

Table S4. Newbler assembly statistics for the samples. Individual assemblies at two different minimum nucleotide identity thresholds (96% and 86%) were computed.

	NY_INDOOR	NY_OUTDOOR	SD_IHOSP	SD_OHOSP	SD_IHOUS	SD_SCRPP
Input Reads	1,433,624	961,778	577,705	824,114	391,761	1,153,701
Input Bases	502,582,263	293,707,031	203,995,362	242,186,832	123,622,093	336,367,571
Assembled Reads	101,165	134,720	376,915	237,068	195,626	229,096
Assembled Bases	24,808,957	28,987,750	139,152,571	78,456,095	70,184,338	69,211,834
%Assembled Reads	7.06%	14.01%	65.24%	28.77%	49.94%	19.86%
%Assembled Bases	4.94%	9.87%	68.21%	32.39%	56.77%	20.58%
#contigs	9119	10573	24,697	21,424	14,383	28,282
Average Contig size	854	791	808	646	685	789
N50 Contig size	869	765	722	589	642	740
#contigs >500 bp	4283	4070	12,884	11,312	7,902	11,130
Largest Contig size	5471	3699	42,057	6,830	11,323	8,678

(A) 96% identity threshold

	NY_INDOOR	NY_OUTDOOR	SD_IHOSP	SD_OHOSP	SD_IHOUS	SD_SCRPP
Input Reads	1,433,624	961,778	577,705	824,114	391,761	1,153,701
Input Bases	502,582,263	293,707,031	203,995,362	242,186,832	123,622,093	336,367,571
Assembled Reads	122,561	164,179	379,767	247,730	200,480	242,346
Assembled Bases	29,327,426	35,836,449	139,649,082	81,066,905	71,300,383	72,400,290
%Assembled Reads	8.55%	17.07%	65.74%	30.06%	51.17%	21.01%
%Assembled Bases	5.84%	12.20%	68.46%	33.47%	57.68%	21.52%
#contigs	11227	13674	25,062	24,078	15,107	31,701
Average Contig size	856	799	808	658	701	793
N50 Contig size	874	784	725	601	659	744
#contigs >500 bp	5252	5631	13,018	12,359	8,238	12,059
Largest Contig size	5645	4058	42,057	6,832	11,323	8,593

(B) 86% identity threshold