

# Characteristic of Przewalski horses population from Askania-Nova reserve based on genetic markers

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**Table S1** The primer sequence and detailed information about analysed polymorphisms in Przewalski horses.

| Region            | Analysed fragment        | Identyfication method             | Primers/Probes                                                                                | Length                    |
|-------------------|--------------------------|-----------------------------------|-----------------------------------------------------------------------------------------------|---------------------------|
| Mitochondrial DNA | Amplicon 1               | Sanger sequencing                 | F: AACGTTTCCTCCCAAGGACT<br>R: GTAGTTGGGAGGGTTGCTGA                                            | 397 bp                    |
|                   | Amplicon 2               | Sanger sequencing                 | F: ACCCCATCCAAGTCAAATCA<br>R: ACCCCATCCAAGTCAAATCA                                            | 462 bp                    |
|                   | Amplicon 3               | Sanger sequencing                 | F: ACCTACCCGCGCAGTAAGCAA<br>R: ACGGGGGAAGAAGGGTTGACA                                          | 306 bp                    |
| Sex chromosomes   | Y chromosome             | Allelic discrimination            | F: AGACCCGCCGGTGC<br>R: CAATTCCTGGAGCCTCTGTAG<br>VIC: AGTCCTGGTGAATGAG<br>FAM: TCCTGGCGAATGAG | 64 bp                     |
|                   | X chromosome             | Real-Time PCR reaction            | F: GTCAGGCCAAGGAGAGTAGCA<br>R: GCACATCCTCCTCCACTTATGC<br>NED: CCCAGTTCTTAGGTCACA              | 73 bp                     |
| TBX gene          | chr8:18,227,267+1,066G>T | Sanger sequencing                 | F: TAAGCCTCCAGACACCCAAG<br>R: CAGCTCCCGTCTCCCTAGAT                                            | 240 bp                    |
|                   | chr8:18,226,905A>G       | Sanger sequencing                 | F: TTCCAGGAACCTGAGCAAAT<br>R: ATAACCAGGCACCCCTTCTC                                            | 155 bp                    |
|                   | chr8:18,227,267, in/del  | Amplification length polymorphism | F: CAAGACGCAAGGCTCTTTCT<br>R: CGTTTCTTTAAGGGCTCGTG                                            | In 1.837 bp<br>Del 215 bp |