MouseTrap2.sh processing details

Schematic is for optimized pipeline

Legend:
- Tool
- Intermediate Results
- Principal Results

Optional (-b)

BAM → samtools sort | samtools fastq → *samp*_1.fastq.gz, *samp*_2.fastq.gz

*samp*_1.fastq.gz, *samp*_2.fastq.gz → bwa mem | samtools view | samtools sort → human.sort.bam

*samp*_1.fastq.gz, *samp*_2.fastq.gz → bwa mem | samtools view | samtools sort → mouse.sort.bam

human.sort.bam, mouse.sort.bam → disambiguate

disambiguate →
- *samp*.disambiguatedSpeciesA.bam
- *samp*.disambiguatedSpeciesB.bam
- *samp*.ambiguousSpeciesA.bam
- *samp*.ambiguousSpeciesB.bam
- *samp*.summary.txt

samp.disambiguatedSpeciesA.bam → samtools sort | samtools fastq → *samp*.disam_1.human.fastq.gz, *samp*.disam_2.human.fastq.gz

samp.disam_1.human.fastq.gz, *samp*.disam_2.human.fastq.gz → bwa mem | picard SortSam → *samp*.SortSam.out

samp.SortSam.out → picard MarkDuplicates →
- *samp*.disambiguate_human.bam
- picard.remdup.metrics.txt

samp.disambiguate_human.bam → samtools index → *samp*.disambiguate_human.bam.bai