Report

# contigs (>= 0 bp) 1978 # contigs (>= 1000 bp) 457 # contigs (>= 1000 bp) 334 # contigs (>= 10000 bp) 286 # contigs (>= 25000 bp) 204 # contigs (>= 50000 bp) 334 Total length (>= 0 bp) 24987397 Total length (>= 1000 bp) 24571185 Total length (>= 1000 bp) 24327298 Total length (>= 1000 bp) 23961066 Total length (>= 25000 bp) 22548009 Total length (>= 50000 bp) 20107292 # contigs 669 Largest contig 494497 Total length (>= 50000 bp) 20107292 # contigs 669 Largest contig 494497 Total length (>= 30000 bp) 34327288 Reference length 32500020 GC (%) 43.72 Reference GC (%) 43.69 N50 159119 NG50 152292 N75 67532 NG75 65000 L50 49 LG50 50 L75 107 LG75 111 # misassemblies 16 # misassembled contigs 16 Misassembled contigs 16 Misassembled contigs 11 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 98.686 Duplication ratio 1.002 # N's per 100 kbp 0.92 Largest alignment 4944497 Total aligned length 2471599 NA50 139195 NA75 66116 NGA75 66500 LA75 13313	Repor	<u>t                                     </u>
# contigs (>= 1000 bp)		sim25M.SpadesH
# contigs (>= 5000 bp)	# contigs (>= 0 bp)	1978
# contigs (>= 10000 bp)	# contigs (>= 1000 bp)	457
# contigs (>= 25000 bp)	# contigs (>= 5000 bp)	334
# contigs (>= 50000 bp)	# contigs (>= 10000 bp)	286
Total length (>= 0 bp)	# contigs (>= 25000 bp)	204
Total length (>= 1000 bp)	# contigs (>= 50000 bp)	134
Total length (>= 5000 bp)	Total length (>= 0 bp)	24987397
Total length (>= 10000 bp)         23961066           Total length (>= 25000 bp)         22548009           Total length (>= 50000 bp)         20107292           # contigs         669           Largest contig         494497           Total length         24713527           Reference length         25000020           GC (%)         43.72           Reference GC (%)         43.69           N50         159119           NG50         152292           N75         67532           NG75         65000           L50         49           LG50         50           L75         107           LG75         111           # misassemblies         16           Misassembled contigs         16           Misassembled contigs length         2215287           # local misassemblies         11           # unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         24.39           # indels per 100 kbp         24.39           # indels per 100 kbp	Total length (>= 1000 bp)	24571185
Total length (>= 25000 bp)  Total length (>= 50000 bp)  # contigs  669  Largest contig  494497  Total length  24713527  Reference length  25000020  GC (%)  43.69  N50  159119  NG50  152292  N75  67532  NG75  65000  L50  49  LG50  50  L75  107  LG75  111  # misassembled contigs  # misassembled contigs length  # local misassemblies  16  # unaligned contigs length  4 unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  24.39  # indels per 100 kbp  1049  NG50  125248009  22548009  24711599  NA50  140014  NGA50  139195  NA75  66116  NGA75  64502  LA50  52  LGA50  53	Total length (>= 5000 bp)	24327298
Total length (>= 50000 bp)         20107292           # contigs         669           Largest contig         494497           Total length         24713527           Reference length         25000020           GC (%)         43.72           Reference GC (%)         43.69           N50         159119           NG50         159119           NG50         152292           N75         67532           NG75         65000           L50         49           LG50         50           L75         107           LG75         111           # misassemblies         16           # misassembled contigs         16           Misassembled contigs length         2215287           # local misassemblies         11           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         2.439           # indels per 100 kbp         2.92           Largest alignment         494497 <t< td=""><td>Total length (&gt;= 10000 bp)</td><td>23961066</td></t<>	Total length (>= 10000 bp)	23961066
# contigs 669 Largest contig 494497 Total length 24713527 Reference length 25000020 GC (%) 43.72 Reference GC (%) 43.69 N50 159119 NG50 152292 N75 67532 NG75 65000 L50 49 LG50 50 L75 111 # misassembled contigs 16 # misassembled contigs 16 Misassembled contigs 16 Misassembled contigs 11 # unaligned mis. contigs 0 # unaligned length 0 Genome fraction (%) 98.686 Duplication ratio 1.002 # N's per 100 kbp 2.02 # mismatches per 100 kbp 0.92 Largest alignment 494497 Total aligned length 24711599 NA50 140014 NGA50 139195 NA75 66116 NGA75 64502 LA50 52 LGA50 53	Total length (>= 25000 bp)	22548009
Largest contig         494497           Total length         24713527           Reference length         25000020           GC (%)         43.72           Reference GC (%)         43.69           N50         159119           NG50         152292           N75         67532           NG75         65000           L50         49           LG50         50           L75         107           LG75         111           # misassemblies         16           # misassembled contigs         16           Misassembled contigs length         2215287           # local misassemblies         11           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         24.39           # indels per 100 kbp         0.92           Largest alignment         494497           Total aligned length         24711599           NA50         140014           NGA50         139195	Total length (>= 50000 bp)	20107292
Total length 24713527  Reference length 25000020  GC (%) 43.72  Reference GC (%) 43.69  N50 159119  NG50 152292  N75 67532  NG75 65000  L50 49  LG50 50  L75 107  LG75 111  # misassembles 16  # misassembled contigs 16  Misassembled contigs length 2215287  # local misassemblies 11  # unaligned mis. contigs 0  # unaligned length 0  Genome fraction (%) 98.686  Duplication ratio 1.002  # N's per 100 kbp 2.02  # mismatches per 100 kbp 0.92  Largest alignment 494497  Total aligned length 24711599  NA50 140014  NGA50 139195  NA75 66116  NGA75 64502  LA50 52  LGA50 53	# contigs	669
Reference length         25000020           GC (%)         43.72           Reference GC (%)         43.69           N50         159119           NG50         152292           N75         67532           NG75         65000           L50         49           LG50         50           L75         107           LG75         111           # misassemblies         16           Misassembled contigs         16           Misassembled contigs length         2215287           # local misassemblies         11           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         24.39           # indels per 100 kbp         0.92           Largest alignment         494497           Total aligned length         24711599           NA50         140014           NGA50         139195           NA75         66116           NGA75         64502           LA50	Largest contig	494497
GC (%)         43.72           Reference GC (%)         43.69           N50         159119           NG50         152292           N75         67532           NG75         65000           L50         49           LG50         50           L75         107           LG75         111           # misassemblies         16           # misassembled contigs         16           Misassembled contigs length         2215287           # local misassemblies         11           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         24.39           # indels per 100 kbp         0.92           Largest alignment         494497           Total aligned length         24711599           NA50         140014           NGA50         139195           NA75         66116           NGA75         64502           LA50         52           LGA50         53	Total length	24713527
Reference GC (%)       43.69         N50       159119         NG50       152292         N75       67532         NG75       65000         L50       49         LG50       50         L75       107         LG75       111         # misassemblies       16         # misassembled contigs       16         Misassembled contigs length       2215287         # local misassemblies       11         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       24.39         # indels per 100 kbp       24.39         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	Reference length	25000020
N50         159119           NG50         152292           N75         67532           NG75         65000           L50         49           LG50         50           L75         107           LG75         111           # misassemblies         16           Misassembled contigs         16           Misassembled contigs length         2215287           # local misassemblies         11           # unaligned mis. contigs         0           # unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         2.439           # indels per 100 kbp         0.92           Largest alignment         494497           Total aligned length         24711599           NA50         140014           NGA50         139195           NA75         66116           NGA75         64502           LA50         52           LGA50         53	GC (%)	43.72
NG50         152292           N75         67532           NG75         65000           L50         49           LG50         50           L75         107           LG75         111           # misassemblies         16           # misassembled contigs         16           Misassembled contigs length         2215287           # local misassemblies         11           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         24.39           # indels per 100 kbp         0.92           Largest alignment         494497           Total aligned length         24711599           NA50         140014           NGA50         139195           NA75         66116           NGA75         64502           LA50         52           LGA50         53	Reference GC (%)	43.69
N75       67532         NG75       65000         L50       49         LG50       50         L75       107         LG75       111         # misassemblies       16         # misassembled contigs       16         Misassembled contigs       2215287         # local misassemblies       11         # unaligned mis. contigs       0         # unaligned length       0         Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	N50	159119
NG75       65000         L50       49         LG50       50         L75       107         LG75       111         # misassemblies       16         # misassembled contigs       16         Misassembled contigs length       2215287         # local misassemblies       11         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	NG50	152292
L50       49         LG50       50         L75       107         LG75       111         # misassemblies       16         # misassembled contigs       16         Misassembled contigs       16         Misassembled contigs       16         # unaligand misassembles       11         # unaligned misassemblies       0         # unaligned misassemblies       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	N75	67532
LG50       50         L75       107         LG75       111         # misassemblies       16         # misassembled contigs       16         Misassembled contigs       16         Misassembled contigs       16         # local misassembles       11         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	NG75	65000
L75       107         LG75       111         # misassemblies       16         # misassembled contigs       16         Misassembled contigs       16         Misassembled contigs       2215287         # local misassemblies       11         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	L50	49
LG75       111         # misassemblies       16         # misassembled contigs       16         Misassembled contigs length       2215287         # local misassemblies       11         # unaligned mis. contigs       0         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	LG50	50
# misassemblies 16 # misassembled contigs 16 Misassembled contigs length 2215287 # local misassemblies 11 # unaligned mis. contigs 0 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.686 Duplication ratio 1.002 # N's per 100 kbp 2.02 # mismatches per 100 kbp 24.39 # indels per 100 kbp 0.92 Largest alignment 494497 Total aligned length 24711599 NA50 140014 NGA50 139195 NA75 66116 NGA75 64502 LA50 52 LGA50 53	L75	107
# misassembled contigs 16  Misassembled contigs length 2215287  # local misassemblies 11  # unaligned mis. contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.686  Duplication ratio 1.002  # N's per 100 kbp 2.02  # mismatches per 100 kbp 24.39  # indels per 100 kbp 0.92  Largest alignment 494497  Total aligned length 24711599  NA50 140014  NGA50 139195  NA75 66116  NGA75 64502  LA50 52  LGA50 53	LG75	111
Misassembled contigs length         2215287           # local misassemblies         11           # unaligned mis. contigs         0           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         24.39           # indels per 100 kbp         0.92           Largest alignment         494497           Total aligned length         24711599           NA50         140014           NGA50         139195           NA75         66116           NGA75         64502           LA50         52           LGA50         53	# misassemblies	16
# local misassemblies 11  # unaligned mis. contigs 0  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 98.686  Duplication ratio 1.002  # N's per 100 kbp 24.39  # indels per 100 kbp 0.92  Largest alignment 494497  Total aligned length 24711599  NA50 140014  NGA50 139195  NA75 66116  NGA75 64502  LAS0 52  LGA50 53	# misassembled contigs	16
# unaligned mis. contigs  # unaligned contigs  0 + 0 part  Unaligned length  0 Genome fraction (%)  98.686  Duplication ratio  1.002  # N's per 100 kbp  2.02  # mismatches per 100 kbp  24.39  # indels per 100 kbp  1.092  Largest alignment  494497  Total aligned length  NA50  140014  NGA50  139195  NA75  66116  NGA75  64502  LA50  52  LGA50  53	Misassembled contigs length	2215287
# unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 98.686 Duplication ratio 1.002 # N's per 100 kbp 2.02 # mismatches per 100 kbp 24.39 # indels per 100 kbp 0.92 Largest alignment 494497 Total aligned length 24711599 NA50 140014 NGA50 139195 NA75 66116 NGA75 64502 LA50 52 LGA50 53	# local misassemblies	11
Unaligned length         0           Genome fraction (%)         98.686           Duplication ratio         1.002           # N's per 100 kbp         2.02           # mismatches per 100 kbp         24.39           # indels per 100 kbp         0.92           Largest alignment         494497           Total aligned length         24711599           NA50         140014           NGA50         139195           NA75         66116           NGA75         64502           LA50         52           LGA50         53	# unaligned mis. contigs	0
Genome fraction (%)       98.686         Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	# unaligned contigs	0 + 0 part
Duplication ratio       1.002         # N's per 100 kbp       2.02         # mismatches per 100 kbp       24.39         # indels per 100 kbp       0.92         Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	Unaligned length	0
# N's per 100 kbp 2.02  # mismatches per 100 kbp 0.92  Largest alignment 494497  Total aligned length 24711599  NA50 140014  NGA50 139195  NA75 66116  NGA75 64502  LA50 52  LGA50 53	Genome fraction (%)	98.686
# mismatches per 100 kbp 24.39  # indels per 100 kbp 0.92  Largest alignment 494497  Total aligned length 24711599  NA50 140014  NGA50 139195  NA75 66116  NGA75 64502  LA50 52  LGA50 53	Duplication ratio	1.002
# indels per 100 kbp 0.92 Largest alignment 494497 Total aligned length 24711599 NA50 140014 NGA50 139195 NA75 66116 NGA75 64502 LA50 52 LGA50 53	# N's per 100 kbp	2.02
Largest alignment       494497         Total aligned length       24711599         NA50       140014         NGA50       139195         NA75       66116         NGA75       64502         LA50       52         LGA50       53	# mismatches per 100 kbp	24.39
Total aligned length         24711599           NA50         140014           NGA50         139195           NA75         66116           NGA75         64502           LA50         52           LGA50         53	# indels per 100 kbp	0.92
NA50     140014       NGA50     139195       NA75     66116       NGA75     64502       LA50     52       LGA50     53	Largest alignment	494497
NGA50         139195           NA75         66116           NGA75         64502           LA50         52           LGA50         53	Total aligned length	24711599
NA75     66116       NGA75     64502       LA50     52       LGA50     53	NA50	140014
NGA75         64502           LA50         52           LGA50         53	NGA50	139195
LA50 52 LGA50 53	NA75	66116
LGA50 53	NGA75	64502
	LA50	52
LA75 113	LGA50	53
	LA75	113
LGA75 116	LGA75	116

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

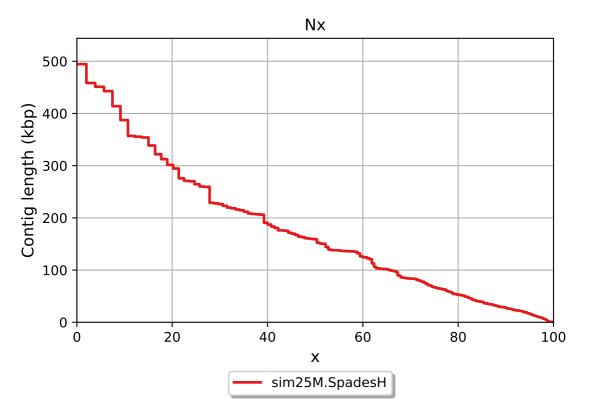
	sim25M.SpadesH
# misassemblies	16
# relocations	16
# translocations	0
# inversions	0
# misassembled contigs	16
Misassembled contigs length	2215287
# local misassemblies	11
# unaligned mis. contigs	0
# mismatches	6018
# indels	227
# indels (<= 5 bp)	202
# indels (> 5 bp)	25
Indels length	985

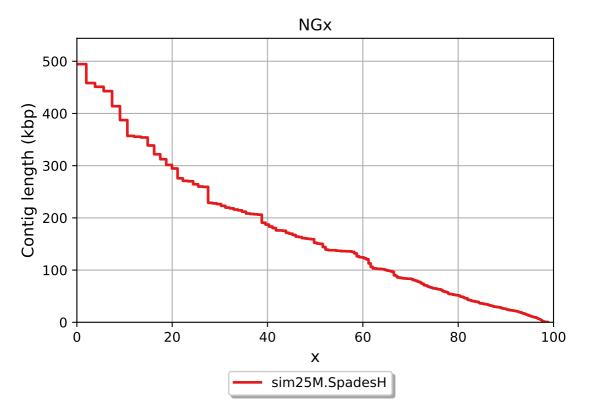
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

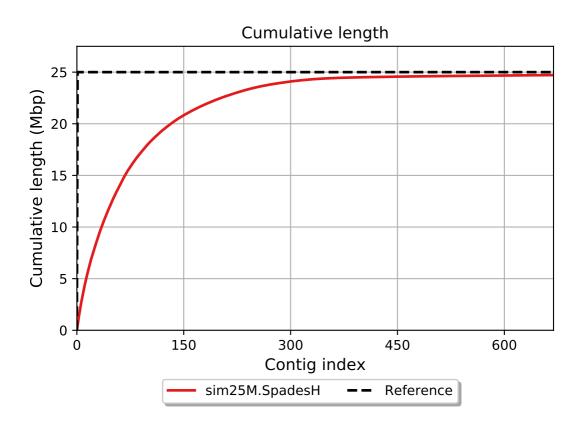
## Unaligned report

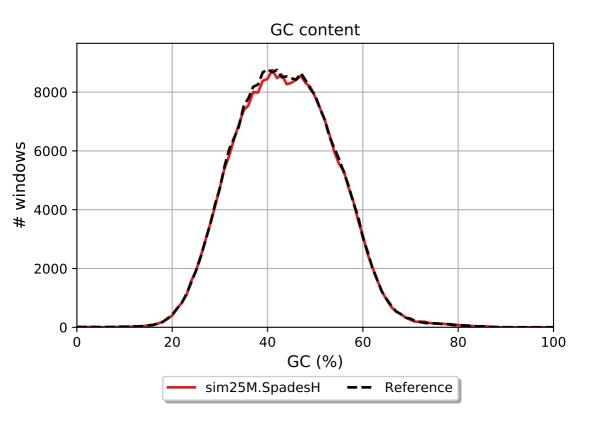
	sim25M.SpadesH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	499

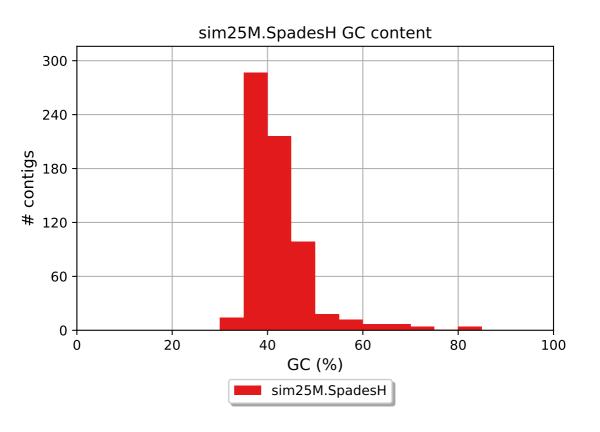
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

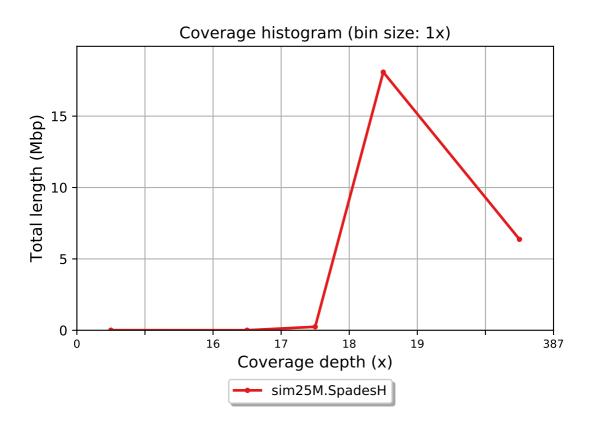












sim25M.SpadesH coverage histogram (bin size: 1x) Total length (Mbp) 0 + 16 17 18 19 387 Coverage depth (x) sim25M.SpadesH

