

Table S3 Statistical association between candidate gene-associated markers and sex at population and family level.

	Wild population		DF family		QF6 family	
	Genotypic	Allelic	Genotypic	Allelic	Genotypic	Allelic
Sma-E79	0.138	0.056	0	0	-	-
Sma-USC270	0.322	0.331	-	-	-	-
<i>dnaj19</i>	0.710	0.387	-	-	0	0.003
SmaUSC-E30	0.074	0.113	0	0	0	0.001
Sma-USC288	0.202	0.222	-	-	-	-
<i>atp11b</i>	0.322	0.623	0	0	-	-
<i>sox2</i>	0.292	0.097	0	0	-	-
<i>fkbp2</i>	-	-	0	0	-	-
<i>ncbp2</i>	0.433	0.182	-	-	-	-
<i>dlg1</i>	0.626	0.951	0	0	0	0.001
Sma-USC254	0.293	0.07	-	-	-	-
Sma-USC65	0.070	0.038	-	-	0	0.001
Sma1-152INRA	0.375	0.237	0	0.002	-	-
Sma-USC191	0.493	0.226	-	-	-	-
Sma-USC247	0.204	0.113	0.001	0	0.180	0.248
YSKr50	0.266	0.738	0.002	0.001	-	-
YSKr54	0.011	0.022	0.002	0.010	-	-
<i>dmrta2</i>	0.876	0.937	0.061	0.188	-	-
Sma-USC198	0.216	0.647	0.053	0.044	-	-
Sma-USC12	0.201	0.142	0.046	0.086	-	-
YSKr178	0.086	0.031	-	-	-	-
Sma-USC278	0.063	0.042	-	-	-	-
Sma-USC88	-	-	-	-	-	-
Sma-USC225	-	-	0	0	-	-
Sma-USC202	0.147	0.081	-	-	-	-
<i>amh</i>	-	-	0.394	0.771	-	-
Sma-E254	0.323	0.300	0.172	0.283	-	-
Sma-USC265	0.080	0.064	-	-	-	-
Sma-USC10	0.361	0.064	0.003	0.236	-	-

P<0.05 in bold characters. Bonferroni correction ($\alpha=0.05$; $k=28$; $P=0.0018$); - non informative markers