

	4478-DNA-S1611-MiSeqKapa	4478-DNA-S1613-MiSeqKapa	4478-DNA-S1616-MiSeqKapa	4478-DNA-S1618-MiSeqKapa
# N's per 100 kbp	0.00	0.00	0.00	0.00
# contigs	2146	157032	122795	98115
# contigs (>= 0 bp)	7221	291686	233529	187446
# contigs (>= 1000 bp)	248	68066	51095	39442
# contigs (>= 10000 bp)	0	2678	1792	1323
# contigs (>= 25000 bp)	0	510	411	326
# contigs (>= 5000 bp)	3	7803	5311	3658
# contigs (>= 50000 bp)	0	151	128	87
# indels per 100 kbp	-	35.42	35.73	33.98
# local misassemblies	-	131	138	106
# misassembled contigs	-	154	163	165
# misassemblies	-	165	179	188
# mismatches per 100 kbp	-	1305.98	1437.66	1208.13
# unaligned contigs	-	153265 + 510 part	117791 + 560 part	95436 + 358 part
# unaligned mis. contigs	-	35	46	32
Duplication ratio	-	1.196	1.171	1.121
GC (%)	48.38			
Genome fraction (%)	-	90.597	73.359	88.469
L50	781	20152	16236	13882
L75	1409	62421	50397	41944
Largest alignment	-	33829	40875	37591
Largest contig	5527	336120	280276	228421
Misassembled contigs length	-	679002	650413	999161
N50	689	2559	2345	2070
N75	580	1073	1010	955
Reference length	-	7052336	10393517	7052336
Total aligned length	-	7399530	8682213	6768965
Total length	1579645	268718963	200790882	152000468
Total length (>= 0 bp)	3466605	319349253	242532181	185720540
Total length (>= 1000 bp)	363644	207382110	151295229	111556300
Total length (>= 10000 bp)	0	56469975	40848293	29490106
Total length (>= 25000 bp)	0	24600947	20480318	14804515
Total length (>= 5000 bp)	16316	91480253	64660508	45267832
Total length (>= 50000 bp)	0	12600805	10879697	6669939
Unaligned length	-	261224533	192001856	145144590
Reads aligned (%)	18.32	86.57	78.71	74.82