

**Table S1.** Genotype for major-effect QTL associated with white spotting.

| QTL*       | ID          | Position ARS_UCD1.2 | Q allele <sup>+</sup> | q allele <sup>#</sup> | BEF2 gen <sup>@</sup> | CC14 gen <sup>&amp;</sup> |
|------------|-------------|---------------------|-----------------------|-----------------------|-----------------------|---------------------------|
| chr2_PAX3  | rs109979909 | chr2:110817975      | A                     | C                     | AC                    | AC                        |
| chr6_KIT   | rs451683615 | chr6:62557125       | A                     | G                     | AA                    | AA                        |
| chr22_MITF | rs209784468 | chr22:31651379      | A                     | G                     | AA                    | AA                        |

\* QTL from Jivanji et al. 2019; positions reference tag variant or candidate mutation

<sup>+</sup> Allele associated with increased spotting

<sup>#</sup> Allele associated with decreased spotting

<sup>@</sup> parental cell line

<sup>&</sup> edited cell line