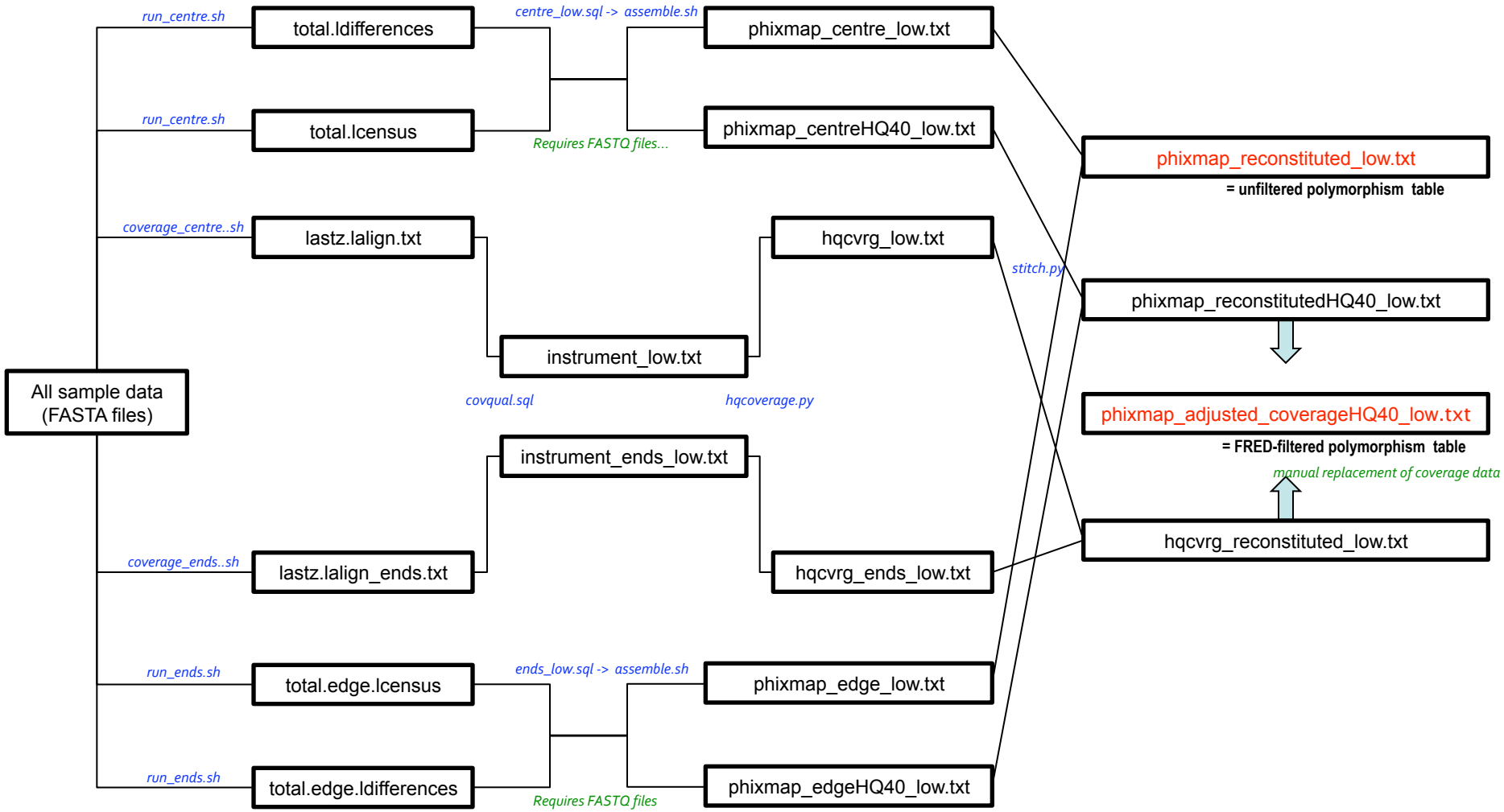
All sample data
(FASTA files)
run_centre.sh
total.ldifferences
run_centre.sh
total.lcensus
centre_low.sql -> assemble.sh
Requires FASTQ files...
phixmap_centre_low.txt
phixmap_centreHQ40_low.txt
coverage_centre..sh
lastz.lalign.txt
instrument_low.txt
covqual.sql
hqcoverage.py
hqcvrg_low.txt
stitch.py
phixmap_reconstituted_low.txt
= unfiltered polymorphism table
phixmap_reconstitutedHQ40_low.txt
phixmap_adjusted_coverageHQ40_low.txt
= FRED-filtered polymorphism table
manual replacement of coverage data
hqcvrg_reconstituted_low.txt
instrument_ends_low.txt
coverage_ends..sh
lastz.lalign_ends.txt
hqcvrg_ends_low.txt
run_ends.sh
total.edge.lcensus
ends_low.sql -> assemble.sh
phixmap_edge_low.txt
run_ends.sh
total.edge.ldifferences
Requires FASTQ files
phixmap_edgeHQ40_low.txt