### Table S5. Primer sequences for Y-SNP verification

4 Top candidates and the Przewlaksi SNP in bold. Frequency of the bases in the breed alignment were 86% G and 14% A for Y-25345, 73% T for Y-45288, the minor allele frequency was about 12 % for the region Y-45701/45997. For Y50869 and 27% T was observed in the lipp pool and 85 % in the breed pool.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **candidate** | **Y-contig/pos** | **amplicon size in bp** | **primer fwd** | **primer reverse** | **mutation** |
| **Y-25345** | **YXX\_24I23/25345** | **246** | **CCTCCGGCCTTTATGTCTTAG** | **TTGGGCTGCAGTATACAACG** | G/A |
| **Y-45288** | **YE3/10594** | **297** | **CCCTCTGCTGAGCATCTAGG** | **TTGGATGAAAGGGACAGTGA** | T/- |
| **Y-45701/997** | **YE3/1107-11315** | **444** | **CCAACACACGTCAACAGCTC** | **GGCTTAGGCCACTGATGGTA** | 20 SNPs and indels |
| **Y-50869** | **YE17/1277** | **264** | **GGCCTAAGTTGTTCGCAGAG** | **TGACTGGTGGTGTCCAGTGT** | T/A |
|  |  |  |  |  |  |  |
| Y-10096  | YXX\_24I23 | 369 | GCACACGAGGACTCTGACAA | AGTTTGGTCTGTGCCACTCC | no SNP |
| Y-34616  | YXX\_24I23 | 300 | TGGGACTGTTGAAATGGAGA | CTTTTCAATGCCATTCCTGA | no SNP |
| Y-360 | YXX\_24I23 | 360 | GATTTGGACCCACCACAGGAG | TTGGTTCTCTGGCACCTCTT | no SNP |
| Y-39624  | YE3 | 290 | GCTGCTCACCAAACACACTG | TATGATTCAGCCAGCACCTG | no SNP |
| Y-40350  | YE3 | 286 | TTCTGAAGAAAGCACCATTTC | AAGCGGAGCATGTTAACCAC | no SNP |
| Y-43717/980  | YE3 | 760 | TGATGGAGAGGTTGTGGAGA | AGCTGTGGCATCATGTTCTG | no SNP |
| Y-68305  | YE3 | 499 | ATCCATGCTTCCTCCCTCTT | GCCACAGGGAACTGTGATTT | no SNP |
| Y-88903  | YM23 | 334 | CCACAGTAACCCCTCCTCAC | CAGGGAACCACTAGCCTGAG | no SNP |
| **Y-90117** | **YM23** | **383** | **GAGCCTTCACCATCTTGTCC** | **TAGCTTTCGTCGCAGAAGGT** | **no SNP, Prz1 G/Prz2 A** |
| Y-94524  | YM23 | 476 | CACAGCTCAGTGGCAGTTGT | GCCCTTGCCAGTTATTCTTG | no SNP |
| Y-95696  | YM23 | 385 | ATGTCTGGGGAGACAGCATC | GACCTGCTGTGCTCATCTTG | no SNP |
| Y-125058  | YNO167 | 469 | AATGGGGTAGGGGATAGGTG | CCAATTTCCCCAAGCATTTA | no SNP |
| Y-151426 | YNO217 | 502 | GAAAGCATGCACTGGCCATATC | GCTCCACCCAGAGAAGATGA | no SNP |
| Y-154256  | YNO217 | 284 | CGAACAAAAGGAGCCACAAT | CTGGGAAGAAAGGGGATTTC | no SNP |
| Y-158936  | YNO217 | 554 | CAAGTCTTTCCAATGGCACA | CCCGGAAAAGACTTCAACTGC | no SNP |
| Y-167086 | YP41 | 382 | ATTCAAGCCCATTGCACATT | TAAGAGCCTCCACCAGGATG | no SNP |
| Y-168785  | YP41 | 531 | TGCCTGTTTTCCAGTTAGGC | CCCATTCATGCTCTTCACCT | no SNP |
|  |  |  |  |  |  |  |
| Y-43647/62.fwd | YE3 | 320 | AATGGGCTGGAGACATGAAC | CAGTAGTGGGATGGCTGGAT | not Y spec |
| Y-119468/973.fwd | YNO167 | 413 | CCTGAGATGGAGTCCTGCTG | AATCCTCATCATACCTATGCCTTA | PCR not working |
|  |  |  |  |  |  |
| Ancient domestic variants discovered by Lippold et al. 2011 in the Bronze Age domestic horse |  |  |  |  |
| Eca SH2-B-17 | BAC-E | 438 | GAGTCCTGCCTTTCCCTCTC | GCCTCAGGCCTCTCTGTCTA | dom C / Prz G |
| Amely-intr2 | contig IV (Paria et al., 2011) | 433 | CTTCACGTTCAAATGTGTGACT | CTCAGAAGTGGCATGCAAAG | dom T / Prz C |