

Supplementary Table 3: *USF1* haplotype frequency distributions in cases and controls in all 7 samples (Online)

(a) European

Haplotype	AM cases n=150	AM controls n=361	FR cases n=259	FR controls n=288	UK cases n=449	UK controls n=450	UT cases n=182	UT controls n=167
2,1,2,1,1,1,2,2	0.289	0.235	0.255	0.261	0.285	0.278	0.264	0.286
1,1,1,1,2,1,1,2	0.279	0.323	0.280	0.264	0.280	0.247	0.284	0.254
2,1,2,2,1,1,2,1,2	0.249	0.215	0.234	0.241	0.204	0.215	0.202	0.244
2,2,2,1,1,2,2,1,1	0.097	0.119	0.135	0.140	0.112	0.148	0.118	0.124
2,1,2,2,1,1,1,2,2	0.047	0.073	0.058	0.069	0.077	0.075	0.079	0.056
2,1,2,1,1,1,2,1,2	0.021	0.023	0.014	0.007	0.031	0.028	0.024	0.026

(b) non-European

Haplotype	HK cases n=64	HK controls n=64	SH cases n=80	SH controls n=80	AZ cases n=200	AZ controls n=199
2,1,2,1,1,1,1,2,2	0.223	0.120	0.169	0.144	0.018	0.015
1,1,1,1,2,1,1,1,2	0.102	0.148	0.206	0.200	0.372	0.334
2,1,2,2,1,1,2,1,2	0.159	0.192	0.106	0.112	0.143	0.151
2,2,2,1,1,2,2,1,1	0.492	0.508	0.519	0.531	0.452	0.485
2,1,2,2,1,1,1,2,2	0.008	not seen	not seen	not seen	0.005	0.005
2,1,2,1,1,1,2,1,2	not seen	0.008	not seen	0.006	not seen	0.003

Haplotype trend regression of the 9-SNP window showed no significant haplotypic association between *USF1* and type 2 diabetes in any of the populations (Amish (AM): $p=0.23$; Pimas (AZ): $p=0.89$; French (FR): $p=0.99$; Hong Kong (HK): $p=0.25$; Shanghai (SH): $p=0.64$; UK: $p=0.31$; Utah (UT): $p=0.59$). SNPs included in this analysis were: rs4339888, rs3766383, rs3737787, rs2516840, rs2073656, rs2073653, rs2516839, rs2516838 and rs1556259. Haplotypes with frequency > 0.02 in at least one population are presented. Allele designations are as provided in table 2.