PCR amplification, sequencing, and *in silico* analysis of holandric genes *TSPY* and *SRY* in Nili Ravi buffalo

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Supplementary Fig. 1. Pair-wise distance (below diagonal) and the respective standard errors (above diagonal) of the *SRY* gene have been displayed in a matrix form. Created using MEGA7 software (dark to light colour indicates less to high pair-wise distance).

Supplementary Fig. 2. Pair-wise distance (below diagonal) and the respective standard errors (above diagonal) of the *TSPY* gene have been displayed in a matrix form. Created using MEGA7 software (dark to light colour indicates high to less pair-wise distance).