SUPPLEMENTARY FILES

SUPPLEMENTARY TABLES

Supplementary Table S1. Characteristics of cervical neoplasia cases in participating study populations.

				Histology			HPV status					
Studies	Cases	Controls	Chip Type	Adeno-carcinoma	Squamous cell carcinoma	Other	HPV16 and 18	HPV16 no 18	HPV18 no 16	Negative for tested HPV types	No HPV16 or HPV18	Not tested
Montreal	95	0	Omni	N/A	N/A	95	N/A	N/A	N/A	N/A	N/A	95
NCI [1]	194	0	660Q	97	88	9	N/A	38	14	93	41	8
NSW [2]	274	0	Omni	10	256	8	11	62	7	67	N/A	127
CerGe [3]	98	0	Omni	N/A	N/A	98	N/A	N/A	N/A	N/A	N/A	98
Seattle [4]	751	0	660Q	424	327	N/A	44	258	112	45	34	258
SUCCEED [1]	313	0	660Q	11	65	237	17	194	18	N/A	69	15
TOMBOLA[5]	324	0	Omni	N/A	N/A	324	16	115	15	177	1	N/A
NIH [3]	94	0	660Q	N/A	N/A	94	N/A	N/A	N/A	N/A	N/A	94
Immunochip	0	13428	Immunochip	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
TOTALS	2143	13428		542	736	865	88	667	166	382	145	695

N/A, not available.

Supplementary Table S2. Allele frequencies of the key SNPs in the intersection between four input datasets and the reference panel of KIR*IMP.

SNPs	**Position**	**Allele0**	**Allele1**	**Omni**[1]	**Ichip1**[1]	**660Q**[1]	**Ichip2**[1]
seq-rs272408	55103603	C	T	0.82	0.82	N/A	N/A
seq-rs7255954	55109883	A	C	0.26	0.26	0.26	0.26
seq-rs272411	55111727	C	T	0.32	0.29	0.31	0.29
rs2363863	55111785	C	T	0.36	0.36	0.36	0.36
seq-rs4806787	55112489	A	C	0.62	0.62	N/A	N/A
rs1000574	55114775	C	T	0.20	0.20	0.20	0.20
seq-rs10411879	55123305	A	G	0.34	0.34	0.34	0.33
seq-rs10423364	55128339	G	A	0.33	0.31	N/A	N/A
seq-rs8102351	55157042	C	T	N/A	N/A	0.90	0.90
seq-rs10419191	55159164	G	A	0.89	0.88	0.88	0.88
seq-rs4806798	55166721	A	G	0.15	0.13	0.15	0.13
seq-rs934434	55172146	C	T	0.52	0.55	N/A	N/A
seq-rs4806802	55173403	G	A	0.15	0.13	0.14	0.13
seq-rs1749313	55173542	G	A	N/A	N/A	0.08	0.08
seq-rs1654668	55174213	T	C	0.56	0.55	0.56	0.55
seq-rs17836409	55183869	C	T	0.12	0.12	0.11	0.12
seq-rs1654656	55183977	C	T	0.49	0.48	0.49	0.48
seq-t1d-19-59878067-G-A	55186255	G	A	0.07	0.07	N/A	N/A
rs1749320	55187279	A	C	0.06	0.06	0.05	0.07
seq-rs912735	55193435	T	C	0.80	0.79	N/A	N/A
seq-rs1654658	55194681	A	G	0.69	0.68	0.70	0.68
seq-rs1654660	55195187	G	A	0.14	0.14	0.13	0.14
seq-rs4806805	55205122	T	C	0.28	0.28	N/A	N/A
rs10422812	55206991	C	T	0.24	0.26	0.27	0.26
rs11084366	55210598	T	G	0.33	0.35	0.37	0.35
rs1952015	55211155	C	T	N/A	N/A	0.86	0.84
seq-rs10426302	55211547	A	G	0.82	0.82	0.83	0.81
seq-rs8109557	55211859	A	G	0.86	0.85	N/A	N/A
seq-rs8107460	55214989	T	C	0.88	0.88	N/A	N/A
seq-rs4436877	55216162	G	A	0.26	0.26	0.28	0.26
seq-rs1325156	55216950	A	G	0.84	0.83	0.85	0.83
rs12151161	55217589	G	A	N/A	N/A	0.90	0.89
seq-rs11666535	55217660	T	G	N/A	N/A	0.53	0.53
rs270771	55220626	C	T	N/A	N/A	0.05	0.05
rs270779	55224260	A	G	N/A	N/A	0.46	0.45
seq-rs2296370	55224785	G	A	0.36	0.37	0.39	0.37
seq-rs2296371	55224885	G	A	0.41	0.41	0.42	0.42
rs10423751	55224967	T	C	0.59	0.58	0.58	0.58
seq-rs11883241	55225613	C	T	0.30	0.29	0.30	0.29
seq-rs6509899	55225835	G	A	0.10	0.10	0.10	0.10
seq-rs1325158	55226402	C	T	0.37	0.37	0.37	0.37
seq-rs7256392	55227879	A	G	0.96	0.96	0.97	0.96
rs4806527	55228948	G	A	0.04	0.03	N/A	N/A
rs587560	55245738	C	T	0.31	0.30	N/A	N/A
rs17207376	55248072	C	A	0.69	0.69	N/A	N/A
seq-rs10409751	55249570	C	G	N/A	N/A	0.33	0.33
seq-rs597598	55315440	G	A	0.18	0.17	0.18	0.17
rs3865507	55322376	C	A	0.03	0.03	N/A	N/A
seq-rs649216	55324635	T	C	N/A	N/A	0.49	0.51
rs145117817	55326739	T	C	0.41	0.43	0.42	0.42
rs12461010	55332601	C	T	0.41	0.43	N/A	N/A
seq-rs1654644	55373362	T	G	0.34	0.34	0.36	0.34
rs3826878	55377211	A	G	0.03	0.04	N/A	N/A
seq-rs17771967	55380214	A	G	N/A	N/A	0.43	0.42
rs11665986	55383941	C	T	0.19	0.19	0.18	0.19
rs12462181	55385435	T	C	0.44	0.44	N/A	N/A

seq-rs3816051	55385604	T	C	0.48	0.48	N/A	N/A
rs10407012	55387953	A	G	0.88	0.88	N/A	N/A
rs7259347	55392755	T	C	N/A	N/A	0.16	0.16
seq-rs4806608	55395582	A	G	0.19	0.20	N/A	N/A
seq-rs1865096	55396900	G	A	0.27	0.28	0.29	0.28
rs1865097	55397217	G	A	0.30	0.32	N/A	N/A
seq-rs16986050	55401170	G	A	0.82	0.82	0.82	0.82
rs7249884	55402691	T	G	0.04	0.04	N/A	N/A
rs10421281	55412835	A	C	0.00	0.00	N/A	N/A
rs2278427	55417731	G	A	0.09	0.08	0.09	0.08
rs2278428	55418054	A	C	0.08	0.08	0.09	0.07
seq-rs1433097	55418458	T	C	0.17	0.16	N/A	N/A
rs16986072	55424307	G	A	0.02	0.01	N/A	N/A
seq-rs1671160	55428459	C	T	0.25	0.26	0.26	0.26
seq-rs11880295	55432529	T	C	0.94	0.94	0.94	0.94
seq-rs775859	55433596	C	T	0.09	0.07	0.09	0.07
seq-rs16986092	55433696	C	T	0.10	0.08	0.08	0.08
rs12461856	55433852	A	G	0.16	0.16	0.17	0.16
rs623383	55434575	A	G	0.52	0.52	0.53	0.52
seq-rs634742	55434818	G	A	0.43	0.45	0.44	0.45
seq-rs269938	55439821	T	G	0.61	0.62	0.61	0.62
seq-rs269939	55439838	G	A	N/A	N/A	0.45	0.45
seq-rs269940	55440357	A	G	N/A	N/A	0.45	0.45
rs269949	55441769	A	G	0.44	0.46	N/A	N/A
seq-rs269950	55441902	C	T	0.44	0.46	N/A	N/A
seq-rs269951	55441995	G	A	0.44	0.46	N/A	N/A
rs269955	55443424	G	A	N/A	N/A	0.41	0.42
seq-rs269957	55445174	T	C	0.27	0.27	0.27	0.28
seq-rs775876	55447572	A	G	0.62	0.62	N/A	N/A
rs7359929	55447595	A	G	0.24	0.22	0.22	0.23
seq-t1d-19-60139424-G-T	55447612	G	T	N/A	N/A	0.22	0.23
rs775879	55449755	G	A	N/A	N/A	0.62	0.62
seq-rs775883	55451797	T	C	0.65	0.65	0.67	0.64
seq-t1d-19-60150968-G-A	55459156	G	A	0.17	0.17	N/A	N/A
rs12460693	55469212	C	A	N/A	N/A	0.16	0.16
seq-t1d-19-60179962-T-C	55488150	T	C	0.16	0.17	N/A	N/A
seq-rs775900	55489349	G	A	N/A	N/A	0.22	0.22
seq-rs7254951	55495106	G	A	0.06	0.06	0.07	0.06
seq-rs1036231	55497843	T	C	0.27	0.27	0.27	0.27
rs10412569	55497855	A	G	N/A	N/A	0.04	0.04

[1] 77 key SNPs in Omni and Ichip1, 66 key SNPs in 660Q and Ichip2 cohort.

Supplementary Table S3. Estimates of the average per-haplotype imputation accuracy for each *KIR* locus in four datasets.

Locus	**Omni (n=791)**	**Ichip1 (n=6703)**	**660Q (n=1352)**	**Ichip2 (n=6725)**
KIR haplotype	86.43	85.18	80.79	82.05
AvsB	97.29	97.08	94.15	94.15
KIR2DS2	98.96	98.96	95.82	95.62
KIR2DL2	98.12	98.33	94.99	95.2
KIR2DL3	98.75	98.75	95.41	95.41
KIR2DP1	91.44	91.86	87.89	88.94
KIR2DL1	91.23	91.44	88.52	88.1
KIR3DP1	96.87	96.87	96.87	96.87
KIR2DL4	97.08	97.08	97.08	97.08
KIR3DL1ex4[1]	97.08	97.08	96.87	96.87
KIR3DL1ex9[1]	96.87	96.87	96.66	96.66
KIR3DS1	96.45	96.45	96.24	96.24
KIR2DL5	89.77	89.77	88.1	88.1
KIR2DS3	91.23	91.44	89.14	88.1
KIR2DS5	96.03	96.24	95.62	95.82
KIR2DS1	97.08	97.08	96.87	96.87
KIR2DS4TOTAL	96.87	96.87	96.66	96.66
KIR2DS4WT	97.91	97.91	97.49	97.49
KIR2DS4DEL	98.75	98.75	98.75	98.75

These data are for the model fitted with the SNP intersection. The estimates are the out-of-bag (OOB) accuracy calculated during the model fitting process [6].

[1] *KIR3DL1* were measured by two different assays, which targeted two different exons, reported as *KIR3DL1ex4* and *KIR3DL1ex9*.

Supplementary Table S4. Estimates of the average per-haplotype imputation accuracy for each *HLA* locus in cases and controls.

Locus	**Omni**	**660Q**	**Ichip**
HLA-A	97.51	97.58	97.51
HLA-B	95.34	95.39	95.34
HLA-C	98.41	98.45	98.41
HLA-DPA1	99.84	99.61	99.84
HLA-DPB1	96.19	95.92	96.19
HLA-DQA1	99.12	99.06	99.12
HLA-DQB1	96.54	96.59	96.54
HLA-DRB1	95	95.09	95
HLA-DRB3	98.98	98.79	98.98
HLA-DRB4	99.37	99.37	99.37
HLA-DRB5	99.67	99.42	99.67

Supplementary Table S5. HLA alleles with $P < 10^{-5}$ in association test with overall cervical neoplasia (cases = 2143, controls = 13428) using three models.

Dosage Model				**Dominant Model**				**Recessive Model**			
HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values
*DRB3*9901*	0.871	1.24	2.49×10^{-9}	*DRB5*0101*	0.255	1.33	4.49×10^{-8}	*DRB5*9901*	0.744	0.75	3.71×10^{-8}
*DRB5*9901*	0.979	0.77	1.90×10^{-8}	*DQB1*0603*	0.106	0.61	5.14×10^{-8}	*DRB3*9901*	0.42	1.25	3.06×10^{-6}
*DRB5*0101*	0.255	1.29	2.26×10^{-8}	*B*0702*	0.268	1.33	6.60×10^{-8}				
*DRB1*1501*	0.27	1.3	4.06×10^{-8}	*DRB1*1501*	0.27	1.34	8.43×10^{-8}				
*DQB1*0603*	0.106	0.63	5.83×10^{-8}	*DRB3*9901*	0.871	1.51	1.91×10^{-7}				
*B*0702*	0.268	1.26	3.13×10^{-7}	*DRB1*1301*	0.11	0.63	8.31×10^{-7}				
*DQA1*0103*	0.113	0.67	7.10×10^{-7}	*DQA1*0103*	0.113	0.66	9.27×10^{-7}				
*DRB1*1301*	0.11	0.65	1.17×10^{-6}	*DRB3*0301*	0.079	0.61	1.94×10^{-6}				
*DQB1*0602*	0.253	1.25	2.04×10^{-6}	*DQB1*0602*	0.253	1.28	2.70×10^{-6}				
*DRB3*0301*	0.079	0.63	4.06×10^{-6}	*C*0702*	0.277	1.24	2.30×10^{-5}				
*C*0702*	0.277	1.21	1.53×10^{-5}	*DQB1*0301*	0.339	1.23	3.07×10^{-5}				
*DQB1*0301*	0.339	1.19	1.62×10^{-5}	*DRB1*1302*	0.087	0.65	3.34×10^{-5}				
*DRB1*1302*	0.087	0.67	5.90×10^{-5}								
*B*1501*	0.12	0.74	8.97×10^{-5}								

In the dosage and dominant models, frequency was calculated as the number of individuals presenting one or two copies of HLA alleles among all individuals. In the recessive model, frequency was calculated as the number of individuals presenting two copies of HLA alleles among all individuals. FRQ, frequency; OR, odds ratio.

Supplementary Table S6. HLA alleles with $P < 10^{-5}$ in association testing with HPV16-related cervical cancer (cases = 667, controls = 13428) using three models.

Dosage Model				**Dominant Model**				**Recessive Model**			
HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values
DRB3*9901	0.868	1.43	1.27×10^{-8}	DRB5*0101	0.252	1.48	5.63×10^{-6}	DRB3*9901	0.418	1.55	6.68×10^{-8}
DRB5*0101	0.252	1.38	1.79×10^{-5}	C*0602	0.171	1.53	9.76×10^{-6}	DRB5*9901	0.748	0.68	6.62×10^{-6}
DRB5*9901	0.98	0.73	2.05×10^{-5}	DRB1*1501	0.266	1.49	1.03×10^{-6}				
DRB1*1501	0.266	1.39	2.59×10^{-5}	B*0702	0.264	1.46	1.85×10^{-5}				
DRB3*0101	0.292	0.7	3.36×10^{-5}	DQB1*0602	0.251	1.43	4.98×10^{-5}				
C*0602	0.171	1.43	5.25×10^{-5}	DRB3*0101	0.292	0.68	5.08×10^{-5}				
DRB1*0301	0.265	0.67	5.55×10^{-5}	DRB1*0301	0.265	0.64	5.43×10^{-5}				

Frequency of individuals presenting HLA alleles among HPV16 infected cases and healthy controls. Frequency for the dosage, dominant and recessive models was calculated as described in Supplementary Table 7. FRQ, frequency; OR, odds ratio.

Supplementary Table S7. HLA alleles with $P < 0.005$ in association testing with HPV18-related cervical cancer (cases = 166, controls = 13428) using three models.

Dosage Model				**Dominant Model**				**Recessive Model**			
HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values
DPA1*0103	0.964	1.89	0.00039	DQB1*0302	0.202	1.74	0.00135	DPA1*0103	0.663	1.99	0.000434
DRB1*1501	0.264	1.64	0.000789	DRB1*1501	0.264	1.76	0.00135	A*2402	0.007	4.54	0.0012
DPA1*0201	0.274	0.52	0.00134	DPA1*0201	0.274	0.51	0.00157				
DQB1*0302	0.202	1.58	0.00302	DRB1*0801	0.045	2.28	0.00456				

Frequency of individuals presenting HLA alleles among HPV18 infected cases and healthy controls. Frequency for the dosage, dominant and recessive models was calculated as described in Supplementary Table 7. FRQ, frequency; OR, odds ratio.

Supplementary Table S8. HLA alleles with $P < 10^{-5}$ in association testing with squamous cell carcinoma (cases = 736, controls = 13428) and adenocarcinoma (cases = 542, controls = 13428) using three models.

	Dosage Model				**Dominant Model**				**Recessive Model**			
	HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values	HLA Alleles	FRQ	OR	*P*-values
Squamous cell carcinoma	DRB5*9901	0.979	0.72	6.57×10^{-6}	DQB1*0301	0.336	1.39	2.80×10^{-5}	DRB5*9901	0.748	0.72	0.000106
	DRB5*0101	0.251	1.38	7.89×10^{-6}	B*1501	0.122	0.54	4.25×10^{-5}				
	DQB1*0301	0.336	1.32	1.95×10^{-5}								
	DQB1*0602	0.25	1.35	3.88×10^{-5}								
	B*1501	0.122	0.55	4.08×10^{-5}								
	DRB1*1501	0.265	1.36	5.54×10^{-5}								
Adenocarcinoma	DRB3*9901	0.868	1.31	7.38×10^{-5}	B*0702	0.263	1.44	0.000182	DPB1*0401	0.198	1.39	0.00162

Frequency of individuals presenting HLA alleles among squamous cell carcinoma cases and healthy controls. Frequency for the dosage, dominant and recessive models was calculated as described in Supplementary Table 7. FRQ, frequency; OR, odds ratio.

Supplementary Table S9. *HLA-Bw4* and *HLA-Bw6* association test with cervical cancer, HPV16-related, HPV18-related cervical cancer, squamous cell carcinoma and adenocarcinoma.

Phenotypes	**Models**	**HLA group**	**Frequency in case group**	**Frequency in control group**	**OR**	**95%CI**	***P*-values**
Cervical cancer	Recessive model	*HLA-Bw4/Bw4*	299/2015(14.8%)	1665/12375(13.5%)	1.12	0.98-1.28	0.10
		HLA-Bw4/Bw6	856/2015 (42.5%)	5143/12375(41.6%)	1.04	0.94-1.14	0.39
		HLA-Bw6/Bw6	650/2015 (32.3%)	3876/12375(31.3%)	1.04	0.94-1.15	0.42
	Dominant model	*HLA-Bw4*	1245/2015(61.8%)	7459/12375(60.3%)	1.07	0.97-1.17	0.18
		HLA-Bw6	1620/2015(80.4%)	9988/12375(80.7%)	0.98	0.87-1.1	0.78
	Dosage model	*HLA-Bw4*	1245/2015(61.8%)	7459/12375(60.3%)	1.06	0.97-1.17	0.076
		HLA-Bw6	1620/2015(80.4%)	9988/12375(80.7%)	1.01	0.87-1.1	0.71
HPV16-related Cervical cancer	Recessive model	*HLA-Bw4/Bw4*	97/623(15.6%)	1665/12375(13.5%)	1.19	0.95-1.48	0.13
		HLA-Bw4/Bw6	286/623(45.9%)	5143/12375(41.6%)	1.2	1.02-1.4	0.029*
		HLA-Bw6/Bw6	188/623(30.2%)	3876/12375(31.3%)	0.94	0.8-1.13	0.53
	Dominant model	*HLA-Bw4*	406/623(65.2%)	7459/12375(60.3%)	1.24	1.04-1.46	0.014*
		HLA-Bw6	502/623(80.6%)	9988/12375(80.7%)	0.99	0.81-1.22	0.94
	Dosage model	*HLA-Bw4*	406/623(65.2%)	7459/12375(60.3%)	1.16	1.04-1.46	0.011*
		HLA-Bw6	502/623(80.6%)	9988/12375(80.7%)	0.97	0.81-1.22	0.64
HPV18-related Cervical cancer	Recessive model	*HLA-Bw4/Bw4*	14/155(9.0%)	1665/12375(13.5%)	0.65	0.37-1.11	0.12
		HLA-Bw4/Bw6	60/155(38.7%)	5143/12375(41.6%)	0.9	0.64-1.23	0.53
		HLA-Bw6/Bw6	59/155(38.1%)	3876/12375(31.3%)	1.34	0.97-1.87	0.079
	Dominant model	*HLA-Bw4*	82/155(52.9%)	7459/12375(60.3%)	0.75	0.54-1.02	0.078
		HLA-Bw6	132/155(85.2%)	9988/12375(80.7%)	1.37	0.88-2.14	0.17
	Dosage model	*HLA-Bw4*	82/155(52.9%)	7459/12375(60.3%)	0.78	0.54-1.02	0.04*
		HLA-Bw6	132/157(85.2%)	9988/12375(80.7%)	1.26	0.88-2.14	0.053
Squamous cell carcinoma	Recessive model	*HLA-Bw4/Bw4*	112/698(16.0%)	1665/12375(13.5%)	1.22	1-1.51	0.062
		HLA-Bw4/Bw6	289/698(41.4%)	5143/12375(41.6%)	1	0.85-1.16	0.97
		HLA-Bw6/Bw6	238/698(34.1%)	3876/12375(31.3%)	1.13	0.97-1.33	0.14
	Dominant model	*HLA-Bw4*	428/698(61.3%)	7459/12375(60.3%)	1.05	0.89-1.22	0.58
		HLA-Bw6	558/698(79.9%)	9988/12375(80.7%)	0.96	0.79-1.15	0.65
	Dosage model	*HLA-Bw4*	428/698(61.3%)	7459/12375(60.3%)	1.08	0.89-1.22	0.18
		HLA-Bw6	558/698(79.9%)	9988/12375(80.7%)	1.04	0.79-1.15	0.47
Adenocarcinoma	Recessive model	*HLA-Bw4/Bw4*	75/507(14.8%)	1665/12375(13.5%)	1.12	0.87-1.43	0.37
		HLA-Bw4/Bw6	205/507(40.4%)	5143/12375(41.6%)	0.97	0.8-1.14	0.73
		HLA-Bw6/Bw6	165/507(32.5%)	3876/12375(31.3%)	1.06	0.88-1.28	0.58
	Dominant model	*HLA-Bw4*	304/507(60.0%)	7459/12375(60.3%)	1	0.82-1.18	0.99
		HLA-Bw6	407/507(80.3%)	9988/12375(80.7%)	0.98	0.78-1.22	0.84
	Dosage model	*HLA-Bw4*	304/507(60.0%)	7459/12375(60.3%)	1.03	0.82-1.18	0.66
		HLA-Bw6	407/507(80.3%)	9988/12375(80.7%)	1.02	0.78-1.22	0.8

*$P < 0.05$.

Three models were applied: a) Dosage model, treating genotypes as 0, 1, or 2 copies, b) dominant model, treating 1 or 2 copy genotypes as present, 0 as absent, c) using recessive model to study the difference of homozygotes and heterozygotes of HLA-B, treating 2 copy genotypes as present, 0 or 1 copy as absent. Frequencies of HLA-B among cases and healthy controls are shown. HLA-Bw4/Bw4 indicates two HLA-Bw4 alleles, HLA-Bw6/Bw6 indicates two HLA-Bw6 alleles, and HLA-Bw4/Bw6 indicates one of each. HLA-Bw4 indicates one or two group Bw4 alleles. *P*-values were calculated by using R code glm model with principal components 1-4; a positive odds ratio indicates a protective association with phenotypes. CI, confidence interval; OR, odds ratio.

Supplementary Table S10. *HLA-C1 and HLA-C2* association testing with cervical cancer, HPV16-related and HPV18-related cervical cancer, squamous cell carcinoma and adenocarcinoma.

Phenotypes	Models	HLA group	Frequency in case group	Frequency in control group	OR	95%CI	*P*-value
Cervical cancer	Recessive model	*HLA-C1/C1*	837/2086(40.1%)	5434/13148(41.3%)	0.96	0.87-1.05	0.389
		HLA-C1/C2	978/2086(46.9%)	6054/13148(46%)	1.03	0.94-1.13	0.539
		HLA-C2/C2	271/2086(13.0%)	1660/13148(12.6%)	1.03	0.9-1.19	0.726
	Dominant model	*HLA-C1*	1815/2086(87.0%)	11488/13148(87.4%)	0.98	0.84-1.11	0.726
		HLA-C2	1249/2086(59.9%)	7714/13148(58.7%)	1.04	0.96-1.15	0.389
	Dosage model	*HLA-C1*	1815/2086(87.0%)	11488/13148(87.4%)	0.97	0.84-1.11	0.424
		HLA-C2	1249/2086(59.9%)	7714/13148(58.7%)	1.03	0.96-1.15	0.424
HPV16-related Cervical cancer	Recessive model	*HLA-C1/C1*	232/649(35.7%)	5434/13148(41.3%)	0.79	0.67-0.93	0.005*
		HLA-C1/C2	326/649(50.2%)	6054/13148(46%)	1.18	1.01-1.38	0.039*
		HLA-C2/C2	91/649(14.0%)	1660/13148(12.6%)	1.13	0.9-1.42	0.29
	Dominant model	*HLA-C1*	558/649(86.0%)	11488/13148(87.4%)	0.88	0.71-1.11	0.29
		HLA-C2	417/649(64.3%)	7714/13148(58.7%)	1.27	1.07-1.49	0.005*
	Dosage model	*HLA-C1*	558/649(86.0%)	11488/13148(87.4%)	0.86	0.71-1.11	0.0103*
		HLA-C2	417/649(64.3%)	7714/13148(58.7%)	1.16	1.07-1.49	0.0103*
HPV18-related Cervical cancer	Recessive model	*HLA-C1/C1*	77/160(48.1%)	5434/13148(41.3%)	1.32	0.96-1.8	0.0786
		HLA-C1/C2	65/160(40.6%)	6054/13148(46%)	0.8	0.58-1.1	0.165
		HLA-C2/C2	18/160(11.2%)	1660/13148(12.6%)	0.88	0.54-1.44	0.599
	Dominant model	*HLA-C1*	142/160(88.8%)	11488/13148(87.4%)	1.14	0.7-1.87	0.599
		HLA-C2	83/160(51.9%)	7714/13148(58.7%)	0.76	0.56-1.04	0.0786
	Dosage model	*HLA-C1*	142/160(88.8%)	11488/13148(87.4%)	1.21	0.7-1.87	0.123
		HLA-C2	83/160(51.9%)	7714/13148(58.7%)	0.83	0.56-1.04	0.123
Squamous cell carcinoma	Recessive model	*HLA-C1/C1*	289/713(40.5%)	5434/13148(41.3%)	0.98	0.83-1.13	0.8
		HLA-C1/C2	341/713(47.8%)	6054/13148(46%)	1.07	0.92-1.25	0.399
		HLA-C2/C2	83/713(11.6%)	1660/13148(12.6%)	0.9	0.72-1.15	0.374
	Dominant model	*HLA-C1*	630/713(88.8%)	11488/13148(87.4%)	1.11	0.87-1.39	0.374
		HLA-C2	424/713(59.5%)	7714/13148(58.7%)	1.02	0.89-1.2	0.8
	Dosage model	*HLA-C1*	630/713(88.8%)	11488/13148(87.4%)	1.01	0.87-1.39	0.799
		HLA-C2	424/713(59.5%)	7714/13148(58.7%)	0.99	0.89-1.2	0.799
Adenocarcinoma	Recessive model	*HLA-C1/C1*	208/530(39.3%)	5434/13148(41.3%)	0.94	0.77-1.1	0.466
		HLA-C1/C2	247/530(46.4%)	6054/13148(46%)	1.01	0.86-1.22	0.906
		HLA-C2/C2	75/530(14.3%)	1660/13148(12.6%)	1.12	0.89-1.46	0.372
	Dominant model	*HLA-C1*	455/530(85.7%)	11488/13148(87.4%)	0.89	0.68-1.13	0.372
		HLA-C2	322/530(60.7%)	7714/13148(58.7%)	1.07	0.91-1.3	0.466
	Dosage model	*HLA-C1*	455/530(85.7%)	11488/13148(87.4%)	0.94	0.68-1.13	0.332
		HLA-C2	322/530(60.7%)	7714/13148(58.7%)	1.07	0.91-1.3	0.332

*$P < 0.05$.

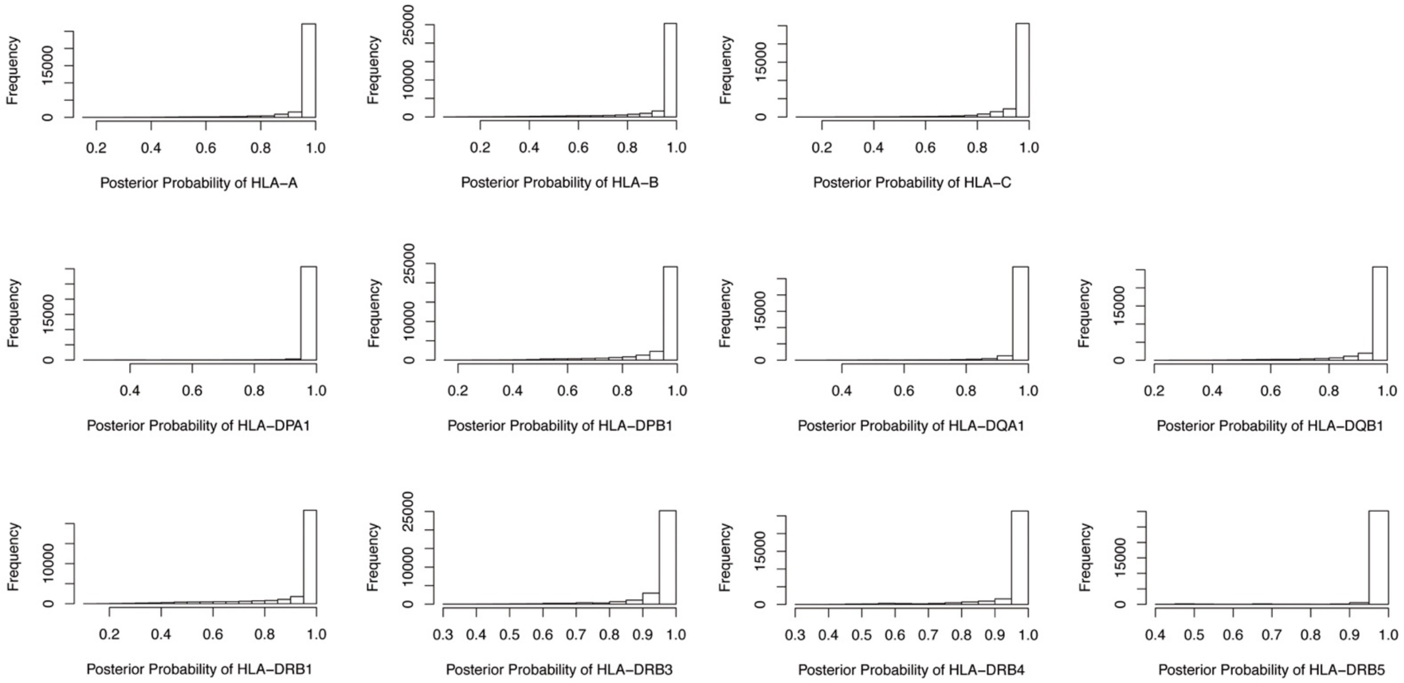
Frequencies of *HLA-C* among cases and healthy controls are shown. In the recessive model, *HLA- C1/C1* indicates two group 1 *HLA-C* alleles, *HLA-C2/C2* indicates two group 2 *HLA-C* alleles, and *HLA-C1/C2* indicates one of each. In the dominant model, *HLA-C1* indicates one or two group *C1* alleles, *HLA-C2* indicates one or two group *C2* alleles. In the dosage model, *HLA-C1* indicates one and two group *C1* alleles, *HLA-C2* indicates one and two group *C2* alleles. *P*-values were calculated by using R code glm model with principal components 1-4; a positive odds ratio indicates a protective association with phenotypes. CI, confidence interval; OR, odds ratio.

Supplementary Table S11. Control-control association test between Ichip1 and Ichip2 imputed data were conducted to check *KIR* imputation concordance using two different groups of key SNPs.

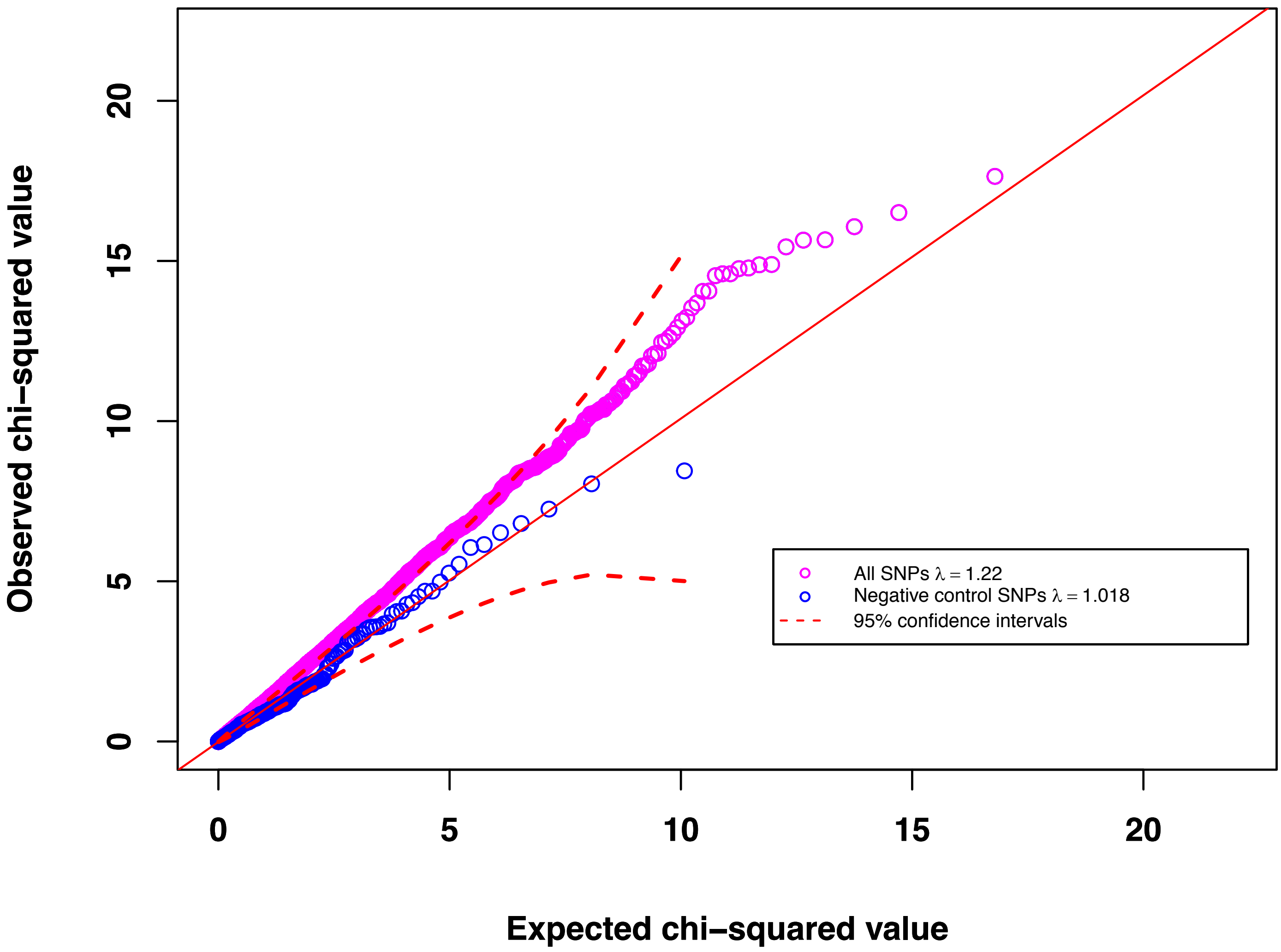
GENE	*P*-value	Ichip1 (number of individuals passed QC)	Ichip2 (number of individuals passed QC)	KIR Frequency in Ichip1	KIR Frequency in Ichip2
KIR2DS3[1]	6.14E-14	5303	5465	0.091	0.138
KIR2DL1[1]	0.000565	5344	5650	0.988	0.979
KIR2DP1[1]	0.00242	5342	5649	0.988	0.981
KIR2DL5[1]	0.0055	5617	5687	0.402	0.427
KIR2DS4DEL	0.101	6721	6696	0.82	0.809
KIR2DS2	0.112	6517	6650	0.519	0.506
KIR2DL2	0.364	6428	6645	0.513	0.506
KIR2DS4WT	0.374	6654	6654	0.376	0.384
KIR2DS5	0.446	6364	6417	0.277	0.283
KIR2DS4TOTAL	0.454	6677	6648	0.956	0.953
KIR3DL1ex4	0.484	6678	6654	0.956	0.953
KIR2DL3	0.493	6523	6665	0.904	0.907
KIR3DL1ex9	0.55	6683	6647	0.956	0.953
KIR2DS1	0.594	6684	6661	0.371	0.376
KIR3DS1	0.902	6542	6499	0.364	0.365

[1] Four *KIR* genes with *P*-value < 0.05 were not analysed further as any apparent interactions could be due to inconsistent imputation results.

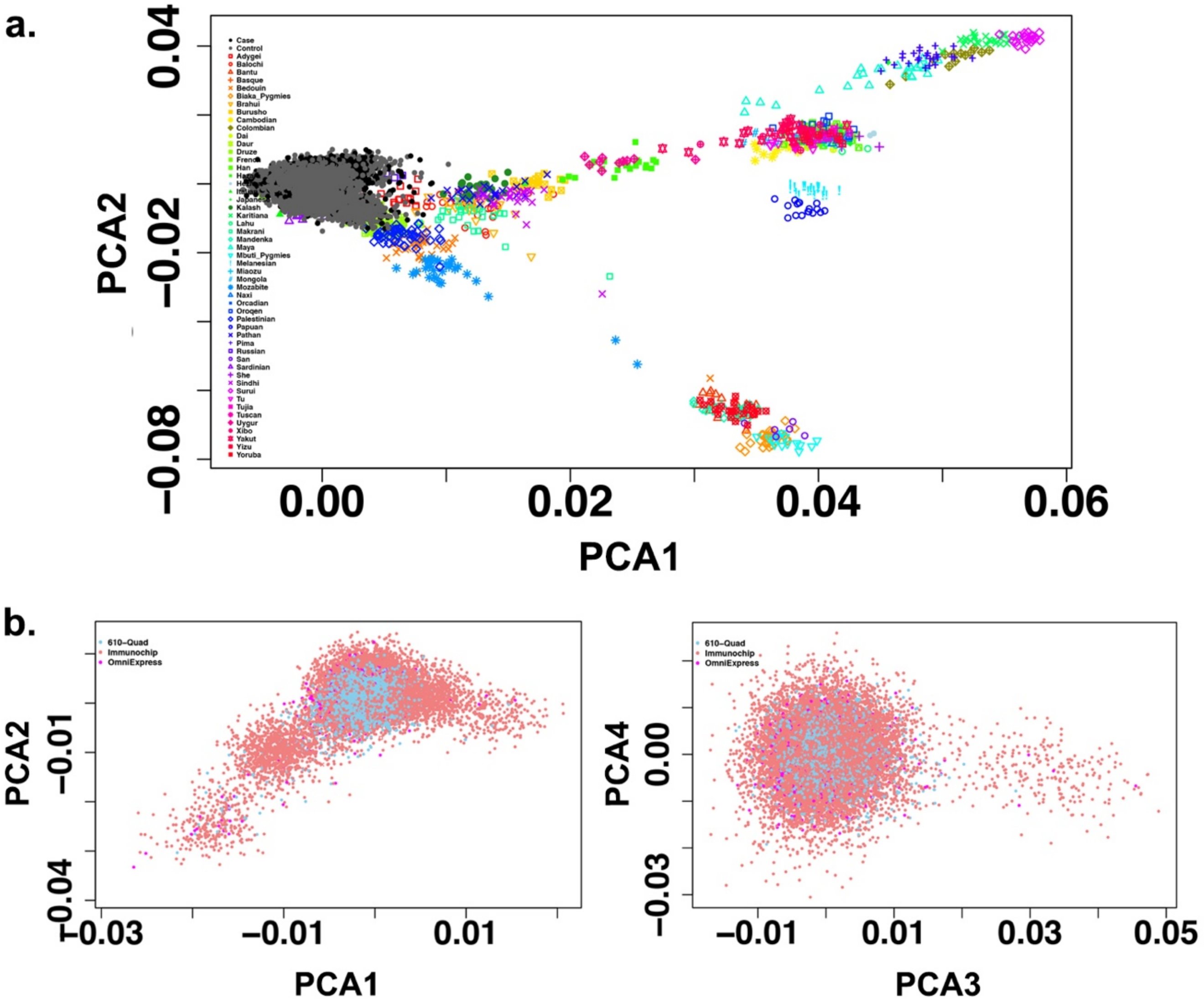
SUPPLEMENTARY FIGURES



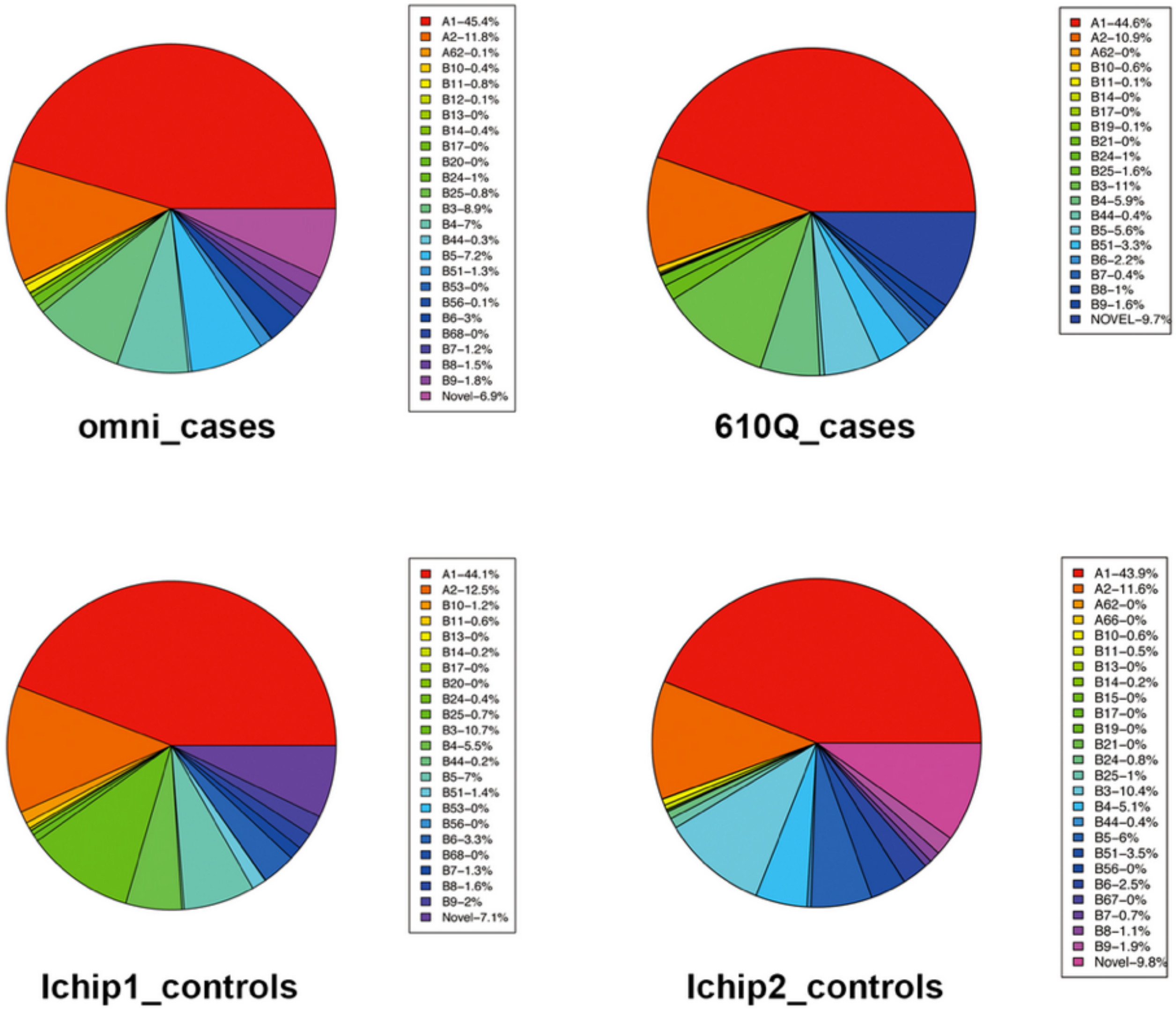
Supplementary Figure S1. Distribution of HLA imputation posterior probability of 11 *HLA* loci in all subjects (n=15571). Individuals with posterior probability < 0.6 were excluded in downstream association testing.



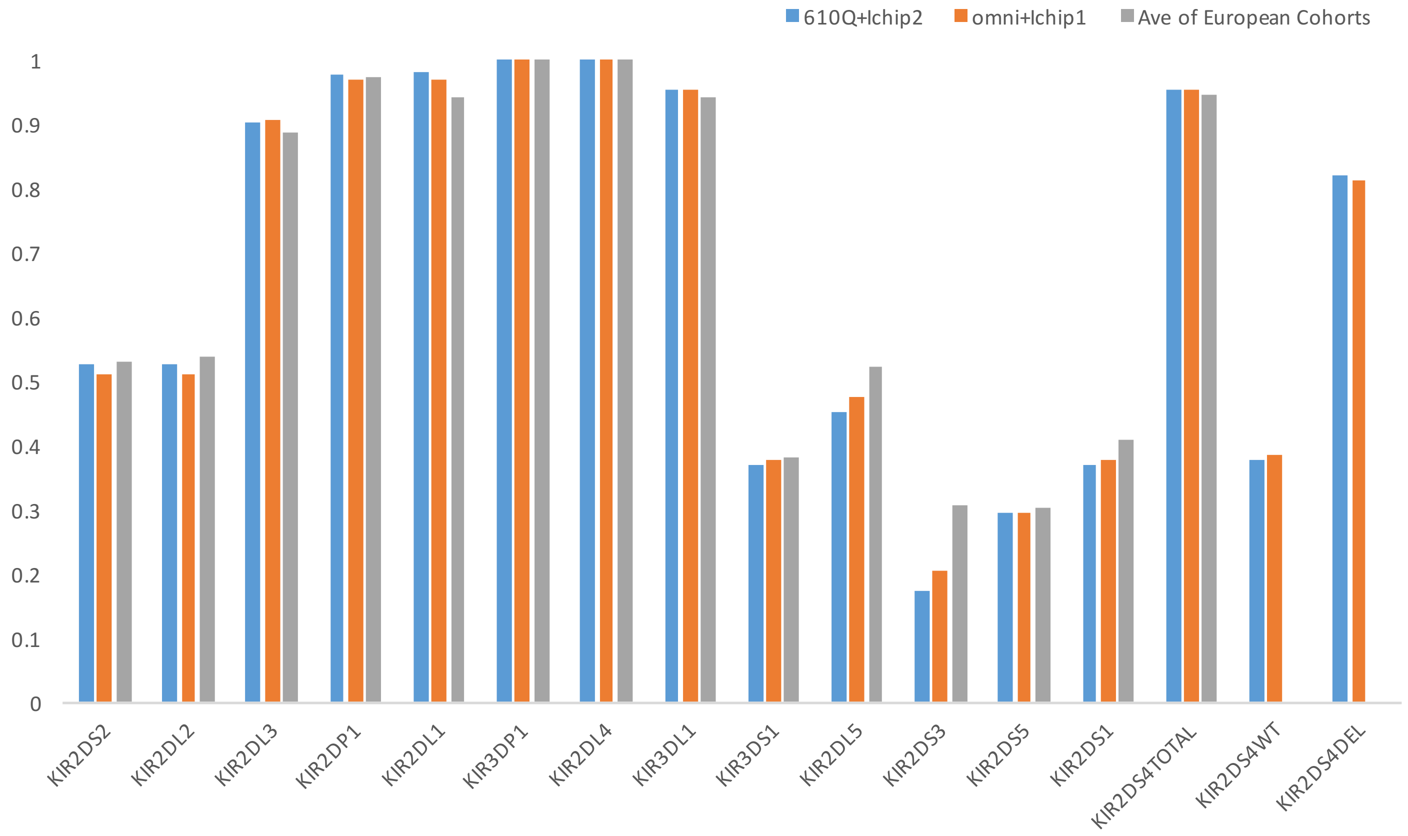
Supplementary Figure S2. Quantile-Quantile plot of observed versus expected chi-squared value for association analysis of cervical neoplasia. Pink, 11980 common SNPs between OmniExpress, 660-Quad and Immunochip datasets. The genomic inflation factor in all common SNPs listed was 1.220. Blue, a negative control set of common SNPs, excluding MHC region, associated with reading and learning disability, schizophrenia and psychosis. The genomic inflation factor in the negative control SNP list was 1.018.



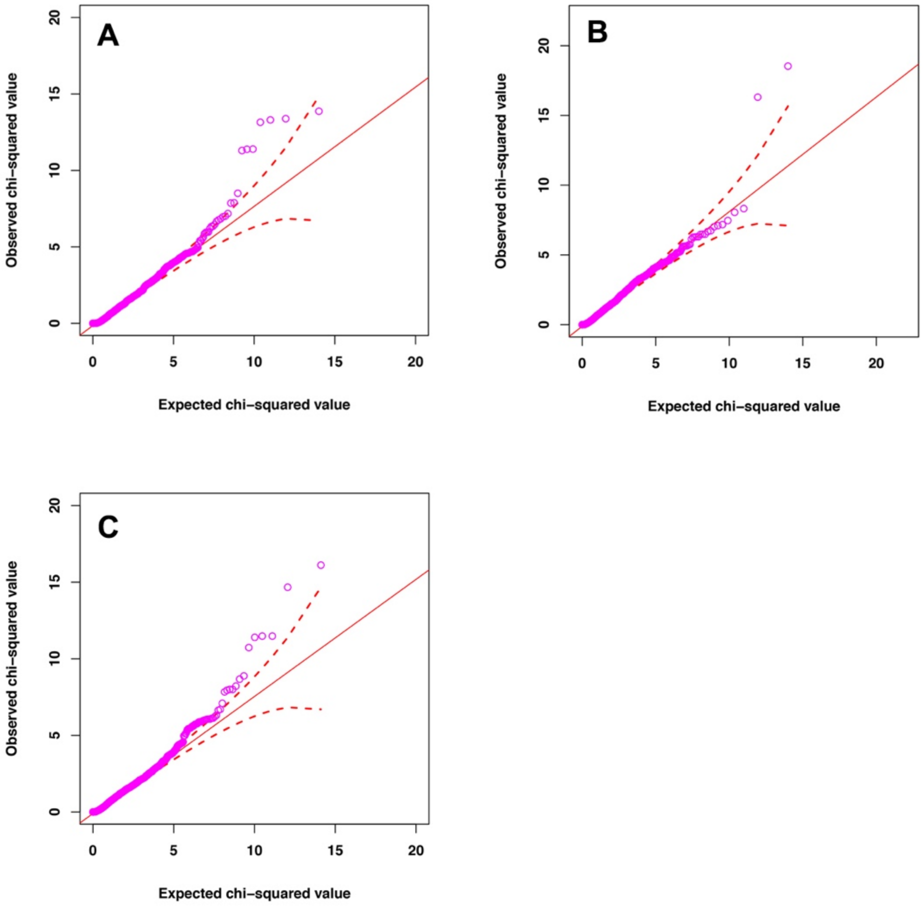
Supplementary Figure S3. PCA plots. All our studies were conducted among majority European descent populations, and no divergence was seen between cases and controls or between different genotype platforms. a, cases and controls are labelled by black and grey, respectively. b, all study subjects, labelled by three different colours, representing each different genotyping platforms.



Supplementary Figure S4. Proportion of KIR A and B haplotype subtypes in cervical neoplasia cases and controls. Haplotypes were numbered according to Jiang *et al.* (2012)[7] based on gene content, and those prefixed with 'N' are considered novel, high-confidence haploptypes that were not reported in this publication.



Supplementary Figure S5. Percentage of Omni-Ichip1 and 660Q-Ichip2 cohorts carrying each *KIR* gene relative to percentages averaged across published European cohorts. Frequencies were calculated by summing the number of individuals that carry at least one copy of a given gene and dividing by the total number of individuals. Published data is the average of KIR gene frequency of Serbia (n=134), England (n=584), Italy (n=217), USA (n=195), Australia (n=50). Details can be found at http://www.allelefrequencies.net/default.asp



Supplementary Figure S6. Quantile-Quantile plots of association for KIR-HLA alleles interaction on cervical neoplasia presented: A) Omni-Ichip1, B) 660Q-Ichip2 and C) meta-analysis of Omni-Ichip1 and 660Q-Ichip2.

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