

Table S1. Accuracy of genomic predictions and standard deviations (in parenthesis) for non-phenotyped cows in the validation set (VS) environment, using the information of their relatives in the training set (TS) environments, via a three-trait animal model over different scenarios. Scenarios consist of high or low linkage disequilibrium (HLD or LLD), different numbers of QTL (60QTL or 300QTL), and different incidences of the binary trait (10% or 30%).

Scenarios	VS	1			2			3			4		
	TS	2	3	4	1	3	4	1	2	4	1	2	3
HLD_60QTL_0.1		0.149 ^{a,A} (0.125)	0.132 ^{a,A} (0.107)	0.121 ^{a,A} (0.154)	0.146 ^{ab,A} (0.132)	0.188 ^{bcd,A} (0.065)	0.188 ^{abc,A} (0.102)	0.141 ^{ab,A} (0.108)	0.188 ^{ab,A} (0.102)	0.184 ^{abcd,A} (0.127)	0.146 ^{a,A} (0.072)	0.157 ^{a,A} (0.120)	0.162 ^{bc,A} (0.097)
HLD_60QTL_0.3		0.205 ^{a,A} (0.086)	0.197 ^{a,A} (0.109)	0.189 ^{a,A} (0.132)	0.263 ^{a,A} (0.088)	0.285 ^{a,A} (0.091)	0.291 ^{a,A} (0.121)	0.244 ^{a,A} (0.131)	0.273 ^{a,A} (0.105)	0.277 ^{a,A} (0.128)	0.196 ^{a,A} (0.064)	0.229 ^{a,A} (0.113)	0.252 ^{ab,A} (0.073)
HLD_300QTL_0.1		0.186 ^{a,A} (0.066)	0.139 ^{a,A} (0.109)	0.119 ^{a,A} (0.111)	0.128 ^{ab,A} (0.088)	0.155 ^{cd,A} (0.100)	0.085 ^{c,A} (0.098)	0.118 ^{ab,A} (0.107)	0.180 ^{ab,A} (0.102)	0.165 ^{bcd,A} (0.089)	0.139 ^{a,A} (0.125)	0.145 ^{a,A} (0.111)	0.156 ^{c,A} (0.104)
HLD_300QTL_0.3		0.211 ^{a,A} (0.102)	0.196 ^{a,A} (0.094)	0.143 ^{a,A} (0.150)	0.192 ^{ab,A} (0.156)	0.267 ^{ab,A} (0.102)	0.248 ^{ab,A} (0.086)	0.167 ^{ab,A} (0.115)	0.241 ^{ab,A} (0.097)	0.248 ^{abc,A} (0.107)	0.126 ^{a,B} (0.093)	0.236 ^{a,A} (0.108)	0.258 ^{a,A} (0.108)
LLD_60QTL_0.1		0.105 ^{a,A} (0.117)	0.103 ^{a,A} (0.079)	0.098 ^{a,A} (0.098)	0.142 ^{ab,A} (0.136)	0.185 ^{bcd,A} (0.093)	0.139 ^{bc,A} (0.148)	0.096 ^{ab,A} (0.149)	0.139 ^{b,A} (0.124)	0.131 ^{d,A} (0.124)	0.103 ^{a,A} (0.162)	0.135 ^{a,A} (0.088)	0.143 ^{c,A} (0.073)
LLD_60QTL_0.3		0.163 ^{a,A} (0.114)	0.162 ^{a,A} (0.077)	0.157 ^{a,A} (0.117)	0.127 ^{ab,A} (0.247)	0.264 ^{ab,A} (0.113)	0.260 ^{a,A} (0.119)	0.149 ^{ab,A} (0.215)	0.263 ^{a,A} (0.084)	0.272 ^{ab,A} (0.112)	0.110 ^{a,B} (0.143)	0.207 ^{a,AB} (0.093)	0.226 ^{abc,A} (0.089)
LLD_300QTL_0.1		0.142 ^{a,A} (0.160)	0.127 ^{a,A} (0.089)	0.075 ^{a,A} (0.125)	0.101 ^{b,A} (0.128)	0.105 ^{d,A} (0.082)	0.083 ^{c,A} (0.117)	0.085 ^{b,A} (0.112)	0.165 ^{ab,A} (0.130)	0.152 ^{cd,A} (0.089)	0.094 ^{a,A} (0.143)	0.128 ^{a,A} (0.113)	0.135 ^{c,A} (0.113)
LLD_300QTL_0.3		0.175 ^{a,A} (0.145)	0.172 ^{a,A} (0.132)	0.138 ^{a,A} (0.141)	0.146 ^{ab,A} (0.179)	0.226 ^{abc,A} (0.110)	0.210 ^{ab,A} (0.123)	0.130 ^{ab,A} (0.202)	0.210 ^{ab,A} (0.138)	0.247 ^{abc,A} (0.077)	0.112 ^{a,A} (0.168)	0.161 ^{a,A} (0.125)	0.211 ^{abc,A} (0.089)

Means followed by the different letters (lowercase letters for comparison within column and uppercase letters for comparison within row) are significantly different ($p < 0.05$).