Table S2. Effects of genetic similarity on female fertility (pregnant yes/no), 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)** MHC antigen sharing ("MHC", yes/no), and **(B)** pairwise genetic relatedness "r" based on 20 polymorphic microsatellite loci. (**C**) Direct comparison of effects of MHC and r in the subsample of 113 mares that allow for such a test. Significant p-values are emphasized in bold.

Model	Effect tested	d.f.	logL	χ^2	P
(A) MHC effects (173 mares)					
MHC + ID		3	-113.8		
ID	MHC sharing	2	-115.5	3.3	0.07[1]
MHC	Stallion ID	2	-113.9	0.02	0.90
MHC + ID + ID x MHC	Stallion ID x MHC	4	-133.7	0.3	0.58
(B) Diversity on microsatellites (113 mares)					
r + ID		3	-75.0		
ID	r	2	-75.1	0.24	0.63
r	Stallion ID	2	-75.0	0	1.0
r + ID + ID x r	Stallion ID x r	4	-75.0	0	1.0
(C) MHC vs microsatellites (113 mares)					
MHC + r+ ID		4	-70.4		
r + ID	MHC sharing	3	-75.0	9.1	**0.003**
MHC + ID	r	3	-70.7	0.6	0.44
MHC + r	Stallion ID	3	-70.4	0	1

[1] p = 0.04 if tested directed (Rice and Gaines 1994 *PNAS.* **91,** 225-226) based on the *a priori* expectancy that MHC-dissimilar stallions are more attractive than MHC-similar stallions