

Table S1. Inference of biological sex using the Ry approach¹

| Sample | Nseqs | NchrY+NchrX | NchrY | R_y | SE | 95% CI | Assignment |
|--------|-------|-------------|-------|--------|--------|---------------|-------------------------------|
| DV 13 | 19598 | 492 | 42 | 0.0854 | 0.0126 | 0.0607-0.1101 | consistent with XY but not XX |
| DV 14 | 18527 | 477 | 31 | 0.065 | 0.0113 | 0.0429-0.0871 | consistent with XY but not XX |
| DV 15 | 15034 | 136 | 7 | 0.0515 | 0.0189 | 0.0143-0.0886 | Not Assigned |

Neqs: Number of total alignments; NchrY+NchrX: Number of alignments to chrX or chrY; NchrY: Number of alignments to chrY

References

- 1 Skoglund, P., Storå, J., Götherström, A. & Jakobsson, M. Accurate sex identification of ancient human remains using DNA shotgun sequencing. *J Archaeol Sci* **40**, 4477-4482, doi:10.1016/j.jas.2013.07.004 (2013).