Table S5

Table S5: CheckV result on individual assemblies. Distribution of contig quality identification by CheckV in regards to phage genome completeness for each of the 11 assemblies

Assembly	Complete/high	Medium	Low	Not determined	Total vOTUs
Baseline metaSPAdes (Assembly 1)	29	51	12,274	2,434	14,788
DC3000 + metaSPAdes (Assembly 2)	17	31	9,865	1,532	11,445
DC3000 + A metaSPAdes (Assembly 3)	6	19	3,805	492	4,916
DC3000 + B metaSPAdes (Assembly 4)	7	20	4,346	582	4,955
DC3000 + C metaSPAdes (Assembly 5)	5	11	2,941	385	3,342
DC3000 – metaSPAdes (Assembly 6)	26	52	17,504	3,204	20,786
DC3000 – A metaSPAdes (Assembly 7)	15	19	7,060	1,048	8,142
DC3000 – B metaSPAdes (Assembly 8)	9	28	6,808	899	7,744
DC3000 – C metaSPAdes (Assembly 9)	12	23	6,912	1,044	7,991
All samples Hybrid metaSPAdes (Assembly 10)	132	196	29,751	6,401	36,480
Baseline Canu (Assembly 11)	116	171	1,595	122	2,004