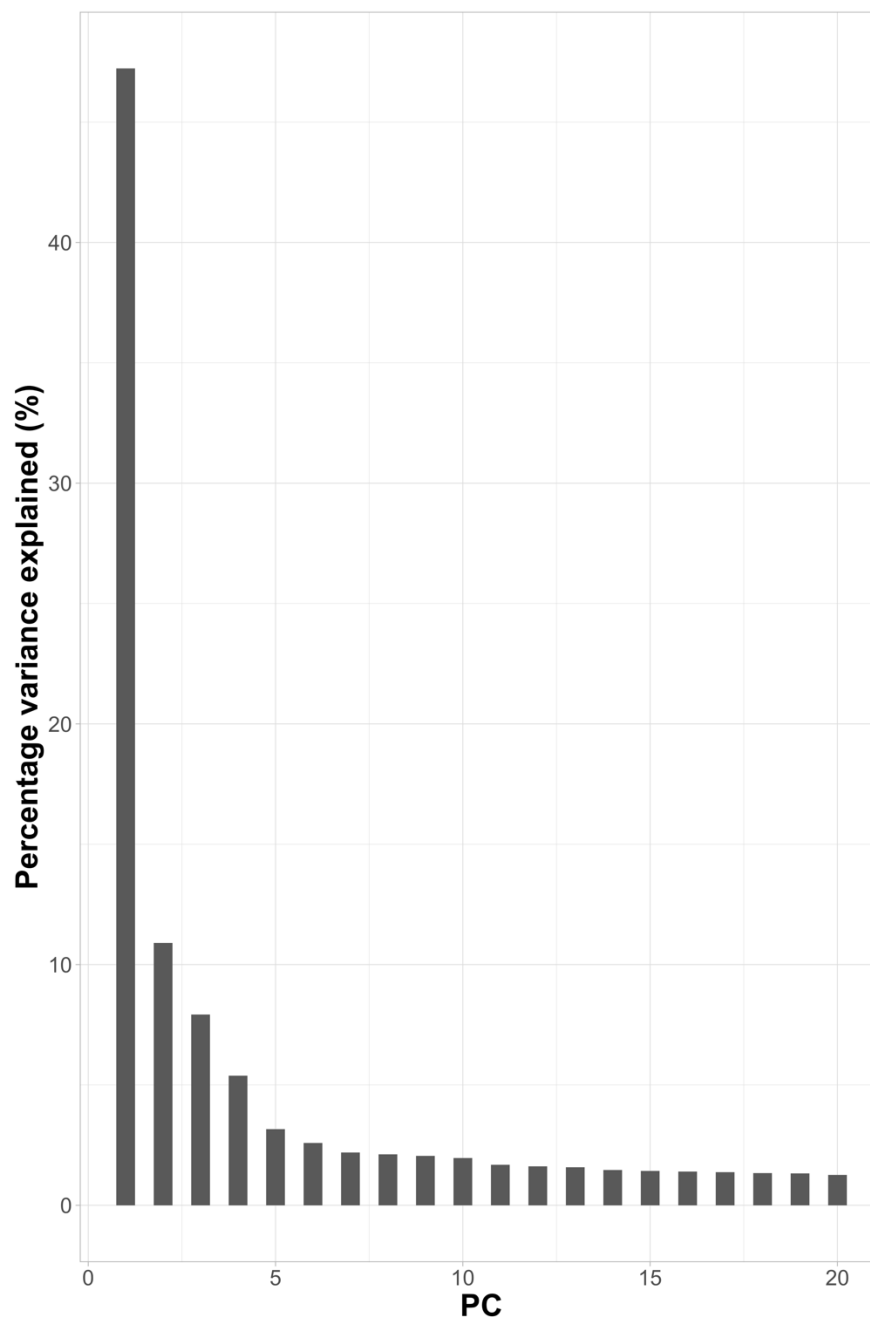


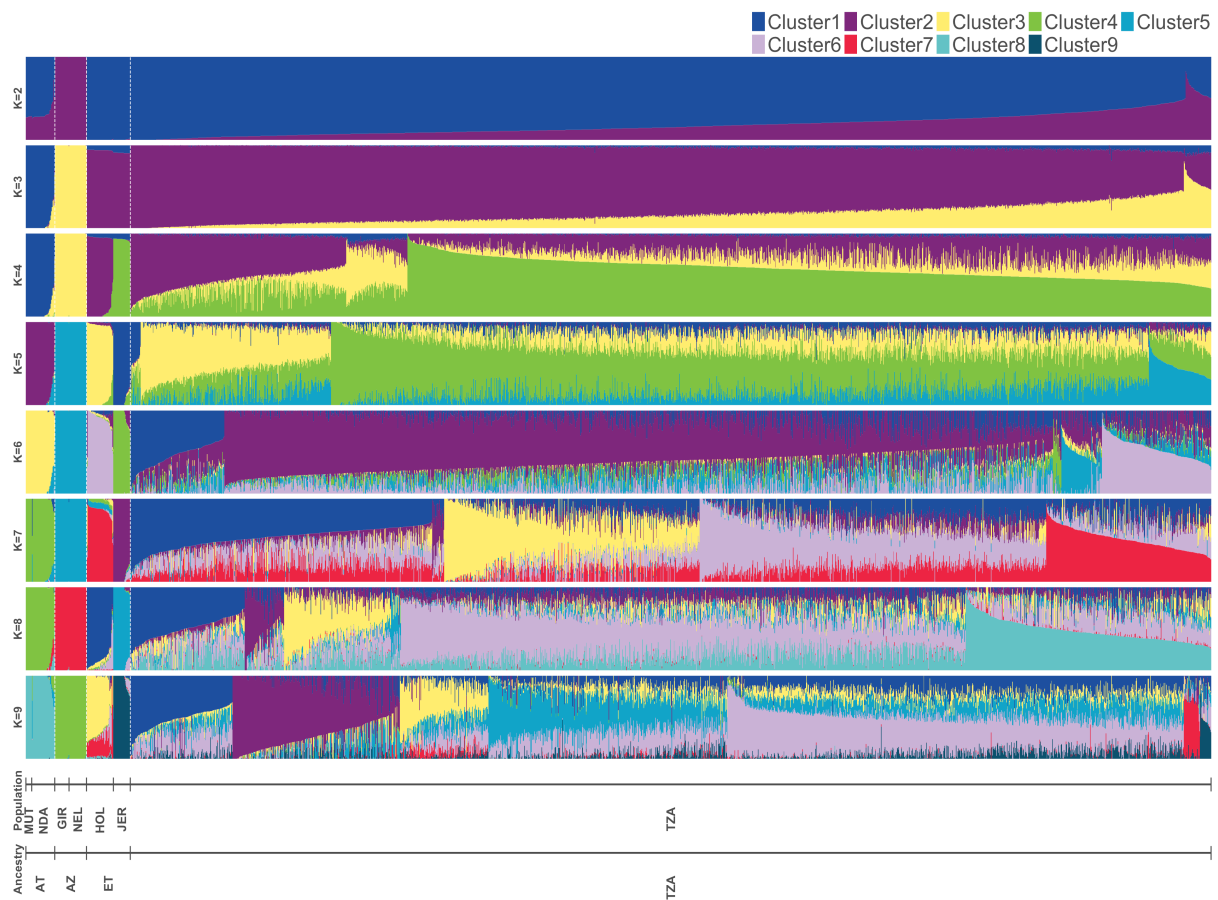
Supplementary Material

1 Supplementary Figures and Tables

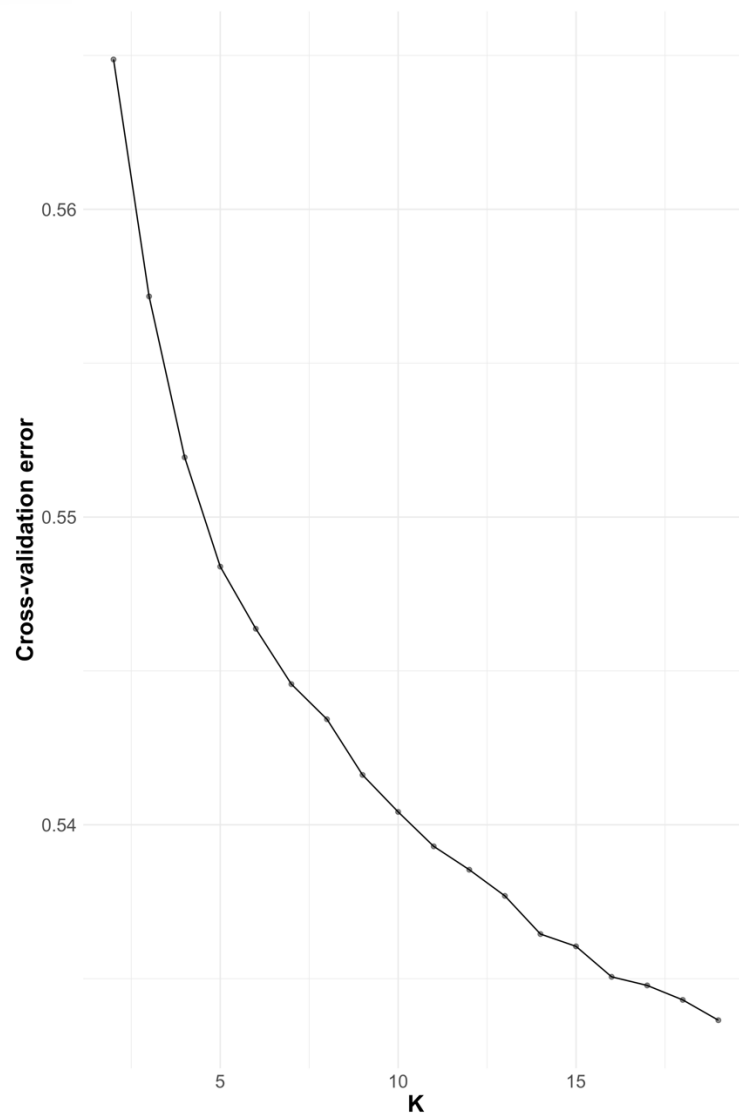
1.1 Supplementary Figures



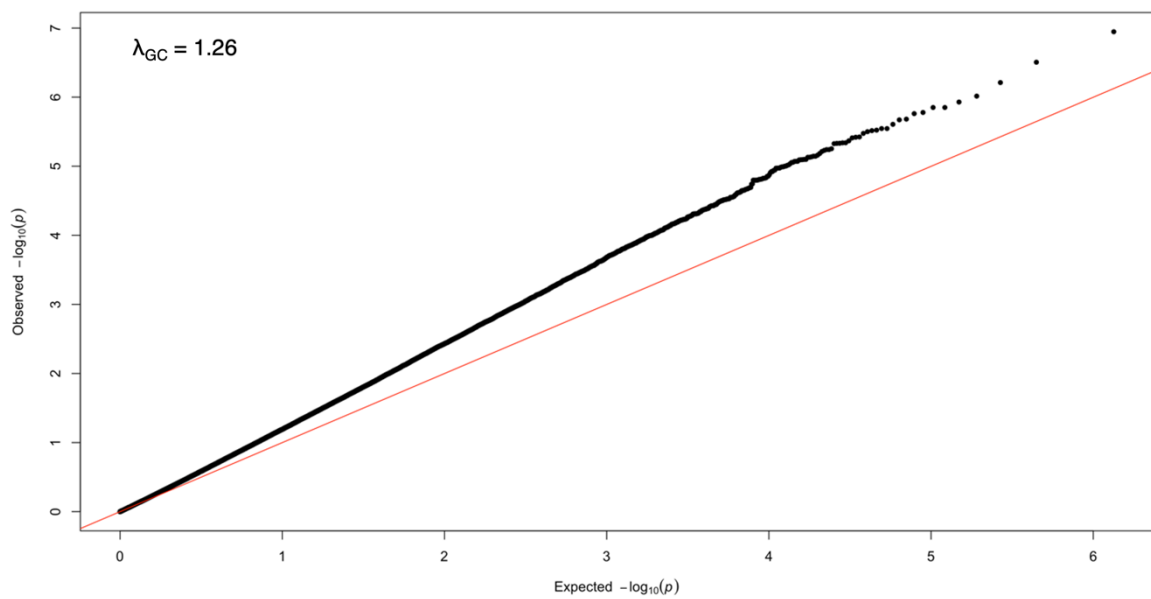
Supplementary Figure 1. Percentage (%) of variance of explained by each of the 20 principal components (PCs) in principal components analysis (PCA) carried out in 1977 Tanzanian animals and 223 reference samples. Bars showed the first and second PCs explaining 47.2% and 10.9% of the total variation.



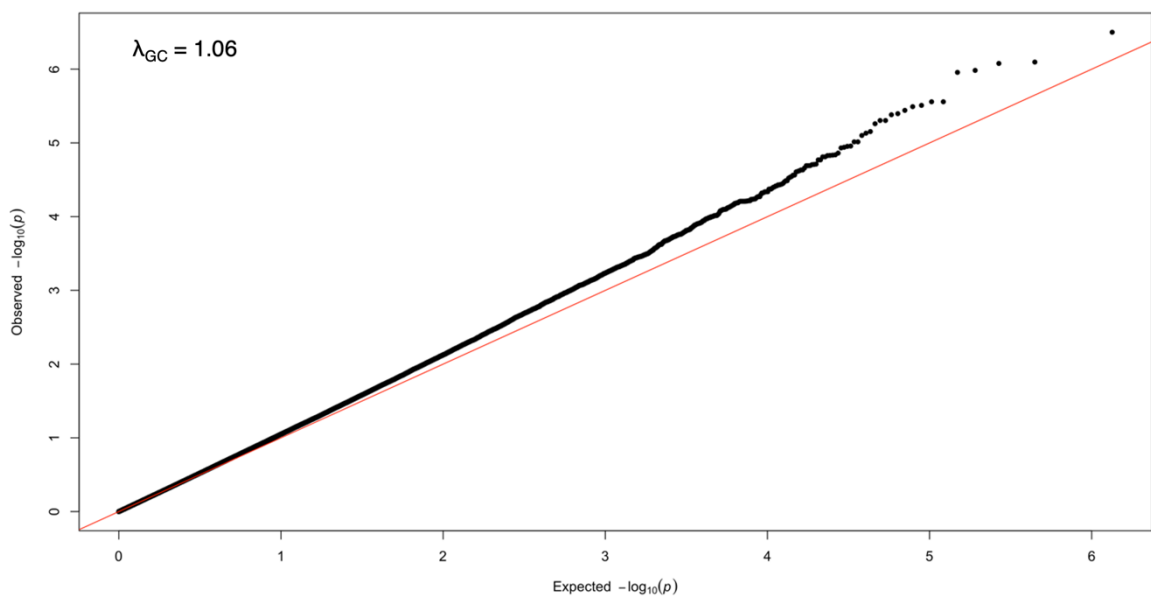
Supplementary Figure 2. Unsupervised admixture bar plot of Tanzanian cattle ancestries assuming $K = 9$ ancestral populations. Bars are split in K colours comparable genomic membership to a given ancestral population.



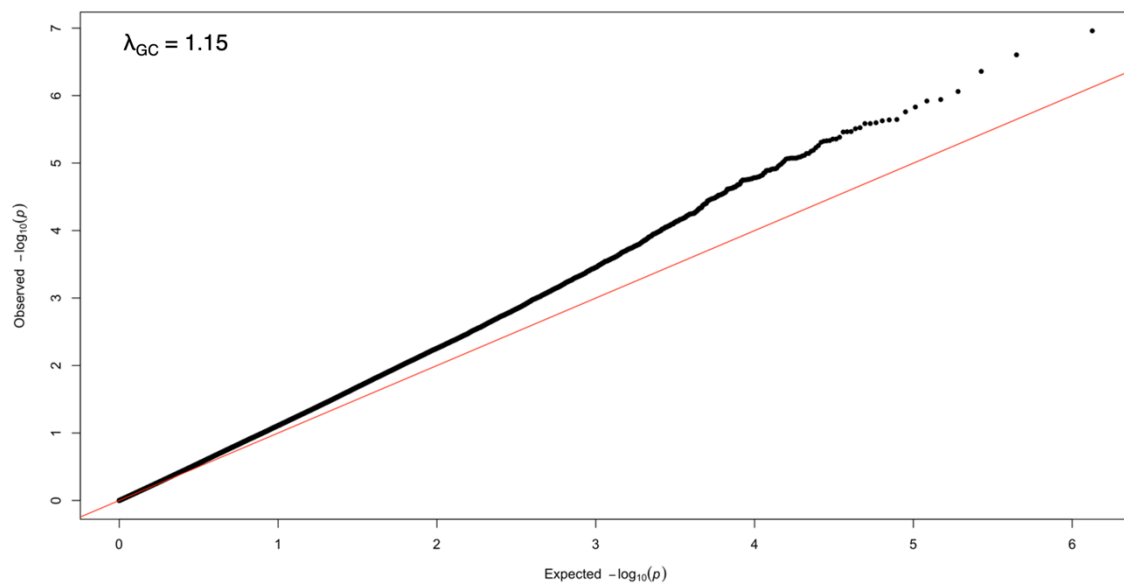
Supplementary Figure 3. Unsupervised admixture analysis cross-validation error plot.
Dots-line shows the cross-validation error for a given value of K , 2 to 23.



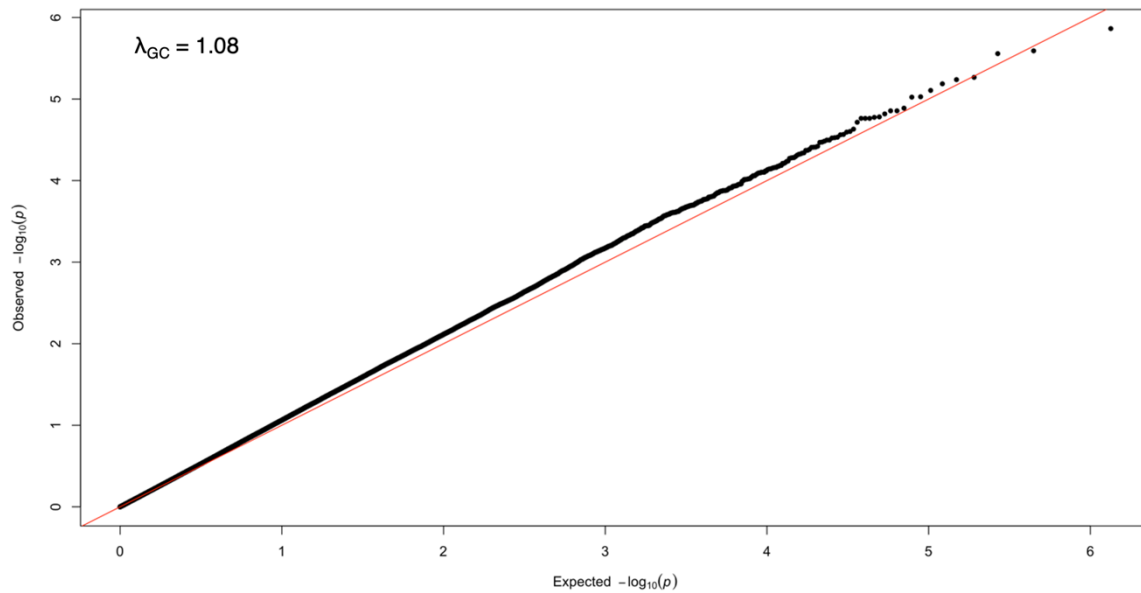
Supplementary Figure 4. QQ plot showing the observed vs expected SNPs $\log^{10}$ p-values distribution from the BVDV GWAS.



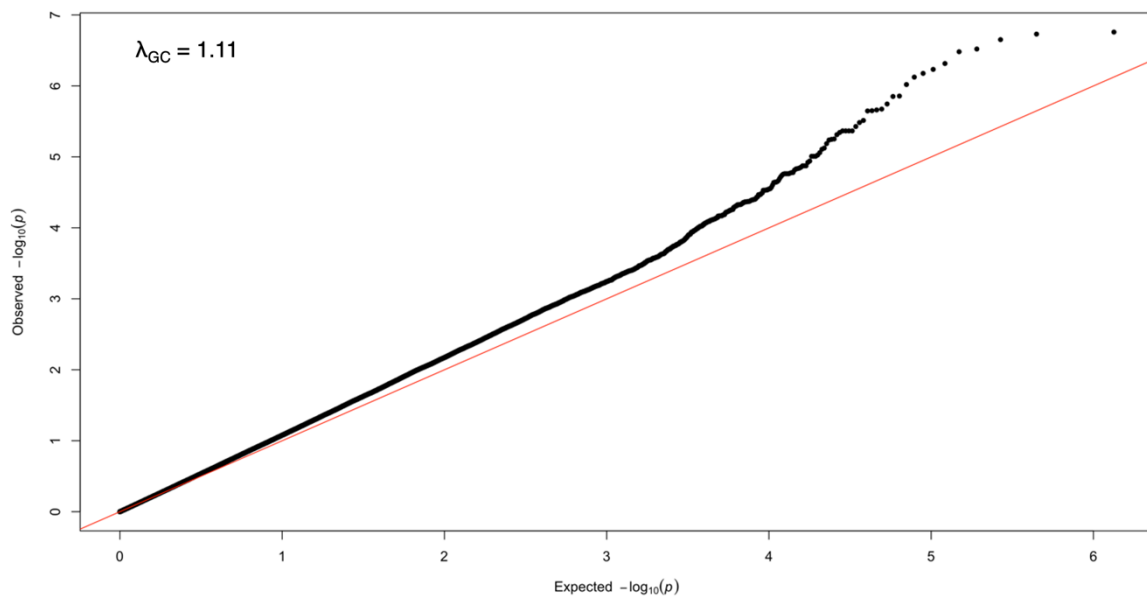
Supplementary Figure 5. QQ plot showing the observed vs expected SNPs $\log^{10}$ p-values distribution from the *Neospora caninum* GWAS.



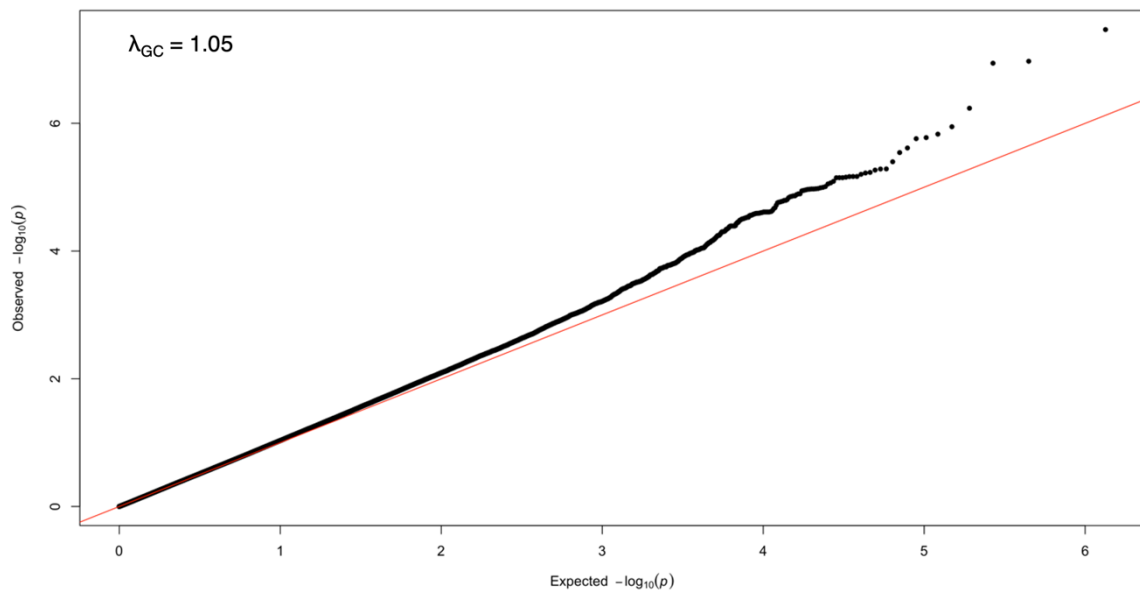
Supplementary Figure 6. QQ plot showing the observed vs expected SNPs $\log^{10}$ p-values distribution from the *Leptospira hardjo* GWAS.



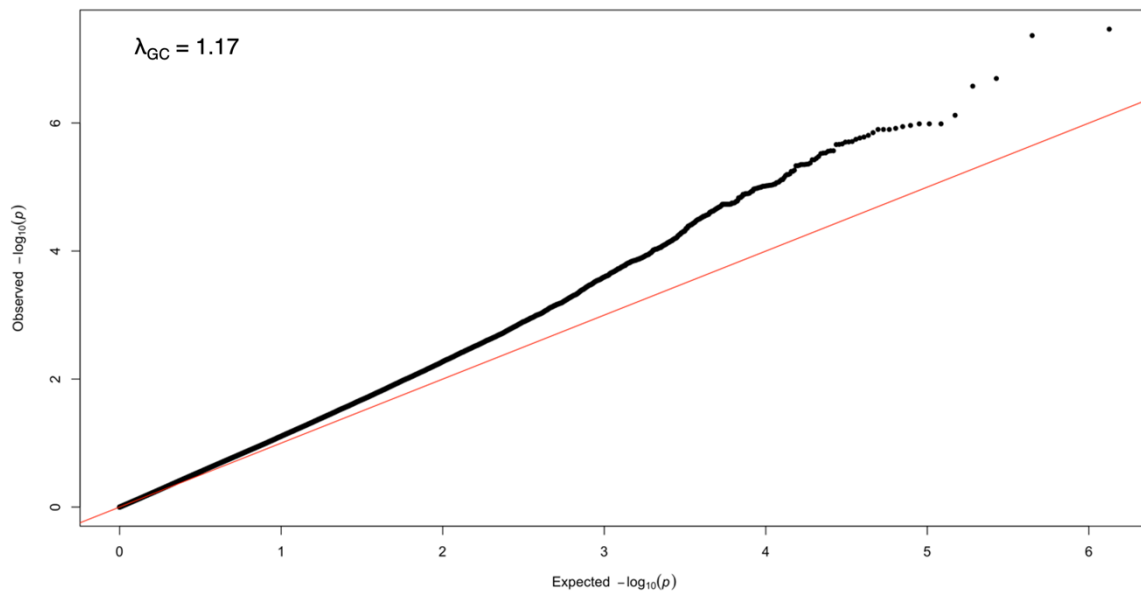
Supplementary Figure 7. QQ plot showing the observed vs expected SNPs $\log^{10}$ p-values distribution from the RVFV GWAS.



Supplementary Figure 8. QQ plot showing the observed vs expected SNPs $\log^{10}$ p-values distribution from the *Toxoplasma gondii* GWAS.



Supplementary Figure 9. QQ plot showing the observed vs expected SNPs $\log^{10}$ p-values distribution from the *Coxiella burnetii* GWAS.



Supplementary Figure 10. QQ plot showing the observed vs expected SNPs $\log^{10}$ p-values distribution from the *Brucella abortus* GWAS.

1.2 Supplementary Tables

S1 Table. Summary of SNP makers density per chromosome.

Chromosome	Total SNPs	Chromosome	Total SNPs
1	42309	16	21811
2	36329	17	20306
3	32488	18	17472
4	31811	19	17155
5	31458	20	19736
6	32489	21	18915
7	30371	22	16559
8	30511	23	13893
9	28529	24	17128
10	27830	25	11656
11	29330	26	13791
12	23677	27	12314
13	21176	28	11917
14	22353	29	13228
15	22369		

S2 Table. Summary statistics of SNP makers showing strong association to serostatus for a given pathogen in GWAS. SNP substitution (**a**) and dominance (**dom**) effects with their standard errors (**SE**) and p-values, proportion of additive genetic (**PvarGen**) and phenotypic (**PvarPhe**) variance and the percentage of genetic variance due to SNP (**% VaSNP**) is provided.

Rs ID	a	p-value (a)	dom	SE (dom)	p-value (dom)	PvarGen	PvarPhe	% VaSNP
BVDv								
rs135177308	0.06	1.24×10^{-4}	0.01	0.02	3.56×10^{-1}	0.02	0.01	0.92
rs42731467	-0.08	5.27×10^{-2}	0.03	0.04	3.36×10^{-1}	0.03	0.01	1.29
Neospora caninum								
rs43566009	-0.29	1.47×10^{-2}	-0.13	0.12	2.15×10^{-1}	0.05	0.01	1.13
rs43680152	-0.07	3.67×10^{-7}	0.00	0.02	3.85×10^{-1}	0.01	0.00	0.21
rs137229140	-0.30	1.16×10^{-1}	-0.10	0.20	3.49×10^{-1}	0.08	0.02	1.76
rs43059701	-0.09	1.37×10^{-2}	-0.01	0.04	3.92×10^{-1}	0.01	0.00	0.27
Leptospira hardjo								
rs137638789	0.05	3.39×10^{-4}	-0.01	0.02	3.43×10^{-1}	0.04	0.01	1.20
rs109573926	-0.06	1.01×10^{-6}	-0.04	0.01	2.31×10^{-2}	0.04	0.01	1.14
Toxoplasma gondii								
rs42429616	0.01	3.96×10^{-1}	0.14	0.12	1.94×10^{-1}	0.07	0.01	1.33
rs110528913	-0.14	4.85×10^{-2}	-0.02	0.07	3.86×10^{-1}	0.05	0.01	0.88
rs41729510	-0.24	5.84×10^{-3}	-0.15	0.09	9.00×10^{-2}	0.06	0.01	1.20
Coxiella burnetii								
rs136314037	0.01		0.15	0.03	4.03×10^{-6}	0.25	0.01	1.21
rs132672447	0.01		0.17	0.03	7.82×10^{-8}	0.34	0.02	1.64
rs137170014	-0.08	1.41×10^{-4}	-0.03	0.02	1.22×10^{-1}	0.29	0.01	1.39
Brucella abortus								
rs43008805	-0.09	9.26×10^{-4}	-0.06	0.03	4.04×10^{-2}	0.07	0.01	0.88