Table S5. Overlap of *cis*- associated genes that were detected using: 1) normalized and PCA-corrected gene expression data, and 2) 'REDUCED' data.

	permutation threshold									
	0.01					0.001				
	REDUCED[a]	non-RED[b]	overlap[c]	proportion REDUCED[d]	proportion non-RED[e]	REDUCED[a]	non-RED[b]	overlap[c]	proportion REDUCED[d]	proportion non-RED[e]
CEU	1966	657	491	0.25	0.75	1253	313	278	0.22	0.89
CHB	1950	774	594	0.30	0.77	1218	378	340	0.28	0.90
GIH	1984	698	514	0.26	0.74	1219	300	277	0.23	0.92
JPT	2131	795	623	0.29	0.78	1327	386	351	0.26	0.91
LWK	1794	773	527	0.29	0.68	962	311	265	0.28	0.85
MEX	1131	472	305	0.27	0.65	528	165	132	0.25	0.80
MKK	2562	947	660	0.26	0.70	1528	411	362	0.24	0.88
YRI	2415	799	559	0.23	0.70	1439	328	300	0.21	0.91

[a] Gene counts detected from the 'REDUCED' analysis.

[b] Gene counts detected from the normalized and PCA-corrected analysis.

[c] The intersection of the gene sets from 'REDUCED' and normalized and PCA-corrected analyses.

[d] The proportion of genes that were detected in the 'REDUCED' analysis that were also detected in the normalized and PCA-corrected analysis.

[e] The proportion of genes that were detected in the normalized and PCA-corrected analysis that were also detected in the 'REDUCED' analysis.