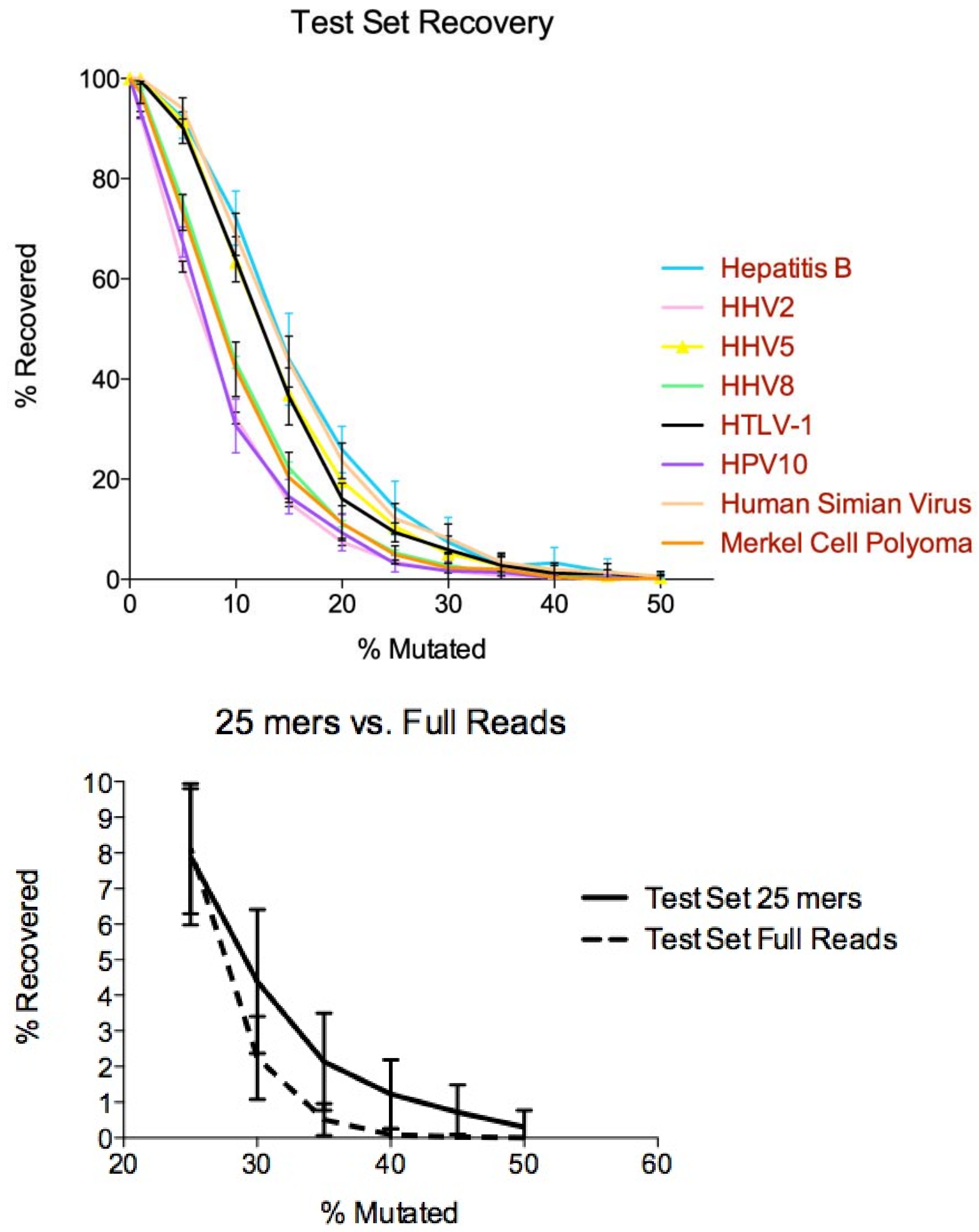

**Figure S1.** Highly mutated genomes can be identified with RINS. a) Genomes from 8 viruses (Hepatitis B, Human herpesvirus 2, Human papilloma virus 10, Merkel Cell Polyomavirus, Human herpesvirus 5, Human Simian Immunodeficiency virus, Human herpesvirus 8, Human T-lymphotrophic virus 1) were each randomly mutated at rates ranging from 1 to 50 %, and the genome was divided into mate paired reads. These reads were used as the template for RINS. Reads could be correctly identified at 35% mutation for all genomes, with some iterations still producing correct identification for all genomes even at 50% mutation. (Error bars shown as mean ± SD, n=10). b) Using sectioned reads improves sensitivity of detecting mutated genomes. Read sets generated from the 8 mutated genomes were tested with RINS after sectioning versus full reads. 25 mer reads were on average significantly more sensitive at identifying the virus ($p < 0.001$) at mutation levels above 25%.

Table S1. RINS accurately generates contigs of verifiable nonhuman sequence on a positive control dataset (SRR073726).

| Step Completed | Reads Remaining | Percent of Total (%) |
|---|---|---|
| Number of Total Reads | 13,654,861 | 100 |
| Blat | 37,364 | 0.27 |
| LZW Compression | 34,785 | 0.25 |
| Alignment to Human | 34,785 | 0.25 |
| Contig Generation | 14,458 | 0.08 |

**Table S2.** Contigs generated by RINS.

| |
|---|
| Human Papillomavirus Serotype 18, CA_HPV_10 cells  (from SRR073726) |
| TTGTACATAAAACCAGCCGTTACAACCCGTGCCCTCCCCGTCTGTACCTTCTGGATCAGCCATTGTTGCTTACTGCTGGGATGCACACCACGGACACACAAAGGACAGGGTGTTCAGAAACAGCTGCTGGAATGCTCGAAGGTCGTCTGCTGAGCTTTCTACTACTAGCTCAATTCTGGCTTCACACTTACAACACATACACAACATTGTGTGACGTTGTGGTTCGGCTCGTCGGGCTGGTAAATGTTGATGATTAACTCCATCTATTTCATCGTTTTCTTCCTCTGAGTCGCTTAATTGCTCGTGACATAGAAGGTCAACCGGAATTTCATTTTGGGGCTCTAAATGCAATACAATGTCTTGCAATGTTGCCTTAGGTCCATGCATACTTAATATTATACTTGTGTTTCTCTGCGTCGTTGGAGTCGTTCCTGTCGTGCTCGGTTGCAGCACGAATGGCACTGGCCTCTATAGTGCCCAGCTATGTTGTGAAATCGTCGTTTTTCATTAAGGTGTCTAAGTTTTTCTGCTGGATTCAACGGTTTCTGAAATTCCGGTTGACCTTCTATG |
| Laboratory contaminant with homology to HIV and lentiviral constructs (from SRA046736) |
| TTATGAGGAAAGGACAGTGGGAGTGGCACCTTCCAGGGTCAAGGAAGGCACGGGGGAGGGGCAAACAACAGATGGCTGGCAACTAGAAGGCACAGTCGAGGCTGATCAGCGGGTTTAAACAATGTCAAGGCCTCTCACTCTCTGATATTCATTTCTTTGCAAGTTATAAATACTGAATAATAAGATGACATGAACTACTACTGCTAGAGATTTTCCACACTGACTAAAAGGGTCTGAGGGATCTCTAGTTACCAGAGTCACACAACAGACGGGCACACACTACTTGAAGCACTCAAGGCAAGCTTTATTGAGGCTTAAGCAGTGGGTTCCCTAGTTAGCCAGAGAGCTCCCAGGCTCAGATCTGGTCTAACCAGAGAGACCCAGTACAAGCAAAAAGCAGATCTTGTCTTCGTTGGGAGTGAATTAGCCCTTCCAGTCCCCTCTTTTCTTTTAAAAAGTGGCTAAGATCTACAGCTGCCTTGTAAGTCATTGGTCTTAAAGGTACCTGAGGTGTGACTGGAAAACCCACCTCCTCCTCCTCTTGTGCTTCTAGCCAGGCACAATCAGCATTGGTAGCTGCTGTATTGCTACTTGTGATTG<br>CTCCATGTTTTTCTAGGTCTCGACTGCAGAATTAATT |