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Table S1. Overview of Sjogren's syndrome and cancer data.

GWAS ID	Trait	Case	Control	Sample size	Year	Consortium	Population
Sjogren's syndrome							
finn-b-M13_SJOGR	Sicca syndrome	1290	213145	214435	2021	FINNGEN	European
ebi-a-GCST9001392	Sjogren's syndrome (Si	NA	NA	407746	2021	NA	European
ebi-a-GCST9001387	Sjogren's syndrome (Fi	NA	NA	407746	2021	NA	European
Lung cancer							
ebi-a-GCST004744	Lung adenocarcinoma	11273	55483	66756	2017	NA	European
ebi-a-GCST004747	Lung cancer in never s	2355	7504	9859	2017	NA	European
ebi-a-GCST004748	Lung cancer	29266	56450	85716	2017	NA	European
ebi-a-GCST004749	Lung cancer in ever sr	23223	16964	40187	2017	NA	European
ebi-a-GCST9001887	Lung cancer	3791	489012	492803	2021	NA	European
finn-b-C3_BRONCH	Malignant neoplasm of	1681	173993	NA	2021	NA	European
finn-b-C3_LUNG_N	Non-small cell lung can	1627	174006	NA	2021	NA	European
finn-b-C3_NSCLC_A	Non-small cell lung can	571	174005	NA	2021	NA	European
finn-b-C3_NSCLC_S	Non-small cell lung can	365	174004	NA	2021	NA	European
finn-b-C3_SCLC_EX	Small cell lung cancer (	179	174006	NA	2021	NA	European
ieu-a-965	Lung adenocarcinoma	3442	14894	18336	2014	ILCCO	European
ieu-a-966	Lung cancer	11348	15861	27209	2014	ILCCO	European
ieu-a-967	Squamous cell lung cai	3275	15038	18313	2014	ILCCO	European
ieu-a-984	Lung adenocarcinoma	11245	54619	65864	NA	TRICL	European
ieu-a-985	Lung cancer	23848	16605	40453	NA	TRICL	European
ieu-a-986	Lung cancer	2303	6995	9298	NA	TRICL	European
ieu-a-987	Lung cancer	29863	55586	85449	NA	TRICL	European
ieu-a-989	Squamous cell lung cai	7704	54763	62467	NA	TRICL	European
ieu-b-4954	Lung cancer	2671	372016	374687	2021	UK Biobank	European
ieu-b-4955	Lung cancer	2671	372016	374687	2021	UK Biobank	European
ukb-a-54	Cancer code self-repor	190	336969	337159	2017	Neale Lab	European
ukb-d-C_RESPIRAT	Cancer of respiratory ir	1944	359250	361194	2018	NA	European
ukb-d-LUNG_CANC	Lung cancer and meso	2007	359187	361194	2018	NA	European
Breast cancer							
ebi-a-GCST007236	Breast cancer	46785	42892	89677	2015	NA	European
ebi-a-GCST004988	Breast cancer	76192	63082	139274	2017	NA	European
ebi-a-GCST9001879	Breast cancer	17389	240341	257730	2021	NA	European
finn-b-C3_BREAST_	Malignant neoplasm of	8401	99321	NA	2021	NA	European
finn-b-C3_BREAST_	Malignant neoplasm of	7355	99321	NA	2021	NA	European
finn-b-C3_BREAST_	Malignant neoplasm of	3092	99267	NA	2021	NA	European

finn-b-C3_BREAST_Malignant neoplasm of	4263	99267	NA	2021	NA	European
finn-b-CD2_INSITU_Carcinoma in situ of br	1131	102391	NA	2021	NA	European
finn-b-CD2_INSITU_Carcinoma in situ of br	1022	102406	NA	2021	NA	European
finn-b-CD2_INSITU_Carcinoma in situ of br	160	102499	NA	2021	NA	European
ieu-a-1126 Breast cancer (Combin	122977	105974	228951	2017	BCAC	European
ieu-a-1127 ER+ Breast cancer (Co	69501	105974	175475	2017	BCAC	European
ieu-a-1128 ER- Breast cancer (Cor	21468	105974	127442	2017	BCAC	European
ieu-a-1129 Breast cancer (Oncoar	61282	45494	106776	2017	BCAC	European
ieu-a-1130 Breast cancer (iCOGS)	46785	42892	89677	2017	BCAC	European
ieu-a-1131 Breast cancer (GWAS)	14910	17588	32498	2017	BCAC	European
ieu-a-1132 ER+ Breast cancer (On	38197	45494	83691	2017	BCAC	European
ieu-a-1133 ER+ Breast cancer (iC	27078	42892	69970	2017	BCAC	European
ieu-a-1134 ER+ Breast cancer (GV	4226	17588	21814	2017	BCAC	European
ieu-a-1135 ER- Breast cancer (On	9655	45494	55149	2017	BCAC	European
ieu-a-1136 ER- Breast cancer (iCC	7333	42892	50225	2017	BCAC	European
ieu-a-1137 ER- Breast cancer (GV	4480	17588	22068	2017	BCAC	European
ieu-a-1160 ER- Breast cancer (iCC	7333	42892	50225	2015	BCAC	European
ieu-a-1161 ER+ Breast cancer (iC	27078	42892	69970	2015	BCAC	European
ieu-a-1162 Breast cancer (iCOGS)	46785	42892	89677	2015	BCAC	European
ieu-a-1163 ER- Breast cancer (Sur	920	5961	6881	2015	BCAC	European
ieu-a-1164 ER+ Breast cancer (Su	1333	21726	23059	2015	BCAC	European
ieu-a-1165 Breast cancer (Survival	2900	35054	37954	2015	BCAC	European
ieu-a-1166 ER- Breast cancer (GV	3611	18084	21695	2015	BCAC	European
ieu-a-1167 ER+ Breast cancer (GV	4202	18084	22286	2015	BCAC	European
ieu-a-1168 Breast cancer (GWAS)	15748	18084	33832	2015	BCAC	European
ieu-b-4810 Breast cancer	13879	198523	212402	2021	UK Biobank	European
ukb-a-55 Cancer code self-repor	7480	329679	337159	2017	Neale Lab	European
ukb-b-6352 Type of cancer: ICD10:	3340	459670	463010	2018	MRC-IEU	European
Genital cancer						
ebi-a-GCST006085 Prostate cancer	79148	61106	140254	2018	NA	European
ebi-a-GCST006464 Endometrial cancer	12906	108979	121885	2018	NA	European
ebi-a-GCST006465 Endometrial cancer (en	8758	46126	54884	2018	NA	European
ebi-a-GCST006466 Endometrial cancer (Nc	1230	35447	36677	2018	NA	European
ebi-a-GCST9001881 Cervical cancer	909	238249	239158	2021	NA	European
ebi-a-GCST9001883 Endometrial cancer	2188	237839	240027	2021	NA	European
ebi-a-GCST9001888 Ovarian cancer	1588	244932	246520	2021	NA	European
ebi-a-GCST9001890 Prostate cancer	11599	199628	211227	2021	NA	European

finn-b-C3_CERVIX_	Malignant neoplasm of	1648	99321	NA	2021	NA	European
finn-b-C3_CORPUS_	Malignant neoplasm of	1053	99321	NA	2021	NA	European
finn-b-C3_FEMALE_	malignant neoplasm of	3665	99321	NA	2021	NA	European
finn-b-C3_FEMALE_	Malignant neoplasm of	106	99321	NA	2021	NA	European
finn-b-C3_MALE_	GE malignant neoplasm of	6542	74685	NA	2021	NA	European
finn-b-C3_OVARY_	E Malignant neoplasm of	719	99321	NA	2021	NA	European
finn-b-C3_PROSTA	1 Malignant neoplasm of	6311	74685	NA	2021	NA	European
finn-b-C3_TESTIS_	E Malignant neoplasm of	199	74685	NA	2021	NA	European
finn-b-CD2_BENIGN	Leiomyoma of uterus (c	18060	88982	NA	2021	NA	European
finn-b-C3_VULVA_	E Malignant neoplasm of	125	99321	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ce	129	102500	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ce	298	102485	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ce	107	102504	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ute	109	102506	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of oth	115	102478	NA	2021	NA	European
ieu-a-1120	Ovarian cancer	25509	40941	66450	2017	OCAC	European
ieu-a-1121	High grade serous ova	13037	40941	53978	2017	OCAC	European
ieu-a-1122	Low grade serous ovar	1012	40941	41953	2017	OCAC	European
ieu-a-1123	Invasive mucinous ova	1417	40941	42358	2017	OCAC	European
ieu-a-1124	Clear cell ovarian canc	1366	40941	42307	2017	OCAC	European
ieu-a-1125	Endometrioid ovarian c	2810	40941	43751	2017	OCAC	European
ieu-a-1228	High grade and low gra	14049	40941	54990	2017	OCAC	European
ieu-a-1229	Serous ovarian cancer:	2966	40941	43907	2017	OCAC	European
ieu-a-1230	Serous ovarian cancer:	1954	40941	42895	2017	OCAC	European
ieu-a-1231	Mucinous ovarian canc	2566	40941	43507	2017	OCAC	European
ieu-a-1232	Low malignant potentia	1149	40941	42090	2017	OCAC	European
ieu-a-1233	Low malignant potentia	3103	40941	47147	2017	OCAC	European
ieu-a-1235	High grade and low gra	NA	NA	0	2017	OCAC	European
ieu-a-1236	High grade serous ova	NA	NA	0	2017	OCAC	European
ieu-a-1237	Ovarian cancer (surviv:	NA	NA	0	2017	OCAC	European
ieu-b-4963	Ovarian cancer	1218	198523	199741	2021	UK Biobank	European
ieu-b-4809	Prostate cancer	9132	173493	182625	2021	UK Biobank	European
ieu-b-4876	cervical cancer	563	198523	199086	2021	NA	European
ieu-b-85	Prostate cancer	79148	61106	NA	2018	PRACTICAL	European
ukb-a-57	Cancer code self-repor	2495	334664	337159	2017	Neale Lab	European
ukb-b-1392	Type of cancer: ICD10:	7847	455163	463010	2018	MRC-IEU	European
ukb-b-14956	Type of cancer: ICD10:	1494	461516	463010	2018	MRC-IEU	European

ukb-b-18157	Malignant neoplasm of	1087	461923	463010	2018	MRC-IEU	European
ukb-d-C_FEMALE_C	Cancer of female genital	2603	358591	361194	2018	NA	European
ukb-d-C_MALE_GE	Cancer of male genital	6795	354399	361194	2018	NA	European
ukb-d-C_URINARY_	Cancer of urinary tract	1841	359353	361194	2018	NA	European
Digestive tract & oral							
ebi-a-GCST003739	Esophageal adenocarc	4112	17159	21271	2016	NA	European
ebi-a-GCST003740	Barrett's esophagus or	6167	4112	27438	2016	NA	European
ebi-a-GCST012234	Oral cavity and pharynx	2342	2329	4671	2016	NA	European
ebi-a-GCST012235	Oral cavity and pharynx	2497	2928	5425	2016	NA	European
ebi-a-GCST012237	Oral cavity cancer	1223	2928	4151	2016	NA	European
ebi-a-GCST012238	Oral cavity cancer	1135	2329	3464	2016	NA	European
ebi-a-GCST012241	Oropharynx cancer	1090	2928	4018	2016	NA	European
ebi-a-GCST012242	Oropharynx cancer	1119	2329	3448	2016	NA	European
ebi-a-GCST012876	Colorectal cancer	11895	14659	26554	2018	NA	European
ebi-a-GCST012877	Colorectal cancer	11835	11856	23691	2018	NA	European
ebi-a-GCST012878	Colorectal cancer	1460	774	2234	2018	NA	European
ebi-a-GCST012879	Colorectal cancer	19948	12124	32072	2018	NA	European
ebi-a-GCST012880	Colorectal cancer	4439	4115	8554	2018	NA	European
ebi-a-GCST9001386	Colorectal cancer (Firth	NA	NA	407746	2021	NA	European
ebi-a-GCST9001386	Colorectal cancer (SPA	NA	NA	407746	2021	NA	European
ebi-a-GCST9001880	Colorectal cancer	6581	463421	470002	2021	NA	European
ebi-a-GCST9001884	Esophageal cancer	998	475308	476306	2021	NA	European
ebi-a-GCST9001884	Gastric cancer	1029	475087	476116	2021	NA	European
ebi-a-GCST9001889	Pharyngeal and larynge	329	355235	355564	2021	NA	European
finn-b-C3_ANUS_A	Malignant neoplasm of	108	174006	NA	2021	NA	European
finn-b-C3_COLON_	Colon adenocarcinoma	1396	174006	NA	2021	NA	European
finn-b-C3_COLON_E	Malignant neoplasm of	1803	174006	NA	2021	NA	European
finn-b-C3_COLORE	Colorectal cancer (all c	3022	174006	NA	2021	NA	European
finn-b-C3_DIGESTI	Malignant neoplasm of	5253	174006	NA	2021	NA	European
finn-b-C3_OESOPH	Malignant neoplasm of	232	174006	NA	2021	NA	European
finn-b-C3_RECTOSI	Malignant neoplasm of	198	174006	NA	2021	NA	European
finn-b-C3_RECTUM	Malignant neoplasm of	1078	174006	NA	2021	NA	European
finn-b-C3_SMALL_I	Malignant neoplasm of	252	174006	NA	2021	NA	European
finn-b-C3_STOMAC	Malignant neoplasm of	633	174006	NA	2021	NA	European
ieu-b-4913	Laryngeal cancer	273	372016	372289	2021	UK Biobank	European
ieu-b-4960	Oesophageal cancer	740	372016	372756	2021	UK Biobank	European
ieu-b-4961	Oral cavity cancer	357	372016	372373	2021	UK Biobank	European

ieu-b-4962	Oral and oropharyngea	839	372016	372855	2021	UK Biobank	European
ieu-b-4965	Colorectal cancer	5657	372016	377673	2021	UK Biobank	European
ieu-b-4968	Oropharyngeal cancer	494	372016	372510	2021	UK Biobank	European
ieu-b-86	Oral cavity and pharynx	2497	2928	5425	2016	Intoarray oral cavity and oropharyngeal cancer	European
ieu-b-87	Oral cavity and pharynx	2342	2329	4671	2016	Intoarray oral cavity and oropharyngeal cancer	European
ieu-b-89	Oral cavity and pharynx	2497	2928	5425	2016	Intoarray oral cavity and oropharyngeal cancer	European
ieu-b-90	Oral cavity and pharynx	2342	2329	4671	2016	Intoarray oral cavity and oropharyngeal cancer	European
ieu-b-93	Oral cavity cancer	1135	2329	3464	2016	Intoarray oral cavity and oropharyngeal cancer	European
ieu-b-94	Oral cavity cancer	1223	2928	4151	2016	Intoarray oral cavity and oropharyngeal cancer	European
ieu-b-96	Oropharyngeal cancer	1090	2928	4018	2016	Intoarray oral cavity and oropharyngeal cancer	European
ieu-b-97	Oropharyngeal cancer	1119	2329	3448	2016	Intoarray oral cavity and oropharyngeal cancer	European
ukb-a-56	Cancer code self-report	156	337003	337159	2017	Neale Lab	European
ukb-b-1251	Type of cancer: ICD10:	1470	461540	463010	2018	MRC-IEU	European
ukb-b-15775	Type of cancer: ICD10:	1241	461769	463010	2018	MRC-IEU	European
ukb-b-4674	Type of cancer: ICD10:	1917	461093	463010	2018	MRC-IEU	European
ukb-d-C_DIGESTIVE	Cancer of digestive org	5690	355504	361194	2018	NA	European
Skin cancer							
ebi-a-GCST9001892	Skin cancer	25928	466275	492203	2021	NA	European
finn-b-C3_MELANOI	Malignant melanoma of	98	174006	NA	2021	NA	European
finn-b-C3_OTHER_5	Other malignant neoplas	10382	174006	NA	2021	NA	European
finn-b-C3_SKIN_EX	Malignant neoplasm of	10384	174006	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi (all c	4035	178083	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi of lip	122	180663	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi of lo	510	180434	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi of ey	123	180668	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi, othe	825	180262	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi of sc	317	180530	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi of tru	1464	179849	NA	2021	NA	European
finn-b-CD2_BENIGN	Melanocytic naevi of up	267	180588	NA	2021	NA	European
finn-b-CD2_INSITU_	Melanoma in situ (all c	393	180622	NA	2021	NA	European
finn-b-CD2_INSITU_	Melanoma in situ of oth	118	180715	NA	2021	NA	European
finn-b-CD2_INSITU_	Melanoma in situ of tru	103	180719	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ski	122	180724	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ski	1379	180245	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ski	749	180489	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ski	167	180699	NA	2021	NA	European
finn-b-CD2_INSITU_	Carcinoma in situ of ski	99	180722	NA	2021	NA	European

finn-b-CD2_INSITU_Carcinoma in situ of ski	154	180703	NA	2021	NA	European
finn-b-CD2_INSITU_Carcinoma in situ of ski	228	180692	NA	2021	NA	European
finn-b-CD2_INSITU_Carcinoma in situ of ski	165	180699	NA	2021	NA	European
ieu-b-4969 Melanoma skin cancer	3751	372016	375767	2021	UK Biobank	European
ukb-a-58 Cancer code self-report	2677	334482	337159	2017	Neale Lab	European
ukb-a-59 Cancer code self-report	3156	334003	337159	2017	Neale Lab	European
ukb-a-60 Cancer code self-report	404	336755	337159	2017	Neale Lab	European
ukb-b-10248 Type of cancer: ICD10:	6034	456976	463010	2018	MRC-IEU	European
ukb-b-15685 Type of cancer: ICD10:	2605	460405	463010	2018	MRC-IEU	European
ukb-b-17174 Type of cancer: ICD10:	1225	461785	463010	2018	MRC-IEU	European
ukb-d-C_SKIN Cancer of skin	16531	344663	361194	2018	NA	European
Other cancer(bile duct, liver, pancreas)						
ebi-a-GCST9001386 Thyroid cancer (Firth c	NA	NA	407746	2021	NA	European
ebi-a-GCST9001386 Thyroid cancer (SPA c	NA	NA	407746	2021	NA	European
ebi-a-GCST9001880 Hepatic bile duct cance	832	475259	476091	2021	NA	European
ebi-a-GCST9001885 Hepatic cancer	379	475259	475638	2021	NA	European
ebi-a-GCST9001889 Pancreatic cancer	1196	475049	476245	2021	NA	European
ebi-a-GCST9001892 Thyroid cancer	1054	490920	491974	2021	NA	European
ebi-a-GCST9008604 Cancer	17131	39506	56637	2021	NA	European
ebi-a-GCST9008604 Cancer	17131	39506	56637	2021	NA	European
ebi-a-GCST9008605 Cancer	17131	39506	56637	2021	NA	European
ebi-a-GCST9008605 Cancer	17131	39506	56637	2021	NA	European
finn-b-C3_BILIARY_Malignant neoplasm of	109	174006	NA	2021	NA	European
finn-b-C3_BLADDEF Malignant neoplasm of	1115	174006	NA	2021	NA	European
finn-b-C3_BRAIN_E Malignant neoplasm of	464	174006	NA	2021	NA	European
finn-b-C3_CONNEC Malignant neoplasm of	275	174006	NA	2021	NA	European
finn-b-C3_ENDOCR Malignant neoplasm of	1069	174006	NA	2021	NA	European
finn-b-C3_EYE_AD Malignant neoplasm of	161	174006	NA	2021	NA	European
finn-b-C3_EYE_BRA Malignant neoplasm of	1446	174006	NA	2021	NA	European
finn-b-C3_GBM_EX Brain glioblastoma (all	91	174006	NA	2021	NA	European
finn-b-C3_HEART_M Malignant neoplasm of	102	174006	NA	2021	NA	European
finn-b-C3_KIDNEY_I Malignant neoplasm of	971	174006	NA	2021	NA	European
finn-b-C3_LARYNX Malignant neoplasm of	180	174005	NA	2021	NA	European
finn-b-C3_LIP_ORAL Malignant neoplasm of	126	174006	NA	2021	NA	European
finn-b-C3_MENINGE Malignant neoplasm of	640	174006	NA	2021	NA	European
finn-b-C3_MESOTHI Mesothelioma (all canc	133	174006	NA	2021	NA	European
finn-b-C3_MESTOTI Malignant neoplasm of	497	174006	NA	2021	NA	European

finn-b-C3_PANCRE/	Malignant neoplasm of	605	174006	NA	2021	NA	European
finn-b-C3_LIVER_INT	Malignant neoplasm of	304	174006	NA	2021	NA	European
finn-b-C3_RESPIRA	Malignant neoplasm of	2074	173985	NA	2021	NA	European
finn-b-C3_SPINAL_(	Malignant neoplasm of	198	174006	NA	2021	NA	European
finn-b-C3_THYROID	Malignant neoplasm of	989	174006	NA	2021	NA	European
finn-b-C3_UNCERT/	Secondary uncertain m	1600	174006	NA	2021	NA	European
finn-b-C3_URINARY	Malignant neoplasm of	2168	174006	NA	2021	NA	European
ieu-b-4874	Bladder cancer	1279	372016	373295	2021	NA	European
ieu-b-4875	brain cancer	606	372016	372622	2021	NA	European
ieu-b-4912	Head and neck cancer	1106	372016	373122	2021	UK Biobank	European
ieu-b-4959	Malignant non-melanor	23694	372016	395710	2021	UK Biobank	European
ieu-b-4964	Pan cancer	50643	372016	422659	2021	UK Biobank	European
ieu-b-4966	Pan cancer	70223	372016	442239	2021	UK Biobank	European
ieu-a-822	Pancreatic cancer	1896	1939	3835	2009	PanScan1	European
ieu-b-4915	Liver & bile duct cancer	350	372016	372366	2021	UK Biobank	European
Blood system and bone							
finn-b-C3_AML_EXA	Acute myeloid leukaem	90	174006	NA	2021	NA	European
finn-b-C3_CLL_EXA	Chronic lymphocytic lei	265	174004	NA	2021	NA	European
finn-b-C3_DLBCL_E	Diffuse large B-cell lym	209	174006	NA	2021	NA	European
finn-b-C3_LYMPHN(	Secondary and unspec	995	174006	NA	2021	NA	European
finn-b-CD2_BENIGN	Haemangioma and lym	1243	179808	NA	2021	NA	European
finn-b-CD2_BENIGN	Haemangioma, any site	1144	179883	NA	2021	NA	European
finn-b-CD2_BENIGN	Lymphangioma, anys s	108	180674	NA	2021	NA	European
finn-b-CD2_FOLLICI	Follicular lymphoma (al	522	180756	NA	2021	NA	European
finn-b-CD2_HODGK	Hodgkin lymphoma (all	369	180756	NA	2021	NA	European
finn-b-CD2_IMMUN(	Malignant immunoprolit	105	180756	NA	2021	NA	European
finn-b-CD2_LEUKAE	Leukaemia of unspecifi	93	180756	NA	2021	NA	European
finn-b-CD2_LYMPH(	Lymphoid leukaemia (a	663	180756	NA	2021	NA	European
finn-b-CD2_MYELOI	Myeloid leukaemia (all	283	180756	NA	2021	NA	European
finn-b-CD2_NONFO	Non-follicular lymphom	1283	180756	NA	2021	NA	European
finn-b-CD2_NONHO	Other and unspecified l	533	180756	NA	2021	NA	European
finn-b-CD2_PRIMAR	Primary lymphoid and	3537	180756	NA	2021	NA	European
finn-b-CD2_PRIMAR	Other and unspecified l	113	180756	NA	2021	NA	European
finn-b-CD2_TNK_LY	Mature T/NK-cell lymph	150	180756	NA	2021	NA	European
ieu-a-1082	Thyroid cancer	649	431	1080	2013	NA	European
ieu-b-4878	haematological cancer	4552	372016	376568	2021	NA	European
ukb-d-C_PRIMARY_	Cancer of primary lym	3030	358164	361194	2018	NA	European

finn-b-C3_BONE_C/ Malignant neoplasm of	119	174006	NA	2021	NA	European
finn-b-CD2_MULTIP Multiple myeloma and r	598	180756	NA	2021	NA	European

Table S2. Characteristics of the single-nucleotide polymorphisms used as instrumental variables of Sjogren's syndrome in forward Mendelian Randomization analyses.

1.IV selection of Sjogren's syndrome using threshold of 5e-8

id.exposure	SNP	chr.exposure	pos.exposure	effect_allele	other_allele	beta.exposure	se.exposure	pval.exposure	F Statistic
finn-b-M13_SJOGREN	rs35407265	6	32591226	G	A	-0.369	0.061	1.79E-09	36.18
	rs2853986	6	31338844	C	T	0.775	0.074	1.43E-25	109.21
	rs9265957	6	31315374	T	C	0.696	0.073	1.37E-21	90.98
	rs3778754	7	128575552	G	C	0.283	0.041	3.16E-12	48.49
	rs496315	20	10047038	C	T	0.225	0.041	3.21E-08	30.52
ebi-a-GCST90013929	rs200801362	6	31555480	C	T	0.756	0.136	2.63E-08	30.96
	rs184318723	6	32558428	C	G	1.507	0.243	5.28E-10	38.57
	rs34713112	6	32608589	TA	T	-0.637	0.082	8.47E-15	60.22
ebi-a-GCST90013879	rs3129962	6	32379383	A	G	0.617	0.083	9.69E-12	55.66
	rs2523495	6	31377978	T	C	0.660	0.078	2.17E-14	70.93

2.IV selection of Sjogren's syndrome using threshold of 5e-6

id.exposure	SNP	chr.exposure	pos.exposure	effect_allele	other_allele	beta.exposure	se.exposure	pval.exposure	F Statistic
finn-b-M13_SJOGREN	rs4853459	2	191962096	C	T	-0.222	0.048	3.70E-06	21.38
	rs138527475	4	6942816	G	C	0.556	0.121	4.57E-06	21.01
	rs2853986	6	31338844	C	T	0.775	0.074	1.43E-25	109.21
	rs2307308	6	24784436	T	C	0.423	0.091	3.48E-06	21.54
	rs34831921	6	32590768	A	C	-0.372	0.061	1.31E-09	36.85
	rs3778754	7	128575552	G	C	0.283	0.041	3.16E-12	48.49
	rs13289503	9	110186251	C	T	-0.224	0.044	3.67E-07	25.87
	rs76882717	10	14768307	T	C	0.430	0.093	4.05E-06	21.24
	rs116898071	11	58601814	G	A	0.999	0.212	2.57E-06	22.11
	rs12888138	18	53822656	T	C	-0.246	0.052	2.09E-06	22.52
	rs10409474	19	850733	G	C	0.352	0.067	1.78E-07	27.29
	rs4630834	20	23740255	T	C	0.191	0.041	2.97E-06	21.89
	rs496315	20	10047038	C	T	0.225	0.041	3.21E-08	30.52
ebi-a-GCST90013929	rs12748886	1	210672483	A	G	0.344	0.074	3.04E-06	21.79
	rs1556984	1	14536104	A	G	-0.573	0.114	4.58E-07	25.43
	rs200801362	6	31555480	C	T	0.756	0.136	2.63E-08	30.96
	rs28631719	6	32625409	G	A	-0.617	0.082	5.74E-14	56.46
	rs1811197	6	31327660	A	G	0.702	0.091	1.46E-14	59.15
	rs76550264	8	59288681	G	T	-0.544	0.119	4.76E-06	20.93
	rs34047862	12	31186482	A	G	-1.196	0.261	4.68E-06	20.96
	rs149449770	12	56539678	C	G	1.183	0.237	5.93E-07	24.94
	rs9516497	13	95597663	T	C	-0.632	0.131	1.34E-06	23.37
	rs55687614	14	34813819	T	C	-0.770	0.155	7.23E-07	24.55
	rs1752404	14	59913751	G	A	-0.346	0.075	3.51E-06	21.52

ebi-a-GCST90013879	rs56666273	16	22728306	G	A	-0.352	0.076	4.22E-06	21.16
	rs7222942	17	13523236	A	G	0.461	0.100	4.10E-06	21.22
	rs17426591	20	46874089	C	T	-0.644	0.140	3.97E-06	21.28
	rs12748886	1	210672483	A	G	0.334	0.071	3.77E-06	21.92
	rs1556984	1	14536104	A	G	-0.626	0.134	8.55E-07	21.88
	rs28631719	6	32625409	G	A	-0.584	0.076	9.54E-14	59.46
	rs200801362	6	31555480	C	T	0.660	0.111	3.10E-08	35.10
	rs1811197	6	31327660	A	G	0.605	0.072	1.20E-14	70.01
	rs149449770	12	56539678	C	G	0.890	0.156	5.41E-07	32.64
	rs9516497	13	95597663	T	C	-0.729	0.168	2.41E-06	18.92
	rs55687614	14	34813819	T	C	-0.930	0.213	1.28E-06	19.10
	rs1752404	14	59913751	G	A	-0.330	0.070	4.31E-06	22.09
	rs7222942	17	13523236	A	G	0.412	0.085	4.15E-06	23.67

Table S3. Overview of significant causality at both two thresholds in forward Mendelian Randomization analyses.

id.exposure	id.outcome	outcome	The MR results of threshold of 5e-8				The MR results of threshold of 5e-6				Heterogeneity		Pleiotropy	
			N SNP	OR	SE	Pval	N SNP	OR	SE	Pval	Q value	P value	Intercept	P value
finn-b-M13_SJOGREN	ebi-a-GCST004744	Lung adenocarcinoma	2	1.124	0.050	0.019	11	1.072	0.032	0.028	NA	NA	NA	NA
	ebi-a-GCST004748	Lung cancer	2	1.198	0.079	0.022	12	1.112	0.038	0.005	NA	NA	NA	NA
	ebi-a-GCST006464	Endometrial cancer	3	0.880	0.027	0.000	12	0.929	0.024	0.002	0.204	0.903	0.011	0.744
	ebi-a-GCST006465	Endometrial cancer (endon	3	0.863	0.032	0.000	12	0.935	0.031	0.029	0.089	0.956	-0.003	0.947
	ieu-a-1123	Invasive mucinous ovarian	3	0.852	0.069	0.021	11	0.888	0.053	0.024	1.927	0.382	-0.100	0.397
	ieu-a-1231	Mucinous ovarian cancer: i	3	0.842	0.067	0.010	11	0.879	0.059	0.028	3.250	0.197	-0.099	0.324
	ieu-b-4809	Prostate cancer	3	0.995	0.002	0.011	12	0.996	0.001	0.001	4.724	0.094	0.002	0.366
	ukb-b-18157	Type of cancer: ICD10: C5	1	1.001	0.001	0.048	3	1.001	0.000	0.019	NA	NA	NA	NA
	ebi-a-GCST003740	Barrett's esophagus or Eso	2	0.878	0.035	0.000	10	0.924	0.029	0.006	NA	NA	NA	NA
	ebi-a-GCST9001386	Colorectal cancer (Firth cor	3	1.098	0.035	0.007	10	1.078	0.027	0.005	1.103	0.576	-0.005	0.912
	ebi-a-GCST9001386	Colorectal cancer (SPA cor	3	1.099	0.036	0.008	10	1.078	0.027	0.005	1.122	0.571	-0.006	0.905
	ieu-b-4961	Oral cavity cancer	3	1.000	0.000	0.000	9	1.000	0.000	0.027	0.619	0.734	0.000	0.588
ebi-a-GCST90013929	finn-b-CD2_NONHOL	Other and unspecified type	3	1.436	0.150	0.016	12	1.277	0.088	0.005	3.130	0.209	-0.137	0.424
	ieu-a-1126	Breast cancer (Combined C	1	0.962	0.018	0.034	12	0.983	0.006	0.007	NA	NA	NA	NA
	ieu-a-1127	ER+ Breast cancer (Combi	1	0.951	0.022	0.022	12	0.983	0.007	0.014	NA	NA	NA	NA
	ieu-a-1130	Breast cancer (iCOGS)	1	0.917	0.030	0.004	12	0.971	0.009	0.001	NA	NA	NA	NA
	ieu-a-1133	ER+ Breast cancer (iCOGS	1	0.888	0.035	0.001	12	0.968	0.011	0.002	NA	NA	NA	NA
	ieu-a-1123	Invasive mucinous ovarian	1	0.777	0.114	0.027	12	0.890	0.031	0.000	NA	NA	NA	NA
	ebi-a-GCST9001386	Colorectal cancer (Firth cor	2	1.068	0.032	0.037	13	1.045	0.016	0.005	NA	NA	NA	NA
	ebi-a-GCST9001386	Colorectal cancer (SPA cor	2	1.068	0.032	0.037	13	1.044	0.016	0.005	NA	NA	NA	NA
ebi-a-GCST90013879	ieu-b-4965	Colorectal cancer	1	1.001	0.001	0.035	12	1.000	0.000	0.014	NA	NA	NA	NA
	ebi-a-GCST004988	Breast cancer	2	0.958	0.012	0.000	9	0.979	0.006	0.001	NA	NA	NA	NA
	ieu-a-1126	Breast cancer (Combined C	1	0.949	0.016	0.001	9	0.979	0.006	0.001	NA	NA	NA	NA
	ieu-a-1127	ER+ Breast cancer (Combi	1	0.944	0.019	0.003	9	0.979	0.007	0.004	NA	NA	NA	NA
	ieu-a-1130	Breast cancer (iCOGS)	1	0.945	0.023	0.013	9	0.965	0.010	0.000	NA	NA	NA	NA
	ebi-a-GCST012880	Colorectal cancer	2	1.138	0.057	0.023	7	1.089	0.032	0.008	NA	NA	NA	NA
	ebi-a-GCST9001386	Colorectal cancer (Firth cor	1	1.135	0.047	0.007	9	1.047	0.018	0.012	NA	NA	NA	NA
	ebi-a-GCST9001386	Colorectal cancer (SPA cor	1	1.137	0.048	0.007	9	1.046	0.018	0.013	NA	NA	NA	NA
finn-b-C3_LIVER_INT		Malignant neoplasm of live	1	1.629	0.237	0.040	7	1.246	0.099	0.026	NA	NA	NA	NA

*The Heterogeneity and Pleiotropy tests were conducted using instrumental variables (IVs) with a threshold of 5e-8.

Table S4. The SNP characteristics of cancers with significant causal relationships in backward Mendelian Randomization analyses.

1.IV selection of cancers using threshold of 5e-8

id.exposure	Trait	SNP	chr.exposure	pos.exposure	effect_allele	other_allele	beta.exposure	se.exposure	pval.exposure	F Statistic
ieu-a-987	ieu-a-987	rs34517439	1	78450517	A	C	0.134	0.020	1.87E-11	45.107
		rs446975	3	9217383	T	G	-0.122	0.018	5.15E-12	47.631
		rs7683574	4	9719148	T	C	0.070	0.013	4.98E-08	29.724
		rs7705526	5	1285974	A	C	0.107	0.013	3.47E-16	66.511
		rs31484	5	1337906	T	A	-0.137	0.012	2.04E-30	131.391
		rs501942	6	31840477	T	C	0.171	0.019	7.33E-19	78.673
		rs6920364	6	167376466	C	G	0.066	0.012	2.90E-08	30.770
		rs2893842	6	26338434	G	T	-0.078	0.012	3.93E-10	39.146
		rs1056562	11	118125625	C	T	-0.072	0.012	1.17E-09	37.010
		rs78853063	11	57250026	T	C	-0.129	0.023	3.44E-08	30.442
		rs7953330	12	998819	C	G	-0.087	0.013	1.03E-11	46.279
		rs11571815	13	32968550	A	G	0.482	0.059	1.69E-16	67.931
		rs55781567	15	78857986	G	C	0.258	0.012	3.64E-101	455.996
		rs77468143	15	49376624	G	T	-0.082	0.014	1.41E-09	36.650
		rs151118057	15	78988620	A	G	-0.290	0.051	1.52E-08	32.033
		rs56113850	19	41353107	C	T	0.127	0.014	3.48E-20	84.687
finn-b-C3_FEMALE_G	finn-b-C3_FEMALE_G	rs28479464	6	32615457	C	T	-0.205	0.032	2.69E-10	39.916
ieu-b-4878	ieu-b-4878	rs6708784	2	111927379	G	A	0.002	0.000	9.60E-10	37.408
		rs34269949	3	27769551	C	A	0.001	0.000	5.30E-09	34.072
		rs539726870	6	32606531	G	A	0.003	0.000	4.20E-12	48.009
ukb-d-C_PRIMARY_L	ukb-d-C_PRIMARY_L	rs6753785	2	111923630	G	T	0.001	0.000	3.39E-08	30.473
		rs34269949	3	27769551	C	A	0.001	0.000	1.52E-08	32.033
		rs539726870	6	32606531	G	A	0.002	0.000	3.89E-11	43.668

2.IV selection of cancers using threshold of 5e-6

id.exposure	Trait	SNP	chr.exposure	pos.exposure	effect_allele	other_allele	beta.exposure	se.exposure	pval.exposure	F Statistic
		rs77045810	1	168505017	C	A	-0.092	0.019	7.86E-07	24.392
		rs75504369	1	230746406	T	C	-0.229	0.047	1.27E-06	23.463
		rs141503707	1	243339168	A	G	-0.339	0.074	4.95E-06	20.858
		rs34517439	1	78450517	A	C	0.134	0.020	1.87E-11	45.107
		rs77710113	1	154618623	C	T	-0.125	0.025	4.06E-07	25.665
		rs79368540	2	45189737	T	C	0.086	0.018	1.42E-06	23.254
		rs11692700	2	67510377	C	T	0.183	0.036	5.17E-07	25.200
		rs4255928	2	182142456	A	G	-0.059	0.012	1.01E-06	23.900
		rs2046308	2	186059597	T	C	0.067	0.015	3.71E-06	21.412

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rs56139148	2	24973767	T	A	0.059	0.013	2.36E-06	22.278
rs1039766	2	65520145	T	C	0.089	0.016	5.97E-08	29.370
rs72899227	2	174238699	G	A	-0.074	0.016	4.81E-06	20.913
rs446975	3	9217383	T	G	-0.122	0.018	5.15E-12	47.631
rs13314271	3	189357602	C	T	-0.059	0.012	6.22E-07	24.844
rs9869622	3	16671821	T	C	-0.076	0.015	6.21E-07	24.846
rs7683574	4	9719148	T	C	0.070	0.013	4.98E-08	29.724
rs111405931	4	100281394	A	C	-0.105	0.022	2.05E-06	22.544
rs11941078	4	111513721	C	G	0.100	0.022	3.88E-06	21.322
rs34357052	5	141195546	C	T	0.065	0.013	7.24E-07	24.548
rs7705526	5	1285974	A	C	0.107	0.013	3.47E-16	66.511
rs31484	5	1337906	T	A	-0.137	0.012	2.04E-30	131.391
rs2816076	6	122427183	A	G	-0.057	0.012	1.40E-06	23.289
rs35452836	6	109699446	T	A	0.061	0.013	2.41E-06	22.235
rs501942	6	31840477	T	C	0.171	0.019	7.33E-19	78.673
rs6920364	6	167376466	C	G	0.066	0.012	2.90E-08	30.770
rs2893842	6	26338434	G	T	-0.078	0.012	3.93E-10	39.146
rs4722166	7	22738762	A	C	-0.058	0.012	2.96E-06	21.844
rs10265693	7	130720805	G	A	0.093	0.020	2.85E-06	21.916
rs71519637	8	27334098	T	C	0.097	0.020	1.49E-06	23.163
rs11780471	8	27344719	A	G	-0.136	0.025	6.92E-08	29.085
rs188586526	8	55495833	A	G	0.258	0.055	2.37E-06	22.265
rs7869680	9	21829604	A	T	0.087	0.019	3.14E-06	21.728
rs28557075	9	22066572	A	G	0.102	0.021	1.36E-06	23.343
rs3025388	9	136503256	G	A	-0.074	0.016	3.34E-06	21.609
rs191205566	9	102587233	T	C	0.308	0.063	8.76E-07	24.182
rs11251039	10	2106207	A	C	-0.243	0.050	1.23E-06	23.534
rs1056562	11	118125625	C	T	-0.072	0.012	1.17E-09	37.010
rs78853063	11	57250026	T	C	-0.129	0.023	3.44E-08	30.442
rs73351723	12	58831070	A	G	0.095	0.018	1.19E-07	28.042
rs6488106	12	33074470	T	C	-0.058	0.012	2.08E-06	22.524
rs55900110	12	102062332	A	G	0.237	0.051	4.13E-06	21.204
rs7953330	12	998819	C	G	-0.087	0.013	1.03E-11	46.279
rs11571815	13	32968550	A	G	0.482	0.059	1.69E-16	67.931
rs61963393	13	76856003	T	C	0.059	0.013	2.66E-06	22.045
rs11157631	14	48852067	A	T	-0.065	0.014	4.00E-06	21.265
rs56377826	15	101827491	C	T	-0.072	0.016	3.82E-06	21.353
rs55781567	15	78857986	G	C	0.258	0.012	3.64E-101	455.996

	rs12593251	15	75063533	G	C	0.142	0.031	4.39E-06	21.085
	rs77468143	15	49376624	G	T	-0.082	0.014	1.41E-09	36.650
	rs4774488	15	47491291	C	T	0.062	0.012	2.45E-07	26.641
	rs151118057	15	78988620	A	G	-0.290	0.051	1.52E-08	32.033
	rs4985771	17	16899251	T	G	0.058	0.012	3.36E-06	21.600
	rs9890128	17	1273646	T	C	-0.062	0.013	4.45E-06	21.061
	rs17181550	17	70299958	G	T	-0.062	0.012	2.61E-07	26.517
	rs631644	18	2280388	G	A	-0.063	0.014	4.36E-06	21.097
	rs56113850	19	41353107	C	T	0.127	0.014	3.48E-20	84.687
	rs34536443	19	10463118	C	G	0.144	0.030	2.29E-06	22.332
	rs7271507	20	49910883	T	A	0.121	0.025	1.11E-06	23.725
	rs1321342	20	19682070	A	T	-0.068	0.015	4.77E-06	20.928
	rs13036436	20	61988382	A	G	-0.080	0.016	5.58E-07	25.052
	rs13054277	22	23626896	A	G	0.065	0.014	3.41E-06	21.574
finn-b-C3_FEMALE_Gfinn-b-C3_FEMALE_G	rs13033424	2	19563477	T	C	0.134	0.029	2.90E-06	21.865
	rs340306	3	158571412	G	A	-0.132	0.029	4.70E-06	20.975
	rs35714416	4	119513594	C	T	0.160	0.034	3.17E-06	21.742
	rs12644386	4	64122826	A	T	-0.116	0.025	2.69E-06	22.018
	rs723186	5	124290808	A	G	0.191	0.038	5.41E-07	25.105
	rs152133	5	1366007	A	G	0.124	0.025	4.13E-07	25.572
	rs9266637	6	31347045	G	C	-0.137	0.030	3.81E-06	21.359
	rs28479464	6	32615457	C	T	-0.205	0.032	2.69E-10	39.916
	rs155491	6	7943686	A	G	-0.158	0.033	1.81E-06	22.735
	rs7090903	10	12430272	C	G	-0.282	0.061	3.25E-06	21.665
	rs7156374	14	33377672	A	C	-0.135	0.027	5.02E-07	25.337
	rs78867459	15	70340033	G	A	0.318	0.067	2.22E-06	22.418
	rs118124186	20	17796358	C	A	0.478	0.099	1.33E-06	23.387
	rs11705163	22	37203961	C	G	0.136	0.030	4.83E-06	20.907
	rs727253	22	45311664	T	C	0.126	0.027	2.83E-06	21.836
	rs3892275	1	181054522	A	G	0.001	0.000	2.20E-07	26.855
	rs72680773	1	70943399	A	C	0.005	0.001	2.70E-07	26.489
	rs2300297	1	168547354	G	A	0.002	0.000	3.60E-06	21.461
	rs1399957	2	172520642	G	A	0.001	0.000	3.00E-06	21.787
	rs6708784	2	111927379	G	A	0.002	0.000	9.60E-10	37.408
	rs34269949	3	27769551	C	A	0.001	0.000	5.30E-09	34.072
	rs115406459	3	167230931	T	C	0.004	0.001	1.70E-06	22.954
	rs117503067	6	133723789	A	G	-0.003	0.001	1.80E-06	22.842
	rs539726870	6	32606531	G	A	0.003	0.000	4.20E-12	48.009

ieu-b-4878	rs41552812	6	32632689	T	C	0.003	0.001	8.90E-08	28.609
	rs62389423	6	421281	A	G	0.002	0.000	2.90E-06	21.890
	rs201094127	6	31974327	T	C	0.005	0.001	1.30E-07	27.846
	rs11763709	7	21925978	C	G	-0.001	0.000	9.50E-07	24.021
	rs2483479	9	134206983	C	A	-0.002	0.000	7.10E-07	24.590
	rs566150748	10	42600304	A	G	0.007	0.001	2.20E-07	26.884
	rs4745915	10	68452234	G	C	0.002	0.000	4.60E-06	21.012
	rs10838696	11	47363285	A	G	-0.001	0.000	2.80E-06	21.929
	rs2859991	11	25880093	C	A	0.001	0.000	2.20E-07	26.888
	rs7960004	12	55926308	A	T	0.001	0.000	3.30E-06	21.620
	rs55837201	15	23922386	T	A	-0.002	0.000	4.40E-06	21.065
	rs150739161	20	59668736	A	G	-0.004	0.001	1.90E-06	22.738
	rs147474280	21	18267110	A	G	0.006	0.001	1.60E-06	23.005
	rs116022655	1	94672023	C	T	0.004	0.001	9.90E-07	23.948
	rs147132052	1	18112275	A	T	0.006	0.001	9.30E-07	24.068
	rs6753785	2	111923630	G	T	0.001	0.000	3.39E-08	30.473
	rs1399957	2	172520642	G	A	0.001	0.000	4.49E-06	21.044
	rs34269949	3	27769551	C	A	0.001	0.000	1.52E-08	32.033
	rs73029915	3	167276947	A	C	0.004	0.001	1.31E-07	27.846
	rs115199771	3	95247695	C	T	0.005	0.001	2.53E-06	22.143
	rs10021991	4	148909585	T	G	0.005	0.001	2.34E-06	22.290
	rs148229976	5	166253714	A	G	0.008	0.002	1.51E-06	23.139
ukb-d-C_PRIMARY_L'	rs79913547	5	113911783	G	A	0.004	0.001	2.15E-06	22.454
	rs539726870	6	32606531	G	A	0.002	0.000	3.89E-11	43.668
	rs1130392	6	32632628	C	G	0.001	0.000	4.26E-06	21.146
	rs17470302	6	30127212	C	T	0.005	0.001	9.31E-07	24.067
	rs79737036	8	126271355	T	G	0.002	0.000	4.39E-06	21.087
	rs150207987	8	108938094	C	T	0.001	0.000	4.22E-06	21.162
	rs72758671	9	113567351	A	G	0.004	0.001	2.98E-06	21.832
	rs148846591	9	26249831	T	C	0.002	0.000	5.35E-07	25.134
	rs62642894	10	42369505	T	A	0.002	0.001	4.34E-06	21.107
	rs139469541	12	85331856	T	G	0.005	0.001	1.08E-06	23.785

Table S5. Overview of significant causality at both two thresholds in backward Mendelian Randomization analyses.

			The MR results of threshold of 5e-8				The MR results of threshold of 5e-6			
id.exposure	Exposure Trait	id.outcome	N SNP	OR	SE	Pval	N SNP	OR	SE	Pval
ieu-a-987	Lung cancer	ebi-a-GCST90013929	12	2.741	0.475	0.034	45	1.744	0.213	0.009
ieu-a-987	Lung cancer	ebi-a-GCST90013879	12	3.230	0.457	0.010	45	1.918	0.214	0.002
finn-b-C3_FEM	Female genital cancer	finn-b-M13_SJOGREN	1	3.851	0.261	0.000	14	1.316	0.121	0.023
finn-b-C3_FEM	Female genital cancer	ebi-a-GCST90013929	1	8.252	0.452	0.000	10	2.215	0.279	0.004
finn-b-C3_FEM	Female genital cancer	ebi-a-GCST90013879	1	8.966	0.497	0.000	10	2.169	0.275	0.005
ieu-b-4878	Hematopoietic cancer	ebi-a-GCST90013929	3	5.95E+71	62.502	0.008	17	9.79E+28	26.5421	0.0119
ieu-b-4878	Hematopoietic cancer	ebi-a-GCST90013879	3	1.69E+71	47.566	0.001	17	2.45E+33	24.8162	0.00195
ukb-d-C_PRIM	Hematopoietic cancer	ebi-a-GCST90013929	3	2.18E+83	86.662	0.027	16	1.57E+26	28.3644	0.03346
ukb-d-C_PRIM	Hematopoietic cancer	ebi-a-GCST90013879	3	3.44E+84	67.576	0.004	16	5.53E+30	28.0726	0.01168

The highlighted causal relationship data were considered abnormal, possibly because they were all derived from summary data from the UK Biobank (UKBB) database, which had a significant overlap in samples. Therefore, these causal relationships were excluded from this study.

Table S6. Overview of significant causality in SMR between eQTL, Sjogren's syndrome and LUAD.

probeID	Gene Symbol	SMR between eQTL and Sjogren's syndrome									SMR between eQTL and LUAD								
		ProbeCh	Probe_bp	topSNP	topSNP_bp	b_SM	se_SM	p_SM	p_HEIDI	nsnp_HE	ProbeCh	Probe_bp	topSNP	topSNP_bp	b_SM	se_SM	p_SM	p_HEIDI	nsnp_HEIDI
ENSG0000009709	SYDE2	1	85644642	rs1874807	85779393	1.381	0.597	0.021	0.062	6	1	85622556	rs973167	85692605	0.193	0.095	0.043	0.552	17
ENSG0000013595	MFSD9	2	103342823	rs955916	1.03E+08	-0.141	0.067	0.036	0.578	5	2	1.03E+08	rs2732830	1.03E+08	-0.317	0.112	0.005	0.120	15
ENSG0000022455	HLA-DPB2	6	33091335	rs743771	32976909	-0.480	0.227	0.034	0.083	6	6	33080228	rs11538659	33033837	-0.074	0.035	0.035	0.064	7
ENSG0000003011	BAK1	6	33544174	rs210130	33533404	-0.321	0.101	0.002	0.369	14	6	33540329	rs511515	33541507	-0.119	0.047	0.012	0.308	20
ENSG0000015716	NRG1	8	32059725	rs4317533	32170767	-0.275	0.128	0.031	0.953	4	8	31496902	rs4422737	32399849	-0.326	0.081	0.000	0.327	20
ENSG0000022675	PSMD5-AS1	9	123601878	rs1076011	1.24E+08	-0.060	0.029	0.037	0.317	12	9	1.24E+08	rs4837796	1.24E+08	-0.045	0.016	0.004	0.790	20
ENSG0000010680	C5	9	123763585	rs1073365	1.24E+08	0.111	0.051	0.031	0.075	19	9	1.24E+08	rs4837805	1.24E+08	0.214	0.099	0.031	0.486	15
ENSG0000024557	BDNF-AS	11	27624053	rs3763965	27528987	0.831	0.416	0.046	0.633	5	11	27528385	rs1083518	27505677	0.203	0.094	0.030	0.988	15
ENSG0000025576	RP11-428G5	12	32035075	rs1666200	32045304	0.140	0.054	0.009	0.293	8	12	32030013	rs1666226	32034338	0.115	0.050	0.021	0.411	20
ENSG0000025870	LINC00638	14	105288796	rs2819469	1.05E+08	0.482	0.245	0.049	0.666	4	14	1.05E+08	rs7263520	1.05E+08	0.125	0.062	0.045	0.441	5

Table S7. The gene list of green module in WGCNA.

Gene Symbol	ENTREZID
HLA-DPB2	3116
HLA-DOA	3111
HLA-DMB	3109
DNAJC5B	85479
C17orf87	
SPN	6693
BTK	695
HLA-DRA	3122
HTRA4	203100
P2RY13	53829
PLEK	5341
NCKAP1L	3071
AMICA1	
TLR8	51311
HLA-DPB1	3115
TFEC	22797
C10orf128	
IGSF6	10261
CLEC4A	50856
MS4A6A	64231
EVI2A	2123
HLA-DPA1	3113
DPEP2	64174
CYBB	1536
CD52	1043
RGS18	64407
FGL2	10875
CD300LF	146722
CD200R1	131450
C1QA	712
TLR7	51284

MNDA	4332
LY86	9450
HLA-DQA1	3117
P2RY12	64805
C1QB	713
CD84	8832
PTPRO	5800
CCR2	729230
CR1	1378
LST1	7940
PRAM1	84106
APOC1	341
HLA-DRB1	3123
MRC1	4360
HSD11B1	3290
CLEC10A	10462
VSIG4	11326
PTCRA	171558
ACSM5	54988
KCNJ5	3762
FOLR2	2350
FZD10	11211
HLA-DQA2	3118
HK3	3101
CCL23	6368
CLEC6A	93978
RASGRF1	5923
ATP6V0D2	245972
AGER	177
SIGLEC11	114132
DNASE2B	58511
TM7SF4	
LOC653786	
APOC2	344

CHIT1	1118
FAM23A	
SCN4A	6329
RAET1G	353091
CCL18	6362
CBR1	873
H19	283120
LRRC36	55282
GPIHBP1	338328
F13A1	2162
HLA-DRB5	3127
RSPO1	284654
HS3ST2	9956
RHOV	171177
MARCO	8685
FGF12	2257
MYCN	4613
LYPD3	27076
EMR1	
SFTPC	6440
MYH2	4620
CD5L	922
C19orf59	
SLC6A4	6532
PKD2L1	9033
HLA-DQB2	3120
FLJ37543	
INHA	3623
PTPRQ	374462
TRPC2	7221
LOC149620	
PCSK2	5126
ATP1A4	480
FIGF	

TMEM90A	
SLC5A12	159963
SCGB3A1	92304
ANGPTL7	10218
OVCH1	341350
LGI3	203190
ADH1B	125
CLC	1178
KRT83	3889
C21orf125	
XG	7499
SLC7A2	6542
CEACAM8	1088
CYP24A1	1591
CLDN18	51208
B4GALNT2	124872
KRT79	338785
NRG4	145957
FAM184B	27146
SERPIND1	3053
C20orf70	
FOXD1	2297
ELANE	1991
ADRA1A	148
S100P	6286
ENO3	2027
NPAS3	64067
APOC1P1	342
HOXA11	3207
VAX1	11023
VSTM1	284415
COL25A1	84570
GLDC	2731
MAGEA1	4100

NXF3	56000
CAV3	859
FXVD4	53828
CYP4F3	4051
PPP2R2C	5522
CRHR2	1395
C13orf36	
CHRNA2	1135
KIAA0408	9729
PKP1	5317
ABCC2	1244
GLTPD2	388323
KCNC2	3747
IGF2BP1	10642
AKR1C2	1646
HOXA11AS	
CYP4F11	57834
EFNA2	1943
CNGB3	54714
C6orf176	
AKR1C1	1645
SP9	1E+08
AKR1B15	441282
PLUNC	
AGXT2L1	
CA1	759
FGL1	2267
PAH	5053
ZFP42	132625
ANTXRL	195977
HOXD11	3237
PNLIPRP3	119548
CALCB	797
EVX1	2128

NR0B1	190
DEFB126	81623
LOC441177	
DLK1	8788
LOC100190940	

*Genes with empty ENTREZIDs indicate that their symbols do not have corresponding ENTREZID mappings.

Table S8. GO enrichment analysis for LUAD.

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0002376	MHC class II protein complex	10/139	16/18614	2.99E-18	3.85E-15	2.82E-15	HLA-DOA	10
BP	GO:0002376	peptide antigen presentation	10/139	16/18614	2.99E-18	3.85E-15	2.82E-15	HLA-DOA	10
BP	GO:0002376	MHC protein complex	10/139	20/18614	6.73E-17	4.33E-14	3.17E-14	HLA-DOA	10
BP	GO:0002376	peptide antigen presentation	10/139	20/18614	6.73E-17	4.33E-14	3.17E-14	HLA-DOA	10
BP	GO:0002376	adaptive immune response	22/139	311/18614	1.41E-15	7.27E-13	5.33E-13	HLA-DOA	22
BP	GO:0002376	antigen processing	11/139	40/18614	5.18E-15	2.22E-12	1.63E-12	HLA-DOA	11
BP	GO:0019898	antigen processing	10/139	31/18614	1.51E-14	5.54E-12	4.06E-12	HLA-DOA	10
BP	GO:0002376	leukocyte mediated immunity	23/139	401/18614	2.76E-14	8.86E-12	6.50E-12	HLA-DOA	23
BP	GO:0002376	antigen processing	10/139	35/18614	6.08E-14	1.58E-11	1.16E-11	HLA-DOA	10
BP	GO:0019898	antigen processing	11/139	49/18614	6.16E-14	1.58E-11	1.16E-11	HLA-DOA	11
BP	GO:0002376	lymphocyte mediated immunity	20/139	300/18614	9.38E-14	2.19E-11	1.61E-11	HLA-DOA	20
BP	GO:0002376	antigen processing	10/139	37/18614	1.14E-13	2.44E-11	1.79E-11	HLA-DOA	10
BP	GO:0048519	antigen processing	12/139	71/18614	1.63E-13	3.23E-11	2.37E-11	HLA-DOA	12
BP	GO:0016067	immunoglobulin mediated immunity	15/139	145/18614	2.42E-13	4.44E-11	3.26E-11	HLA-DOA	15
BP	GO:0019898	B cell mediated immunity	15/139	148/18614	3.28E-13	5.62E-11	4.12E-11	HLA-DOA	15
BP	GO:0019898	antigen processing	13/139	114/18614	2.89E-12	4.65E-10	3.41E-10	HLA-DOA	13
BP	GO:0002376	immunoglobulin mediated immunity	11/139	75/18614	8.79E-12	1.33E-09	9.75E-10	HLA-DOA	11
BP	GO:0050671	regulation of T cell mediated immunity	19/139	377/18614	5.47E-11	7.74E-09	5.68E-09	HLA-DOA	19
BP	GO:1903066	regulation of leukocyte mediated immunity	19/139	378/18614	5.72E-11	7.74E-09	5.68E-09	HLA-DOA	19
BP	GO:0007275	leukocyte cell-cell adhesion	19/139	415/18614	2.79E-10	3.59E-08	2.63E-08	HLA-DOA	19
BP	GO:0002376	negative regulation of immune response	14/139	202/18614	3.57E-10	4.37E-08	3.20E-08	SPN/BTK	14
BP	GO:0002376	production of immune response	17/139	328/18614	3.95E-10	4.62E-08	3.38E-08	HLA-DOA	17
BP	GO:0022614	regulation of cytokine production	20/139	491/18614	7.05E-10	7.88E-08	5.78E-08	HLA-DOA	20
BP	GO:0050671	negative regulation of T cell mediated immunity	14/139	225/18614	1.46E-09	1.57E-07	1.15E-07	SPN/BTK	14
BP	GO:1903066	positive regulation of leukocyte mediated immunity	15/139	273/18614	2.05E-09	2.11E-07	1.54E-07	HLA-DOA	15
BP	GO:0050671	regulation of lymphocyte mediated immunity	14/139	239/18614	3.20E-09	3.16E-07	2.32E-07	HLA-DME	14
BP	GO:0032479	regulation of neutrophil mediated immunity	14/139	243/18614	3.96E-09	3.77E-07	2.76E-07	HLA-DME	14
BP	GO:0050671	positive regulation of leukocyte mediated immunity	14/139	249/18614	5.41E-09	4.97E-07	3.65E-07	HLA-DOA	14
BP	GO:0070491	regulation of leukocyte mediated immunity	14/139	268/18614	1.38E-08	1.22E-06	8.98E-07	HLA-DME	14
BP	GO:0022614	positive regulation of cytokine production	15/139	321/18614	1.82E-08	1.56E-06	1.14E-06	HLA-DOA	15
BP	GO:0051601	positive regulation of leukocyte mediated immunity	15/139	327/18614	2.33E-08	1.93E-06	1.42E-06	HLA-DOA	15

BP	GO:0002614 regulation of immune system process	16/139	384/1861	2.97E-08	2.38E-06	1.75E-06	HLA-DME	16
BP	GO:0050821 positive regulation of cell growth	16/139	394/1861	4.24E-08	3.30E-06	2.42E-06	HLA-DOA	16
BP	GO:0051972 negative regulation of cell growth	11/139	168/1861	5.37E-08	4.06E-06	2.98E-06	SPN/BTK	11
BP	GO:0002614 regulation of immune system process	12/139	212/1861	6.54E-08	4.81E-06	3.52E-06	HLA-DOA	12
BP	GO:0046601 lymphocyte proliferation	14/139	306/1861	7.26E-08	5.18E-06	3.80E-06	HLA-DME	14
BP	GO:0032089 mononuclear cell differentiation	14/139	313/1861	9.60E-08	6.67E-06	4.89E-06	HLA-DME	14
BP	GO:0042110 regulation of T cell activation	11/139	183/1861	1.29E-07	8.71E-06	6.39E-06	HLA-DME	11
BP	GO:0002614 negative regulation of immune system process	17/139	487/1861	1.38E-07	9.13E-06	6.69E-06	HLA-DOA	17
BP	GO:0002614 positive regulation of immune system process	15/139	377/1861	1.50E-07	9.64E-06	7.07E-06	HLA-DOA	15
BP	GO:0070491 leukocyte proliferation	14/139	348/1861	3.50E-07	2.19E-05	1.61E-05	HLA-DME	14
BP	GO:0042110 T cell proliferation	11/139	213/1861	5.91E-07	3.62E-05	2.65E-05	HLA-DME	11
BP	GO:0045119 positive regulation of cell growth	16/139	482/1861	6.48E-07	3.87E-05	2.84E-05	HLA-DOA	16
BP	GO:0002614 regulation of immune system process	10/139	190/1861	1.65E-06	9.65E-05	7.08E-05	BTK/HLA-	10
BP	GO:0002614 regulation of immune system process	11/139	246/1861	2.42E-06	0.00014	0.0001	BTK/HLA-	11
BP	GO:0032089 type II interferon production	8/139	118/1861	2.90E-06	0.00016	0.00012	TLR8/HLA-	8
BP	GO:0032089 regulation of type II interferon production	8/139	118/1861	2.90E-06	0.00016	0.00012	TLR8/HLA-	8
BP	GO:0002614 regulation of immune system process	10/139	205/1861	3.27E-06	0.00018	0.00013	BTK/HLA-	10
BP	GO:0002614 dendritic cell activation	4/139	15/1861	3.81E-06	0.0002	0.00015	HLA-DRA	4
BP	GO:0001825 positive regulation of cell growth	15/139	489/1861	3.90E-06	2.01E-04	1.47E-04	SPN/BTK	15
BP	GO:0050821 negative regulation of cell growth	7/139	88/1861	4.27E-06	2.15E-04	1.58E-04	SPN/BTK	7
BP	GO:0002614 T cell mediated immunity	8/139	125/1861	4.46E-06	2.19E-04	1.61E-04	HLA-DRA	8
BP	GO:0002614 activation of immune system process	15/139	495/1861	4.52E-06	2.19E-04	1.61E-04	BTK/NCK	15
BP	GO:0032089 negative regulation of type II interferon production	7/139	89/1861	4.60E-06	0.00022	1.61E-04	SPN/BTK	7
BP	GO:0070491 negative regulation of cell growth	7/139	96/1861	7.62E-06	0.00036	0.00026	SPN/BTK	7
BP	GO:0034087 chylomicron remnant catabolic process	3/139	6/1861	8.02E-06	0.00036	0.00027	APOC1/A	3
BP	GO:0071555 triglyceride-rich lipoprotein catabolic process	3/139	6/1861	8.02E-06	0.00036	0.00027	APOC1/A	3
BP	GO:0002614 regulation of T cell activation	7/139	97/1861	8.2E-06	0.00036	0.00027	HLA-DRA	7
BP	GO:0002614 regulation of immune system process	9/139	184/1861	1E-05	0.00044	0.00032	BTK/HLA-	9
BP	GO:0002614 leukocyte activation	11/139	296/1861	1.4E-05	0.0006	0.00044	HLA-DME	11
BP	GO:0002614 cell activation	11/139	300/1861	1.6E-05	0.00067	0.00049	HLA-DME	11
BP	GO:0031334 regulation of cell growth	7/139	110/1861	1.9E-05	0.00077	0.00057	HLA-DRA	7
BP	GO:0001825 negative regulation of cell growth	12/139	371/1861	2.3E-05	0.00092	0.00068	BTK/NCK	12
CC	GO:0042110 MHC class II peptide binding	10/142	17/19518	5.6E-18	1.3E-15	8.9E-16	HLA-DOA	10
CC	GO:0042110 MHC protein complex	10/142	25/19518	9E-16	1E-13	7.1E-14	HLA-DOA	10

CC	GO:00981 lumenal side c 8/142	29/19518	2.4E-11	1.9E-09	1.3E-09	HLA-DRA	8
CC	GO:00981 lumenal side c 8/142	36/19518	1.6E-10	9.5E-09	6.5E-09	HLA-DRA	8
CC	GO:00121 ER to Golgi tra 8/142	63/19518	1.8E-08	8.2E-07	5.7E-07	HLA-DRA	8
CC	GO:00451 clathrin-coated 9/142	92/19518	2.3E-08	8.9E-07	6.1E-07	HLA-DRA	9
CC	GO:00301 clathrin-coated 8/142	73/19518	5.8E-08	1.9E-06	1.3E-06	HLA-DRA	8
CC	GO:00301 endocytic vesi 11/142	196/19518	2E-07	5.8E-06	4E-06	HLA-DRA	11
CC	GO:00301 endocytic vesi 14/142	347/19518	2.5E-07	6.4E-06	4.4E-06	HLA-DRA	14
CC	GO:00301 COPII-coated 8/142	93/19518	3.9E-07	9E-06	6.2E-06	HLA-DRA	8
CC	GO:00321 trans-Golgi ne 8/142	102/19518	7.9E-07	1.7E-05	1.1E-05	HLA-DRA	8
CC	GO:00051 lysosomal mer 14/142	415/19518	2.1E-06	3.7E-05	2.6E-05	HLA-DOA	14
CC	GO:00981 lytic vacuole n 14/142	415/19518	2.1E-06	3.7E-05	2.6E-05	HLA-DOA	14
CC	GO:00051 vacuolar mem 14/142	460/19518	6.9E-06	0.00011	7.3E-05	HLA-DOA	14
CC	GO:00301 clathrin-coated 8/142	136/19518	6.9E-06	0.00011	7.3E-05	HLA-DRA	8
CC	GO:00051 trans-Golgi ne 10/142	255/19518	1.8E-05	0.00026	0.00018	HLA-DRA	10
CC	GO:00301 clathrin-coated 9/142	215/19518	2.8E-05	0.00039	0.00027	HLA-DRA	9
MF	GO:00231 MHC class II p 10/141	27/18369	3.9E-15	1.8E-12	1.2E-12	HLA-DOA	10
MF	GO:00231 MHC protein c 10/141	36/18369	1.1E-13	2.4E-11	1.7E-11	HLA-DOA	10
MF	GO:00321 MHC class II r 7/141	10/18369	1.6E-13	2.4E-11	1.7E-11	HLA-DOA	7
MF	GO:01401 immune recep 10/141	141/18369	1.4E-07	1.6E-05	1.1E-05	HLA-DOA	10
MF	GO:00421 peptide antige 6/141	39/18369	4.9E-07	4.5E-05	3.1E-05	HLA-DRA	6
MF	GO:00331 amide binding 14/141	400/18369	2.5E-06	0.00019	0.00013	HLA-DRA	14

Table S9. KEGG enrichment analysis of LUAD.

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa05330	Allograft rejection	9/64	39/5894	1.93E-10	5.46E-09	4.26E-09	3111/3109/	9
hsa04612	Antigen processing	9/64	78/5894	1.19E-07	7.79E-07	6.08E-07	3111/3109/	9
hsa05310	Asthma	9/64	31/5894	1.96E-11	8.33E-10	6.50E-10	3111/3109/	9
hsa05320	Autoimmune	9/64	54/5894	4.26E-09	4.02E-08	3.14E-08	3111/3109/	9
hsa04514	Cell adhesion	11/64	136/5894	1.72E-07	1.05E-06	8.17E-07	3111/3109/	11
hsa04610	Complement	5/64	69/5894	0.00085	0.00451	0.00352	712/713/13	5
hsa05332	Graft-versus-	9/64	43/5894	4.96E-10	1.05E-08	8.22E-09	3111/3109/	9
hsa04672	Intestinal immu	9/64	49/5894	1.72E-09	2.43E-08	1.90E-08	3111/3109/	9
hsa05140	Leishmania in	10/64	73/5894	4.01E-09	4.02E-08	3.14E-08	3111/3109/	10
hsa05322	Systemic lup	12/64	138/5894	1.95E-08	1.51E-07	1.17E-07	3111/3109/	12
hsa04940	Type I diabetes	9/64	45/5894	7.66E-10	1.30E-08	1.02E-08	3111/3109/	9
hsa05416	Viral myocard	10/64	72/5894	3.49E-09	4.02E-08	3.14E-08	3111/3109/	10

Table S10. GO enrichment analysis of 107 downregulated genes in HLA-DPB1-high memory B cells.

ONTOLOGY ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	geneID	Count
BP	GO:004677 protein autoph	9/101	227/1861	4.02E-06	0.00968	EIF2AK3/PIK	9
BP	GO:001657 histone modifi	12/101	475/1861	1.01E-05	0.01218	JMJD1C/PRI	12
BP	GO:001810 peptidyl-serine	9/101	309/1861	4.67E-05	0.02734	EIF2AK3/PIK	9
BP	GO:003560 protein deacyl	6/101	127/1861	6.69E-05	0.02734	DYRK1A/HD	6
BP	GO:001820 peptidyl-serine	9/101	327/1861	7.22E-05	0.02734	EIF2AK3/PIK	9
BP	GO:190332 regulation of p	8/101	255/1861	7.49E-05	0.02734	CBLB/CTNNI	8
BP	GO:009873 macromolecul	6/101	131/1861	7.94E-05	0.02734	DYRK1A/HD	6
BP	GO:004831 mitochondrion	3/101	17/1861	9.98E-05	0.03004	MEF2A/TRAF	3
BP	GO:004316 proteasome-n	10/101	439/1861	0.00014	0.03368	RNF19A/UBE	10
BP	GO:003139 regulation of p	7/101	213/1861	0.00016	0.03368	CBLB/UBR5/	7
BP	GO:000276 immune respc	10/101	450/1861	0.00017	0.03368	CBLB/MAP3k	10
BP	GO:005164 mitochondrion	4/101	51/1861	0.00017	0.03368	MEF2A/TRAF	4
BP	GO:003450 protein localiz	8/101	304/1861	0.00025	0.04266	EIF2AK3/PIK	8
BP	GO:000660 protein import	6/101	163/1861	0.00026	0.04266	CBLB/RANBI	6
BP	GO:003085 regulation of e	6/101	166/1861	0.00029	0.04266	NCOA3/CTN	6
BP	GO:005117 import into nu	6/101	168/1861	0.00031	0.04266	CBLB/RANBI	6
BP	GO:009026 positive regul	5/101	110/1861	0.00033	0.04266	ZEB2/UBR5/	5
BP	GO:200006 positive regul	5/101	111/1861	0.00035	0.04266	RNF19A/UBC	5
BP	GO:003599 response to r	3/101	26/1861	0.00037	0.04266	CTNNB1/PT	3
BP	GO:000020 protein polyub	7/101	244/1861	0.00037	0.04266	RNF19A/UBE	7
BP	GO:000691 nucleocytopla	8/101	328/1861	0.00042	0.04266	AKAP13/CBL	8
BP	GO:005116 nuclear transp	8/101	328/1861	0.00042	0.04266	AKAP13/CBL	8
BP	GO:000647 protein deace	5/101	116/1861	0.00042	0.04266	DYRK1A/HD	5
BP	GO:000276 immune respc	8/101	329/1861	0.00042	0.04266	CBLB/MAP3k	8
BP	GO:000275 immune respc	9/101	423/1861	0.00049	0.04694	CBLB/TRAF3	9
BP	GO:003139 positive regul	5/101	121/1861	0.00051	0.04694	CBLB/UBQL	5
BP	GO:006082 regulation of c	7/101	260/1861	0.00054	0.04694	ZEB2/CTNNE	7
BP	GO:001972 calcium-medi	6/101	187/1861	0.00055	0.04694	EIF2AK3/CAI	6
CC	GO:009856 cytoplasmic si	7/101	193/1951	6.51E-05	0.01493	CYTH1/MTS	7
CC	GO:000989 cytoplasmic si	6/101	159/1951	0.00018	0.01493	CYTH1/MTS	6
CC	GO:000015 ubiquitin ligas	8/101	307/1951	0.00019	0.01493	RNF19A/TRA	8

CC	GO:001623 inclusion body	4/101	74/19518	0.00059	0.03385	RANBP2/UBI	4
CC	GO:003146 Cul3-RING ub	3/101	36/19518	0.00085	0.03902	SPOPL/KLHL	3
CC	GO:000581 spindle	8/101	421/19518	0.00154	0.04864	EML4/MAPR	8
CC	GO:004240 nuclear inclus	2/101	12/19518	0.00169	0.04864	RANBP2/NUI	2
CC	GO:004461 nuclear pore r	2/101	12/19518	0.00169	0.04864	RANBP2/NUI	2
MF	GO:000467 protein serine	12/100	421/18369	3.06E-06	0.00098	EIF2AK3/PIK	12
MF	GO:010631 protein serine	10/100	363/18369	2.87E-05	0.00462	EIF2AK3/PIK	10
MF	GO:001990 phosphatase l	7/100	187/18369	7.30E-05	0.00626	EIF2AK3/CTI	7
MF	GO:003559 signaling ada	5/100	83/18369	8.97E-05	0.00626	AKAP13/ABI	5
MF	GO:001679 phosphatase	8/100	265/18369	1.00E-04	0.00626	PIKFYVE/PP	8
MF	GO:001990 protein phosp	6/100	140/18369	0.00012	0.00626	EIF2AK3/CTI	6
MF	GO:000472 phosphoprote	6/100	168/18369	0.00031	0.01443	PPP1CB/PTK	6
MF	GO:004696 nuclear thyro	3/100	29/18369	0.00052	0.02077	JMJD1C/NCC	3
MF	GO:004257 phosphoric es	8/100	352/18369	0.00068	0.02418	PIKFYVE/PP	8
MF	GO:001701 myosin phosp	4/100	76/18369	0.00079	0.0253	PPP1CB/CD	4
MF	GO:004216 SH2 domain t	3/100	41/18369	0.00144	0.04204	PAG1/SYK/P	3
MF	GO:000471 non-membran	3/100	43/18369	0.00165	0.04293	DYRK1A/SYK	3
MF	GO:000472 protein serine	4/100	94/18369	0.00173	0.04293	PPP1CB/CD	4

Table S11. KEGG enrichment analysis of 107 downregulated genes in HLA-DPB1-high memory B cells.

category	subcateg ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	geneID	Count
Environmental Signal tra	hsa04012	ErbB signaling pathway	4/43	87/5894	0.00352	0.03772	CBLB/CA	4
Organismal Sy Immune s	hsa04662	B cell receptor signaling pathway	4/43	75/5894	0.00205	0.03772	NFAT5/S	4
Organismal Sy Endocrine	hsa04910	Insulin signaling pathway	5/43	138/5894	0.00308	0.03772	CBLB/PP	5
Organismal Sy Nervous s	hsa04720	Long-term potentiation	4/43	70/5894	0.00159	0.03772	PPP1CB/	4
Human Diseases Infectious	hsa05100	Bacterial invasion of epithelial cells	4/43	71/5894	0.00167	0.03772	CBLB/CT	4
Environmental Signal tra	hsa04310	Wnt signaling pathway	5/43	151/5894	0.00454	0.0416	CTNNB1/	5
Genetic Inform Folding s	hsa04120	Ubiquitin mediated proteolysis	5/43	139/5894	0.00318	0.03772	CBLB/UB	5
Cellular Process Cell growth	hsa04114	Oocyte meiosis	4/43	114/5894	0.00917	0.06541	PPP1CB/	4
Human Diseases Cancer: o	hsa05200	Pathways in cancer	7/43	327/5894	0.00868	0.06541	CBLB/CT	7
Environmental Signal tra	hsa04370	VEGF signaling pathway	3/43	76/5894	0.01757	0.07355	NFAT5/P	3
Cellular Process Cell motility	hsa04810	Regulation of actin cytoskeleton	5/43	214/5894	0.01887	0.07355	PIKFYVE,	5
Organismal Sy Immune s	hsa04664	Fc epsilon RI signaling pathway	3/43	79/5894	0.01947	0.07355	SYK/PIK3	3
Organismal Sy Nervous s	hsa04722	Neurotrophin signaling pathway	4/43	127/5894	0.01326	0.07355	MAP3K1/	4
Organismal Sy Developm	hsa04380	Osteoclast differentiation	4/43	128/5894	0.01362	0.07355	SYK/PIK3	4
Human Diseases Cancer: s	hsa05216	Thyroid cancer	2/43	29/5894	0.01863	0.07355	CTNNB1/	2
Human Diseases Cancer: s	hsa05220	Chronic myeloid leukemia	3/43	73/5894	0.01578	0.07355	CBLB/PIK	3
Human Diseases Infectious	hsa05160	Hepatitis C	4/43	135/5894	0.01628	0.07355	EIF2AK3/	4
Human Diseases Cancer: s	hsa05222	Small cell lung cancer	3/43	85/5894	0.0236	0.08419	TRAF3/P	3
Organismal Sy Endocrine	hsa04914	Progesterone-mediated oocyte maturation	3/43	87/5894	0.02508	0.08474	PRKX/CD	3
Human Diseases Cancer: s	hsa05215	Prostate cancer	3/43	89/5894	0.0266	0.08539	CTNNB1/	3
Organismal Sy Immune s	hsa04666	Fc gamma R-mediated phagocytosis	3/43	95/5894	0.03146	0.09619	SYK/PIK3	3
Metabolism Lipid metabolism	hsa00600	Sphingolipid metabolism	2/43	40/5894	0.03404	0.09835	UGCG/SC	2
Organismal Sy Endocrine	hsa04912	GnRH signaling pathway	3/43	101/5894	0.03676	0.09835	MAP3K1/	3
Organismal Sy Endocrine	hsa04916	Melanogenesis	3/43	101/5894	0.03676	0.09835	CTNNB1/	3

Table S12. GO enrichment analysis of 79 upregulated genes in HLA-DPB1-high memory B cells.

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	geneID	Count
CC	GO:00057	mitochondrial r	8/73	484/1951	0.00044	0.03296	ISCA2/GL	8
CC	GO:00057	mitochondrial i	8/73	497/1951	0.00053	0.03296	STOML2/	8