

Scripts	Function
passfilterreads.py	Remove reads that failed Illumina filter
conc.py	Concatenate read files for each samples
runfastqc.py	Run FastQC pre-cleanup
cleanreadsmulti.py	Remove adapters and trim ends/poor quality
runfastqc_postclean.py	Run FastQC post-cleanup
3-generateAssemblies_XSEDE_ML.pl	Generate batch files for trinity
blastx_batchscript.sh, tblastn_batchscript.sh, mtdna_blastx_batch.sh, mtdna_tblastn_batch.sh	Batch files for BLAST (nuclear and mtDNA)
theblastparser.py	Parse BLAST results and get RBH
hbirds_biomart.r	Parse RBH, get gene information
cutalign.py and sn5talign.py	Trim un-alignable regions, align with Mafft and transAlign
samprename.py	Rename sequence names within a file
fasta2Nexus.py, nexus2phylip.py, convertNconcat.py	File conversion scripts used to do the file conversion and concatenate sequences (for concatenated species tree)
nullbatruncodeml.py, posbatruncodeml.py, rerun_codeml.py	Run null and test models of codeml, plus rerun any that fail to converge in the first run
Calc_LRT.r	Calculate LRT, grab gene ontology information, NMDS