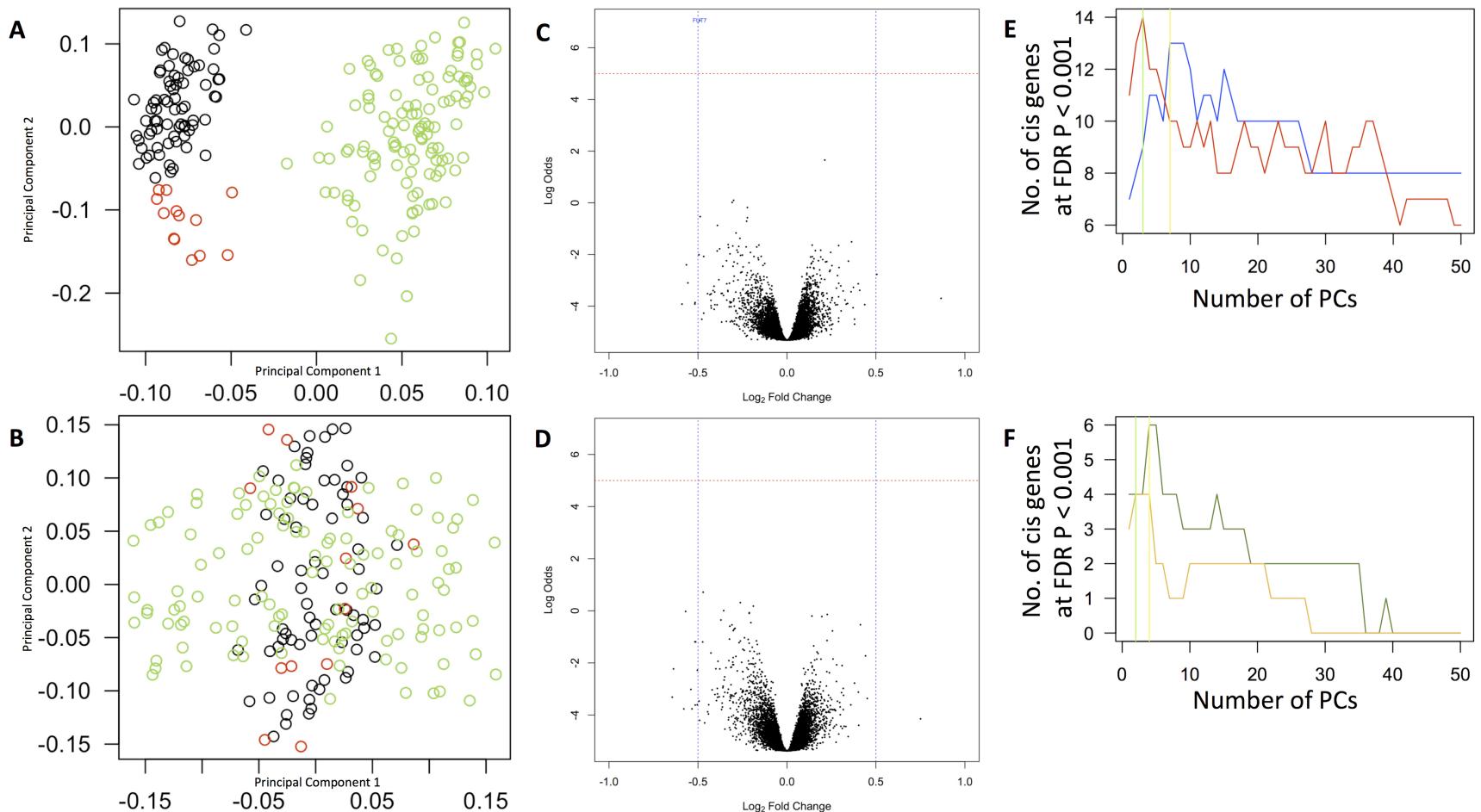


SUPPLEMENTARY INFORMATION



1
2

3 **Supplementary Figure 1. Principle component analysis of EBV-B basal cell samples.** Analysis of principle components that define
4 batch effects: (A) A cross plot between PC1 and PC2 that separate the samples into three technical batches in which samples were
5 processed (B) A cross plot between PC1 and PC2 after batch effect removal. **Comparison of gene expression in EBV-B cells from**
6 **cases and controls.** Analysis of differential gene expression in (C) unstimulated and (D) PMA-stimulated B-EBV-B cells from cases
7 ($n=136$) and controls ($n=25$). Differences (\log_2 fold change) in gene expression are shown on the X axis; Y axis shows B score (30).
8 **PCA analysis for detecting eQTLs at FDR P < 0.001.** (E) Blue and red line corresponds to EBV-B basal and PMA stimulated cell
9 line samples. The x-axis corresponds to number of PCs added as covariates and y-axis corresponds to number of *cis*-genes identified
10 at FDR P < 0.001 as a result of covariate addition. Threshold lines are drawn at ideal number of PCs as covariate to maximize *cis*-gene
11 identification. (F) Green and orange lines represent CD4+ and CD8+ cell samples. Analysis is repeated similar to that of EBV-B
12 samples.

Supplementary Table I.

Cell type	EBV-B	EBV-B	CD4+	CD8+
	Basal	PMA		
N	202	202	102	84
Females	48.5%	47.5%	36.4%	36.6%
Unaffected	46	49	6	6
Affected	156	153	96	78
GAD+	63	63	45	34
IA2+	95	94	42	36
TPO+	60	59	20	15
TG+	11	10	4	4
OH21+	2	2	1	0
ATPASE+	45	44	10	9
Total AB+	134	131	71	57
HLA DR34	26	26	30	24
HLA DR4X	126	123	42	36
HLA DR3X	4	4	15	12
HLA DRXX	0	0	5	5

(i). Summary of Gender, HLA and auto-antibody statuses of samples utilized in this study.

	FDR P	EBV-Basal		EBV-PMA		CD4+		CD8+	
		RUV	PCA	RUV	PCA	RUV	PCA	RUV	PCA
<i>Cis</i>	P < 0.001	20	13	17	14	11	6	9	4
	P < 0.05	36	28	37	21	20	15	19	8
<i>Trans</i>	P < 0.001	29	22	47	22	29	23	30	26
	P < 0.05	1071	57	1605	37	60	25	66	33

(ii). Table compares number of cis and trans genes identified by correction methods RUV-2 and PCA at FDR P value thresholds 0.001 and 0.05.

ID	T1D SNPs	Gene	Functional variants in LD ($r^2 > 0.8$)	P-value of T1D SNP	P-value of Func. SNP
32	rs10877012	<i>TSFM</i>	rs2014886 (splice donor)	0.44	N/A
42	rs4788084	<i>ATXN2L</i>	rs55719896 (splice acceptor)	0.0001	2.59×10^{-5}
45	rs2290400	<i>GSDMB</i>	rs11078928 (splice acceptor)	0.0017	0.0006
51	rs679574	<i>FUT2</i>	rs601338 (stop gain)	3.59×10^{-6}	N/A

(iii). Splice-region and stop-gain variant SNPs found in LD ($r^2 > 0.8$) with 4 T1D loci. T1D loci identifiers as in Table I. N/A – SNP genotypes not available

Supplementary Table II.

ID	T1D SNP (Effect allele)	Gene	EBV-B basal	EBV-B PMA	CD4+	CD8+
1	rs2269241 (C)	<i>PGM1</i>	ns	↓ *	ns	ns
6	rs2165738 (C)	<i>SF3B14</i>	↓ *	ns	ns	ns
7	rs363609 (C)	<i>NCOA1</i>	ns	↑ *	ns	ns
8	rs9653442 (C)	<i>AUPI</i>	↑ *	ns	ns	ns
9	rs6543134 (C)	<i>CHST10</i>	ns	↓ **	ns	ns
11	rs231727 (T)	<i>CTLA4</i>	ns	ns	ns	↓ *
17	rs597325 (C)	<i>ANKRD6</i>	ns	↓ *	ns	ns
19	rs2327832 (C)	<i>HEBP2</i>	↓ *	ns	ns	ns
20	rs1738074 (C)	<i>TCP1</i>	ns	ns	↓ *	ns
23	rs7020673 (C)	<i>GLIS3</i>	ns	↓ *	ns	ns
25	rs10758593 (T)	<i>PPAPDC2</i>	ns	ns	↓ *	ns
26	rs947474 (C)	<i>PFKFB3</i>	↑ **	↑ *	ns	ns
27	rs722988 (C)	<i>ITGB1</i>	ns	ns	ns	↑ **
27	rs10509540 (T)	<i>PTEN</i>	ns	ns	ns	↓ **
29	rs3764021 (T)	<i>CLEC2B</i>	↑ **	ns	ns	ns
		<i>CD69</i>	↑ **	ns	ns	ns
	rs10466829 (T)	<i>DDX12</i>	↓ *	ns	ns	ns
		<i>CLEC1A</i>	ns	ns	↓ *	ns
		<i>P42G4</i>	↑ *	ns	ns	ns
30	rs705704 (T)	<i>STAT2</i>	↓ *	↓ **	ns	ns
		<i>ESYT1</i>	ns	↓ *	ns	ns
	rs2292239 (T)	<i>ATPSB</i>	↓ *	ns	ns	ns
		<i>BLOC1S1</i>	ns	ns	↓ **	ns
32	rs10877012 (C)	<i>TSPN3J</i>	ns	ns	↑ **	↑ **
		<i>SLC26A10</i>	ns	ns	ns	↑ *
33	rs1265565 (T)	<i>HVCNJ</i>	ns	↑ *	ns	ns
		<i>TMEM116</i>	ns	↓ *	ns	ns
34	rs17696736 (C)	<i>OAS2</i>	↑ **	ns	ns	ns
		<i>SH2B3</i>	ns	↑ **	ns	ns
		<i>C12ORF30</i>	ns	ns	ns	↓ *
42	rs4788084 (C)	<i>IL27</i>	ns	↓ *	ns	ns
45	rs2290400 (T)	<i>CCR7</i>	ns	↑ *	ns	ns
46	rs7221109 (C)	<i>MED24</i>	↑ *	ns	ns	ns
		<i>KRT9</i>	↑ *	ns	ns	ns
47	rs1893217 (C)	<i>PTPN2</i>	↓ *	ns	ns	ns
49	rs2304256 (C)	<i>PDE4A</i>	ns	↓ *	ns	ns
51	rs679574 (C)	<i>CD37</i>	ns	ns	ns	↓ *
53	rs11203203 (T)	<i>WDR4</i>	ns	↓ *	ns	ns
		<i>UCRC</i>	↓ **	↓ *	ns	ns
54	rs5753037 (T)	<i>EWSR1</i>	↓ *	ns	ns	ns
		<i>NIPSNAPI</i>	ns	↑ *	ns	ns
55	rs229541 (T)	<i>APOL2</i>	↑ *	ns	ns	ns
58	rs2611215 (A)	<i>TMEM192</i>	↓ **	ns	ns	ns

(i) List of *cis* gene interaction detected at below FDR $P < 0.05$. ** $P < 0.01$, * $P < 0.05$, ns – not significant, ↓ risk allele decreases expression, ↑ risk allele increases expression

CHR	T1D SNP	Trans genes identified at FDR P < 0.01
1p31.3	rs2269241	<i>C4orf34, OPTN, RPL34, TP53TG1, WDR33, ZNF786</i>
1q31.2	rs2816316	<i>FGR</i>
2p24.3	rs1534422	<i>C1orf226, PLAC1, RHOBTB2, ST6GAL1</i>
2p23.3	rs2165738	<i>AASDH, CCDC106, GABPB2, SLC2A5</i>
2p13.1	rs363609	<i>EIF2B2, LOC645018, TLR10</i>
2q11.2	rs9653442	<i>SCAPER</i>
2q12.1	rs6543134	<i>ADK, FANCE, FXR2, LOC728532, MAPK13, PRRT3, TNFRSF8</i>
2q24.2	rs1990760	<i>JUND, LOC392285, LOC643997, LOC649946, OMA1, REL</i>
2q24.2	rs3747517	<i>LOC649946, UFM1</i>
2q33.2	rs11571291	<i>CCDC86, LOC729148, RYK, ST6GALNAC4, TDPI, TJAP1, TMUB2, ZNF549</i>
2q33.2	rs3087243	<i>LOC729148, SENP6, TDPI, TMUB2, ZNF549</i>
2q33.2	rs231727	<i>BIRC2, FADS2, MOBK2A, TDPI, ZNF549, ZNF69</i>
2q35	rs3731865	<i>C1orf106, CENPM, DYNC1HI, FEZ1, ID3, JAM2, NOTCH1, SLAMF6</i>
3p21.31	rs11711054	<i>C11orf73, G3BP1, GRAMD1B, NME4, SLC35B2</i>
4p15.2	rs10517086	<i>HMGB1L</i>
4q27	rs4505848	<i>ATG9A, CDC2L5, NT5DC3, PDCD10, SIX3</i>
4q27	rs17388568	<i>SIX3</i>
4q27	rs2069763	<i>ATG9A, CDC2L5, PDCD10, SIX3</i>
5p13.2	rs6897932	<i>ARHGAP17, BCL7C, CDC4EPI5, GLDC, KLF10, MNX1</i>
6q15	rs597325	<i>NTSE, TBC1D9, TNK</i>
6q15	rs56297233	<i>DBI, EDEMI, LRP5L, NR2F2</i>
6q22.32	rs9388489	<i>C18orf56</i>
6q23.3	rs2327832	<i>CHD2, PCCA</i>
6q23.3	rs10499194	<i>EHD1, LOC728661, TUBB6</i>
6q25.3	rs1738074	<i>EXOSC7, LOC388436</i>
7p15.2	rs7804356	<i>GPM6A, LHX3, NCAPD2, NME7, POLA2, RRP15, SAR1B, SEC61G, SERPIN49, SLC39A8, SPAG1, TYMS</i>
7p12.2	rs10272724	<i>HES1, SGCE, SMAP1</i>
9p24.2	rs7020673	<i>FHL3, LOC646939, PLCB2</i>
9p24.2	rs10758593	<i>PICALM, ZNF695</i>
10p15.1	rs12251307	<i>C14orf68, CAMK2D, DERA, SASS6, ZNF326</i>
10p15.1	rs947474	<i>GLB1, MEIS2, NOL12, PTP4A3</i>
11p15.5	rs7928968	<i>TLC1D</i>
11p15.5	rs3842727	<i>CD276, ID2, LOC347292, NLRP2, TRIP6</i>
11p15.5	rs7111341	<i>FCGR2A, G3BP1, TUBB4O</i>
12p13.31	rs3764021	<i>SNORA24, SPDYA, SYNE2</i>
12p13.31	rs10466829	<i>COCH, NFATC1, SNORA24, SPDYA, SYNE2</i>
12q13.2	rs705704	<i>HES4, IP6K2, LOC100129552, LOC389386, LOC641768, LOC728823, LOC728873, LOC92659, MIR130A, MIR1471, RPS26P10, RPS26P11, RTTN</i>

...cont

CHR	T1D SNP	Trans genes identified at FDR P < 0.01
12q13.2	rs11171739	<i>IP6K2, LOC100129552, LOC389386, LOC641768, LOC728823, LOC728873, LOC92659, MIR130A, MIR1471, OASL, RPS26P10, RPS26P11</i>
12q13.2	rs2292239	<i>DDIT4, IP6K2, LOC100129552, LOC389386, LOC641768, LOC728823, LOC728873, LOC92659, MIR130A, MIR1471, NRP2, RPS26P10, RPS26P11</i>
12q13.3	rs3809114	<i>BEX5, LITAF, SLC9A3R1, SNRNP25</i>
12q14.1	rs10877012	<i>ECGF1</i>
12q24.12	rs1265565	<i>DCUN1D5, NCOA7, ZMYM5</i>
12q24.12	rs3184504	<i>EIF2AK2, NCOA7, TBX15, TPCN2, UBE2L6</i>
12q24.13	rs17696736	<i>IFI16, IRF8, MI33, NCOA7, SP110, TBX15</i>
13q32.3	rs9585056	<i>AHCTF1, CKS2, IFI1H1, MARCKS, MRPL35</i>
14q24.1	rs1465788	<i>CCDC50, DLGAP4, LHFP, SRM</i>
14q32.2	rs4900384	<i>EIF5B, PLP2, RASSF6, RBMS1, SSPN</i>
14q32.2	rs56994090	<i>BATF, TXNRD2</i>
15q14	rs17574546	<i>FBXO48, HES4, LUZP1, NAT9, NSBP1</i>
15q14	rs12908309	<i>BCL2L1, CD99, ELL3, FAHD1, HMHB1, JAM2, RNF13, STAT5A, TMCO1, ZMAT5</i>
15q25.1	rs3825932	<i>ASNS, CLDN12, MORF4L2, PCK2, SLC1A5, TRIT1, UBXN2A</i>
16p13.13	rs12708716	<i>CSTF3, LOC642828, SAFB, SNRNP25</i>
16p13.13	rs12927355	<i>CSTF3, LARP7, LOC642828, SMOX, SNRNP25, TAFID, VAMP4</i>
16p13.13	rs416603	<i>BHLHB2, CD86, DAP, IL10RA, OXTR, SORL1</i>
16p11.2	rs4788084	<i>PRKDC</i>
16p11.2	rs9924471	<i>DUSP5, LOC440926, LRRC33, PHC2, RRP7A, ZNF681</i>
16q23.1	rs7202877	<i>FAM71F2, LOC100134708</i>
16q23.1	rs8056814	<i>HS467627</i>
17p13.1	rs16956936	<i>HLA-DRB4</i>
17q12	rs2290400	<i>TEX9</i>
17q12	rs7221109	<i>SMAD7, USP14</i>
18p11.21	rs1893217	<i>CDC2L5, KDM3B, MCM3AP, PDGFA</i>
18q22.2	rs763361	<i>ATM, IL16, P2RY11, RIOK1, TADA2A</i>
19p13.2	rs2304256	<i>CAMKK2, USP24, ZNF280D</i>
19q13.32	rs425105	<i>ACP5, C6orf72, CCL5, CYBRD1, GAPDHL6, LRIG1, PIK3R6, PSMC4, PTK7, SAL2, SLAIN1</i>
19q13.33	rs679574	<i>EIF5A, HLA-DRB4, HLA-H, SLFN11, TMEM55A, ZC3HC1</i>
20p13	rs2281808	<i>BRD3, DDX41, MAPKAPK3, MED4, SLFN11, WTAP</i>
21q22.3	rs11203203	<i>PRKAR1B</i>
21q22.3	rs876498	<i>CAT, CYBRD1, PRKAR1B</i>
22q12.2	rs5753037	<i>ABC46, ANXA6, CCDC53, SLC35B2</i>
22q12.3	rs229541	<i>BIRC3, SV2B</i>

(ii) List of all *trans* gene interaction detected at below FDR $P < 0.01$ in cells tested.

cont...

Supplementary Table III.