Report

# contigs (>= 0 bp)		M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# contigs (>= 5000 bp)	# contigs (>= 0 bp)	42	56	18	7028
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	14	36	11	621
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	11	22	8	3
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	10	18	8	0
Total length (>= 0 bp)	# contigs (>= 25000 bp)	10	14	7	0
Total length (>= 0 bp)	# contigs (>= 50000 bp)	8	12	4	0
Total length (>= 5000 bp)	Total length (>= 0 bp)	1831657	1965102	1811331	3320808
Total length (>= 10000 bp)	Total length (>= 1000 bp)	1821194	1955209	1808761	1071265
Total length (>= 25000 bp)	Total length (>= 5000 bp)	1816377	1924256	1802504	16099
Total length (>= 50000 bp) 1739635 1787121 1700270 0 # contigs 19 45 12 1590 Largest contig 545971 305868 1150911 5936 Total length 1824603 1961709 1809438 173815 Reference length 1850897 1850897 1850897 1850897 GC (%) 37.88 38.25 37.91 38.00 Reference GC (%) 38.16 38.16 38.16 38.16 38.16 N50 444952 200368 1150911 1206 NG50 444952 200368 1150911 1149 N75 179754 79547 311459 786 NG75 179754 112073 311459 7709 L50 2 4 1 4 4 1 437 L650 2 4 4 1 437 L650 2 4 4 1 485 L75 4 8 2 884 LG75 4 7 7 2 997 # misassembled contigs length 1782615 902633 1741348 982 # local misassembles 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part 10 L032 # wisassembled contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part 10 L032 # N's per 100 kbp 59.52 57.45 38.30 84.60 # wisastendel sper 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251647 - 532 NGA75 24858 61870	Total length (>= 10000 bp)	1810330	1897645	1802504	0
# contigs 19 45 12 1590 Largest contig 545971 305868 1150911 5936 Total length 1824603 1961709 1809438 1738815 Reference length 1850897 1850897 1850897 1850897 GC (%) 37.88 38.25 37.91 38.009 Reference GC (%) 38.16 38.16 38.16 38.16 38.16 N50 444952 200368 1150911 1206 NG50 444952 200368 1150911 1149 N75 179754 79547 311459 786 NG75 179754 79547 311459 709 L50 2 4 1 1 485 L75 4 8 2 884 LG75 4 7 7 84 11 485 L75 4 8 2 884 LG75 4 7 7 84 11 # misassembled contigs 9 6 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassembles 66 24 43 10 # unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # misp per 100 kbp 59.52 57.45 38.30 84.64 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10283 884 NA50 12 5 388 520 LGA50 12 5 38 520	Total length (>= 25000 bp)	1810330	1840422	1792310	0
Largest cortig 545971 305868 1150911 5936 Total length 1824603 1961709 1809438 1738815 Reference length 1850897 1850897 1850897 1850897 GC (%) 37.88 38.25 37.91 38.00 Reference GC (%) 38.16 38.16 38.16 38.16 38.16 N50 444952 200368 1150911 1109 N75 179754 79547 311459 786 NG75 179754 112073 311459 709 L50 2 4 1 1 437 LG50 2 4 1 1 485 L75 4 8 2 884 LG75 4 7 7 2 997 # misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.44 Largest alignment 157918 251457 51332 5936 NG50 44468 140605 10283 884 Largest alignment 157918 251457 51332 5936 NG675 1.13169 74.88 NG75 1.13169 74.88 NG75 1.13169 74.88 NG75 1.13169 74.88 NG75 1.13169 75.88 NG75 1.1316 75.88 LA75 1.1316	Total length (>= 50000 bp)	1739635	1787121	1700270	0
Total length 1824603 1961709 1809438 1738815 Reference length 1850897 1850897 1850897 1850897 GC (%) 37.88 38.25 37.91 38.00 Reference GC (%) 38.16 38.16 38.16 38.16 38.16 NS50 444952 200368 1150911 1109 NG50 444952 200368 1150911 1149 NF5 179754 79547 311459 786 NG75 179754 112073 311459 709 L50 2 4 1 437 LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 <	# contigs	19	45	12	1590
Reference length 1850897 1850897 1850897 1850897 GC (%) 37.88 38.25 37.91 38.00 Reference GC (%) 38.16 38.16 38.16 38.16 38.16 N50 444952 200368 1150911 1206 NG50 444952 200368 1150911 1149 NT5 179754 79547 311459 786 NG75 179754 112073 311459 709 L50 2 4 1 437 LG50 2 4 1 437 LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # Local misas	Largest contig	545971	305868	1150911	5936
GC (%) 37.88 38.25 37.91 38.00 Reference GC (%) 38.16 38.16 38.16 38.16 38.16 N50 444952 200368 1150911 1206 NG50 444952 200368 1150911 1149 N75 179754 79547 311459 786 NG75 179754 112073 311459 709 L50 2 4 1 437 LG50 2 4 1 485 LG75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part </td <td>Total length</td> <td>1824603</td> <td>1961709</td> <td>1809438</td> <td>1738815</td>	Total length	1824603	1961709	1809438	1738815
Reference GC (%) 38.16 38.14 38.14 38.14 38.14 39.20 39.20 39.20 39.20 39.20 39.20 39.20 39.20 39.20 39.20 39.20	Reference length	1850897	1850897	1850897	1850897
N50 444952 200368 1150911 1206 NG50 444952 200368 1150911 1149 N75 179754 79547 311459 786 NG75 179754 112073 311459 709 L50 2 4 1 437 LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassembles 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644	GC (%)	37.88	38.25	37.91	38.00
NG50 444952 200368 1150911 1149 N75 179754 79547 311459 786 NG75 179754 112073 311459 709 L50 2 4 1 437 LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.95 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082	Reference GC (%)	38.16	38.16	38.16	38.16
N75 179754 79547 311459 786 NG75 179754 112073 311459 709 L50 2 4 1 437 LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.	N50	444952	200368	1150911	1206
NG75 179754 112073 311459 709 L50 2 4 1 437 LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 63.11 24.83 85.80	NG50	444952	200368	1150911	1149
L50 2 4 1 437 LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83<	N75	179754	79547	311459	786
LG50 2 4 1 485 L75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468	NG75	179754	112073	311459	709
L75 4 8 2 884 LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10283 884 NA75 <t< td=""><td>L50</td><td>2</td><td>4</td><td>1</td><td>437</td></t<>	L50	2	4	1	437
LG75 4 7 2 997 # misassemblies 47 7 84 1 # misassembled contigs 9 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10283 884	LG50	2	4	1	485
# misassemblies	L75	4	8	2	884
# misassembled contigs 9 6 6 6 1 Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 111 - 1136	LG75	4	7	2	997
Misassembled contigs length 1782615 902633 1741348 982 # local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - -	# misassemblies	47	7	84	1
# local misassemblies 66 24 43 10 # unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 111 - 1136	# misassembled contigs	9	6	6	1
# unaligned contigs 2 + 1 part 5 + 7 part 0 + 3 part 306 + 85 part Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	Misassembled contigs length	1782615	902633	1741348	982
Unaligned length 4970 53728 34736 364041 Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	# local misassemblies	66	24	43	10
Genome fraction (%) 86.802 95.975 60.264 68.644 Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	# unaligned contigs	2 + 1 part	5 + 7 part	0 + 3 part	306 + 85 part
Duplication ratio 1.133 1.074 1.591 1.082 # N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	Unaligned length	4970	53728	34736	364041
# N's per 100 kbp 59.52 57.45 38.30 84.60 # mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	Genome fraction (%)	86.802	95.975	60.264	68.644
# mismatches per 100 kbp 2478.49 744.82 3589.10 1429.26 # indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	Duplication ratio	1.133	1.074	1.591	1.082
# indels per 100 kbp 63.11 24.83 85.80 28.18 Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	# N's per 100 kbp	59.52	57.45	38.30	84.60
Largest alignment 157918 251457 51332 5936 NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	# mismatches per 100 kbp	2478.49	744.82	3589.10	1429.26
NA50 44468 140605 10860 961 NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	# indels per 100 kbp	63.11	24.83	85.80	28.18
NGA50 44468 140605 10283 884 NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	Largest alignment	157918	251457	51332	5936
NA75 25261 48366 - 532 NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	NA50	44468	140605	10860	961
NGA75 24858 61870 - - LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	NGA50	44468	140605	10283	884
LA50 12 5 38 520 LGA50 12 5 40 581 LA75 25 11 - 1136	NA75	25261	48366	-	532
LGA50 12 5 40 581 LA75 25 11 - 1136	NGA75	24858	61870	-	-
LA75 25 11 - 1136	LA50	12	5	38	520
	LGA50	12	5	40	581
LGA75 26 9	LA75	25	11	-	1136
1 1 1	LGA75	26	9	-	-

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

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# misassemblies	47	7	84	1
# relocations	46	7	84	1
# translocations	0	0	0	0
# inversions	1	0	0	0
# misassembled contigs	9	6	6	1
Misassembled contigs length	1782615	902633	1741348	982
# local misassemblies	66	24	43	10
# mismatches	39820	13231	40034	18159
# indels	1014	441	957	358
# short indels	898	360	866	313
# long indels	116	81	91	45
Indels length	3243	2164	2250	1196

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

	M05964_contigs	M07572_contigs	M10540_contigs	M16180_contigs
# fully unaligned contigs	2	5	0	306
Fully unaligned length	3605	30703	0	322661
# partially unaligned contigs	1	7	3	85
# with misassembly	0	3	2	2
# both parts are significant	1	3	1	8
Partially unaligned length	1365	23025	34736	41380
# N's	1086	1127	693	1471

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).



















