## **Supplementary Information**

## Variola virus genome sequenced from an eighteenth-century museum specimen supports the recent origin of smallpox

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## Supplementary Figures

Supplementary Figure S1: Metagenomic composition of all libraries for sample P328, library and extraction blanks at the order level. All P328 libraries show a high amount of Poxviridae (turquoise), which is completely absent in the blank.



Supplementary Figure S2: Damage profiles of the reads mapping to VARV reference genome for all six P328 libraries. The reads were assigned with MALT to the VARV reference genome.



0.04

Supplementary Figure S3: Uncollapsed Maximum Likelihood tree including 57 Orthopoxvirus genomes. Bootstrap values are given as node labels. The historic genomes are in bold, the newly added genome in red.



Supplementary Figure S4: Dated Bayesian Maximum Clade Credibility tree reconstructed with BEAST 2.5.5 (using a strict clock and constant population size) excluding strains V1588 and V563. The nodes are labelled with the 95% HPD interval. Historic genomes are in bold, the newly added genome in red. Posterior values are given as node labels in grey.