Table 4: Details for genome analyses in lieu of EBI Pipeline

Data	Program	Parameters or VEuPathDB GitHub repository	Version
BLAT against NRDB	BLAT	-nohead -maxIntron=1000 -t=dnax -q=prot -dots=10 -minScore=25 -minIdentity=20	35
Computed Open Reading Frames	orfFinder	--minPepLength 50 https://github.com/VEuPathDB/.../orfFinder	
DNA Repeat regions	Tandem Repeats Finder	2 7 7 80 20 50 500	4.04
EST alignments	BLAT	-nohead -maxIntron=1000 -t=dna -q=dna -dots=10	35
Signal peptide predictions	SignalP	-t euk -f short -m nn+hmm -q -trunc 70	3.0
Synteny	Mercator and MAVID	-p <PATH TO MERCATOR DIRECTORY> -t <tree string> -m <MAVID_EXE> -c <CNDSRC_DIR> -d draftGenome1... -d draftGemoneN -n nonDraftGeome1... -n nonDraftGenomeN -r referenceGenome https://github.com/VEuPathDB/.../runMercator	Mercator mapmaker 0.4 (2016-01-21) Mavid Version 2.0.4
Transmembrane domain prediction	TMHMM	Nice -short	2.0c