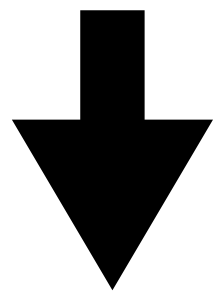


HS Rats Genotyping Pipeline

Pipeline Summary Report Design

Pipeline Overview

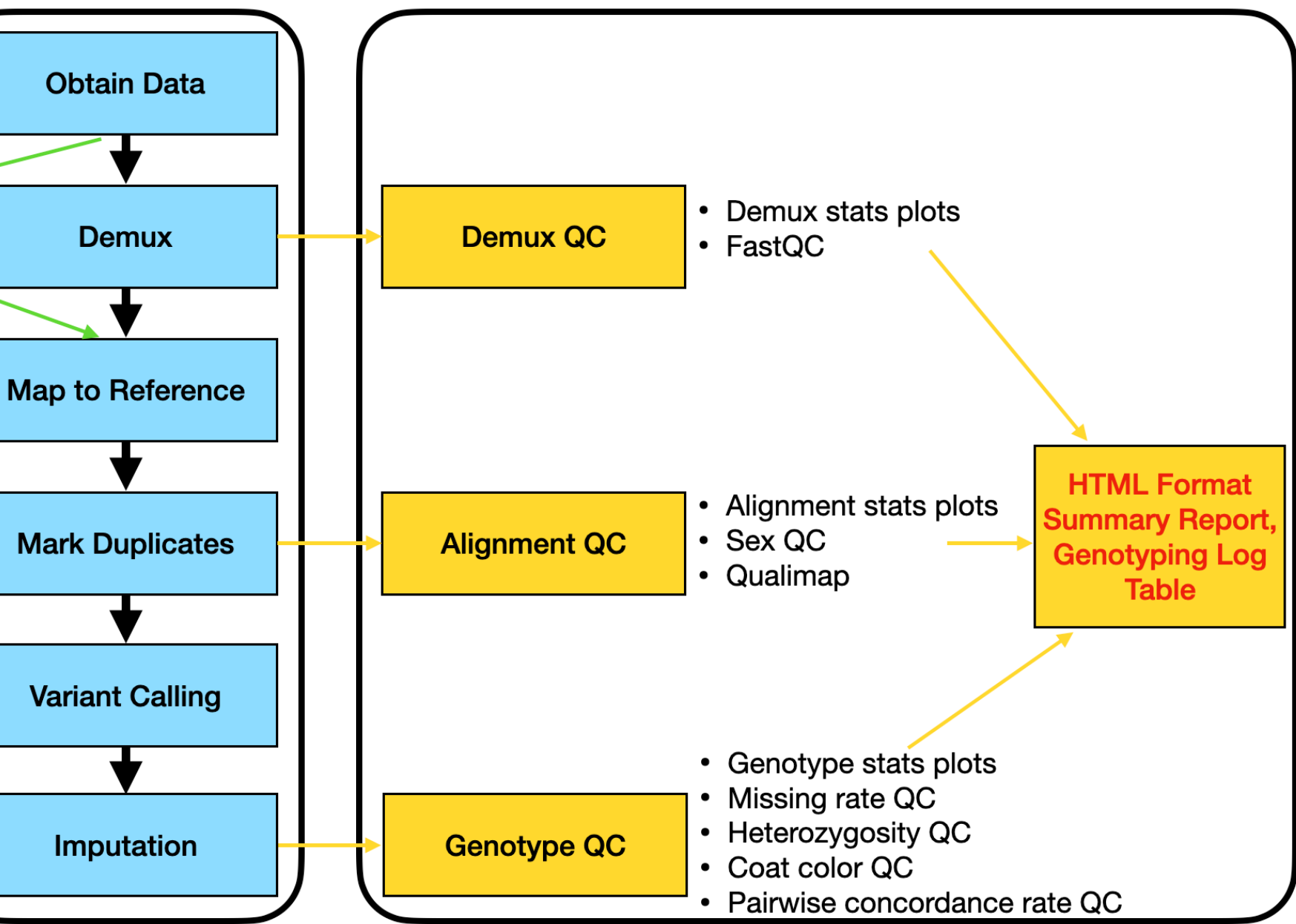
Submission Script



Before Genotyping

Genotyping

Quality Control



Flowchart

Genotyping Summary Report

Palmer Lab
Behavioral Genetics of Mice, Rats and Men

Palmer Lab
January 21, 2021

1 Pipeline Overview

1.1 Pipeline workflow

The pipeline flow chart is shown in figure 1.

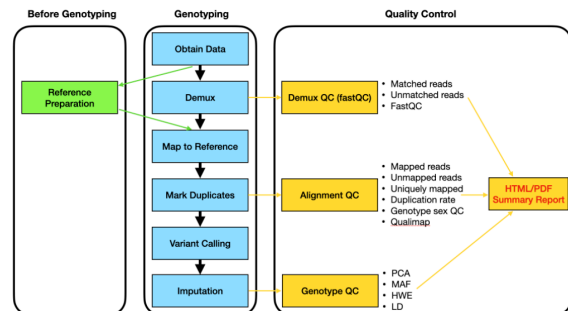


Figure 1: Pipeline flow chart

- 1 Pipeline Overview
- 2 Data
- 2.1 Sequence Data
- 2.2 Reference Data
- 3 Demultiplex Results
- 4 Alignment Results
- 5 MultiQC Summary for Demultiplex and Alignment Steps
- 6 Genotype Results
- 7 Outliers Report
- 8 Appendix A. Relevant Softwares
- 9 Appendix B. Preparation for Reference Data

2 Data

2.1 Sequence Data

Sample strain: Heterogenous stock
Number of samples: 376
Flow cell run ID(s): 201218_A00953_0203_BHNSHYDSXY
Riptide library preparation: Riptide31, Riptide32, Riptide39, Riptide40
Metadata: /projects/ps-palmer/hs_rats/201218_A00953_0203_BHNSHYDSXY/data/kn04_fastq_sample_metadata_n952.csv

Run ID	Library ID	Sample Project	Number of Samples
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_olivier_george_cocaine	1
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_olivier_george_oxycodone	83
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_olivier_george_scrub	4
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_suzanne_mitchell	3
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_tom_jhou	5
201218_A00953_0203_BHNSHYDSXY	Riptide32	u01_olivier_george_cocaine	91
201218_A00953_0203_BHNSHYDSXY	Riptide32	u01_olivier_george_scrub	5
201218_A00953_0203_BHNSHYDSXY	Riptide39	u01_olivier_george_oxycodone	8
201218_A00953_0203_BHNSHYDSXY	Riptide39	u01_peter_kalivas_italy	88
201218_A00953_0203_BHNSHYDSXY	Riptide40	u01_peter_kalivas_italy	88

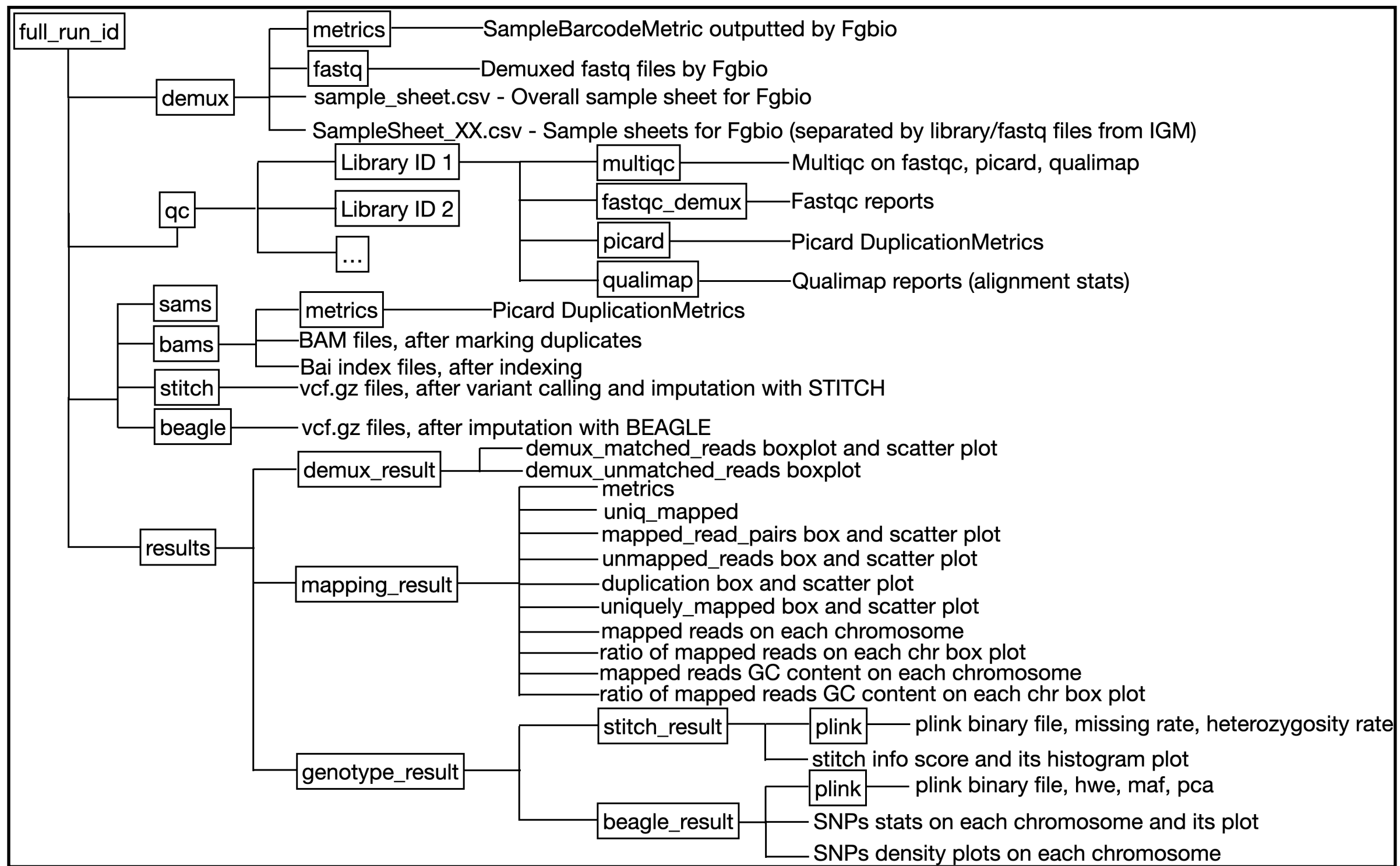
2.2 Reference Data

Reference genome for alignment: /projects/ps-palmer/hs_rats/reference_genome/rn6.fa
STITCH variant calling reference panel: /projects/ps-palmer/hs_rats/reference_genome/rn6_refPnls
BEAGLE imputation genetic map: /projects/ps-palmer/hs_rats/reference_genome/map_files

Summary Report

Genotyping Log Table

hs_rats_n1912_01202021_genotype_log																
rid	demux_reads	mapped_read_pairs	unmapped_reads_ratio	duplication_ratio	unq_mapped_ratio	QC_reads	QC_sas	data	missing_rate	QC_missing	heterozygosity_rate	QC_heterozygosity	coatcolor	QC_coat_color	afhms	QC_pnls
0007E79AF	445456	398341	0.012942477904693	0.004919	0.8028939971803	pass	pass	pass	1202021	0.003717	pass	0.311291208191811	pass	pass	pass	pass
0007E79AC3	4860719	4884948	0.011624348712951	0.104058	0.8089846932902	pass	pass	pass	1202021	0.049789	pass	0.3176026325217	pass	pass	pass	pass
0007E79C0F	2382093	2282840	0.0118620048198031	0.001802	0.81887073687461	pass	pass	pass	1202021	0.048487	pass	0.320733781058203	pass	pass	pass	pass
0007E79C40	124685	910484	0.010180158216618	0.005505	0.81026780250772	pass	pass	pass	1202021	0.048411	pass	0.30602780250772	pass	pass	pass	pass
0007E79C86	3129639	2084025	0.011851786884543	0.0038	0.7987269061687	pass	pass	pass	1202021	0.058843	pass	0.31602131345758	pass	pass	pass	pass
0007E79C8B	484849	4743309	0.01157831838884	0.00424	0.811732017141373	pass	pass	pass	1202021	0.0484171	pass	0.314478482326371	pass	pass	pass	pass
0007E79D3F	3518739	344481	0.0115091824343483	0.00477	0.802646323214919	pass	pass	pass	1202021	0.051897	pass	0.3190494456582	pass	pass	pass	pass
0007E79D10	2238122	2238121	0.011851786884543	0.00303	0.80527562809443	pass	pass	pass	1202021	0.000685	pass	0.312180388143481	pass	pass	pass	pass
0007E79E41	4476238	4284181	0.0116730208312053	0.00406	0.8027918293252	pass	pass	pass	1202021	0.052188	pass	0.30211208881028	pass	pass	pass	pass
0007E79E4C	3475400	3416295	0.010803393120705	0.00388	0.78784607781891	pass	pass	pass	1202021	0.052514	pass	0.306178021488453	pass	pass	pass	pass
0007E79E4F	1367196	2844455	0.011443217102168	0.002021	0.8214717071688	pass	pass	pass	1202021	0.056403	pass	0.296716261500507	pass	pass	pass	pass
0007E79E78	2865547	2891900	0.011208464575505	0.00375	0.7861151899892	pass	pass	pass	1202021	0.056884	pass	0.3028108443438	pass	pass	pass	pass
0007E79E8C	9729221	9538678	0.011804473239993	0.00757	0.82480437228816	pass	pass	pass	1202021	0.0417072	pass	0.32008402658689	pass	pass	pass	pass
0007E79EAD	3160900	3105685	0.0114081071823157	0.00241	0.80437388494348	pass	pass	pass	1202021	0.030968	pass	0.312174743896151	pass	pass	pass	pass
0007E79EAE	322904	3198543	0.0110257916468138	0.002579	0.8088118054058	pass	pass	pass	1202021	0.019444	pass	0.28441789238113	pass	pass	pass	pass
0007E79E85	2020119	581687	0.01102023886101	0.005138	0.8021802061164	pass	pass	pass	1202021	0.048823	pass	0.29800037246784	pass	pass	pass	pass
0007E79E8A	332506	3208819	0.0123729135814963	0.0051	0.80515219155239	pass	pass	pass	1202021	0.024737	pass	0.314488481703918	pass	pass	pass	pass
0007E79E8C	3170785	2714257	0.011246895118758	0.00417	0.81165157288187	pass	pass	pass	1202021	0.0517864	pass	0.324505820202088	pass	pass	pass	pass
0007E79E81	3149597	2102846	0.0118026778915807	0.00129	0.79688351870276	pass	pass	pass	1202021	0.087152	pass	0.2975468842109	pass	pass	pass	pass
0007E79E8E	4735197	4648179	0.011281848164	0.00408	0.8038218478486	pass	pass	pass	1202021	0.0487808	pass	0.29025388410274	pass	pass	pass	pass
0007E79F10	4884802	481108	0.0107214871891977	0.00404	0.7988777487313	pass	pass	pass	1202021	0.047179	pass	0.3077594188021	pass	pass	pass	pass
0007E79FAC	3448889	2883899	0.0112317233551752	0.00364	0.808916221198513	pass	pass	pass	1202021	0.054884	pass	0.2980003870707	pass	pass	pass	pass
0007E79F8C	2849187	2385189	0.013438055185708	0.00791	0.813432578257814	pass	pass	pass	1202021	0.056609	pass	0.31278208416883	pass	pass	pass	pass
0007E79F89	551188	5443439	0.012320388218854	0.00361	0.81882862747028	pass	pass	pass	1202021	0.047808	pass	0.31888802837396	pass	pass	pass	pass
0007E79F86	482280	4782856	0.0110271812118863	0.002027	0.81888302891448	pass	pass	pass	1202021	0.047808	pass	0.3264067818741	pass	pass	pass	pass
0007E79F88	2229703	2182242	0.01222534448683	0.00489	0.807863037177795	pass	pass	pass	1202021	0.0584238	pass	0.3028108443438	pass	pass	pass	pass
0007E79F8A	2790608	2744811	0.0114473311527058	0.0026	0.80354843283516	pass	pass	pass	1202021	0.050278	pass	0.31881802778074	pass	pass	pass	pass
0007E79F83	3884847	3884847	0.0110271812118863	0.00471	0.802388151961802	pass	pass	pass	1202021	0.081803	pass	0.311291208191811	pass	pass	pass	pass
0007E79F81	2785882	2775882	0.0132058884442888	0.00388	0.8144758830314206	pass	pass	pass	1202021	0.0487802	pass	0.29881124848705	pass	pass	pass	pass
0007E79F84	4810556	4828891	0.010581814084954	0.00485	0.811728304142812	pass	pass	pass	1202021	0.0480051	pass	0.32278208416883	pass	pass	pass	pass
0007E79F8E	2827887	2878227	0.0120421487184885	0.00293	0.78789804898908	pass	pass	pass	1202021	0.057296	pass	0.30642741488481	pass	pass	pass	pass
0007E79F8D	3260140	1888175	0.0110271812118863	0.00194	0.784431870257428	pass	pass	pass	1202021	0.067805	pass	0.30418283818181	pass	pass	pass	pass
0007E79F82	3488034	2415455	0.0128828144824819	0.00332	0.81905147198552	pass	pass	pass	1202021	0.058059	pass	0.3088108820202	pass	pass	pass	pass
0007E79F85	3188202	3188202	0.011873882022738	0.00008	0.8074283028793	pass	pass	pass	1202021	0.0547332	pass	0.308478832323232	pass	pass	pass	pass
0007E79F87	1004021	8895972	0.0101271812118863	0.00387	0.80200848793284	pass	pass	pass	1202021	0.044313	pass	0.218432323232323	pass	pass	pass	pass
0007E79F80	4812645	3844005	0.0108612288311837	0.00406	0.79481341688381	pass	pass	pass	1202021	0.0513868	pass	0.2838188117783	pass	pass	pass	pass
0007E79F81	2358877	2488508	0.0115370197295709	0.002138	0.787780488488313	pass	pass	pass	1202021	0.056507	pass	0.311720880200587	pass	pass	pass	pass
0007E79F8C	3848507	3823124	0.0101271812118863	0.00288	0.8155815501587	pass	pass	pass	1202021	0.050342	pass	0.29012088818873	pass	pass	pass	pass



Directory Structure

Pipeline Arguments

Line 1: home directory

Line 2: Flow cell directory

Line 3: Flow cell metadata Line 4: Sequencing data directory

Line 5: Reference genome

Line 6: Reference panels for STITCH

Line 7: Genetic map for BEAGLE

Line 8: Directory where you keep the code for the pipeline

Line 9: The general name of this run

previous_flow_cells_metadata

Paths to previous flow cells' metadata.

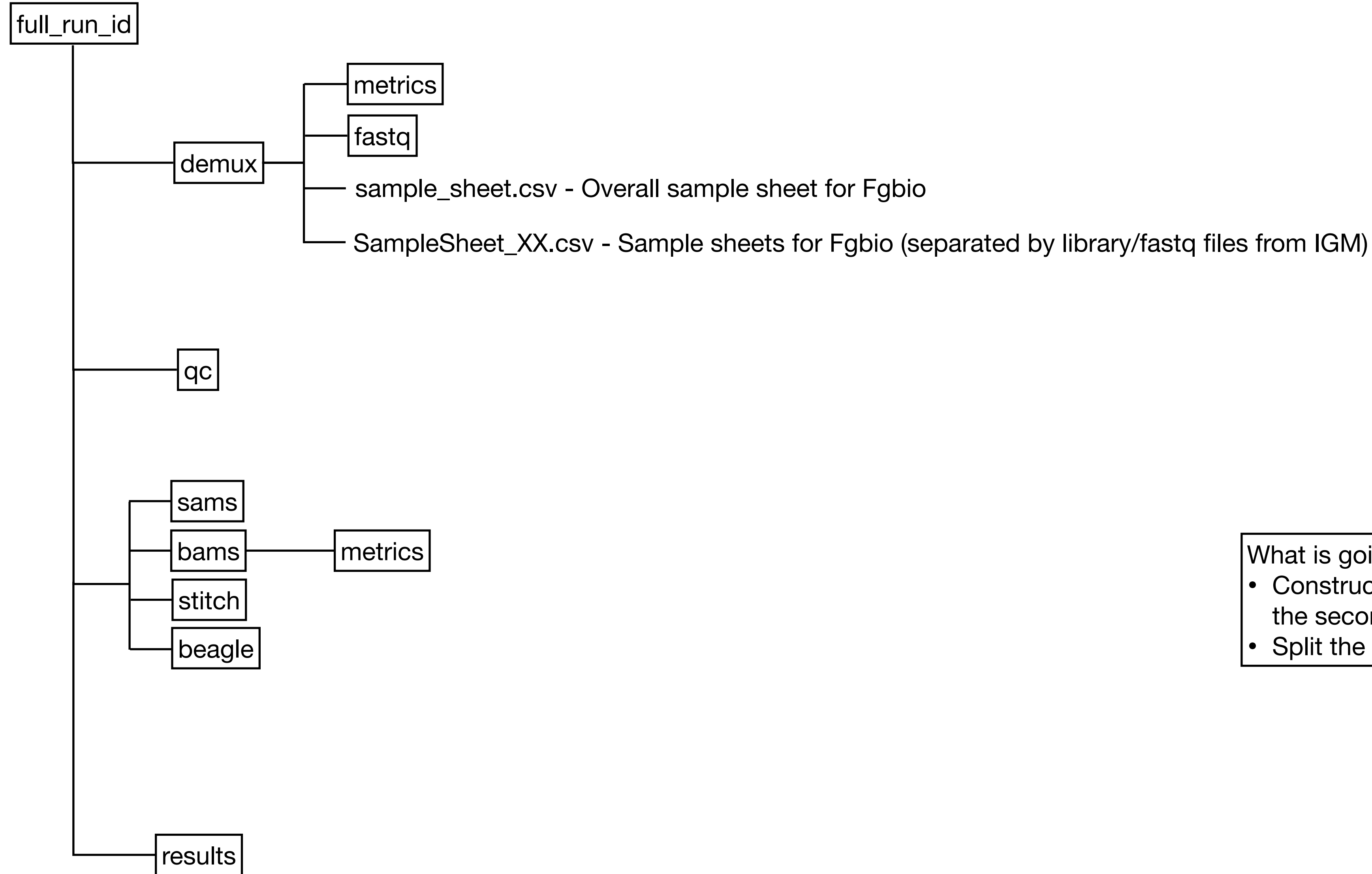
previous_flow_cells_bams

Paths to previous flow cells' BAM files.

pedigree_data

Paths to all flow cells' pedigree data.

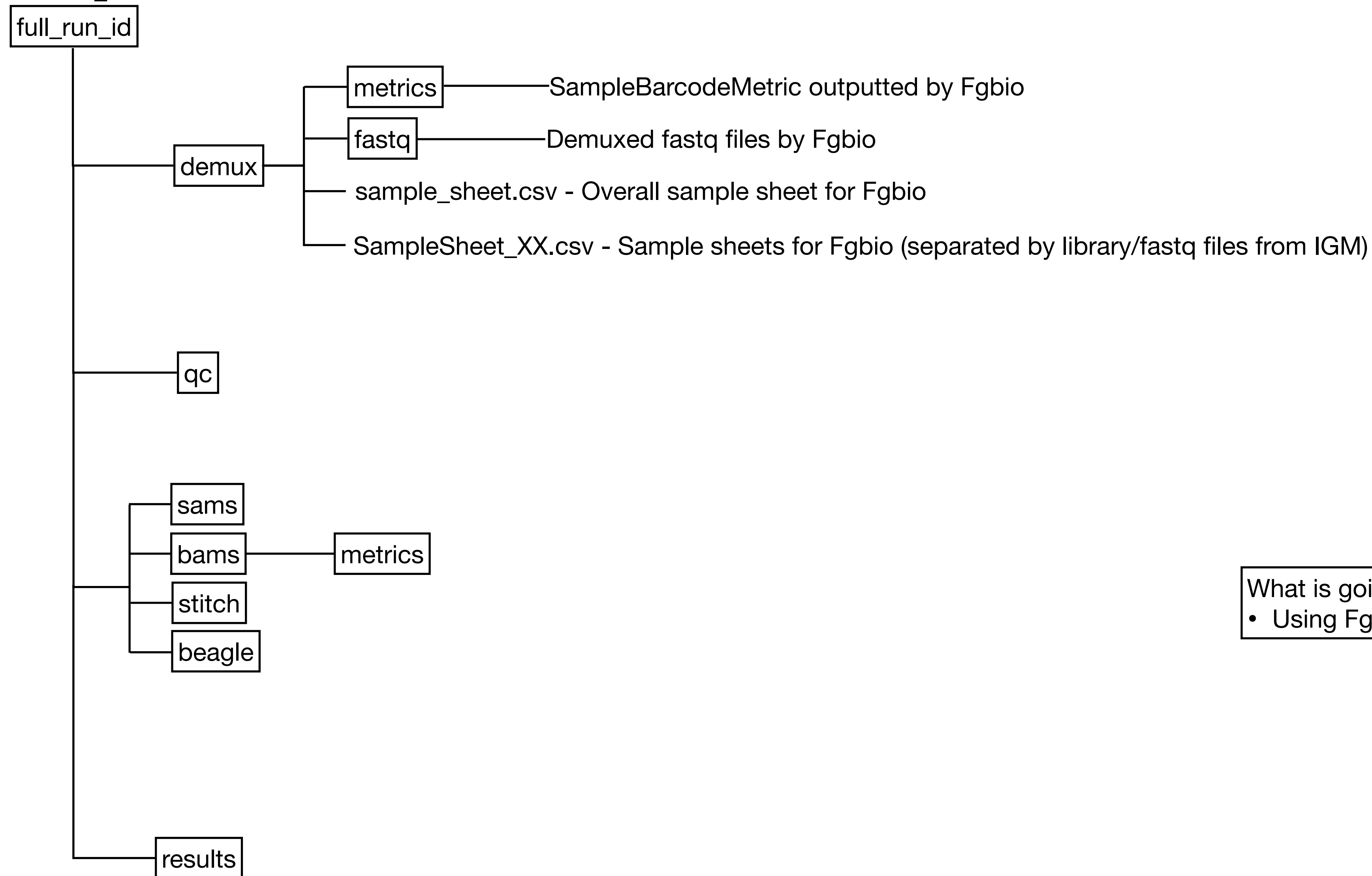
Step 1 - Preparation



What is going on:

- Construct the basic structure of the directory from the second line of the Pipeline Argument file
- Split the sample sheet for each library prep for Fgbio

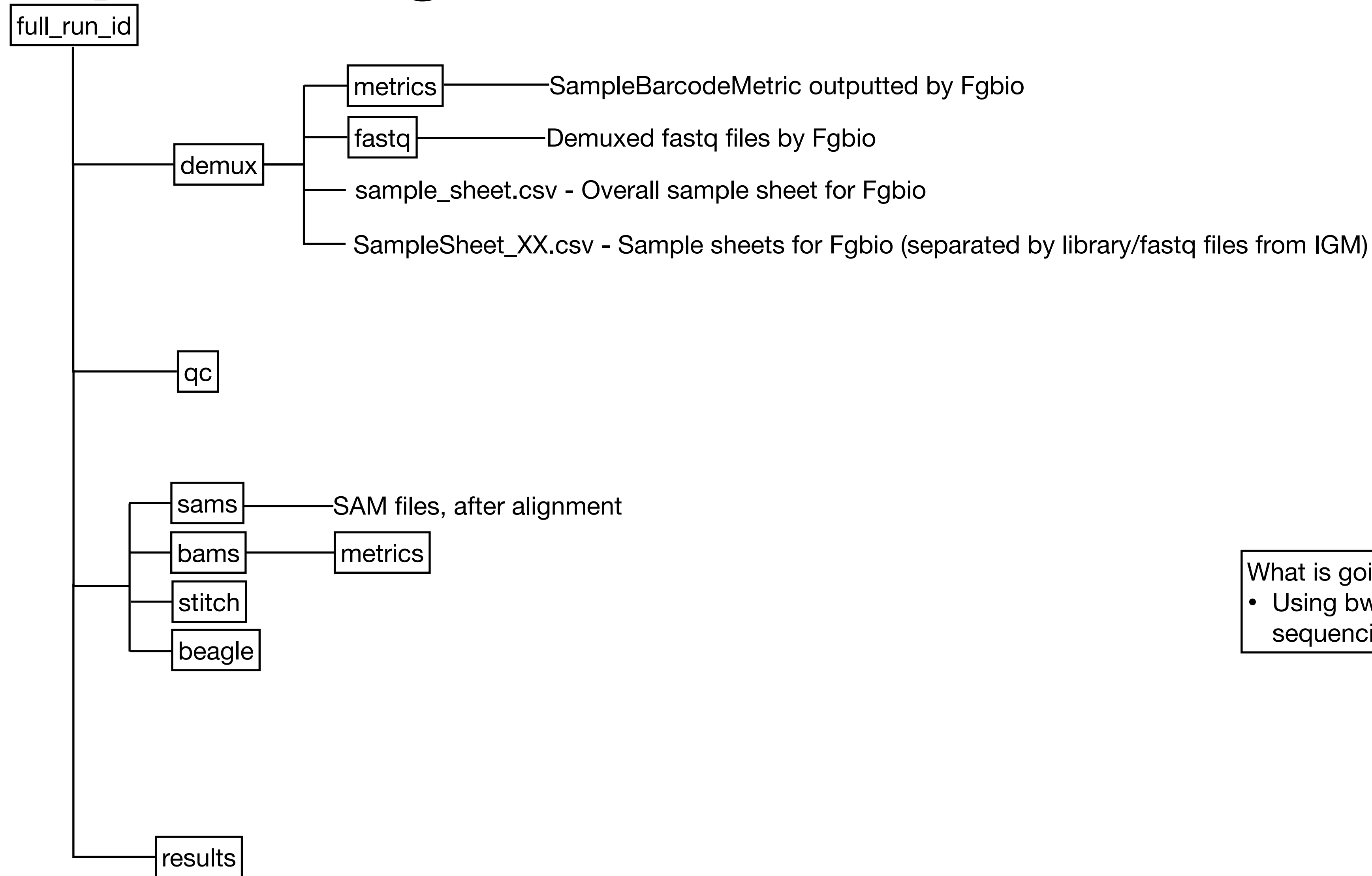
Step 2 - Demux



What is going on:

- Using Fgbio to demultiplex the fastq files

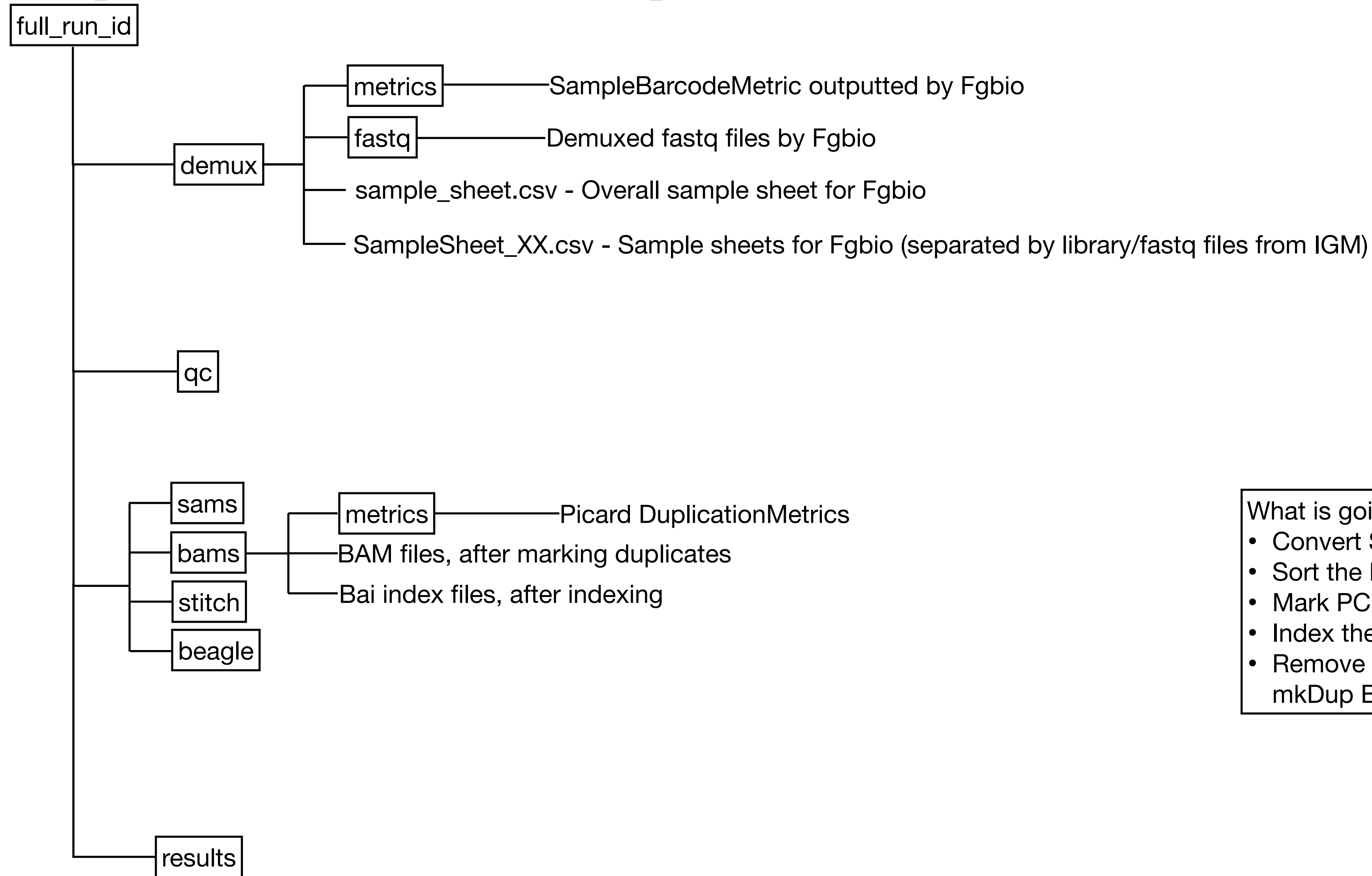
Step 3 - Alignment



What is going on:

- Using bwa mem to map the demultiplexed sequencing reads to reference genome

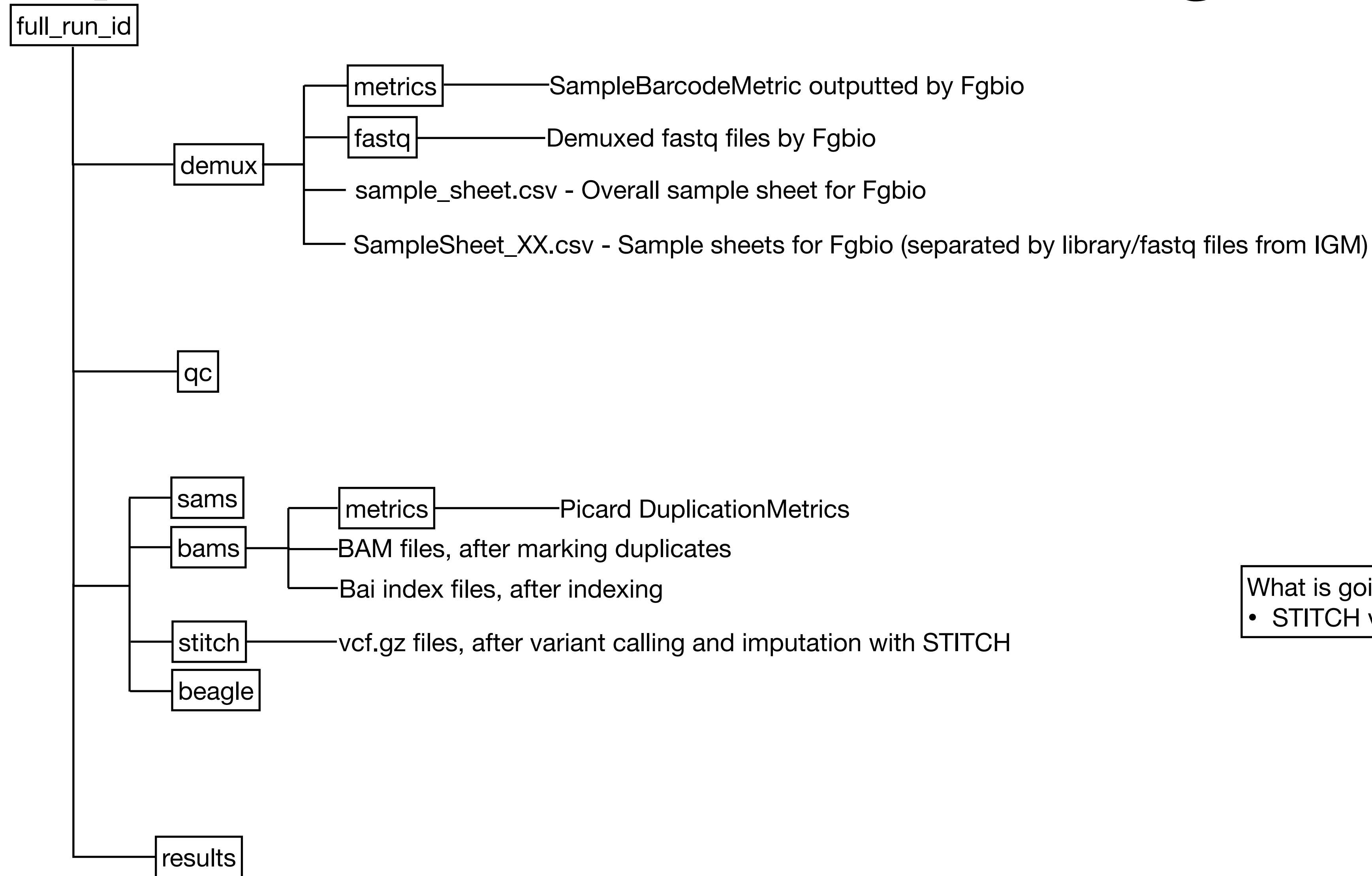
Step 4 - Mark Duplicates



What is going on:

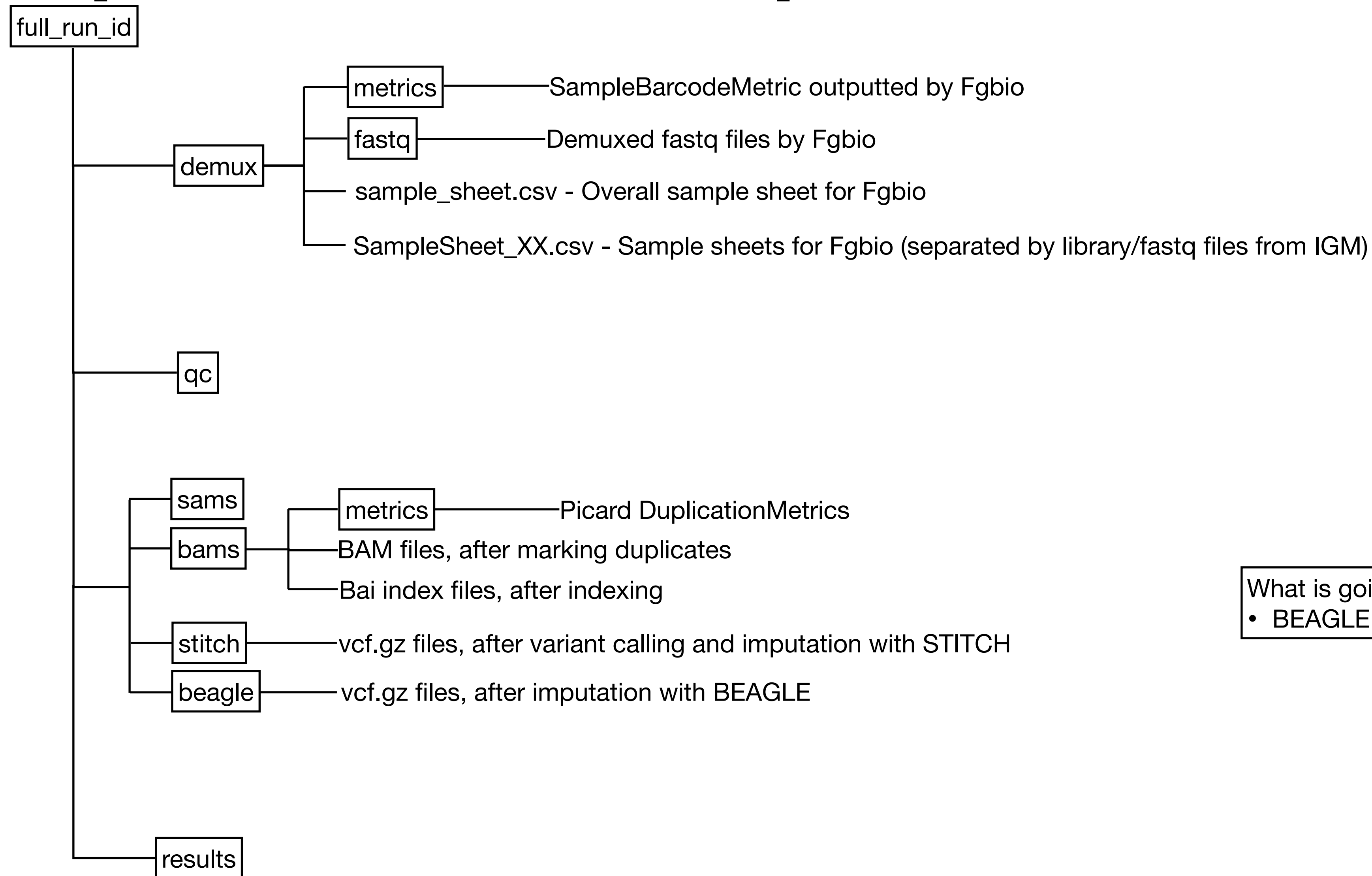
- Convert SAM files to BAM files
- Sort the BAM files
- Mark PCR duplicates
- Index the marked duplicates BAM files
- Remove the SAM files, unsorted BAM files, and non-mkDup BAM files

Step 5 - STITCH Variant Calling



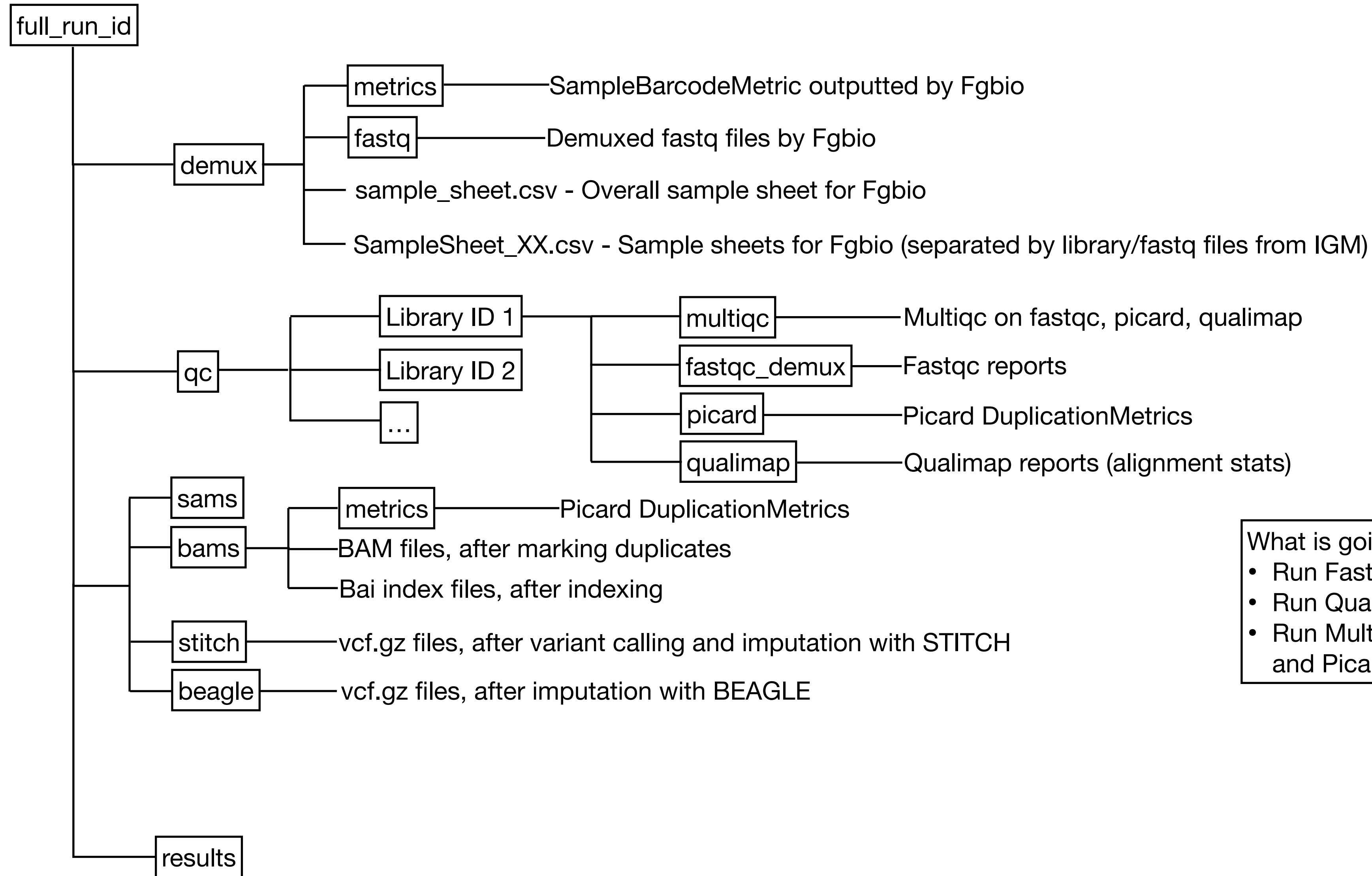
What is going on:
• STITCH variant calling

Step 6 - BEAGLE Imputation



What is going on:
• BEAGLE imputation

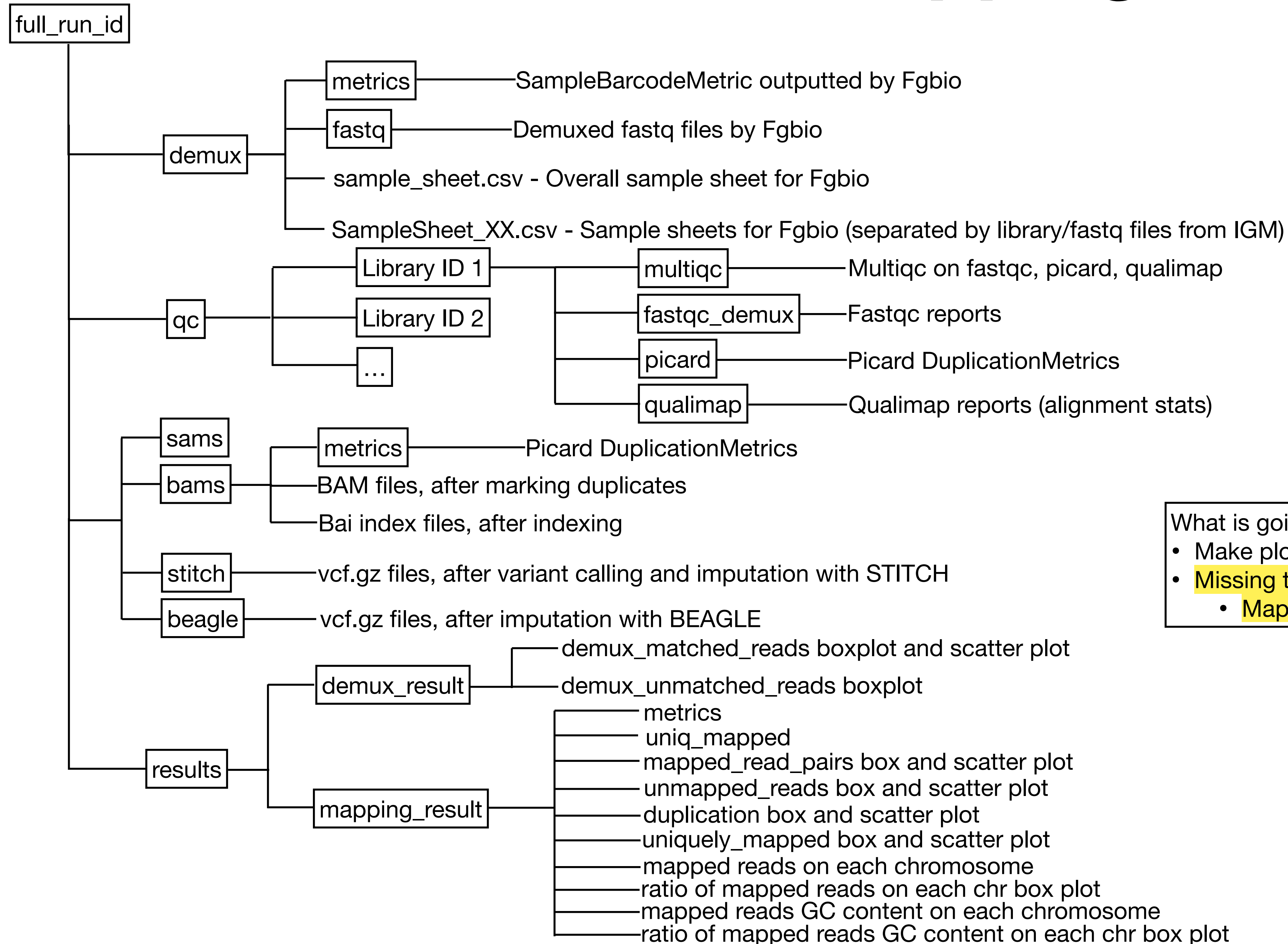
Result 1 - MultiQC



What is going on:

- Run FastQC on each library's fastq files
- Run Qualimap on each library's mapped bam files
- Run MultiQC on each library's FastQC, Qualimap, and Picard DuplicationMetrics results

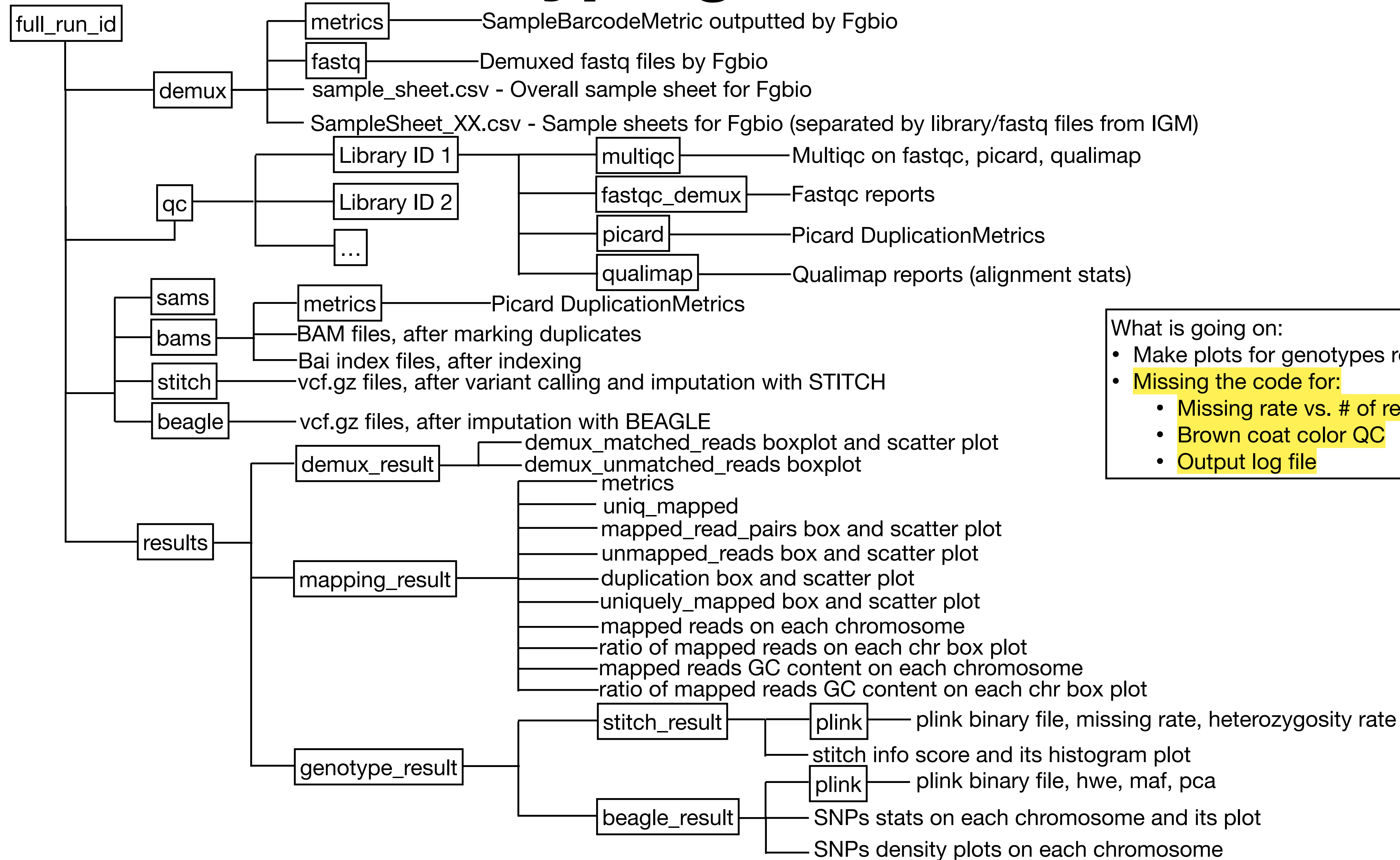
Result 2 - Demux and Mapping Results



What is going on:

- Make plots for demux result and mapping result
- Missing the code for:
 - Mapping quality histogram

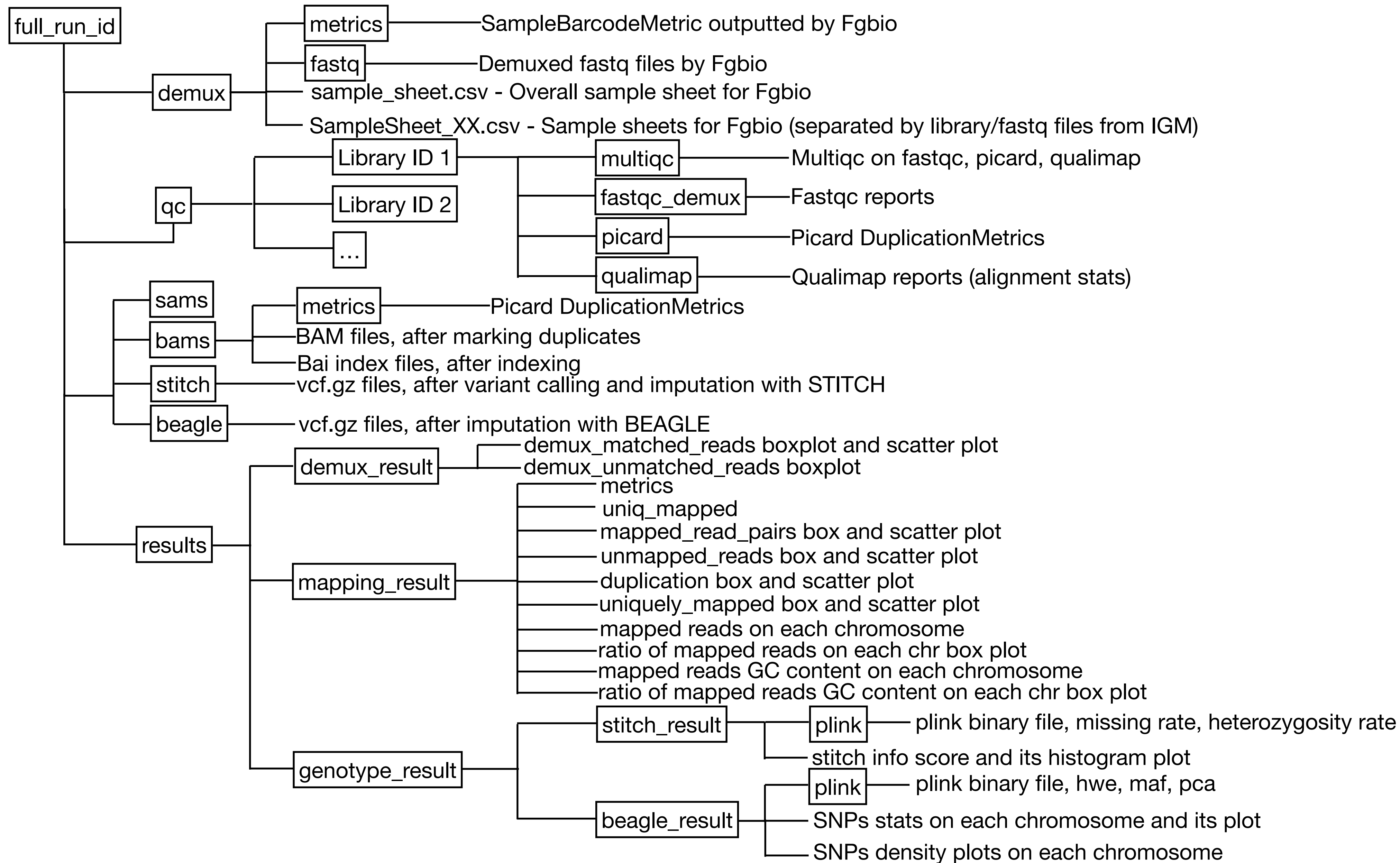
Result 3 - Genotyping Results



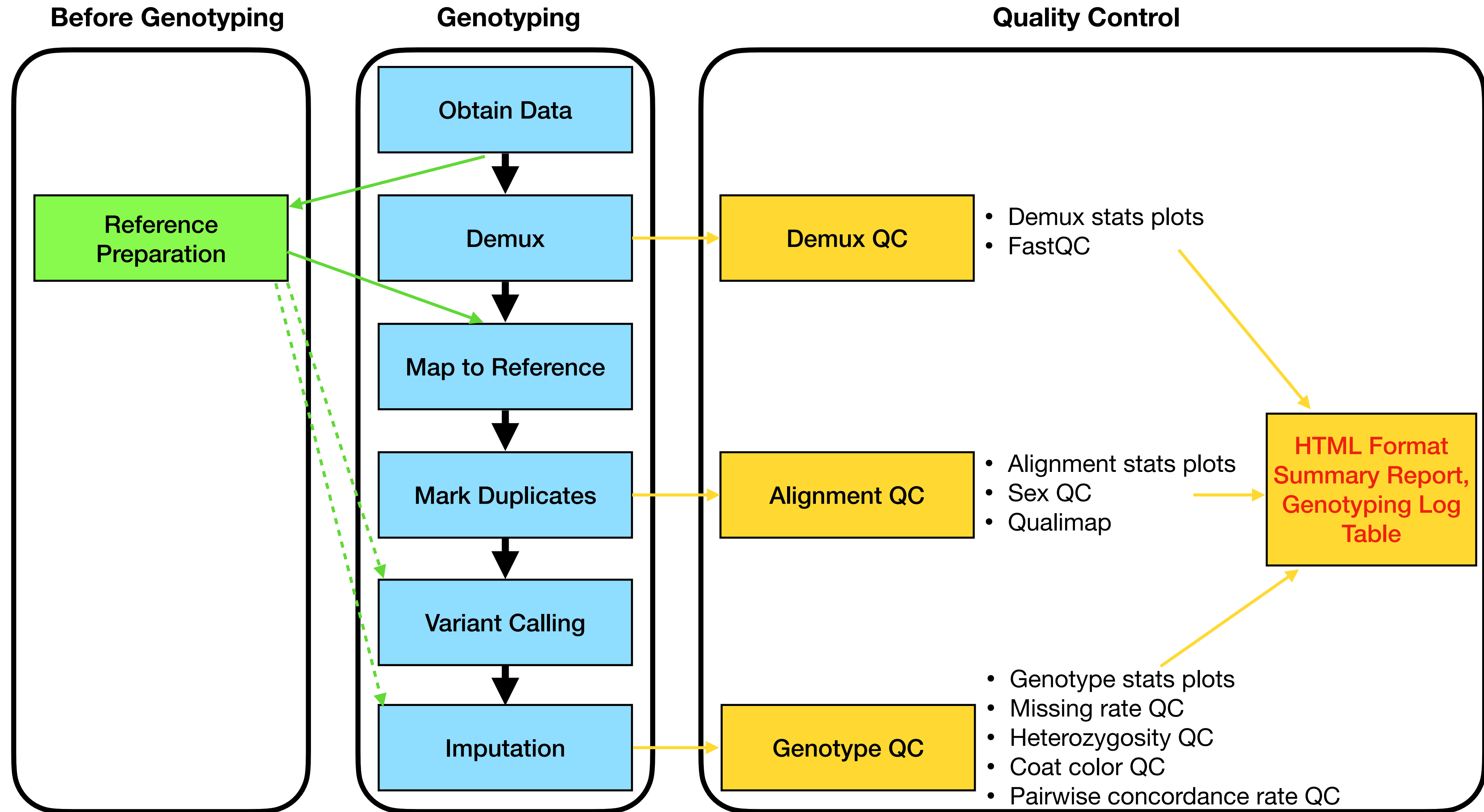
What is going on:

- Make plots for genotypes result
- Missing the code for:
 - Missing rate vs. # of reads
 - Brown coat color QC
 - Output log file

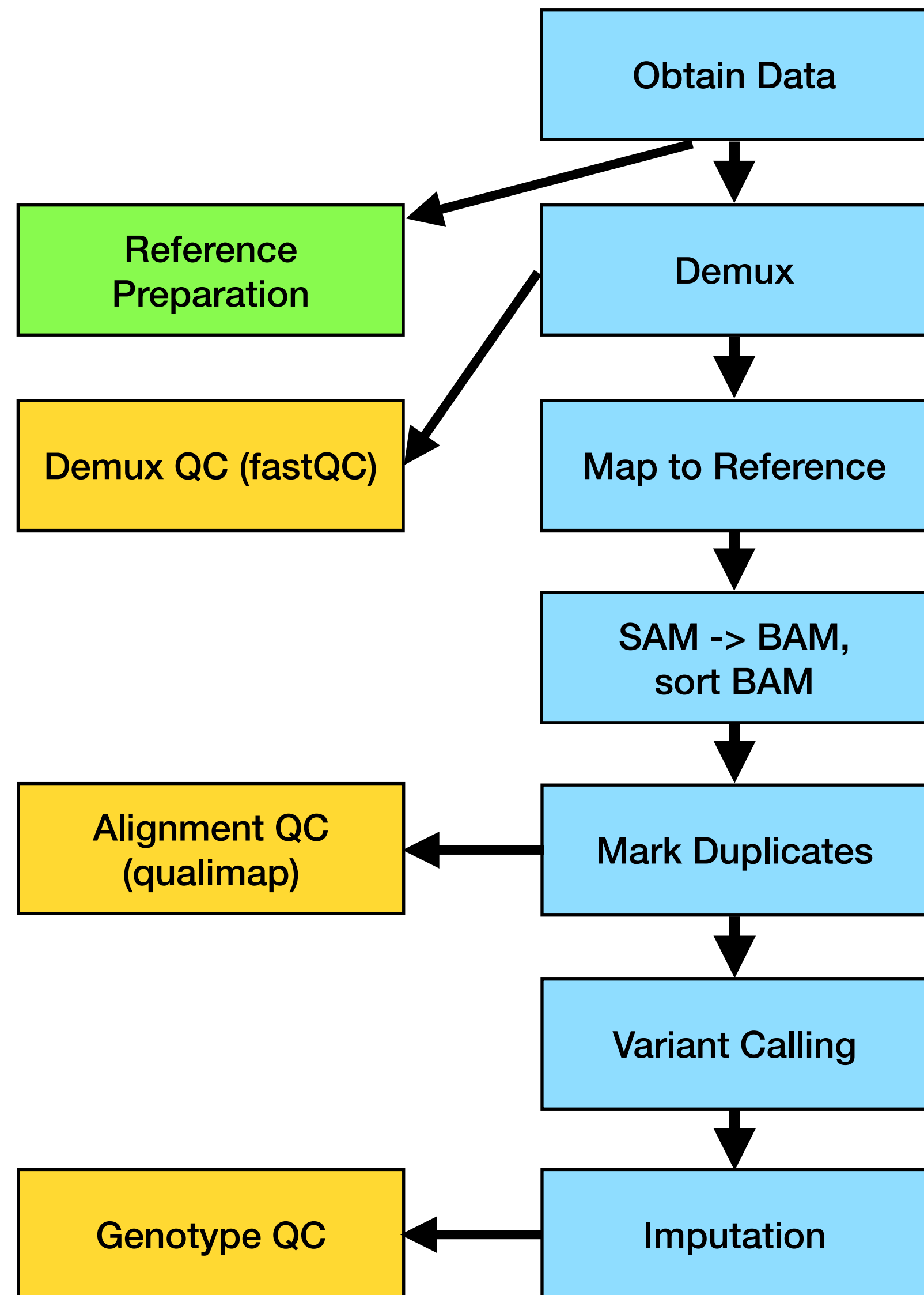
TSCC Directory Structure



Pipeline Overview



Pipeline Flowchart



```
java -Xmx40G -XX:+AggressiveOpts -XX:+AggressiveHeap \  
-jar /projects/ps-palmer/software/local/src/fgbio-1.2.0/fgbio-1.2.0.jar DemuxFastqs \  
--inputs ${pre_demux_fastq_R1} ${pre_demux_fastq_R2} \  
--metadata ${sample_sheet} \  
--read-structures 8B12M+T 8M+T \  
--output-type=Fastq \  
--threads $ncpu \  
--output ${out_path}/demux/fastq \  
--metrics ${out_path}/demux/metrics/${fastq_temp}demux_barcode_metrics.txt
```

```
/projects/ps-palmer/software/local/src/bwa-0.7.12/bwa mem -aM -t 2\  
-R "@RG\tID:${instrument_name}.${run_id}.${flowcell_id}.${flowcell_lane}\tLB:${library_id}\tPL:ILLUMINA\tSM:${sample_id}\tPU:${flowcell_id}.${flowcell_lane}.${sample_barcode}" \  
${reference_data} ${demux_data}/${f}_R1.fastq.gz \  
${demux_data}/${f}_R2.fastq.gz > ${out_path}/sams/${f}.sam &
```

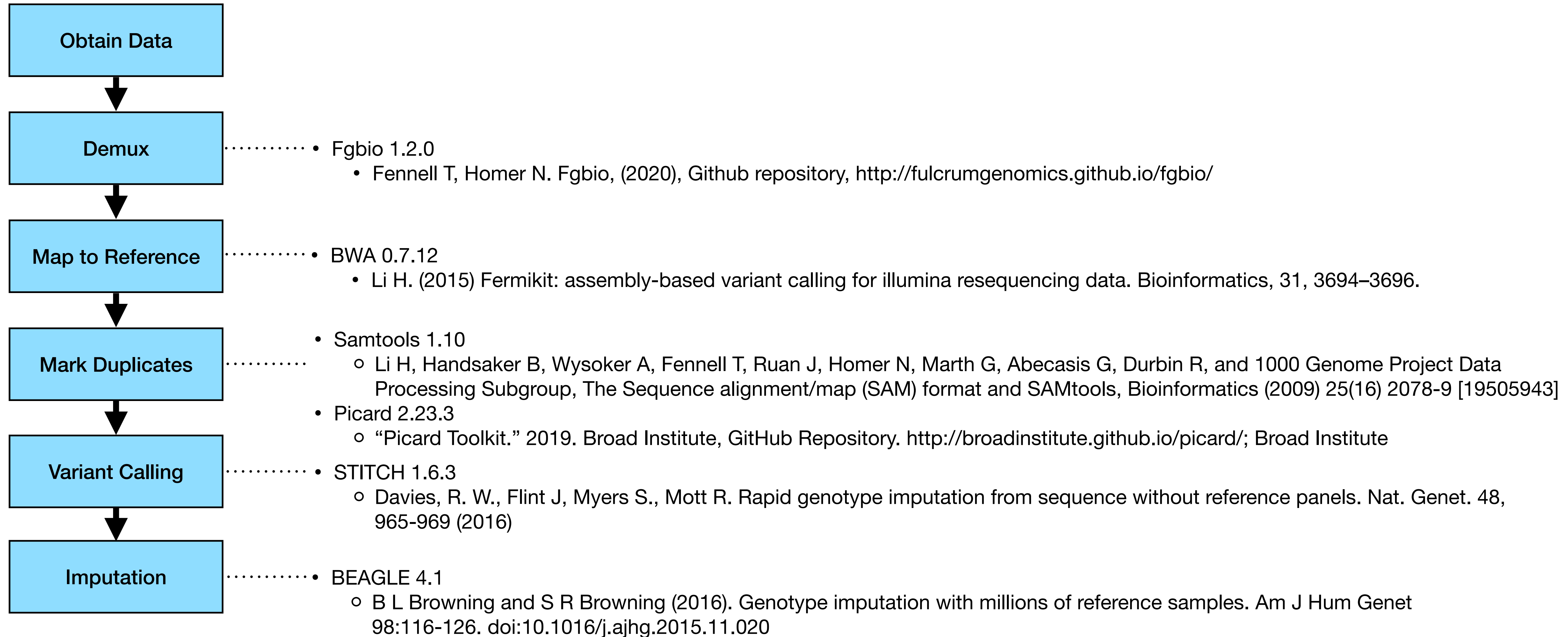
```
/projects/ps-palmer/software/local/src/samtools-1.10/samtools view -h -b \  
-t ${reference_data} -o ${out_path}/bams/${f}.bam ${mapped_data}/${f}.sam
```

```
/projects/ps-palmer/software/local/src/samtools-1.10/samtools sort -m 30G \  
-o ${out_path}/bams/${f}_sorted.bam ${out_path}/bams/${f}.bam
```

```
java -Xmx20G -XX:+AggressiveOpts -XX:+AggressiveHeap\  
-jar /projects/ps-palmer/software/local/src/picard-2.23.3/picard.jar MarkDuplicates \  
--INPUT ${out_path}/bams/${f}_sorted.bam \  
--REMOVE_DUPLICATES false \  
--ASSUME_SORTED true \  
--METRICS_FILE ${out_path}/bams/metrics/${f}_sorted_mkDup_metrics.txt \  
--OUTPUT ${out_path}/bams/${f}_sorted_mkDup.bam &
```

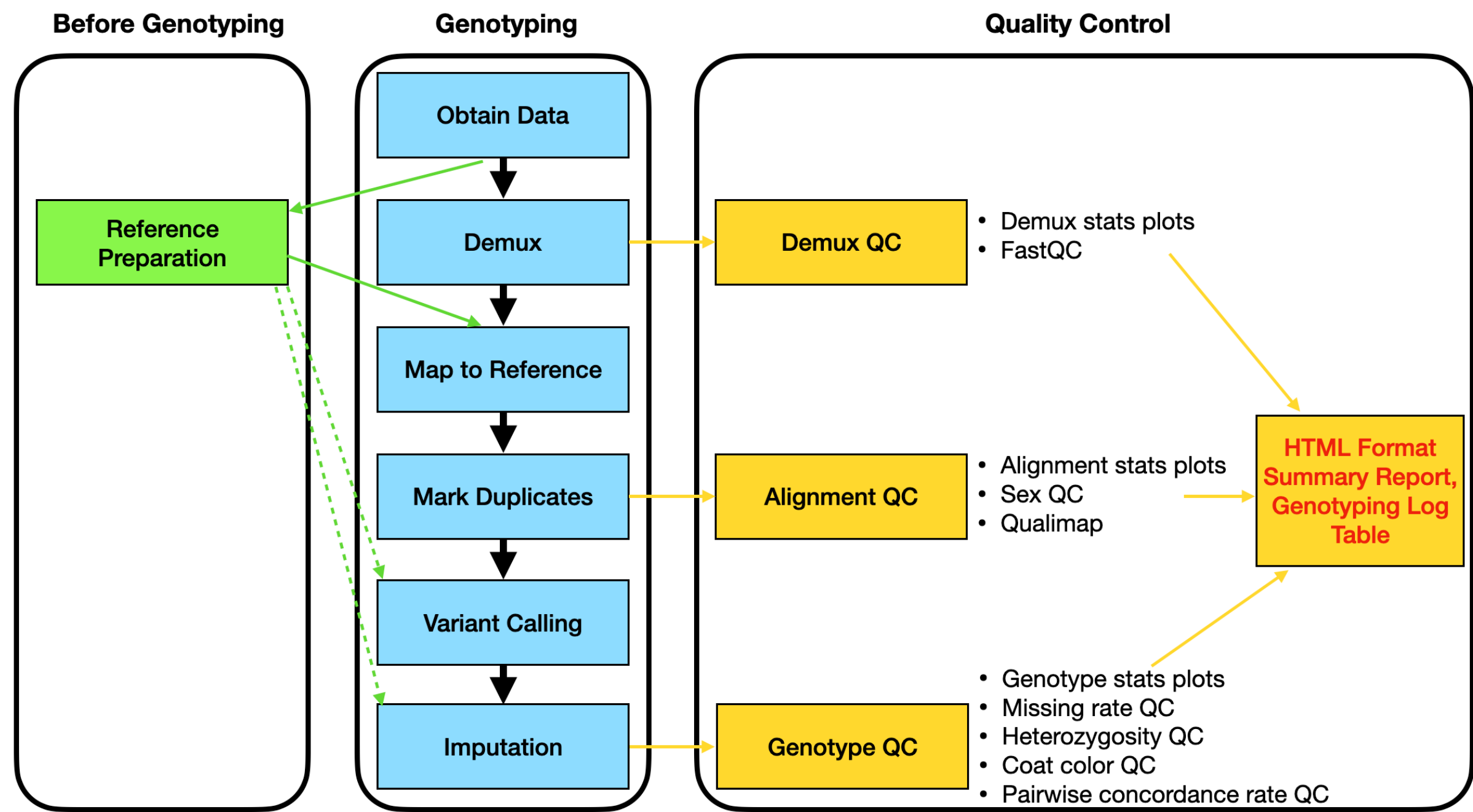
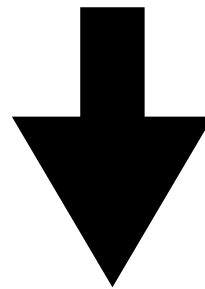
```
/projects/ps-palmer/software/local/src/samtools-1.10/samtools index \  
${out_path}/bams/${f}_sorted_mkDup.bam ${out_path}/bams/${f}_sorted_mkDup.bai
```

Relevant Software



Pipeline on TSCC

Submission Script



Flowchart

1 Pipeline Overview	2 Data
2.1 Sequence Data	2.2 Reference Data
3 Demultiplex Results	4 Alignment Results
5 MultiQC Summary for Demultiplex and Alignment Steps	6 Genotype Results
7 Outliers Report	8 Appendix A. Relevant Softwares
9 Appendix B. Preparation for Reference Data	

PALMER LAB
Behavioral Genetics of Mice, Rats and Men

Genotyping Summary Report

Palmer Lab
January 21, 2021

1 Pipeline Overview

1.1 Pipeline workflow

The pipeline flow chart is shown in figure 1.

Figure 1: Pipeline flow chart

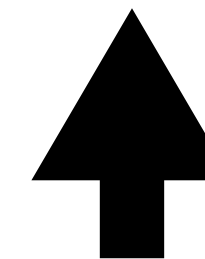
Sample strain: Heterogenous stock
Number of samples: 376
Flow cell run ID(s): 201218_A00953_0203_BHNSHYDSXY
Riptide library preparation: Riptide31, Riptide32, Riptide39, Riptide40
Metadata: /projects/ps-palmer/hs_rats/201218_A00953_0203_BHNSHYDSXY/data/kn04_fastq_sample_metadata_n952.csv

Run ID	Library ID	Sample Project	Number of Samples
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_olivier_george_cocaine	1
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_olivier_george_oxycodone	83
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_olivier_george_scrub	4
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_suzanne_mitchell	3
201218_A00953_0203_BHNSHYDSXY	Riptide31	u01_tom_jhou	5
201218_A00953_0203_BHNSHYDSXY	Riptide32	u01_olivier_george_cocaine	91
201218_A00953_0203_BHNSHYDSXY	Riptide32	u01_olivier_george_scrub	5
201218_A00953_0203_BHNSHYDSXY	Riptide39	u01_olivier_george_oxycodone	8
201218_A00953_0203_BHNSHYDSXY	Riptide39	u01_peter_kalivas_italy	88
201218_A00953_0203_BHNSHYDSXY	Riptide40	u01_peter_kalivas_italy	88

2.2 Reference Data

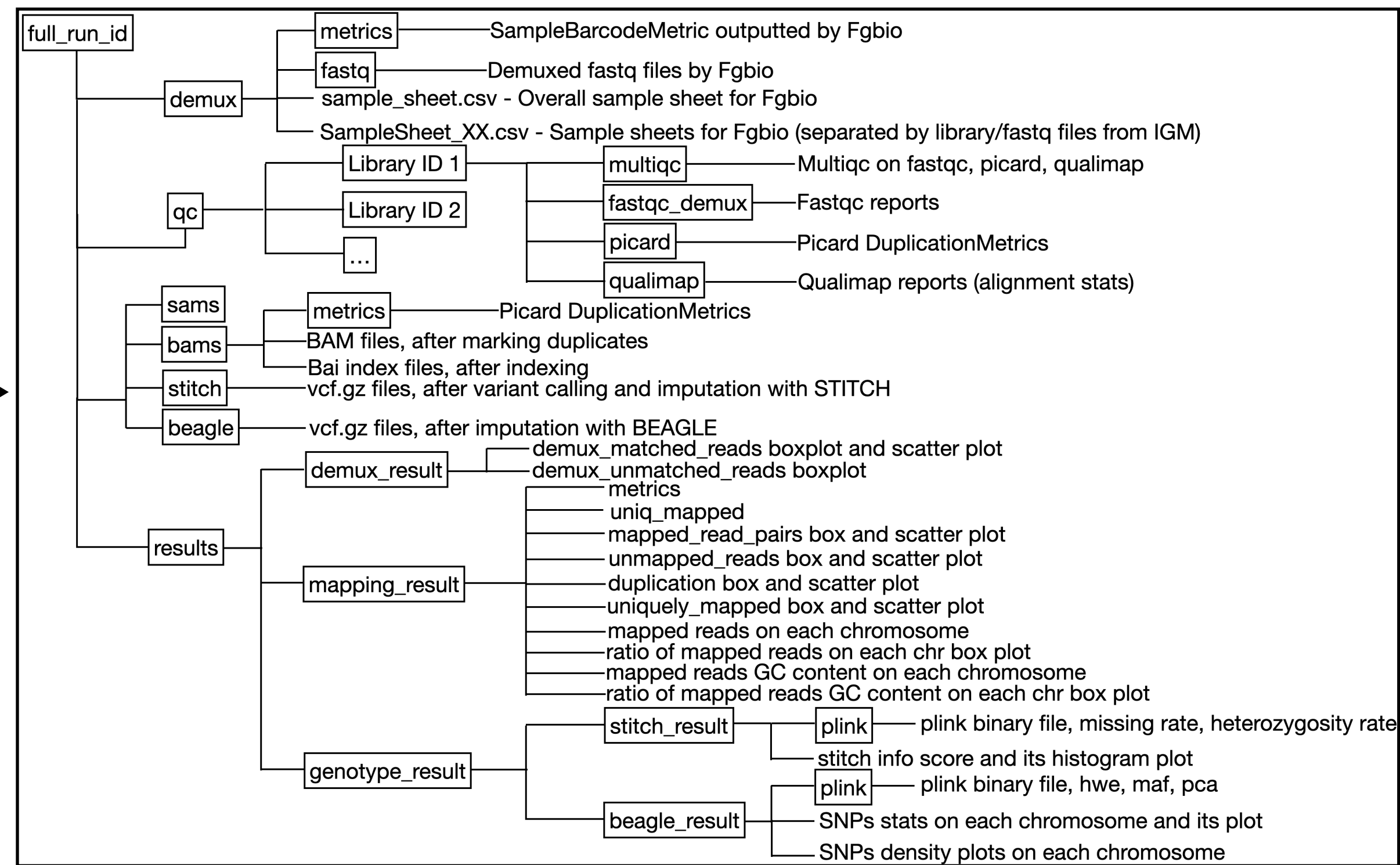
Reference genome for alignment: /projects/ps-palmer/hs_rats/reference_genome/rn6.fa
STITCH variant calling reference panel: /projects/ps-palmer/hs_rats/reference_genome/rn6_refPnls
BEAGLE imputation genetic map: /projects/ps-palmer/hs_rats/reference_genome/map_files

Summary Report



rs_id	demux_reads	mapped_read_pairs	unmapped_reads_ratio	duplication_ratio	uniquely_mapped_ratio	QC_reads	QC_data	missing_rate	QC_missing	heterozygosity_rate	QC_heterozygosity	coatcolor	QC_coat_color	afibio	QC_afibio
00077E9F	464089	398345	0.01294247704669	0.004919	0.8028939071803	pass	pass	1202021	0.003717	pass	0.311291208191811	pass	pass	pass	pass
00077EAC	4860719	486049	0.01142434812951	0.104091	0.8089666032902	pass	pass	1202021	0.049189	pass	0.31160263202147	pass	pass	pass	pass
00077E07	4480227	4412550	0.010871562706198	0.008468	0.79973502634055	pass	pass	1202021	0.048807	pass	0.320133761405051	pass	pass	pass	pass
00077E0F	2382093	2202840	0.011862004819001	0.001802	0.8188737687461	pass	pass	1202021	0.061005	pass	0.328718814370201	pass	pass	pass	pass
00077E0D	124685	2102846	0.010120140214616	0.005509	0.81026786502072	pass	pass	1202021	0.048411	pass	0.30602786502072	pass	pass	pass	pass
00077E08	2129639	2092425	0.0118517869884543	0.0038	0.7987269061687	pass	pass	1202021	0.058843	pass	0.316021313457158	pass	pass	pass	pass
00077E0B	484849	4743309	0.01157831838864	0.00424	0.811732011741373	pass	pass	1202021	0.048171	pass	0.31447840232671	pass	pass	pass	pass
00077E09	318719	344881	0.0115091824348483	0.00477	0.80266320214919	pass	pass	1202021	0.051897	pass	0.319040494456502	pass	pass	pass	pass
00077E1D	2208122	2208117	0.011851102402094	0.00021	0.80025760208443	pass	pass	1202021	0.000689	pass	0.312103898143481	pass	pass	pass	pass
00077E41	4476238	4284181	0.0116730208312053	0.00406	0.80279182925252	pass	pass	1202021	0.052188	pass	0.30211208881028	pass	pass	pass	pass
00077EAC	3475400	3416295	0.010802393120705	0.000884	0.78784607781891	pass	pass	1202021	0.052514	pass	0.3068176021488453	pass	pass	pass	pass
00077E0F	1260786	2844455	0.011443217102116	0.000201	0.8217417011658	pass	pass	1202021	0.056403	pass	0.296716261050057	pass	pass	pass	pass
00077E07	2865547	2891900	0.011206464575505	0.00075	0.78611918998962	pass	pass	1202021	0.056884	pass	0.3028410843434028	pass	pass	pass	pass
00077E0E	9729221	9336878	0.011804473239993	0.00757	0.824804372208116	pass	pass	1202021	0.0417072	pass	0.320004020550689	pass	pass	pass	pass
00077EAD	2160900	2105685	0.0114081071432317	0.00044	0.80437398494548	pass	pass	1202021	0.030968	pass	0.312174145896151	pass	pass	pass	pass
00077EAC	232904	2198543	0.0110257916468138	0.00079	0.80881180540508	pass	pass	1202021	0.019414	pass	0.28441789238113	pass	pass	pass	pass
00077E05	2020119	581667	0.01102023886101	0.00138	0.80210820011644	pass	pass	1202021	0.048823	pass	0.29800037246734	pass	pass	pass	pass
00077E0A	332506	3208819	0.0123729135814961	0.0001	0.80515219155239	pass	pass	1202021	0.024737	pass	0.31448884720978	pass	pass	pass	pass
00077E0C	2170785	2714257	0.011246069118738	0.00417	0.81165157268187	pass	pass	1202021	0.051704	pass	0.324505050202098	pass	pass	pass	pass
00077E0B	2149597	2102846	0.0118026778915007	0.00129	0.79686931970276	pass	pass	1202021	0.059752	pass	0.2975489842109	pass	pass	pass	pass
00077E0E	4720197	4684179	0.011281848164	0.00408	0.80386216748686	pass	pass	1202021	0.0487008	pass	0.29023088450734	pass	pass	pass	pass
00077E1D	4884002	4811006	0.0107214871891977	0.00404	0.79887774673713	pass	pass	1202021	0.0471719	pass	0.3177094186021	pass	pass	pass	pass
00077EAC	2448699	2893899	0.0112317233551752	0.00044	0.808916221108513	pass	pass	1202021	0.054804	pass	0.29890030707071	pass	pass	pass	pass
00077E0F	2849187	2395189	0.0131408501167038	0.00701	0.813432762578164	pass	pass	1202021	0.056609	pass	0.312780284168083	pass	pass	pass	pass
00077E09	551188	5404439	0.0123203882189541	0.00061	0.81862860274008	pass	pass	1202021	0.047808	pass	0.319168603873787	pass	pass	pass	pass
00077E08	4822840	4782636	0.0110271912118863	0.00027	0.819895020919448	pass	pass	1202021	0.047808	pass	0.3266007819741	pass	pass	pass	pass
00077E0B	2229703	2182242	0.0122023544446803	0.00489	0.807863037177795	pass	pass	1202021	0.0584239	pass	0.30287998150584	pass	pass	pass	pass
00077E0A	2790608	2744811	0.0114473311327058	0.00026	0.80034843008316	pass	pass	1202021	0.0502878	pass	0.318816027760716	pass	pass	pass	pass
00077E1D	3884847	3895847	0.0110460091470711	0.00471	0.802386119611802	pass	pass	1202021	0.0818033	pass	0.31170191868008	pass	pass	pass	pass
00077E1B	2780548	2773882	0.0132058848440288	0.00088	0.81447580314206	pass	pass	1202021	0.0487802	pass	0.298881124486705	pass	pass	pass	pass
00077E1A	4810056	4828891	0.010501814004054	0.00485	0.811728304142812	pass	pass	1202021	0.0480051	pass	0.32278431338548	pass	pass	pass	pass
00077E1E	2627687	2573237	0.0120421487148857	0.00029	0.78789048948908	pass	pass	1202021	0.072296	pass	0.30662734148649	pass	pass	pass	pass
00077E0D	2060140	1888175	0.0110271088671217	0.00194	0.784431870231428	pass	pass	1202021	0.0670105	pass	0.304162082818181	pass	pass	pass	pass
00077E0E	2486034	2415455	0.0128028143824819	0.00032	0.81905141788552	pass	pass	1202021	0.058059	pass	0.308810882022031	pass	pass	pass	pass
00077E07	2180202	2106887	0.011873380227738	0.00006	0.8027420300793	pass	pass	1202021	0.0547332	pass	0.3094708323203	pass	pass	pass	pass
00077E07	1204021	6891972	0.010121718104871381	0.00071	0.800004879070264	pass	pass	1202021	0.0442137	pass	0.2104323321781418	pass	pass	pass	pass
00077E07	4812645	3844005	0.0108612238311837	0.00406	0.79481341688391	pass	pass	1202021	0.0513688	pass	0.28381686117783	pass	pass	pass	pass
00077E09	2338877	2488508	0.0115370197295705	0.00138	0.787780489488313	pass	pass	1202021	0.056507	pass	0.311720080200587	pass	pass	pass	pass
00077E0C	3848507	3823124	0.0121670204602116	0.00280	0.81558155011627	pass	pass	1202021	0.050042	pass	0.29612088818873	pass	pass	pass	pass

Genotyping Log Table



Directory Structure

Pipeline with Docker - step1 preparation

AWS

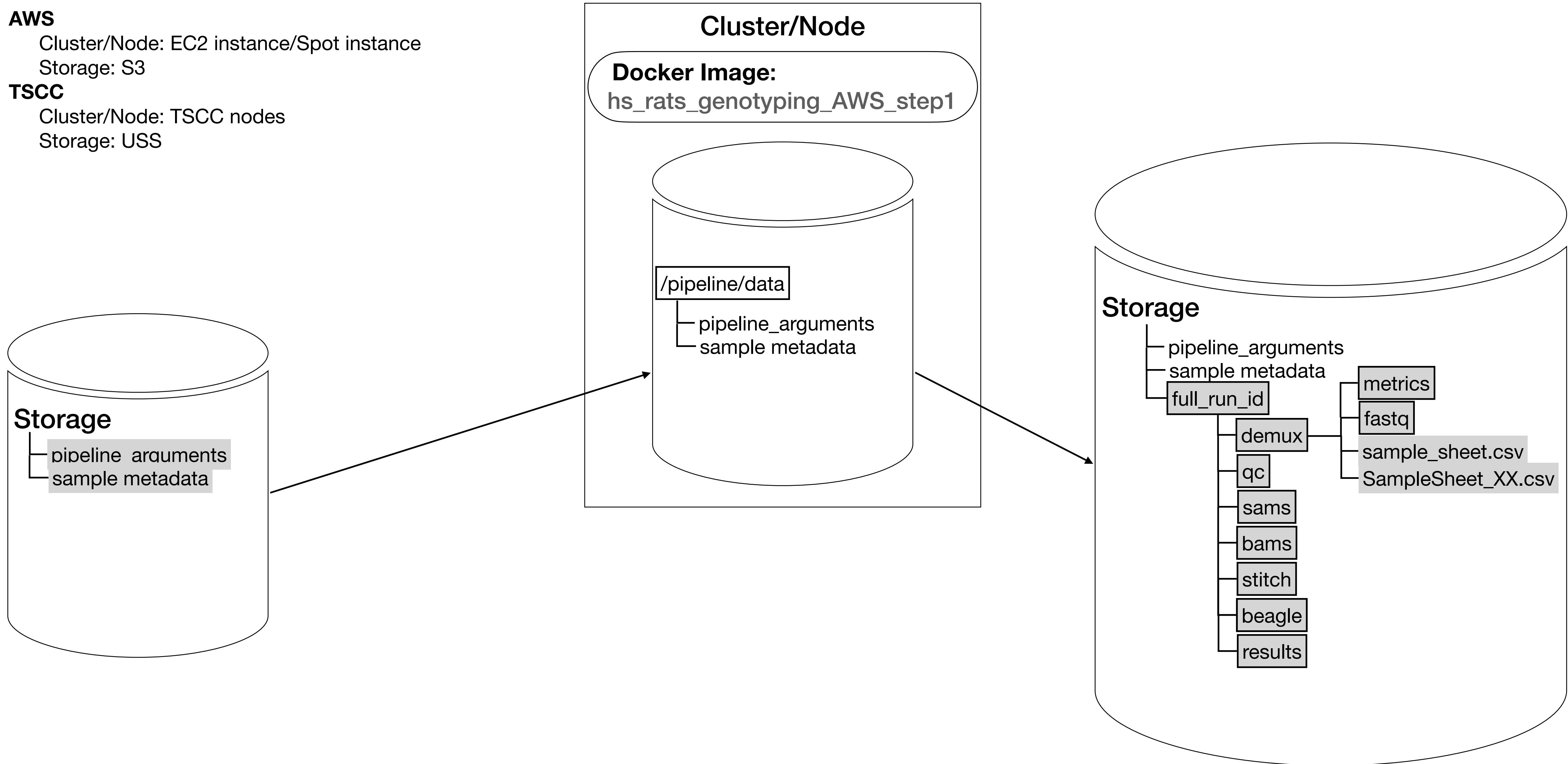
Cluster/Node: EC2 instance/Spot instance

Storage: S3

TSCC

Cluster/Node: TSCC nodes

Storage: USS



Pipeline with Docker - step2 demultiplex

AWS

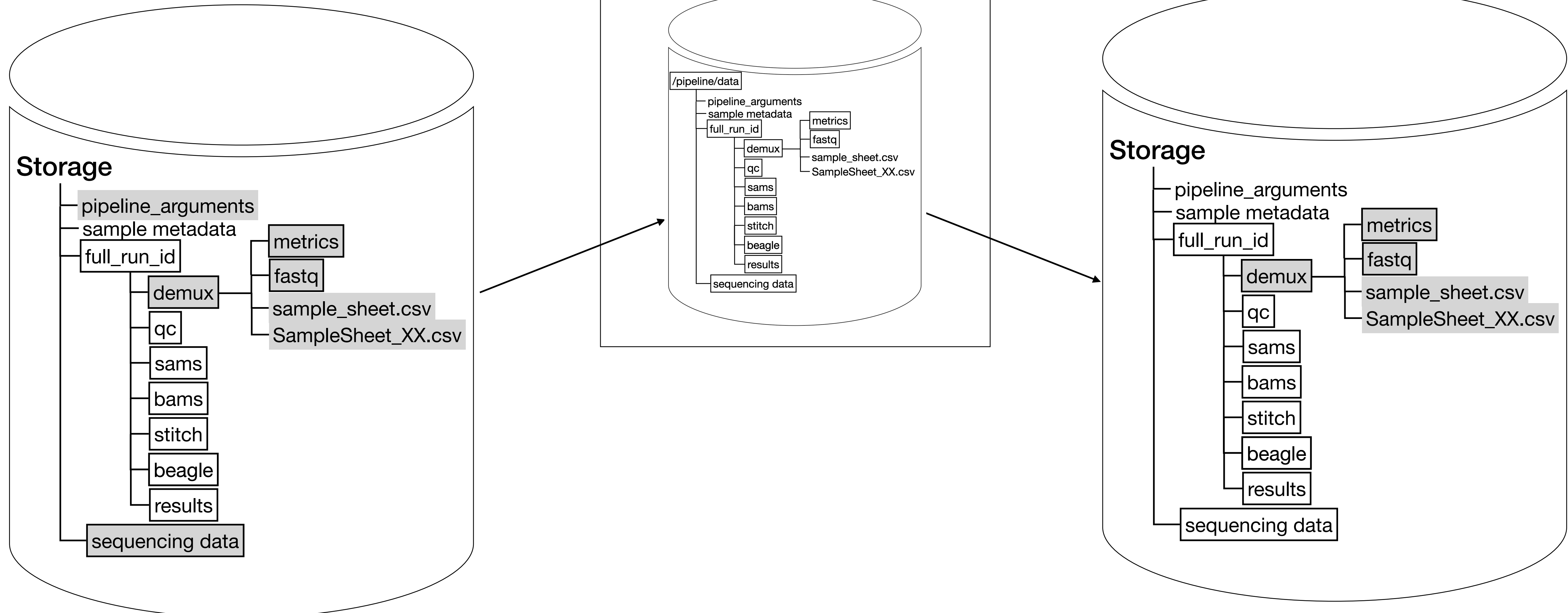
Cluster/Node: EC2 instance/Spot instance

Storage: S3

TSCC

Cluster/Node: TSCC nodes

Storage: USS



Pipeline with Docker - step3 alignment

AWS

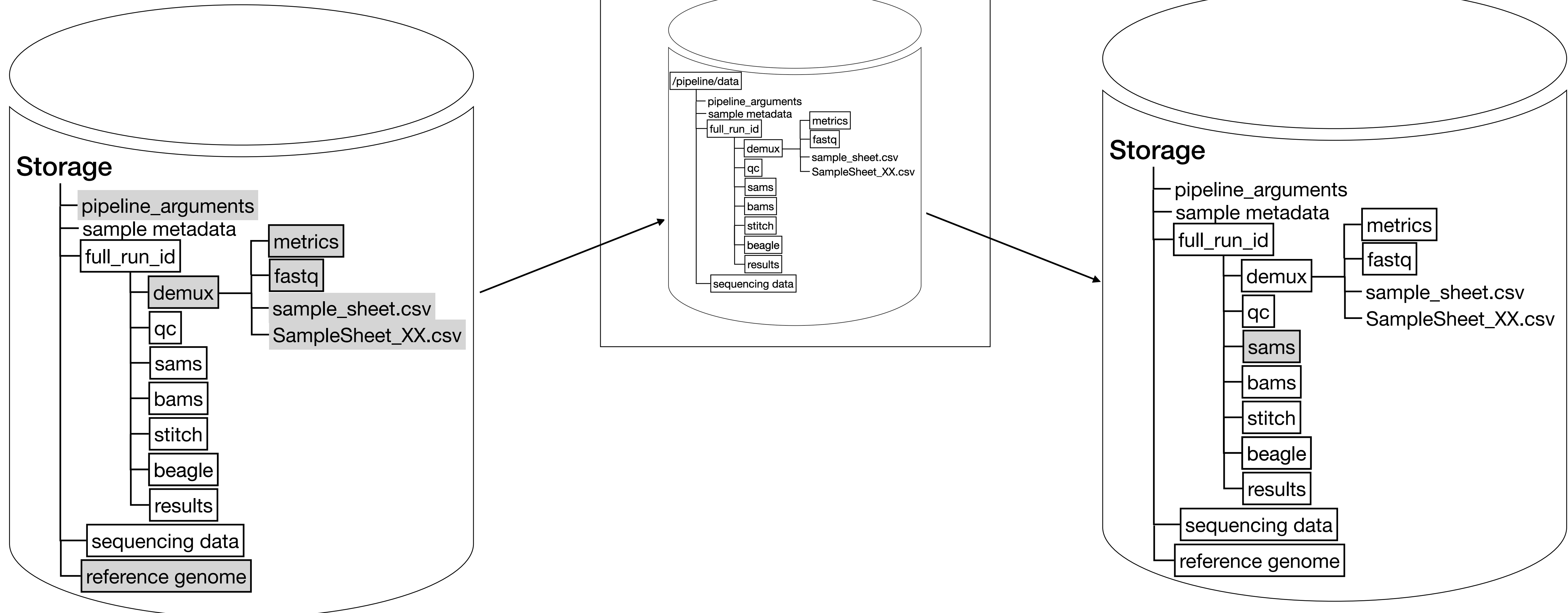
Cluster/Node: EC2 instance/Spot instance

Storage: S3

TSCC

Cluster/Node: TSCC nodes

Storage: USS



Pipeline with Docker - step4 mark duplicates

AWS

Cluster/Node: EC2 instance/Spot instance

Storage: S3

TSCC

Cluster/Node: TSCC nodes

Storage: USS

