Table S9. Partitioning contribution of androgen- (AR) and estrogen- (ER) responsive genes and of sex-heterogeneous markers to sex-combined, male and female heritability in WTCCC diseases

	AR$			ER$			Heterogeneous SNPs$			P$
Diseases	*All h²$_g$* (SE)	*M h²$_g$* (SE)	*F h²$_g$* (SE)	*All h²$_g$* (SE)	*M h²$_g$* (SE)	*F h²$_g$* (SE)	*All h²$_g$* (SE)	*M h²$_g$* (SE)	*F h²$_g$* (SE)	
AS*	4% (4%)	8% (6%)	1% (8%)	4% (4%)	5% (5%)	2% (6%)	-1% (2%)	3% (4%)	7% (6%)	NS
BD	6% (5%)	7% (14%)	9% (8%)	-6% (3%)	-4% (10%)	-0.6% (5%)	-1% (3%)	-3% (8%)	-4% (5%)	NS
CAD	20% (10%)	2% (14%)	21% (12%)*	7% (7%)	-4% (1%)	25% (11%)***	1% (6%)	6% (8%)	-7% (6%)	NS
CD*	16% (6%)	6% (12%)	-	6% (4%)	3% (9%)	-	1% (3%)	2% (7%)	-	-
HT	2% (6%)	22% (40%)	0% (7%)	5% (5%)	32% (4%)	6% (5%)	-2% (3%)	60% (76%)	-6% (4%)	NS
MS*	5% (2%)	8% (3%)	3% (2%)	2% (1%)	6% (2%)	1% (1%)	1% (9%)	3% (3%)	2% (1%)	1.0×10^{-2}
RA*	19% (14%)	-18% (18%)	37% (26%)**	12% (9%)	-2% (11%)	14% (14%)	-9% (7%)	6% (1%)	-14% (12%)	3.0×10^{-2}
T1D*	14% (9%)	27% (15%)	46% (47%)	17% (8%)	10% (10%)	51% (43%)	2% (5%)	4% (7%)	-3% (16%)	NS
T2D	6% (6%)	2% (13%)	17% (11%)	2% (4%)	-6% (9%)	8% *8%)	1% (3%)	-7% (7%)	11% (7%)	3.0×10^{-2}

Abbreviations: h2g heritability; P p-value; SE standard error; NS not significant

$ Empirical p-value for difference between M and F h2g, estimation based on 1,000 permutations

* HLA locus was tested separately from the rest of the autosomes

% h2g computed as (h2g in category) / (h2g total) with corresponding standard error estimated using delta method

AR and ER genes covered 6% and 3% of SNPs, respectively. Heterogeneous SNPs were 0.01% of all SNPs

*** P<0.001; ** P<0.01; * P<0.05; dashes indicate that estimates did not converge