

Sexton_Supp. Table 1**Nucleosome Distribution Microarray Gene Annotations**

Gene Name	Accession #	Chr. #	TSS	Start	Stop
SERPINC1	NM_000488	chr1	173886516	173885516	173887516
IL10	NM_000572	chr1	206945839	206944839	206946839
ADORA1	NM_000674	chr1	203096836	203095836	203097836
TNFRSF1B	NM_001066	chr1	12227060	12226060	12228060
F11R	NM_144503	chr1	160,965,002	160964002	160966002
CD53	NM_000560	chr1	111415722	111414722	111416722
C8A	NM_000562	chr1	57320443	57319443	57321443
IL6R	NM_000565	chr1	154377669	154376669	154378669
CRP	NM_000567	chr1	159684379	159683379	159685379
CR1	NM_000573	chr1	207669473	207668473	207670473
CD55	NM_000574	chr1	207494817	207493817	207495817
FASLG	NM_000639	chr1	172628185	172627185	172629185
SELL	NM_000655	chr1	169680843	169679843	169681843
CD247	NM_000734	chr1	167487847	167486847	167488847
CSF1	NM_000757	chr1	110453233	110452233	110454233
CSF3R	NM_000760	chr1	36948509	36947509	36949509
PTAFR	NM_000952	chr1	28503455	28502455	28504455
PTGS2	NM_000963	chr1	186649559	186648559	186650559
TNFRSF8	NM_001243	chr1	12123434	12122434	12124434
IL12RB2	NM_001559	chr1	67773047	67772047	67774047
TNFRSF9	NM_001561	chr1	8000887	7999887	8001887
PARP1	NM_001618	chr1	226595801	226594801	226596801
APCS	NM_001639	chr1	159557616	159556616	159558616
APOA2	NM_001643	chr1	161193418	161192418	161194418
CD1B	NM_001764	chr1	158301321	158300321	158302321
CD1C	NM_001765	chr1	158259563	158258563	158260563
CD1D	NM_001766	chr1	158149737	158148737	158150737
CD58	NM_001779	chr1	117113715	117112715	117114715
CR2	NM_001877	chr1	207627645	207626645	207628645
GADD45A	NM_001924	chr1	68150883	68149883	68151883
F3	NM_001993	chr1	95007371	95006371	95008371
HSPA6	NM_002155	chr1	161494036	161493036	161495036
JUN	NM_002228	chr1	59249785	59248785	59250785
PRDX1	NM_002574	chr1	45987609	45986609	45988609
PIK3C2B	NM_002646	chr1	204459474	204458474	204460474
XCL1	NM_002995	chr1	168545856	168544856	168546856
TLR5	NM_003268	chr1	223316624	223315624	223317624
TNFSF4	NM_003326	chr1	173176471	173175471	173177471
TNFRSF4	NM_003327	chr1	1149512	1148512	1150512
CHIT1	NM_003465	chr1	203198860	203197860	203199860
TNFRSF25	NM_003790	chr1	6526255	6525255	6527255
TNFRSF14	NM_003820	chr1	2487805	2486805	2488805

TNFRSF18	NM_004195	chr1	1142089	1141089	1143089
DFFA	NM_004401	chr1	10532613	10531613	10533613
TNFSF18	NM_005092	chr1	173020103	173019103	173021103
LMNA	NM_005572	chr1	156084461	156083461	156085461
S100A12	NM_005621	chr1	153348075	153347075	153349075
IL20	NM_018724	chr1	207039154	207038154	207040154
PGLYRP4	NM_020393	chr1	153321022	153320022	153322022
PGLYRP3	NM_052891	chr1	153283194	153282194	153284194
NLRP3	NM_183395	chr1	247581351	247580351	247582351
IL2RA	NM_000417	chr10	6104272	6103272	6105272
FAS	NM_000043	chr10	90750288	90749288	90751288
MBL2	NM_000242	chr10	54531460	54530460	54532460
CXCL12	NM_000609	chr10	44880542	44879542	44881542
ALOX5	NM_000698	chr10	45869629	45868629	45870629
CHUK	NM_001278	chr10	101989344	101988344	101990344
IL15RA	NM_002189	chr10	6019537	6018537	6020537
NFKB2	NM_002502	chr10	104155432	104154432	104156432
MAPK8	NM_002750	chr10	49609687	49608687	49610687
SFTPD	NM_003019	chr10	81708861	81707861	81709861
BMPR1A	NM_004329	chr10	88516396	88515396	88517396
DMBT1	NM_004406	chr10	124320181	124319181	124321181
BLNK	NM_013314	chr10	98031333	98030333	98032333
BTRC	NM_033637	chr10	103113825	103112825	103114825
F2	NM_000506	chr11	46740743	46739743	46741743
CD44	NM_000610	chr11	35160417	35159417	35161417
TIRAP	NM_001039661	chr11	126152982	126151982	126153982
CASP4	NM_001225	chr11	104839325	104838325	104840325
IL10RA	NM_001558	chr11	117857106	117856106	117858106
IL18	NM_001562	chr11	112034840	112033840	112035840
IRF7	NM_001572	chr11	615999	614999	616999
CXCR5	NM_001716	chr11	118754541	118753541	118755541
PAK1	NM_002576	chr11	77185108	77184108	77186108
PRG2	NM_002728	chr11	57158130	57157130	57159130
CHST1	NM_003654	chr11	45687172	45686172	45688172
MADD	NM_003682	chr11	47291199	47290199	47292199
FADD	NM_003824	chr11	70049269	70048269	70050269
BANF1	NM_003860	chr11	65769550	65768550	65770550
BAD	NM_004322	chr11	64052176	64051176	64053176
TRAF6	NM_004620	chr11	36531822	36530822	36532822
GPR44	NM_004778	chr11	60623444	60622444	60624444
HRAS	NM_005343	chr11	535550	534550	536550
NFRKB	NM_006165	chr11	129762904	129761904	129763904
TSG101	NM_006292	chr11	18548489	18547489	18549489
HTATIP2	NM_006410	chr11	20385231	20384231	20386231
TOLLIP	NM_019009	chr11	1330839	1329839	1331839
CARD18	NM_021571	chr11	105009806	105008806	105010806
SIGIRR	NM_021805	chr11	417397	416397	418397
RELA	NM_021975	chr11	65430443	65429443	65431443
RELT	NM_032871	chr11	73087713	73086713	73088713
TRIM5	NM_033093	chr11	5706293	5705293	5707293
CASP1	NM_033292	chr11	104972158	104971158	104973158

TNFRSF1A	NM_001065	chr12	6451261	6450261	6452261
LYZ	NM_000239	chr12	69742134	69741134	69743134
CD4	NM_000616	chr12	6898651	6897651	6899651
IFNG	NM_000619	chr12	68553521	68552521	68554521
ARHGDIB	NM_001175	chr12	15114562	15113562	15115562
CCNT1	NM_001240	chr12	49110781	49109781	49111781
CD27	NM_001242	chr12	6554051	6553051	6555051
C1R	NM_001733	chr12	7245043	7244043	7246043
CD69	NM_001781	chr12	9913497	9912497	9914497
GAPDH	NM_002046	chr12	6643657	6642657	6644657
KLRD1	NM_002262	chr12	10460417	10459417	10461417
LALBA	NM_002289	chr12	48963829	48962829	48964829
LTBR	NM_002342	chr12	6493357	6492357	6494357
UBE2N	NM_003348	chr12	93836026	93835026	93837026
CRADD	NM_003805	chr12	94071151	94070151	94072151
C3AR1	NM_004054	chr12	8218955	8217955	8219955
ACVR1B	NM_004302	chr12	52345486	52344486	52346486
TFCP2	NM_005653	chr12	51566664	51565664	51567664
IRAK3	NM_007199	chr12	66582978	66581978	66583978
CBX5	NM_012117	chr12	54673915	54672915	54674915
TBK1	NM_013254	chr12	64845937	64844937	64846937
CLEC4E	NM_014358	chr12	8693558	8692558	8694558
IRAK4	NM_016123	chr12	44152747	44151747	44153747
IL22	NM_020525	chr12	68647281	68646281	68648281
AMHR2	NM_020547	chr12	53817639	53816639	53818639
CLEC7A	NM_022570	chr12	10282868	10281868	10283868
DCD	NM_053283	chr12	55042149	55041149	55043149
RB1	NM_000321	chr13	48877883	48876883	48878883
HMGB1	NM_002128	chr13	31040081	31039081	31041081
TNFSF11	NM_003701	chr13	43148291	43147291	43149291
TNFSF13B	NM_006573	chr13	108921977	108920977	108922977
TNFRSF19	NM_018647	chr13	24153639	24152639	24154639
SERPINA1	NM_000295	chr14	94855153	94854153	94856153
BDKRB1	NM_000710	chr14	96722559	96721559	96723559
RNASE3	NM_002935	chr14	21359562	21358562	21360562
TRAF3	NM_003300	chr14	103243816	103242816	103244816
YY1	NM_003403	chr14	100705102	100704102	100706102
FOS	NM_005252	chr14	75745481	75744481	75746481
BATF	NM_006399	chr14	75988784	75987784	75989784
NFKBIA	NM_020529	chr14	35873960	35872960	35874960
PELI2	NM_021255	chr14	56585093	56584093	56586093
BCL11B	NM_022898	chr14	99737822	99736822	99738822
RNASE7	NM_032572	chr14	21510385	21509385	21511385
APEX1	NM_080649	chr14	20923290	20922290	20924290
LTB4R	NM_181657	chr14	24782313	24781313	24783313
CD276	NM_025240	chr15	73976622	73975622	73977622
B2M	NM_004048	chr15	45003685	45002685	45004685
IL16	NM_004513	chr15	81587467	81586467	81588467
CX3CL1	NM_002996	chr16	57406414	57405414	57407414
CIITA	NM_000246	chr16	10971055	10970055	10972055
ITGAX	NM_000887	chr16	31366509	31365509	31367509

TNFRSF17	NM_001192	chr16	12058964	12057964	12059964
CTF1	NM_001330	chr16	30907928	30906928	30908928
CCL17	NM_002987	chr16	57438679	57437679	57439679
CCL22	NM_002990	chr16	57392718	57391718	57393718
TRADD	NM_003789	chr16	67193812	67192812	67194812
CREBBP	NM_004380	chr16	3930121	3929121	3931121
RBL2	NM_005611	chr16	53468351	53467351	53469351
VPS4A	NM_013245	chr16	69345287	69344287	69346287
IL17C	NM_013278	chr16	88705001	88704001	88706001
MAPK8IP3	NM_015133	chr16	1756221	1755221	1757221
TNFRSF12A	NM_016639	chr16	3070313	3069313	3071313
CMTM2	NM_144673	chr16	66613351	66612351	66614351
CMTM1	NM_181269	chr16	66600294	66599294	66601294
CKLF	NM_181641	chr16	66586472	66585472	66587472
NOS2	NM_000625	chr17	26127555	26126555	26128555
CSF3	NM_000759	chr17	38171688	38170688	38172688
CCL4L1	NM_001001435	chr17	34538468	34537468	34539468
CCR7	NM_001838	chr17	38721724	38720724	38722724
NGFR	NM_002507	chr17	47572655	47571655	47573655
MAP2K3	NM_002756	chr17	21194781	21193781	21195781
MAP2K6	NM_002758	chr17	67410838	67409838	67411838
CCL1	NM_002981	chr17	32690252	32689252	32691252
CCL2	NM_002982	chr17	32582296	32581296	32583296
CCL3	NM_002983	chr17	34417506	34416506	34418506
CCL4	NM_002984	chr17	34431220	34430220	34432220
CCL5	NM_002985	chr17	34207377	34206377	34208377
CCL11	NM_002986	chr17	32612687	32611687	32613687
CCL18	NM_002988	chr17	34391643	34390643	34392643
MAP2K4	NM_003010	chr17	11924135	11923135	11925135
STAT3	NM_003150	chr17	40540513	40539513	40541513
TNFSF13	NM_003808	chr17	7461609	7460609	7462609
TNFSF12	NM_003809	chr17	7452375	7451375	7453375
MAP3K14	NM_003954	chr17	43394414	43393414	43395414
ERBB2	NM_004448	chr17	37856254	37855254	37857254
CCL16	NM_004590	chr17	34308523	34307523	34309523
CCL23	NM_005064	chr17	34345005	34344005	34346005
CCL13	NM_005408	chr17	32683471	32682471	32684471
CCL8	NM_005623	chr17	32646066	32645066	32647066
CCL7	NM_006273	chr17	32597240	32596240	32598240
TNFRSF13B	NM_012452	chr17	16875402	16874402	16876402
SARM1	NM_015077	chr17	26698987	26697987	26699987
CCR10	NM_016602	chr17	40833845	40832845	40834845
CCL3L1	NM_021006	chr17	34625730	34624730	34626730
CXCL16	NM_022059	chr17	4643223	4642223	4644223
CCL15	NM_032965	chr17	34329100	34328100	34330100
BCL2	NM_000633	chr18	60986613	60985613	60987613
TNFRSF11A	NM_003839	chr18	59992548	59991548	59993548
PSMG2	NM_020232	chr18	12703064	12702064	12704064
COLEC12	NM_130386	chr18	500729	499729	501729
NFATC1	NM_172390	chr18	77155772	77154772	77156772
C3	NM_000064	chr19	6720662	6719662	6721662

C3	NM_000064	chr19	6720662	6719662	6721662
EPOR	NM_000121	chr19	11495019	11494019	11496019
AMH	NM_000479	chr19	2249113	2248113	2250113
IL11	NM_000641	chr19	55881814	55880814	55882814
TGFB1	NM_000660	chr19	41859816	41858816	41860816
CD70	NM_001252	chr19	6591163	6590163	6592163
FLT3LG	NM_001459	chr19	49977486	49976486	49978486
IRF3	NM_001571	chr19	50169132	50168132	50170132
AZU1	NM_001700	chr19	827831	826831	828831
CD22	NM_001771	chr19	35820079	35819079	35821079
CD97	NM_001784	chr19	14519533	14518533	14520533
CLC	NM_001828	chr19	40228668	40227668	40229668
ELA2	NM_001972	chr19	852291	851291	853291
FCAR	NM_002000	chr19	55385549	55384549	55386549
NFKBIB	NM_002503	chr19	39390615	39389615	39391615
TNFSF14	NM_003807	chr19	6670599	6669599	6671599
TNFSF9	NM_003811	chr19	6531010	6530010	6532010
BAX	NM_004324	chr19	49458117	49457117	49459117
CRLF1	NM_004750	chr19	18717660	18716660	18718660
PGLYRP1	NM_005091	chr19	46526323	46525323	46527323
IL12RB1	NM_005535	chr19	18197697	18196697	18198697
CCL25	NM_005624	chr19	8117934	8116934	8118934
EBI3	NM_005755	chr19	4229540	4228540	4230540
PRDX2	NM_005809	chr19	12912694	12911694	12913694
RELB	NM_006509	chr19	45504712	45503712	45505712
RPL13A	NM_012423	chr19	49990865	49989865	49991865
KIR3DL1	NM_013289	chr19	55327893	55326893	55328893
ZBTB7A	NM_015898	chr19	4066816	4065816	4067816
ECSIT	NM_016581	chr19	11639987	11638987	11640987
CD209	NM_021155	chr19	7812464	7811464	7813464
HAMP	NM_021175	chr19	35773410	35772410	35774410
LMNB2	NM_032737	chr19	2456958	2455958	2457958
PGLYRP2	NM_052890	chr19	15590315	15589315	15591315
TICAM1	NM_182919	chr19	4831737	4830737	4832737
PROC	NM_000312	chr2	128176017	128175017	128177017
IL1A	NM_000575	chr2	113542971	113541971	113543971
IL1B	NM_000576	chr2	113594356	113593356	113595356
IL1RN	NM_000577	chr2	113875470	113874470	113876470
SLC11A1	NM_000578	chr2	219246752	219245752	219247752
IL8RA	NM_000634	chr2	219031716	219030716	219032716
IL1R1	NM_000877	chr2	102770402	102769402	102771402
ASB1	NM_001040445	chr2	239335626	239334626	239336626
ACVR1	NM_001105	chr2	158731623	158730623	158732623
BMPR2	NM_001204	chr2	203241050	203240050	203242050
CASP8	NM_001228	chr2	202098166	202097166	202099166
IL8RB	NM_001557	chr2	218990746	218989746	218991746
ACVR2A	NM_001616	chr2	148602570	148601570	148603570
FN1	NM_002026	chr2	216300791	216299791	216301791
GPC1	NM_002081	chr2	241375115	241374115	241376115
HSPD1	NM_002156	chr2	198364640	198363640	198365640
MAL	NM_002371	chr2	95691479	95690479	95692479

EIF2AK2	NM_002759	chr2	37384190	37383190	37385190
REL	NM_002908	chr2	61108752	61107752	61109752
RPS27A	NM_002954	chr2	55459635	55458635	55460635
RPS27A	NM_002954	chr2	55459635	55458635	55460635
XPO1	NM_003400	chr2	61765418	61764418	61766418
CXCR4	NM_003467	chr2	136875725	136874725	136876725
PRKRA	NM_003690	chr2	179315958	179314958	179316958
IL1RL2	NM_003854	chr2	102803433	102802433	102804433
IL18R1	NM_003855	chr2	102979097	102978097	102980097
CAD	NM_004341	chr2	27440258	27439258	27441258
AGFG1	NM_004504	chr2	228336888	228335888	228337888
CCL20	NM_004591	chr2	228678558	228677558	228679558
IL1R2	NM_004633	chr2	102608306	102607306	102609306
MAP4K4	NM_004834	chr2	102314488	102313488	102315488
GLI2	NM_005270	chr2	121554867	121553867	121555867
CD28	NM_006139	chr2	204571198	204570198	204572198
GNLY	NM_006433	chr2	85921414	85920414	85922414
STAT1	NM_007315	chr2	191878976	191877976	191879976
IL1F5	NM_012275	chr2	113816685	113815685	113817685
IL1F6	NM_014440	chr2	113763449	113762449	113764449
IL1F9	NM_019618	chr2	113735606	113734606	113736606
CYP26B1	NM_019885	chr2	72374963	72373963	72375963
PELI1	NM_020651	chr2	64371605	64370605	64372605
NLRC4	NM_021209	chr2	32490801	32489801	32491801
IL1F10	NM_173161	chr2	113825547	113824547	113826547
IL1F8	NM_173178	chr2	113810440	113809440	113811440
IL1F7	NM_173205	chr2	113672770	113671770	113673770
BMP2	NM_001200	chr20	6748745	6747745	6749745
CD40	NM_001250	chr20	44746906	44745906	44747906
BMP7	NM_001719	chr20	55841707	55840707	55842707
BPI	NM_001725	chr20	36932552	36931552	36933552
HCK	NM_002110	chr20	30640057	30639057	30641057
SLPI	NM_003064	chr20	43883206	43882206	43884206
TNFRSF6B	NM_003823	chr20	62328021	62327021	62329021
LBP	NM_004139	chr20	36974885	36973885	36975885
CEBPB	NM_005194	chr20	48807376	48806376	48808376
PLUNC	NM_016583	chr20	31823802	31822802	31824802
UBE2V1	NM_021988	chr20	48732494	48731494	48733494
DEFB118	NM_054112	chr20	29956428	29955428	29957428
DEFB127	NM_139074	chr20	138186	137186	139186
ATRN	NM_139321	chr20	3451665	3450665	3452665
IL10RB	NM_000628	chr21	34638672	34637672	34639672
MX2	NM_002463	chr21	42733950	42732950	42734950
IFNGR2	NM_005534	chr21	34775202	34774202	34776202
FAM3B	NM_058186	chr21	42688661	42687661	42689661
ADORA2A	NM_000675	chr22	24823530	24822530	24824530
APOL3	NM_014349	chr22	3653637	3652637	3654637
CSF2RB	NM_000395	chr22	37309675	37308675	37310675
NCF4	NM_000631	chr22	37257030	37256030	37258030
IL2RB	NM_000878	chr22	37545962	37544962	37546962
EP300	NM_001429	chr22	41488614	41487614	41489614

TYMP	NM_001953	chr22	50968514	50967514	50969514
HMOX1	NM_002133	chr22	35777087	35776087	35778087
LIF	NM_002309	chr22	30642796	30641796	30643796
MIF	NM_002415	chr22	24236565	24235565	24237565
MAPK11	NM_002751	chr22	50708779	50707779	50709779
MAPK12	NM_002969	chr22	50700089	50699089	50701089
SMARCB1	NM_003073	chr22	24129150	24128150	24130150
PPARA	NM_005036	chr22	46546499	46545499	46547499
MAP3K7IP1	NM_006116	chr22	39795759	39794759	39796759
IL17RA	NM_014339	chr22	17565849	17564849	17566849
APOBEC3G	NM_021822	chr22	39473025	39472025	39474025
APOL2	NM_030882	chr22	36635689	36634689	36636689
TNFRSF13C	NM_052945	chr22	42322821	42321821	42323821
APOBEC3F	NM_145298	chr22	39436673	39435673	39437673
CD47	NM_001777	chr3	107809935	107808935	107810935
TLR9	NM_017442	chr3	52260179	52259179	52261179
IL5RA	NM_000564	chr3	3152058	3151058	3153058
CCR5	NM_000579	chr3	46411633	46410633	46412633
CCR2	NM_000648	chr3	46395235	46394235	46396235
IL12A	NM_000882	chr3	159706629	159705629	159707629
ACVR2B	NM_001106	chr3	38495790	38494790	38496790
CCR1	NM_001295	chr3	46249832	46248832	46250832
CX3CR1	NM_001337	chr3	39321527	39320527	39322527
IRAK2	NM_001570	chr3	10206563	10205563	10207563
AHSG	NM_001622	chr3	186330850	186329850	186331850
BCL6	NM_001706	chr3	187463475	187462475	187464475
CCR3	NM_001837	chr3	46283872	46282872	46284872
IL1RAP	NM_002182	chr3	190231891	190230891	190232891
LTF	NM_002343	chr3	46506395	46505395	46507395
MYD88	NM_002468	chr3	38179969	38178969	38180969
PAK2	NM_002577	chr3	196466728	196465728	196467728
NR2C2	NM_003298	chr3	14989236	14988236	14990236
TNFSF10	NM_003810	chr3	172241269	172240269	172242269
CCRL2	NM_003965	chr3	46448721	46447721	46449721
CAMP	NM_004345	chr3	48264862	48263862	48265862
CD80	NM_005191	chr3	119243142	119242142	119244142
CCR8	NM_005201	chr3	39371197	39370197	39372197
XCR1	NM_005283	chr3	46068979	46067979	46069979
CCR4	NM_005508	chr3	32993066	32992066	32994066
CXCR6	NM_006564	chr3	45984973	45983973	45985973
CCR9	NM_006641	chr3	45928051	45927051	45929051
CD86	NM_006889	chr3	121796750	121795750	121797750
STAB1	NM_015136	chr3	52529356	52528356	52530356
CCRL1	NM_016557	chr3	132316094	132315094	132317094
FGF12	NM_021032	chr3	192126838	192125838	192127838
IL2	NM_000586	chr4	123377650	123376650	123378650
TLR2	NM_003264	chr4	154605441	154604441	154606441
TLR3	NM_003265	chr4	186990309	186989309	186991309
SPP1	NM_000582	chr4	88896802	88895802	88897802
IL8	NM_000584	chr4	74606275	74605275	74607275
IL15	NM_000585	chr4	142557754	142556754	142558754

BMP3	NM_001201	chr4	81952119	81951119	81953119
BMPR1B	NM_001203	chr4	95679128	95678128	95680128
CXCL1	NM_001511	chr4	74735109	74734109	74736109
CXCL10	NM_001565	chr4	76942273	76941273	76943273
AREG	NM_001657	chr4	75480629	75479629	75481629
CXCL2	NM_002089	chr4	74964997	74963997	74965997
CXCL3	NM_002090	chr4	74904490	74903490	74905490
IRF2	NM_002199	chr4	185395726	185394726	185396726
CXCL9	NM_002416	chr4	76928641	76927641	76929641
PF4	NM_002619	chr4	74847715	74846715	74848715
PPBP	NM_002704	chr4	74853900	74852900	74854900
MAPK10	NM_002753	chr4	87374283	87373283	87375283
ABCE1	NM_002940	chr4	146019156	146018156	146020156
CXCL6	NM_002993	chr4	74702273	74701273	74703273
CXCL5	NM_002994	chr4	74864416	74863416	74865416
TLR1	NM_003263	chr4	38806412	38805412	38807412
NFKB1	NM_003998	chr4	103422486	103421486	103423486
TMPRSS11D	NM_004262	chr4	68749716	68748716	68750716
CASP3	NM_004346	chr4	185570629	185569629	185571629
SCYE1	NM_004757	chr4	107236853	107235853	107237853
CXCL11	NM_005409	chr4	76954842	76953842	76955842
TLR6	NM_006068	chr4	38831160	38830160	38832160
CXCL13	NM_006419	chr4	78432907	78431907	78433907
IL21	NM_021803	chr4	123542211	123541211	123543211
TLR10	NM_030956	chr4	38784589	38783589	38785589
IL6ST	NM_002184	chr5	55290763	55289763	55291763
IL3	NM_000588	chr5	131396347	131395347	131397347
IL4	NM_000589	chr5	132009373	132008373	132010373
IL9	NM_000590	chr5	135231516	135230516	135232516
CD14	NM_000591	chr5	140013010	140012010	140014010
CSF2	NM_000758	chr5	131409485	131408485	131410485
IL5	NM_000879	chr5	131879214	131878214	131880214
CAST	NM_001042440	chr5	95997941	95996941	95998941
CDK7	NM_001799	chr5	68530622	68529622	68531622
HSPA4	NM_002154	chr5	132387662	132386662	132388662
IL12B	NM_002187	chr5	158757481	158756481	158758481
IL13	NM_002188	chr5	131993865	131992865	131994865
IRF1	NM_002198	chr5	131826465	131825465	131827465
MAPK9	NM_002752	chr5	179719071	179718071	179720071
CD74	NM_004355	chr5	149792323	149791323	149793323
DUSP1	NM_004417	chr5	172198203	172197203	172199203
FGF10	NM_004465	chr5	44388784	44387784	44389784
CXCL14	NM_004887	chr5	134914969	134913969	134915969
DOCK2	NM_004946	chr5	169064251	169063251	169065251
CSF1R	NM_005211	chr5	149492935	149491935	149493935
LMNB1	NM_005573	chr5	126112833	126111833	126113833
CD180	NM_005582	chr5	66492617	66491617	66493617
MAP3K1	NM_005921	chr5	56110900	56109900	56111900
ERAP1	NM_016442	chr5	96143892	96142892	96144892
ERBB2IP	NM_018695	chr5	65222384	65221384	65223384
TICAM2	NM_021649	chr5	114938109	114937109	114939109

LEAP2	NM_052971	chr5	132209358	132208358	132210358
CCL28	NM_148672	chr5	43412488	43411488	43413488
HMGA1	NM_145904	chr6	34,207,070	34206070	34208070
C2	NM_000063	chr6	31895266	31894266	31896266
CDKN1A	NM_000389	chr6	36646459	36645459	36647459
IFNGR1	NM_000416	chr6	137540567	137539567	137541567
TNF	NM_000594	chr6	31543350	31542350	31544350
LTA	NM_000595	chr6	31540093	31539093	31541093
ABCF1	NM_001090	chr6	30539170	30538170	30540170
MAPK14	NM_001315	chr6	35995454	35994454	35996454
GABBR1	NM_001470	chr6	29600962	29599962	29601962
AIF1	NM_001623	chr6	31583033	31582033	31584033
CFB	NM_001710	chr6	31913721	31912721	31914721
HLA-A	NM_002116	chr6	29910331	29909331	29911331
HLA-C	NM_002117	chr6	31239855	31238855	31240855
IL17A	NM_002190	chr6	52051185	52050185	52052185
LTB	NM_002341	chr6	31548337	31547337	31549337
MAPK13	NM_002754	chr6	36098262	36097262	36099262
MAP3K7	NM_003188	chr6	91296907	91295907	91297907
LY86	NM_004271	chr6	6588934	6587934	6589934
CCR6	NM_004367	chr6	167525295	167524295	167526295
NFKBIE	NM_004556	chr6	44233525	44232525	44234525
NFKBIL1	NM_005007	chr6	31515353	31514353	31516353
HSPA1A	NM_005345	chr6	31783291	31782291	31784291
HLA-E	NM_005516	chr6	30457271	30456271	30458271
MAP3K5	NM_005923	chr6	137113656	137112656	137114656
CRISP3	NM_006061	chr6	49712056	49711056	49713056
TNFAIP3	NM_006290	chr6	138188581	138187581	138189581
TNFRSF21	NM_014452	chr6	47277680	47276680	47278680
MAP3K7IP2	NM_015093	chr6	149639063	149638063	149640063
TREM1	NM_018643	chr6	41254457	41253457	41255457
C4A	NM_007293	chr6	31949834	31948834	31950834
IL6	NM_000600	chr7	22766766	22765766	22767766
SERPINE1	NM_000602	chr7	100770379	100769379	100771379
EPO	NM_000799	chr7	100318423	100317423	100319423
CCL24	NM_002991	chr7	75443033	75442033	75444033
CCL26	NM_006072	chr7	75419064	75418064	75420064
COPS6	NM_006833	chr7	99686583	99685583	99687583
PPIA	NM_021130	chr7	44836241	44835241	44837241
CASP2	NM_032982	chr7	142985402	142984402	142986402
IL7	NM_000880	chr8	79717758	79716758	79718758
IKBKB	NM_001556	chr8	42128829	42127829	42129829
DEFA4	NM_001925	chr8	6795786	6794786	6796786
DEFA6	NM_001926	chr8	6783598	6782598	6784598
EPHX2	NM_001979	chr8	27348645	27347645	27349645
TNFRSF11B	NM_002546	chr8	119964383	119963383	119965383
RIPK2	NM_003821	chr8	90769975	90768975	90770975
TNFRSF10D	NM_003840	chr8	23021540	23020540	23022540
TNFRSF10C	NM_003841	chr8	22960434	22959434	22961434
TNFRSF10B	NM_003842	chr8	22926700	22925700	22927700
TNFRSF10A	NM_003844	chr8	23082680	23081680	23083680

PTK2B	NM_004103	chr8	27168999	27167999	27169999
BAG4	NM_004874	chr8	38034106	38033106	38035106
DEFB4	NM_004942	chr8	7752199	7751199	7753199
DEFB1	NM_005218	chr8	6735529	6734529	6736529
BMP1	NM_006129	chr8	22022675	22021675	22023675
PRKDC	NM_006904	chr8	48872743	48871743	48873743
NFKBIL2	NM_013432	chr8	145669812	145668812	145670812
LY96	NM_015364	chr8	74903587	74902587	74904587
DEFA5	NM_021010	chr8	6914259	6913259	6915259
TLR4	NM_138554	chr9	120466460	120465460	120467460
IFNA2	NM_000605	chr9	21385396	21384396	21386396
ANXA1	NM_000700	chr9	75766781	75765781	75767781
TNFSF8	NM_001244	chr9	117692770	117691770	117693770
CDK9	NM_001261	chr9	130548305	130547305	130549305
C5	NM_001735	chr9	123812554	123811554	123813554
CNTFR	NM_001842	chr9	34589722	34588722	34590722
IFNB1	NM_002176	chr9	21077943	21076943	21078943
CCL21	NM_002989	chr9	34710147	34709147	34711147
SPTAN1	NM_003127	chr9	131314866	131313866	131315866
IKBKAP	NM_003640	chr9	111696608	111695608	111697608
IL11RA	NM_004512	chr9	34653932	34652932	34654932
PTGES	NM_004878	chr9	132515344	132514344	132516344
TNFSF15	NM_005118	chr9	117568408	117567408	117569408
S1PR3	NM_005226	chr9	91606362	91605362	91607362
CER1	NM_005454	chr9	14722715	14721715	14723715
NFIB	NM_005596	chr9	14313945	14312945	14314945
TRAF1	NM_005658	chr9	123689173	123688173	123690173
CCL19	NM_006274	chr9	34691274	34690274	34692274
CCL27	NM_006664	chr9	34662689	34661689	34663689
IFNK	NM_020124	chr9	27526494	27525494	27527494
TRAF2	NM_021138	chr9	139780965	139779965	139781965
IFNA1	NM_024013	chr9	21440440	21439440	21441440
TLR7	NM_016562	chrX	12885202	12884202	12886202
BTK	NM_000061	chrX	100641212	100640212	100642212
CD40LG	NM_000074	chrX	135730336	135729336	135731336
F8	NM_000132	chrX	154250998	154249998	154251998
HPRT1	NM_000194	chrX	133594175	133593175	133595175
IL2RG	NM_000206	chrX	70331403	70330403	70332403
CYBB	NM_000397	chrX	37639270	37638270	37640270
IL13RA2	NM_000640	chrX	114252207	114251207	114253207
EDA	NM_001399	chrX	68835911	68834911	68836911
CXCR3	NM_001504	chrX	70838367	70837367	70839367
IL13RA1	NM_001560	chrX	117861559	117860559	117862559
IRAK1	NM_001569	chrX	153285342	153284342	153286342
CFP	NM_002621	chrX	47489704	47488704	47490704
IKBKG	NM_003639	chrX	153776062	153775062	153777062
FIGF	NM_004469	chrX	15402577	15401577	15403577
ELK1	NM_005229	chrX	47510003	47509003	47511003
CSF2RA	NM_006140	chrX	1387693	1386693	1388693
HTATSF1	NM_014500	chrX	135579671	135578671	135580671
IL1RAPL2	NM_017416	chrX	103810996	103809996	103811996

EDA2R	NM_021783	chrX	65835873	65834873	65836873
TLR8	NM_138636	chrX	12924739	12923739	12925739
CRLF2	NM_001012288	chrY	1281527	1280527	1282527
IL9R	NM_002186	chrY	59330252	59329252	59331252