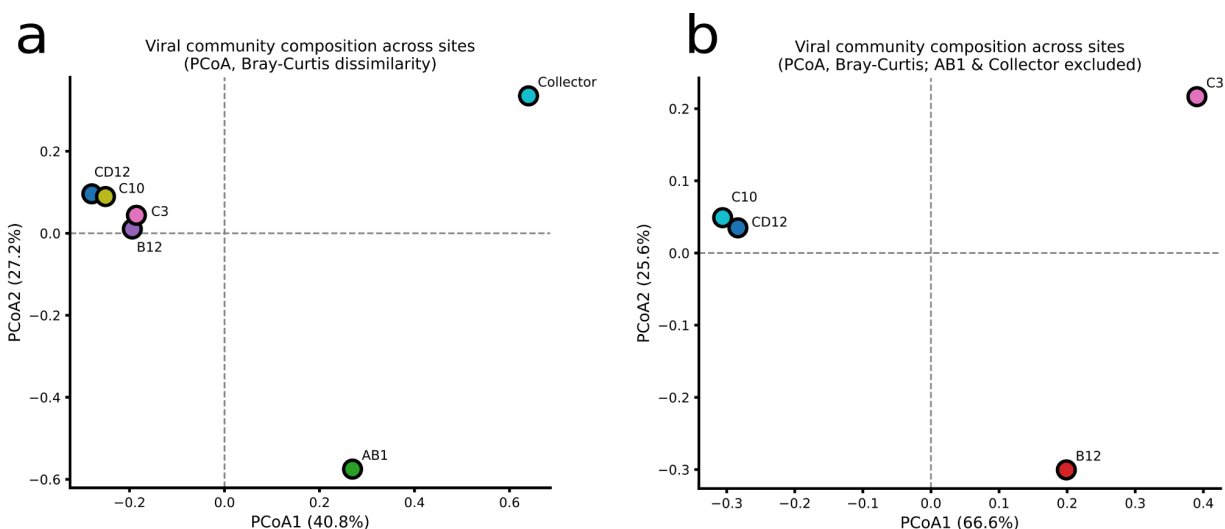
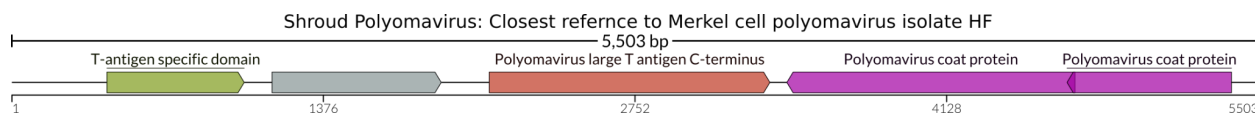


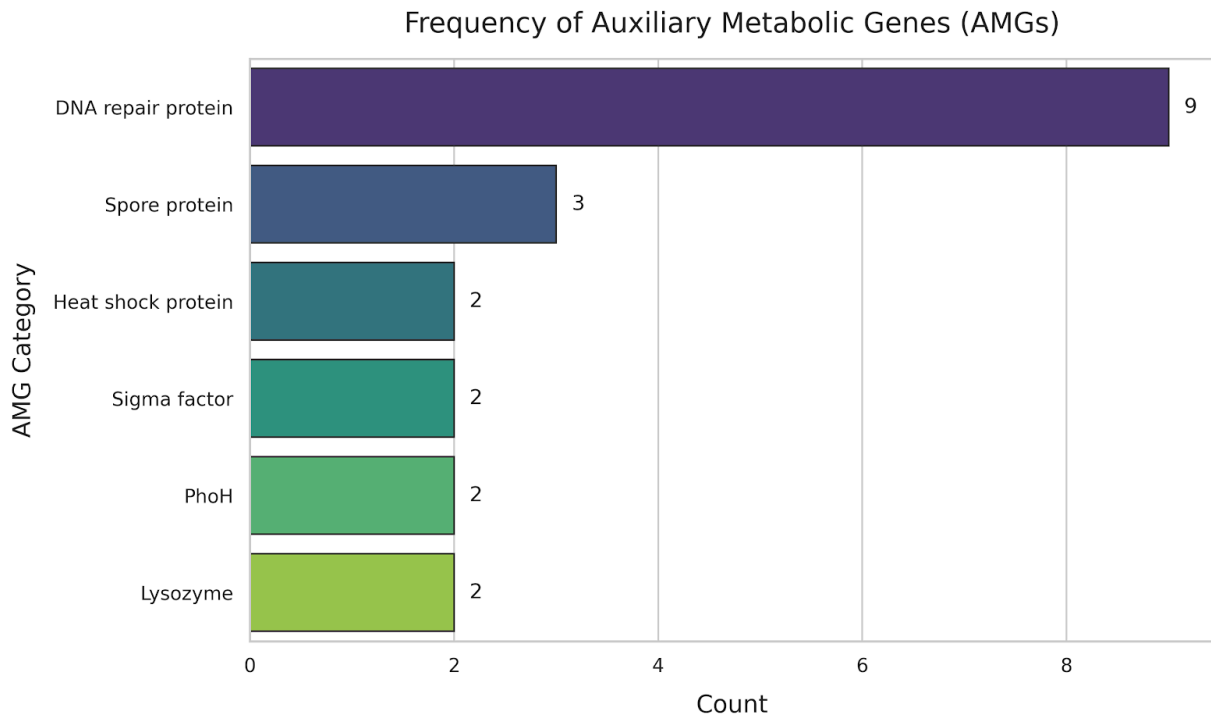
# Supplemental Information for “The first comprehensive analysis of the viruses associated with the Shroud of Turin”



**Figure S1. PCoA analysis of the Bray-Curtis dissimilarity between the different viral communities of the Shroud of Turin.** Clustering is based on the abundance (RPKM) values of all viruses in each sample (AB1: feet, C3: hand, C10: glutei, CD12: feet, B12: feet, Collector: collector metagenome). PCoA plots that include (a) all samples and (b) outlier samples removed are both shown here.



**Figure S2. Genome map for the Shroud Polyomavirus.** This genome map represents the 5.5 kb Polyomavirus genome with direct terminal repeats (DTR). Genes were annotated using the Pfam database, and the map was visualized using lovis4u.



**Figure S3. Auxiliary metabolic genes (AMGs) in Shroud of Turin viruses.** Selected AMGs involved in processes relevant to the Shroud's history were selected for visualization. Gene annotations were done using DRAM-v and included DNA repair proteins (MutS2, RadA, RadD), spore proteins (ssp), heat shock proteins (Hsp70), sigma factor, PhoH, and lysozyme (tail lysozyme).

| Contig                      | Site | Length | Best hit                    |
|-----------------------------|------|--------|-----------------------------|
| AB1_assembly.fa_k119_239443 | AB1  | 1189   | Debaryomyces hansenii virus |
| AB1_assembly.fa_k119_223936 | AB1  | 499    | Debaryomyces hansenii virus |
| AB1_assembly.fa_k119_70043  | AB1  | 479    | Debaryomyces hansenii virus |
| AB1_assembly.fa_k119_463282 | AB1  | 453    | Debaryomyces hansenii virus |
| k119_65323                  | B12  | 825    | Group K retrovirus          |
| k119_75988                  | B12  | 2847   | Group K retrovirus          |

**Table S1. Riboviria viruses found associated with the Shroud of Turin.** Each viral contig and its length are shown here, along with the BLASTn best match.

| Name                                                               | NCBI Accession | Species                      | Length (bp) | Isolation source                 |
|--------------------------------------------------------------------|----------------|------------------------------|-------------|----------------------------------|
| Atripovirus timinis isolate ctdb796                                | MH617332.1     | <i>Atripovirus timinis</i>   | 6405        | Minnow tissue                    |
| CRESS virus sp. ctin15                                             | MN582096.1     | <i>Meliavirus jackflis</i>   | 5223        | Jackson Spring, Florida          |
| Oreadivirus manflis isolate ctJ1A291                               | MW202570.1     | <i>Oreadivirus manflis</i>   | 9070        | Manatee Spring, Florida          |
| Oreiadivirus spriflis isolate ctOGJ943                             | MW202822.1     | <i>Oreiadivirus spriflis</i> | 6235        | Manatee Spring, Florida          |
| Lake Sarah-associated circular virus-28 isolate LScCV-28-LSLA-2013 | KP153453.1     | <i>Satyrivirus cordulis</i>  | 6380        | Procordulia grayi in New Zealand |
| Sthenivirus nowtis isolate ctce741                                 | MH617353.1     | <i>Sthenivirus nowtis</i>    | 6979        | Minnow tissue                    |
| Thisbivirus naringis isolate ctntl873                              | MW202729.1     | <i>Thisbivirus naringis</i>  | 5925        | Manatee Spring, Florida          |
| Thyavirus flanatis isolate ctCcl689                                | MW202851.1     | <i>Thyavirus flanatis</i>    | 7644        | Manatee Spring, Florida          |

**Table S2. Reference viruses of the family *Gandrviridae*.** All reference sequences were obtained from NCBI and can be accessed there using the accession numbers.