


QUAST

Quality Assessment Tool for Genome Assemblies by CAB

24 January 2018, Wednesday, 23:03:33

[View in Icarus contig browser](#)All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Aligned to "GRCm38_p5_no_chrY" | 2 639 127 076 bp | 65 fragments | 41.76% G+C


 Show heatmap

Genome statistics	B6Eve	B6Eve_broken
Genome fraction (%)	96.848	96.841
Duplication ratio	1.123	1.017
# genomic features	22 994 + 2144 part	22 953 + 2182 part
Largest alignment	5 570 225	4 577 372
Total aligned length	2 526 660 255	2 525 333 977
NG50	1 390 099	371 965
NG75	439 613	151 056
NA50	422 265	384 295
NA75	115 689	168 024
NCA50	476 164	365 098
NCA75	146 696	146 364
LG50	524	1757
LG75	1281	4525
LA50	1516	1657
LA75	4821	4140
LGA50	1336	1793
LGA75	3885	4626
Misassemblies		
# misassemblies	2590	1306
# relocations	1735	557
# translocations	827	724
# inversions	28	25
# misassembled contigs	1714	1166
Misassembled contigs length	1 509 562 627	220 209 949
# local misassemblies	3529	2962
# scaffold gap size mis.	88	-
# possible MGEs	18	16
# unaligned mis. contigs	69	51
Unaligned		
# fully unaligned contigs	166	21 642
Fully unaligned length	3 719 105	3 869 437
# partially unaligned contigs	2456	1793
Partially unaligned length	7 251 439	6 820 765
Mismatches		
# mismatches	321 280	320 246
# indels	494 061	492 931
Indels length	3 818 564	2 606 030
# mismatches per 100 kbp	12.93	12.89
# indels per 100 kbp	19.89	19.85
# indels (≤ 5 bp)	465 708	464 749
# indels (> 5 bp)	28 353	28 182
# N's	263 669 715	422
# N's per 100 kbp	9412.42	0.02
Statistics without reference		
# contigs	12 658	36 182
# contigs (≥ 0 bp)	12 661	-
# contigs (≥ 1000 bp)	12 661	-
# contigs (≥ 5000 bp)	12 656	14 704
# contigs (≥ 10000 bp)	12 645	14 693
# contigs (≥ 25000 bp)	9722	11 770
# contigs (≥ 50000 bp)	6787	8835
Largest contig	9 177 662	4 577 433
Total length	2 801 295 686	2 537 626 393
Total length (≥ 0 bp)	2 801 301 292	-
Total length (≥ 1000 bp)	2 801 301 292	-
Total length (≥ 5000 bp)	2 801 286 582	2 537 466 957
Total length (≥ 10000 bp)	2 801 206 759	2 537 387 134
Total length (≥ 25000 bp)	2 741 388 976	2 477 569 351
Total length (≥ 50000 bp)	2 638 542 761	2 374 723 136
N50	1 291 016	391 273
N75	233 769	172 412
L50	585	1624
L75	1674	4053
GC (%)	41.8	41.8
K-mer-based statistics		
K-mer-based completeness	97.38	97.38
K-mer-based cor. length (%)	74.76	87.29
K-mer-based mis. length (%)	24.45	11.86
K-mer-based undef. length (%)	0.78	0.85
# k-mer-based misjoins	1568	1493
# k-mer-based translocations	1091	1024
# k-mer-based 100kbp relocations	477	469
Similarity statistics		
# similar correct contigs	9448	9448
# similar misassembled blocks	3598	3598

[Short report](#)

