

POPULATION	N	MNA	SD	PA	R <sub>t</sub>	SD	H <sub>o</sub>	SD	H <sub>e</sub>	SD	f <sub>m</sub>	F <sub>is</sub>	HWEd	LD
<b>Autochthonous</b>														
Alentejana	50	6.7	2.1	1	5.8	1.5	0.642	0.123	0.680	0.121	0.327	0.056**	7	1
Algarvia	33 <sup>a</sup>	6.0	1.6	10	5.7	1.4	0.635	0.188	0.691	0.102	0.322	0.083***	10	
Arouquesa	50	7.2	2.6	1	6.4	2.1	0.716	0.131	0.725	0.111	0.282	0.012	5	
Barrosã	50	6.7	1.9	2	5.9	1.5	0.666	0.150	0.689	0.144	0.318	0.034*	3	
Brava de Lide	40	5.8	1.9		5.3	1.6	0.544	0.170	0.637	0.167	0.371	0.148***	15	4
Garvonesa	29	6.5	2.2	5	6.2	2.0	0.680	0.177	0.715	0.136	0.296	0.050*	6	
Marinhua	51	6.7	1.9	1	5.8	1.3	0.667	0.111	0.688	0.097	0.319	0.031*	6	
Maronesa	47	6.5	2.2	1	5.8	1.9	0.725	0.120	0.709	0.100	0.299	-0.023	0	
Mertolenga	50	7.7	2.5	2	6.8	2.0	0.684	0.102	0.739	0.107	0.269	0.074***	9	
Minhota	50	7.5	2.3	1	6.6	1.8	0.690	0.134	0.715	0.110	0.293	0.035**	2	
Mirandesa	50	5.7	1.3		4.9	0.9	0.621	0.114	0.637	0.099	0.369	0.026	1	2
Preta	47	7.1	2.8	7	6.3	2.2	0.636	0.132	0.714	0.087	0.294	0.110***	13	4
<b>Exotic</b>														
Charolais	45	6.7	2.2	1	6.0	1.8	0.677	0.171	0.686	0.149	0.321	0.014	3	1
Friesian	35	7.0	2.3	4	6.4	1.8	0.702	0.141	0.712	0.101	0.298	0.015	4	
Limousin	48	7.0	2.7	2	6.2	1.9	0.709	0.089	0.717	0.081	0.291	0.011	2	
<b>Overall<sup>b</sup></b>	<b>642</b>	<b>6.8</b>	<b>0.6</b>	<b>28</b>	<b>6.0</b>	<b>1.8</b>	<b>0.668</b>	<b>0.047</b>	<b>0.697</b>	<b>0.030</b>	<b>0.310</b>	<b>0.042</b>	<b>76</b>	<b>12</b>

<sup>a</sup>Animals identified as belonging to the core group to recover *Algarvia*; <sup>b</sup>Overall values across breeds without *Algarvia*; \*( $P < 0.05$ ); \*\*( $P < 0.01$ ); \*\*\*( $P < 0.001$ ); N: sample size; MNA: mean number of alleles; PA: number of population-specific alleles; R<sub>t</sub>: allelic richness; H<sub>o</sub>: observed heterozygosity; H<sub>e</sub>: unbiased expected heterozygosity; f<sub>m</sub>: molecular coancestry; F<sub>is</sub>: inbreeding coefficient; HWEd: number of loci showing significant ( $P < 0.05$ ) HWE deviation due to heterozygote deficit; LD: number of loci pairs showing significant ( $P < 0.001$ ) linkage disequilibrium; SD: standard deviation