R	۵	n	Λ	rt
г	ᆫ	v	v	ıι

# contigs (>= 0 bp) 634 625 # contigs (>= 1000 bp) 666 56 # contigs (>= 10000 bp) 38 29 # contigs (>= 25000 bp) 30 23 # contigs (>= 25000 bp) 22 19 # contigs (>= 25000 bp) 22 19 # contigs (>= 50000 bp) 20 16 Total length (>= 0 bp) 4174333 4174432 Total length (>= 1000 bp) 3939294 3938252 Total length (>= 10000 bp) 3812943 3834948 Total length (>= 10000 bp) 3812943 3834948 Total length (>= 50000 bp) 3812943 3839948  # contigs 157 149 Largest contig 384004 573239 Total length (>= 39000 bp) 3996348 3996360 Reference length 2961149 2961149 GC (%) 47.33 47.33 Reference GC (%) 47.70 47.70 N50 243364 350399 NG50 262473 508069 N75 105216 132765 NG75 216166 350399 L50 7 5 LG50 5 3 L75 13 99 LG75 8 5 # misassembled contigs 1 1 1 # misassembled contigs 1 1 1 # misassembled contigs 1 1 1 # scaffold gap ext. mis. 1 1 # scaffold gap ext. mis. 1 1 # unaligned mis. contigs 2 2 # unaligned length 1077789 1079151 Genome fraction (%) 98.284 98.288 # pupilication ratio 1.002 # N's per 100 kbp 1.239 12.39 # mismatches per 100 kbp 1.27 9.86 # indels per 100 kbp 2.10 2.10 Largest alignment 383873 573239 Total aligned length 2917031 2916589 NA50 215940 246267 NGA50 5 4 LGA75 9 6		report .	
# contigs (>= 1000 bp)		· -	
# contigs (>= 5000 bp) 38 29 # contigs (>= 10000 bp) 30 23 # contigs (>= 25000 bp) 22 19 # contigs (>= 50000 bp) 20 16 Total length (>= 0 bp) 4174333 4174432 Total length (>= 1000 bp) 3939294 3938252 Total length (>= 1000 bp) 3872333 3875815 Total length (>= 1000 bp) 3812943 3834948 Total length (>= 5000 bp) 3681650 3781002 Total length (>= 5000 bp) 3592797 3656854 # contigs 157 149 Largest contig 384004 573239 Total length (>= 50000 bp) 399348 3996360 Reference length 3996348 3996360 Reference length 2961149 2961149 GC (%) 47.33 47.33 Reference GC (%) 47.70 47.70 N50 243364 350399 NG50 262473 50869 NG50 262473 50869 L50 7 5 5 LG50 5 3 L75 105216 132765 NG75 216166 350399 L50 7 5 5 LG50 5 3 L75 13 99 L50 7 5 5 LG50 5 3 L75 13 99 L50 1 1 1 Misassembled contigs 1 1 1 1 Misassembled contigs 1 1 2 1 Misassembled 1 1 1 Misassembled 1 1 1 Misassembled 1 1 1 Misassembled 1 1 1 1 Misassembled 1 1 1 1 Misassembled 1 1 1 1 1 Misassembled 1 1 1 1 1 Misassembled 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
# contigs (>= 10000 bp) 30 23  # contigs (>= 25000 bp) 22 19  # contigs (>= 50000 bp) 20 16  Total length (>= 0 bp) 4174333 4174432  Total length (>= 1000 bp) 3939294 3938252  Total length (>= 50000 bp) 3872333 3875816  Total length (>= 10000 bp) 3812943 3834948  Total length (>= 50000 bp) 3812943 3834948  Total length (>= 50000 bp) 3681650 3781002  Total length (>= 50000 bp) 3592797 365685  # contigs 157 149  Largest contig 384004 573239  Total length (>= 39000 bp) 399294 3993600  Reference length 3996348 3996360  Reference length 2961149 2961149  GC (%) 47.33 47.33  Reference GC (%) 47.70 47.70  N50 243364 350399  NG50 262473 508069  N75 105216 132765  NG75 216166 350399  L50 7 5  LG50 5 3  L75 13 9  LG75 8 5  LG75 8 5  H misassembled contigs 1 1  # misassembled contigs 1 1  # misassembled contigs 1 1  # scaffold gap ext. mis. 1 1  # scaffold gap ext. mis. 1 1  # scaffold gap ext. mis. 1 1  # unaligned length 1077789 1079151  Genome fraction (%) 98.284 98.288  Duplication ratio 1.003 1.0002  # N's per 100 kbp 12.39 12.39  # mismatches per 100 kbp 2.10 2.10  Largest alignment 383873 573239  NG50 16800 15 44			
# contigs (>= 25000 bp)			
# contigs (>= 50000 bp)			
Total length (>= 0 bp)         4174333         4174432           Total length (>= 1000 bp)         3939294         3938252           Total length (>= 5000 bp)         3872333         3875816           Total length (>= 10000 bp)         3812943         3834948           Total length (>= 50000 bp)         3681650         3781002           Total length (>= 50000 bp)         3592797         3656854           # contigs         157         149           Largest contig         384004         573239           Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # misassembled			
Total length (>= 1000 bp)         3939294         3938252           Total length (>= 5000 bp)         3872333         3875816           Total length (>= 10000 bp)         3812943         3834948           Total length (>= 25000 bp)         3681650         3781002           Total length (>= 50000 bp)         3592797         3656854           # contigs         157         149           Largest contig         384004         573239           Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           NS0         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # local misassemblies         1         1           # scaffold gap ext. mis. <td># contigs (&gt;= 50000 bp)</td> <td>20</td> <td>16</td>	# contigs (>= 50000 bp)	20	16
Total length (>= 5000 bp)         3872333         3875816           Total length (>= 10000 bp)         3812943         3834948           Total length (>= 25000 bp)         3681650         3781002           Total length (>= 50000 bp)         3592797         3656854           # contigs         157         149           Largest contig         384004         573239           Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassembled contigs         1         1           # local misassemblies         1         1           # local misassemblies         1         1           # caffold gap ext. mis.	Total length (>= 0 bp)	4174333	4174432
Total length (>= 10000 bp)         3812943         3834948           Total length (>= 25000 bp)         3681650         3781002           Total length (>= 50000 bp)         3592797         3656854           # contigs         157         149           Largest contig         384004         573239           Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # misassembled contigs         1         1           Misassembled contigs length         166802         166802           # local misassemblies         1         1           # scaffold gap loc. mis.         1		3939294	
Total length (>= 25000 bp)         3681650         3781002           Total length (>= 50000 bp)         3592797         3656854           # contigs         157         149           Largest contig         384004         573239           Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # misassembled contigs         1         1           # local misassemblies         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap kext. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned length         1077789         1079151	Total length (>= 5000 bp)	3872333	3875816
Total length (>= 50000 bp)         3592797         3656854           # contigs         157         149           Largest contig         384004         573239           Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassembled contigs         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap loc. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.	Total length (>= 10000 bp)		3834948
# contigs 157 149 Largest contig 384004 573239 Total length 3996348 3996360 Reference length 2961149 2961149 GC (%) 47.33 47.33 Reference GC (%) 47.70 47.70 N50 243364 350399 NG50 262473 508069 N75 105216 132765 NG75 216166 350399 L50 7 5 LG50 5 3 L75 13 9 LG75 8 5 # misassemblies 1 1 1 # misassembled contigs 1 1 1 # misassembled contigs 1 1 1 # scaffold gap ext. mis. 1 1 1 # scaffold gap ext. mis. 1 1 1 # scaffold gap loc. mis. 1 1 1 # unaligned mis. contigs 2 2 # unaligned contigs 110 + 15 part 112 + 13 part Unaligned length 1077789 1079151 Genome fraction (%) 98.284 98.288 Duplication ratio 1.003 1.002 # N's per 100 kbp 12.39 12.39 # mismatches per 100 kbp 10.27 9.86 # indels per 100 kbp 2.10 2.10 Largest alignment 383873 573239 Total aligned length 2917031 2916589 NA50 215940 246267 NGA50 262398 350300 NGA75 115075 229773 LA50 7 5 LGA50 7 5	Total length (>= 25000 bp)	3681650	3781002
Largest contig         384004         573239           Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # local misassemblies         1         1           # local misassemblies         1         1           # scaffold gap loc. mis.         1         1           # scaffold gap loc. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.284           Duplication ratio         1.003         1.002 <td>Total length (&gt;= 50000 bp)</td> <td>3592797</td> <td>3656854</td>	Total length (>= 50000 bp)	3592797	3656854
Total length         3996348         3996360           Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # local misassemblies         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap loc. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.002           # N's per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10	# contigs	157	149
Reference length         2961149         2961149           GC (%)         47.33         47.33           Reference GC (%)         47.70         47.70           N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # local misassemblies         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap ext. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned bength         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.002           # N's per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10           Largest alignment         383873         573239	Largest contig	384004	573239
GC (%)       47.33       47.33         Reference GC (%)       47.70       47.70         N50       243364       350399         NG50       262473       508069         N75       105216       132765         NG75       216166       350399         L50       7       5         LG50       5       3         L75       13       9         LG75       8       5         # misassemblies       1       1         # local misassemblies       1       1         # scaffold gap ext. mis.       1       1         # scaffold gap ext. mis.       1       1         # unaligned mis. contigs       2       2         # unaligned contigs       110 + 15 part       112 + 13 part         Unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       12.39       12.39         # mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239 <td>Total length</td> <td>3996348</td> <td>3996360</td>	Total length	3996348	3996360
Reference GC (%)       47.70       47.70         N50       243364       350399         NG50       262473       508069         N75       105216       132765         NG75       216166       350399         L50       7       5         LG50       5       3         L75       13       9         LG75       8       5         # misassemblies       1       1         # misassembled contigs       1       1         Misassembled contigs length       166802       166802         # local misassemblies       1       1         # scaffold gap ext. mis.       1       1         # scaffold gap loc. mis.       1       1         # unaligned mis. contigs       2       2         # unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       10.39       12.39         # mismatches per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589	Reference length	2961149	2961149
N50         243364         350399           NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # misassembled contigs         1         1           Misassembled contigs length         166802         166802           # local misassemblies         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap loc. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.002           # N's per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10           Largest alignment         383873         573239           Total aligned length         2917031	GC (%)	47.33	47.33
NG50         262473         508069           N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # misassembled contigs         1         1           Misassembled contigs length         166802         166802           # local misassemblies         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap loc. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.002           # N's per 100 kbp         12.39         12.39           # mismatches per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10           Largest alignment         383873         573239           Total aligned length	Reference GC (%)	47.70	47.70
N75         105216         132765           NG75         216166         350399           L50         7         5           LG50         5         3           L75         13         9           LG75         8         5           # misassemblies         1         1           # misassembled contigs         1         1           Misassembled contigs length         166802         166802           # local misassemblies         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap loc. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned contigs         110 + 15 part         112 + 13 part           Unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.002           # N's per 100 kbp         12.39         12.39           # indels per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10           Largest alignment         383873         573239           Total ali	N50	243364	350399
NG75       216166       350399         L50       7       5         LG50       5       3         L75       13       9         LG75       8       5         # misassemblies       1       1         # misassembled contigs       1       1         Misassembled contigs length       166802       166802         # local misassemblies       1       1         # scaffold gap ext. mis.       1       1         # scaffold gap loc. mis.       1       1         # unaligned mis. contigs       2       2         # unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       12.39       12.39         # mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589         NA50       215940       246267         NGA50       262398       350300         NGA75       115075       2297	NG50	262473	508069
L50       7       5         LG50       5       3         L75       13       9         LG75       8       5         # misassemblies       1       1         # misassembled contigs       1       1         Misassembled contigs length       166802       166802         # local misassemblies       1       1         # scaffold gap ext. mis.       1       1         # scaffold gap loc. mis.       1       1         # unaligned mis. contigs       2       2         # unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       12.39       12.39         # mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589         NA50       215940       246267         NGA50       262398       350300         NGA75       115075       229773         LA50       7       5	N75	105216	132765
LG50       5       3         L75       13       9         LG75       8       5         # misassemblies       1       1         # misassembled contigs       1       1         Misassembled contigs length       166802       166802         # local misassemblies       1       1         # scaffold gap ext. mis.       1       1         # scaffold gap loc. mis.       1       1         # unaligned mis. contigs       2       2         # unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       12.39       12.39         # mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589         NA50       215940       246267         NGA50       262398       350300         NGA75       115075       229773         LA50       7       5         LGA50       5       4	NG75	216166	350399
L75       13       9         LG75       8       5         # misassemblies       1       1         # misassembled contigs       1       1         Misassembled contigs length       166802       166802         # local misassemblies       1       1         # scaffold gap ext. mis.       1       1         # scaffold gap loc. mis.       1       1         # unaligned mis. contigs       2       2         # unaligned contigs       110 + 15 part       112 + 13 part         Unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       12.39       12.39         # mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589         NA50       215940       246267         NGA50       262398       350300         NGA75       115075       229773         LA50       7       5         LGA50 <td>L50</td> <td>7</td> <td>5</td>	L50	7	5
LG75       8       5         # misassemblies       1       1         # misassembled contigs       1       1         Misassembled contigs length       166802       166802         # local misassemblies       1       1         # scaffold gap ext. mis.       1       1         # scaffold gap loc. mis.       1       1         # unaligned mis. contigs       2       2         # unaligned contigs       110 + 15 part       112 + 13 part         Unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       12.39       12.39         # mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589         NA50       215940       246267         NGA50       262398       350300         NGA75       115075       229773         LA50       7       5         LGA50       5       4	LG50	5	3
# misassemblies 1 1 1  # misassembled contigs 1 1 1  Misassembled contigs length 166802 166802  # local misassemblies 1 1 1  # scaffold gap ext. mis. 1 1 1  # scaffold gap loc. mis. 1 1 1  # unaligned mis. contigs 2 2  # unaligned contigs 110 + 15 part 112 + 13 part 1	L75	13	9
# misassembled contigs 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LG75	8	5
Misassembled contigs length         166802         166802           # local misassemblies         1         1           # scaffold gap ext. mis.         1         1           # scaffold gap loc. mis.         1         1           # unaligned mis. contigs         2         2           # unaligned contigs         110 + 15 part         112 + 13 part           Unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.002           # N's per 100 kbp         12.39         12.39           # mismatches per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10           Largest alignment         383873         573239           Total aligned length         2917031         2916589           NA50         215940         246267           NGA50         262398         350300           NGA75         115075         229773           LA50         7         5           LGA50         5         4	# misassemblies	1	1
# local misassemblies 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	# misassembled contigs	1	1
# scaffold gap ext. mis. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Misassembled contigs length	166802	166802
# scaffold gap loc. mis. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	# local misassemblies	1	1
# unaligned mis. contigs 2 2  # unaligned contigs 110 + 15 part 112 + 13 part  Unaligned length 1077789 1079151  Genome fraction (%) 98.284 98.288  Duplication ratio 1.003 1.002  # N's per 100 kbp 12.39 12.39  # mismatches per 100 kbp 10.27 9.86  # indels per 100 kbp 2.10 2.10  Largest alignment 383873 573239  Total aligned length 2917031 2916589  NA50 215940 246267  NGA50 262398 350300  NGA75 115075 229773  LA50 7 5  LGA50 5 4	# scaffold gap ext. mis.	1	1
# unaligned contigs       110 + 15 part       112 + 13 part         Unaligned length       1077789       1079151         Genome fraction (%)       98.284       98.288         Duplication ratio       1.003       1.002         # N's per 100 kbp       12.39       12.39         # mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589         NA50       215940       246267         NGA50       262398       350300         NGA75       115075       229773         LA50       7       5         LGA50       5       4	# scaffold gap loc. mis.	1	1
Unaligned length         1077789         1079151           Genome fraction (%)         98.284         98.288           Duplication ratio         1.003         1.002           # N's per 100 kbp         12.39         12.39           # mismatches per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10           Largest alignment         383873         573239           Total aligned length         2917031         2916589           NA50         215940         246267           NGA50         262398         350300           NGA75         115075         229773           LA50         7         5           LGA50         5         4	# unaligned mis. contigs	2	2
Genome fraction (%) 98.284 98.288  Duplication ratio 1.003 1.002  # N's per 100 kbp 12.39 12.39  # mismatches per 100 kbp 10.27 9.86  # indels per 100 kbp 2.10 2.10  Largest alignment 383873 573239  Total aligned length 2917031 2916589  NA50 215940 246267  NGA50 262398 350300  NGA75 115075 229773  LA50 7 5  LGA50 5 4	# unaligned contigs	110 + 15 part	112 + 13 part
Duplication ratio         1.003         1.002           # N's per 100 kbp         12.39         12.39           # mismatches per 100 kbp         10.27         9.86           # indels per 100 kbp         2.10         2.10           Largest alignment         383873         573239           Total aligned length         2917031         2916589           NA50         215940         246267           NGA50         262398         350300           NGA75         115075         229773           LA50         7         5           LGA50         5         4	Unaligned length	1077789	1079151
# N's per 100 kbp 12.39 12.39  # mismatches per 100 kbp 10.27 9.86  # indels per 100 kbp 2.10 2.10  Largest alignment 383873 573239  Total aligned length 2917031 2916589  NA50 215940 246267  NGA50 262398 350300  NGA75 115075 229773  LA50 7 5  LGA50 5 4	Genome fraction (%)	98.284	98.288
# mismatches per 100 kbp       10.27       9.86         # indels per 100 kbp       2.10       2.10         Largest alignment       383873       573239         Total aligned length       2917031       2916589         NA50       215940       246267         NGA50       262398       350300         NGA75       115075       229773         LA50       7       5         LGA50       5       4	Duplication ratio	1.003	1.002
# indels per 100 kbp 2.10 2.10 Largest alignment 383873 573239 Total aligned length 2917031 2916589 NA50 215940 246267 NGA50 262398 350300 NGA75 115075 229773 LA50 7 5 LGA50 5 4	# N's per 100 kbp	12.39	12.39
Largest alignment         383873         573239           Total aligned length         2917031         2916589           NA50         215940         246267           NGA50         262398         350300           NGA75         115075         229773           LA50         7         5           LGA50         5         4	# mismatches per 100 kbp	10.27	9.86
Total aligned length 2917031 2916589  NA50 215940 246267  NGA50 262398 350300  NGA75 115075 229773  LA50 7 5  LGA50 5 4	# indels per 100 kbp	2.10	2.10
NA50         215940         246267           NGA50         262398         350300           NGA75         115075         229773           LA50         7         5           LGA50         5         4	Largest alignment	383873	573239
NGA50         262398         350300           NGA75         115075         229773           LA50         7         5           LGA50         5         4	Total aligned length	2917031	2916589
NGA75         115075         229773           LA50         7         5           LGA50         5         4	NA50	215940	246267
LA50 7 5 LGA50 5 4	NGA50	262398	350300
LGA50 5 4	NGA75	115075	229773
	LA50	7	5
LGA75 9 6	LGA50	5	4
	LGA75	9	6

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

	spades_scf	mulksg_scf
# misassemblies	1	1
# contig misassemblies	1	1
# c. relocations	1	1
# 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	1	1
Misassembled contigs length	166802	166802
# local misassemblies	1	1
# scaffold gap ext. mis.	1	1
# scaffold gap loc. mis.	1	1
# unaligned mis. contigs	2	2
# mismatches	299	287
# indels	61	61
# indels (<= 5 bp)	56	56
# indels (> 5 bp)	5	5
Indels length	268	268

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

	spades_scf	mulksg_scf
# fully unaligned contigs	110	112
Fully unaligned length	196614	197677
# partially unaligned contigs	15	13
Partially unaligned length	881175	881474
# N's	495	495

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).

































