

			Allele Frequency (%)	
GWAS1	HLADQA1 rs2187668	CC	357516/487208 (73.4%)	
		CT	118070/487208 (24.2%)	
		TT	11622/487208 (2.4%)	
		MAF	14.5%	
	PLA2R1 rs4664308	AA	174588/487208 (35.8%)	
		AG	230759/487208 (47.4%)	
		GG	81861/487208 (16.8%)	
		MAF	40.5%	
	GWAS2	HLADQA1 rs9272729	GG	351417/479895 (73.2%)
			GA	117731/479895 (24.5%)
AA			10747/479895 (2.2%)	
MAF			14.5%	
PLA2R1 rs17830558		TT	105620/472780 (22.3%)	
		TG	228842/472780 (48.4%)	
		GG	138318/472780 (29.3%)	
		MAF	46.5%	
GWAS3		HLADRB1/DQA1 rs9271573	CC	170192/486978 (34.9%)
			AC	234411/486978 (48.1%)
	AA		82375/486978 (16.9%)	
	MAF		41%	
	PLA2R1 rs17831251	CC	172495/481109 (35.9%)	
		CT	227843/481109 (47.4%)	
		TT	80771/481109 (16.8%)	
		MAF	40.5%	
	NFKB1 rs230540	TT	205265/481333 (42.6%)	
		CT	216576/481333 (45.0%)	
CC		59492/481333 (12.4%)		
MAF		34.9%		
IRF4 rs9405192	GG	259096/474386 (54.6%)		
	GA	182247/474386 (38.4%)		
	AA	33043/474386 (7.0%)		
	MAF	26.2%		

Table S2 – Allele counts at the lead SNPs from GWAS1⁴, GWAS2⁵, and GWAS3⁶ in all UK Biobank participants using the imputed UK Biobank datasets. GWAS – Genome-Wide Association Study, MAF – minor allele frequency, SNP – single nucleotide polymorphism