

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 Percentile Cov.	Bases >= Q40	% GC	Runtime
ATCC_31615	305	305	9,115,013	1,573,165	339,243	6,376,808	6,120,268	95.98	1,913,042,400	1,324,218,266	69.22	209.88	145.28	174	123	8,960,535	71.1	5:10
BKM_A840	2360	2360	9,721,547	700,630	240,716	15,984,844	15,396,825	96.32	4,795,453,200	3,360,311,933	70.07	493.28	345.66	488	3	8,069,790	71.8	14:33
DSM_40763	178	178	8,087,573	798,222	386,799	4,517,426	4,335,036	95.96	1,355,227,800	894,127,750	65.98	167.57	110.56	132	94	8,002,307	72.6	3:34
H021	631	631	8,922,734	761,529	309,232	8,047,424	7,727,689	96.03	2,414,227,200	1,682,127,738	69.68	270.57	188.52	232	187	8,500,802	71.3	7:05
PGAG4	92	92	9,039,361	1,092,651	395,988	7,894,854	7,629,881	96.64	2,368,456,200	1,666,553,376	70.36	262.02	184.37	201	164	9,010,551	71.5	6:33

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		

* 5 samples on 1 lane of MiSeq 2x300bp v3
* Yield = Clusters x 300bp x 2 (PE)

Taxonomy Info

Strain	Tax ID	Species
ATCC_31615	33899	S. gallilaeus
BKM_A840	1914	S. lavendulae
DSM_40663	67257	S. albus
H021	1519486	?
PGAG4	?	?