**S2 METHODS. Vipie platform (1) analysis parameters.**

1. Quality control
	1. Trim left/right: 10 / 10
	2. Qual cutoff: 10
	3. Insert/read length: 150
	4. MAPQ/Phred: 10
	5. Subsample: 0.80
2. De novo assembly
	1. De novo assembly algorithm: Velvet
	2. Amos: No
	3. Kmer length: 31
	4. Expected coverage/cutoff: auto / 20
	5. Min contig length: auto
3. BLAST parameters
	1. Min percent similar: 80
	2. E value: 0.0001
	3. Number of alignments: 10
4. REMAP/Reduction parameters
	1. Minimum total matches: 2
	2. Remapping of hits PER: 1,000,000
	3. Apply blacklist (vector/synthetic refs): yes
	4. Remove ribosomes (bacteria/others): yes
5. Viral Dark Matter
	1. Allow unmapped viral reads for further analysis: yes

**REFERENCES**

1. Lin J, Kramna L, Autio R, Hyoty H, Nykter M, Cinek O. Vipie: web pipeline for parallel characterization of viral populations from multiple NGS samples. BMC Genomics. 2017;18(1):378.