dnaseq.py -t mugqic

Legend:
- Hexagon: Step per reasdet
- Filled hexagon: Step on multiple reasets/samples
- File
- Arrow: Input/output
- Circle arrow: Alternative entry
- Dash-dot arrow: Step dependency

Files:
- .bam
- .fastq

Steps:
1. Picard Sam to Fastq
2. Skewer trimming
3. Bwa mem picard sort sam
4. Sambamba merge sam files
5. Gatk indel realigner
6. Sambamba merge realigned
7. Fix mate by coordinate
8. Picard mark duplicates
9. Recalibration
10. sym link final bam
11. Metrics dna picard metrics
12. Metrics dna sample qualimap
13. Metrics dna sambamba flagstat
14. Metrics dna fastqc
15. Picard calculate hs metrics
16. Gatk callable loci
17. Extract common snp freq
18. Baf plot
19. Gatk haplotype caller
20. Merge and call individual gvcf
21. Combine gvcf
22. Merge and call combined gvcf
23. Variant recalibrator
24. Haplotype caller filter nstretches
25. Haplotype caller flag mappability
26. Haplotype caller snp id annotation
27. Haplotype caller snp effect
28. Haplotype caller dbnsfp annotation
29. Haplotype caller metrics vcf stats
30. Haplotype caller metrics snv graph metrics