

Supplemental Table 1: Oligonucleotide primers used in this study

Primer Use (Abbreviation)	Sequence
PCR: exon 1 (Ex1F)	F: 5' CCCTTGGTGTTCTGCCATAA 3'
PCR/expression: exon 2 (Ex2F)	F: 5' CATTCTGGATTGCTGTCTGTC 3'
PCR: exon 3 (Ex3F)	F: 5' GAAGCTACCAGAACCACATC 3'
PCR/expression: start of 3' UTR (UTR1R)	R: 5' AGTTCTCACATCCAGGATC 3'
PCR: end of 3' UTR (UTR2R)	R: 5' GGTCTGTGAGATCATTTCAGC 3'
5' RACE: 3' UTR (RACE_OUT)	R: 5' CCAGGCCAGCAGCAGGTTCTCACATC 3'
5' RACE: exon 3 (RACE_IN)	R: 5' GCTTCTCCACCCAGGACTGAGCAGG 3'

Supplemental Table 4: HLA-DR/DQ stratified analysis for rs1233478

We performed a stratified analysis for rs1233478, restricting the analysis to *HLA-DR/DQ* groups with more than 100 chromosomes. The overall case/control association is also presented so the direction of odds ratios can be compared.

HLA-DR/DQ	Total	Case A	Control A	Case C	Control C	p-value	Odds Ratio
Overall (all groups)	8191	1394	433	4044	2320	3.2E-25	1.85
DRB1*0101-DQB1*0501	446	40	17	227	162	0.1	1.68
DRB1*0301-DQB1*0201	1579	566	141	737	135	0.023	0.74
DRB1*0401-DQB1*0302	1132	206	14	834	78	0.3	1.38
DRB1*0401-DQB1*0301	221	14	9	102	96	0.5	1.46
DRB1*0402-DQB1*0302	164	13	1	130	20	1	2
DRB1*0404-DQB1*0302	308	34	6	224	44	1	1.11
DRB1*0405-DQB1*0302	146	35	1	97	13	0.2	4.69
DRB1*0701-DQB1*0201	367	16	21	147	183	1	0.95
DRB1*0801-DQB1*0402	145	29	4	72	40	9.6E-03	4.03
DRB1*1101-DQB1*0301	199	5	12	49	133	0.8	1.13
DRB1*1301-DQB1*0603	164	8	12	44	100	0.4	1.52
DRB1*1302-DQB1*0604	222	21	9	127	65	0.8	1.19
DRB1*1501-DQB1*0602	337	10	29	36	262	0.043	2.51
DRB1*1601-DQB1*0502	125	5	2	65	53	0.5	2.04

Supplemental Table 5: Expression results from Taqman quantitative PCR.

Taqman was performed using 40 cycles for experiments 1 and 2, and 45 cycles for experiment 3. Results are expressed as Ct, the number of PCR cycles required for the transcript to appear. *LOC729653* is present at low levels in many tissues. Results are grouped by the number of experiments (out of 3) in which a tissue expressed the transcript.

Sample Name	Experiment 1 (40 cycles)	Experiment 2 (40 cycles)	Experiment 3 (45 cycles)	Mean Ct
Found in 3 of 3 experiments				
epididymis	33	33.16	30.3	32.2
intestine (small)	35.09	35.28	32.29	34.2
stomach	34.89	35	34.77	34.9
uterus	35.1	35.3	34.29	34.9
duodenum (descending)	34.36	35.76	35.13	35.1
vagina	34.61	35.57	35.44	35.2
lung	35.91	36.4	33.39	35.2
rectum	35.71	35.52	34.81	35.3
thymus	35.03	34.94	36.11	35.4
urinary bladder	35.54	35	35.56	35.4
prostate	36.16	37.52	36.15	36.6
fat	37.67	36.21	36.16	36.7
lymph node	39.19	36.96	35.48	37.2
testis	37.57	38.63	36.3	37.5
urethra	39.21	37.31	37.27	37.9
cervix	39.58	39.3	35.28	38.1
bone marrow	39.85	38.6	37.21	38.6
whole pancreas (purified)	39.72	39.42	39.99	39.7
colon	39.32	39.14	40.71	39.7
Found in 2 of 3 experiments				
retina	>40	37.77	36.53	38.1

seminal vesicles	>40	36.4	38.36	38.3
trachea	38.36	>40	37.18	38.5
penis	39.54	>40	36.01	38.5
spleen	>40	39.44	37.59	39.0
pancreas	39.35	>40	37.74	39.0
ovary	>40	39.58	37.6	39.1
vena cava	>40	38.97	38.66	39.2
skin	>40	39.54	38.82	39.5
heart	39.86	39.97	>45	41.6
Found in 1 of 3 experiments				
esophagus	>40	>40	35.19	38.4
nasal mucosa	>40	>40	37.49	39.2
tongue	>40	>40	37.57	39.2
kidney	>40	>40	38.76	39.6
spinal cord	>40	>40	38.97	39.7
tonsil	>40	>40	39.04	39.7
uvula	>40	>40	39.25	39.8
thyroid	>40	>40	39.54	39.8
pituitary	>40	>40	39.89	40.0
adrenal gland	39.87	>40	>45	41.6
Found in 0 of 3 experiments				
brain	>40	>40	>45	41.7
intercranial artery	>40	>40	>45	41.7
liver	>40	>40	>45	41.7
PBL (plasma blood leukocytes)	>40	>40	>45	41.7
mammary gland	>40	>40	>45	41.7
muscle	>40	>40	>45	41.7
optic nerve	>40	>40	>45	41.7
pericardium	>40	>40	>45	41.7

oviduct	>40	>40	>45	41.7
placenta	>40	>40	>45	41.7
adult islets (purified)	>40	>40	>45	41.7
negative control	>40	>40	>45	41.7

Supplemental Table 6: Additional sequencing for 8 T1DGC individuals across *LOC729653*.

Orange is a SNP that is heterozygous in individuals that are homozygous for one of the haplotypes, and yellow points out rs1233478, the only SNP that has one allele in all the low risk and neutral individuals and the opposite allele in all the high risk individuals.

SNP	Position	Location in <i>LOC729653</i>	Low Risk Haplotype Individual 1	Low Risk Haplotype Individual 2	Neutral Haplotype Individual 1	Neutral Haplotype Individual 2	High Risk Haplotype #1 Individual 1	High Risk Haplotype #1 Individual 2	High Risk Haplotype #2 Individual 1	High Risk Haplotype #2 Individual 2
rs1233489	29571022	5' of gene	TT	TT	TT	TT	AA	AA	TT	TT
rs11961131	29571259	5' of gene	TT	TT	TT	TT	TT	TT	TT	TT
rs11407246	29571275	5' of gene	-/-	-/-	-/-	-/-	-/-	-/-	AA	AA
rs9257870	29572945	5' of gene	CC	CC	CC	CC	CC	CC	CC	CC
rs6932526	29572948	5' of gene	AA	AA	AA	AA	AA	AA	AA	AA
rs13437558	29573251	intron 1	CC	CC	CC	CC	CC	CC	CC	CC
rs2746147	29574587	intron 1	CC	CC	TT	TT	CC	CC	CC	CC
rs1233487	29576788	intron 1	AA	AA	AA	AA	GG	GG	AA	AA
rs1233486	29577631	intron 1	CC	CC	TT	TT	CC	CC	CC	CC
rs3131019	29578964	intron 1	CC	CC	AA	AA	AA	AA	AA	AA
rs11961013	29579913	intron 1	GG	GG	GG	GG	GG	GG	GG	GG
rs757256	29580895	intron 1	CC	CC	TT	CT	TT	CT	TT	TT
rs3130858	29581480	intron 2	TT	TT	TT	TT	TT	TT	TT	TT
rs734961	29583018	exon 3	GG	GG	GG	GG	GG	GG	GG	GG
rs734960	29583121	3' UTR, part 1	CC	CC	CC	CC	CC	CC	CC	CC
rs6919091	29583303	3' UTR, part 1	GG	GG	GG	GG	GG	GG	GG	GG
rs1002187	29583446	intron 3' UTR	GG	GG	CC	CC	CC	CC	CC	CC
rs1233482	29583661	intron 3' UTR	CC	CC	AA	AA	CC	CC	CC	CC
rs3131020	29583881	intron 3' UTR	GG	GG	AA	AA	AA	AA	AA	AA
rs9257877	29584487	intron 3' UTR	GG	GG	GG	GG	GG	GG	GG	GG
rs3131022	29584663	intron 3' UTR	CC	CC	GG	GG	GG	GG	GG	GG
rs35174396	29584811	intron 3' UTR	TT	TT	TT	TT	TT	TT	CC	CC
rs2158282	29584997	intron 3' UTR	GG	GG	GG	GG	GG	GG	GG	GG
rs35617617	29585112	intron 3' UTR	GG	GG	GG	GG	GG	GG	AA	AA
rs28675319	29585194	intron 3' UTR	TT	TT	TT	TT	TT	TT	TT	TT
rs1557820	29585219	intron 3' UTR	CC	CC	TT	TT	TT	TT	TT	TT

