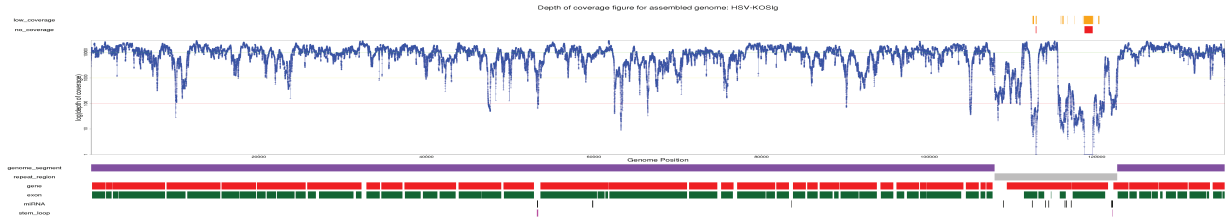
Supplemental Figure S4. Excerpts from a VirGA output summary.

====VirGA HSV-KOSLarge Report Summary====

Genome name	HSV-KOSlg.fa
Genome annotation	HSV-KOSlg.gff
Genome length (trimmed)	135295 bp
Genome name (with TRL/TRS)	full-length_HSV-KOSlg.fa
Genome annotation (with TRL/TRS)	full-length_HSV-KOSlg.gff
Genome length (with TRL/TRS)	150147 bp
Number of bases with >=100 depth support	129239 (95.52%)

Number of gaps	4
Number of Ns	1081
Complete protein annotations	70
Incomplete protein annotations	4
Reference name	HSV-17_trimmed.fa
Reference annotation	HSV-17_trimmed.gff

Coverage plot demonstrating read depth across the new genome



The following proteins were correctly assembled and annotated from the HSV-KOSlg genome

gene_RL1: Gene|ORF|AA No errors	gene_UL1: Gene|ORF|AA No errors	gene_UL2: Gene|ORF|AA No errors
gene_UL3: Gene|ORF|AA No errors	gene_UL4: Gene|ORF|AA No errors	gene_UL5: Gene|ORF|AA No errors
gene_UL6: Gene|ORF|AA No errors	gene_UL7: Gene|ORF|AA No errors	gene_UL8: Gene|ORF|AA No errors

Proteins requiring review due to potential assembly defects or substantial biological variation:

gene_RL2: Gene|ORF|AA (Gaps found)

gene_RS1: Gene|ORF|AA (Deviation of percent identity is >= 20%) (Gaps found)

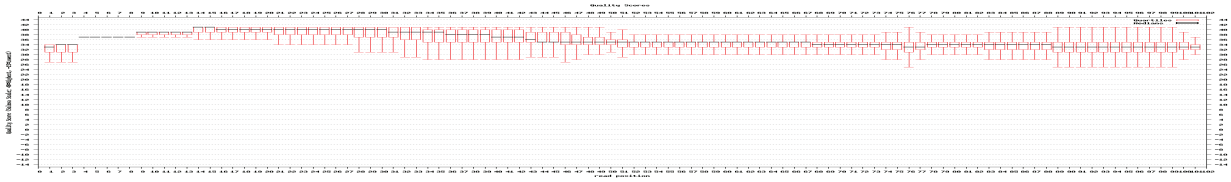
The following genome features are not proteins and were aligned to the reference for comparison

gene_LAT: None	gene_US12_start_in_IRS: DNA	hsv1-mir-H1: DNA
hsv1-mir-H2: DNA	hsv1-mir-H3: DNA	hsv1-mir-H4: DNA

===VirGA Detailed Report===

Procedure: 'after_stats'

Purpose: Create histograms of raw read quality and other metrics



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

Supplemental Figure S4. Example of a VirGA output summary. As part of its output, VirGA generates an interactive html file for each draft genome assembly, which can be opened in any web browser. This file summarizes statistics about the assembly, and links to additional files. This image includes excerpted sections from a full VirGA output. Complete records of all VirGA outputs from this paper are archived at: https://scholarsphere.psu.edu/collections/sf268c193. The "VirGA Report Summary" includes statistics about the new draft genome, such as length, percent with coverage depth >100-fold, number of gaps, and number of intact (gap-free) proteins. Links are provided to alignments of each gene and protein vs. the reference genome; these are grouped into those without errors (green text) and those needing user attention (red text). Alignments for non-coding features are included as well. Below the summary, an extensive "VirGA detailed report" includes statistics on the number of sequence reads filtered out during the preprocessing steps, the number of contigs produced during SSAKE and Celera assembly, the gaps closed by GapFiller, and the results of quality assessment when the sequence reads are aligned to the new draft genome. From this extensive summary, only a histogram of sequence read quality per base is shown here.

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