.521	-0.523	0.574	-1.046	-0.160	-0.756	-0.458	0.233	0.661	-0.972	-1.189	-0.053	-1.273	-0.266	0.977	-1.092	-0.682	-0.636	-0.786	-0.065	0.829	-0.481	-1.481	-0.106	-0.697	-0.200	0.186	-0.954	-1.836	-0.517	-0.525	0.400	0.651	-1.103	-1.817	0.020	-0.329	-0.718
110	TNF	TNF	7124	-0.551	-1.171	-0.919	-1.976	-1.157	-1.200	-0.518	-0.585	-0.658	-0.336	-1.014	-0.277	-0.044	-1.344	-0.998	-0.515	-1.854	-3.319	0.042	-1.026	-0.804	-1.156	-0.811	-2.167	0.050	-2.141	-2.058	-0.129	-1.894	-3.231	-1.061	-0.804	-1.870	0.028	-1.254	-3.191	-0.850	-0.876	-3.621	-0.095	-1.525	-2.709
111	CCL3	CCL3	6348	-0.634	-0.261	-0.267	-0.186	-0.003	-0.299	-1.282	-0.192	-0.650	-0.617	0.870	-1.246	-1.213	-0.313	0.051	-0.208	-0.486	-0.156	0.144	-0.655	0.088	-0.677	0.524	-0.622	-1.800	-0.193	-0.180	0.046	-0.357	0.197	-2.045	0.164	-0.047	0.042	0.188	-0.676	-0.336	-0.672	-0.755	-0.175	0.500	-0.262
112	CXCL11	CXCL11	6373	-0.425	-0.517	-0.452	0.184	-0.411	-0.149	-2.746	-0.026	0.265	-0.460	-1.547	-0.390	-1.627	0.088	-0.298	-0.510	-0.857	-0.525	-1.526	-0.531	0.254	-0.374	-2.212	-0.353	-0.918	0.452	0.202	0.215	-0.225	0.166	-1.953	0.007	-0.111	-0.297	-0.524	-0.648	-1.973	-0.155	-0.126	-0.187	-0.143	-0.066
113	CXCL9	CXCL9	4283	-0.581	-0.858	-0.957	-0.501	-0.645	-0.336	-1.949	-0.778	0.562	-2.628	-0.385	0.616	-0.764	-0.951	-1.160	-1.245	-0.097	0.131	-1.650	-0.582	0.709	-2.353	1.337	-1.332	-0.052	-0.871	-1.324	-1.495	-0.132	0.115	-1.060	-0.212	-0.942	-2.114	-0.348	0.437	-2.570	-0.121	-0.551	-2.449	0.185	1.279
114	RP105	CD180	4064	-0.336	-0.538	-0.732	-0.325	0.174	-0.383	-0.280	-0.393	-0.903	-0.957	0.767	0.315	-0.510	-0.456	-1.203	-0.565	-1.303	-0.186	-0.682	-0.704	-2.529	-1.084	-0.759	-0.260	-0.597	-0.616	0.061	-0.054	-1.115	0.005	0.113	0.235	-1.994	0.690	-0.011	1.042	0.575	-0.055	-0.928	-0.711	-0.823	0.167
115	MD1	LY86	9450	-0.605	-0.579	-1.131	-0.053	-0.233	-0.235	-0.438	-1.418	-0.551	-1.209	-0.658	-0.193	0.196	-0.510	-0.647	-2.145	-0.757	-0.445	0.795	-1.431	-0.595	-1.980	-1.654	-0.831	0.310	-0.107	0.000	-1.083	-0.449	0.146	-0.376	-0.710	0.033	-2.006	-0.089	0.061	0.158	-0.078	0.005	-3.092	-0.442	-0.392
116	TIR8	SIGIRR	59307	-0.346	-0.782	-0.133	-0.526	-0.260	0.120	-0.428	-0.405	-0.287	0.196	-0.434	-0.238	-0.182	-0.676	-0.889	-0.992	1.033	-0.895	0.441	-0.531	-0.285	-0.310	1.412	0.019	-0.257	0.638	-0.950	-1.348	0.959	-0.795	-0.460	0.451	-1.080	-0.159	1.755	-0.360	0.182	0.058	-0.158	0.196	1.350	-0.594
117	ST2	IL1RL1	9173	-0.122	-0.442	-0.023	-0.488	-0.520	-0.542	-0.189	-1.061	0.561	0.778	-0.207	-0.055	-0.564	-1.256	-0.321	-0.020	-2.705	-0.096	0.001	-0.534	0.355	1.001	-2.574	-0.047	-0.647	-1.398	0.042	0.450	-2.347	-0.329	-0.398	-1.732	-0.643	0.763	-1.592	-0.163	-0.704	-0.380	-0.239	1.048	-1.187	-0.842
118	IRAK3	IRAK3	11213	-0.135	-0.402	-0.087	-0.444	-0.458	-0.448	0.085	-0.753	-0.022	0.654	-0.543	-0.249	0.311	-0.614	0.093	-0.191	-0.732	-0.614	1.473	0.298	0.057	-0.470	-0.232	-0.423	-0.796	-0.304	0.262	-0.440	-0.506	-0.447	-0.340	-0.613	-0.406	-0.568	-0.510	-0.336	-0.691	-0.623	-0.273	0.200	-0.710	0.103
119	SHP1	PTPN6	5777	-0.900	-0.443	-0.653	-0.764	-1.126	-1.038	-1.368	0.942	-0.431	-1.519	-1.450	-0.301	-0.473	0.434	-0.349	-1.850	-1.007	-0.413	-0.779	0.144	-0.528	-1.167	-0.864	-0.160	-0.012	0.310	-0.371	-2.132	-1.219	-1.158	-1.064	1.151	-0.176	-1.690	-1.607	-1.188	-1.122	0.242	0.139	-1.690	-1.321	-0.954
120	Cyld	CYLD	1540	-1.987	-0.141	-0.662	0.146	-1.460	-1.071	-2.811	-4.249	-0.363	-0.998	-2.245	-1.728	-0.176	-0.758	0.274	-0.106	0.254	-0.587	-0.531	-1.466	1.037	-0.793	-0.991	-0.455	0.362	-0.835	0.895	0.090	0.202	-1.119	-1.609	-2.576	-0.665	-0.564	-1.310	-1.686	-1.219	-0.613	-1.171	-0.418	-0.972	-1.314
121	A20	TNFAIP3	7128	-0.825	-0.624	0.844	-0.810	-1.180	-1.790	-2.784	-0.511	-2.321	-0.162	1.201	-1.140	-0.701	0.760	-0.548	-0.808	-0.156	-1.638	0.829	0.860	1.792	0.527	1.028	-0.972	-0.549	-0.166	-1.150	-1.072	0.259	-1.734	-1.945	-0.360	-3.256	-0.767	0.270	-1.594	-2.370	-1.222	-2.938	-1.405	0.478	-2.175
122	DUSP2	DUSP2	1844	-0.236	0.143	-0.707	-0.243	-0.398	-0.101	-0.521	0.029	-3.521	-0.115	-0.196	-0.276	0.132	0.184	-2.814	0.154	0.209	0.094	-1.094	-0.305	-1.513	1.122	-0.633	-0.781	0.209	-0.663	-3.429	-0.240	-0.245	0.172	-0.372	-0.850	-3.923	0.245	0.064	-0.424	-0.055	-0.074	-4.273	0.164	-0.128	-0.446
123	AIP1	DAB2IP	153090	-0.747	-0.984	-0.941	-0.741	-0.923	-0.555	-1.031	0.131	1.342	-2.489	-0.463	-2.627	-1.115	-1.686	1.168	-0.853	-1.269	0.364	-0.729	-1.678	0.878	-1.153	-1.253	-0.393	-0.522	-1.368	0.030	-1.015	-0.961	0.972	-1.003	-1.175	1.126	-1.962	-0.843	-0.563	-0.600	-0.239	1.322	-1.228	-0.814	-0.510
124	Tollip	TOLLIP	54472	-0.691	-0.767	-0.830	-0.403	-0.801	-0.345	-1.177	-0.538	-0.006	-2.909	-0.499	-0.843	-1.398	-0.473	0.126	-1.062	-1.187	-0.445	-1.285	-1.656	1.061	-1.146	0.474	-0.515	-0.397	-0.408	0.029	-1.779	-1.165	1.024	-1.291	-0.172	0.044	-5.431	-0.418	-1.184	-1.343	-0.789	0.814	-2.399	0.098	0.522
125	MKP1	DUSP1	1843	0.574	0.098	-0.002	0.050	0.540	-0.102	0.422	0.682	1.534	0.816	0.207	0.466	-0.498	1.225	-0.244	1.193	-1.048	0.441	-0.729	-0.226	1.337	0.222	-0.891	0.955	-0.248	1.119	-0.599	1.603	-0.592	0.348	0.526	1.231	0.555	0.864	0.333	0.466	-0.138	-0.248	-0.011	1.185	-0.432	-0.066
126	RIP3	RIPK3	11035	-0.118	-0.496	-0.191	-0.203	-0.084	-0.095	-0.335	-0.327	0.092	-0.642	0.459	0.280	-0.701	-0.602	0.804	-0.130	-0.931	-0.390	-0.183	-0.199	0.388	-0.622	-0.310	0.115	0.155	-0.831	0.624	-0.345	-0.691	-0.062	-0.055	-0.850	0.102	-0.464	-0.114	0.044	0.368	-0.302	0.575	-0.624	-0.239	0.049

TABLE S2 MOUSE SCREEN SCORES)

Gene#	Name	Gene Symbol	Gene ID	LPS-mTNF_Median	P3C-mTNF_Median	R848-mTNF_Median	LPS-mNFKB_Median	P3C-mNFKB_Median	R848-mNFKB_Median	LPS-mTNF_siRNA1	LPS-mTNF_siRNA2	LPS-mTNF_siRNA3	LPS-mTNF_siRNA4	LPS-mTNF_siRNA5	LPS-mTNF_siRNA6	P3C-mTNF_siRNA1	P3C-mTNF_siRNA2	P3C-mTNF_siRNA3	P3C-mTNF_siRNA4	P3C-mTNF_siRNA5	P3C-mTNF_siRNA6	R848-mTNF_siRNA1	R848-mTNF_siRNA2	R848-mTNF_siRNA3	R848-mTNF_siRNA4	R848-mTNF_siRNA5	R848-mTNF_siRNA6	LPS-mNFKB_siRNA1	LPS-mNFKB_siRNA2	LPS-mNFKB_siRNA3	LPS-mNFKB_siRNA4	LPS-mNFKB_siRNA5	LPS-mNFKB_siRNA6	P3C-mNFKB_siRNA1	P3C-mNFKB_siRNA2	P3C-mNFKB_siRNA3	P3C-mNFKB_siRNA4	P3C-mNFKB_siRNA5	P3C-mNFKB_siRNA6	R848-mNFKB_siRNA1	R848-mNFKB_siRNA2	R848-mNFKB_siRNA3	R848-mNFKB_siRNA4	R848-mNFKB_siRNA5	R848-mNFKB_siRNA6
1	TLR1	Tlr1	21897	-0.011	0.237	-0.092	-0.014	-0.493	-0.213	0.608	0.164	-0.206	0.565	-0.187	-0.851	0.302	0.318	0.132	0.498	0.172	-0.149	0.696	0.250	-0.483	0.390	-0.435	-0.558	0.744	-0.086	0.058	-0.559	-1.351	0.153	0.270	-0.457	-1.176	-0.530	0.900	-1.498	0.172	-0.582	-0.127	-0.203	-0.223	-0.481
2	TLR2	Tlr2	24088	0.082	-0.368	0.454	0.334	-1.785	0.238	0.103	-0.346	1.382	0.924	-1.052	0.060	-0.447	-0.257	-0.290	0.968	-1.004	-1.027	0.023	-0.222	1.256	0.885	-0.861	1.088	-0.553	-0.963	0.925	0.410	0.966	0.258	-3.303	-2.242	-1.096	-1.880	2.087	-1.691	-0.323	-1.002	1.109	0.800	-0.698	0.998
3	TLR3	Tlr3	142980	0.455	-0.185	0.108	-0.359	-0.090	-0.046	0.314	-2.188	-0.186	0.688	0.596	1.192	-0.209	-1.667	-0.222	-0.162	0.749	0.805	-0.426	-1.928	-0.396	0.646	0.836	0.612	1.028	-0.600	-0.932	0.347	-0.615	-0.118	0.190	1.297	0.421	-0.370	-0.927	-1.114	1.062	-0.798	-0.657	-0.194	0.176	0.102
4	TLR4	Tlr4	21898	-1.072	0.284	0.591	-2.605	0.440	0.267	-0.841	-1.008	-1.625	-1.136	-0.527	-1.542	-0.325	0.405	0.163	0.142	0.661	0.405	-0.353	0.556	-1.001	1.379	0.626	1.079	-0.302	-2.059	-3.151	-3.357	-1.541	-4.140	0.567	0.725	0.478	0.401	-0.363	-1.303	0.044	0.704	-0.528	0.331	0.203	0.933
5	TLR5	Tlr5	53791	-0.237	0.262	0.303	0.393	-0.127	-0.062	-0.369	1.827	-0.104	1.009	-0.668	-0.369	-0.988	1.377	0.495	0.631	-0.453	0.029	0.143	1.000	-0.178	0.462	-0.846	0.781	-0.596	0.451	0.429	-0.965	1.172	0.358	-1.146	0.996	-0.109	-0.144	1.090	-1.339	-0.165	0.743	0.210	-0.139	-1.215	0.015
6	TLR6	Tlr6	21899	-0.170	-0.364	0.527	0.178	-1.474	0.033	0.504	1.512	-1.881	0.113	-0.474	-0.453	-0.313	1.279	-1.968	-0.880	0.252	-0.415	0.502	0.768	-1.342	0.553	0.827	0.104	0.310	0.094	-1.121	0.263	0.418	-0.138	-2.584	-1.500	-3.054	1.117	-1.218	-1.448	0.013	0.037	-1.378	0.028	0.856	0.038
7	TLR7	Tlr7	170743	-0.302	-0.314	-1.798	-0.111	-0.730	-2.652	-0.987	-1.327	-0.452	0.385	-0.152	0.336	-1.121	-1.326	-0.522	0.355	1.052	-0.107	-1.689	-1.907	-2.488	-1.659	-1.926	-1.365	-0.709	-2.596	1.031	-0.510	0.601	0.288	-1.043	-1.789	2.001	-0.417	-1.045	1.598	-2.199	-3.409	-3.104	-1.153	-3.853	-2.186
8	TLR8	Tlr8	170744	-0.083	0.365	-0.198	-0.053	-0.004	0.374	1.074	-0.341	-0.340	0.784	-2.050	0.174	1.899	0.629	-0.159	0.592	-1.839	0.138	0.944	0.327	-0.651	0.071	-0.468	-0.468	-0.126	0.649	-0.497	0.170	-2.285	0.021	-0.686	0.409	-0.082	0.073	-1.303	1.777	0.649	0.711	-0.319	0.652	0.099	-0.989
9	TLR9	Tlr9	81897	-0.282	-0.576	-0.455	-0.516	-0.644	-0.522	-0.103	-2.141	1.593	-0.051	-0.461	-1.313	-0.738	-1.327	1.298	-0.247	-1.674	-0.414	0.168	-1.480	0.988	-0.119	-0.791	-0.840	-1.189	-0.770	-0.293	-0.739	0.541	-0.164	-0.617	-0.904	0.054	-0.670	0.268	-1.332	-0.223	-0.050	-0.617	-0.427	-1.034	-1.320
10	LBP	Lbp	16803	-0.253	0.243	0.107	-0.244	-0.541	0.073	-0.073	0.116	-0.578	-0.550	0.774	-0.433	0.211	1.464	0.268	-2.600	0.631	0.218	0.702	-0.035	-0.568	-0.140	0.248	0.840	-0.202	-1.832	0.978	-0.754	1.032	-0.286	-0.526	-1.446	0.929	-0.609	1.676	-0.557	-0.127	-1.321	0.989	-1.435	0.274	0.402
11	MD2	Ly96	17087	-0.842	-0.457	0.262	-0.967	-0.287	-0.008	0.063	-2.108	-0.861	-0.650	-1.074	-0.823	1.124	-0.794	-0.671	0.546	-0.243	-0.674	0.954	-1.054	0.299	0.571	0.226	0.147	-0.422	-2.922	-0.838	-2.277	-0.619	-1.097	0.298	-0.042	-0.260	-0.860	-0.468	-0.313	-0.072	0.371	0.120	-0.089	-0.636	0.055
12	CD14	Cd14	12475	-1.725	-1.594	-1.357	-1.719	-0.742	-1.591	-1.764	-2.082	-1.686	0.342	-1.849	0.107	-1.952	-1.860	-1.792	-1.210	-1.395	0.836	-1.537	-2.220	-0.946	-1.582	-1.177	0.684	-2.239	-2.381	-1.819	-1.323	-1.618	-0.484	-0.830	-2.121	-1.405	2.898	1.083	-0.654	-0.712	-2.524	-2.469	-2.723	-0.508	0.478
13	CD11b	Itgam	16409	0.038	-0.366	-0.390	-0.324	-0.668	-0.287	0.492	-0.547	0.446	0.345	-0.269	-1.114	-1.293	-0.762	0.028	0.291	-0.266	-0.466	-0.376	-0.681	-0.088	0.239	-0.745	-0.404	0.037	-0.290	-0.359	0.643	-1.112	-0.915	0.423	-0.408	-1.550	0.724	-1.113	-0.929	-0.389	-0.289	0.097	-0.286	-0.209	-1.519
14	CD11c	Itgax	16411	-0.232	0.197	0.346	-0.739	-0.374	-0.598	1.585	-0.298	-0.919	0.275	-0.165	-0.456	1.015	-0.060	-1.169	0.048	0.758	0.345	0.767	-0.337	-1.384	0.021	0.973	0.670	-0.606	-0.821	-1.465	-0.607	-0.777	-0.700	-0.088	-1.509	-1.185	0.634	1.125	-0.659	-0.734	0.269	-1.434	-2.229	-0.461	0.215
15	ARF6	Arf6	11845	1.002	0.618	0.429	-0.390	-0.703	-0.493	-0.735	0.938	0.641	1.067	2.301	1.816	-0.313	0.841	0.009	0.394	1.481	0.883	0.054	0.641	-0.270	0.953	0.705	0.217	-0.455	-0.324	-0.714	-0.262	-0.222	-0.918	-0.567	-0.324	-1.420	-0.792	-0.613	-1.550	-0.334	-0.705	-1.071	-0.651	1.321	0.254
16	MyD88	Myd88	17874	-0.951	-1.431	-2.119	-1.154	-0.583	-3.608	-1.060	-2.208	-0.842	-1.521	-0.573	0.176	-1.392	-1.895	-1.528	-1.469	-1.390	-0.386	-1.940	-2.283	-1.954	-2.545	-2.463	-0.076	-0.028	-2.167	-0.498	-1.721	-1.162	-1.145	0.436	-1.647	-2.780	-0.248	0.072	-0.919	-2.362	-3.874	-3.342	-4.158	-4.441	-0.616
17	Mal	Tirap	117149	-1.472	-1.471	0.401	-2.096	-1.615	0.186	-1.047	-0.948	-1.949	-1.897	-0.860	-2.548	-2.048	-1.141	-1.129	-1.801	0.166	-2.492	0.515	0.287	-1.402	1.487	0.636	-0.687	-2.046	-0.640	-1.625	-3.133	-2.147	-2.455	-1.885	-0.108	-3.382	-1.345	0.215	-1.906	0.290	0.222	0.504	0.149	0.014	-0.060
18	IRAK1	Irak1	16179	-0.226	-0.268	-0.108	-0.359	-0.825	-0.972	-0.995	0.926	-0.393	1.541	-0.059	-0.785	-0.516	0.590	-0.544	-0.010	-0.077	-0.460	-0.865	0.538	-0.413	1.634	0.197	-0.704	-0.890	0.232	-0.542	-1.086	0.577	-0.175	-1.375	0.458	-1.552	-1.152	-0.499	1.424	-1.777	-0.068	-1.186	-1.228	0.019	-0.757
19	IRAK2	Irak2	108960	-1.229	-1.752	-2.006	-1.107	-0.619	-2.889	-0.279	-0.937	-1.521	-0.182	-1.789	-1.629	-0.923	-1.797	-1.802	-1.476	-1.707	-1.926	-1.589	-1.722	-2.345	-1.993	-2.260	-2.020	-2.029	-0.959	-2.224	-1.088	-1.127	-0.450	-1.269	-0.295	-1.818	-0.701	-0.538	0.227	-2.878	-1.544	-3.429	-2.502	-2.899	-3.649
20	IRAK4	Irak4	266632	-1.362	-1.790	-2.169	-1.290	-1.233	-1.545	0.692	-1.613	-1.441	-1.393	-1.330	-1.088	0.021	-2.344	-1.418	-2.162	-2.281	-1.395	-1.283	-2.418	-1.945	-2.394	-3.861	-1.581	0.494	-3.136	-2.049	-0.894	1.247	-1.685	-1.049	-2.765	-2.266	-1.416	3.157	1.430	-0.129	-3.775	-2.674	-1.909	-1.181	-0.051
21	Pellino	Peli1	67245	0.372	0.337	0.341	-0.566	-0.317	-0.677	1.461	0.476	0.268	2.587	-1.220	-0.644	1.010	0.271	0.402	1.893	-0.313	-1.150	0.563	0.119	0.668	1.270	-0.961	-1.793	-0.385	-0.571	-0.560	0.786	-1.599	-0.840	-0.982	-0.544	-0.091	0.404	-1.759	0.816	-0.528	-0.555	-0.798	2.027	-0.808	-0.799
22	Uev1a	Ube2v1	66589	-0.225	0.214	0.049	-0.326	-0.193	0.034	-0.432	-0.018	0.139	-0.494	2.334	-1.976	-0.408	0.420	0.203	0.224	2.626	-2.565	0.102	-0.004	-0.640	0.163	2.256	-1.310	1.575	-1.212	0.160	-0.813	0.846	-1.203	1.454	-0.685	-0.077	-1.498	-0.308	1.890	1.233	-1.053	-0.399	0.466	0.730	-1.352
23	Ubc13	Ube2n	93765	-0.317	-0.436	-0.340	0.086	0.036	-0.030	-0.108	-1.055	0.083	-0.466	-0.167	-0.820	-0.248	-0.532	-0.536	-0.340	0.094	-0.654	-0.054	-1.020	-0.111	-0.259	-0.836	-0.421	0.179	-1.104	0.690	0.027	-2.009	0.144	-0.136	-0.409	0.209	0.500	-0.726	0.844	-0.161	-1.094	0.455	0.230	-1.419	0.101
24	TRAF6	Traf6	22034	-0.579	-0.888	-1.342	-1.765	-1.578	-2.495	-0.350	-0.740	-1.331	0.187	-0.418	-0.834	-0.833	-1.611	-2.688	-0.516	-0.814	-0.942	-0.355	-1.862	-2.122	-0.488	-1.284	-1.399	-2.256	-1.220	-1.933	-0.967	-1.598	-2.409	-2.504	-2.738	-0.848	-1.453	-1.702	-0.964	-2.532	-2.575	-2.883	-1.646	-2.105	-2.458
25	TRAF3	Traf3	22031	-0.351	-0.336	-0.559	0.274	-0.071	-0.362	-0.156	-0.919	-0.547	0.583	-1.033	-0.026	-0.899	-0.569	-0.103	0.309	-1.407	0.005	0.005	-1.098	-0.844	-0.274	-1.373	0.490	0.296	-0.083	0.252	0.028	2.078	0.782	0.178	-0.200	-0.297	0.533	-0.403	0.058	-0.034	-0.690	0.486	-0.711	-1.575	1.241
26	TAK1	Map3k7	26409	-0.487	-0.532	-0.599	0.566	-0.851	-0.758	-0.322	0.799	-0.860	0.622	-0.653	-1.715	-1.027	0.266	-0.734	0.592	-0.331	-1.759	-0.016	-0.093	-1.104	0.202	-1.448	-2.169	0.456	0.677	-2.294	0.071	1.411	3.092	-0.953	-0.748	-1.288	-1.152	-0.122	-0.536	-0.019	-0.168	-1.362	0.448	-1.665	-1.347
27	TAB1	Tab1	66513	-1.080	-0.638	-0.669	-0.553	-0.422	-1.281	0.929	-2.274	-0.732	-1.550	2.195	-1.428	0.386	-1.499	-0.431	-1.113	1.416	-0.845	-0.187	-1.943	-0.868	-0.470	1.343	-1.597	-0.134	-0.484	-0.667	-0.622	-1.789	-0.068	-0.348	-0.496	-0.258	-0.527	-0.902	0.037	-0.677	-1.175	-1.430	-1.386	-0.115	-1.820
28	TAB2	Tab2	68652	-0.321	-0.395	-0.475	-0.056	-0.503	-0.139	-0.124	0.031	-0.518	0.244	-1.062	-1.157	-0.180	-0.198	-0.322	-0.468	-0.474	-0.736	0.318	0.098	-0.961	-1.074	-0.811	-0.138	-0.550	-1.042	0.241	0.947	0.797	-0.354	-0.638	-0.368	-0.045	-0.989	0.375	-0.833	-1.232	-0.801	0.114	-0.173	-0.014	-0.105
29	TAB3	Tab3	66724	-0.254	-0.410	-0.755	0.254	-0.376	-0.406	-0.434	-0.256	-0.885	0.767	-0.252	-0.093	-1.337	-0.576	-0.819	0.482	0.425	-0.245	-0.849	-0.600	-0.891	1.270	-0.870	-0.661	-0.091	0.233	-0.944	0.275	1.633	1.131	-0.415	-1.142	-0.595	0.105	0.279	-0.337	-0.459	-0.263	-1.283	0.364	-1.012	-0.353
30	NEMO	Ikbkg	16151	-1.386	-0.736	-0.784	-1.084	-0.810	-2.139	0.221	-1.546	-1.227	-3.027	-1.837	-0.812	0.418	-1.509	-0.764	-2.323	-0.709	-0.456	0.028	-1.237	-0.330	-1.837	-1.504	-0.017	-1.580	-0.825	0.249	-2.362	-1.344	1.301	-1.185	-0.061	-0.856	-1.551	-0.765	-0.397	-2.223	-2.056	-0.204	-2.637	-2.441	-0.007
31	IKKa	Chuk	12675	-0.708	-0.181	0.076	0.363	-0.296	-0.804	0.886	-1.196	1.344	-2.262	-1.234	-0.220	0.695	-1.978	0.660	-1.079	-0.175	-0.188	0.418	-2.043	0.964	-1.075	-0.170	0.321	1.326	-0.993	0.548	3.565	-1.577	0.178	-0.072	-1.820	0.253	1.475	-1.842	-0.521	0.554	-2.159	0.120	-1.936	-1.728	1.087
32	IKKb	Ikbkb	16150	-1.067	-0.972	-0.987	-0.535	-1.105	-1.620	-0.832	-2.006	-1.367	-0.502	-1.255	-0.878	-0.734	-1.765	-0.752	-0.420	-1.192	-1.255	-1.100	-1.889	-0.875	0.436	-1.398	-0.395	0.867	-1.122	-1.644	-0.935	0.146	-0.136	-0.188	-1.228	-2.030	-1.260	-0.981	0.060	0.985	-1.212	-2.212	-0.785	-2.049	-2.027
33	IkBa	Nfkbia	18035	0.340	0.644	-0.045	-1.379	-1.560	-1.447	1.242	-1.680	1.491	-0.281	0.575	0.104	-0.421	0.360	1.958	0.929	1.636	-1.042	0.087	-1.595	0.837	-0.176	0.482	-1.226	-1.733	-2.871	-1.054	-0.867	-1.705	0.274	-1.772	-3.111	-1.622	0.038	-1.498	-0.952	-1.677	-3.395	-0.874	-2.054	-1.217	-0.045
34	IkBb	Nfkbib	18036	-0.742	-0.458	-0.614	0.438	-0.031	-0.971	0.004	-0.753	0.070	-0.850	-1.311	-0.731	-1.069	-0.184	1.743	-0.732	-2.688	0.129	-0.537	-0.691	0.999	-0.813	-0.184	-0.837	-0.780	0.354	0.523	0.555	-0.739	0.577	-1.182	-0.314	0.531	0.253	12.303	-0.550	-1.304	0.170	0.880	-0.639	-1.826	-1.669
35	IkBe	Nfkbie	18037	-0.382	-0.116	-0.800	-1.251	-0.642	-0.883	-0.879	-1.062	0.428	-0.487	-0.277	0.361	-1.075	-0.428	0.157	-0.167	-0.065	0.364	-1.030	-1.586	0.224	-0.775	-0.824	0.529	-1.981	-0.603	-0.964	-1.537	-1.620	-0.624	0.144	-0.637	-1.023	1.307	-0.829	-0.646	-0.793	-0.715	-0.974	-1.631	-1.423	-0.354
36	Nfkb1	Nfkb1	18033	0.105	-1.177	-0.785	0.103	0.299	0.400	0.326	-1.127	0.197	0.951	-0.362	0.013	-0.190	-1.804	-0.222	-1.313	-1.673	-1.040	-0.900	-2.202	-0.441	-0.497	-1.395	-0.671	2.116	0.117	0.727	-0.391	0.088	-0.364	0.335	0.263	0.239	0.663	-0.612	0.699	1.146	-0.168	0.178	0.888	-0.156	0.621
37	NFkb2	Nfkb2	18034	-0.693	-0.764	-0.614	0.600	0.011	0.044	-0.532	-0.855	-1.408	0.525	1.291	-1.372	-0.815	-0.713	-0.909	-0.019	0.062	-1.977	-0.124	-1.114	-1.103	0.179	-0.016	-2.083	0.451	-0.373	0.748	0.918	-0.264	2.169	0.110	-0.088	-0.543	1.335	-0.895	0.916	0.420	-0.333	0.729	1.173	-1.660	-0.794
38	RelA	Rela	19697	-0.558	-1.204	-1.406	-0.911	-0.329	-1.711	-0.301	0.564	-1.124	-1.806	-0.224	-0.814	-0.894	0.275	-1.281	-2.231	-1.126	-1.418	-0.381	0.113	-2.259	-1.657	-1.311	-1.501	-1.236	-1.008	0.341	2.378	-2.202	-0.814	-1.230	-0.305	-0.354	2.051	-1.225	-0.260	-1.534	-1.336	-0.261	-1.889	-3.261	-2.456
39	RelB	Relb	19698	-0.611	-0.723	-0.357	-0.797	-0.522	-0.339	-0.284	-0.030	-1.275	0.688	-2.234	-0.939	-0.161	0.290	-1.504	0.836	-2.459	-1.286	-0.230	0.283	-1.465	0.587	-1.472	-0.484	-0.010	-0.437	-2.415	0.272	-1.157	-1.582	-0.680	0.028	-2.334	-0.364	1.469	-0.685	-0.636	-0.218	-0.460	0.209	-0.502	0.435
40	cRel	Rel	19696	-0.458	-0.468	-0.323	-0.280	-0.098	0.121	-0.528	-0.127	-0.306	-0.387	-0.842	-1.012	-1.146	0.754	0.219	-0.050	-1.217	-0.885	-0.467	-0.054	-0.248	-0.360	-0.286	-0.449	-0.639	0.679	1.033	-0.115	-0.508	-0.445	0.067	-0.264	0.893	1.171	-1.299	-0.287	-0.417	0.396	2.030	-0.677	1.088	-0.155
41	Tpl2	Map3k8	26410	-0.037	-0.173	-0.419	0.146	0.041	0.111	-0.021	0.804	-1.003	0.543	-0.052	-1.244	0.020	0.331	-0.876	0.392	-0.369	-0.366	-0.513	0.174	-1.579	0.608	-0.326	-0.642	0.111	0.181	0.386	-0.636	0.206	-0.373	0.223	1.259	-0.190	-0.062	-0.251	0.144	-0.400	0.122	-0.225	0.101	0.711	0.273
42	Mekk1	Map3k1	26401	0.024	-0.042	0.058	0.113	-0.071	0.274	-0.148	-2.401	0.492	1.183	-0.309	0.196	-0.077	-2.820	0.627	0.125	-0.006	-0.752	0.779	-1.370	-1.518	0.682	-0.232	0.348	0.656	-1.290	0.745	-0.430	2.834	-0.450	1.334	-0.420	-0.543	-0.792	0.711	0.279	1.971	-1.986	0.216	0.176	0.331	0.379
43	Mkk1	Map2k1	26395	-0.780	-0.680	-0.414	0.261	-0.355	0.612	0.130	-0.902	-0.977	-0.074	-1.720	-0.658	0.426	-0.998	-0.737	0.183	-0.623	-0.973	-0.320	-0.794	-1.113	0.354	-0.399	-0.429	0.634	0.169	-0.145	0.205	0.658	0.317	0.052	-0.626	-0.765	-0.084	0.356	-1.105	0.641	0.182	-0.583	1.781	0.584	1.051
44	Mkk2	Map2k2	26396	-0.531	-0.854	-0.887	-0.217	-0.323	-1.031	0.620	-1.164	-0.661	-0.402	-0.041	-1.849	0.398	-0.813	-0.894	-0.694	-0.920	-1.106	-0.088	-1.202	-0.858	-0.917	-1.313	0.154	0.585	-0.666	-0.247	2.720	-0.187	-0.672	0.227	-0.781	-0.489	2.911	-0.157	-0.797	-0.016	-1.344	-1.020	-1.042	-1.205	-0.846
45	Erk1	Mapk3	26417	0.032	-0.461	-0.139	-0.291	-0.949	-0.304	-0.128	2.126	-0.749	0.192	-1.303	0.343	-1.692	1.520	-0.680	-0.242	-1.250	0.800	-1.300	0.901	-0.152	-0.125	-0.911	0.772	-1.644	0.736	-0.228	0.312	-0.484	-0.355	-1.343	1.122	-0.110	-0.962	-1.128	-0.936	-1.432	0.845	0.036	-0.528	-0.624	-0.081
46	Erk2	Mapk1	26413	-0.575	-0.826	-0.989	0.157	-0.784	-1.036	-0.843	-1.500	-1.514	-0.306	-0.036	0.017	-1.169	-2.069	-2.224	-0.483	-0.067	-0.425	-1.192	-2.116	-1.174	-0.804	0.088	-0.001	-0.325	-0.922	-0.519	0.877	0.639	3.894	-0.992	-1.208	-1.139	-0.577	-0.022	-0.047	-0.772	-2.488	-1.300	0.005	-0.485	-2.439
47	Mkk3	Map2k3	26397	-0.212	-0.451	-0.808	-0.349	0.174	-0.115	-0.409	0.073	-0.016	-0.652	-1.306	1.501	-0.242	-0.660	0.178	-1.115	-0.862	0.346	-0.791	-0.825	0.224	-1.185	-0.937	0.253	0.530	-0.186	-0.340	-0.563	-1.477	-0.357	-0.352	0.278	0.069	2.387	-0.993	0.842	0.244	-0.271	-0.066	-1.111	0.595	-0.165
48	Mkk6	Map2k6	26399	-0.211	-0.146	-0.018	-0.026	-0.333	-0.676	-0.454	0.032	-0.469	1.659	-0.930	0.911	-0.777	0.415	-0.819	0.359	-0.651	1.046	-0.267	0.231	-0.663	0.876	-0.689	0.849	-1.563	-1.451	0.047	-0.099	4.635	0.516	-1.551	-1.297	-0.103	-0.564	1.067	0.215	-1.560	-1.262	-0.090	0.755	-1.522	0.032
49	p38a	Mapk14	26416	-0.139	-0.667	-0.344	0.587	-0.248	-0.292	0.057	0.850	0.270	-0.341	-0.438	-0.334	-0.697	0.413	-0.140	-0.637	-1.237	-1.179	-0.156	0.273	-0.331	-0.358	-1.660	-0.720	1.620	0.630	0.544	-0.842	-0.931	2.947	0.459	-0.258	-0.238	-1.283	-1.095	0.311	1.450	0.299	0.210	-0.895	-1.675	-0.795
50	p38b	Mapk11	19094	-0.295	-0.135	-0.414	0.411	-0.013	0.262	0.696	-1.415	1.208	-0.333	-1.579	-0.258	0.648	-0.295	0.025	-0.335	-1.178	0.164	1.113	-0.793	-0.428	-0.401	-0.510	0.558	0.841	-0.353	1.032	-0.555	-0.018	0.857	0.883	-0.649	-0.267	0.242	-0.950	0.412	0.540	-0.539	1.656	-0.863	-0.016	0.809
51	MK2	Mapkapk2	17164	-0.362	-0.676	-0.034	-0.544	-0.328	0.152	-2.349	0.572	-0.304	-1.174	1.808	-0.420	-2.333	0.891	-0.979	-1.429	1.698	-0.373	-2.769	0.511	-1.025	-0.091	1.387	0.022	-1.389	0.486	-0.525	-1.563	-0.211	-0.564	-1.769	0.488	1.132	-1.342	0.514	-1.145	-2.242	1.007	-0.530	-0.420	0.725	1.425
52	Mkk4	Map2k4	26398	-0.145	-0.220	-0.171	-0.152	0.299	-0.068	0.725	-0.175	-0.114	0.800	-1.214	-1.038	0.599	-0.510	0.069	0.537	-1.059	-1.218	-0.117	0.354	-0.226	0.365	-0.790	-1.343	0.731	-0.339	0.035	-1.616	-0.855	0.187	1.003	0.499	0.184	-1.070	0.414	-0.893	0.225	-0.079	-0.056	-1.792	-0.612	0.103
53	Mkk7	Map2k7	26400	-0.672	-0.821	-0.854	-0.588	0.225	-0.631	2.471	-0.857	-1.115	-0.566	0.369	-0.778	1.880	-1.214	-1.414	-0.580	0.253	-1.063	1.264	-0.104	-1.541	-0.917	-1.014	-0.791	1.111	-0.410	-0.701	-1.567	-0.475	-0.762	0.969	-0.769	0.037	0.761	0.413	-1.285	1.184	-0.281	-0.413	-1.254	-1.030	-0.850
54	Jnk1	Mapk8	26419	-0.077	-0.183	0.064	-0.430	-0.640	-1.011	1.945	0.366	-1.262	0.197	-0.352	-0.956	2.195	1.086	0.144	-0.616	-1.075	-0.511	0.975	0.095	0.033	-0.609	-1.619	0.302	1.168	-0.509	0.156	-0.351	-0.899	-0.891	0.882	-0.926	0.251	-0.354	-1.425	-1.591	0.774	-1.342	-1.042	-0.534	-1.557	-0.981
55	Jnk2	Mapk9	26420	-0.694	-0.057	-0.127	0.014	0.171	-0.312	-0.333	-1.054	-1.504	0.935	-1.201	1.148	-0.106	-0.007	-1.270	0.821	-0.794	0.365	0.055	-0.308	-1.705	0.762	-0.553	0.430	0.122	0.020	-0.530	0.458	-1.971	0.008	0.576	0.753	0.332	0.010	-1.121	-1.067	-0.884	-0.003	-0.620	0.180	-0.693	0.334
56	Jnk3	Mapk10	26414	0.245	0.386	0.604	-0.654	-0.331	0.022	2.144	0.897	-1.169	0.548	-0.058	-1.091	1.627	1.394	-0.635	0.968	-0.767	-0.196	0.977	1.199	-0.798	1.283	-0.928	0.232	1.246	0.189	-0.911	-0.645	-0.663	-1.158	0.799	0.994	-1.434	0.170	-0.832	-1.221	0.908	-0.118	0.001	0.526	-0.332	0.043
57	Erk3	Mapk12	29857	-0.356	-0.159	-0.336	-0.531	-0.268	-0.394	0.313	-0.314	-1.108	2.153	-0.398	-1.369	-0.072	-0.247	0.169	1.552	-0.532	-1.647	0.522	-0.842	-1.609	0.630	0.171	-1.575	0.165	-0.507	-0.799	-0.498	-0.776	-0.555	-0.221	-0.116	0.571	-0.324	-0.314	-0.431	-0.026	-0.820	-1.454	0.283	-0.142	-0.646
58	p38d	Mapk13	26415	-1.139	-1.127	-0.810	-0.331	-0.735	-0.669	-0.999	-1.384	-0.708	-1.279	-0.549	-1.875	-1.466	-1.186	-0.851	-1.068	-0.637	-1.277	-2.220	-1.694	-0.731	-0.889	-0.405	-0.490	-0.903	-2.085	-0.231	0.201	0.588	-0.431	-0.749	-1.735	-0.721	-0.918	1.267	0.835	-1.757	-2.444	0.319	-0.399	0.712	-0.939
59	TRIF	Ticam1	106759	-0.986	0.142	-0.385	-0.483	0.041	-0.449	-0.895	1.403	-0.407	-1.078	-1.189	-1.758	0.283	1.269	0.159	-0.858	0.126	-1.636	0.331	0.858	-0.287	-1.527	-0.482	-1.247	-2.054	-0.351	-0.946	2.198	0.088	-0.615	-1.615	0.237	-0.488	-0.093	1.253	0.176	-2.098	0.313	-0.628	0.168	-0.271	-2.295
60	TRAM	Ticam2	225471	-0.862	-1.151	-0.858	-0.435	-0.600	-0.111	-0.850	-0.874	-1.715	-0.488	-0.746	-1.452	-1.151	-1.151	-2.394	-0.194	-0.655	-2.951	-0.788	-0.598	-2.847	0.009	-0.927	-1.534	-1.399	-0.702	0.571	-0.168	0.228	-1.718	0.008	0.211	-2.301	-0.855	-1.644	-0.345	-1.702	0.762	-0.075	0.005	-0.146	-0.963
61	RIP1	Ripk1	19766	0.396	0.353	0.035	0.402	0.103	0.033	-0.828	-0.321	1.113	3.757	-1.003	2.373	-1.572	-0.417	1.122	1.199	-0.532	2.223	-0.791	-0.149	0.219	0.275	-0.588	1.700	-1.514	0.130	0.676	-1.400	0.673	1.467	-0.654	0.282	0.621	-1.286	-0.076	0.910	-1.463	1.031	0.962	-0.520	-1.088	0.585
62	FADD	Fadd	14082	-0.547	-0.664	-0.538	-0.618	-0.659	-0.657	-0.307	-2.255	-0.787	0.743	-0.888	0.145	-0.702	-2.263	-0.627	0.503	-0.564	-0.934	-0.209	-1.302	-1.341	1.065	-0.511	-0.564	-0.156	-1.268	-1.363	-0.827	-0.409	-0.091	-0.782	-0.217	-0.728	-0.590	-1.563	-0.219	-1.050	-0.704	-1.472	-0.610	-0.476	0.147
63	Caspase 8	Casp8	12370	0.250	0.356	-0.192	-0.841	-0.842	-0.876	-0.610	-1.209	0.131	0.370	0.776	0.918	0.132	-1.097	-0.224	0.581	1.149	0.624	0.344	-1.139	-0.229	-0.543	-0.155	0.502	0.864	-1.217	-0.908	0.320	-3.434	-0.774	0.085	-1.063	-0.693	0.313	-1.722	-0.992	0.516	-1.682	-1.139	-0.613	-2.242	0.266
64	TBK1	Tbk1	56480	0.067	0.301	0.389	-0.038	-0.314	0.432	-0.114	0.112	-0.149	0.982	0.023	1.225	-0.381	0.329	-0.322	0.274	0.473	1.135	-0.700	0.281	-0.186	0.498	0.818	1.446	-0.063	-0.013	-0.169	0.294	-1.643	1.401	-1.347	1.556	-0.709	0.080	-1.163	0.512	0.418	0.446	-0.765	0.611	-0.503	0.620
65	IKKe	Ikbke	56489	-1.367	-0.655	-1.029	-0.773	-0.453	-0.126	-1.366	-0.853	-1.369	-1.921	-0.247	-1.569	-1.725	-1.278	-0.701	-0.331	-0.498	-0.608	-0.982	-2.192	-0.538	-1.076	-0.158	-1.808	-0.738	-0.850	-1.286	0.233	1.104	-0.808	-0.667	-0.318	-0.587	-0.156	-0.819	1.431	-0.005	-0.247	-0.410	0.086	0.326	-1.172
66	IRF3	Irf3	54131	-0.366	-0.036	-0.105	0.649	-0.263	-0.402	1.393	-0.331	-1.686	-1.714	-0.402	0.515	1.233	0.785	-2.320	-1.207	-0.458	0.387	1.883	0.182	-2.701	-1.710	-0.393	1.155	-1.128	1.545	-2.105	3.721	0.723	0.575	-0.227	1.929	-0.921	0.178	-0.298	-0.834	-1.049	1.771	-2.689	-0.617	0.294	-0.188
67	Duba	Otud5	54644	-0.950	-0.943	-0.791	-0.022	0.374	-0.161	0.067	0.151	-0.564	-1.340	-1.336	-2.395	0.177	-1.454	-0.576	-0.755	-1.131	-1.216	0.112	-1.337	-0.899	-0.683	-1.584	-0.600	-0.515	0.186	-0.391	0.971	-0.231	0.885	-0.907	1.816	0.124	-0.114	0.623	2.232	-0.358	-0.069	0.419	0.317	-1.140	-0.254
68	TRADD	Tradd	71609	-0.086	0.076	0.300	-0.445	-0.657	-0.341	3.348	-0.474	0.187	0.528	-0.785	-0.360	2.446	-0.652	0.195	0.749	-0.309	-0.043	2.302	-0.955	-0.066	0.666	-1.200	1.392	-1.044	-0.453	-0.778	-0.230	-0.436	0.842	-2.400	1.114	-0.778	0.454	-0.844	-0.536	-0.392	-0.290	-1.554	-1.145	-0.207	1.439
69	TANK	Tank	21353	0.496	0.564	0.694	0.105	0.739	1.264	-0.532	1.409	0.685	1.291	0.006	0.306	-1.427	1.466	0.548	0.580	1.298	0.366	-1.839	1.621	0.219	1.184	0.505	0.883	-0.294	3.971	0.504	-0.441	1.562	-0.338	1.257	3.949	0.589	-0.593	0.888	-0.924	-0.553	4.182	0.828	1.537	2.844	0.992
70	SINTBAD	Tbkbp1	73174	0.281	0.141	0.512	0.279	-0.547	0.160	0.449	-0.559	0.649	0.153	0.409	-0.218	-0.321	-0.846	0.968	0.375	0.889	-0.094	0.463	-1.492	0.716	0.877	0.561	-0.132	0.238	-0.599	0.972	-0.305	1.267	0.320	-0.829	-1.507	1.074	8.113	-0.266	-1.511	-0.166	-0.533	1.682	0.145	0.175	0.410
71	BTK	Btk	12229	-0.605	-0.620	-0.952	-0.775	-0.207	-1.545	-0.181	-1.435	-1.028	-0.150	-1.115	-0.054	-0.004	-1.638	-0.762	-0.596	-0.645	0.144	-0.208	-1.064	-0.839	-0.666	-2.449	-3.115	-0.099	-0.720	-1.418	-2.301	-0.830	-0.005	-0.182	-0.232	-1.022	-0.510	3.767	1.602	-0.474	0.878	-1.820	-1.753	-2.168	-1.336
72	NIK	Map3k14	53859	-0.435	-0.266	-0.049	-0.134	0.452	-0.703	-0.024	1.350	-1.291	0.195	-2.479	-0.847	0.578	0.822	-0.856	0.323	-1.342	-1.223	0.018	1.258	-0.076	-0.022	-1.059	-3.158	-0.553	0.887	-1.266	0.286	5.747	-1.482	-1.037	1.322	-0.417	-0.876	7.470	3.370	-0.251	0.315	-0.618	-0.788	-3.494	-1.471
73	AKT1	Akt1	11651	-0.548	-0.273	-0.098	-1.209	-0.794	-1.288	0.398	-1.308	0.616	-0.148	-0.948	-1.404	0.024	-1.185	0.205	0.113	-0.780	-0.571	1.038	-1.769	0.492	0.002	-1.114	-0.198	-1.558	-2.668	0.427	3.897	-1.315	-1.104	-1.112	-2.135	-0.135	4.019	-1.155	-0.477	-1.403	-2.691	0.741	-0.360	-1.357	-1.219
74	AKT2	Akt2	11652	-0.847	-1.062	-0.711	0.034	1.113	-0.005	-0.448	-2.326	-0.454	-2.064	-1.078	-0.615	-1.662	-0.599	-0.812	-1.812	-0.654	-1.313	-1.375	-0.713	-0.011	-0.736	-0.709	-0.266	-1.051	-0.467	0.534	0.721	-1.092	1.533	-0.977	0.447	0.060	1.780	7.869	2.054	-1.192	1.023	0.989	-1.592	0.227	-0.238
75	AKT3	Akt3	23797	-0.494	-1.045	-0.660	-0.577	-0.771	-0.495	-0.632	-0.356	-1.453	-0.075	-1.263	-0.240	-1.359	0.909	-1.686	-0.731	-0.705	-1.492	-1.134	0.819	-0.729	-0.590	-0.027	-0.981	0.721	0.363	-0.422	-0.731	-0.917	-0.973	0.573	-0.130	-0.835	-1.485	-0.707	-0.869	0.214	-0.348	-0.642	-1.627	-0.004	-1.754
76	PIK3CA	Pik3ca	18706	0.127	0.394	-0.575	-0.330	-0.574	-0.297	0.242	1.184	0.012	-2.510	-0.839	0.952	0.683	0.667	0.121	-1.294	-1.386	1.439	-0.142	0.877	-0.186	-0.965	-1.770	-3.103	-0.808	0.228	0.132	-0.793	-1.930	1.130	-0.504	0.019	0.260	-1.571	-0.644	-0.675	-1.524	-0.106	-0.013	0.146	-1.920	-0.488
77	PIK3CB	Pik3cb	74769	-1.148	-0.889	-0.579	-0.769	0.072	-0.488	1.557	-0.998	-1.299	-0.379	-2.538	-1.676	0.098	-2.186	-0.224	0.866	-1.717	-1.553	0.617	-1.856	-0.498	0.303	-3.778	-0.659	-0.077	-0.962	-0.583	-0.540	-0.956	-1.517	0.976	-1.706	-1.124	0.451	0.988	-0.307	-0.341	-1.993	-0.380	-0.595	-3.708	0.121
78	PIK3CD	Pik3cd	18707	-0.879	-0.374	-0.817	0.252	-0.189	-0.349	-0.620	-1.275	-0.685	-0.164	-1.453	-1.074	-0.326	-0.733	-0.336	-0.413	-0.241	-1.039	-0.018	-1.502	-0.826	-1.403	-0.034	-0.808	0.018	0.486	-0.105	0.611	-1.293	1.976	0.217	-0.821	-0.311	0.873	-0.526	-0.067	0.132	-0.728	-0.766	-0.167	-0.087	-0.532
79	PIK3CG	Pik3cg	30955	-0.063	-0.186	-1.636	-0.389	-0.138	-0.988	2.311	-1.754	0.623	0.522	-0.648	-1.967	1.273	-1.852	0.601	1.068	-0.973	-2.233	0.918	-2.767	-0.104	-0.505	-3.900	-3.368	-0.416	-1.964	-0.362	1.166	-0.275	-1.840	-0.013	-0.884	-0.263	0.490	-0.305	3.130	-0.424	-2.378	-1.253	0.395	-0.723	-2.375

TABLE S2 MOUSE SCREEN SCORES)

Gene#	Name	Gene Symbol	Gene ID	LPS-mTNF_Median	P3C-mTNF_Median	R848-mTNF_Median	LPS-mNFKB_Median	P3C-mNFKB_Median	R848-mNFKB_Median	LPS-mTNF_siRNA1	LPS-mTNF_siRNA2	LPS-mTNF_siRNA3	LPS-mTNF_siRNA4	LPS-mTNF_siRNA5	LPS-mTNF_siRNA6	P3C-mTNF_siRNA1	P3C-mTNF_siRNA2	P3C-mTNF_siRNA3	P3C-mTNF_siRNA4	P3C-mTNF_siRNA5	P3C-mTNF_siRNA6	R848-mTNF_siRNA1	R848-mTNF_siRNA2	R848-mTNF_siRNA3	R848-mTNF_siRNA4	R848-mTNF_siRNA5	R848-mTNF_siRNA6	LPS-mNFKB_siRNA1	LPS-mNFKB_siRNA2	LPS-mNFKB_siRNA3	LPS-mNFKB_siRNA4	LPS-mNFKB_siRNA5	LPS-mNFKB_siRNA6	P3C-mNFKB_siRNA1	P3C-mNFKB_siRNA2	P3C-mNFKB_siRNA3	P3C-mNFKB_siRNA4	P3C-mNFKB_siRNA5	P3C-mNFKB_siRNA6	R848-mNFKB_siRNA1	R848-mNFKB_siRNA2	R848-mNFKB_siRNA3	R848-mNFKB_siRNA4	R848-mNFKB_siRNA5	R848-mNFKB_siRNA6
80	PIK3R1	Pik3r1	18708	-0.419	-0.171	-0.653	-1.332	-0.830	-0.767	-0.521	-0.473	-0.130	-0.009	-0.449	-0.390	-1.387	0.086	0.228	0.210	-0.427	-1.276	-1.590	-0.167	-0.178	0.869	-1.129	-1.487	-1.679	-1.253	0.626	-0.068	-1.411	-1.425	-0.550	-0.660	-0.072	-1.672	-1.000	-1.379	-2.087	-1.057	-0.075	-0.018	-1.927	-0.476
81	PIK3R2	Pik3r2	18709	-0.290	-0.603	-0.037	0.034	0.382	-0.402	-0.080	-0.501	-0.500	0.994	0.400	-0.579	-0.837	-0.660	-0.593	0.879	0.750	-0.613	0.211	-0.227	-1.554	0.137	0.265	-0.212	-0.807	0.047	0.056	-0.275	1.296	0.021	-0.184	0.319	-2.479	0.444	0.623	0.707	-0.882	-1.026	-0.181	-0.561	-0.244	0.226
82	PIK3R3	Pik3r3	18710	-0.822	-0.254	-0.211	0.303	-0.291	-0.590	-0.865	-0.429	-0.779	-1.253	-0.083	-1.176	-1.573	-0.114	0.067	-0.394	0.252	-0.679	-0.894	0.917	0.060	-0.483	0.397	-0.690	0.381	0.225	1.550	-1.624	0.139	0.886	1.077	0.184	-0.766	-1.777	-1.896	3.858	1.558	1.826	-1.069	-0.112	-1.693	-1.172
83	PIK3R5	Pik3r5	320207	-0.737	-0.581	-0.793	-0.021	0.263	-0.787	0.276	-0.067	-1.827	-0.962	-1.520	-0.511	0.217	-0.008	-0.500	-0.662	-1.586	-0.792	-0.141	-1.322	-1.448	-0.264	-1.901	0.131	0.464	0.664	-0.445	0.403	-1.774	-1.291	0.529	2.114	0.047	0.479	-2.203	-0.347	0.317	-0.016	-1.360	-1.909	-2.536	-0.214
84	RAC1	Rac1	19353	-0.036	0.003	0.047	-0.456	-0.613	-0.170	0.618	0.549	0.147	-0.219	-0.947	-0.299	0.261	1.453	-1.512	-0.436	-0.255	0.806	0.126	1.117	-0.786	0.260	-3.152	-0.031	1.768	0.227	-2.312	-0.151	-0.762	-1.302	2.052	0.461	-1.490	-0.799	-0.599	-0.626	2.049	-0.143	-2.699	-0.197	-0.513	-0.141
85	IRF5	Irf5	27056	-0.360	-0.264	-0.402	-0.238	-0.491	-0.302	-0.806	-0.219	0.045	-1.238	-0.502	-0.128	-2.222	-0.331	0.232	-0.949	-0.197	0.363	-3.281	0.250	0.127	-0.637	-0.167	-0.749	-0.506	-0.032	-0.110	-0.077	-0.366	-2.360	-0.017	-0.791	-0.216	0.163	-0.767	-2.729	-1.220	-0.199	-0.404	0.615	0.613	-2.746
86	IRF7	Irf7	54123	-0.157	-0.332	-0.630	-0.527	0.218	-0.153	-1.841	-0.638	-0.245	0.861	-0.068	0.147	-2.000	-1.235	-0.667	0.935	0.141	0.003	-2.646	-0.866	0.959	-0.517	-0.482	-0.743	-0.569	0.150	0.122	-0.646	-0.777	-0.486	-1.599	1.717	1.026	-0.590	2.329	-1.126	-0.377	0.068	0.978	-0.955	-0.374	0.460
87	STAT1	Stat1	20846	-0.128	-0.448	-0.373	0.023	-0.305	0.471	0.490	0.727	0.141	-0.398	-0.765	-1.727	0.402	0.376	-0.764	-0.133	-0.886	-1.954	0.792	0.091	-0.529	-0.618	-0.217	-1.617	-0.102	0.984	0.289	-1.232	0.148	-0.718	-0.316	0.701	-2.081	-0.295	-1.425	0.367	0.543	1.187	0.262	0.564	0.399	-1.114
88	Fos	Fos	14281	-0.553	-0.351	-0.292	-0.893	-0.181	-0.614	-1.110	-0.740	1.073	-0.502	-0.604	0.059	-1.970	-0.405	0.895	-0.297	-0.766	0.085	-0.140	-1.176	-0.421	0.518	-0.239	-0.345	-3.629	-0.179	-0.590	-1.328	-0.732	-1.053	-3.005	-0.346	0.325	-1.414	-0.015	0.461	-0.606	-0.859	-0.817	-0.379	-0.622	-0.352
89	Jun	Jun	16476	-1.017	-0.371	-0.480	-1.139	-0.682	-1.100	-1.507	-1.050	-0.983	-0.853	-1.075	-0.153	-1.261	-0.505	-0.040	-0.399	-0.343	1.110	0.193	-1.779	-0.139	-1.265	-0.821	0.155	-0.392	-2.730	-0.525	-2.039	-1.754	-0.199	-0.943	-2.317	-0.421	-1.287	0.310	-0.127	0.472	-2.935	-0.488	-1.845	-1.712	-0.423
90	PYK2	Ptk2b	19229	-0.490	0.062	-0.235	-0.133	0.336	0.546	-0.137	0.802	-0.583	-1.860	-0.534	-0.446	-0.428	1.383	-0.695	-0.535	0.666	0.552	-0.064	1.166	-1.020	-0.452	1.158	-0.407	1.051	1.148	-0.126	-0.468	-0.196	-0.140	1.071	1.284	-0.202	0.455	0.218	-0.823	0.788	1.254	0.025	0.370	0.051	0.722
91	ETS1	Ets1	23871	-0.434	-0.526	0.222	0.223	0.002	0.940	-0.451	0.823	-0.418	0.944	-1.735	-0.745	-0.567	1.558	-0.577	1.041	-0.486	-1.397	0.183	0.883	-1.093	1.586	0.262	-0.980	0.473	0.209	-0.740	1.394	-2.241	0.237	0.155	0.876	-1.531	2.824	-2.172	-0.151	0.927	0.952	-2.079	1.088	1.668	0.135
92	ELK1	Elk1	13712	-0.858	-1.668	-1.775	-0.923	-0.226	-0.818	-1.163	0.020	0.007	-2.115	-1.678	-0.553	-1.333	0.984	-0.034	-3.671	-2.188	-2.003	-1.580	0.121	0.074	-3.006	-3.457	-1.971	-0.614	-0.540	-1.248	-1.233	0.177	-2.026	-0.121	-0.602	0.902	4.245	-0.332	-0.594	-0.555	-0.979	-0.657	-2.831	-3.058	-0.586
93	ELK4	Elk4	13714	-0.257	-0.354	-0.578	-0.818	-0.013	-0.379	-0.114	-0.049	-0.400	0.525	-1.316	-1.257	-1.270	0.529	-0.652	0.085	-0.216	-0.491	-0.887	0.240	-0.795	0.304	-0.390	-0.766	-2.109	-0.228	-0.268	-1.123	-0.802	-0.834	-1.085	0.340	0.249	0.280	-0.274	-1.013	-1.999	-0.240	-0.518	-0.136	0.015	-0.742
94	SP1	Sp1	20683	-1.276	-1.417	-1.326	-0.191	-1.222	-0.791	-1.232	-1.320	-1.793	-0.753	0.023	-1.933	-1.017	-1.295	2.375	-1.540	-0.791	-1.863	-0.966	-1.426	-2.471	-1.226	0.113	-1.827	-0.539	-1.836	0.386	-0.304	-0.077	0.357	-0.771	-1.384	-2.337	-1.215	2.580	-1.228	-0.449	0.960	-1.440	0.001	-1.243	-1.134
95	EGR1	Egr1	13653	-1.210	-1.048	-1.138	-0.085	-0.562	-0.295	-0.923	-2.189	-2.250	-0.147	-1.497	-0.367	-0.780	-1.993	-1.341	0.039	-1.316	-0.294	-1.404	-0.871	-1.703	0.379	-2.669	-0.174	0.356	-1.544	-1.181	0.088	0.164	-0.257	-1.001	-0.183	-0.536	-0.588	3.462	-0.831	-0.622	-0.669	-0.667	0.174	0.675	0.032
96	EGR2	Egr2	13654	-1.983	-1.415	-2.150	-1.029	-0.362	-0.649	-0.816	-2.150	-1.815	-3.362	-2.506	-0.098	-0.496	-1.596	-1.346	-3.049	-1.484	-0.332	-0.086	-1.794	-2.138	-2.761	-2.996	-2.163	-1.155	-0.243	-1.980	-0.968	0.838	-1.090	-0.948	-0.218	-1.425	2.751	-0.506	2.041	-0.445	-0.212	-1.415	-2.941	-0.854	-0.231
97	ATF2	Atf2	11909	-0.645	-0.691	-1.192	-0.383	-0.811	-0.515	-0.937	-1.108	-0.353	1.570	-2.171	0.304	-1.508	-0.865	-0.409	1.598	-1.345	-0.518	-2.484	-1.827	-0.081	0.388	-1.807	-0.577	-1.376	-0.870	0.105	-1.349	0.816	0.443	-0.634	-1.028	-1.405	-0.856	-0.766	-0.223	-0.544	-1.235	-0.044	-0.486	-0.566	0.456
98	ATF7	Atf7	223922	-1.159	-0.842	-0.982	-0.466	0.024	-0.721	-0.447	-1.556	-1.255	0.055	-1.760	-1.063	-1.177	-0.425	-0.718	0.525	-1.586	-0.965	-1.110	-0.268	-1.160	0.644	-0.855	-1.532	-1.430	-0.582	-0.128	-0.350	0.338	-0.846	-1.711	-1.063	0.097	-0.017	6.522	0.065	-1.376	-1.817	-0.076	0.407	-0.406	-1.036
99	CBP	Crebbp	12914	-1.109	-1.214	-1.111	-0.579	-0.517	-1.508	0.832	-1.491	-1.594	0.284	-1.569	-0.727	0.734	-1.590	-1.106	-0.535	-3.161	-1.322	0.679	-2.354	-1.762	-0.186	-3.765	-0.459	-0.398	-2.640	-0.760	-0.812	0.174	0.338	-0.481	-1.275	-0.714	-0.554	4.111	-0.088	0.106	-2.250	-1.802	-0.722	-3.604	-1.214
100	p300	Ep300	328572	-0.400	-0.388	-1.299	-1.268	-0.618	-1.194	-1.680	-0.482	0.376	-0.318	-0.711	-0.233	-2.253	-0.791	1.335	-0.031	0.107	-0.746	-1.473	-1.126	0.009	0.078	-2.029	-1.671	-2.524	-1.310	-0.800	-1.096	-1.226	-1.342	-0.810	-0.766	-1.688	2.068	-0.101	-0.469	-0.716	-1.104	-1.369	-0.269	-1.538	-1.284
101	ISGF3G	Irf9	16391	0.583	0.994	0.756	-0.398	-1.111	0.163	2.221	0.413	0.044	0.753	1.179	-0.615	1.310	0.896	0.060	1.091	1.785	-1.098	0.962	-0.554	0.551	1.908	1.830	-0.218	-0.585	-1.402	0.624	-0.210	0.031	-1.909	-0.274	-1.765	-0.038	-0.805	-1.850	-1.416	-0.898	-1.392	0.416	0.785	0.356	-0.030
102	ELF4	Elf4	56501	-0.591	-0.304	-1.103	-0.537	-0.868	-0.635	-0.655	-0.726	-0.276	-0.526	-1.554	-0.170	-0.135	-0.474	-1.994	-0.094	-1.374	0.466	-0.866	-1.339	-2.889	0.041	-1.427	1.399	0.066	-0.951	-1.185	-0.124	-1.074	0.192	-0.870	0.151	-0.866	-1.482	-0.271	-1.645	0.143	-1.382	-0.645	-0.626	-1.560	-0.328
103	IFNAR1	Ifnar1	15975	-1.037	-1.057	-0.878	-0.468	-0.557	-0.975	-1.026	-1.263	-0.703	1.676	-1.076	-1.048	-1.128	0.038	-0.986	1.599	-1.182	-1.610	-0.661	-0.417	-1.363	0.929	-1.860	-1.095	-1.434	0.417	-1.362	1.143	-0.095	-0.842	-0.337	1.538	-1.337	-0.776	-0.181	-1.069	-1.316	0.637	-1.473	1.414	-0.634	-1.315
104	IFNAR2	Ifnar2	15976	-0.421	-0.292	-0.334	0.010	1.240	0.293	-0.767	-0.799	-0.101	0.166	0.341	-0.742	-1.135	-0.485	-0.099	0.219	-0.029	-1.216	-0.412	-0.553	0.022	0.325	-0.256	-1.814	2.078	-1.110	1.246	-0.580	0.600	-1.717	2.141	-0.324	0.647	1.834	0.059	3.326	3.587	0.410	1.513	0.176	-0.296	-2.317
105	IFNB1	Ifnb1	15977	-0.923	-0.877	-0.835	-0.386	-0.065	-0.085	1.554	-1.636	-1.068	1.717	-1.775	-0.777	1.022	-0.803	-1.212	1.267	-0.951	-1.097	1.426	-1.310	-0.653	0.683	-1.116	-1.017	1.186	0.122	-1.507	-0.227	-0.620	-0.545	1.696	0.296	-1.549	0.676	-0.894	-0.426	1.124	-0.522	1.272	0.107	-0.276	-0.828
106	IL12A	Il12a	16159	-1.014	-0.728	-0.828	-0.153	-0.103	-0.594	0.553	-1.822	-1.768	-0.261	-1.813	0.614	0.492	-1.867	-0.930	-0.525	-1.516	0.563	-0.009	-0.814	-1.008	-0.842	-0.878	-0.200	-0.272	-0.306	-0.034	0.030	-0.875	0.448	-0.300	-0.637	0.663	0.094	1.134	-0.963	-0.477	-0.143	-0.789	-0.710	-1.093	0.071
107	IL12B	Il12b	16160	-0.130	-0.514	-0.612	-0.250	-0.387	-0.177	-2.140	-0.047	-0.213	0.876	-1.113	0.184	-1.586	-0.395	-0.633	1.006	-1.512	0.154	-1.254	-0.847	-0.443	-0.068	-0.781	1.142	-0.736	0.992	0.091	-0.591	-1.339	0.333	0.020	1.471	0.089	-0.795	-1.800	-1.411	-0.741	2.051	-0.088	-0.231	-1.201	-0.123
108	IL1B	Il1b	16176	0.038	0.063	-0.158	-0.090	0.185	-0.249	0.346	-1.555	-0.805	-0.270	1.003	0.384	0.179	-0.642	-0.007	0.245	0.132	-0.263	0.605	-1.333	-0.200	0.787	-0.352	-0.116	0.425	-0.342	0.161	1.816	-0.385	-0.573	0.620	0.260	0.109	1.473	-0.688	-1.299	0.819	-1.166	0.284	-0.280	-0.824	-0.218
109	IL6	Il6	16193	0.211	0.026	0.056	0.015	-0.367	-0.189	0.427	-0.891	0.639	-0.747	0.503	-0.005	-0.676	-0.811	0.569	-0.037	0.507	0.089	-0.531	0.113	0.747	-0.263	-0.001	0.787	-0.222	0.155	0.174	-1.017	0.465	-0.125	-0.997	-0.200	0.178	0.748	-0.683	-0.534	0.075	-0.484	-0.452	-1.335	0.171	0.206
110	TNF	Tnf	21926	-0.389	-1.033	-0.229	-0.488	-1.178	0.032	-0.232	1.064	-1.023	-0.547	-0.191	-2.248	-0.363	0.679	-1.267	-0.799	-1.445	-2.376	-0.376	1.300	-0.437	-0.081	0.426	-1.620	-0.577	-0.162	-0.398	-1.031	-0.368	-1.038	-1.283	-1.073	-0.922	-2.112	-1.740	-0.185	-0.007	0.070	1.431	-0.338	1.364	-1.391
111	CCL3	Ccl3	20302	-0.673	-0.565	-0.324	-0.268	-0.197	-0.676	-0.497	-0.371	-1.674	-0.858	-0.202	-0.849	-0.642	0.379	-0.813	-0.488	-0.172	-1.664	-0.564	-0.083	-1.039	1.151	1.002	-3.158	-1.833	-0.214	-0.653	0.107	-0.323	4.735	-1.939	0.087	-0.481	0.163	-0.591	5.372	-2.857	-0.455	-0.897	1.191	0.124	-1.589
112	CXCL11	Cxcl11	56066	-0.284	-0.515	-0.653	-0.326	-0.114	-0.503	-0.323	-0.585	0.109	-0.217	-0.245	-1.561	-0.409	-0.907	0.605	0.510	-1.344	-0.620	-0.609	-0.697	-0.212	0.273	-1.547	-1.558	-0.439	0.688	-0.006	-1.577	-1.083	-0.213	-0.037	0.917	1.015	-0.729	-0.192	-0.454	-0.701	1.147	-0.306	-0.115	-2.503	1.184
113	CXCL9	Cxcl9	17329	0.116	-0.059	-0.093	-0.640	-0.620	-0.338	-1.112	0.536	0.278	-1.335	-0.047	0.450	-1.973	-0.020	-0.094	-0.977	0.554	-0.024	-0.062	-0.390	-0.011	-0.123	-0.325	0.195	-0.554	-0.935	-0.328	-0.818	-0.725	-0.415	-1.093	-0.623	-0.354	0.011	-0.617	-1.408	-0.467	-1.773	-0.624	0.225	-0.209	-0.034
114	RP105	Cd180	17079	-0.485	-0.640	-0.460	0.261	-0.561	0.171	0.000	0.341	-0.675	-1.309	-1.571	-0.295	-0.980	0.099	-0.056	-0.740	-1.227	-0.541	-1.043	0.259	0.081	-0.734	-1.033	-0.186	-2.054	0.640	0.936	0.275	-1.314	0.247	-0.997	0.425	1.204	-0.379	-0.742	-0.802	-2.975	0.588	1.148	1.637	-2.035	-0.246
115	MD1	Ly86	17084	0.034	0.055	-0.115	-0.348	-0.304	0.159	-0.150	0.218	-1.203	0.792	1.223	-0.310	-0.001	0.111	-0.255	1.165	1.184	-0.854	0.176	-0.727	-0.406	0.595	1.521	-1.229	0.111	-1.856	-0.610	-1.779	1.516	-0.085	-0.421	-1.470	-0.129	-0.188	0.163	-0.920	0.448	-1.875	-0.130	-1.188	1.141	0.670
116	TIR8	Sigirr	24058	-0.547	-0.126	-0.462	-1.271	-0.765	-1.005	-1.151	-0.532	-1.231	0.559	-0.562	0.484	-0.993	-0.565	-0.118	0.912	-0.133	1.216	0.534	-1.399	-0.080	-1.384	-0.843	0.892	-2.053	-2.564	-0.878	-1.509	-1.032	-0.692	-1.669	-2.146	-0.691	-0.244	-0.839	-0.514	-1.067	-2.682	-0.717	-1.813	-0.944	-0.706
117	ST2	Il1rl1	17082	-0.126	-0.755	-0.647	-1.263	-0.641	-1.071	1.909	-1.360	-0.273	1.015	-1.697	0.021	1.028	-1.044	-0.961	-0.549	-1.138	-0.069	1.852	-0.940	-1.022	0.590	-1.102	-0.355	-0.421	-1.241	-0.846	-1.285	-1.695	-1.287	-1.064	-0.655	-0.886	-0.327	-0.421	-0.627	-1.236	-1.106	-0.414	-1.036	-1.728	-0.938
118	IRAK3	Irak3	73914	-0.645	-0.395	-0.206	-0.800	-0.825	-0.937	-0.770	-0.520	-0.036	-0.017	-0.919	-1.546	-0.610	-1.464	0.573	-0.107	-0.180	-1.218	-0.808	-0.805	0.394	0.163	0.016	-0.427	-1.512	-1.124	-0.371	-0.306	-0.475	-1.835	-0.533	0.017	-1.401	-1.117	0.680	-1.660	-1.104	-1.476	-0.462	-0.770	-1.638	-0.199
119	SHP1	Ptpn6	15170	-0.466	-0.671	-0.507	-0.498	-0.187	-1.524	0.681	0.157	-0.238	-0.694	-1.874	-2.147	0.753	0.240	-0.606	-0.737	-1.106	-3.603	0.886	0.692	-0.911	-0.103	-1.084	-2.986	0.008	0.386	-2.821	-1.004	1.671	-2.197	-0.763	-0.890	-3.106	0.389	0.749	2.957	0.514	0.367	-3.022	-2.079	-1.488	-1.560
120	Cyld	Cyld	74256	1.175	0.058	0.035	-0.243	-0.387	0.336	1.549	-0.717	-0.424	0.890	1.965	1.460	-0.043	-0.065	-0.100	0.158	2.099	0.904	0.121	-0.052	-0.508	0.989	-2.814	0.815	0.654	-0.878	0.273	-0.352	-0.577	-0.134	0.198	-0.344	0.030	-1.100	-1.376	-0.431	-0.243	0.280	0.825	-0.887	1.091	0.393
121	A20	Tnfaip3	21929	0.726	0.745	0.271	-0.362	-0.184	1.028	1.281	-0.375	-0.327	0.312	1.141	1.249	1.387	0.200	-0.242	0.698	0.793	0.896	1.070	-0.046	0.312	0.060	2.294	0.229	0.095	-1.192	1.457	0.379	-0.818	-1.728	0.381	-1.650	1.476	0.840	-1.087	-0.749	0.849	-1.085	2.427	1.579	0.640	1.206
122	DUSP2	Dusp2	13537	0.147	-0.368	-0.098	-0.962	-0.367	-0.473	0.668	-2.001	2.286	0.734	-0.374	-0.688	-0.599	-2.028	2.797	0.837	-0.294	-0.441	-0.090	-0.831	1.224	0.129	-1.032	-0.105	-0.566	-4.918	-1.357	0.936	-1.530	0.609	-0.406	-2.073	-0.187	-0.329	0.613	-1.210	-0.546	0.321	-0.756	0.082	-1.051	-0.399
123	AIP1	Dab2ip	69601	-0.261	-0.380	-0.020	-0.295	-0.076	-0.808	0.163	-0.685	1.410	-1.243	-1.400	1.060	-0.144	-0.616	1.617	-1.554	-0.771	1.194	0.385	-0.019	1.586	-2.698	-1.088	-0.021	-0.412	0.937	-1.219	2.502	-0.345	-0.245	-0.834	0.503	-0.979	6.104	1.961	-0.654	0.449	-0.059	-0.994	-2.432	-0.915	-0.702
124	Tollip	Tollip	54473	-0.556	-0.247	-0.498	-0.886	-1.046	-0.720	0.865	-1.581	-1.124	-0.252	1.422	-0.861	0.050	-0.287	-1.915	-0.207	1.644	-1.708	0.174	-1.169	-2.095	0.333	0.520	-3.903	0.799	-1.173	-2.551	-0.667	-0.510	-1.105	-0.067	-0.793	-2.523	-1.299	-1.347	0.633	0.661	-0.818	-2.902	-0.623	0.341	-1.209
125	MKP1	Dusp1	19252	0.142	-0.338	0.253	-0.127	0.027	-0.150	1.259	0.104	-0.572	0.180	0.262	-0.928	-0.407	0.283	-0.591	1.063	-0.661	-0.268	0.782	0.294	0.418	0.211	-0.694	-0.942	0.153	-0.227	-0.028	0.406	-1.541	-1.471	0.375	0.022	0.033	1.240	-0.978	-0.858	0.430	1.613	-0.178	-0.332	-0.122	-0.425
126	RIP3	Ripk3	56532	-0.018	0.074	-0.138	-0.206	-0.255	-0.440	-0.404	0.206	0.110	-0.145	0.977	-1.863	-0.514	0.060	0.087	0.098	1.618	-0.739	-0.200	-0.076	0.775	-0.615	1.125	-1.310	-0.246	0.452	-0.740	-0.418	-0.166	1.579	-0.270	0.784	-0.465	-0.240	-0.572	2.869	0.031	0.305	-1.049	-0.912	0.201	-2.620

TABLE S3

Gene#	Name	Human Gene Symbol	Human Gene ID	Mouse Gene Symbol	Mouse Gene ID	Module	Human rank TNFa	Human rank TNFa SUM	Mouse rank NF-kB	Mouse rank NF-kB SUM	Mouse rank TNFa	Mouse rank TNFa SUM	LPS-hTNF_rank	P3C-hTNF_rank	R848-hTNF_rank	P2C-hTNF_rank	PGN-hTNF_rank	FLG-hTNF_rank	LPS-mNFKB_rank	P3C-mNFKB_rank	R848-mNFKB_rank	LPS-mTNF_rank	P3C-mTNF_rank	R848-mTNF_rank	LPS-hTNF_z-score	P3C-hTNF_z-score	R848-hTNF_z-score	P2C-hTNF_z-score	PGN-hTNF_z-score	FLG-hTNF_z-score	LPS-mNFKB_z-score	P3C-mNFKB_z-score	R848-mNFKB_z-score	LPS-mTNF_z-score	P3C-mTNF_z-score	R848-mTNF_z-score
1	TLR1	TLR1	7096	Tlr1	21897	TLR	68	440	80	226	109	304	99	47	79	82	67	66	95	52	79	101	111	92	-0.092	-0.600	-0.338	-0.265	-0.370	-0.425	-0.014	-0.493	-0.213	-0.011	0.237	-0.092
2	TLR2	TLR2	7097	Tlr2	24088	TLR	58	394	82	230	101	293	93	35	124	40	5	97	117	1	112	108	65	120	-0.143	-0.748	0.367	-0.720	-2.648	-0.170	0.334	-1.785	0.238	0.082	-0.368	0.454
3	TLR3	TLR3	7098	Tlr3	142980	TLR	82	469	92	247	113	314	57	93	112	58	82	67	61	93	93	121	85	108	-0.543	-0.180	-0.015	-0.448	-0.259	-0.397	-0.359	-0.090	-0.046	0.455	-0.185	0.108
4	TLR4	TLR4	7099	Tlr4	21898	TLR	64	410	83	237	91	252	1	92	97	63	75	82	1	122	114	15	114	123	-4.482	-0.182	-0.168	-0.413	-0.309	-0.301	-2.605	0.440	0.267	-1.072	0.284	0.591
5	TLR5	TLR5	7100	Tlr5	53791	TLR	50	341	113	300	111	308	23	91	85	91	50	1	119	89	92	81	113	114	-1.076	-0.201	-0.278	-0.196	-0.614	-3.659	0.393	-0.127	-0.062	-0.237	0.262	0.303
6	TLR6	TLR6	10333	Tlr6	21899	TLR	71	445	72	212	95	277	67	94	117	114	12	41	108	5	99	87	68	122	-0.447	-0.178	0.139	0.117	-1.549	-0.757	0.178	-1.474	0.033	-0.170	-0.364	0.527
7	TLR7	TLR7	51284	Tlr7	170743	TLR	101	525	28	116	44	151	82	104	93	78	80	88	86	27	3	72	74	5	-0.305	-0.014	-0.201	-0.316	-0.271	-0.271	-0.111	-0.730	-2.652	-0.302	-0.314	-1.798
8	TLR8	TLR8	51311	Tlr8	170744	TLR	73	449	115	309	102	293	71	106	2	96	96	78	90	101	118	95	119	79	-0.378	0.006	-2.731	-0.149	-0.089	-0.324	-0.053	-0.004	0.374	-0.083	0.365	-0.198
9	TLR9	TLR9	54106	Tlr9	81897	TLR	125	686	34	130	54	180	104	126	100	125	115	116	45	33	52	76	45	59	-0.034	0.957	-0.138	0.497	0.134	0.119	-0.516	-0.644	-0.522	-0.282	-0.576	-0.455
10	LBP	LBP	3929	Lbp	16803	Proximal	104	538	79	226	107	299	79	96	54	95	108	106	75	48	103	80	112	107	-0.330	-0.138	-0.545	-0.156	0.022	-0.072	-0.244	-0.541	0.073	-0.253	0.243	0.107
11	MD2	LY96	23643	Ly96	17087	Proximal	95	508	59	188	66	193	12	116	105	87	95	93	18	75	95	28	54	111	-1.344	0.160	-0.097	-0.211	-0.094	-0.183	-0.967	-0.287	-0.008	-0.842	-0.457	0.262
12	CD14	CD14	929	Cd14	12475	Proximal	117	629	4	37	4	15	65	121	99	109	114	121	4	25	8	2	4	9	-0.450	0.265	-0.142	0.025	0.113	0.235	-1.719	-0.742	-1.591	-1.725	-1.594	-1.357
13	CD11b	ITGAM	3684	Itgam	16409	Proximal	61	405	55	176	86	236	78	62	78	55	79	53	69	30	77	105	67	64	-0.333	-0.495	-0.363	-0.493	-0.273	-0.573	-0.324	-0.668	-0.287	0.038	-0.366	-0.390
14	CD11c	ITGAX	3687	Itgax	16411	Proximal	31	213	38	139	110	307	32	37	39	21	32	52	31	59	49	82	109	116	-0.885	-0.707	-0.679	-1.042	-0.864	-0.592	-0.739	-0.374	-0.598	-0.232	0.197	0.346
15	ARF6	ARF6	382	Arf6	11845	Proximal	124	685	40	140	124	367	117	100	118	124	104	122	56	28	56	125	123	119	0.202	-0.056	0.157	0.380	-0.009	0.260	-0.390	-0.703	-0.493	1.002	0.618	0.429
16	MyD88	MYD88	4615	Myd88	17874	Proximal	21	187	9	56	6	30	4	84	1	85	11	2	13	42	1	21	6	3	-1.949	-0.246	-3.301	-0.236	-1.583	-3.569	-1.154	-0.583	-3.608	-0.951	-1.431	-2.119
17	Mal	TIRAP	114609	Tirap	117149	Proximal	18	176	27	115	34	126	2	16	70	3	1	84	2	2	111	3	5	118	-2.870	-1.188	-0.441	-3.240	-5.061	-0.292	-2.096	-1.615	0.186	-1.472	-1.471	0.401
18	IRAK1	IRAK1	3654	Irak1	16179	Proximal	3	29	22	104	89	248	9	3	4	4	4	5	62	17	25	83	78	87	-1.568	-2.780	-2.413	-2.685	-3.026	-2.119	-0.359	-0.825	-0.972	-0.226	-0.268	-0.108
19	IRAK2	IRAK2	3656	Irak2	108960	Proximal	118	639	8	55	3	14	112	79	111	98	121	118	15	38	2	8	2	4	0.096	-0.298	-0.019	-0.128	0.295	0.127	-1.107	-0.619	-2.889	-1.229	-1.752	-2.006
20	IRAK4	IRAK4	51135	Irak4	266632	Proximal	93	503	2	22	1	8	108	114	71	74	73	63	7	6	9	6	1	1	-0.019	0.148	-0.436	-0.326	-0.345	-0.462	-1.290	-1.233	-1.545	-1.362	-1.790	-2.169
21	Pellino	PELI1	57162	Peli1	67245	Proximal	89	488	43	147	121	350	77	107	51	104	59	90	38	69	40	119	116	115	-0.335	0.010	-0.573	-0.058	-0.478	-0.236	-0.566	-0.317	-0.677	0.372	0.337	0.341
22	Uev1a	UBE2V1	7335	Ube2v1	66589	Proximal	112	595	94	251	105	296	107	115	73	107	97	96	67	83	101	84	110	102	-0.024	0.153	-0.425	0.003	-0.085	-0.174	-0.326	-0.193	0.034	-0.225	0.214	0.049
23	Ubc13	UBE2N	7334	Ube2n	93765	Proximal	110	576	114	302	70	197	114	46	103	99	112	102	102	106	94	71	57	69	0.144	-0.609	-0.133	-0.126	0.094	-0.107	0.086	0.036	-0.030	-0.317	-0.436	-0.340
24	TRAF6	TRAF6	7189	Traf6	22034	Proximal	1	17	1	10	19	75	5	1	5	1	2	3	3	3	4	43	22	10	-1.858	-3.617	-1.993	-3.883	-3.292	-2.956	-1.765	-1.578	-2.495	-0.579	-0.888	-1.342
25	TRAF3	TRAF3	7187	Traf3	22031	Proximal	49	338	103	276	64	192	39	70	59	108	26	36	114	96	66	69	72	51	-0.779	-0.432	-0.529	0.010	-1.027	-0.831	0.274	-0.071	-0.362	-0.351	-0.336	-0.559
26	TAK1	MAP3K7	6885	Map3k7	26409	Proximal	2	20	52	173	43	148	6	2	3	2	3	4	123	14	36	54	47	47	-1.795	-3.448	-2.469	-3.498	-3.075	-2.760	0.566	-0.851	-0.758	-0.487	-0.532	-0.599
27	TAB1	TAB1	10454	Tab1	66513	Proximal	11	124	23	109	27	93	29	10	19	24	25	17	39	55	15	14	41	38	-0.915	-1.415	-1.094	-0.946	-1.046	-1.221	-0.553	-0.422	-1.281	-1.080	-0.638	-0.669
28	TAB2	TAB2	23118	Tab2	68652	Proximal	4	47	78	226	57	186	19	5	6	5	6	6	89	51	86	70	60	56	-1.138	-2.074	-1.992	-2.049	-2.102	-1.929	-0.056	-0.503	-0.139	-0.321	-0.395	-0.475
29	TAB3	TAB3	257397	Tab3	66724	Proximal	105	543	81	230	52	173	100	81	77	115	85	85	111	58	61	79	58	36	-0.089	-0.297	-0.366	0.123	-0.250	-0.290	0.254	-0.376	-0.406	-0.254	-0.410	-0.755
30	NEMO	IKBKG	8517	Ikbkg	16151	NFkB	36	257	5	41	17	69	55	24	88	26	39	25	16	20	5	4	30	35	-0.556	-0.902	-0.228	-0.905	-0.747	-1.056	-1.084	-0.810	-2.139	-1.386	-0.736	-0.784
31	IKKa	CHUK	1147	Chuk	12675	NFkB	53	373	77	223	80	226	97	43	65	71	54	43	118	73	32	33	87	106	-0.099	-0.639	-0.493	-0.364	-0.540	-0.749	0.363	-0.296	-0.804	-0.708	-0.181	0.076
32	IKKb	IKBKB	3551	Ikbkb	16150	NFkB	116	620	11	59	11	54	122	109	44	113	113	119	42	10	7	16	19	19	0.426	0.081	-0.639	0.078	0.102	0.138	-0.535	-1.105	-1.620	-1.067	-0.972	-0.987
33	IkBa	NFKBIA	4792	Nfkbia	18035	NFkB	60	398	3	22	117	336	87	77	63	54	52	65	5	4	13	118	124	94	-0.235	-0.348	-0.508	-0.497	-0.564	-0.438	-1.379	-1.560	-1.447	0.340	0.644	-0.045
34	IkBb	NFKBIB	4793	Nfkbib	18036	NFkB	55	374	91	246	36	128	63	83	49	61	69	49	122	98	26	31	53	44	-0.467	-0.253	-0.586	-0.431	-0.366	-0.644	0.438	-0.031	-0.971	-0.742	-0.458	-0.614
35	IkBe	NFKBIE	4794	Nfkbie	18037	NFkB	6	60	18	73	61	189	8	14	7	16	7	8	11	34	28	64	94	31	-1.630	-1.275	-1.633	-1.199	-1.795	-1.799	-1.251	-0.642	-0.883	-0.382	-0.116	-0.800
36	Nfkb1	NFKB1	4790	Nfkb1	18033	NFkB	57	392	125	339	46	154	84	51	120	44	70	23	103	117	119	109	11	34	-0.266	-0.572	0.200	-0.649	-0.365	-1.066	0.103	0.299	0.400	0.105	-1.177	-0.785
37	NFkb2	NFKB2	4791	Nfkb2	18034	NFkB	96	509	120	330	31	108	59	103	95	103	102	47	125	103	102	35	28	45	-0.501	-0.025	-0.191	-0.079	-0.021	-0.702	0.600	0.011	0.044	-0.693	-0.764	-0.614
38	RelA	RELA	5970	Rela	19697	NFkB	10	111	19	93	16	63	16	8	48	9	19	11	21	66	6	45	10	8	-1.204	-1.540	-0.604	-1.848	-1.225	-1.266	-0.911	-0.329	-1.711	-0.558	-1.204	-1.406
39	RelB	RELB	5971	Relb	19698	NFkB	111	589	42	145	41	139	61	78	81	120	126	123	27	49	69	40	32	67	-0.471	-0.318	-0.316	0.207	0.746	0.365	-0.797	-0.522	-0.339	-0.611	-0.723	-0.357
40	cRel	REL	5966	Rel	19696	NFkB	54	373	99	269	55	181	53	41	46	66	66	101	72	92	105	57	51	73	-0.573	-0.649	-0.610	-0.397	-0.393	-0.119	-0.280	-0.098	0.121	-0.458	-0.468	-0.323
41	Tpl2	MAP3K8	1326	Map3k8	26410	MAPK	5	56	117	317	88	246	22	4	8	7	8	7	106	107	104	98	88	60	-1.110	-2.191	-1.507	-1.961	-1.711	-1.832	0.146	0.041	0.111	-0.037	-0.173	-0.419
42	Mekk1	MAP3K1	4214	Map3k1	26401	MAPK	34	239	116	315	108	303	30	42	25	60	45	37	105	95	115	102	97	104	-0.913	-0.647	-0.933	-0.439	-0.675	-0.819	0.113	-0.071	0.274	0.024	-0.042	0.058
43	Mkk1	MAP2K1	5604	Map2k1	26395	MAPK	79	460	112	299	35	126	109	66	115	29	68	73	113	63	123	30	34	62	0.007	-0.456	0.114	-0.843	-0.368	-0.342	0.261	-0.355	0.612	-0.780	-0.680	-0.414
44	Mkk2	MAP2K2	5605	Map2k2	26396	MAPK	103	534	49	166	28	97	105	58	125	34	103	109	78	68	20	51	24	22	-0.033	-0.524	0.409	-0.764	-0.012	-0.035	-0.217	-0.323	-1.031	-0.531	-0.854	-0.887
45	Erk1	MAPK3	5595	Mapk3	26417	MAPK	24	193	47	155	87	238	43	23	20	14	53	40	71	12	72	103	52	83	-0.731	-0.980	-1.089	-1.277	-0.544	-0.763	-0.291	-0.949	-0.304	0.032	-0.461	-0.139
46	Erk2	MAPK1	5594	Mapk1	26413	MAPK	102	530	44	148	25	88	91	88	87	45	99	120	107	22	19	44	26	18	-0.185	-0.236	-0.243	-0.589	-0.060	0.171	0.157	-0.784	-1.036	-0.575	-0.826	-0.989
47	Mkk3	MAP2K3	5606	Map2k3	26397	MAPK	17	174	96	263	51	170	24	36	61	22	15	16	63	112	88	85	55	30	-1.066	-0.725	-0.522	-1.013	-1.327	-1.241	-0.349	0.174	-0.115	-0.212	-0.451	-0.808
48	Mkk6	MAP2K6	5608	Map2k6	26399	MAPK	115	608	67	197	94	275	110	117	45	121	120	95	92	64	41	86	91	98	0.015	0.214	-0.633	0.246	0.198	-0.178	-0.026	-0.333	-0.676	-0.211	-0.146	-0.018
49	p38a	MAPK14	1432	Mapk14	26416	MAPK	9	93	105	279	67	195	37	6	17	10	10	13	124	79	76	90	37	68	-0.805	-1.949	-1.112	-1.775	-1.608	-1.261	0.587	-0.248	-0.292	-0.139	-0.667	-0.344
50	p38b	MAPK11	5600	Mapk11	19094	MAPK	74	450	122	333	81	226	75	101	69	67	78	60	121	99	113	73	92	61	-0.339	-0.042	-0.443	-0.395	-0.275	-0.525	0.411	-0.013	0.262	-0.295	-0.135	-0.414
51	MK2	MAPKAPK2	9261	Mapkapk2	17164	MAPK	81	466	73	213	69	197	66	53	92	76	93	86	40	67	106	66	35	96	-0.448	-0.560	-0.205	-0.323	-0.137	-0.279	-0.544	-0.328	0.152	-0.362	-0.676	-0.034
52	Mkk4	MAP2K4	6416	Map2k4	26398	MAPK	91	492	110	291	92	253	102	65	84	84	100	57	82	118	91	89	83	81	-0.065	-0.472	-0.279	-0.236	-0.031	-0.544	-0.152	0.299	-0.068	-0.145	-0.220	-0.171
53	Mkk7	MAP2K7	5609	Map2k7	26400	MAPK	14	150	65	197	26	89	21	15	34	39	17	24	35	115	47	37	27	25	-1.127	-1.269	-0.782	-0.722	-1.271	-1.059	-0.588	0.225	-0.631	-0.672	-0.821	-0.854
54	Jnk1	MAPK8	5599	Mapk8	26419	MAPK	114	602	25	111	97	287	89	105	91	93	111	113	54	36	21	96	86	105	-0.200	-0.001	-0.218	-0.176	0.087	0.018	-0.430	-0.640	-1.011	-0.077	-0.183	0.064
55	Jnk2	MAPK9	5601	Mapk9	26420	MAPK	83	470	106	279	78	215	98	87	43	57	91	94	97	111	71	34	96	85	-0.098	-0.236	-0.652	-0.471	-0.190	-0.180	0.014	0.171	-0.312	-0.694	-0.057	-0.127
56	Jnk3	MAPK10	5602	Mapk10	26414	MAPK	109	569	62	194	122	359	92	75	80	106	116	100	32	65	97	115	120	124	-0.180	-0.389	-0.336	-0.016	0.155	-0.133	-0.654	-0.331	0.022	0.245	0.386	0.604
57	Erk3	MAPK12	6300	Mapk12	29857	MAPK	72	448	57	183	82	228	90	72	55	80	89	62	43	76	64	68	90	70	-0.195	-0.410	-0.543	-0.281	-0.208	-0.512	-0.531	-0.268	-0.394	-0.356	-0.159	-0.336
58	p38d	MAPK13	5603	Mapk13	26415	MAPK	29	210	36	134	10	54	42	54	58	11	16	29	65	26	43	12	13	29	-0.745	-0.555	-0.529	-1.645	-1.281	-0.963	-0.331	-0.735	-0.669	-1.139	-1.127	-0.810
59	TRIF	TICAM1	148022	Ticam1	106759	TRIF	48	336	74	215	65	193	7	55	121	47	71	35	48	108	59	20	108	65	-1.775	-0.538	0.236	-0.572	-0.360	-0.853	-0.483	0.041	-0.449	-0.986	0.142	-0.385
60	TRAM	TICAM2	353376	Ticam2	225471	TRIF	66	434	56	183	14	61	11	69	75	94	106	79	53	41	89	25	12	24	-1.371	-0.441	-0.375	-0.171	0.002	-0.318	-0.435	-0.600	-0.111	-0.862	-1.151	-0.858
61	RIP1	RIPK1	8737	Ripk1	19766	TRIF	63	410	121	330	118	337	103	39	30	72	74	92	120	110	100	120	117	100	-0.059	-0.704	-0.833	-0.360	-0.338	-0.233	0.402	0.103	0.033	0.396	0.353	0.035

TABLE S3

Gene#	Name	Human Gene Symbol	Human Gene ID	Mouse Gene Symbol	Mouse Gene ID	Module	Human rank TNFa	Human rank TNFa SUM	Mouse rank NF-kB	Mouse rank NF-kB SUM	Mouse rank TNFa	Mouse rank TNFa SUM	LPS-hTNF_rank	P3C-hTNF_rank	R848-hTNF_rank	P2C-hTNF_rank	PGN-hTNF_rank	FLG-hTNF_rank	LPS-mNFKB_rank	P3C-mNFKB_rank	R848-mNFKB_rank	LPS-mTNF_rank	P3C-mTNF_rank	R848-mTNF_rank	LPS-hTNF_z-score	P3C-hTNF_z-score	R848-hTNF_z-score	P2C-hTNF_z-score	PGN-hTNF_z-score	FLG-hTNF_z-score	LPS-mNFKB_z-score	P3C-mNFKB_z-score	R848-mNFKB_z-score	LPS-mTNF_z-score	P3C-mTNF_z-score	R848-mTNF_z-score
62	FADD	FADD	8772	Fadd	14082	TRIF	62	406	24	109	40	139	49	71	33	46	109	98	34	31	44	49	38	52	-0.631	-0.411	-0.795	-0.583	0.069	-0.161	-0.618	-0.659	-0.657	-0.547	-0.664	-0.538
63	Caspase 8	CASP8	841	Casp8	12370	TRIF	87	476	15	68	114	314	83	76	50	86	94	87	24	15	29	116	118	80	-0.298	-0.351	-0.583	-0.227	-0.136	-0.272	-0.841	-0.842	-0.876	0.250	0.356	-0.192
64	TBK1	TBK1	29110	Tbk1	56480	TRIF	76	454	107	281	119	339	111	50	119	27	92	55	91	70	120	107	115	117	0.076	-0.577	0.189	-0.880	-0.142	-0.564	-0.038	-0.314	0.432	0.067	0.301	0.389
65	IKKe	IKBKE	9641	Ikbke	56489	TRIF	84	472	51	170	15	61	70	86	15	100	77	124	29	54	87	5	39	17	-0.397	-0.238	-1.145	-0.123	-0.302	0.465	-0.773	-0.453	-0.126	-1.367	-0.655	-1.029
66	IRF3	IRF3	3661	Irf3	54131	TRIF	33	236	97	265	90	251	13	74	13	33	44	59	126	77	62	65	98	88	-1.254	-0.397	-1.228	-0.798	-0.681	-0.536	0.649	-0.263	-0.402	-0.366	-0.036	-0.105
67	Duba	OTUD5	55593	Otud5	54644	TRIF	23	191	111	296	20	75	26	25	53	8	31	48	93	120	83	22	20	33	-1.021	-0.865	-0.566	-1.849	-0.917	-0.692	-0.022	0.374	-0.161	-0.950	-0.943	-0.791
68	TRADD	TRADD	8717	Tradd	71609	TRIF	46	325	45	152	112	313	106	38	52	12	72	45	52	32	68	94	106	113	-0.032	-0.706	-0.569	-1.432	-0.351	-0.709	-0.445	-0.657	-0.341	-0.086	0.076	0.300
69	TANK	TANK	10010	Tank	21353	TRIF	107	555	126	354	125	369	62	125	114	77	88	89	104	124	126	122	122	125	-0.471	0.909	0.061	-0.323	-0.220	-0.264	0.105	0.739	1.264	0.496	0.564	0.694
70	SINTBAD	TBKBP1	9755	Tbkbp1	73174	TRIF	119	645	100	270	120	345	126	124	101	65	119	110	115	47	108	117	107	121	0.782	0.613	-0.136	-0.400	0.190	-0.026	0.279	-0.547	0.160	0.281	0.141	0.512
71	BTK	BTK	695	Btk	12229	PI3K	85	474	30	119	29	104	120	57	60	89	37	111	28	81	10	41	42	21	0.261	-0.537	-0.524	-0.201	-0.754	-0.025	-0.775	-0.207	-1.545	-0.605	-0.620	-0.952
72	NIK	MAP3K14	9020	Map3k14	53859	PI3K	122	669	90	245	83	230	121	108	90	101	124	125	83	123	39	58	79	93	0.377	0.069	-0.224	-0.112	0.576	0.475	-0.134	0.452	-0.703	-0.435	-0.266	-0.049
73	AKT1	AKT1	207	Akt1	11651	PI3K	99	519	6	47	76	214	40	97	68	117	83	114	12	21	14	48	77	89	-0.776	-0.137	-0.446	0.159	-0.257	0.087	-1.209	-0.794	-1.288	-0.548	-0.273	-0.098
74	AKT2	AKT2	208	Akt2	11652	PI3K	90	490	118	321	22	78	34	119	72	122	63	80	100	125	96	27	14	37	-0.863	0.236	-0.433	0.288	-0.433	-0.307	0.034	1.113	-0.005	-0.847	-1.062	-0.711
75	AKT3	AKT3	10000	Akt3	23797	PI3K	108	557	26	115	32	108	116	111	82	90	107	51	37	23	55	52	17	39	0.166	0.131	-0.309	-0.201	0.014	-0.618	-0.577	-0.771	-0.495	-0.494	-1.045	-0.660
76	PIK3CA	PIK3CA	5290	Pik3ca	18706	PI3K	98	516	58	183	96	282	113	85	83	79	87	69	66	43	74	111	121	50	0.097	-0.238	-0.302	-0.284	-0.226	-0.373	-0.330	-0.574	-0.297	0.127	0.394	-0.575
77	PIK3CB	PIK3CB	5291	Pik3cb	74769	PI3K	80	465	64	196	23	80	101	99	89	52	49	75	30	109	57	11	21	48	-0.084	-0.094	-0.227	-0.514	-0.618	-0.339	-0.769	0.072	-0.488	-1.148	-0.889	-0.579
78	PIK3CD	PIK3CD	5293	Pik3cd	18707	PI3K	67	440	95	261	33	115	44	118	36	126	90	26	110	84	67	24	63	28	-0.717	0.230	-0.711	0.550	-0.199	-1.043	0.252	-0.189	-0.349	-0.879	-0.374	-0.817
79	PIK3CG	PIK3CG	5294	Pik3cg	30955	PI3K	41	282	50	168	60	188	64	49	67	36	51	15	57	88	23	97	84	7	-0.451	-0.578	-0.451	-0.763	-0.577	-1.256	-0.389	-0.138	-0.988	-0.063	-0.186	-1.636
80	PIK3R1	PIK3R1	5295	Pik3r1	18708	PI3K	121	667	10	57	62	190	119	102	104	118	117	107	6	16	35	61	89	40	0.253	-0.028	-0.106	0.183	0.164	-0.062	-1.332	-0.830	-0.767	-0.419	-0.171	-0.653
81	PIK3R2	PIK3R2	5296	Pik3r2	18709	PI3K	69	442	108	285	75	212	58	113	116	38	40	77	101	121	63	74	43	95	-0.537	0.143	0.116	-0.735	-0.716	-0.333	0.034	0.382	-0.402	-0.290	-0.603	-0.037
82	PIK3R3	PIK3R3	8503	Pik3r3	18710	PI3K	47	327	85	241	59	187	80	90	23	42	58	34	116	74	51	29	81	77	-0.325	-0.226	-0.945	-0.681	-0.481	-0.877	0.303	-0.291	-0.590	-0.822	-0.254	-0.211
83	PIK3R5	PIK3R5	23533	Pik3r5	320207	PI3K	52	366	88	244	30	108	85	29	108	81	33	30	94	116	34	32	44	32	-0.250	-0.802	-0.045	-0.279	-0.824	-0.947	-0.021	0.263	-0.787	-0.737	-0.581	-0.793
84	RAC1	RAC1	5879	Rac1	19353	PI3K	97	510	53	173	106	299	73	98	62	102	101	74	51	40	82	99	99	101	-0.351	-0.133	-0.515	-0.086	-0.030	-0.341	-0.456	-0.613	-0.170	-0.036	0.003	0.047
85	IRF5	IRF5	3663	Irf5	27056	TF	35	242	68	203	74	210	88	28	22	15	18	71	77	53	73	67	80	63	-0.212	-0.810	-0.955	-1.260	-1.260	-0.353	-0.238	-0.491	-0.302	-0.360	-0.264	-0.402
86	IRF7	IRF7	3665	Irf7	54123	TF	16	162	86	242	72	204	47	27	11	17	27	33	44	114	84	88	73	43	-0.640	-0.832	-1.301	-1.125	-1.014	-0.883	-0.527	0.218	-0.153	-0.157	-0.332	-0.630
87	STAT1	STAT1	6772	Stat1	20846	TF	100	523	109	291	77	214	69	120	109	111	60	54	99	71	121	92	56	66	-0.413	0.245	-0.026	0.050	-0.460	-0.567	0.023	-0.305	0.471	-0.128	-0.448	-0.373
88	Fos	FOS	2353	Fos	14281	TF	113	599	48	157	63	191	125	60	122	70	110	112	22	87	48	47	70	74	0.659	-0.516	0.237	-0.366	0.085	-0.016	-0.893	-0.181	-0.614	-0.553	-0.351	-0.292
89	Jun	JUN	3725	Jun	16476	TF	25	198	12	60	39	137	14	31	74	23	24	32	14	29	17	18	64	55	-1.237	-0.784	-0.413	-0.955	-1.058	-0.885	-1.139	-0.682	-1.100	-1.017	-0.371	-0.480
90	PYK2	PTK2B	2185	Ptk2b	19229	TF	22	189	119	325	84	231	28	34	29	25	42	31	84	119	122	53	103	75	-0.982	-0.752	-0.845	-0.935	-0.690	-0.893	-0.133	0.336	0.546	-0.490	0.062	-0.235
91	ETS1	ETS1	2113	Ets1	23871	TF	45	317	123	335	79	216	60	40	76	62	41	38	109	102	124	59	48	109	-0.480	-0.661	-0.370	-0.418	-0.712	-0.792	0.223	0.002	0.940	-0.434	-0.526	0.222
92	ELK1	ELK1	2002	Elk1	13712	TF	30	212	33	130	7	35	35	13	28	68	22	46	20	80	30	26	3	6	-0.861	-1.304	-0.871	-0.379	-1.131	-0.706	-0.923	-0.226	-0.818	-0.858	-1.668	-1.775
93	ELK4	ELK4	2005	Elk4	13714	TF	42	285	60	190	68	196	51	30	57	48	57	42	25	100	65	78	69	49	-0.582	-0.798	-0.536	-0.556	-0.502	-0.754	-0.818	-0.013	-0.379	-0.257	-0.354	-0.578
94	SP1	SP1	6667	Sp1	20683	TF	75	452	31	120	5	25	118	64	123	32	34	81	80	7	33	7	7	11	0.243	-0.476	0.294	-0.810	-0.818	-0.303	-0.191	-1.222	-0.791	-1.276	-1.417	-1.326
95	EGR1	EGR1	1958	Egr1	13653	TF	7	75	69	207	9	39	17	7	12	20	9	10	88	44	75	9	16	14	-1.183	-1.706	-1.263	-1.077	-1.669	-1.483	-0.085	-0.562	-0.295	-1.210	-1.048	-1.138
96	EGR2	EGR2	1959	Egr2	13654	TF	13	149	32	124	2	11	15	9	27	18	36	44	17	62	45	1	8	2	-1.204	-1.424	-0.872	-1.085	-0.773	-0.741	-1.029	-0.362	-0.649	-1.983	-1.415	-2.150
97	ATF2	ATF2	1386	Atf2	11909	TF	56	384	35	131	24	84	54	89	98	30	43	70	59	19	53	38	33	13	-0.562	-0.227	-0.163	-0.836	-0.686	-0.364	-0.383	-0.811	-0.515	-0.645	-0.691	-1.192
98	ATF7	ATF7	11016	Atf7	223922	TF	20	185	61	191	12	55	45	20	10	41	48	21	50	104	37	10	25	20	-0.704	-1.070	-1.326	-0.699	-0.625	-1.071	-0.466	0.024	-0.721	-1.159	-0.842	-0.982
99	CBP	CREBBP	1387	Crebbp	12914	TF	126	692	20	98	8	37	123	123	94	112	125	115	36	50	12	13	9	15	0.437	0.573	-0.195	0.057	0.682	0.094	-0.579	-0.517	-1.508	-1.109	-1.214	-1.111
100	p300	EP300	2033	Ep300	328572	TF	120	655	14	64	38	135	115	122	47	123	122	126	9	39	16	62	61	12	0.146	0.286	-0.608	0.302	0.540	0.633	-1.268	-0.618	-1.194	-0.400	-0.388	-1.299
101	ISGF3G	IRF9	10379	Irf9	16391	TF	27	202	54	173	126	375	27	18	14	43	61	39	55	9	109	123	126	126	-0.986	-1.158	-1.227	-0.674	-0.459	-0.785	-0.398	-1.111	0.163	0.583	0.994	0.756
102	ELF4	ELF4	2000	Elf4	56501	TF	8	86	21	100	37	133	10	12	9	13	14	28	41	13	46	42	75	16	-1.505	-1.334	-1.329	-1.413	-1.417	-0.964	-0.537	-0.868	-0.635	-0.591	-0.304	-1.103
103	IFNAR1	IFNAR1	3454	Ifnar1	15975	Cytokine	44	297	29	119	13	55	25	52	56	69	76	19	49	46	24	17	15	23	-1.054	-0.565	-0.539	-0.368	-0.303	-1.170	-0.468	-0.557	-0.975	-1.037	-1.057	-0.878
104	IFNAR2	IFNAR2	3455	Ifnar2	15976	Cytokine	26	199	124	338	73	207	18	21	32	49	29	50	96	126	116	60	76	71	-1.179	-1.005	-0.801	-0.545	-0.932	-0.640	0.010	1.240	0.293	-0.421	-0.292	-0.334
105	IFNB1	IFNB1	3456	Ifnb1	15977	Cytokine	19	178	89	245	18	72	33	11	18	50	46	20	58	97	90	23	23	26	-0.885	-1.358	-1.109	-0.544	-0.667	-1.094	-0.386	-0.065	-0.085	-0.923	-0.877	-0.835
106	IL12A	IL12A	3592	Il12a	16159	Cytokine	94	505	76	222	21	77	72	80	64	97	84	108	81	91	50	19	31	27	-0.368	-0.297	-0.493	-0.147	-0.252	-0.050	-0.153	-0.103	-0.594	-1.014	-0.728	-0.828
107	IL12B	IL12B	3593	Il12b	16160	Cytokine	15	156	71	212	58	187	38	19	38	19	28	14	74	57	81	91	50	46	-0.799	-1.132	-0.702	-1.083	-1.011	-1.259	-0.250	-0.387	-0.177	-0.130	-0.514	-0.612
108	IL1B	IL1B	3553	Il1b	16176	Cytokine	38	268	104	278	100	292	20	63	107	28	38	12	87	113	78	106	104	82	-1.128	-0.485	-0.075	-0.859	-0.752	-1.263	-0.090	0.185	-0.249	0.038	0.063	-0.158
109	IL6	IL6	3569	Il6	16193	Cytokine	51	356	84	239	115	317	81	45	41	73	55	61	98	61	80	114	100	103	-0.309	-0.619	-0.659	-0.341	-0.521	-0.523	0.015	-0.367	-0.189	0.211	0.026	0.056
110	TNF	TNF	7124	Tnf	21926	Cytokine	12	144	46	153	48	157	56	17	26	6	21	18	47	8	98	63	18	76	-0.551	-1.171	-0.919	-1.976	-1.157	-1.200	-0.488	-1.178	0.032	-0.389	-1.033	-0.229
111	CCL3	CCL3	6348	Ccl3	20302	Cytokine	92	496	66	197	47	154	48	82	86	92	105	83	73	82	42	36	46	72	-0.634	-0.261	-0.267	-0.186	-0.003	-0.299	-0.268	-0.197	-0.676	-0.673	-0.565	-0.324
112	CXCL11	CXCL11	6373	Cxcl11	56066	Cytokine	86	475	70	212	50	165	68	59	66	119	64	99	68	90	54	75	49	41	-0.425	-0.517	-0.452	0.184	-0.411	-0.149	-0.326	-0.114	-0.503	-0.284	-0.515	-0.653
113	CXCL9	CXCL9	4283	Cxcl9	17329	Cytokine	39	275	39	140	104	296	52	26	21	53	47	76	33	37	70	110	95	91	-0.581	-0.858	-0.957	-0.501	-0.645	-0.336	-0.640	-0.620	-0.338	0.116	-0.059	-0.093
114	RP105	CD180	4064	Cd180	17079	Regulator	65	428	98	267	45	153	76	56	35	75	118	68	112	45	110	55	40	58	-0.336	-0.538	-0.732	-0.325	0.174	-0.383	0.261	-0.561	0.171	-0.485	-0.640	-0.460
115	MD1	LY86	9450	Ly86	17084	Regulator	59	396	87	243	99	291	50	48	16	105	86	91	64	72	107	104	101	86	-0.605	-0.579	-1.131	-0.053	-0.233	-0.235	-0.348	-0.304	0.159	0.034	0.055	-0.115
116	TIR8	SIGIRR	59307	Sigirr	24058	Regulator	77	457	7	54	71	200	74	32	102	51	81	117	8	24	22	50	93	57	-0.346	-0.782	-0.133	-0.526	-0.260	0.120	-1.271	-0.765	-1.005	-0.547	-0.126	-0.462
117	ST2	IL1RL1	9173	Il1rl1	17082	Regulator	70	443	13	63	49	164	95	68	110	56	56	58	10	35	18	93	29	42	-0.122	-0.442	-0.023	-0.488	-0.520	-0.542	-1.263	-0.641	-1.071	-0.126	-0.755	-0.647
118	IRAK3	IRAK3	11213	Irak3	73914	Regulator	78	458	16	71	53	176	94	73	106	59	62	64	26	18	27	39	59	78	-0.135	-0.402	-0.087	-0.444	-0.458	-0.448	-0.800	-0.825	-0.937	-0.645	-0.395	-0.206
119	SHP1	PTPN6	5777	Ptpn6	15170	Regulator	32	225	41	142	42	145	31	67	42	35	23	27	46	85	11	56	36	53	-0.900	-0.443	-0.653	-0.764	-1.126	-1.038	-0.498	-0.187	-1.524	-0.466	-0.671	-0.507
120	Cyld	CYLD	1540	Cyld	74256	Regulator	43	289	93	249	116	327	3	95	40	116	13	22	76	56	117	126	102	99	-1.987	-0.141	-0.662	0.146	-1.460	-1.071	-0.243	-0.387	0.336	1.175	0.058	0.035
121	A20	TNFAIP3	7128	Tnfaip3	21929	Regulator	37	266	101	271	123	361	36	44	126	31	20	9	60	86	125	124	125	112	-0.825	-0.624	0.844	-0.810	-1.180	-1.790	-0.362	-0.184	1.028	0.726	0.745	0.271
122	DUSP2	DUSP2	1844	Dusp2	13537	Regulator	88	487	37	137	93	269	86	112	37	83	65	104	19	60	58	113	66	90	-0.236	0.143	-0.707	-0.243	-0.398	-0.101	-0.962	-0.367	-0.473	0.147	-0.368	-0.098

TABLE S3

Gene#	Name	Human Gene Symbol	Human Gene ID	Mouse Gene Symbol	Mouse Gene ID	Module	Human rank TNFa	Human rank TNFa SUM	Mouse rank NF-kB	Mouse rank NF-kB SUM	Mouse rank TNFa	Mouse rank TNFa SUM	LPS-hTNF_rank	P3C-hTNF_rank	R848-hTNF_rank	P2C-hTNF_rank	PGN-hTNF_rank	FLG-hTNF_rank	LPS-mNFKB_rank	P3C-mNFKB_rank	R848-mNFKB_rank	LPS-mTNF_rank	P3C-mTNF_rank	R848-mTNF_rank	LPS-hTNF_z-score	P3C-hTNF_z-score	R848-hTNF_z-score	P2C-hTNF_z-score	PGN-hTNF_z-score	FLG-hTNF_z-score	LPS-mNFKB_z-score	P3C-mNFKB_z-score	R848-mNFKB_z-score	LPS-mTNF_z-score	P3C-mTNF_z-score	R848-mTNF_z-score
123	AIP1	DAB2IP	153090	Dab2ip	69601	Regulator	28	210	63	195	85	236	41	22	24	37	30	56	70	94	31	77	62	97	-0.747	-0.984	-0.941	-0.741	-0.923	-0.555	-0.295	-0.076	-0.808	-0.261	-0.380	-0.020
124	Tollip	TOLLIP	54472	Tollip	54473	Regulator	40	281	17	72	56	182	46	33	31	64	35	72	23	11	38	46	82	54	-0.691	-0.767	-0.830	-0.403	-0.801	-0.345	-0.886	-1.046	-0.720	-0.556	-0.247	-0.498
125	MKP1	DUSP1	1843	Dusp1	19252	Regulator	123	683	102	275	103	293	124	110	113	110	123	103	85	105	85	112	71	110	0.574	0.098	-0.002	0.050	0.540	-0.102	-0.127	0.027	-0.150	0.142	-0.338	0.253
126	RIP3	RIPK3	11035	Ripk3	56532	Regulator	106	544	75	217	98	289	96	61	96	88	98	105	79	78	60	100	105	84	-0.118	-0.496	-0.191	-0.203	-0.084	-0.095	-0.206	-0.255	-0.440	-0.018	0.074	-0.138

TABLE S4

Gene#	Name	Human Gene Symbol	Human Gene ID	Mouse Gene Symbol	Mouse Gene ID	Module	LPS-hTNF_z-score	P3C-hTNF_z-score	R848-hTNF_z-score	LPS-mTNF_z-score	P3C-mTNF_z-score	R848-mTNF_z-score	LPS/hTNF-mTNF	P3C/hTNF-mTNF	R848/hTNF-mTNF	Median hTNF-mTNF
1	TLR1	TLR1	7096	Tlr1	21897	TLR	-0.092	-0.600	-0.338	-0.011	0.237	-0.092	-0.081	-0.837	-0.245	-0.245
2	TLR2	TLR2	7097	Tlr2	24088	TLR	-0.143	-0.748	0.367	0.082	-0.368	0.454	-0.225	-0.379	-0.087	-0.225
3	TLR3	TLR3	7098	Tlr3	142980	TLR	-0.543	-0.180	-0.015	0.455	-0.185	0.108	-0.997	0.005	-0.123	-0.123
4	TLR4	TLR4	7099	Tlr4	21898	TLR	-4.482	-0.182	-0.168	-1.072	0.284	0.591	-3.410	-0.466	-0.759	-0.759
5	TLR5	TLR5	7100	Tlr5	53791	TLR	-1.076	-0.201	-0.278	-0.237	0.262	0.303	-0.839	-0.463	-0.580	-0.580
6	TLR6	TLR6	10333	Tlr6	21899	TLR	-0.447	-0.178	0.139	-0.170	-0.364	0.527	-0.277	0.186	-0.388	-0.277
7	TLR7	TLR7	51284	Tlr7	170743	TLR	-0.305	-0.014	-0.201	-0.302	-0.314	-1.798	-0.003	0.301	1.597	0.301
8	TLR8	TLR8	51311	Tlr8	170744	TLR	-0.378	0.006	-2.731	-0.083	0.365	-0.198	-0.295	-0.359	-2.533	-0.359
9	TLR9	TLR9	54106	Tlr9	81897	TLR	-0.034	0.957	-0.138	-0.282	-0.576	-0.455	0.247	1.533	0.316	0.316
10	LBP	LBP	3929	Lbp	16803	Proximal	-0.330	-0.138	-0.545	-0.253	0.243	0.107	-0.076	-0.381	-0.652	-0.381
11	MD2	LY96	23643	Ly96	17087	Proximal	-1.344	0.160	-0.097	-0.842	-0.457	0.262	-0.502	0.617	-0.360	-0.360
12	CD14	CD14	929	Cd14	12475	Proximal	-0.450	0.265	-0.142	-1.725	-1.594	-1.357	1.275	1.858	1.214	1.275
13	CD11b	ITGAM	3684	Itgam	16409	Proximal	-0.333	-0.495	-0.363	0.038	-0.366	-0.390	-0.371	-0.130	0.028	-0.130
14	CD11c	ITGAX	3687	Itgax	16411	Proximal	-0.885	-0.707	-0.679	-0.232	0.197	0.346	-0.654	-0.904	-1.024	-0.904
15	ARF6	ARF6	382	Arf6	11845	Proximal	0.202	-0.056	0.157	1.002	0.618	0.429	-0.800	-0.674	-0.272	-0.674
16	MyD88	MYD88	4615	Myd88	17874	Proximal	-1.949	-0.246	-3.301	-0.951	-1.431	-2.119	-0.998	1.184	-1.182	-0.998
17	Mal	TIRAP	114609	Tirap	117149	Proximal	-2.870	-1.188	-0.441	-1.472	-1.471	0.401	-1.399	0.283	-0.841	-0.841
18	IRAK1	IRAK1	3654	Irak1	16179	Proximal	-1.568	-2.780	-2.413	-0.226	-0.268	-0.108	-1.342	-2.512	-2.305	-2.305
19	IRAK2	IRAK2	3656	Irak2	108960	Proximal	0.096	-0.298	-0.019	-1.229	-1.752	-2.006	1.325	1.454	1.987	1.454
20	IRAK4	IRAK4	51135	Irak4	266632	Proximal	-0.019	0.148	-0.436	-1.362	-1.790	-2.169	1.343	1.938	1.733	1.733
21	Pellino	PELI1	57162	Peli1	67245	Proximal	-0.335	0.010	-0.573	0.372	0.337	0.341	-0.707	-0.326	-0.914	-0.707
22	Uev1a	UBE2V1	7335	Ube2v1	66589	Proximal	-0.024	0.153	-0.425	-0.225	0.214	0.049	0.201	-0.061	-0.474	-0.061
23	Ubc13	UBE2N	7334	Ube2n	93765	Proximal	0.144	-0.609	-0.133	-0.317	-0.436	-0.340	0.461	-0.173	0.207	0.207
24	TRAF6	TRAF6	7189	Traf6	22034	Proximal	-1.858	-3.617	-1.993	-0.579	-0.888	-1.342	-1.280	-2.730	-0.652	-1.280
25	TRAF3	TRAF3	7187	Traf3	22031	Proximal	-0.779	-0.432	-0.529	-0.351	-0.336	-0.559	-0.428	-0.096	0.030	-0.096
26	TAK1	MAP3K7	6885	Map3k7	26409	Proximal	-1.795	-3.448	-2.469	-0.487	-0.532	-0.599	-1.308	-2.916	-1.871	-1.871
27	TAB1	TAB1	10454	Tab1	66513	Proximal	-0.915	-1.415	-1.094	-1.080	-0.638	-0.669	0.165	-0.777	-0.426	-0.426
28	TAB2	TAB2	23118	Tab2	68652	Proximal	-1.138	-2.074	-1.992	-0.321	-0.395	-0.475	-0.817	-1.680	-1.518	-1.518
29	TAB3	TAB3	257397	Tab3	66724	Proximal	-0.089	-0.297	-0.366	-0.254	-0.410	-0.755	0.165	0.113	0.390	0.165
30	NEMO	IKBKG	8517	Ikbkg	16151	NFkB	-0.556	-0.902	-0.228	-1.386	-0.736	-0.784	0.830	-0.166	0.556	0.556
31	IKKa	CHUK	1147	Chuk	12675	NFkB	-0.099	-0.639	-0.493	-0.708	-0.181	0.076	0.609	-0.457	-0.568	-0.457
32	IKKb	IKBKB	3551	Ikbkb	16150	NFkB	0.426	0.081	-0.639	-1.067	-0.972	-0.987	1.492	1.054	0.348	1.054
33	IkBa	NFKBIA	4792	Nfkbia	18035	NFkB	-0.235	-0.348	-0.508	0.340	0.644	-0.045	-0.574	-0.992	-0.463	-0.574
34	IkBb	NFKBIB	4793	Nfkbib	18036	NFkB	-0.467	-0.253	-0.586	-0.742	-0.458	-0.614	0.275	0.205	0.028	0.205
35	IkBe	NFKBIE	4794	Nfkbie	18037	NFkB	-1.630	-1.275	-1.633	-0.382	-0.116	-0.800	-1.247	-1.160	-0.833	-1.160
36	Nfkb1	NFKB1	4790	Nfkb1	18033	NFkB	-0.266	-0.572	0.200	0.105	-1.177	-0.785	-0.371	0.605	0.985	0.605
37	NFkb2	NFKB2	4791	Nfkb2	18034	NFkB	-0.501	-0.025	-0.191	-0.693	-0.764	-0.614	0.192	0.739	0.423	0.423
38	RelA	RELA	5970	Rela	19697	NFkB	-1.204	-1.540	-0.604	-0.558	-1.204	-1.406	-0.646	-0.336	0.801	-0.336
39	RelB	RELB	5971	Relb	19698	NFkB	-0.471	-0.318	-0.316	-0.611	-0.723	-0.357	0.141	0.405	0.040	0.141
40	cRel	REL	5966	Rel	19696	NFkB	-0.573	-0.649	-0.610	-0.458	-0.468	-0.323	-0.116	-0.181	-0.287	-0.181
41	Tpl2	MAP3K8	1326	Map3k8	26410	MAPK	-1.110	-2.191	-1.507	-0.037	-0.173	-0.419	-1.073	-2.018	-1.088	-1.088
42	Mekk1	MAP3K1	4214	Map3k1	26401	MAPK	-0.913	-0.647	-0.933	0.024	-0.042	0.058	-0.937	-0.605	-0.991	-0.937
43	Mkk1	MAP2K1	5604	Map2k1	26395	MAPK	0.007	-0.456	0.114	-0.780	-0.680	-0.414	0.787	0.224	0.528	0.528
44	Mkk2	MAP2K2	5605	Map2k2	26396	MAPK	-0.033	-0.524	0.409	-0.531	-0.854	-0.887	0.499	0.330	1.296	0.499
45	Erk1	MAPK3	5595	Mapk3	26417	MAPK	-0.731	-0.980	-1.089	0.032	-0.461	-0.139	-0.763	-0.519	-0.950	-0.763
46	Erk2	MAPK1	5594	Mapk1	26413	MAPK	-0.185	-0.236	-0.243	-0.575	-0.826	-0.989	0.389	0.590	0.746	0.590
47	Mkk3	MAP2K3	5606	Map2k3	26397	MAPK	-1.066	-0.725	-0.522	-0.212	-0.451	-0.808	-0.853	-0.274	0.286	-0.274
48	Mkk6	MAP2K6	5608	Map2k6	26399	MAPK	0.015	0.214	-0.633	-0.211	-0.146	-0.018	0.226	0.360	-0.615	0.226
49	p38a	MAPK14	1432	Mapk14	26416	MAPK	-0.805	-1.949	-1.112	-0.139	-0.667	-0.344	-0.667	-1.282	-0.768	-0.768
50	p38b	MAPK11	5600	Mapk11	19094	MAPK	-0.339	-0.042	-0.443	-0.295	-0.135	-0.414	-0.043	0.093	-0.028	-0.028
51	MK2	MAPKAPK2	9261	Mapkapk2	17164	MAPK	-0.448	-0.560	-0.205	-0.362	-0.676	-0.034	-0.086	0.116	-0.171	-0.086
52	Mkk4	MAP2K4	6416	Map2k4	26398	MAPK	-0.065	-0.472	-0.279	-0.145	-0.220	-0.171	0.079	-0.251	-0.107	-0.107
53	Mkk7	MAP2K7	5609	Map2k7	26400	MAPK	-1.127	-1.269	-0.782	-0.672	-0.821	-0.854	-0.455	-0.448	0.072	-0.448
54	Jnk1	MAPK8	5599	Mapk8	26419	MAPK	-0.200	-0.001	-0.218	-0.077	-0.183	0.064	-0.123	0.182	-0.282	-0.123
55	Jnk2	MAPK9	5601	Mapk9	26420	MAPK	-0.098	-0.236	-0.652	-0.694	-0.057	-0.127	0.596	-0.180	-0.526	-0.180
56	Jnk3	MAPK10	5602	Mapk10	26414	MAPK	-0.180	-0.389	-0.336	0.245	0.386	0.604	-0.425	-0.775	-0.940	-0.775
57	Erk3	MAPK12	6300	Mapk12	29857	MAPK	-0.195	-0.410	-0.543	-0.356	-0.159	-0.336	0.161	-0.251	-0.207	-0.207

TABLE S4

Gene#	Name	Human Gene Symbol	Human Gene ID	Mouse Gene Symbol	Mouse Gene ID	Module	LPS-hTNF_z-score	P3C-hTNF_z-score	R848-hTNF_z-score	LPS-mTNF_z-score	P3C-mTNF_z-score	R848-mTNF_z-score	LPS/hTNF-mTNF	P3C/hTNF-mTNF	R848/hTNF-mTNF	Median hTNF-mTNF
58	p38d	MAPK13	5603	Mapk13	26415	MAPK	-0.745	-0.555	-0.529	-1.139	-1.127	-0.810	0.394	0.573	0.281	0.394
59	TRIF	TICAM1	148022	Ticam1	106759	TRIF	-1.775	-0.538	0.236	-0.986	0.142	-0.385	-0.789	-0.680	0.621	-0.680
60	TRAM	TICAM2	353376	Ticam2	225471	TRIF	-1.371	-0.441	-0.375	-0.862	-1.151	-0.858	-0.509	0.710	0.482	0.482
61	RIP1	RIPK1	8737	Ripk1	19766	TRIF	-0.059	-0.704	-0.833	0.396	0.353	0.035	-0.455	-1.056	-0.868	-0.868
62	FADD	FADD	8772	Fadd	14082	TRIF	-0.631	-0.411	-0.795	-0.547	-0.664	-0.538	-0.084	0.253	-0.257	-0.084
63	Caspase 8	CASP8	841	Casp8	12370	TRIF	-0.298	-0.351	-0.583	0.250	0.356	-0.192	-0.548	-0.707	-0.391	-0.548
64	TBK1	TBK1	29110	Tbk1	56480	TRIF	0.076	-0.577	0.189	0.067	0.301	0.389	0.008	-0.878	-0.201	-0.201
65	IKKe	IKBKE	9641	Ikbke	56489	TRIF	-0.397	-0.238	-1.145	-1.367	-0.655	-1.029	0.970	0.417	-0.116	0.417
66	IRF3	IRF3	3661	Irf3	54131	TRIF	-1.254	-0.397	-1.228	-0.366	-0.036	-0.105	-0.888	-0.361	-1.123	-0.888
67	Duba	OTUD5	55593	Otud5	54644	TRIF	-1.021	-0.865	-0.566	-0.950	-0.943	-0.791	-0.071	0.077	0.225	0.077
68	TRADD	TRADD	8717	Tradd	71609	TRIF	-0.032	-0.706	-0.569	-0.086	0.076	0.300	0.054	-0.782	-0.869	-0.782
69	TANK	TANK	10010	Tank	21353	TRIF	-0.471	0.909	0.061	0.496	0.564	0.694	-0.966	0.345	-0.632	-0.632
70	SINTBAD	TBKBP1	9755	Tbkbp1	73174	TRIF	0.782	0.613	-0.136	0.281	0.141	0.512	0.501	0.473	-0.648	0.473
71	BTK	BTK	695	Btk	12229	PI3K	0.261	-0.537	-0.524	-0.605	-0.620	-0.952	0.866	0.084	0.428	0.428
72	NIK	MAP3K14	9020	Map3k14	53859	PI3K	0.377	0.069	-0.224	-0.435	-0.266	-0.049	0.813	0.335	-0.176	0.335
73	AKT1	AKT1	207	Akt1	11651	PI3K	-0.776	-0.137	-0.446	-0.548	-0.273	-0.098	-0.228	0.137	-0.348	-0.228
74	AKT2	AKT2	208	Akt2	11652	PI3K	-0.863	0.236	-0.433	-0.847	-1.062	-0.711	-0.017	1.298	0.278	0.278
75	AKT3	AKT3	10000	Akt3	23797	PI3K	0.166	0.131	-0.309	-0.494	-1.045	-0.660	0.661	1.176	0.350	0.661
76	PIK3CA	PIK3CA	5290	Pik3ca	18706	PI3K	0.097	-0.238	-0.302	0.127	0.394	-0.575	-0.030	-0.632	0.274	-0.030
77	PIK3CB	PIK3CB	5291	Pik3cb	74769	PI3K	-0.084	-0.094	-0.227	-1.148	-0.889	-0.579	1.064	0.794	0.352	0.794
78	PIK3CD	PIK3CD	5293	Pik3cd	18707	PI3K	-0.717	0.230	-0.711	-0.879	-0.374	-0.817	0.163	0.604	0.106	0.163
79	PIK3CG	PIK3CG	5294	Pik3cg	30955	PI3K	-0.451	-0.578	-0.451	-0.063	-0.186	-1.636	-0.388	-0.393	1.185	-0.388
80	PIK3R1	PIK3R1	5295	Pik3r1	18708	PI3K	0.253	-0.028	-0.106	-0.419	-0.171	-0.653	0.673	0.143	0.547	0.547
81	PIK3R2	PIK3R2	5296	Pik3r2	18709	PI3K	-0.537	0.143	0.116	-0.290	-0.603	-0.037	-0.247	0.747	0.154	0.154
82	PIK3R3	PIK3R3	8503	Pik3r3	18710	PI3K	-0.325	-0.226	-0.945	-0.822	-0.254	-0.211	0.497	0.028	-0.734	0.028
83	PIK3R5	PIK3R5	23533	Pik3r5	320207	PI3K	-0.250	-0.802	-0.045	-0.737	-0.581	-0.793	0.487	-0.221	0.749	0.487
84	RAC1	RAC1	5879	Rac1	19353	PI3K	-0.351	-0.133	-0.515	-0.036	0.003	0.047	-0.315	-0.136	-0.562	-0.315
85	IRF5	IRF5	3663	Irf5	27056	TF	-0.212	-0.810	-0.955	-0.360	-0.264	-0.402	0.148	-0.546	-0.553	-0.546
86	IRF7	IRF7	3665	Irf7	54123	TF	-0.640	-0.832	-1.301	-0.157	-0.332	-0.630	-0.484	-0.500	-0.672	-0.500
87	STAT1	STAT1	6772	Stat1	20846	TF	-0.413	0.245	-0.026	-0.128	-0.448	-0.373	-0.284	0.694	0.348	0.348
88	Fos	FOS	2353	Fos	14281	TF	0.659	-0.516	0.237	-0.553	-0.351	-0.292	1.212	-0.165	0.530	0.530
89	Jun	JUN	3725	Jun	16476	TF	-1.237	-0.784	-0.413	-1.017	-0.371	-0.480	-0.220	-0.413	0.067	-0.220
90	PYK2	PTK2B	2185	Ptk2b	19229	TF	-0.982	-0.752	-0.845	-0.490	0.062	-0.235	-0.492	-0.814	-0.609	-0.609
91	ETS1	ETS1	2113	Ets1	23871	TF	-0.480	-0.661	-0.370	-0.434	-0.526	0.222	-0.045	-0.135	-0.593	-0.135
92	ELK1	ELK1	2002	Elk1	13712	TF	-0.861	-1.304	-0.871	-0.858	-1.668	-1.775	-0.003	0.365	0.905	0.365
93	ELK4	ELK4	2005	Elk4	13714	TF	-0.582	-0.798	-0.536	-0.257	-0.354	-0.578	-0.325	-0.445	0.042	-0.325
94	SP1	SP1	6667	Sp1	20683	TF	0.243	-0.476	0.294	-1.276	-1.417	-1.326	1.519	0.941	1.620	1.519
95	EGR1	EGR1	1958	Egr1	13653	TF	-1.183	-1.706	-1.263	-1.210	-1.048	-1.138	0.027	-0.658	-0.125	-0.125
96	EGR2	EGR2	1959	Egr2	13654	TF	-1.204	-1.424	-0.872	-1.983	-1.415	-2.150	0.778	-0.009	1.278	0.778
97	ATF2	ATF2	1386	Atf2	11909	TF	-0.562	-0.227	-0.163	-0.645	-0.691	-1.192	0.083	0.465	1.029	0.465
98	ATF7	ATF7	11016	Atf7	223922	TF	-0.704	-1.070	-1.326	-1.159	-0.842	-0.982	0.455	-0.228	-0.344	-0.228
99	CBP	CREBBP	1387	Crebbp	12914	TF	0.437	0.573	-0.195	-1.109	-1.214	-1.111	1.546	1.787	0.916	1.546
100	p300	EP300	2033	Ep300	328572	TF	0.146	0.286	-0.608	-0.400	-0.388	-1.299	0.546	0.674	0.691	0.674
101	ISGF3G	IRF9	10379	Irf9	16391	TF	-0.986	-1.158	-1.227	0.583	0.994	0.756	-1.569	-2.152	-1.983	-1.983
102	ELF4	ELF4	2000	Elf4	56501	TF	-1.505	-1.334	-1.329	-0.591	-0.304	-1.103	-0.914	-1.029	-0.226	-0.914
103	IFNAR1	IFNAR1	3454	Ifnar1	15975	Cytokine	-1.054	-0.565	-0.539	-1.037	-1.057	-0.878	-0.017	0.492	0.339	0.339
104	IFNAR2	IFNAR2	3455	Ifnar2	15976	Cytokine	-1.179	-1.005	-0.801	-0.421	-0.292	-0.334	-0.758	-0.713	-0.467	-0.713
105	IFNB1	IFNB1	3456	Ifnb1	15977	Cytokine	-0.885	-1.358	-1.109	-0.923	-0.877	-0.835	0.038	-0.481	-0.274	-0.274
106	IL12A	IL12A	3592	Il12a	16159	Cytokine	-0.368	-0.297	-0.493	-1.014	-0.728	-0.828	0.646	0.431	0.335	0.431
107	IL12B	IL12B	3593	Il12b	16160	Cytokine	-0.799	-1.132	-0.702	-0.130	-0.514	-0.612	-0.670	-0.619	-0.090	-0.619
108	IL1B	IL1B	3553	Il1b	16176	Cytokine	-1.128	-0.485	-0.075	0.038	0.063	-0.158	-1.166	-0.547	0.083	-0.547
109	IL6	IL6	3569	Il6	16193	Cytokine	-0.309	-0.619	-0.659	0.211	0.026	0.056	-0.520	-0.645	-0.715	-0.645
110	TNF	TNF	7124	Tnf	21926	Cytokine	-0.551	-1.171	-0.919	-0.389	-1.033	-0.229	-0.162	-0.138	-0.690	-0.162
111	CCL3	CCL3	6348	Ccl3	20302	Cytokine	-0.634	-0.261	-0.267	-0.673	-0.565	-0.324	0.039	0.305	0.057	0.057
112	CXCL11	CXCL11	6373	Cxcl11	56066	Cytokine	-0.425	-0.517	-0.452	-0.284	-0.515	-0.653	-0.141	-0.003	0.201	-0.003
113	CXCL9	CXCL9	4283	Cxcl9	17329	Cytokine	-0.581	-0.858	-0.957	0.116	-0.059	-0.093	-0.697	-0.798	-0.864	-0.798
114	RP105	CD180	4064	Cd180	17079	Regulator	-0.336	-0.538	-0.732	-0.485	-0.640	-0.460	0.148	0.103	-0.272	0.103

TABLE S4																
Gene#	Name	Human Gene Symbol	Human Gene ID	Mouse Gene Symbol	Mouse Gene ID	Module	LPS-hTNF_z-score	P3C-hTNF_z-score	R848-hTNF_z-score	LPS-mTNF_z-score	P3C-mTNF_z-score	R848-mTNF_z-score	LPS/hTNF-mTNF	P3C/hTNF-mTNF	R848/hTNF-mTNF	Median hTNF-mTNF
115	MD1	LY86	9450	Ly86	17084	Regulator	-0.605	-0.579	-1.131	0.034	0.055	-0.115	-0.639	-0.634	-1.016	-0.639
116	TIR8	SIGIRR	59307	Sigirr	24058	Regulator	-0.346	-0.782	-0.133	-0.547	-0.126	-0.462	0.201	-0.657	0.328	0.201
117	ST2	IL1RL1	9173	Il1rl1	17082	Regulator	-0.122	-0.442	-0.023	-0.126	-0.755	-0.647	0.004	0.313	0.624	0.313
118	IRAK3	IRAK3	11213	Irak3	73914	Regulator	-0.135	-0.402	-0.087	-0.645	-0.395	-0.206	0.509	-0.007	0.118	0.118
119	SHP1	PTPN6	5777	Ptpn6	15170	Regulator	-0.900	-0.443	-0.653	-0.466	-0.671	-0.507	-0.433	0.228	-0.146	-0.146
120	Cyld	CYLD	1540	Cyld	74256	Regulator	-1.987	-0.141	-0.662	1.175	0.058	0.035	-3.162	-0.199	-0.697	-0.697
121	A20	TNFAIP3	7128	Tnfaip3	21929	Regulator	-0.825	-0.624	0.844	0.726	0.745	0.271	-1.552	-1.370	0.574	-1.370
122	DUSP2	DUSP2	1844	Dusp2	13537	Regulator	-0.236	0.143	-0.707	0.147	-0.368	-0.098	-0.383	0.511	-0.609	-0.383
123	AIP1	DAB2IP	153090	Dab2ip	69601	Regulator	-0.747	-0.984	-0.941	-0.261	-0.380	-0.020	-0.486	-0.603	-0.921	-0.603
124	Tollip	TOLLIP	54472	Tollip	54473	Regulator	-0.691	-0.767	-0.830	-0.556	-0.247	-0.498	-0.134	-0.521	-0.333	-0.333
125	MKP1	DUSP1	1843	Dusp1	19252	Regulator	0.574	0.098	-0.002	0.142	-0.338	0.253	0.432	0.436	-0.255	0.432
126	RIP3	RIPK3	11035	Ripk3	56532	Regulator	-0.118	-0.496	-0.191	-0.018	0.074	-0.138	-0.100	-0.569	-0.053	-0.100