

Supplemental Table 1. Sequencing Statistics

	454		Ion Torrent		Combined	
	CA	CA6	CA	CA6	CA	CA6
Total Reads	607,789	568,103	463,121	452,254	1,070,910	1,020,357
Used Reads (%)	606,450 (99.8%)	566,774 (99.8%)	424,539 (91.7%)	424,875 (93.9%)	1,030,989 (96.3%)	991,649 (97.2%)
Mean Read Length	412.2	429.5	214.3	214.2	330.7	337.2
	± 126.3	± 113.3	± 37.3	± 41	± 139.4	± 139.3
Read Length Range	40-597	40-595	14-394	14-393	14-597	14-595
Mean Depth	46.8 \pm 13	45.6 \pm 14.4	18.9 \pm 14.1	19.2 \pm 15.6	66.1 \pm 22.7	65.4 \pm 25.8
Depth Range	0-160	0-139	0-106	0-108	0-190	0-228
Coverage	47	46	17	17	64	63

Supplemental Table 2. Variations Discovered in Genome Comparison. Position column contains nucleotide position in DJ. * - stop codon. Variant Frequency refers to percentage of sequencing reads showing each variation.

Locus Tag	Gene Function	Position	CDS Position	Base/AA Change	Variant Frequency	
Mutations in CA6						
AvCA6_14900	Glycerol-3-phosphate acyltransferase	1470474	854/987	G:A/G:D	100%	
AvCA6_27910	Flagellar biosynthesis	2871708	1568/2085	G:A/E:*	100%	
		3868591		C:T	56%	
	many	5102868-5144962		-42095bp/many genes	100%	
Mutations in CA						
		500008		+ATTCCTTC	100%	
AvCA_11230	cation transporter	1072498	765/1071	+GACCAT/+DH	96%	
AvCA_12720	Peptidase, modulator of DNA gyrase	1240550	896/1443	C:T/Q:*	100%	
AvCA_18210	hypothetical protein	1805893	375/762	-GC/Frameshift	94%	
AvCA_24220	Flagellar motor switch	2417604	144/996	G:A/E:*	98%	
AvCA_36670	TolQ proton channel	3728269	481/696	G:A	100%	
		4686485		+1053bp	100%	
Mutations in DJ					CA	CA6
Avin_02860	Hypothetical	270373	163/369	C:T/P:L	98%	100%
		278677		C:T	100%	97%
Avin_06870	Hybrid histidine kinase	650766	2715/2802	G:C/H:D	100%	99%
Avin_06870	Hybrid histidine kinase	652277	807/2802	-AGGGCG/-AL	100%	100%
Avin_07570	Membrane bound protease regulator	716487	564/870	-CGCGAG/-RE	100%	100%
		1504215		-A	81%	78%
		2199316		+G	98%	97%
Avin_22710	Heavy metal translocating P-type ATPase	2265546	357/2160	G:A/A:T	100%	100%
		3182849		+TGGCGGATGGCGGA	100%	100%
Avin_33130	TonB-dependent vitamin B12 receptor	3387906	2009/3072	-G/Frameshift	97%	93%
Avin_40360	Chaperone HscA	4087773	1518/1866	+GCA/+L	100%	100%
Avin_44040	Enoyl-(Acyl carrier protein) reductase	4455982	601/783	C:T/P:L	100%	100%
		4492914		+C	98%	100%
Avin_45560	proline iminopeptidase	4626694	673/968	+CG/Frameshift	99%	100%

Avin_46380	major facilitator superfamily	4713376	1121/1558	+CATGAT/+IM	100%	100%
Avin_52160	F0F1 ATP synthase subunit beta	5330589	653/1377	G:A/A:V	99%	100%