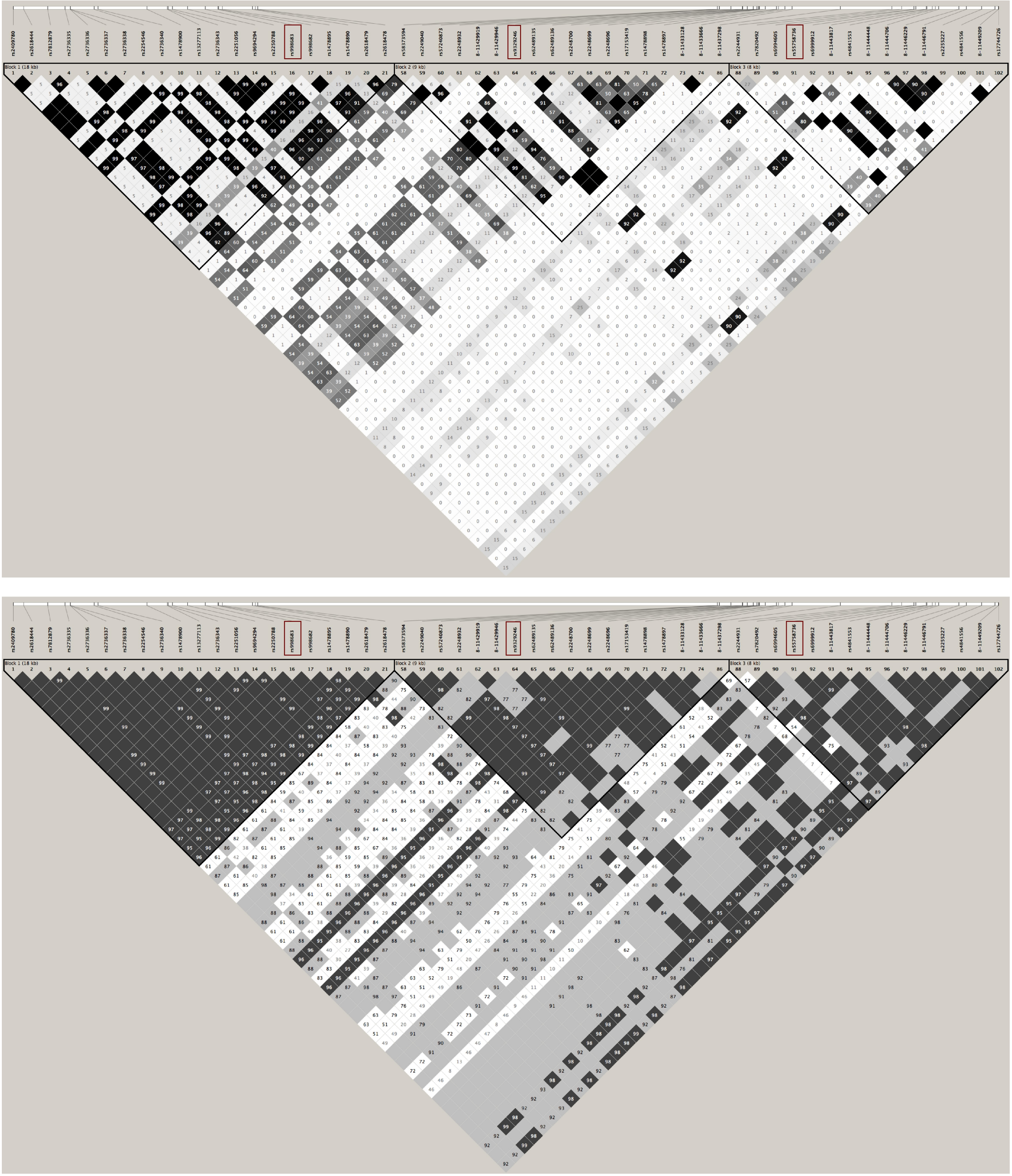

Figure S1. **Linkage disequilibrium (LD) plots of the three blocks of BLK associated with systemic lupus erythematosus.** The haplotype window analysis defined three gene regions that coincide with three haplotype blocks in the *BLK* locus. The blocks were defined using the "Solid Spine of LD" method implemented in Haploview version 4.1. For clarity, only the SNPs comprised within the associated blocks are displayed and the LD values between them in terms of r^2 (top) and D' values (bottom) are shown. The representative SNPs of each block are enclosed in red rectangles.

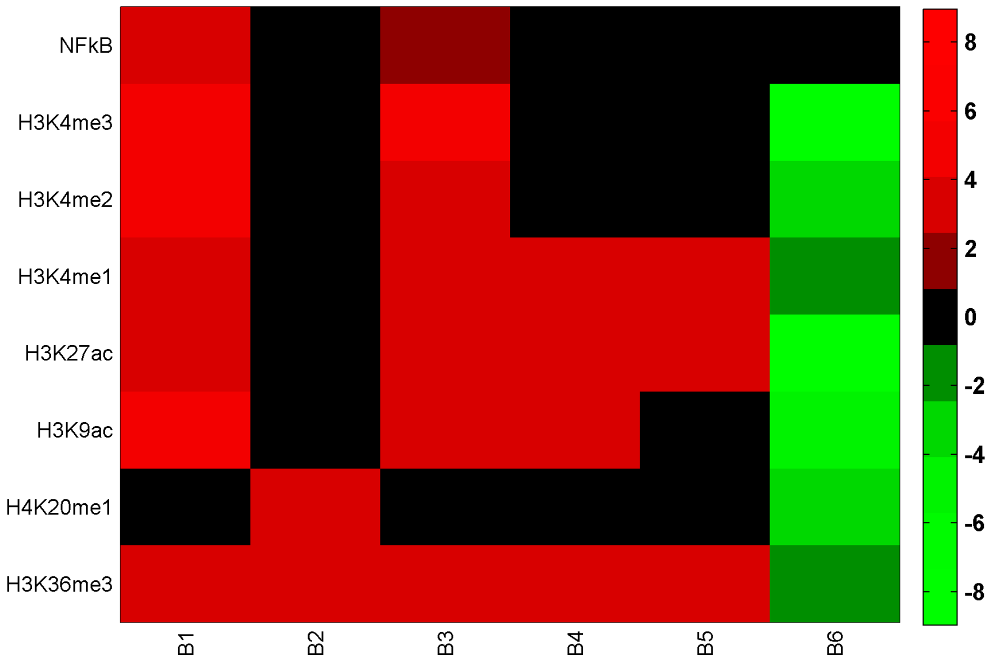

Figure S2. Heat map of –log10 p-values of enrichment of transcription factor binding sites and genomic features within haplotype block SNPs. Green/Red gradients indicate the level of under-/over-representation of the enrichment, respectively. Overall, associated regions (B1, B3) were enriched in genomic features while not associated regions were either not enriched or under-represented in these genomic features.

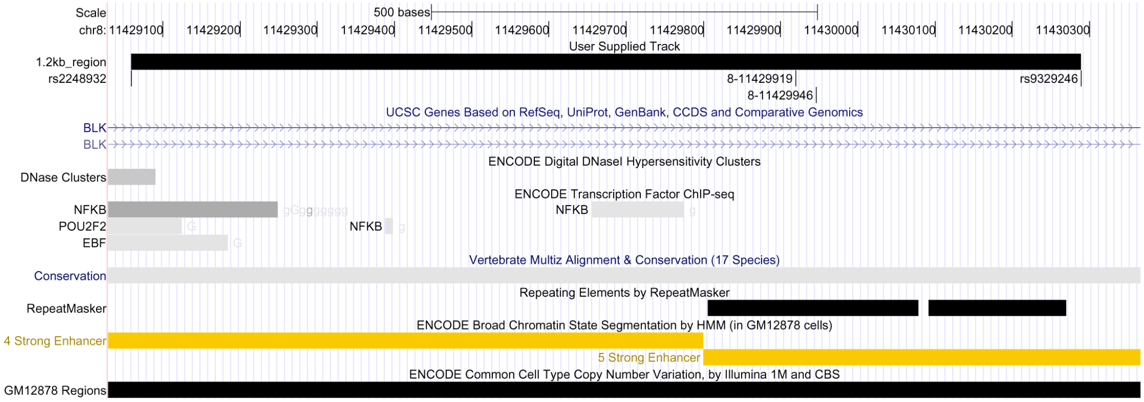

Figure S3. **Schematic description of the best-associated haplotype window.** The 1.2Kb genomic section tracks extracted from UCSC genome database showing the features identified in this segment. A strong NFkB site lies precisely under SNP rs2248932. The region includes also two strong enhancer elements.

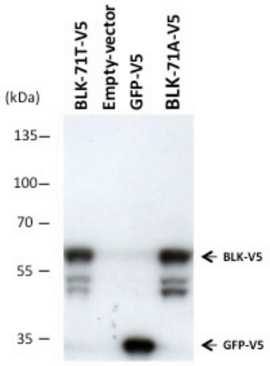

Figure S4. **Detection specificity of the constructs targeted with the epitope tag V5.** Extracts from cells transfected with different constructs were interrogated with anti-mouse V5 antibody (Invitrogen). The BLK variants targeted with V5 at the C-terminal show specific bands at the expected size (60 kDa). Two minor bands probably representing posttranslational modifications are also visible at lower molecular weight. A construct expressing the GFP protein targeted with V5 (positive control) shows a single band at the expected size (29 kDa).

Table S1 *Association analysis of BLK single-nucleotide polymorphisms with systemic lupus erythematosus*

SNP	Position*	Allele 1 / Allele 2	Frequency allele 1 cases	Frequency allele 1 controls	OR**	L95	U95	P_{CMH}	$P_{CMH\text{-}corrected}$	$P_{Breslow\text{-}Day}$
rs2409780	11374997	C/T	0.3070	0.2532	1.35	1.18	1.54	**8.09E-06**	**1.16E-04**	0.9879
rs2618444	11375780	C/A	0.3070	0.2532	1.35	1.18	1.54	**8.09E-06**	**1.16E-04**	0.9879
rs7812879	11377591	T/C	0.1212	0.1242	0.96	0.80	1.15	0.6823	0.7985	0.0835
rs2736335	11378897	A/G	0.1145	0.1187	0.94	0.78	1.14	0.5464	0.6851	0.0996
rs2736336	11379280	T/G	0.3075	0.2530	1.36	1.19	1.55	**5.89E-06**	**1.05E-04**	0.9881
rs2736337	11379290	C/T	0.3075	0.2530	1.36	1.19	1.55	**5.89E-06**	**1.05E-04**	0.9881
rs2736338	11379293	C/A	0.3050	0.2491	1.36	1.19	1.56	**5.06E-06**	**1.05E-04**	0.9757
rs2254546	11381089	A/G	0.1184	0.1198	0.98	0.82	1.18	0.8389	0.9079	0.0516
rs2736340	11381382	T/C	0.3019	0.2477	1.36	1.19	1.55	**3.73E-06**	**1.05E-04**	0.9672
rs1478900	11385069	C/T	0.1196	0.1200	0.99	0.83	1.19	0.9288	0.9654	0.0619
rs13277113	11386595	A/G	0.2978	0.2442	1.36	1.19	1.55	**3.84E-06**	**1.05E-04**	0.9448
rs2736343	11386659	C/T	0.1194	0.1210	0.98	0.82	1.17	0.8063	0.9035	0.1305
rs2251056	11386985	C/A	0.1194	0.1210	0.98	0.82	1.17	0.8063	0.9035	0.1305
rs9694294	11388130	C/G	0.1194	0.1202	0.99	0.82	1.18	0.8773	0.9180	0.0685
rs2250788	11389465	A/G	0.1197	0.1210	0.98	0.82	1.17	0.8247	0.9049	0.1331
rs998683	11390409	A/G	0.2914	0.2370	1.38	1.21	1.58	**2.12E-06**	**1.05E-04**	0.9426
rs998682	11390461	A/G	0.1182	0.1174	1.00	0.83	1.21	0.9713	0.9817	0.0402
rs1478895	11390744	G/C	0.1205	0.1176	1.03	0.85	1.23	0.7843	0.8915	0.0345
rs1478890	11393011	C/G	0.4978	0.4456	1.27	1.13	1.42	**6.46E-05**	**6.38E-04**	0.7613
rs2618479	11393230	A/G	0.1132	0.1155	1.00	0.83	1.21	0.9755	0.9817	0.0909
rs2618478	11393411	C/A	0.0975	0.0966	1.02	0.84	1.25	0.8181	0.9039	0.0077
rs10100215	11399681	T/G	0.3088	0.2754	1.17	1.03	1.33	**0.0151**	**0.0398**	0.4466
rs2618461	11403101	C/T	0.0108	0.0048	2.10	1.04	4.22	**0.0348**	0.0734	NA
rs11997711	11403312	G/A	0.0048	0.0024	1.69	0.64	4.49	0.2800	0.3881	NA
rs2736353	11404447	C/T	0.1238	0.1302	0.95	0.80	1.14	0.6016	0.7378	0.3771
rs2252729	11405628	A/G	0.1264	0.1376	0.90	0.76	1.07	0.2467	0.3512	0.2377
rs2736354	11406140	T/C	0.1273	0.1405	0.89	0.75	1.06	0.1943	0.2894	0.3240
rs2618458	11406477	A/G	0.1264	0.1390	0.89	0.75	1.06	0.1860	0.2854	0.2805
rs2618457	11406586	A/G	0.1264	0.1390	0.89	0.75	1.06	0.1860	0.2854	0.2805
rs4841545	11406645	C/G	0.3512	0.3782	0.84	0.74	0.94	**3.76E-03**	**0.0135**	0.9525
rs2736355	11407186	T/C	0.1321	0.1422	0.92	0.77	1.09	0.3176	0.4252	0.2391
rs6993775	11407398	G/T	0.1393	0.1497	0.91	0.77	1.08	0.2762	0.3862	0.1938
rs2618456	11408142	G/C	0.1216	0.1348	0.88	0.74	1.05	0.1662	0.2679	0.2700
rs2618455	11408287	A/G	0.1218	0.1383	0.86	0.73	1.03	0.0959	0.1629	0.3105
rs12674768	11408956	T/C	0.2691	0.2371	1.23	1.07	1.41	**2.66E-03**	**0.0108**	0.6036
rs11990277	11409494	C/T	0.2747	0.2416	1.24	1.08	1.41	**1.73E-03**	**8.39E-03**	0.7194
rs2736359	11409508	A/G	0.1189	0.1283	0.92	0.77	1.10	0.3578	0.4751	0.3672
rs11250142	11409942	G/A	0.1190	0.1275	0.93	0.78	1.12	0.4627	0.5944	0.2411
rs12677903	11410046	C/T	0.2751	0.2418	1.24	1.09	1.42	**1.54E-03**	**8.08E-03**	0.6958
rs17153385	11410673	T/C	0.0979	0.1032	0.96	0.79	1.17	0.7018	0.8153	0.3358
rs4841546	11411516	T/C	0.2738	0.2409	1.24	1.08	1.41	**1.95E-03**	**9.07E-03**	0.6835
chr8:11411637	11411637	T/C	0.1180	0.1276	0.92	0.77	1.11	0.3886	0.5116	0.4169
rs55903839	11411696	G/A	0.0197	0.0173	1.21	0.78	1.88	0.4173	0.5404	0.1115
rs2618450	11414199	A/G	0.2474	0.2393	1.08	0.94	1.23	0.2900	0.3950	0.6808
rs2729940	11419776	A/G	0.4360	0.4017	1.19	1.06	1.34	**3.96E-03**	**0.0136**	0.3732
rs2252797	11420068	G/C	0.3867	0.4255	0.81	0.72	0.91	**4.71E-04**	**4.01E-03**	0.4680
chr8:11421060	11421060	C/T	0.0052	0.0108	0.46	0.22	0.94	**0.0292**	0.0640	NA
chr8:11421946	11421946	C/T	0.0061	0.0108	0.55	0.28	1.09	0.0820	0.1456	NA
rs2618443	11421965	T/C	0.4719	0.4289	1.22	1.09	1.37	**8.32E-04**	**5.94E-03**	0.3692
chr8:11422004	11422004	T/C	0.0061	0.0108	0.55	0.28	1.09	0.0820	0.1456	NA
chr8:11422232	11422232	A/T	0.0061	0.0108	0.55	0.28	1.09	0.0820	0.1456	NA
rs11250144	11423685	C/G	0.3218	0.2856	1.23	1.08	1.40	**1.68E-03**	**8.39E-03**	0.9429
rs2249275	11425691	T/C	0.0111	0.0059	1.78	0.91	3.47	0.0910	0.1563	NA
rs2264866	11426062	T/C	0.3313	0.3456	0.90	0.80	1.02	0.0899	0.1563	0.1470
chr8:11426473	11426473	A/G	0.0065	0.0108	0.60	0.31	1.16	0.1199	0.1974	NA
chr8:11426486	11426486	T/G	0.0065	0.0108	0.60	0.31	1.16	0.1199	0.1974	NA
rs4841550	11426633	C/G	0.4351	0.4557	0.88	0.79	0.99	**0.0388**	0.0766	0.9930
rs58373594	11428036	T/A	0.1015	0.1022	1.02	0.84	1.25	0.8178	0.9039	0.1569
rs2249040	11428188	A/T	0.3967	0.3417	1.32	1.17	1.49	**5.98E-06**	**1.05E-04**	0.9349
rs57240873	11428190	G/C	0.1011	0.1022	1.02	0.84	1.25	0.8386	0.9079	0.1505
rs2248932	11429059	A/G	0.3970	0.3452	1.30	1.15	1.47	**1.84E-05**	**2.23E-04**	0.9507
chr8:11429919	11429919	T/C	0.0065	0.0114	0.55	0.29	1.06	0.0680	0.1279	NA
chr8:11429946	11429946	C/A	0.0065	0.0114	0.55	0.29	1.06	0.0680	0.1279	NA
rs9329246	11430289	C/T	0.3685	0.3326	1.23	1.09	1.39	**8.65E-04**	**5.94E-03**	0.9809
rs62489135	11430738	C/A	0.1020	0.1042	1.01	0.83	1.23	0.9564	0.9813	0.1192
rs62489136	11431026	C/G	0.1020	0.1042	1.01	0.83	1.23	0.9564	0.9813	0.1192
rs2248700	11431154	G/A	0.3977	0.3424	1.33	1.18	1.50	**4.26E-06**	**1.05E-04**	0.9468
rs2248699	11431173	A/G	0.5148	0.4633	1.29	1.14	1.45	**3.61E-05**	**3.88E-04**	0.4005
rs2248696	11431212	C/T	0.3977	0.3424	1.33	1.18	1.50	**4.26E-06**	**1.05E-04**	0.9468
rs17153419	11431642	G/A	0.3227	0.2913	1.21	1.06	1.38	**3.95E-03**	**0.0136**	0.9927
rs1478898	11432488	G/A	0.5148	0.4633	1.29	1.14	1.45	**3.69E-05**	**3.88E-04**	0.4018
rs1478897	11432641	T/A	0.4057	0.3540	1.30	1.16	1.47	**1.40E-05**	**1.84E-04**	0.8964
chr8:11433128	11433128	G/A	0.0065	0.0114	0.55	0.29	1.06	0.0680	0.1279	NA
chr8:11433666	11433666	A/G	0.0065	0.0114	0.55	0.29	1.06	0.0680	0.1279	NA
rs7014565	11434227	T/C	0.1036	0.1095	0.93	0.77	1.13	0.4800	0.6117	0.0869
rs2409784	11434265	C/A	0.4867	0.4482	1.22	1.08	1.37	**1.31E-03**	**7.15E-03**	0.6660
rs2169889	11434323	C/T	0.0079	0.0112	0.66	0.36	1.23	0.1904	0.2893	NA
rs7004267	11434383	A/T	0.1012	0.1027	1.02	0.84	1.24	0.8509	0.9109	0.1373
rs6981617	11434992	T/C	0.1012	0.1027	1.02	0.83	1.24	0.8588	0.9109	0.1381
rs9657551	11435592	G/A	0.3724	0.3336	1.24	1.10	1.40	**5.97E-04**	**4.72E-03**	0.9671
rs35451117	11435744	A/C	0.1008	0.1025	1.02	0.83	1.24	0.8590	0.9109	0.1374
rs4366049	11435913	G/A	0.3806	0.3433	1.24	1.09	1.40	**8.14E-04**	**5.94E-03**	0.9428
chr8:11436013	11436013	C/G	0.0065	0.0094	0.64	0.33	1.25	0.1855	0.2854	NA
chr8:11436018	11436018	C/T	0.0065	0.0094	0.64	0.33	1.25	0.1855	0.2854	NA
chr8:11437211	11437211	C/T	0.0065	0.0094	0.64	0.33	1.25	0.1847	0.2854	NA

chr8:11437298	11437298	T/C	0.0148	0.0068	2.12	1.17	3.82	**0.0101**	**0.0297**	0.6504
chr8:11438059	11438059	A/G	0.0061	0.0094	0.61	0.31	1.21	0.1447	0.2357	NA
rs2244931	11441178	G/C	0.4680	0.4664	1.03	0.92	1.16	0.6305	0.7547	0.2052
rs7820492	11441923	A/G	0.4645	0.4906	0.84	0.75	0.95	**3.67E-03**	**0.0135**	0.9755
rs6994605	11442846	G/A	0.0066	0.0087	0.69	0.35	1.36	0.2732	0.3854	NA
rs55758736	11442985	A/G	0.0217	0.0092	2.27	1.37	3.75	**1.30E-03**	**7.15E-03**	0.4600
rs6999912	11443766	A/G	0.3909	0.4151	0.86	0.77	0.97	**0.0139**	**0.0380**	0.5293
chr8:11443817	11443817	A/G	0.0217	0.0092	2.27	1.37	3.76	**1.30E-03**	**7.15E-03**	0.4614
rs4841553	11444224	C/T	0.4896	0.4587	1.19	1.06	1.34	**3.47E-03**	**0.0133**	0.9488
chr8:11444448	11444448	C/A	0.0062	0.0087	0.64	0.32	1.28	0.1936	0.2894	NA
chr8:11444706	11444706	T/C	0.0217	0.0092	2.27	1.37	3.76	**1.28E-03**	**7.15E-03**	0.4645
chr8:11446229	11446229	T/C	0.0237	0.0109	2.13	1.32	3.44	**1.75E-03**	**8.39E-03**	0.7329
chr8:11446791	11446791	T/G	0.0220	0.0090	2.29	1.38	3.81	**1.16E-03**	**7.15E-03**	0.5059
rs2255227	11447947	C/T	0.0220	0.0090	2.29	1.38	3.80	**1.19E-03**	**7.15E-03**	0.5091
rs4841556	11448952	T/A	0.2978	0.3383	0.80	0.71	0.91	**4.69E-04**	**4.01E-03**	0.8678
chr8:11449209	11449209	C/T	0.0062	0.0087	0.64	0.32	1.28	0.1960	0.2894	NA
rs17744726	11449232	A/G	0.2978	0.3381	0.80	0.71	0.91	**4.82E-04**	**4.01E-03**	0.8652
chr8:11451210	11451210	A/C	0.0053	0.0083	0.56	0.27	1.18	0.1167	0.1962	NA
rs7007439	11453203	T/A	0.4101	0.3870	1.15	1.02	1.30	**0.0232**	0.0533	0.6664
rs6983727	11453221	T/C	0.4551	0.4879	0.85	0.76	0.96	**7.01E-03**	**0.0213**	0.5927
rs7011778	11453580	T/C	0.4101	0.3870	1.15	1.02	1.30	**0.0203**	**0.0485**	0.6753
chr8:11455041	11455041	C/A	0.1127	0.1081	1.05	0.87	1.26	0.6181	0.7476	0.0430
chr8:11455750	11455750	T/C	0.0049	0.0083	0.51	0.24	1.09	0.0727	0.1335	NA
rs62490888	11456175	A/G	0.1126	0.1081	1.05	0.87	1.26	0.6198	0.7476	0.0456
rs4841561	11456182	T/C	0.3811	0.3661	1.11	0.98	1.25	0.0910	0.1563	0.8478
rs11250148	11457261	C/T	0.3853	0.3593	1.17	1.03	1.32	**0.0125**	**0.0350**	0.6305
rs10109802	11457270	G/T	0.3696	0.3467	1.14	1.01	1.29	**0.0339**	0.0724	0.5620
rs35401006	11457513	G/C	0.3841	0.3591	1.16	1.03	1.31	**0.0145**	**0.0389**	0.5754
rs13262953	11457630	A/G	0.3639	0.3409	1.16	1.02	1.31	**0.0234**	0.0533	0.6500
rs7834638	11457704	C/T	0.3840	0.3597	1.16	1.03	1.31	**0.0155**	**0.0400**	0.5772
rs11776201	11458307	G/A	0.0152	0.0154	1.08	0.67	1.75	0.7456	0.8537	0.8009
rs2279169	11458425	A/G	0.3821	0.3577	1.16	1.03	1.31	**0.0177**	**0.0437**	0.5424
rs62490890	11458663	T/C	0.1156	0.1091	1.06	0.88	1.28	0.5381	0.6801	0.0607
rs10097005	11458767	A/C	0.3817	0.3572	1.16	1.03	1.31	**0.0166**	**0.0416**	0.5656
rs10097015	11458793	T/C	0.3817	0.3572	1.16	1.03	1.31	**0.0166**	**0.0416**	0.5656
rs1042689	11459202	T/C	0.3807	0.3571	1.15	1.02	1.30	**0.0199**	**0.0483**	0.5281
rs2250986	11459698	C/G	0.3827	0.3568	1.17	1.03	1.32	**0.0126**	**0.0350**	0.4920
rs62490891	11459834	T/A	0.1162	0.1115	1.04	0.87	1.25	0.6771	0.7984	0.0267
rs7840748	11459853	A/G	0.0057	0.0010	5.95	1.47	24.06	**5.72E-03**	**0.0185**	NA
rs12549144	11460270	G/C	0.4969	0.4719	1.14	1.02	1.28	**0.0262**	0.0583	0.7217
rs12549150	11460345	T/C	0.4956	0.4716	1.14	1.01	1.28	**0.0304**	0.0657	0.6614
rs12541800	11460481	G/A	0.4944	0.4718	1.13	1.01	1.27	**0.0373**	0.0747	0.6910
chr8:11460552	11460552	T/A	0.1182	0.1121	1.05	0.87	1.26	0.6023	0.7378	0.0308
rs10094362	11460790	G/T	0.1174	0.1107	1.06	0.88	1.27	0.5535	0.6886	0.0283
rs34379689	11460843	G/A	0.3725	0.3519	1.14	1.01	1.29	**0.0374**	0.0747	0.5974
rs755320	11460848	G/A	0.1358	0.1221	1.11	0.93	1.32	0.2460	0.3512	0.0354
rs62490892	11460924	T/C	0.1176	0.1139	1.02	0.84	1.22	0.8746	0.9180	0.0217
rs62490893	11460927	A/G	0.1033	0.1023	1.00	0.82	1.22	0.9868	0.9868	0.0182
rs35067819	11460946	A/G	0.3582	0.3389	1.12	0.99	1.27	0.0691	0.1285	0.7052
rs11786268	11461601	T/C	0.1182	0.1125	1.04	0.87	1.25	0.6666	0.7919	0.0355
rs4841563	11462490	T/G	0.3718	0.3504	1.14	1.01	1.29	**0.0371**	0.0747	0.6314
rs13280813	11462514	T/G	0.4562	0.4897	0.85	0.76	0.96	**8.36E-03**	**0.0249**	0.6330
rs4841564	11463218	G/T	0.4684	0.5048	0.84	0.75	0.94	**3.53E-03**	**0.0133**	0.6926
rs10093314	11463522	C/T	0.0176	0.0153	1.21	0.76	1.94	0.4165	0.5404	0.5392
rs10093575	11463731	T/C	0.1177	0.1129	1.03	0.86	1.24	0.7444	0.8537	0.0353
rs35370321	11463809	G/T	0.3789	0.3543	1.15	1.02	1.30	**0.0236**	0.0533	0.6570
rs1382562	11464027	A/G	0.0176	0.0146	1.30	0.81	2.08	0.2877	0.3950	0.3367
rs1382563	11464199	C/G	0.4671	0.5027	0.85	0.76	0.96	**6.30E-03**	**0.0199**	0.7650
rs9650661	11464542	T/G	0.4684	0.5069	0.84	0.75	0.94	**2.96E-03**	**0.0117**	0.7095
rs12547947	11464750	G/T	0.3573	0.3324	1.16	1.02	1.32	**0.0208**	**0.0491**	0.9015
rs10107563	11464901	A/G	0.0167	0.0142	1.28	0.79	2.07	0.3172	0.4252	0.4553
rs7831039	11465046	T/A	0.4627	0.5030	0.83	0.74	0.94	**2.19E-03**	**9.12E-03**	0.8291
rs11991139	11465804	T/C	0.4691	0.5090	0.83	0.74	0.94	**2.16E-03**	**9.12E-03**	0.7614
rs899366	11467894	A/G	0.3420	0.3087	1.21	1.07	1.37	**2.14E-03**	**9.12E-03**	0.8288
rs61199332	11468050	T/C	0.0156	0.0118	1.38	0.83	2.29	0.2100	0.3072	0.6903
rs12679960	11468399	T/C	0.3511	0.3223	1.20	1.05	1.36	**5.67E-03**	**0.0185**	0.6945
rs11776081	11468631	A/G	0.1138	0.1129	1.00	0.83	1.20	0.9667	0.9817	0.0480
rs4841566	11469847	C/G	0.3421	0.3084	1.21	1.07	1.38	**2.18E-03**	**9.12E-03**	0.8591
rs35353728	11469862	T/C	0.3274	0.3010	1.18	1.04	1.34	**0.0110**	**0.0316**	0.9001
chr8:11470221	11470221	G/C	0.1452	0.1311	1.12	0.94	1.33	0.2152	0.3120	0.0350
rs2127128	11472338	C/T	0.3313	0.3045	1.19	1.05	1.36	**6.92E-03**	**0.0213**	0.8362
rs968179	11475473	T/G	0.3301	0.3021	1.19	1.05	1.35	**5.67E-03**	**0.0185**	0.8900
rs3802235	11475653	A/G	0.0103	0.0056	2.12	1.04	4.31	**0.0358**	0.0743	0.6982

Single marker association tests of genotyped (underlined) and imputed SNPs. *Positions on chr8 obtained from the National Center for Biotechnology Information (NCBI) Build 36. **Odds ratios (ORs) and 95% confidence intervals (defined by L95 -lower limit- and U95 –upper limit-) were calculated for the allele 1of each SNP by a meta-analysis with the country of origin as the stratification variable. The value P_{CMH} indicates the significance of the allelic association determined by the Cochran-Mantel-Haenszel test, while $P_{\text{CMH-corrected}}$ displays the association after adjustment for false discovery rate, and $P_{\text{Breslow-Day}}$ is the P value determined using the Breslow-Day test for homogeneity of the ORs. The analyses were performed using PLINK software, version 1.07.

Table S2 *Conditional association analysis*

SNP	Position	MAF	N	OR	Step 1 - Meta-analysis	Step 2 - MA conditioning on rs998683	Step 3 - MA conditioning on rs998683 + chr8:11446791	Step 4 - MA conditioning on rs998683 + chr8:11446791 + chr8:11437298	Step 5 - MA conditioning on rs998683 + chr8:11446791 + chr8:11437298 + rs4841553	r2 rs13277113	r2 Ala71Thr
rs2409780	11374997	0.2767	2523	1.61	7.92E-06					99.9%	0.4%
rs2618444	11375780	0.2767	2523	1.61	7.92E-06					99.9%	0.4%
rs7812879	11377591	0.1229	2527	0.94						5.3%	0.2%
rs2736335	11378897	0.1169	2520	0.90						5.0%	0.3%
rs2736336	11379280	0.2768	2527	1.62	5.69E-06					99.9%	0.4%
rs2736337	11379290	0.2768	2527	1.62	5.69E-06					99.9%	0.4%
rs2736338	11379293	0.2735	2506	1.62	4.86E-06					100.0%	0.3%
rs2254546	11381089	0.1192	2559	0.97						5.0%	0.2%
rs2736340	11381382	0.2714	2646	1.62	3.50E-06					99.8%	0.4%
rs1478900	11385069	0.1198	2558	0.99						5.0%	0.2%
rs13277113	11386595	0.2676	2612	1.63	3.65E-06					100.0%	0.3%
rs2736343	11386659	0.1203	2552	0.96						5.1%	0.1%
rs2251056	11386985	0.1203	2552	0.96						5.1%	0.1%
rs9694294	11388130	0.1198	2516	0.97						5.2%	0.1%
rs2250788	11389465	0.1204	2553	0.96						5.1%	0.1%
rs998683	11390409	0.2609	2507	1.66	***1.61E-06***					99.7%	0.3%
rs998682	11390461	0.1177	2544	1.01						5.0%	0.1%
rs1478895	11390744	0.1189	2557	1.05						5.0%	0.2%
rs1478890	11393011	0.4684	2646	1.47	6.06E-05					36.5%	1.4%
rs2618479	11393230	0.1145	2481	1.01						4.2%	0.2%
rs2618478	11393411	0.0970	2496	1.04						3.8%	0.2%
rs10100215	11399681	0.2900	2645	1.31	0.0141					43.6%	0.5%
rs2618461	11403101	0.0074	2580	2.65	0.0390	0.0243				0.5%	31.9%
rs11997711	11403312	0.0035	2591	2.23						0.2%	13.0%
rs2736353	11404447	0.1273	2521	0.92						2.1%	0.2%
rs2252729	11405628	0.1327	2592	0.83						2.1%	0.1%
rs2736354	11406140	0.1347	2617	0.81						2.1%	0.1%
rs2618458	11406477	0.1335	2596	0.80						2.1%	0.1%
rs2618457	11406586	0.1335	2596	0.80						2.1%	0.1%
rs4841545	11406645	0.3664	2646	0.68	0.0036		0.0349	0.0199		15.2%	1.9%
rs2736355	11407186	0.1377	2476	0.84						2.6%	0.1%
rs6993775	11407398	0.1451	2646	0.84						2.6%	0.4%
rs2618456	11408142	0.1290	2570	0.79						2.1%	0.1%
rs2618455	11408287	0.1311	2608	0.75						2.3%	0.2%
rs12674768	11408956	0.2511	2581	1.40	0.0026					47.3%	0.5%
rs11990277	11409494	0.2560	2646	1.41	0.0017					43.6%	0.5%
rs2736359	11409508	0.1242	2573	0.85						2.0%	0.1%
rs11250142	11409942	0.1237	2542	0.88						2.0%	0.1%
rs12677903	11410046	0.2563	2608	1.42	0.0016					45.4%	0.6%
rs17153385	11410673	0.1009	2558	0.93						2.1%	0.3%
rs4841546	11411516	0.2552	2578	1.41	0.0020					46.4%	0.5%
chr8:11411637	11411637	0.1234	2532	0.86						2.0%	0.1%
rs55903839	11411696	0.0183	2617	1.35						4.9%	0.0%
rs2618450	11414199	0.2428	2646	1.14		0.0362	0.0253			1.9%	0.3%
rs2729940	11419776	0.4167	2646	1.34	0.0037					31.8%	0.1%
rs2252797	11420068	0.4085	2646	0.63	4.39E-04	0.0368		0.0409		15.7%	1.1%
chr8:11421060	11421060	0.0083	2635	-0.09	0.0282	0.0487				0.2%	0.1%
chr8:11421946	11421946	0.0087	2637	0.12						0.2%	0.1%
rs2618443	11421965	0.4476	2645	1.39	7.88E-04					31.4%	2.1%
chr8:11422004	11422004	0.0087	2637	0.12						0.2%	0.1%
chr8:11422232	11422232	0.0087	2637	0.12						0.2%	0.1%
rs11250144	11423685	0.3014	2465	1.40	0.0018					57.8%	0.4%
rs2249275	11425691	0.0082	2511	2.23		0.0308				0.2%	48.6%
rs2264866	11426062	0.3394	2646	0.80						14.7%	0.7%
chr8:11426473	11426473	0.0089	2637	0.21						0.2%	0.1%
chr8:11426486	11426486	0.0089	2637	0.21						0.2%	0.1%
rs4841550	11426633	0.4467	2646	0.78	0.0406					22.0%	0.3%
rs58373594	11428036	0.1019	2484	1.04						2.0%	0.2%
rs2249040	11428188	0.3657	2617	1.54	7.75E-06					47.1%	3.8%
rs57240873	11428190	0.1017	2483	1.04						2.0%	0.2%
rs2248932	11429059	0.3678	2640	1.51	2.06E-05					43.0%	3.4%
chr8:11429919	11429919	0.0093	2643	0.10						0.3%	0.1%
chr8:11429946	11429946	0.0093	2643	0.10						0.3%	0.1%
rs9329246	11430289	0.3483	2646	1.40	8.32E-04					52.2%	0.3%
rs62489135	11430738	0.1032	2485	1.01						1.9%	0.2%
rs62489136	11431026	0.1032	2485	1.01						1.9%	0.2%
rs2248700	11431154	0.3666	2638	1.55	5.39E-06					47.2%	3.7%
rs2248699	11431173	0.4858	2473	1.47	5.36E-05					34.5%	2.4%
rs2248696	11431212	0.3666	2638	1.55	5.39E-06					47.2%	3.7%
rs17153419	11431642	0.3050	2487	1.38	0.0040					55.5%	0.4%
rs1478898	11432488	0.4858	2473	1.47	5.46E-05					34.3%	2.4%
rs1478897	11432641	0.3766	2646	1.52	1.63E-05					44.2%	3.5%
chr8:11433128	11433128	0.0093	2643	0.10						0.3%	0.1%
chr8:11433666	11433666	0.0093	2643	0.10						0.3%	0.1%
rs7014565	11434227	0.1069	2586	0.88						1.9%	0.3%
rs2409784	11434265	0.4649	2533	1.37	0.0015					37.9%	0.1%
rs2169889	11434323	0.0098	2615	0.34						0.3%	0.4%
rs7004267	11434383	0.1020	2475	1.03						1.8%	0.2%
rs6981617	11434992	0.1021	2474	1.03						1.8%	0.2%
rs9657551	11435592	0.3504	2583	1.41	6.10E-04					53.0%	0.0%
rs35451117	11435744	0.1017	2472	1.03						1.8%	0.2%

rs4366049	11435913	0.3593	2534	1.41	8.59E-04				50.6%	0.1%
chr8:11436013	11436013	0.0082	2637	0.28					0.3%	0.1%
chr8:11436018	11436018	0.0082	2637	0.28					0.3%	0.1%
chr8:11437211	11437211	0.0082	2636	0.28					0.3%	0.1%
chr8:11437298	11437298	0.0103	2472	2.84	0.0111	0.0040	***0.0044***		0.2%	0.3%
chr8:11438059	11438059	0.0080	2635	0.21					0.3%	0.0%
rs2244931	11441178	0.4671	2644	1.05					10.4%	1.4%
rs7820492	11441923	0.4792	2644	0.69	0.0033		0.0183	0.0160	7.1%	1.3%
rs6994605	11442846	0.0078	2574	0.37					0.3%	0.0%
rs55758736	11442985	0.0146	2605	2.99	0.0012	4.00E-04			0.3%	100.0%
rs6999912	11443766	0.4045	2645	0.73	0.0125			0.0347	11.6%	1.5%
chr8:11443817	11443817	0.0146	2602	2.98	0.0012	3.98E-04			0.4%	100.0%
rs4841553	11444224	0.4722	2646	1.34	0.0031		0.0229	***0.0156***	8.2%	1.1%
chr8:11444448	11444448	0.0076	2572	0.26					0.2%	0.0%
chr8:11444706	11444706	0.0146	2597	3.01	0.0011	3.96E-04			0.4%	100.0%
chr8:11446229	11446229	0.0165	2517	2.84	0.0016	4.75E-04			0.4%	90.8%
chr8:11446791	11446791	0.0146	2565	3.05	0.0010	***3.57E-04***			0.3%	100.0%
rs2255227	11447947	0.0146	2563	3.05	0.0011	3.67E-04			0.3%	100.0%
rs4841556	11448952	0.3206	2645	0.62	5.52E-04	0.0418			13.6%	1.1%
chr8:11449209	11449209	0.0076	2569	0.26					0.2%	0.0%
rs17744726	11449232	0.3205	2644	0.62	5.67E-04	0.0425			13.6%	1.0%
chr8:11451210	11451210	0.0070	2565	0.09					0.2%	0.0%
rs7007439	11453203	0.3972	2494	1.26	0.0231				23.8%	0.8%
rs6983727	11453221	0.4735	2581	0.71	0.0069				25.4%	0.2%
rs7011778	11453580	0.3972	2558	1.27	0.0202				23.2%	0.8%
chr8:11455041	11455041	0.1101	2575	1.09					1.2%	0.0%
chr8:11455750	11455750	0.0068	2564	-0.03					0.2%	0.0%
rs62490888	11456175	0.1100	2581	1.09					1.2%	0.0%
rs4841561	11456182	0.3726	2646	1.19					21.5%	0.6%
rs11250148	11457261	0.3706	2628	1.29	0.0129				20.0%	0.1%
rs10109802	11457270	0.3567	2575	1.27	0.0318				17.1%	0.0%
rs35401006	11457513	0.3700	2639	1.29	0.0149				20.0%	0.1%
rs13262953	11457630	0.3509	2532	1.28	0.0234				22.9%	0.1%
rs7834638	11457704	0.3703	2645	1.28	0.0157				19.3%	0.0%
rs11776201	11458307	0.0153	2580	1.15					0.8%	0.0%
rs2279169	11458425	0.3683	2628	1.28	0.0181				20.7%	0.1%
rs62490890	11458663	0.1119	2596	1.11					1.4%	0.0%
rs10097005	11458767	0.3678	2622	1.28	0.0170				20.9%	0.1%
rs10097015	11458793	0.3678	2622	1.28	0.0170				20.9%	0.1%
rs1042689	11459202	0.3674	2616	1.27	0.0204				21.2%	0.1%
rs2250986	11459698	0.3681	2611	1.29	0.0131				21.5%	0.0%
rs62490891	11459834	0.1135	2607	1.07					1.2%	0.1%
rs7840748	11459853	0.0031	2598	5.76	0.0056	0.0027			0.2%	15.6%
rs12549144	11460270	0.4827	2607	1.25	0.0264				26.3%	0.7%
rs12549150	11460345	0.4820	2617	1.25	0.0306				26.4%	0.7%
rs12541800	11460481	0.4817	2645	1.23	0.0370				25.7%	0.8%
chr8:11460552	11460552	0.1148	2596	1.09					1.2%	0.1%
rs10094362	11460790	0.1136	2593	1.10					1.3%	0.1%
rs34379689	11460843	0.3609	2548	1.24	0.0376				23.2%	0.5%
rs755320	11460848	0.1281	2596	1.20					0.3%	0.3%
rs62490892	11460924	0.1155	2467	1.03					1.2%	0.1%
rs62490893	11460927	0.1028	2496	1.00					0.9%	0.1%
rs35067819	11460946	0.3473	2491	1.23					19.8%	0.4%
rs11786268	11461601	0.1150	2539	1.08					1.3%	0.1%
rs4841563	11462490	0.3597	2488	1.24	0.0380				23.8%	0.5%
rs13280813	11462514	0.4749	2593	0.72	0.0082				24.7%	0.3%
rs4841564	11463218	0.4888	2585	0.70	0.0036				27.3%	0.2%
rs10093314	11463522	0.0163	2551	1.37					0.7%	0.0%
rs10093575	11463731	0.1150	2531	1.06					1.3%	0.1%
rs35370321	11463809	0.3650	2519	1.27	0.0241				22.0%	0.1%
rs1382562	11464027	0.0159	2549	1.50					0.8%	0.0%
rs1382563	11464199	0.4872	2646	0.71	0.0064				25.8%	0.3%
rs9650661	11464542	0.4900	2595	0.69	0.0031				27.1%	0.3%
rs12547947	11464750	0.3434	2452	1.27	0.0214				26.6%	0.5%
rs10107563	11464901	0.0153	2547	1.48					0.8%	0.0%
rs7831039	11465046	0.4854	2631	0.68	0.0023				26.0%	0.3%
rs11991139	11465804	0.4916	2561	0.68	0.0022				27.4%	0.3%
rs899366	11467894	0.3233	2645	1.38	0.0021				26.3%	0.1%
rs61199332	11468050	0.0135	2566	1.67					0.6%	0.0%
rs12679960	11468399	0.3350	2454	1.35	0.0055				26.5%	0.1%
rs11776081	11468631	0.1133	2569	0.99					0.7%	0.1%
rs4841566	11469847	0.3230	2619	1.37	0.0022				27.3%	0.1%
rs35353728	11469862	0.3124	2585	1.31	0.0111				30.3%	0.4%
chr8:11470221	11470221	0.1373	2462	1.21					1.7%	0.1%
rs2127128	11472338	0.3161	2493	1.34	0.0075				31.5%	0.8%
rs968179	11475473	0.3143	2604	1.34	0.0057				29.5%	0.7%
rs3802235	11475653	0.0076	2551	2.67	0.0349				0.3%	0.1%

Conditional analysis of SNPs done by logistic regression using GenABEL's score test. By specifying the country of origin as the *strata* argument, we performed a structured test of association for all the SNPs. In a step-wise manner, the SNP with higher *P*-value was identified in each step and then used as a covariate for the next association step. This analysis demonstrated that the association of BLK could be summarized by the independent associations of SNPs rs998683 and "chr8:11446791". After conditioning by these 2 SNPs, some variants displayed significant although weaker nominal associations (step 3) and thus we continued until no SNP remained associated. GenABEL package was run using R version 2.9.2.

Table S3. *Statistical analysis for the enrichment of transcription factor binding sites and epigenetic marks in BLK associated and non associated haplotype blocks within the promoter region of BLK.*

Red – chi-square p-value for over-representation; Green – under-representation; empty cell – not significant. Marginal – significant if tested against whole genome

	B1 assoc	B2 not assoc	B3 assoc	B4 not assoc
NFkB	1.86e-04		Marginal	
PAX5-C20/N19				
IRF4	2.97E-02			
H3K4me2	2.09E-04		1.05E-03	
H3K4me3	4.25E-04		1.05E-03	
H3K9ac	4.54E-04	Marginal	4.46E-03	Marginal
H3K27ac	3.02E-03		2.87E-03	2.45E-03
H4K20me1		Marginal	7.66E-03	9.34E-03

NFkB binding sites were identified using Chip-Seq in the ENCODE Project with the antibody described in their information site: http://genome.ucsc.edu/cgi-bin/hgEncodeVocab?ra=encode%2Fcv.ra&target="NFKB"

Table S4. Characterization of 1.2kb haplotype window between SNPs rs2248932 and rs9329246 in B3; Coordinates (hg18): chr8:11429059-11430289

1.2kb region SNPs	**DNAse site**	**TFBS**	**Chromatin state segmentation**	**RepeatMasker regions**	**CNV**
rs2248932	Yes	NFKB|POU2F2|EBF	Strong Enhancer		normal
chr8:11429919			Strong Enhancer	Alu:SINE	normal
chr8:11429946			Strong Enhancer	Alu:SINE	normal
rs9329246			Strong Enhancer	Near Simple repeat	normal

All information retrieved is for the GM12878 lymphoblastoid cell line. The whole 1.2kb region shows evidence for conservation by having low probability of insertions and deletions, as defined by Cons Indels MmCf (consIndelsHgMmCanFam) Track.