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Supplementary Table 1: Extent of common variation captured in 40 candidate genes in populations of European or African descent

GENE	Targeted region (NCBI 36)	n tag SNPs	HapMap CEU (European)				HapMap YRI (African)			
			r ² ≥0.8	r ² ≥0.5	mean r ²	lowest r ²	r ² ≥0.8	r ² ≥0.5	mean r ²	lowest r ²
<i>ABCC8</i>	chr11:17361008-17475025	84	99%	99%	0.970	0.209	92%	98%	0.933	0.315
<i>ADIPOQ</i>	chr3:188023157-188068946	25	85%	100%	0.928	0.502	80%	83%	0.836	0.118
<i>ADIPOR1</i>	chr1:201166584-201214323	22	96%	100%	0.961	0.786	96%	100%	0.911	0.633
<i>ADIPOR2</i>	chr12:1650508-1778106	31	98%	100%	0.967	0.658	95%	98%	0.908	0.382
<i>CAPN10</i>	chr2:241154818-241197193	33	84%	84%	0.867	0.096	92%	92%	0.900	0.067
<i>CREB1</i>	chr2:208082861-208188527	13	97%	100%	0.981	0.738	96%	100%	0.963	0.666
<i>CYP3A4</i>	chr7:99182540-99239744	15	71%	85%	0.731	0.009	84%	87%	0.867	0.212
<i>FOXO1A</i>	chr13:40017801-40158734	35	98%	98%	0.964	0.210	96%	100%	0.947	0.626
<i>GCG</i>	chr2:162697634-162737003	13	100%	100%	0.960	0.839	92%	92%	0.894	0.371
<i>GCK</i>	chr7:44140395-44215547	37	98%	98%	0.980	0.292	92%	96%	0.948	0.348
<i>HNF1A</i>	chr12:119880932-119934695	20	100%	100%	0.976	0.832	87%	91%	0.854	0.174
<i>HNF1B</i>	chr17:33110547-33199209	74	94%	97%	0.938	0.335	92%	95%	0.930	0.177
<i>HNF4A</i>	chr20:42397855-42501725	66	94%	97%	0.954	0.228	85%	92%	0.890	0.123
<i>ITLN1</i>	chr1:159102954-159141584	11	100%	100%	0.977	0.826	84%	97%	0.800	0.255
<i>ITLN2</i>	chr1:159171440-159211213	15	83%	87%	0.871	0.368	76%	86%	0.812	0.018
<i>KCNJ11</i>	chr11:17353374-17387454	9	94%	100%	0.952	0.686	74%	92%	0.879	0.239
<i>MC4R</i>	chr18:56179544-56210981	21	100%	100%	0.937	0.803	89%	93%	0.847	0.089
<i>MEF2A</i>	chr15:97903656-98084150	38	96%	98%	0.934	0.143	92%	95%	0.889	0.356
<i>MEF2D</i>	chr1:154690143-154757153	16	95%	95%	0.899	0.060	97%	97%	0.921	0.321
<i>NEUROD1</i>	chr2:182239439-182273626	14	100%	100%	0.979	0.877	92%	100%	0.936	0.682
<i>PCK1</i>	chr20:55549543-55584919	37	96%	97%	0.935	0.373	95%	98%	0.948	0.158
<i>PCK2</i>	chr14:23613323-23653179	14	92%	92%	0.921	0.402	83%	88%	0.868	0.071
<i>PDX1</i>	chr13:27372168-27408451	13	100%	100%	0.991	0.941	88%	88%	0.891	0.206
<i>PKLR</i>	chr1:153515708-153557849	10	100%	100%	0.994	0.960	93%	93%	0.916	0.229
<i>PPARA</i>	chr22:44905163-45028317	63	91%	94%	0.922	0.034	89%	95%	0.910	0.085
<i>PPARG</i>	chr3:12284349-12460855	59	97%	98%	0.966	0.182	91%	99%	0.894	0.370
<i>PPARGC1A</i>	chr4:23392742-23520798	79	98%	100%	0.965	0.603	98%	99%	0.946	0.459
<i>PPARGC1B</i>	chr5:149070057-149217462	96	98%	100%	0.962	0.571	88%	98%	0.905	0.127
<i>PRKAA1</i>	chr5:40785238-40854054	9	84%	84%	0.848	0.251	100%	100%	0.954	0.804
<i>PRKAA2</i>	chr1:56863578-56963596	18	91%	93%	0.909	0.099	95%	98%	0.870	0.103
<i>PRKAB1</i>	chr12:118570144-118613812	10	95%	95%	0.938	0.053	92%	96%	0.902	0.018

<i>PRKAB2</i>	chr1:145083309-145130753	13	70%	83%	0.828	0.259	93%	96%	0.884	0.491
<i>PRKAG1</i>	chr12:47672322-47718859	7	100%	100%	0.991	0.897	57%	100%	0.799	0.534
<i>PRKAG2*</i>	chr7:150874134-151021682	53	94%	99%	0.956	0.171	95%	98%	0.921	0.268
<i>PRKAG3</i>	chr2:219385350-219424756	11	85%	85%	0.880	0.161	100%	100%	0.980	0.867
<i>PTPN1</i>	chr20:48540298-48644493	27	98%	100%	0.972	0.748	100%	100%	0.940	0.802
<i>SLC22A1</i>	chr6:160442853-160509740	47	96%	100%	0.982	0.528	88%	97%	0.894	0.143
<i>SLC22A2</i>	chr6:160547782-160619949	44	98%	98%	0.969	0.307	92%	94%	0.907	0.243
<i>SLC47A1</i>	chr17:19357759-19432938	29	94%	94%	0.946	0.133	81%	86%	0.858	0.159
<i>STK11</i>	chr19:1136798-1189434	10	72%	72%	0.788	0.121	69%	76%	0.750	0.048

Tagger was used to select tag SNPs designed to capture all common (minor allele frequency >5%) variants at $r^2 \geq 0.8$ in 40 candidate genes (plus 20 kb upstream and 10 kb downstream) for both HapMap CEU and YRI populations. Actual coverage obtained by working SNPs is shown for $r^2 \geq 0.8$ and $r^2 \geq 0.5$. (*) Because of weak linkage disequilibrium (LD) across a substantial segment in the *PRKAG2* gene region, only a subset marked by strong LD was targeted.

Supplementary Table 2: Full association dataset

[Excel spreadsheet]

Supplementary Table 3: SNPs imputed in DPP non-Hispanic white participants

[Excel spreadsheet]