

Table S1 - SNPs per phenotype, WTCCC study associated loci (HS) and *Gentrepid* predicted candidate genes per phenotype

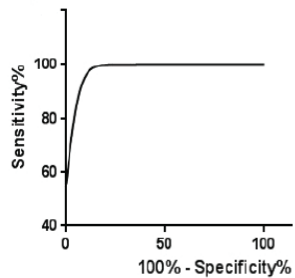
Phenotype	WS $p \leq 1 \times 10^{-3}$ SNPs (Clusters)	MWS $p \leq 1 \times 10^{-4}$ SNPs (Clusters)	MHS $p \leq 1 \times 10^{-5}$ SNPs (Clusters)	HS $p \leq 5 \times 10^{-7}$ SNPs (Clusters)	Loci in the original WTCCC Study	<i>Gentrepid</i> predicted candidate genes
CAD	757 (436)	134 (86)	43 (22)	25 (10)	1	264
HT	799 (460)	110 (61)	5 (5)	0 (0)	0	219
T2D	725 (421)	125 (70)	45 (15)	19 (2)	3	291
T1D	966 (442)	276 (103)	162 (43)	92 (24)	7	358
RA	699 (429)	104 (75)	27 (14)	11 (5)	3	200
CD	1064 (501)	261 (112)	102 (23)	63 (10)	9	378
BD	797 (513)	138 (94)	23 (10)	0 (0)	1	212

Abbreviations - T2D - Type 2 Diabetes; BD - Bipolar Disorder; CD - Crohn's Disease; HT -

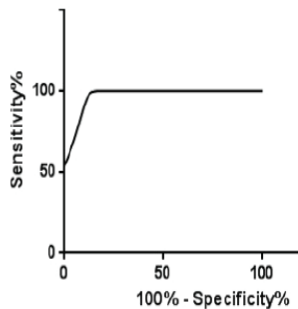
Hypertension; T1D - Type 1 Diabetes; CAD - Coronary Artery Disease; RA - Rheumatoid Arthritis; SNP - Single Nucleotide Polymorphism; WTCCC - Wellcome Trust Case-Control Consortium; WS: Weakly Significant Set; MWS: Moderately-Weak Significant Set; MHS: Moderately-High Significant set; HS: Highly Significant Set.



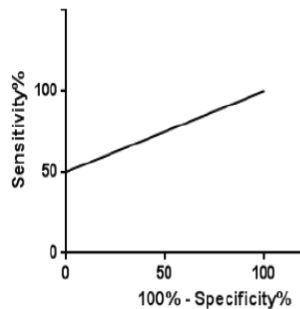
BD



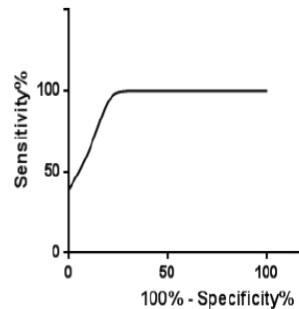
T1D



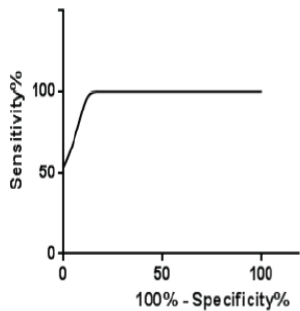
CD



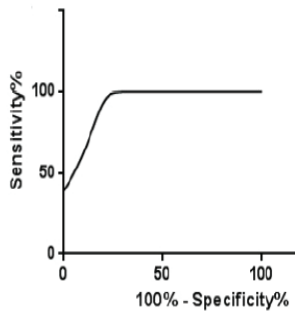
RA



CAD



HT



T2D

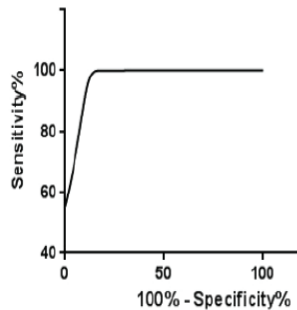
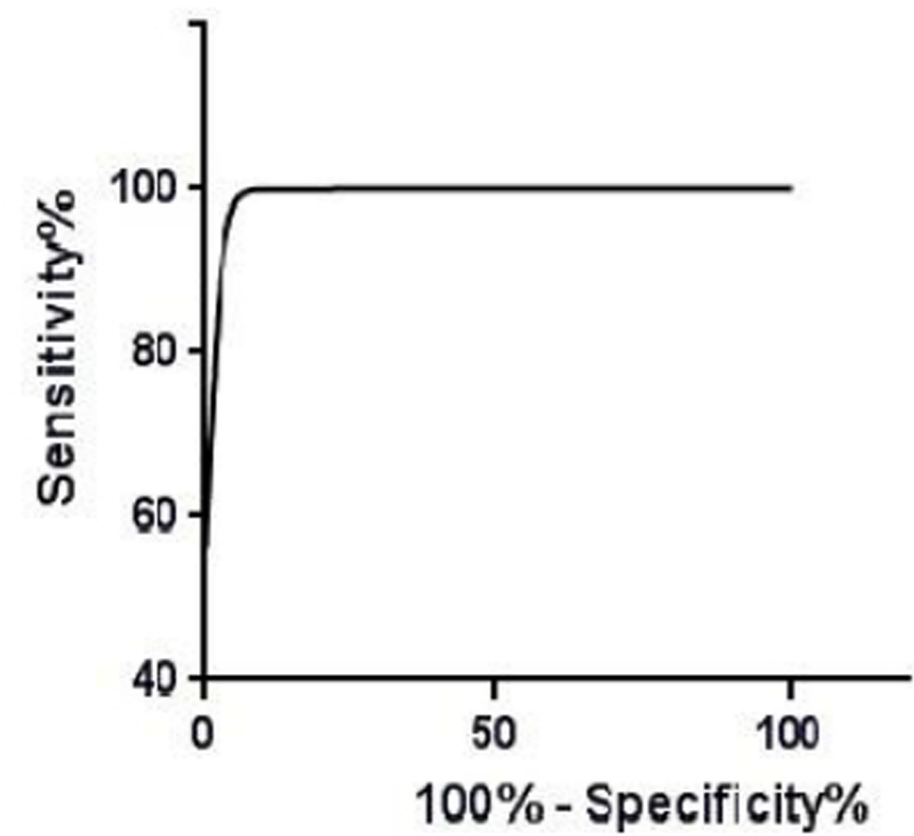
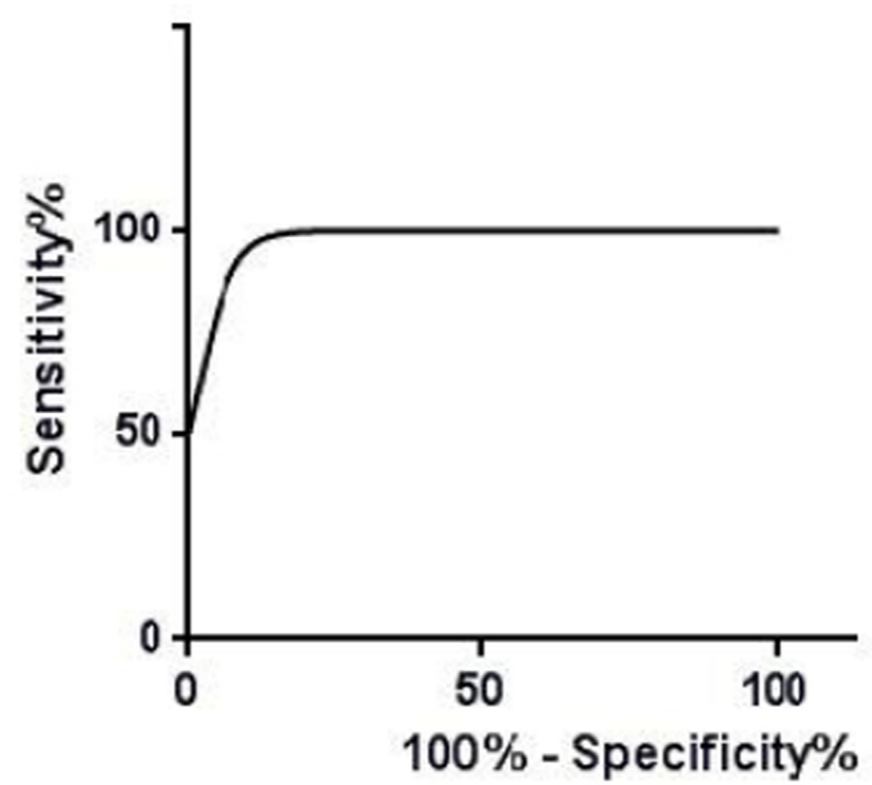
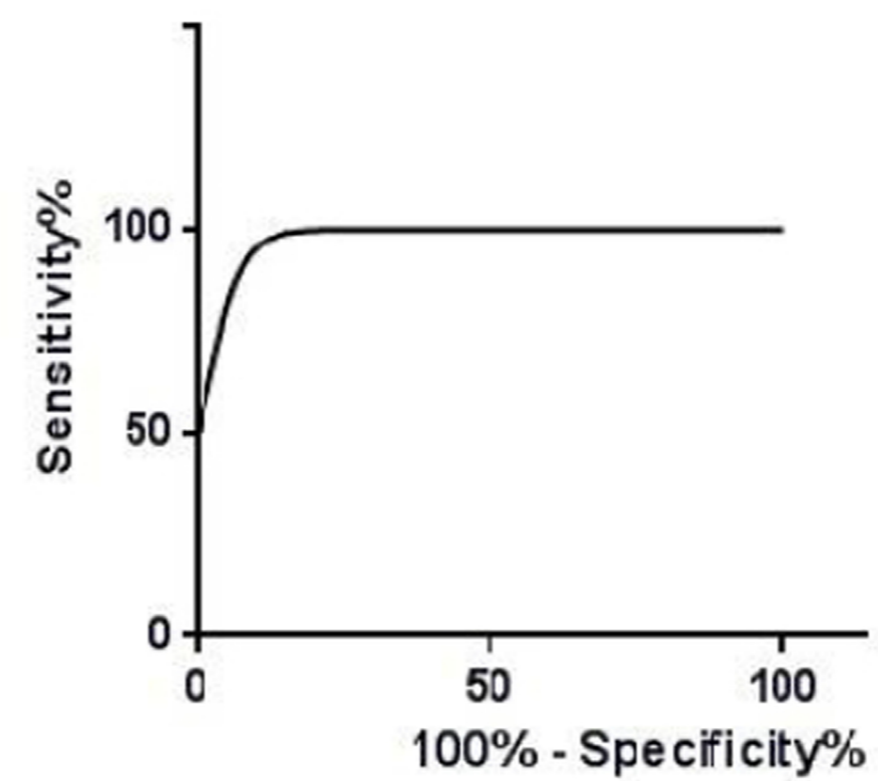
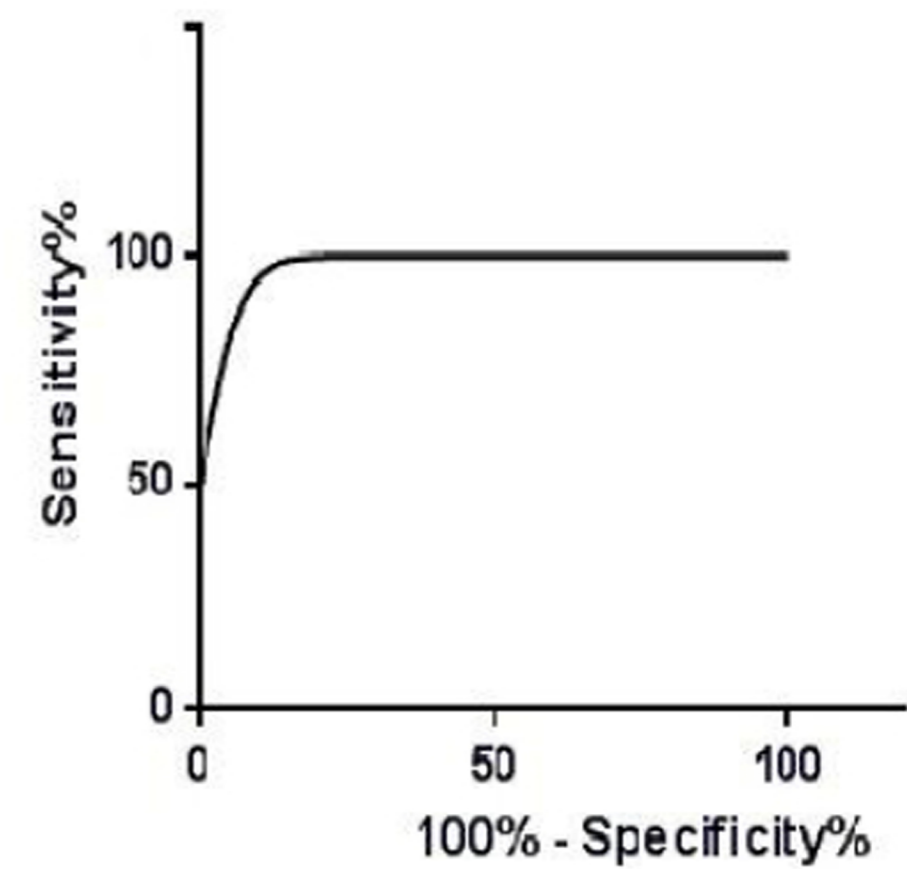
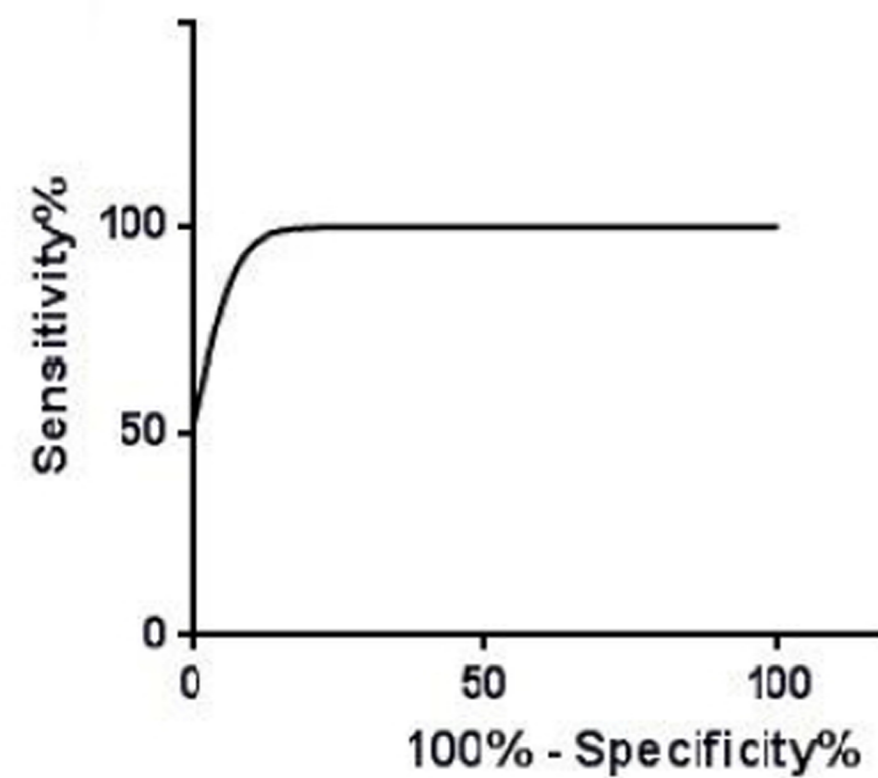
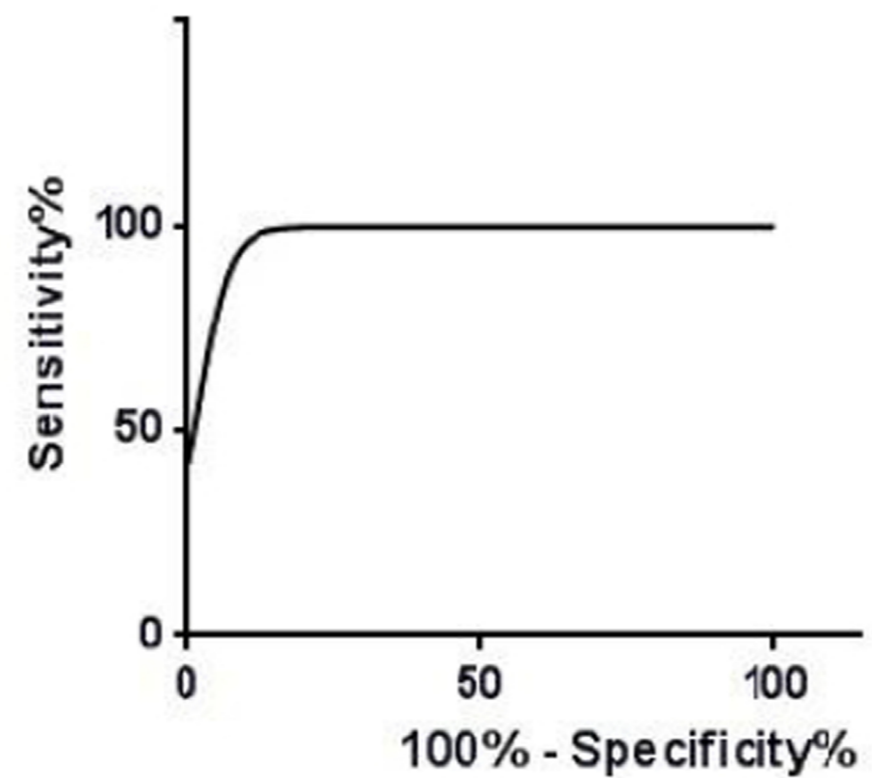


Table S2 - AUC values for ROC curves

Phenotype	AUC (figure S1)	AUC (figure S2)
T2D	0.98	0.95
T1D	0.97	0.97
RA	0.95	0.97
HT	0.95	0.97
BD	0.98	0.98
CD	0.99	0.97
CAD	0.97	0.97

Abbreviations - T2D - Type 2 Diabetes; BD - Bipolar Disorder; CD - Crohn's Disease; HT - Hypertension; T1D - Type 1 Diabetes; CAD - Coronary Artery Disease; RA - Rheumatoid Arthritis; AUC - Area under curve.

BD**CAD****HT****CD****T1D****RA****T2D**