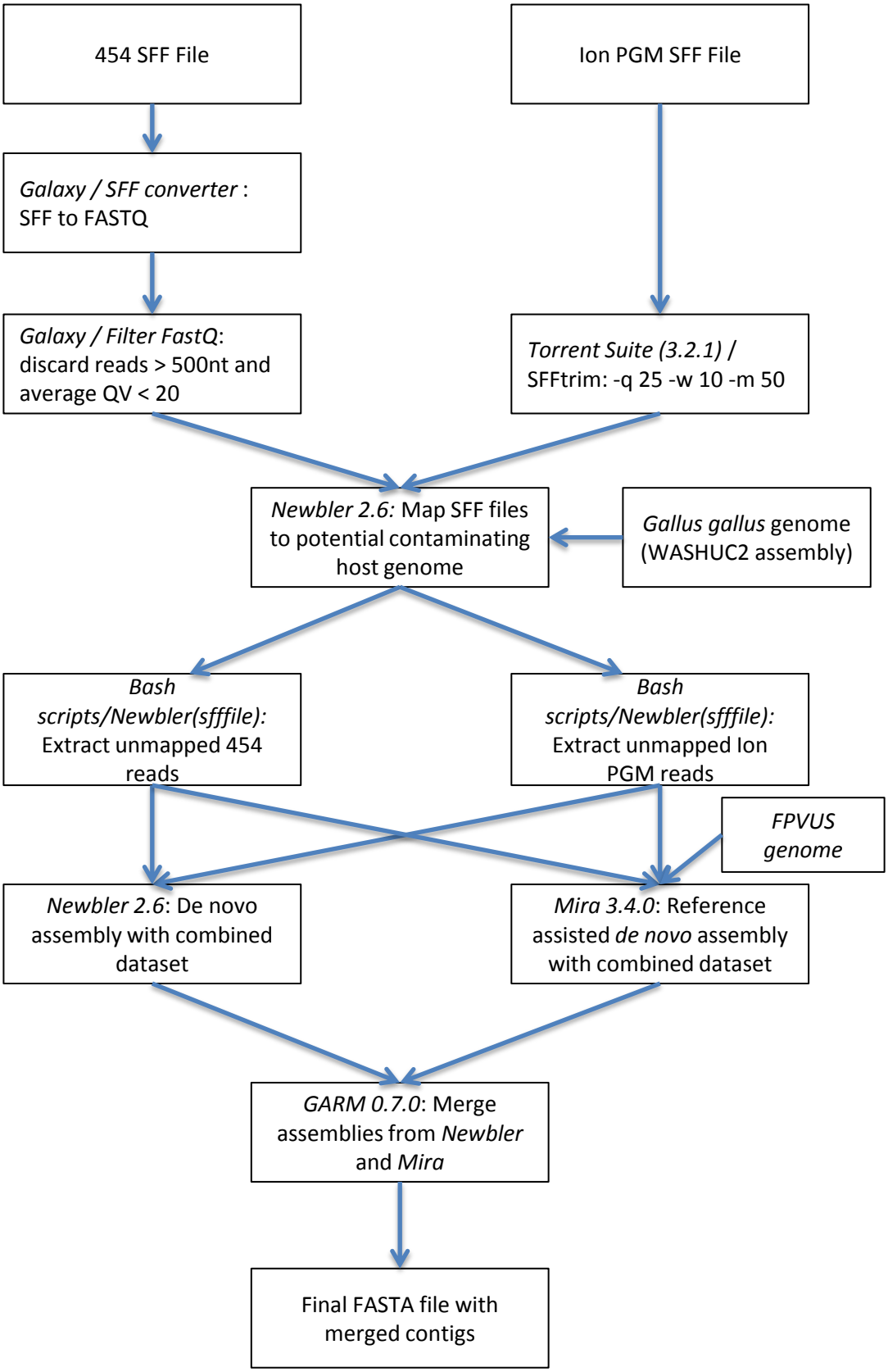
454 SFF File
Ion PGM SFF File
Galaxy / SFF converter : SFF to FASTQ
Galaxy / Filter FastQ: discard reads > 500nt and average QV < 20
Torrent Suite (3.2.1) / SFFtrim: -q 25 -w 10 -m 50
Newbler 2.6: Map SFF files to potential contaminating host genome
Gallus gallus genome (WASHUC2 assembly)
Bash scripts/Newbler(sfffile): Extract unmapped 454 reads
Bash scripts/Newbler(sfffile): Extract unmapped Ion PGM reads
FPVUS genome
Newbler 2.6: De novo assembly with combined dataset
Mira 3.4.0: Reference assisted *de novo* assembly with combined dataset
GARM 0.7.0: Merge assemblies from *Newbler* and *Mira*
Final FASTA file with merged contigs