

**Table S5. Effects of genetic similarity on female fertility (pregnant yes/no), based on numbers of shared MHC antigens instead of the dichotomous sharing/no sharing and restricting the analyses to only warmblood mares (N=173).**

Likelihood ratio tests comparing GLMMs and GLMs with genetic markers (fixed factors) and/or stallion identity (“ID”, random factor) and reference models (indicated in italics) to test the effects of **(A)** number of shared MHC antigens (“MHC”, range 0 to 3), and **(B)** the effects of the number of shared MHC antigens and r in the subsample of 113 mares that allow for a direct comparison. Significant p-values are emphasized in bold.

Model	Effect tested	d.f.	logL	$\chi^2$	P
<b>(A) MHC effects (173 mares)</b>					
<i>MHC + ID</i>		3	-114.7		
ID	MHC sharing	2	-115.5	1.6	0.20
MHC	Stallion ID	2	-114.7	0	1.0
MHC + ID + ID x MHC	Stallion ID x MHC	4	-114.6	0.1	0.78
<b>(B) MHC vs microsatellites (113 mares)</b>					
<i>MHC + r + ID</i>		4	-70.6		
r + ID	MHC sharing	3	-75.0	8.8	<b>0.003</b>
MHC + ID	r	3	-71.0	0.9	0.35
MHC + r	Stallion ID	3	-70.6	0	1