## Report

# contigs (>= 1000 bp)		[ Einel eenkine]
# contigs (>= 5000 bp)	# continue (s 1000 hm)	
# contigs (>= 10000 bp)		
# contigs (>= 25000 bp)		<del></del>
# contigs (>= 50000 bp) Total length (>= 1000 bp) Total length (>= 5000 bp) Total length (>= 5000 bp) Total length (>= 10000 bp) Total length (>= 25000 bp) Total length (>= 25000 bp) Total length (>= 50000 bp)  # contigs  Largest contig Total length Reference length  GC (%) Total length Reference length  N50 S0.74 Reference GC (%) N50 N75 N850 N75 N850 N75 N84 NG75 LG50 LG75 LG50 LG75 LG75 LG75 LG75 PMisassemblies Pmisassembled contigs Pmisass		<del></del>
Total length (>= 1000 bp)         2312290           Total length (>= 5000 bp)         5476           Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         3828           Largest contig         5476           Total length         3974624           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         1117           NG50         996           N75         784           NG75         642           L50         1195           LG50         1512           L75         2260           LG75         2963           # misassemblies         1           # misassembled contigs         1           Misassembled contigs length         3047           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         81.896           Duplication ratio         1.046           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00		0
Total length (>= 5000 bp) 5476  Total length (>= 10000 bp) 0  Total length (>= 25000 bp) 0  Total length (>= 50000 bp) 0  # contigs 3828  Largest contig 5476  Total length 3974624  Reference length 4641652  GC (%) 50.74  Reference GC (%) 50.79  N50 1117  NG50 996  N75 784  NG75 642  L50 1195  LG50 1512  L75 2260  LG75 2963  # misassembled contigs 1  Misassembled contigs 1  Misassembled contigs 10  # local misassemblies 0  # unaligned contigs 10  H unaligned length 0  Genome fraction (%) 81.896  Duplication ratio 1.046  # N's per 100 kbp 0.00  # mismatches per 100 kbp 39.28  # indels per 100 kbp 0.00  Largest alignment 5476  NA50 1117  NGA50 996  NA75 784  NGA75 642  LA50 1195  LGA50 1512  LA75 2260  LGA50 1512		
Total length (>= 10000 bp)         0           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         3828           Largest contig         5476           Total length         3974624           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         1117           NG50         996           N75         784           NG75         642           L50         1195           LG50         1512           L75         2260           LG75         2963           # misassemblies         1           # misassembled contigs         1           Misassembled contigs         0           Unaligned length         0           Genome fraction (%)         81.896           Duplication ratio         1.046           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         5476           NA50         996           NA75		2312290
Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         3828           Largest contig         5476           Total length         3974624           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         1117           NG50         996           N75         784           NG75         642           L50         1195           LG50         1512           L75         2260           LG75         2963           # misassemblies         1           # misassembled contigs         1           Misassembled contigs length         3047           # local misassemblies         0           # unaligned length         0           Genome fraction (%)         81.896           Duplication ratio         1.046           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         5476           NA50         1117           NGA50         996           NA75         784           NGA75         642		5476
Total length (>= 50000 bp)       0         # contigs       3828         Largest contig       5476         Total length       3974624         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512 <td></td> <td>0</td>		0
# contigs       3828         Largest contig       5476         Total length       3974624         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LA50       1512		0
Largest contig       5476         Total length       3974624         Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # local misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260 <td>Total length (&gt;= 50000 bp)</td> <td>0</td>	Total length (>= 50000 bp)	0
Total length         3974624           Reference length         4641652           GC (%)         50.74           Reference GC (%)         50.79           N50         1117           NG50         996           N75         784           NG75         642           L50         1195           LG50         1512           L75         2260           LG75         2963           # misassemblies         1           # local misassembled contigs         1           Misassembled contigs length         3047           # local misassemblies         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         81.896           Duplication ratio         1.046           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.00           Largest alignment         5476           NA50         1117           NGA50         996           NA75         784           NGA75         642           LA50         1195           LGA50         1512	# contigs	3828
Reference length       4641652         GC (%)       50.74         Reference GC (%)       50.79         N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # local misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	Largest contig	5476
GC (%)       50.74         Reference GC (%)       50.79         N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs       0         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	Total length	3974624
Reference GC (%)       50.79         N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	Reference length	4641652
N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	GC (%)	50.74
N50       1117         NG50       996         N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	Reference GC (%)	50.79
N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		1117
N75       784         NG75       642         L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	NG50	996
L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	N75	
L50       1195         LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260	NG75	642
LG50       1512         L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
L75       2260         LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
LG75       2963         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
# misassemblies 1 # misassembled contigs 1 Misassembled contigs length 3047 # local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.896 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 39.28 # indels per 100 kbp 0.00 Largest alignment 5476 NA50 1117 NGA50 996 NA75 784 NGA75 642 LA50 1195 LGA50 1512 LA75		
# misassembled contigs 1  Misassembled contigs length 3047  # local misassemblies 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 81.896  Duplication ratio 1.046  # N's per 100 kbp 0.00  # mismatches per 100 kbp 39.28  # indels per 100 kbp 0.00  Largest alignment 5476  NA50 1117  NGA50 996  NA75 784  NGA75 642  LA50 1195  LGA50 1512  LA75		
Misassembled contigs length       3047         # local misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
# local misassemblies 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.896 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 39.28 # indels per 100 kbp 0.00 Largest alignment 5476 NA50 1117 NGA50 996 NA75 784 NGA75 642 LA50 1195 LGA50 1512 LA75		
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 81.896 Duplication ratio 1.046 # N's per 100 kbp 0.00 # mismatches per 100 kbp 39.28 # indels per 100 kbp 0.00 Largest alignment 5476 NA50 1117 NGA50 996 NA75 784 NGA75 642 LA50 1195 LGA50 1512 LA75 2260		
Unaligned length       0         Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
Genome fraction (%)       81.896         Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
Duplication ratio       1.046         # N's per 100 kbp       0.00         # mismatches per 100 kbp       39.28         # indels per 100 kbp       0.00         Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
# N's per 100 kbp 0.00 # mismatches per 100 kbp 39.28 # indels per 100 kbp 0.00 Largest alignment 5476 NA50 1117 NGA50 996 NA75 784 NGA75 642 LA50 1195 LGA50 1512 LA75 2260		
# mismatches per 100 kbp 39.28 # indels per 100 kbp 0.00 Largest alignment 5476 NA50 1117 NGA50 996 NA75 784 NGA75 642 LA50 1195 LGA50 1512 LA75 2260	·	
# indels per 100 kbp 0.00 Largest alignment 5476 NA50 1117 NGA50 996 NA75 784 NGA75 642 LA50 1195 LGA50 1512 LA75 2260		
Largest alignment       5476         NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
NA50       1117         NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
NGA50       996         NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
NA75       784         NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
NGA75       642         LA50       1195         LGA50       1512         LA75       2260		
LA50     1195       LGA50     1512       LA75     2260		
LGA50 1512 LA75 2260		
LA75 2260		
LGA75 2963		
	LGA75	2963

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

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# mismatches	1493
# indels	0
# short indels	0
# long indels	0
Indels length	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

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	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).















