

Supplementary Figures

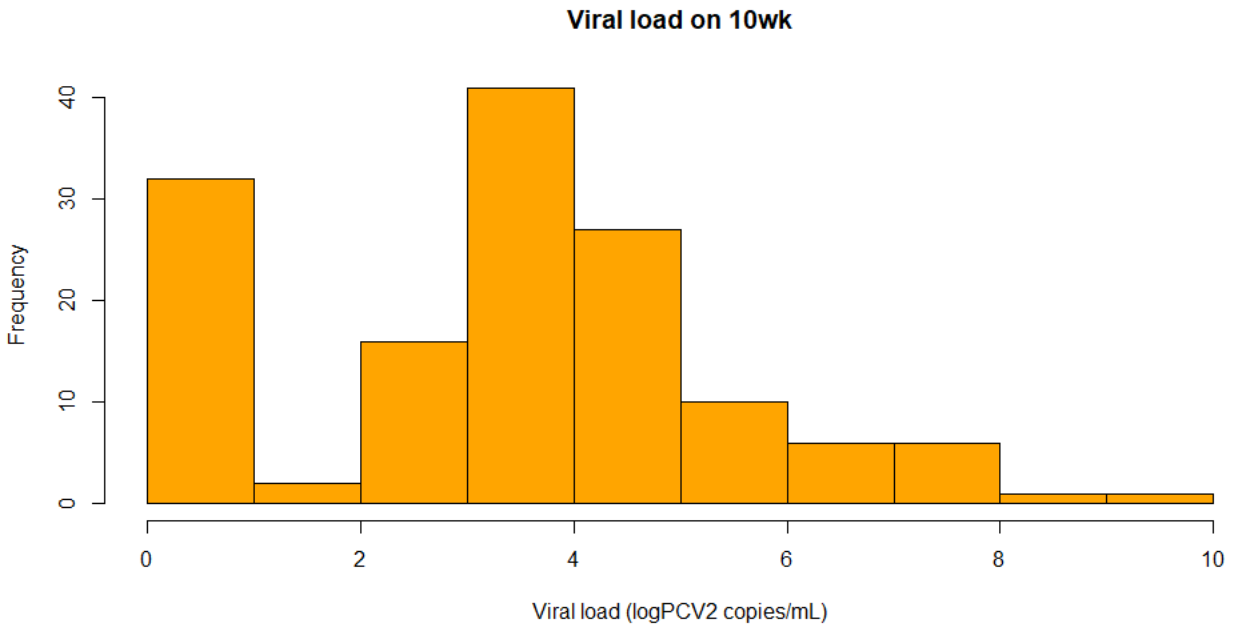


Fig. S1. Histogram for the animal population against PCV2 viral load. The interval of the viral load was set by positive integer values.

(a)

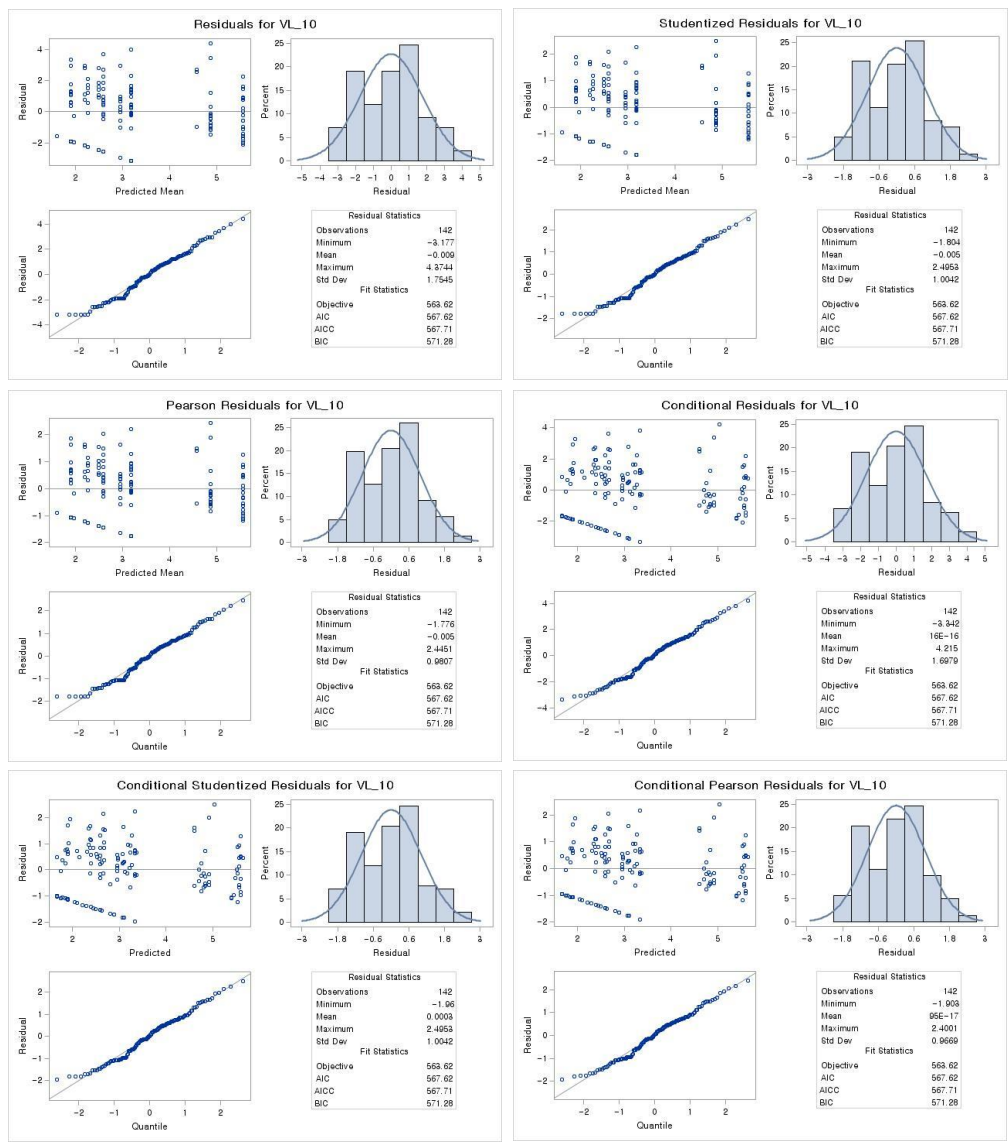


Fig. S2. The results of residual normality test. (a) The result of normality test between genotypes of rs332913874 in RGS16 and PCV2 viral load (VL₁₀). (b) The result of normality test between genotypes of rs326071195 in RGS16 and PCV2 viral load (VL₁₀). (c) The result of normality test between genotypes of rs318298586 in RGS16 and PCV2 viral load (VL₁₀).

(b)

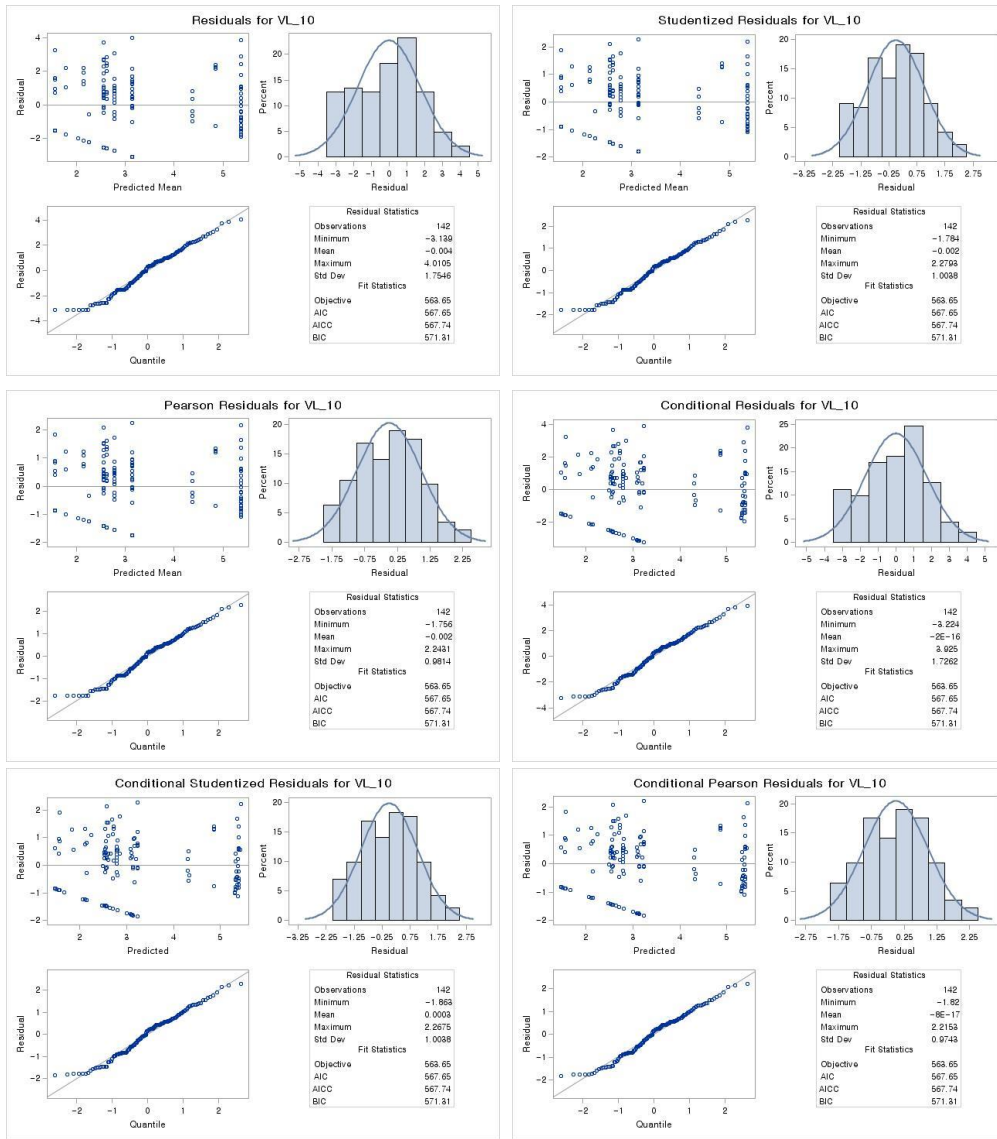


Fig. S2. The results of residual normality test (continued)

(c)

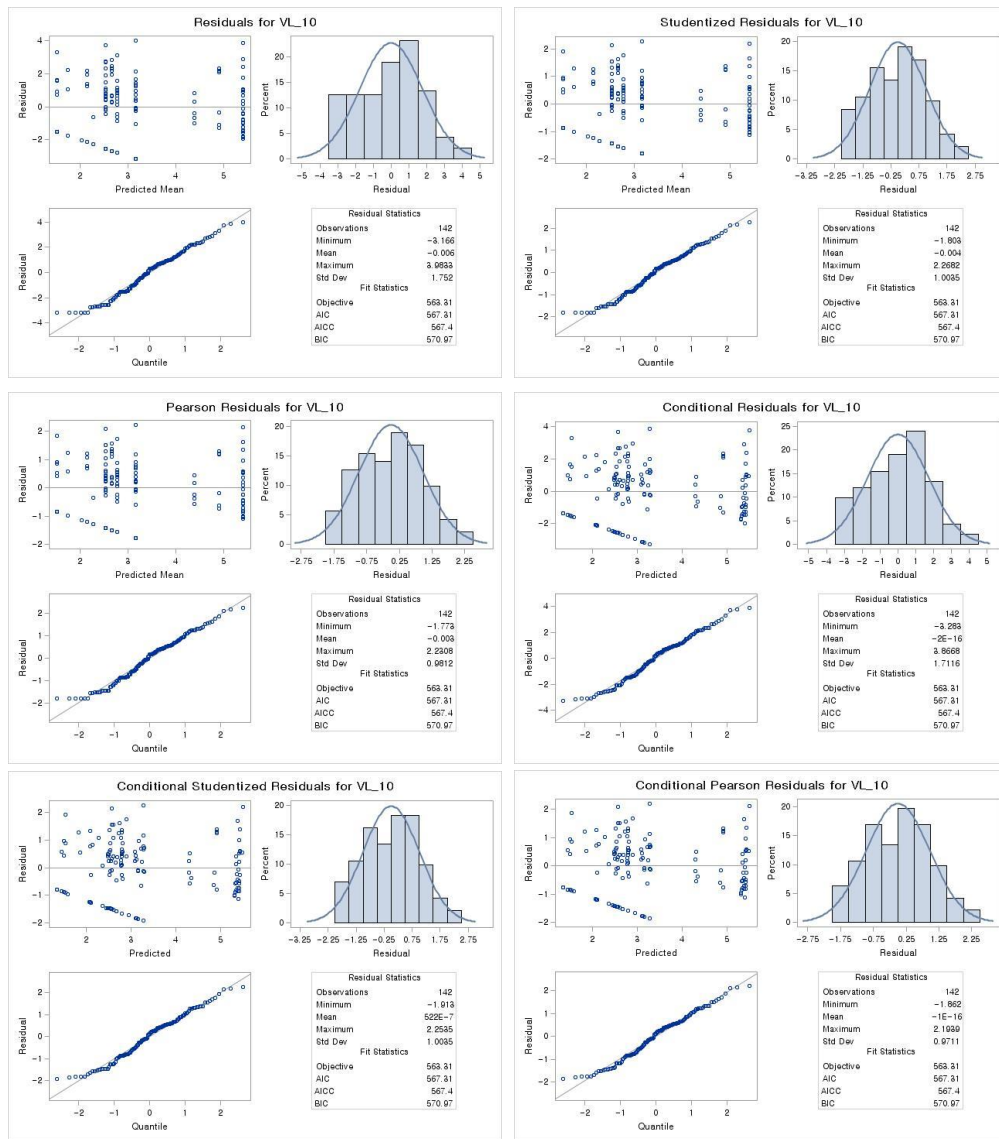


Fig. S2. The results of residual normality test (continued)

Supplementary Tables

Table S1. The registered SNP list on dbSNP

rsID	ssID	dbSNP Nomenclature	Submitter
rs344080032	ss836189292	NC_010451.4:g.123921466C>A	KUAMG
rs332913874	ss836189293	NC_010451.4:g.123921385C>T	KUAMG
rs333806279	ss836189294	NC_010451.4:g.123921254T>C	KUAMG
rs332574546	ss836189295	NC_010451.4:g.123920718T>C	KUAMG
rs431825270	ss836189296	NC_010451.4:g.123920674C>T	KUAMG
rs337489711	ss836189297	NC_010451.4:g.123920649A>C	KUAMG
rs336711794	ss836189298	NC_010451.4:g.123920520G>A	KUAMG
rs326071195	ss836189299	NC_010451.4:g.123920503A>G	KUAMG
rs345370257	ss836189300	NC_010451.4:g.123919650T>C	KUAMG
rs321011720	ss836189301	NC_010451.4:g.123919018T>C	KUAMG
rs318298586	ss836189302	NC_010451.4:g.123918537A>T	KUAMG
rs328561328	ss836189303	NC_010451.4:g.123918268G>A	KUAMG
rs81416935	ss836189304	NC_010451.4:g.123918221T>C	KUAMG
rs339895779	ss836189305	NC_010451.4:g.123918187T>A	KUAMG
rs431825271	ss836189306	NC_010451.4:g.123918182C>A	KUAMG
rs325900938	ss836189307	NC_010451.4:g.123918180T>C	KUAMG
rs431825272	ss836189308	NC_010451.4:g.123918177T>C	KUAMG
rs344750119	ss836189309	NC_010451.4:g.123918148T>C	KUAMG
rs334394495	ss836189310	NC_010451.4:g.123918120T>C	KUAMG
rs81416934	ss836189311	NC_010451.4:g.123917480A>T	KUAMG
rs336159360	ss836189312	NC_010451.4:g.123917061C>G	KUAMG
rs344134561	ss836189313	NC_010451.4:g.123916810C>T	KUAMG

Table S2. Diplootype combination from the three SNPs of the *RGS16* gene

Diplotype	Allele combination	Counts	Frequency
Haplo1/Haplo1	GTA/GTA	25	0.176
Haplo1/Haplo2	GTA/GTT	2	0.014
Haplo1/Haplo3	GTA/GCA	1	0.007
Haplo1/Haplo4	GTA/GCT	24	0.169
Haplo1/Haplo5	GTA/ACA	1	0.007
Haplo1/Haplo6	GTA/ACT	66	0.465
Haplo2/Haplo4	GTT/GCT	2	0.014
Haplo2/Haplo6	GTT/ACT	1	0.007
Haplo4/Haplo6	GCT/ACT	6	0.042
Haplo6/Haplo6	ACT/ACT	14	0.099

Table S3. Diplotypes of top 4 combinations effect of polymorphisms in RGS16 on the PCV2 viral load in 142 Yorkshire pigs

Trait	Diplotype combinations				<i>p</i>-value
	Haplo1/Haplo1 (GTA/GTA)	Haplo1/Haplo4 (GTA/GCT)	Haplo1/Haplo6 (GTA/ACT)	Haplo6/Haplo6 (ACT/ACT)	
Viral load					
LSM ± SE (Log PCV2 copies/mL)	2.46 ± 0.37 ^b	3.32 ± 0.37 ^{ab}	3.57 ± 0.22 ^a	2.54 ± 0.49 ^{ab}	0.01