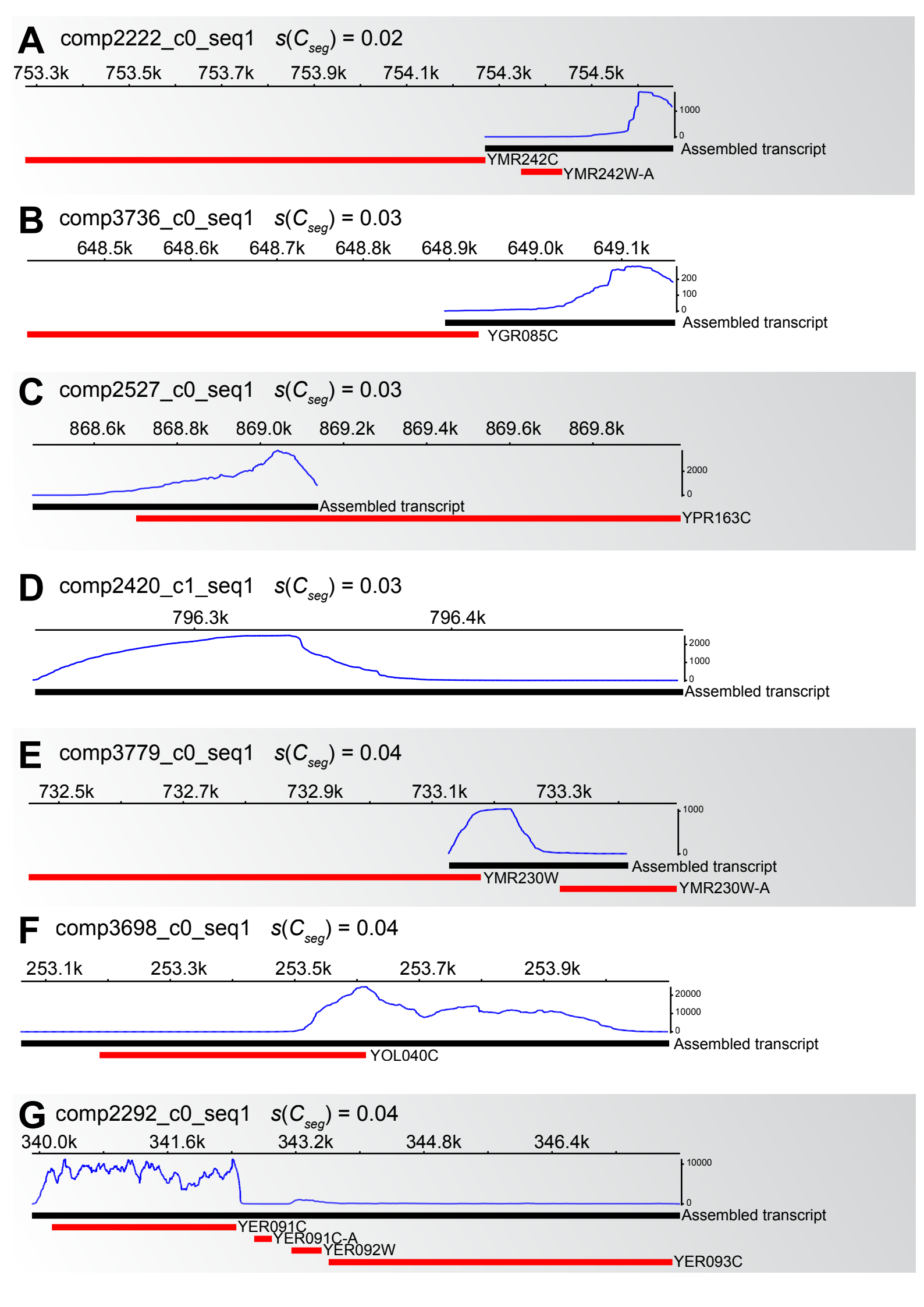
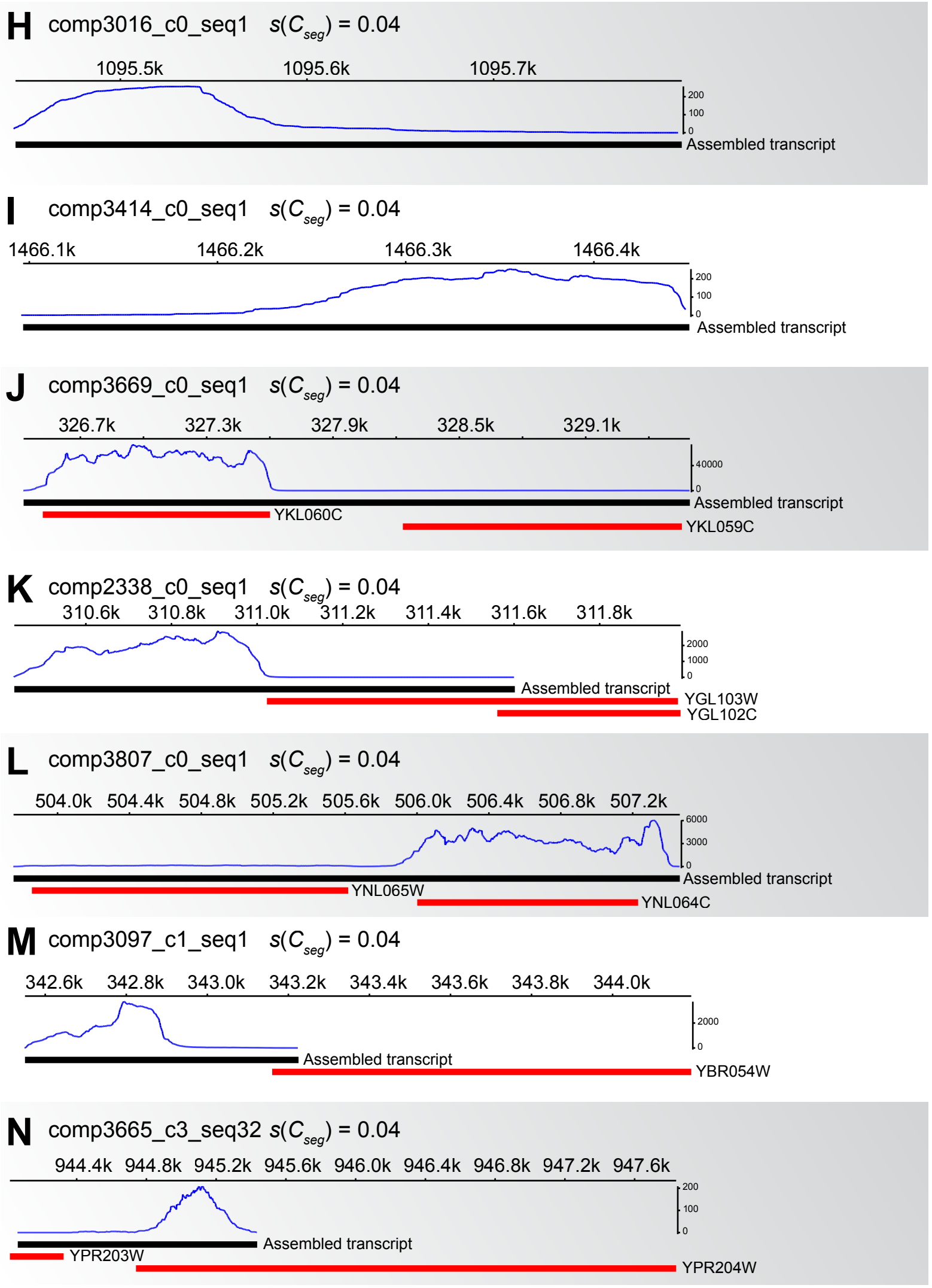

A comp2222_c0_seq1 s(C_seg) = 0.02
753.3k 753.5k 753.7k 753.9k 754.1k 754.3k 754.5k
1000
0
Assembled transcript
YMR242C
YMR242W-A
B comp3736_c0_seq1 s(C_seg) = 0.03
648.5k 648.6k 648.7k 648.8k 648.9k 649.0k 649.1k
200
100
0
Assembled transcript
YGR085C
C comp2527_c0_seq1 s(C_seg) = 0.03
868.6k 868.8k 869.0k 869.2k 869.4k 869.6k 869.8k
2000
0
Assembled transcript
YPR163C
D comp2420_c1_seq1 s(C_seg) = 0.03
796.3k 796.4k
2000
1000
0
Assembled transcript
E comp3779_c0_seq1 s(C_seg) = 0.04
732.5k 732.7k 732.9k 733.1k 733.3k
1000
0
Assembled transcript
YMR230W
YMR230W-A
F comp3698_c0_seq1 s(C_seg) = 0.04
253.1k 253.3k 253.5k 253.7k 253.9k
20000
10000
0
Assembled transcript
YOL040C
G comp2292_c0_seq1 s(C_seg) = 0.04
340.0k 341.6k 343.2k 344.8k 346.4k
10000
0
Assembled transcript
YER091C
YER091C-A
YER092W
YER093C


H comp3016_c0_seq1 s(C_seg) = 0.04
1095.5k
1095.6k
1095.7k
200
100
0
Assembled transcript
I comp3414_c0_seq1 s(C_seg) = 0.04
1466.1k
1466.2k
1466.3k
1466.4k
200
100
0
Assembled transcript
J comp3669_c0_seq1 s(C_seg) = 0.04
326.7k
327.3k
327.9k
328.5k
329.1k
40000
0
Assembled transcript
YKL060C
YKL059C
K comp2338_c0_seq1 s(C_seg) = 0.04
310.6k
310.8k
311.0k
311.2k
311.4k
311.6k
311.8k
2000
1000
0
Assembled transcript
YGL103W
YGL102C
L comp3807_c0_seq1 s(C_seg) = 0.04
504.0k
504.4k
504.8k
505.2k
505.6k
506.0k
506.4k
506.8k
507.2k
6000
3000
0
Assembled transcript
YNL065W
YNL064C
M comp3097_c1_seq1 s(C_seg) = 0.04
342.6k
342.8k
343.0k
343.2k
343.4k
343.6k
343.8k
344.0k
2000
0
Assembled transcript
YBR054W
N comp3665_c3_seq32 s(C_seg) = 0.04
944.4k
944.8k
945.2k
945.6k
946.0k
946.4k
946.8k
947.2k
947.6k
200
100
0
Assembled transcript
YPR203W
YPR204W

Supplemental Fig S2. Visualization of genome alignment evidence for the 24 worst scoring contigs for the $s(C_{seg})$ contig score component. The black lines indicate the de novo assembled transcripts, red lines indicate annotated genes in the yeast genome. Read coverage depth is indicated above the assembled transcript.