Supplemental Table 1. Gene sets enriched in SLE patients with risk haplotypes. Gene sets with an FDR of <25% are not included in this table, instead are presented in the main body. Gene sets with nominal P values <0.01 are included.

NAME	SIZE	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
HSC_INTERMEDIATEPROGENITORS_FETAL	149	-1.6999	<0.001	0.253795	0.84	3179
HSA00052_GALACTOSE_METABOLISM	32	-1.61557	0.002	0.305292	0.968	2123
REFRACTORY_GASTRIC_UP	80	-1.52912	0.002092	0.345095	0.994	4300
ZHAN_MULTIPLE_MYELOMA_SUBCLASSES_DIFF	28	-1.64872	0.003937	0.308918	0.941	1744
TOLLPATHWAY	32	-1.62693	0.003945	0.348624	0.961	2274
HSC_INTERMEDIATEPROGENITORS_SHARED	123	-1.57143	0.008	0.359105	0.986	3179
AGUIRRE_PANCREAS_CHR22	54	-1.59091	0.00818	0.361323	0.982	4004

Supplemental table 2: Gene sets enriched in controls with risk haplotypes. Gene sets with an FDR of <25% are not included in this table, instead are presented in the main body. Gene sets with nominal P values <0.01 are included.

NAME	SIZE	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
GERY_CEBP_TARGETS	109	-1.81319	<0.001	0.275938	0.488	3221
V$AP1_Q2_01	243	-1.43992	<0.001	0.347928	1	2732
V$AP1_Q6	228	-1.48634	<0.001	0.373109	1	2835
LEE_MYC_E2F1_UP	54	-1.84568	<0.001	0.435867	0.373	4284
STAEGE_EFTS_UP	29	-1.56459	0.001942	0.315071	0.992	3743
BRG1_ALAB_UP	38	-1.70861	0.003717	0.257094	0.821	4685
CIS_XPC_UP	144	-1.60351	0.003745	0.274163	0.977	4561
AGED_MOUSE_CEREBELLUM_UP	58	-1.63976	0.004016	0.267618	0.938	1894
V$CP2_02	204	-1.34375	0.005484	0.426902	1	4937
CIS_RESIST_GASTRIC_UP	15	-1.65266	0.00565	0.259019	0.92	2363
LEE_ACOX1_UP	63	-1.62756	0.005747	0.265578	0.955	2861
LEE_MYC_TGFA_UP	58	-1.61086	0.005747	0.284531	0.972	2861
NI2_MOUSE_UP	39	-1.82372	0.006135	0.397077	0.448	2833
UVB_NHEK1_UP	171	-1.67952	0.007435	0.280447	0.873	3450
ADIP_DIFF_CLUSTER5	37	-1.70904	0.007463	0.269807	0.821	3467
BUT_TSA_UP	18	-1.70194	0.007874	0.262453	0.826	2471
HDACI_COLON_CLUSTER9	60	-1.66699	0.008114	0.254092	0.9	3132
ET743_HELA_UP	53	-1.67516	0.009488	0.261475	0.882	3090
STRIATED_MUSCLE_CONTRACTION	34	-1.68601	0.009634	0.271933	0.858	6386

Supplemental Table 3: Gene sets enriched in SLE patients with non-risk IRF 5 haplotypes compared to patients with the Risk haplotype. Gene sets with a nominal p value of less than 0.01 are included.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
CSKPATHWAY	21	0.666287	1.870454	0	0.407342	0.273	3742
TENEDINI_MEGAKARYOCYTIC_GENES	54	0.511938	1.786157	0	0.425361	0.617	3338
V$AP1_Q2	239	0.328148	1.41691	0	0.456004	1	3572
V$AP1FJ_Q2	244	0.337882	1.48669	0	0.471216	1	3305
SMOOTH_MUSCLE_CONTRACTION	146	0.372629	1.545349	0	0.474066	0.999	3988
AMIPATHWAY	21	0.666287	1.870454	0	0.814685	0.273	3742
HSA04630_JAK_STAT_SIGNALING_PATHWAY	151	0.325419	1.464096	0.001767	0.461325	1	5371
CCAWNWWNNNGGC_UNKNOWN	69	0.402963	1.542663	0.001818	0.470765	0.999	1526
CHIARETTI_T_ALL_DIFF	253	0.449471	1.736445	0.001832	0.571742	0.798	4613
CHIARETTI_T_ALL	233	0.455962	1.724574	0.001835	0.578779	0.829	4613
HSA05131_PATHOGENIC_ESCHERICHIA_COLI_INFECTION_EPEC	44	0.484547	1.639318	0.001855	0.399826	0.958	1754
HSA05130_PATHOGENIC_ESCHERICHIA_COLI_INFECTION_EHEC	44	0.484547	1.639318	0.001855	0.413153	0.958	1754
HSA05210_COLORECTAL_CANCER	83	0.381618	1.530341	0.001873	0.45464	1	4458
WNT_SIGNALING	61	0.435306	1.638039	0.00188	0.392309	0.958	4323
SPRYPATHWAY	18	0.525617	1.689199	0.003617	0.463204	0.902	2119
AGED_MOUSE_NEOCORTEX_UP	65	0.407376	1.626143	0.00367	0.389216	0.969	2531
MENSE_HYPOXIA_UP	100	0.489513	1.801542	0.003711	0.538363	0.547	4161
HYPOXIA_REVIEW	80	0.41852	1.612287	0.003759	0.402516	0.979	5326
UVC_HIGH_D2_DN	35	0.594234	1.700157	0.003861	0.507861	0.883	3022
LINDSTEDT_DEND_UP	49	0.468639	1.646219	0.005245	0.480557	0.951	5503
V$NFY_01	211	0.283507	1.34383	0.005415	0.43691	1	4613
CTATGCA,MIR-153	208	0.359483	1.504467	0.005464	0.460001	1	5005
TAVOR_CEBP_UP	49	0.456658	1.699041	0.005484	0.47757	0.886	2284
ZHAN_MM_CD138_MS_VS_REST	41	0.55605	1.704728	0.005556	0.573807	0.877	3113
CMV_HCMV_TIMECOURSE_20HRS_DN	38	0.552308	1.817208	0.005556	0.58786	0.48	3627
TTANWNANTGGM_UNKNOWN	49	0.474865	1.681922	0.005629	0.468083	0.911	5856
IGF1_NIH3T3_UP	35	0.559457	1.674902	0.005671	0.449658	0.921	5211
V$AML1_Q6	211	0.302969	1.373787	0.00692	0.440082	1	4134
V$AML1_01	211	0.302969	1.373787	0.00692	0.441801	1	4134
KIM_TH_CELLS_DN	16	0.722009	1.614114	0.007105	0.405474	0.978	3383
CALCIUM_REGULATION_IN_CARDIAC_CELLS	139	0.365563	1.528075	0.007299	0.445209	1	3824
GLEEVECPATHWAY	21	0.500399	1.645783	0.007313	0.463973	0.952	4323
IL6PATHWAY	21	0.491444	1.642442	0.007519	0.427253	0.958	2155
PARK_HSC_VS_MPP_DN	15	0.668124	1.738739	0.007547	0.636853	0.79	2447
IRITANI_ADPROX_UP	25	0.554791	1.706344	0.007561	0.6189	0.87	1488
VERNELL_PRB_CLSTR2	20	0.57965	1.674946	0.007752	0.474329	0.921	2071
V$FXR_IR1_Q6	99	0.355864	1.475467	0.008681	0.478204	1	4613
UVC_HIGH_D9_DN	24	0.584352	1.790693	0.009452	0.483812	0.596	2758
TGF_BETA_SIGNALING_PATHWAY	50	0.502144	1.623769	0.00994	0.389268	0.975	4552

Supplemental Table 4: Gene sets enriched in controls with non-risk haplotypes compared to controls with risk haplotypes. Gene sets with a nominal p value of less than 0.01 are included.

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
V$AR_Q6	206	0.340263	1.508151	0	0.318034	1	3688
CACTGCC,MIR-34A,MIR-34C,MIR-449	260	0.270111	1.34264	0	0.436335	1	2304
AGTCAGC,MIR-345	57	0.554175	1.863005	0	0.495772	0.294	3241
UV-CMV_UNIQUE_HCMV_6HRS_DN	78	0.399057	1.717096	0	0.50321	0.775	3301
NICK_RHAPC_UP	32	0.62646	1.893779	0	0.650289	0.225	3652
GTACAGG,MIR-486	55	0.444743	1.742531	0	0.793029	0.696	2389
GTAAACC,MIR-299-5P	51	0.474455	1.722654	0.001988	0.598143	0.755	2843
AATGGAG,MIR-136	75	0.417531	1.607454	0.002033	0.396443	0.963	3204
HDACI_COLON_CLUSTER6	41	0.484505	1.749171	0.00207	0.920742	0.669	2981
V$NFY_Q6	220	0.268103	1.37565	0.002088	0.409294	1	3839
GGGATGC,MIR-324-5P	48	0.507847	1.663359	0.002088	0.595669	0.91	2537
AACATTC,MIR-409-3P	133	0.392304	1.644786	0.002092	0.465639	0.928	2625
V$NFMUE1_Q6	201	0.336825	1.602082	0.003914	0.390644	0.972	4044
AGGTGCA,MIR-500	95	0.46492	1.787601	0.003968	0.814696	0.542	3138
HSA00563_GLYCOSYLPHOSPHATIDYLINOSITOL_ANCHOR_BIOSYNTHESIS	21	0.548717	1.68209	0.003992	0.584356	0.877	4221
GTTTGTT,MIR-495	234	0.363304	1.547093	0.004115	0.349654	0.999	5208
V$NFY_Q6_01	219	0.276807	1.429326	0.004444	0.39202	1	3504
ST_DICTYOSTELIUM_DISCOIDEUM_CAMP_CHEMOTAXIS_PATHWAY	31	0.484055	1.562924	0.005736	0.382973	0.996	3231
KCCGNSWTTT_UNKNOWN	92	0.422236	1.736122	0.00578	0.704391	0.727	3807
GTATGAT,MIR-154,MIR-487	62	0.479539	1.734639	0.005964	0.610813	0.734	4452
V$PAX5_02	15	0.632917	1.656221	0.005988	0.522398	0.921	2926
AAGCAAT,MIR-137	203	0.370809	1.567534	0.006098	0.385252	0.995	3010
ST_WNT_CA2_CYCLIC_GMP_PATHWAY	19	0.572863	1.720111	0.00616	0.544048	0.764	3231
CMV-UV_HCMV_6HRS_DN	102	0.334174	1.518252	0.006316	0.327895	1	3781
GTATTAT,MIR-369-3P	199	0.390514	1.6264	0.007952	0.394448	0.945	3587
CTGTTAC,MIR-194	98	0.420709	1.662515	0.008081	0.524477	0.911	3098
ACACTGG,MIR-199A,MIR-199B	151	0.393323	1.629722	0.008097	0.411399	0.943	4060
AAAGGGA,MIR-204,MIR-211	207	0.399147	1.640456	0.00818	0.441223	0.933	2307
GCTGAGT,MIR-512-5P	50	0.379575	1.555463	0.008316	0.338814	0.998	3578
YKACATTT_UNKNOWN	244	0.275524	1.367366	0.008565	0.420582	1	3358
TGGTGCT,MIR-29A,MIR-29B,MIR-29C	485	0.323705	1.523993	0.008584	0.339233	1	3307
V$IRF1_Q6	223	0.265861	1.328382	0.008639	0.452129	1	3677
V$MYCMAX_02	231	0.29708	1.37937	0.008715	0.404388	1	3903
ACAWNRNSRCGG_UNKNOWN	56	0.445959	1.649523	0.009709	0.470336	0.925	4366
V$SP1_Q4_01	204	0.262791	1.372438	0.009823	0.412572	1	2389

Supplemental Table 5. Gene sets enriched after EBV infection, for all samples. Gene sets are listed first by FDR Q value <0.25, then by nominal P value. Gene sets with a nominal P value <0.01 are included.

GENE SET NAME	SIZE	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
COLLER_MYC_UP	20	2.061405	<0.001	0.012466	0.019	1458
MYC_TARGETS	41	2.10619	<0.001	0.014556	0.01	2567
ADIP_VS_FIBRO_UP	34	1.939168	<0.001	0.01639	0.135	3406
PENG_RAPAMYCIN_DN	189	1.941526	<0.001	0.017186	0.132	2262
CANCER_UNDIFFERENTIATED_META_UP	67	1.930825	<0.001	0.017772	0.161	3498
HDACI_COLON_CLUSTER5	23	1.966754	0.001992	0.018121	0.094	1867
PENG_GLUTAMINE_DN	254	1.977151	<0.001	0.018152	0.081	4308
ZELLER_MYC_UP	24	1.941613	<0.001	0.018414	0.132	2567
DER_IFNG_UP	61	1.924572	0.001919	0.018504	0.172	3705
STRESS_TPA_SPECIFIC_UP	42	2.063957	<0.001	0.018698	0.019	2070
SCHUMACHER_MYC_UP	52	1.943548	<0.001	0.018766	0.126	1820
TENEDINI_MEGAKARYOCYTIC_GENES	54	1.956904	<0.001	0.018924	0.105	1883
GENOTOXINS_ALL_4HRS_REG	24	1.979833	<0.001	0.019587	0.077	1132
CMV_ALL_UP	92	1.946134	<0.001	0.019663	0.119	1768
IFNALPHA_NL_UP	27	1.980039	<0.001	0.022029	0.076	1646
SHEPARD_CRASH_AND_BURN_MUT_VS_WT_UP	157	1.905434	<0.001	0.023324	0.209	3314
PENG_LEUCINE_DN	140	1.981576	<0.001	0.025275	0.074	3054
HDACI_COLON_SUL_UP	123	1.596451	<0.001	0.111061	0.986	5018
MYC_ONCOGENIC_SIGNATURE	183	1.722319	<0.001	0.0681	0.815	3024
FERNANDEZ_MYC_TARGETS	170	1.709666	<0.001	0.068374	0.851	3696
LI_FETAL_VS_WT_KIDNEY_DN	151	1.70729	<0.001	0.067493	0.855	2179
ET743_SARCOMA_DN	255	1.737493	<0.001	0.062753	0.78	2430
ET743_SARCOMA_72HRS_DN	213	1.786378	<0.001	0.05263	0.613	3135
FSH_OVARY_MCV152_UP	57	1.784702	<0.001	0.051037	0.617	1865
TARTE_PLASMA_BLASTIC	289	1.988238	<0.001	0.027665	0.066	3303
FLECHNER_KIDNEY_TRANSPLANT_WELL_PBL_DN	41	1.805854	<0.001	0.048858	0.526	1876
METHOTREXATE_PROBCELL_UP	18	1.762165	<0.001	0.056202	0.704	2180
HSA00251_GLUTAMATE_METABOLISM	29	1.852667	<0.001	0.034607	0.372	2497
CMV_24HRS_UP	71	1.841986	<0.001	0.037211	0.403	1768
ZHAN_MMPC_PC	23	1.817264	<0.001	0.049328	0.489	1033
CELLCYCLEPATHWAY	23	1.877971	<0.001	0.032479	0.273	1520
HBX_HEP_UP	18	1.876098	<0.001	0.03158	0.277	870
ZMPSTE24_KO_UP	32	1.795409	<0.001	0.051946	0.576	2689
GENOTOXINS_ALL_24HRS_REG	27	1.996537	<0.001	0.030231	0.062	1183
HBX_HCC_UP	15	1.859713	<0.001	0.035531	0.336	1883
UV-CMV_UNIQUE_HCMV_6HRS_UP	100	1.674703	0.001818	0.078753	0.905	3768
CMV-UV_HCMV_6HRS_UP	117	1.748971	0.001828	0.061469	0.749	3308
TARTE_PC	72	1.717831	0.001845	0.06686	0.83	2262
LU_IL4BCELL	68	1.754807	0.001848	0.060765	0.728	3919

BYSTRYKH_HSC_BRAIN_TRANS_GLOCUS	155	1.534042	0.001852	0.154286	0.996	2572
CELL_CYCLE_ARREST	31	1.707601	0.001866	0.068129	0.855	3104
BRENTANI_DEATH	71	1.679511	0.001873	0.078632	0.896	2244
UEDA_MOUSE_SCN	81	1.848583	0.001883	0.03583	0.384	2756
PENG_LEUCINE_UP	105	1.777879	0.001887	0.052308	0.646	3002
ESR_FIBROBLAST_DN	17	1.772798	0.00189	0.05361	0.662	1108
YU_CMYC_UP	29	1.816237	0.001894	0.048443	0.491	3124
HEARTFAILURE_VENTRICLE_DN	66	1.764685	0.001901	0.056681	0.695	1323
IFN_GAMMA_UP	38	1.866335	0.001901	0.033704	0.313	3705
BLEO_MOUSE_LYMPH_LOW_24HRS_DN	27	1.854611	0.001901	0.035767	0.356	1063
OLDAGE_DN	47	1.771335	0.001919	0.053302	0.671	4890
BRCA_BRCA1_POS	101	1.720164	0.001931	0.067792	0.821	3192
APOPTOSIS_KEGG	48	1.738276	0.001938	0.063394	0.779	2955
IFNALPHA_NL_HCC_UP	18	1.85651	0.001961	0.036304	0.349	1398
CELL_CYCLE	78	1.625128	0.001976	0.100241	0.966	1520
AS3_FIBRO_C4	18	1.802538	0.003656	0.049855	0.543	2863
STTTCRNTTT_V$IRF_Q6	162	1.692885	0.003704	0.075508	0.877	3010
ET743_SARCOMA_48HRS_DN	177	1.692807	0.003711	0.074698	0.877	3659
FERRARI_4HPR_UP	22	1.744434	0.003724	0.061245	0.758	605
IRS1_KO_ADIP_UP	87	1.491775	0.003731	0.186374	0.999	4781
HSP27PATHWAY	15	1.774761	0.003738	0.053442	0.656	913
HDACI_COLON_CLUSTER4	15	1.72163	0.003745	0.067528	0.816	593
IDX_TSA_UP_CLUSTER1	24	1.852964	0.003745	0.035733	0.369	3658
SANA_IFNG_ENDOTHELIAL_UP	71	1.793802	0.003774	0.051643	0.58	3160
KRETZSCHMAR_IL6_DIFF	135	1.815595	0.003817	0.045867	0.493	2870
BROCKE_IL6	135	1.815595	0.003817	0.047257	0.493	2870
CMV_8HRS_UP	32	1.87101	0.003861	0.032263	0.295	882
HESS_HOXAANMEIS1_UP	59	1.60366	0.003876	0.107399	0.981	3397
HESS_HOXAANMEIS1_DN	59	1.60366	0.003876	0.10814	0.981	3397
GUO_HEX_DN	57	1.578358	0.003945	0.122771	0.988	3347
AGED_MOUSE_CORTEX_UP	30	1.730665	0.003945	0.066412	0.798	3057
MUNSHI_MM_VS_PCS_UP	73	1.654787	0.003953	0.08498	0.937	2360
PDGF_ES_UP	17	1.806553	0.003992	0.049815	0.523	2891
HDACI_COLON_BUT_DN	242	1.481133	0.005587	0.194265	0.999	5068
CIRCADIAN_EXERCISE	41	1.743573	0.005607	0.060794	0.76	5258
AMINOACYL_TRNA_BIOSYNTHESIS	22	1.783188	0.005792	0.050736	0.625	1670
HDACI_COLON_CUR48HRS_UP	60	1.796235	0.005825	0.052806	0.571	2140
CANCERDRUGS_PROBCELL_UP	20	1.745479	0.005906	0.061694	0.756	2180
UVC_HIGH_ALL_UP	18	1.715446	0.005929	0.066985	0.832	1425
HSA04130_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	28	1.74619	0.005952	0.062174	0.754	1895
TRANSLATION_FACTORS	45	1.778666	0.005964	0.052768	0.644	4076
MUNSHI_MM_UP	64	1.628538	0.006	0.097769	0.965	2858
4NQO_UNIQUE_FIBRO_UP	22	1.785094	0.006	0.052036	0.617	1714
TAKEDA_NUP8_HOXA9_10D_UP	173	1.576563	0.007156	0.123916	0.989	4287
VHL_NORMAL_UP	407	1.40451	0.007246	0.261186	1	3079
HDACI_COLON_CUR_UP	105	1.729479	0.007394	0.066299	0.799	5028

BREASTCA_THREE_CLASSES	40	1.674891	0.007435	0.079397	0.904	2603
TGANNYRGCA_V$TCF11MAFG_01	261	1.359197	0.007519	0.299275	1	3437
BRENTANI_IMMUNE_FUNCTION	53	1.664875	0.007576	0.081998	0.921	3008
DAC_BLADDER_UP	27	1.749521	0.00759	0.062211	0.748	3768
ZHAN_MMPC_EARLYVS	46	1.657075	0.007634	0.084347	0.932	602
HSA00970_AMINOACYL_TRNA_BIOSYNTHESIS	31	1.789253	0.007648	0.052331	0.603	3494
GILDEA_BLADDER_UP	29	1.658191	0.007692	0.084183	0.931	1398
BREASTCA_TWO_CLASSES	132	1.624543	0.007722	0.100026	0.966	5162
GLYCINE_SERINE_AND_THREONINE_METABOLISM	35	1.643408	0.008048	0.089887	0.949	3865
NADLER_OBESITY_DN	36	1.719923	0.008147	0.066958	0.821	3082
HDACI_COLON_SUL24HRS_UP	62	1.648374	0.009174	0.088971	0.945	2034
SERUM_FIBROBLAST_CELLCYCLE	124	1.525365	0.009259	0.159301	0.996	4414
ZHAN_MM_MOLECULAR_CLASSI_UP	56	1.679381	0.009328	0.077915	0.896	3363
ADIP_VS_PREADIP_UP	35	1.624362	0.009381	0.098654	0.966	2732
APOPTOSIS_GENMAPP	40	1.651681	0.009416	0.086756	0.939	2814
APOPTOSIS	65	1.764204	0.009434	0.055965	0.698	2814
LEE_TCELLS6_UP	24	1.645311	0.009434	0.089795	0.948	2859
TNFALPHA_4HRS_UP	37	1.599594	0.009506	0.110143	0.983	4231
HDACI_COLON_BUT48HRS_DN	115	1.592986	0.009597	0.111788	0.987	2496
BRENTANI_CELL_CYCLE	81	1.525288	0.009615	0.158569	0.996	2797
UVB_NHEK3_ALL	385	1.537201	0.009671	0.153778	0.996	3775
UVB_NHEK3_C3	17	1.728242	0.009728	0.065035	0.803	3338
LEE_TCELLS1_UP	169	1.542012	0.009862	0.150325	0.996	4535
LEE_TCELLS8_UP	169	1.542012	0.009862	0.15117	0.996	4535
LEE_TCELLS10_UP	169	1.542012	0.009862	0.152024	0.996	4535