## a5 Assembly Stats

File Name	Contigs	Scaffolds	Genome Size	Longest Scaffold	N50	Raw Reads	EC Reads	% Reads Passing EC	Raw nt	EC nt	% nt passing EC	Raw Cov.	EC Cov.	Median Cov. 10th Per	rcentile Cov.	Bases >= Q40 %	6 GC	Runtime	_
ATCC_31615	30	5 25	5 9,123,520	6 1,579,490	947,108	6,376,808	6,120,268	95.98	1,913,042,400	1,324,218,266	69.2	209.68	145.14	128	90	8,954,890	7:	l. <b>1</b> 5:1	14
BKM_A840	236	0 233	1 9,775,54	5 704,664	280,754	15,984,844	15,396,825	96.32	4,795,453,200	3,360,311,933	70.0	490.56	343.75	367	2	7,896,772	7:	1.8 14:3	30
BKM (norm)	12	0 9	8 7,754,948	8 981,968	3 447,215	7,197,432	7,196,183	99.98	1,571,351,722	1,571,307,956	99.99	202.63	202.62	199	180	7,717,832	72	2.2 6:2	22
DSM_40763	17	8 16	2 8,090,646	6 804,804	488,914	4,517,426	4,335,036	95.96	1,355,227,800	894,127,750	65.9	167.51	110.51	100	70	7,999,729	72	2.6 3:5	58
H021	63	1 60	0 8,936,389	9 1,609,583	498,848	8,047,424	7,727,689	96.03	2,414,227,200	1,682,127,738	69.6	3 270.16	188.23	177	137	8,482,395	7:	1.3 6:2	26
H021 (norm)	8	1 5	7 8,470,51	1,610,840	552,887	5,981,342	5,980,277	99.98	1,304,491,716	1,304,453,870	99.99	9 154	154	147	132	8,459,074	7:	1.5 5:1	15
PGAG4	9	2 6	6 9,040,703	3 1,889,106	1,237,475	7,894,854	7,629,881	96.64	2,368,456,200	1,666,553,376	70.30	261.98	184.34	151	119	9,009,106	71	1.5 6:3	30

## Raw Stats

Sample	Yield (Mbp)	Clusters	%Q30	Mean Q
ATCC_31615	1,913	3,188,404	63.15	27.02
BKM_A840	4,795	7,992,422	64.27	27.38
DSM_40663	1,355	2,258,713	62.71	26.62
H021	2,414	4,023,712	64.38	27.37
PGAG4	2,368	3,947,427	64.66	27.5
	12,845	21,410,678		

<sup>\* 5</sup> samples on 1 lane of MiSeq 2x300bp v3

## Taxonomy Info

Strain	Tax ID	Species
ATCC_31615	33899	S. galilaeus
BKM_A840	1914	S. lavendulae
DSM_40663	67257	S. albus
H021	1519486	?
DCVCA	2	2

<sup>\*</sup> Yield = Clusters x 300bp x 2 (PE)