Supplementary Table 1: Genetic Variants Found to Meet Criteria								
Health Condition	**Gene Symbol**	**Variant**	**Risk Allele[1]**	**Risk Allele Frequency[2]**			**Example of a published association**	**Reference**
				A.Am.	**Cau.**	**As.**		
Cancer	CYP1A1	I462V rs1048943	 G	 .0	 .05	 .21	OR 1.44 (1.17-1.78) Esophageal cancer	[1,2]
	GSTM1	Null	Null	.32	.43	.43	OR 1.27 (1.13-1.42) Head and neck cancer	[3,4]
	GSTM1	Null	Null	.32	.43	.43	OR 1.13 (1.04-1.25) Lung cancer	[3,5]
	GSTM1	Null	Null	.32	.43	.43	OR 1.44 (1.23-1.68) Bladder cancer	[3,6]
	GSTT1	Null	Null	.26	.21	.40	OR 1.42 (1.21-1.66) Colorectal cancer	[3,7]
	MC1R	RHC rs1805006 rs11547464 rs1805007 rs1805008 rs1805009	 A A T T C	.04	.21	.0	OR 2.0 (1.6-2.6) Cutaneous malignant melanoma	[1,8]
	MPO	-463G->A rs2333227	 C	 .50	 .83	 .85	OR 0.68 (0.50-0.93) Lung cancer	[1,9]
	MTHFR	677C->T rs1801133	 C	 .88	 .67	 .62	OR 0.82 (0.72-0.93) Colorectal cancer	[1,10]
	NAT2	Slow	Slow	-	.11	.56	OR 1.4 (1.2-1.7) Bladder cancer	[11]
Heart Disease	ADD1	G460W rs4961	 T	 .15	 .21	 .53	OR 1.55 (1.03-2.43) Hypertension	[1,12]
	AGT	M235T rs699	 C	 .83	 .43	 .80	OR 1.21 (1.11-1.32) Hypertension	[1,13]
	APOB	Xba1 rs693	 C	 .82	 .51	 .94	OR 0.80 (0.66-0.96) Ischemic heart disease	[1,14]
	APOB	Sp I/D	D	-	.32	-	OR 1.30 (1.08-1.58) Ischemic heart diseases	[14]

	CETP	Taq1B rs708272	C	.75	.57	.65	OR 0.78 (0.66-0.93) Coronary artery disease	[1,15]
	LIPC	-514C->T rs1800588	C	.46	.70	.56	WMD 0.09 (0.07-0.12) High Density Lipoprotein	[1,16]
	NOS3	E298D rs1799983	T	.08	.39	.10	OR 1.31 (1.13-1.51) Heart disease	[1,17]
	PON1	Q192R rs662	G	.59	.26	.62	OR 1.15 (1.09-1.22) Coronary heart disease	[1,18]
Ischemic Stroke	MTHFR	677C->T rs1801133	T	.12	.31	.38	OR 1.24 (1.08-1.42) Ischemic stroke	[1,19]
Osteoporosis	COL1A1	Sp1 rs1800012	T	.04	.18	-	OR 1.37 (1.15-1.64) Vertebral fracture risk	[1,20]
	CYP19A1	$(TTTA)_n$	≠A2	-	.85	-	OR 0.27 (0.09-0.79) Fracture risk	[21]
	ESR1	Xba1 rs9340799	A	.62	.67	.78	OR 0.63 (0.44-0.90) Fracture risk	[1,22]
	IL6	-174G->C rs1800795	G	.96	.47	.99	OR 1.46 (1.08-1.97) Fracture risk	[1,23]
Type 2 Diabetes	CAPN10	SNP44 rs2975760	C	.02	.15	.09	OR 1.17 (1.02-1.34) Type 2 diabetes	[1,24]
	CAPN10	SNP43 rs3792267	G	.89	.70	.90	OR 1.19 (1.07-1.33) Type 2 Diabetes	[1,25]
	KCNJ11	E23K rs5219	T	.08	.32	.27	OR 1.37 (1.21-1.54) Type 2 Diabetes	[1,26]
	PPARG	P12A rs1801282	C	.97	.92	.95	OR 1.25 (p 0.002) Type 2 Diabetes	[1,27]
	TCF7L2	rs12255372	T	.27	.22	.01	OR 1.45 (1.26-1.67) Type 2 Diabetes	[1,28]

Notes:

[1] The risk allele is defined as the allele that is associated with higher risk for the health condition (or is not protective).

[2] This is the approximate frequency of the allele of the genetic variant that is associated with greater risk for the health condition (i.e. when the risk information is protective, the frequency information will be for the non-protective allele). The abbreviations are African American (A.Am.), Caucasian (Cau.), and Asian (As.). For MC1R, prevalence information was combined for the different genetic variants. This information was obtained from dbSNP (www.ncbi.nlm.nih.gov/SNP/) whenever possible, otherwise it was extracted from papers.

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