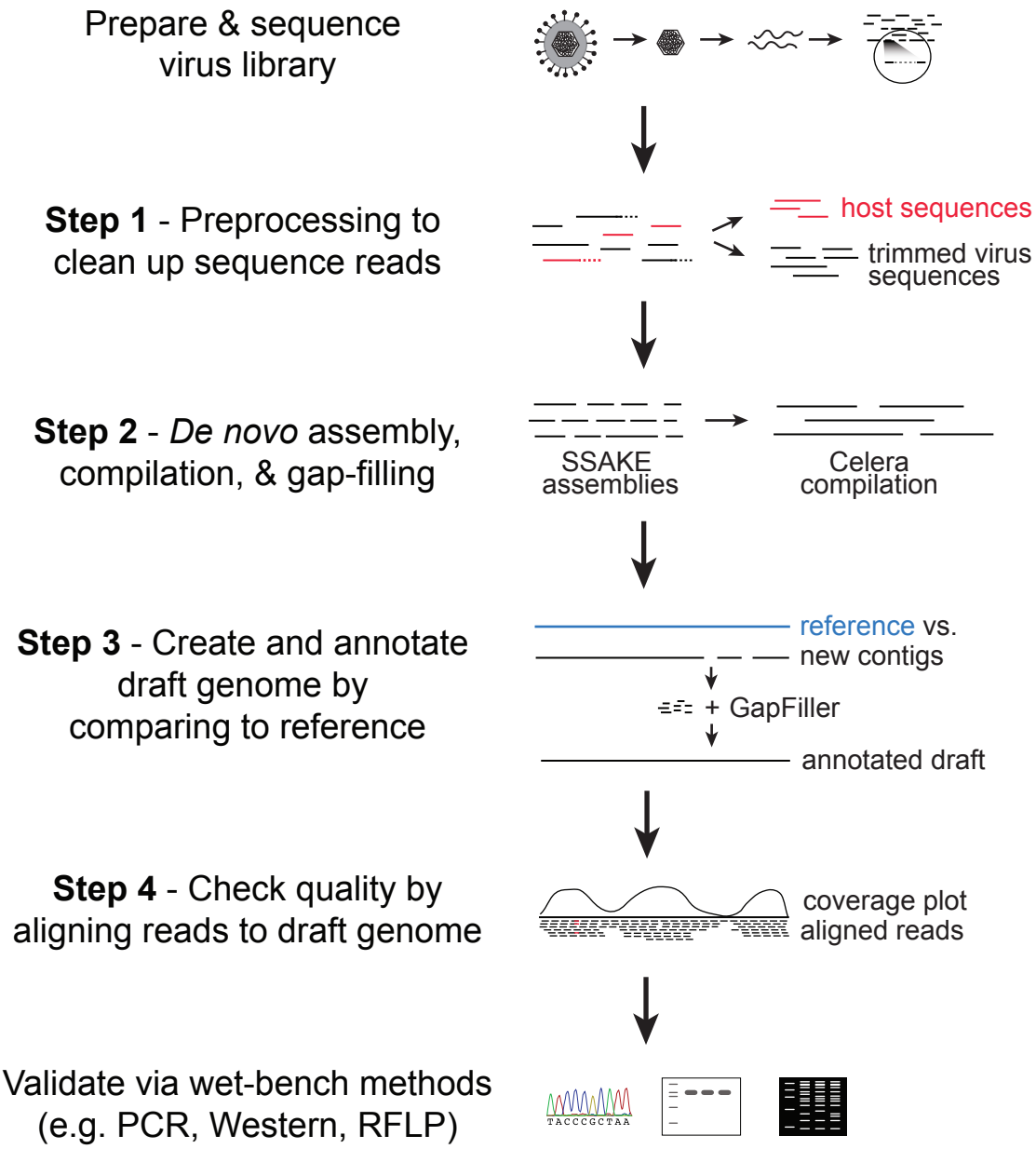
Supplemental Figure S3. Overview of HSV genome sequencing using the Viral Genome Assembly (VirGA) workflow.



Parsons *et al., mBio* (2015).
Rapid genome assembly and comparison decodes intra-strain variation in human alpha-herpesviruses

Supplemental Figure S3. Overview of HSV genome sequencing using the Viral Genome Assembly (VirGA) workflow. The VirGA workflow requires an input of high-throughput Illumina sequence read data from the viral genome of interest. We generate this by expanding a viral stock, isolating viral nucleocapsid DNA, preparing a library of genome fragments, and collecting high-throughput, paired-end sequence reads using an Illumina HiSeq or MiSeq instrument. In VirGA **Step 1**, host sequences and quality-reducing contaminants are removed. In **Step 2**, the viral sequences are assembled into long stretches of continuous sequence (contigs) by the use of two de novo assemblers, SSAKE and Celera. In **Step 3**, these long stretches of sequence are arranged in order by comparison to a reference genome. Gaps can be closed by using the GapFiller™ program to search for overlapping sequences in the input data. Annotations are transferred from the reference genome to the new draft genome at this stage. In **Step 4**, the original sequence reads are aligned to the draft consensus to check the assembly quality. Best practices in HSV genome assembly involve wet-bench validations of each assembly, such as PCR verification of key differences or RFLP analysis of genome orientation.

Parsons *et al., mBio* (2015).
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