

	EST6_S1_L001	OL6_S3_L001	OLDE56_S4_L001	PAL6_S2_L001
# N's per 100 kbp	0.00	0.00	0.00	0.00
# contigs	158962	167679	141461	149486
# contigs (>= 0 bp)	269259	301973	258605	249642
# contigs (>= 1000 bp)	54757	58359	48473	48551
# contigs (>= 10000 bp)	1072	1250	1221	966
# contigs (>= 25000 bp)	191	195	206	172
# contigs (>= 5000 bp)	3675	4427	4032	3271
# contigs (>= 50000 bp)	52	47	35	39
# indels per 100 kbp	20.97	21.81	19.20	17.99
# local misassemblies	45	88	76	42
# misassembled contigs	88	197	165	86
# misassemblies	95	208	175	87
# mismatches per 100 kbp	607.84	1138.29	898.12	572.64
# unaligned contigs	157539 + 165 part	160773 + 460 part	133578 + 380 part	147797 + 209 part
# unaligned mis. contigs	16	34	23	18
Duplication ratio	1.118	1.099	1.068	1.143
GC (%)				
Genome fraction (%)	91.090	51.230	46.366	91.833
L50	30186	30700	24667	28952
L75	78759	81888	68102	75390
Largest alignment	21582	18605	31325	23252
Largest contig	165310	114545	157288	100744
Misassembled contigs length	256679	323518	278508	202033
N50	1465	1515	1553	1380
N75	798	811	815	772
Reference length	3026645	15897113	20428964	3026645
Total aligned length	2936758	8646921	9773162	3035355
Total length	202801485	218444940	187250445	184564422
Total length (>= 0 bp)	245103504	268861328	231427448	223102892
Total length (>= 1000 bp)	130819175	142770228	122804017	115075522
Total length (>= 10000 bp)	21055547	23611474	23125246	18684516
Total length (>= 25000 bp)	8380598	8311228	8375220	7081355
Total length (>= 5000 bp)	38691783	45047082	42296213	34302308
Total length (>= 50000 bp)	3746286	3215821	2630751	2580626
Unaligned length	199827248	209653731	177344794	181490122
Reads aligned (%)	77.61	73.85	71.80	