# Marlais et al. Comparative ‘omics’ discovery of Strongyloides stercoralis coproantigens for diagnostics development

## List of supplementary files

* **S1**: Sources and details of open access data used in this study.
* **S2:** Number of sequences used on phylogenetic trees.
* **S3:** DE 328 *S. stercoralis* genes differentially expressed in gut-dwelling versus non-gut-dwelling life stages of the nematode and those containing predicted epitopes. Transcriptomic data from Stoltzfus et al. (2012). Gene accession numbers (starting SSTP) are given for WormBase Parasite or UniProtKB and life stage transcriptomic data accession numbers (starting ERR) for NCBI SRA. Expression levels are in normalized read counts.
* **S4:** BLAST results listing *S. stercoralis* orthologues of *S. ratti* E/S proteins at 1e-50.
* **S5:** E/S 1057*S. stercoralis* orthologues of *S. ratti* E/S proteins – TPM, protein families, epitope predictions and signal peptide predictions.
* **S6**: Predicted epitopes from E/S orthologues and DE genes using two different prediction tools, with length, position in parent proteins and overlapping predictions.
* **S7:** All pedicted epitope sequences in fasta format, from DE and E/S orthologues data sets.
* **S8:** Table of details of candidate coproantigens.
* **S9:** Candidate coproantigen sequences in fasta format.