

Amplification of museum specimens
via PCR

Bin samples according to quality

High Quality
Museum Specimens

Low Quality
Museum Specimens

Repeat until 3 successful genotypes are recovered
-consider PCR optimization for LQMS

Library preparation, Illumina Sequencing

prinseq-lite
QC

CHIIMP
Output

*-use prinseq-lite results
to inform manual
evaluation of genotypes*

Calculate % of
reads per allele

Compare allele calls,
if shifted evaluate repeat
motif and primer sequences

Alleles with less
than 500 total reads

if less than 1/3 other
allele and one motif
smaller = stutter

manually adjust
genotypes

discard genotype

Final genotypes