Re _l	port toy_r_k35	toy_r_k45
# contigs (>= 0 bp)	4	1
# contigs (>= 1000 bp)	0	1
# contigs (>= 5000 bp)	0	0
# contigs (>= 10000 bp)	0	0
# contigs (>= 25000 bp)	0	0
# contigs (>= 50000 bp)	0	0
Total length (>= 0 bp)	1136	1040
Total length (>= 1000 bp)	0	1040
Total length (>= 5000 bp)	0	0
Total length (>= 10000 bp)	0	0
Total length (>= 25000 bp)	0	C
Total length (>= 50000 bp)	0	C
# contigs	1	1
Largest contig	914	1040
Total length	914	1040
Reference length	1040	1040
GC (%)	51.64	51.25
Reference GC (%)	51.25	51.25
N50	914	1040
NG50	914	1040
N90	914	1040
NG90	314	1040
auN	914.0	1040.0
	1	
auNG	803.3	1040.0
L50	1	1
LG50	1	1
L90	1	1
LG90	-	1
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	87.885	100.000
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.00
# indels per 100 kbp	0.00	0.00
Largest alignment	914	1040
Total aligned length	914	1040
NA50	914	1040
NGA50	914	1040
NA90	914	1040
NGA90	-	1040
auNA	914.0	1040.0
auNGA	803.3	1040.0
	1	1
LA50		1
LA50 LGA50	1	
	1	1
LGA50		

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	toy_r_k35	toy_r_k45
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	0	0
# indels	0	0
# indels (<= 5 bp)	0	0
# indels (> 5 bp)	0	0
Indels length	0	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	toy_r_k35	toy_r_k45
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

























