

Table S6. Summary of the analyses of polymorphism and frequency spectrum tests of neutrality in both rabbit subspecies for three different datasets.

Type of data/Site class	Subspecies	Locus	π (%) ^a	θ_w (%) ^b	D_T ^c
Sanger ¹	<i>O. c. algirus</i>	Autosomes	0.633	0.777	-0.77
Introns		X-chromosome	0.420	0.471	-0.58
	<i>O. c. cuniculus</i>	Autosomes	0.617	0.677	-0.39
		X-chromosome	0.358	0.381	-0.27
Illumina - Sequence capture ²	<i>O. c. algirus</i>	Autosomes	0.674	0.775	-0.61
Introns		X-chromosome	0.312	0.355	-0.55
	<i>O. c. cuniculus</i>	Autosomes	0.508	0.537	-0.26
		X-chromosome	0.197	0.200	-0.03
Illumina - Transcriptome ³	<i>O. c. algirus</i>	Autosomes	0.829	0.931	-0.38
Synonymous sites		X-chromosome	0.416	0.434	-0.12
	<i>O. c. cuniculus</i>	Autosomes	0.756	0.842	-0.36
		X-chromosome	0.385	0.388	-0.32

¹Unweighted average values across 27 X-linked loci and 17 autosomal loci. Values obtained from Carneiro *et al.* [26].

²Unweighted average values across all genes. Only positions with data for all individuals were considered. by bootstrapping a 1,000 times by locus

³Unweighted average values across all fragments. Only positions with data for all individuals were considered. by bootstrapping a 1,000 times by locus

^aAverage number of pairwise differences in a sample [68].

^bProportion of segregating sites in a sample [67].

^cTajima's D [69].