

Supplemental Table 4. DOB alleles. Related to Figures 6 and 7.

Chrom	Position	RSID	Ref	Alt	Protein Consequence	Transcript Consequence	Annotation	Number of Homozygotes	Allele Frequency
6	32782883	.	G	A	p.Ala100Val	c.299C>T	missense	0	0.00002472
6	32782931	.	G	A	p.Ala84Val	c.251C>T	missense	0	0.000008237
6	32782827	.	T	C	p.Arg119Gly	c.355A>G	missense	0	0.00001656
6	32782826	rs143319753	C	T	p.Arg119Lys	c.356G>A	missense	0	0.001093
6	32782246	.	C	A	p.Arg165Ile	c.494G>T	missense	0	0.000008579
6	32784676	rs2071554	C	T	p.Arg18Gln	c.53G>A	missense	343	0.06776
6	32781586	.	C	T	p.Arg223Lys	c.668G>A	missense	0	0.00003937
6	32782989	rs147835586	G	A	p.Arg65Cys	c.193C>T	missense	0	0.00002471
6	32782988	rs144504518	C	T	p.Arg65His	c.194G>A	missense	0	0.00003295
6	32782913	.	C	T	p.Arg90Gln	c.269G>A	missense	0	0.000008238
6	32782913	.	C	A	p.Arg90Leu	c.269G>T	missense	0	0.000008238
6	32782914	.	G	A	p.Arg90Trp	c.268C>T	missense	0	0.00001648
6	32782896	.	T	C	p.Arg96Gly	c.286A>G	missense	0	0.00004119
6	32782325	rs139684832	T	G	p.Asn139His	c.415A>C	missense	0	0.000008605
6	32782213	.	T	C	p.Asn176Ser	c.527A>G	missense	0	0.0001543
6	32781221	rs143706496	T	C	p.Asn261Ser	c.782A>G	missense	0	0.00000859
6	32782877	.	T	A	p.Asp102Val	c.305A>T	missense	0	0.00001648
6	32782285	.	T	A	p.Asp152Val	c.455A>T	missense	0	0.00005158
6	32784646	.	T	C	p.Asp28Gly	c.83A>G	missense	0	0.000008614
6	32782983	.	C	T	p.Asp67Asn	c.199G>A	missense	0	0.000008237
6	32782935	.	C	A	p.Asp83Tyr	c.247G>T	missense	0	0.000008237
6	32780998	.	A	G	p.Cys273Arg	c.817T>C	missense	0	0.000008601
6	32782376	.	G	A	p.Gln122Ter	c.364C>T	stop gained	0	0.000008656
6	32782330	.	T	C	p.Gln137Arg	c.410A>G	missense	0	0.000008606
6	32782255	.	T	C	p.Gln162Arg	c.485A>G	missense	0	0.000008583
6	32781234	.	G	C	p.Gln257Glu	c.769C>G	missense	0	0.000008592
6	32784655	.	T	C	p.Gln25Arg	c.74A>G	missense	0	0.000008611
6	32782924	.	C	A	p.Gln86His	c.258G>T	missense	0	0.000008237
6	32782926	rs142229094	G	T	p.Gln86Lys	c.256C>A	missense	0	0.0005437
6	32782885	.	C	A	p.Gln99His	c.297G>T	missense	0	0.000008239
6	32782887	.	G	A	p.Gln99Ter	c.295C>T	stop gained	0	0.00001648
6	32782251	.	C	A	p.Glu163Asp	c.489G>T	missense	0	0.00002574
6	32782250	rs142148406	C	G	p.Glu164Gln	c.490G>C	missense	0	0.0001201
6	32782102	.	T	C	p.Glu213Gly	c.638A>G	missense	0	0.000008624
6	32781219	.	C	T	p.Glu262Lys	c.784G>A	missense	0	0.00004295
6	32783001	.	C	T	p.Glu61Lys	c.181G>A	missense	0	0.000008237
6	32782929	.	C	T	p.Glu85Lys	c.253G>A	missense	0	0.000008238
6	32782874	rs144814623	C	A	p.Gly103Val	c.308G>T	missense	1	0.0003791
6	32782224	.	GC	G	p.Gly172AlafsTer14	c.515delG	frameshift	0	0.0004802

6	32781500	.	C	T	p.Gly252Arg	c.754G>A	missense	0	0.0004295
6	32783046	.	C	T	p.Gly46Arg	c.136G>A	missense	0	0.00005767
6	32783045	.	C	T	p.Gly46Glu	c.137G>A	missense	0	0.00008238
6	32782863	.	G	T	p.His107Asn	c.319C>A	missense	0	0.00008243
6	32782334	.	G	A	p.His136Tyr	c.406C>T	missense	0	0.00008608
6	32782316	.	G	A	p.His142Tyr	c.424C>T	missense	0	0.00008603
6	32782276	.	A	G	p.Ile155Thr	c.464T>C	missense	0	0.00008593
6	32782220	.	T	A	p.Ile174Phe	c.520A>T	missense	0	0.00001715
6	32782219	.	A	G	p.Ile174Thr	c.521T>C	missense	0	0.0000343
6	32782336	.	A	G	p.Leu135Pro	c.404T>C	missense	0	0.0001549
6	32782318	.	A	G	p.Leu141Pro	c.422T>C	missense	0	0.00001721
6	32782142	.	G	T	p.Leu200Ile	c.598C>A	missense	0	0.00008589
6	32781554	rs2070121	G	T	p.Leu234Ile	c.700C>A	missense	0	0.0009835
6	32781554	rs2070121	G	A	p.Leu234Phe	c.700C>T	missense	143	0.114
6	32782904	.	A	T	p.Leu93His	c.278T>A	missense	0	0.00008238
6	32782279	.	T	C	p.Lys154Arg	c.461A>G	missense	0	0.00008594
6	32784728	.	T	C	p.Met1?	c.1A>G	start lost	0	0.00001729
6	32782182	.	C	A	p.Met186Ile	c.558G>T	missense	0	0.00001715
6	32782182	.	C	T	p.Met186Ile	c.558G>A	missense	0	0.00001715
6	32782183	.	A	G	p.Met186Thr	c.557T>C	missense	0	0.00008573
6	32782173	.	C	T	p.Met189Ile	c.567G>A	missense	0	0.00008576
6	32784662	.	T	C	p.Met23Val	c.67A>G	missense	0	0.00002583
6	32782298	.	A	T	p.Phe148Ile	c.442T>A	missense	0	0.0000086
6	32783028	.	A	G	p.Phe52Leu	c.154T>C	missense	0	0.00008237
6	32782355	.	G	A	p.Pro129Ser	c.385C>T	missense	0	0.00003448
6	32784710	.	G	C	p.Pro7Ala	c.19C>G	missense	0	0.00001724
6	32784664	.	G	A	p.Ser22Phe	c.65C>T	missense	0	0.00006027
6	32781227	.	G	C	p.Ser259Cys	c.776C>G	missense	0	0.0000859
6	32782836	.	T	C	p.Thr116Ala	c.346A>G	missense	0	0.00008267
6	32782304	.	T	A	p.Thr146Ser	c.436A>T	missense	0	0.00008601
6	32784679	.	G	A	p.Thr17Ile	c.50C>T	missense	0	0.00001722
6	32782146	.	GGT	G	p.Thr198LeufsTer21	c.592_593delAC	frameshift	0	0.00008587
6	32781236	.	G	T	p.Thr256Lys	c.767C>A	missense	0	0.00008593
6	32781236	.	G	A	p.Thr256Met	c.767C>T	missense	0	0.00001719
6	32782270	rs146350950	C	A	p.Trp157Leu	c.470G>T	missense	0	0.00006872
6	32782270	rs146350950	C	T	p.Trp157Ter	c.470G>A	stop gained	0	0.0000859
6	32781588	.	C	T	p.Trp222Ter	c.666G>A	stop gained	0	0.00003966
6	32782922	.	C	A	p.Trp87Leu	c.260G>T	missense	0	0.00008237
6	32784707	.	A	G	p.Trp8Arg	c.22T>C	missense	0	0.00008619
6	32782295	.	A	G	p.Tyr149His	c.445T>C	missense	0	0.0000344
6	32782832	.	A	G	p.Val117Ala	c.350T>C	missense	0	0.00008273
6	32782832	.	A	C	p.Val117Gly	c.350T>G	missense	0	0.00008273
6	32782833	.	C	G	p.Val117Leu	c.349G>C	missense	0	0.00002481
6	32782367	.	C	T	p.Val125Met	c.373G>A	missense	0	0.00008634

6	32782189	.	A	G	p.Val184Ala	c.551T>C	missense	0	0.00008573
6	32782186	.	A	G	p.Val185Ala	c.554T>C	missense	0	0.00008573
6	32782153	.	A	T	p.Val196Asp	c.587T>A	missense	0	0.00008581
6	32782112	rs150697393	C	T	p.Val210Ile	c.628G>A	missense	80	0.02834
6	32782105	.	A	G	p.Val212Ala	c.635T>C	missense	0	0.00004309
6	32781524	rs148095098	C	T	p.Val244Ile	c.730G>A	missense	25	0.03823
6	32783025	.	C	G	p.Val53Leu	c.157G>C	missense	0	0.00008237
6	32782096	.	C	A		c.643+1G>T	splice donor	0	0.00008648
6	32781030	.	T	C		c.787-2A>G	splice acceptor	0	0.000086
6	32783091	.	C	T		c.92-1G>A	splice acceptor	0	0.00008256

All single nucleotide variants found in human HLA-DOB from ExAC. <http://exac.broadinstitute.org/gene/ENSG00000241106>.

Ref, DOB*0101 common allele. RSID, SNP. Highlighted, alleles used in Figures 6 and S3).