

Figure S1

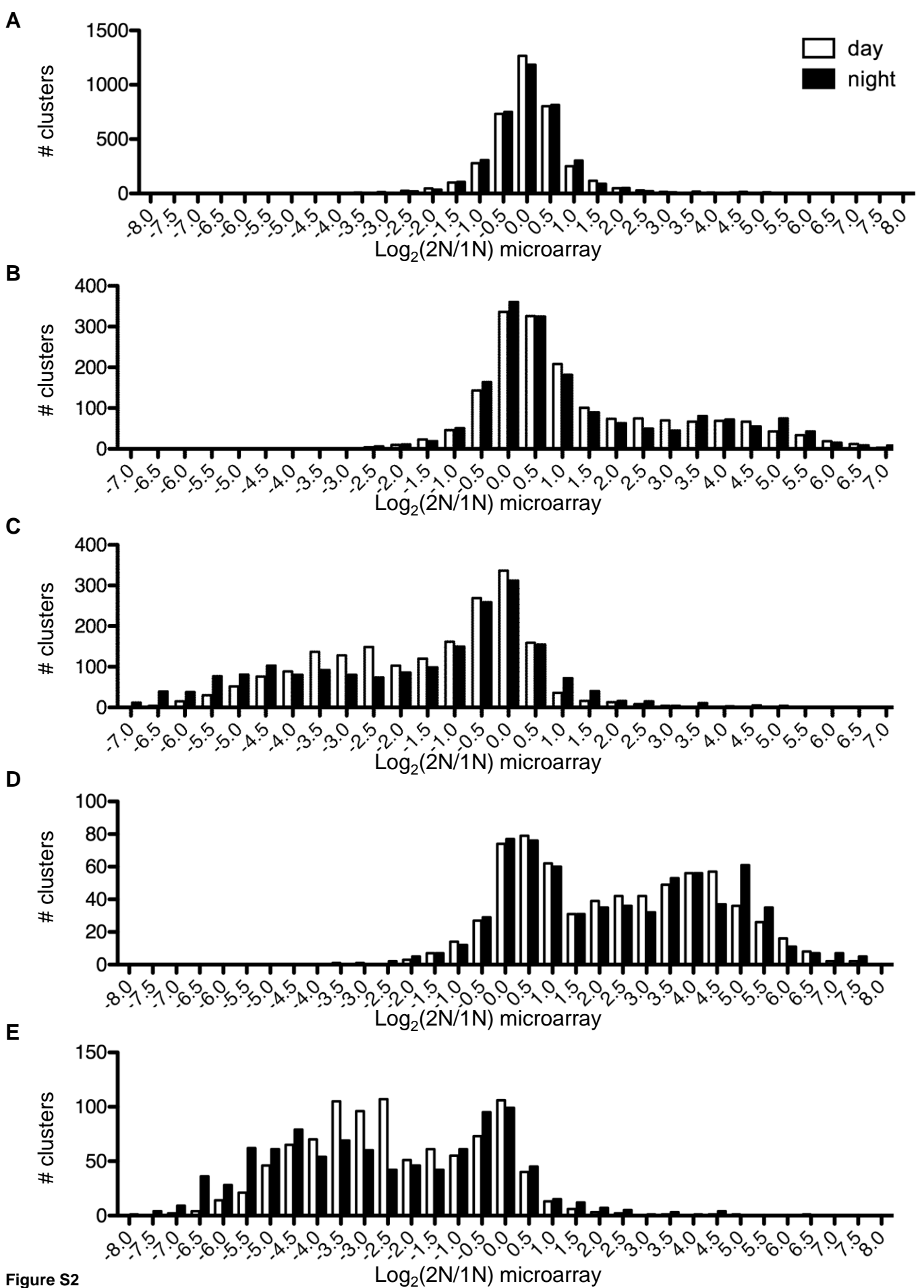


Figure S2

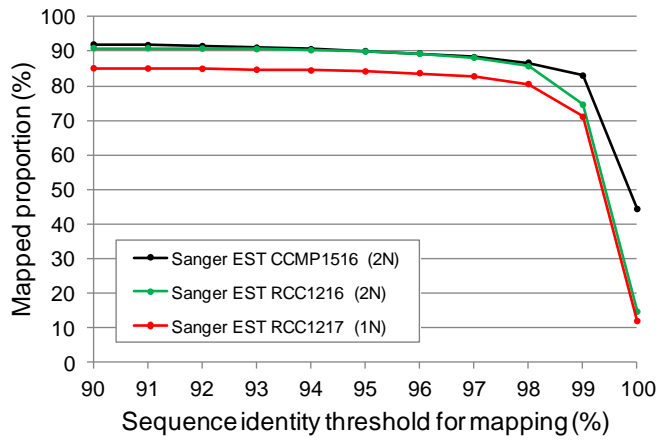
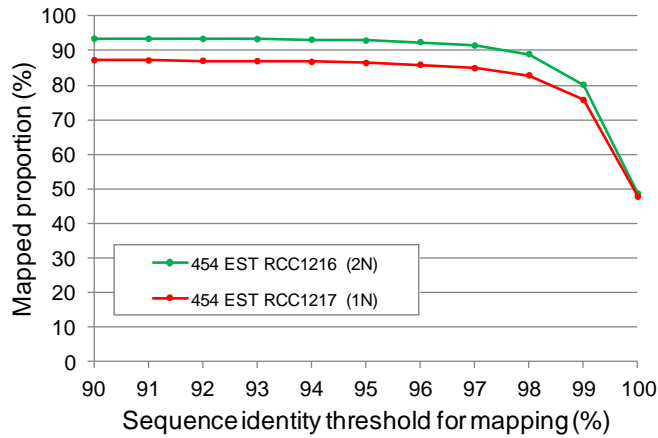
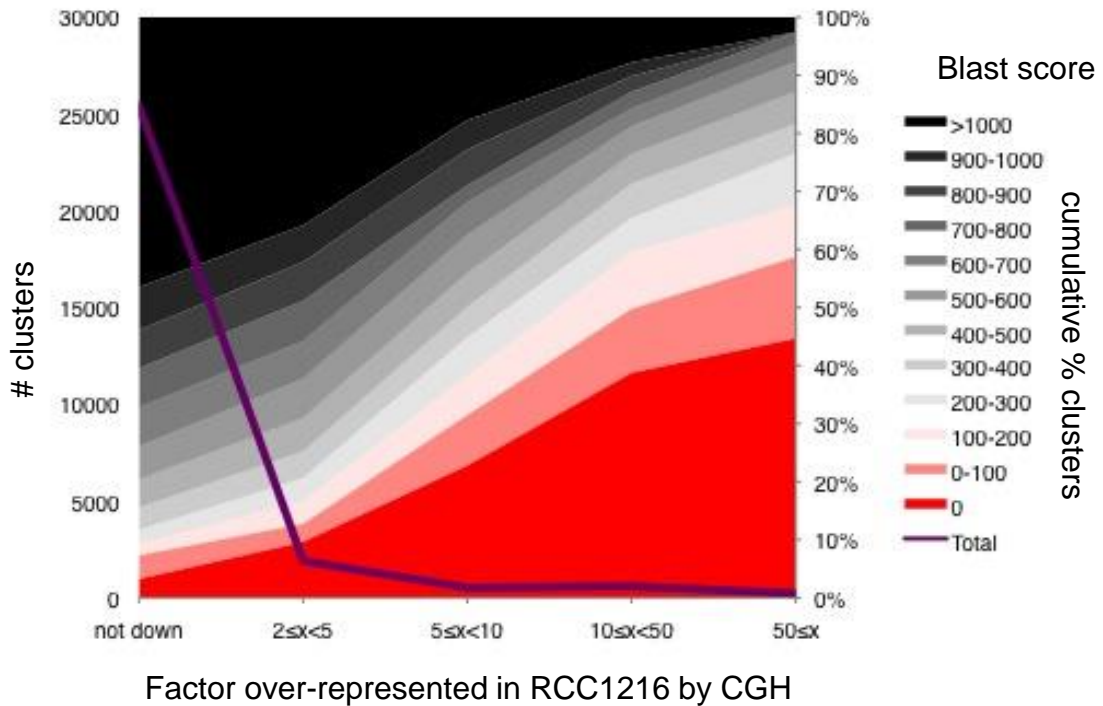
A**B****C**

Figure S3

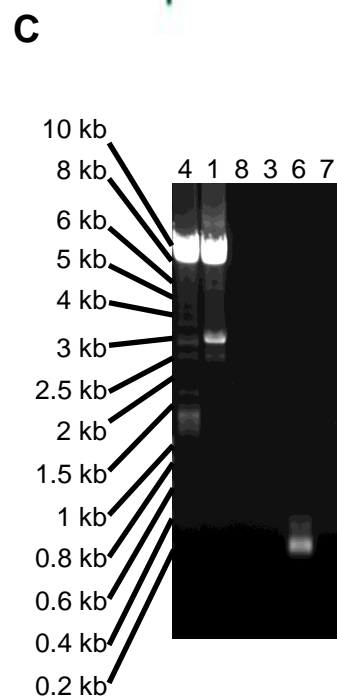
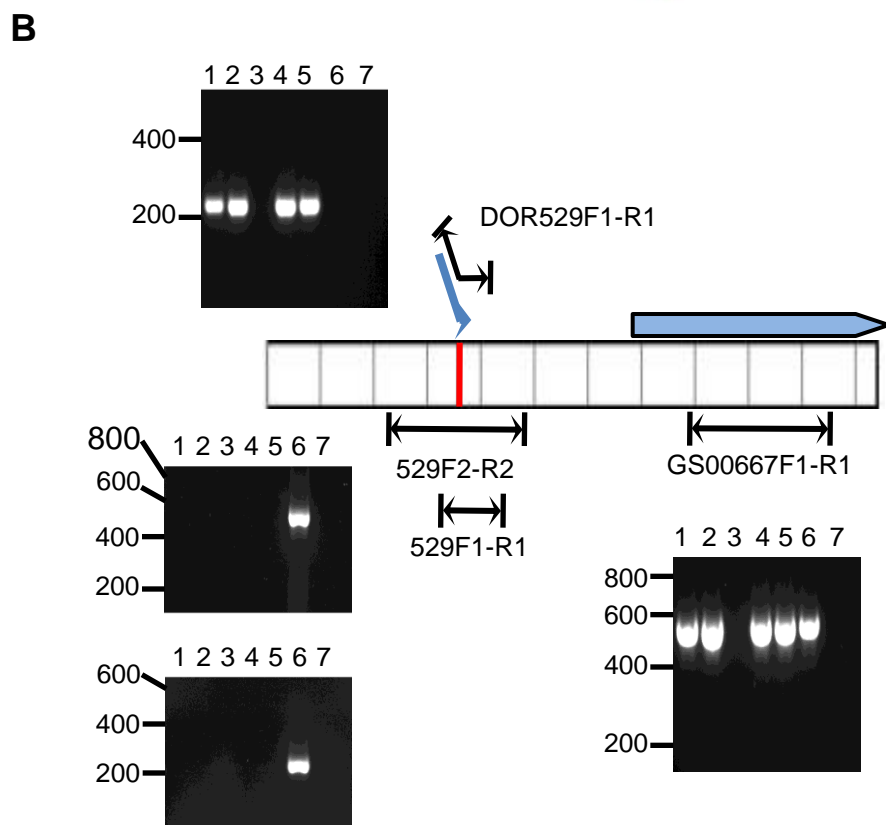
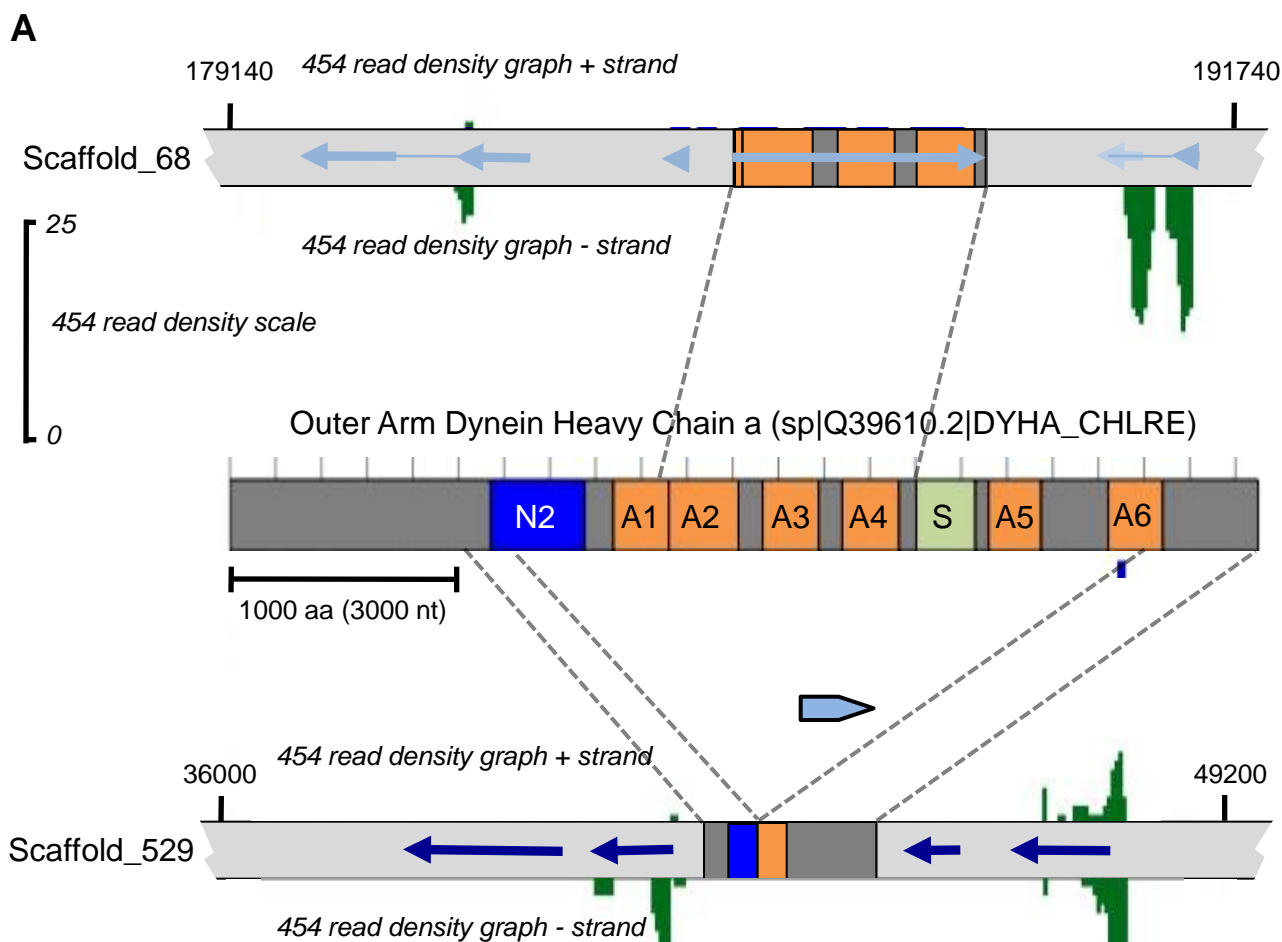


Figure S4

>gDNAb529F1_-_C01_2010-05-12_id_3364_005.ab1
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TCGAGTTTAAATTCGACAGGCACGCGGAGACGGAGTTTACCTCATCCGGATGCAGGAGGAAGACTTCGAGATGCTTGAGG
ACAACCAGCTGGTGGTGCAGGGGATGATGGCCTCCAAGTACCTGGCCACCTTCGAGGAGCCCGTCACGCGATGGCAGAAG
GACCTTTCCTCCGTGTCAGACGTGCTCGGTATTATGCTGGATGTGCAGCGCAAGTGGGCCTATCTCGAGACGCTATTTCATCG
GCTCAGAGGAGGTGAAGCGTGAGCTGCCGGCGGAC

>[sp|Q39610.2|DYHA_CHLRE](#) RecName: Full=Dynein alpha chain, flagellar outer arm; AltName: Full=DHC alpha Length=4499
Score = 147 bits (372), Expect = 7e-39 Identities = 67/117 (58%), Positives = 93/117 (80%), Gaps = 0/117 (0%) Frame = +2
Query 2 GEVVDQATKEDKMEQLTKLEETWKDIEFKFDRHAETEYVYLIRMQEEDFEMLEDNQLVVQ 181
GE+VD+A KE+KME +KL +TW +EF+F RH+ +V+ ++M EEDFE LEDNQ+ VQ
Sbjct 1270 GEIVDRAQKEEKMEIAIRKLNLDTWTRVEFQFHRHKDYDVHTVKMAEEDFEALDNQVQVQ 1329

Query 182 GMMASKYLATFEFPVTRWQKDLSSVSDVLGIMLDVQRKWAYLETFIGSEEVKRELP 352
GM+A++Y+ATF+++ WQK L+ V+DV IM ++QR WAYLE+LFI SEEVK+ELP
Sbjct 1330 GMIANRYMATFKDEILGWQKLNLDVADVQNQIMAEIQRWAYLESLEFIHSEEVKKELP 1386

>gDNAb529R1_-_F01_2010-05-12_id_3364_011.ab1
GACTGCATGATACCCTCGGGCAGGGTCTGCATGTCGGGCAGCGGTGGAGGCTCGGCCGAGAGGAAGCAGCGGAAATTCCT
GTGTCCACCTCAGCCGCAATCTCCAGCTTTCGCTCGAGTATCGGCAACCATGACTGCATGAGGTGGACGTTTTGCAGAAAG
ACCCAGCCGCCGTCGCGGTTGAAGCGGTGAGTACGTTCTCGGCATTCTTCTCCTGCCCTGGCCCATGGAGATTGAGACG
TACTGCTGATTGGCCTCGGTGTACCCTAGCTTTGCGCCAGGTTCTCGATATCGACGCCCGGTTCAACACCGGGGAAGAGG
ACAAAGAAGAGCGGCGTCCGAAAGTGGAGTCCGCAACGTTGCTGTCATGTCGAACGTAGGCTGCGACATGTAGCGCTCG
CCCATCTCCTGCACGATGTACCTCGTACGCGCGG

>[sp|Q39610.2|DYHA_CHLRE](#) RecName: Full=Dynein alpha chain, flagellar outer arm; AltName: Full=DHC alpha Length=4499
Score = 149 bits (377), Expect = 3e-39 Identities = 76/146 (53%), Positives = 94/146 (65%), Gaps = 1/146 (0%) Frame = -3
Query 437 AVTRYIVQEMGERYSQPTFDMDDTFADSTFATPLFFVLPFGVDPGVDIENLGAKLGYTE 258
A+ + MG Y++Q F +S+ ATP+FF+LFPG P +IE KGY+
Sbjct 3842 ALQNFCEHMMGSDYVNVQDAFSPAAMMDESSATPIFFILFPGYSPSKEIEVYANKCGYSV 3901

Query 257 ANQQYVSISMGQGQEKNAENVLD RFTADGGWVFLQNVHLMQSWLPILERKLEIAAEVGHK 78
AN+ ISMGQGQE AE VLD++T +GGWVFL NVHLMQ W+P LERKLEIAAE H
Sbjct 3902 ANGRCLISMGGQEAPEAEVLDKYTREGGWVFLDNVHLMQGWIPKLERKLEIAAESAH 3961

Query 77 NFRCFLSAEP-PPLPDMQTVPEGIMQ 3
+FRCF SAEP P +PE I+Q
Sbjct 3962 DFRCFSAEPINGAPHANIIPESILQ 3987

Score = 19.6 bits (39), Expect = 4.2 Identities = 6/7 (86%), Positives = 7/7 (100%), Gaps = 0/7 (0%) Frame = -3
Query 323 LFPGVDP 303
LFPG+DP
Sbjct 1965 LFPGIDP 1971

Score = 19.2 bits (38), Expect = 5.5 Identities = 5/9 (56%), Positives = 8/9 (89%), Gaps = 0/9 (0%) Frame = -2
Query 360 CRLHLCDAA 334
CR+ +CDA+
Sbjct 1667 CRIRICDAS 1675

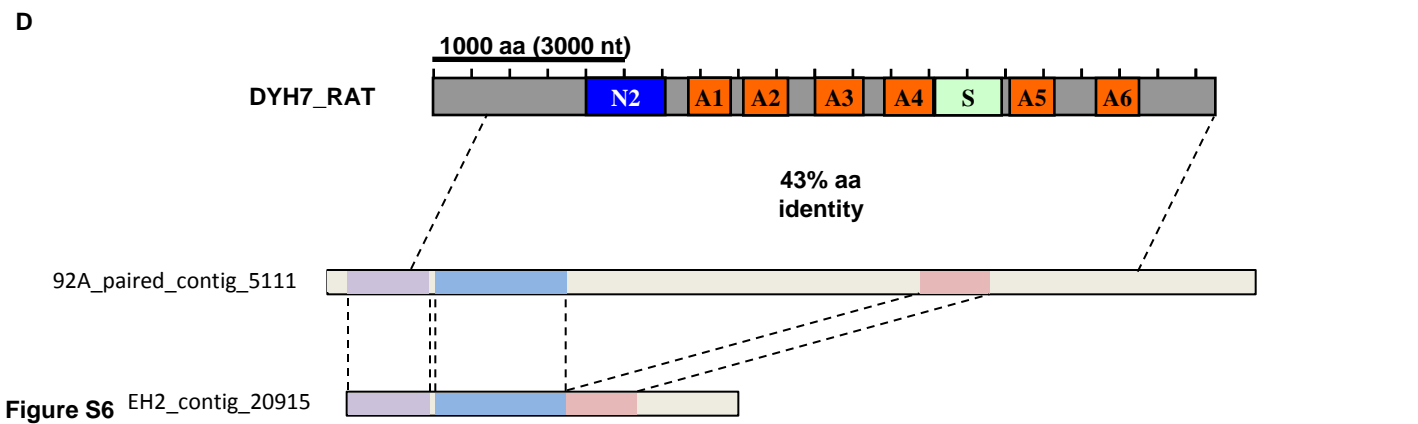
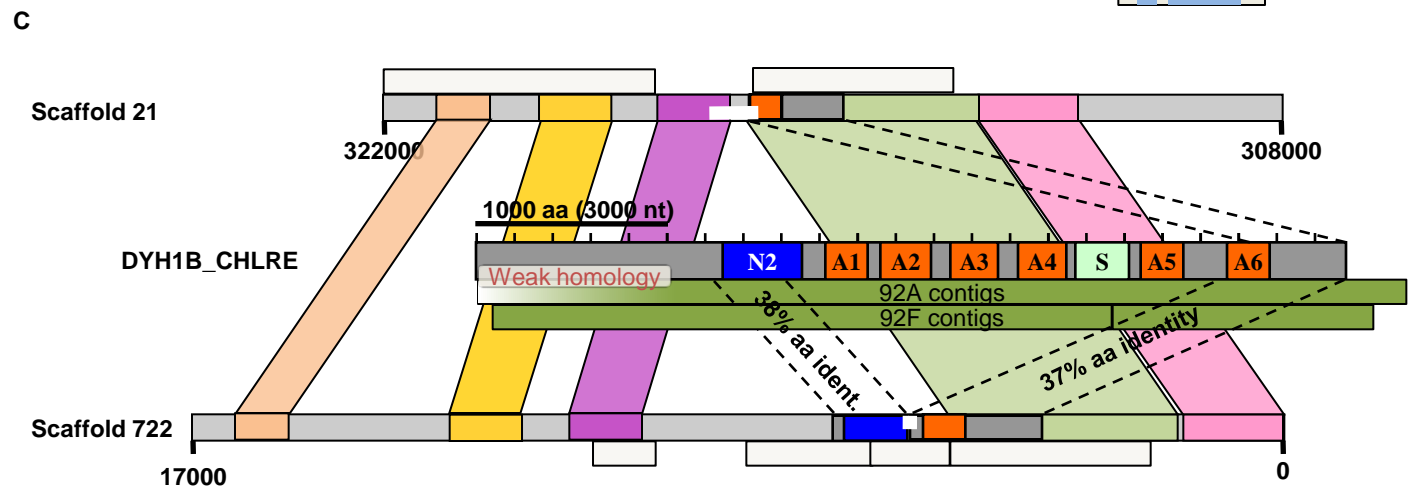
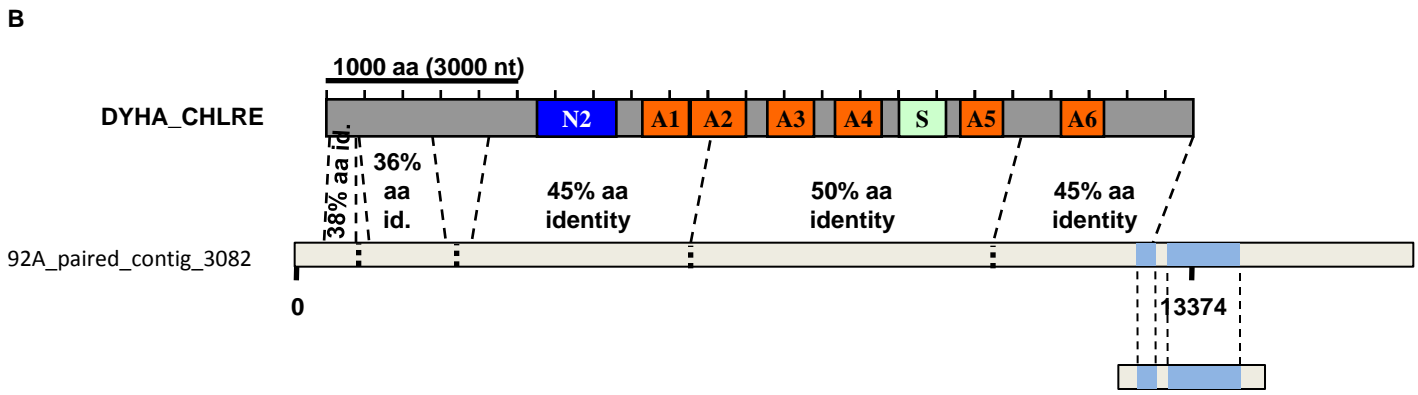
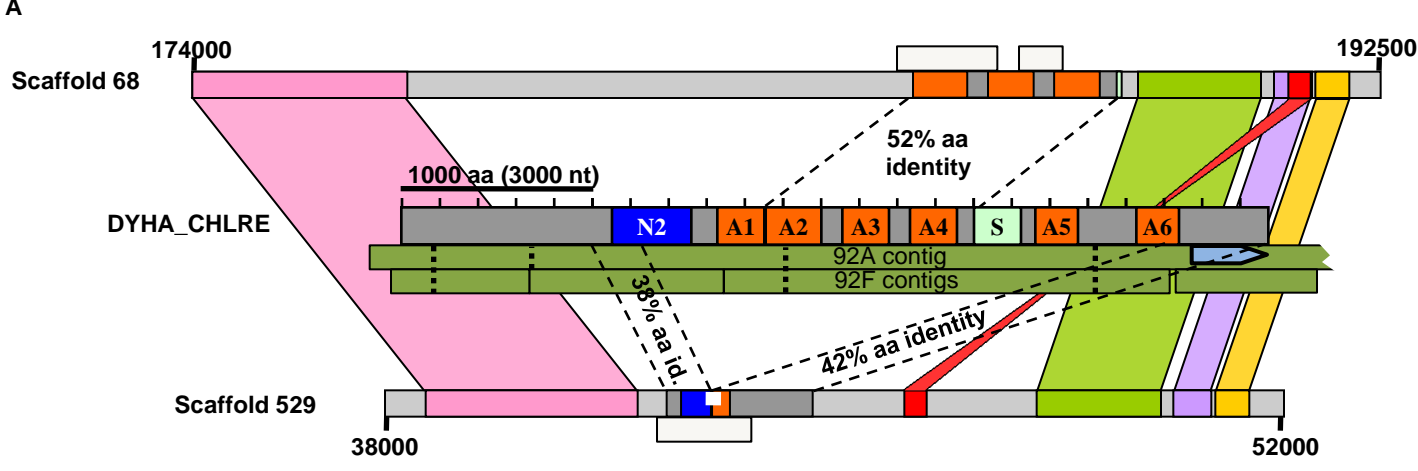
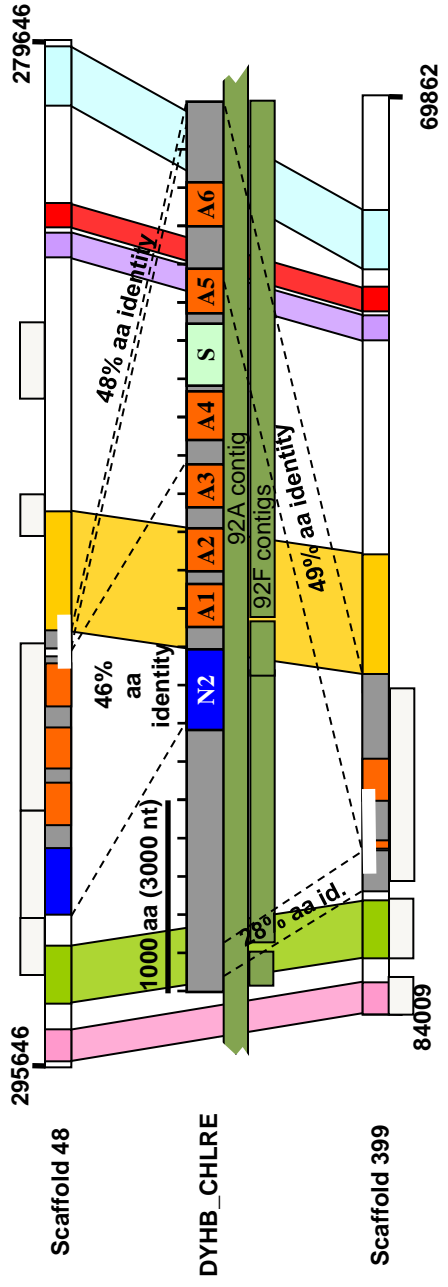


Figure S6 EH2_contig_20915

A



B

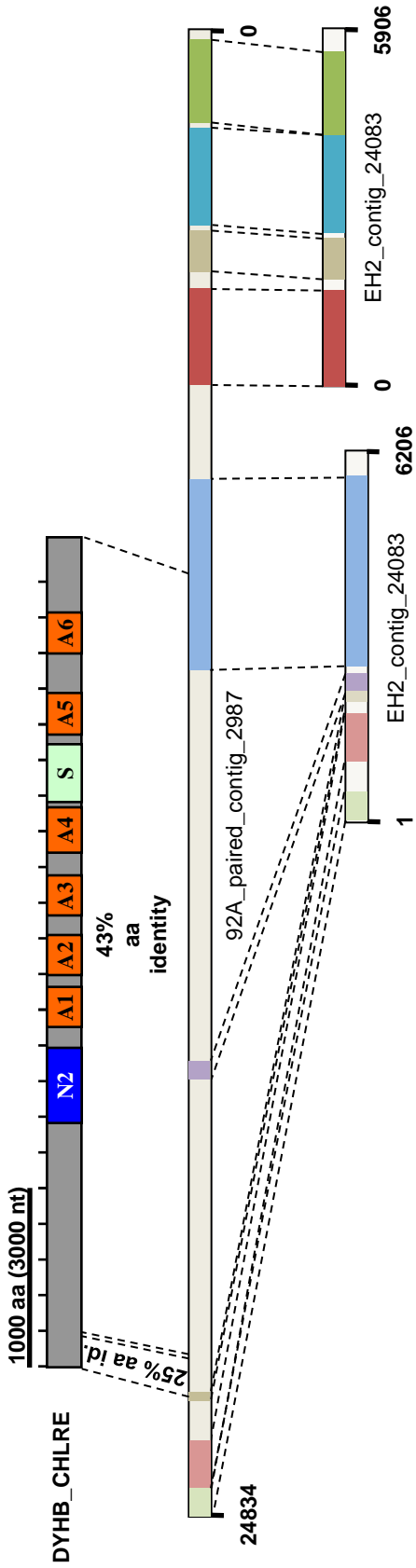
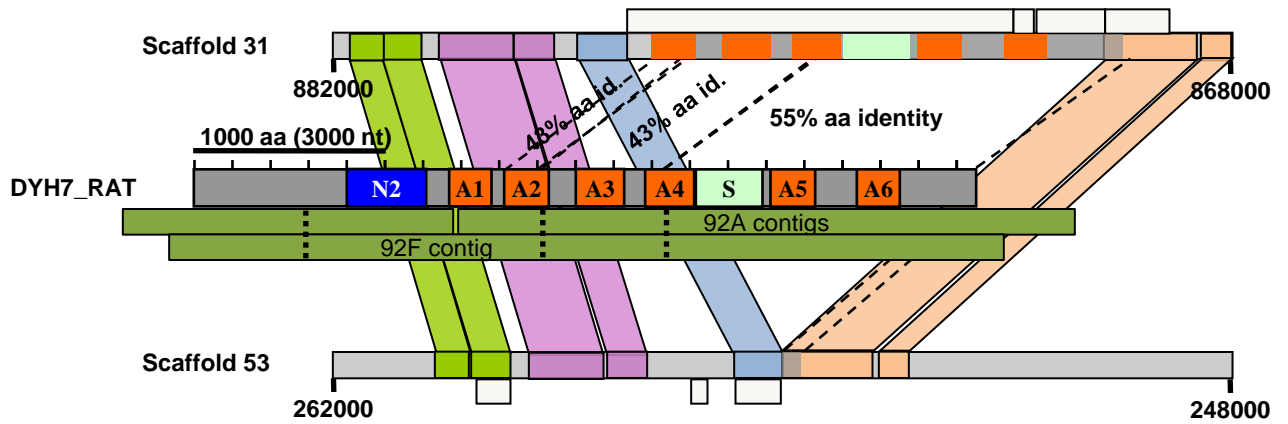


Figure S7

A



B

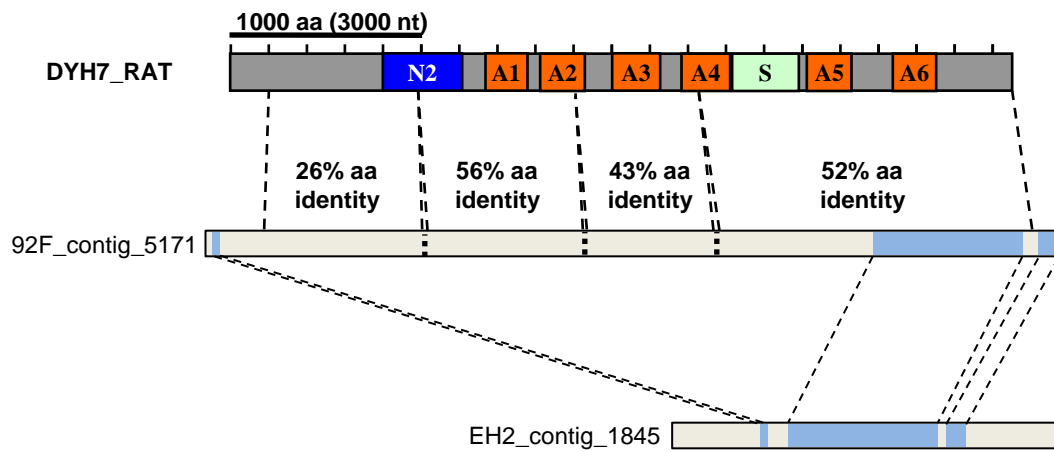


Figure S8

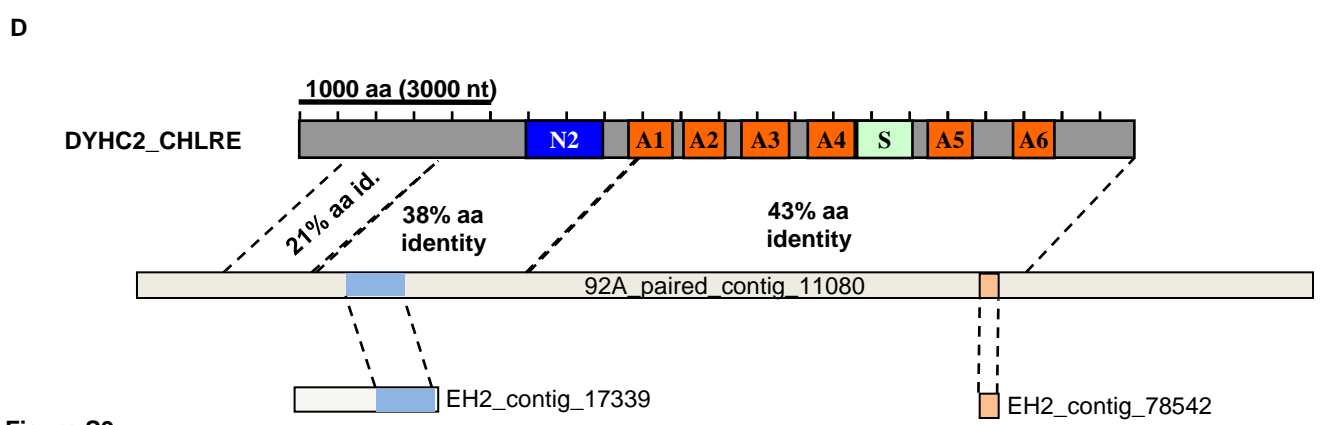
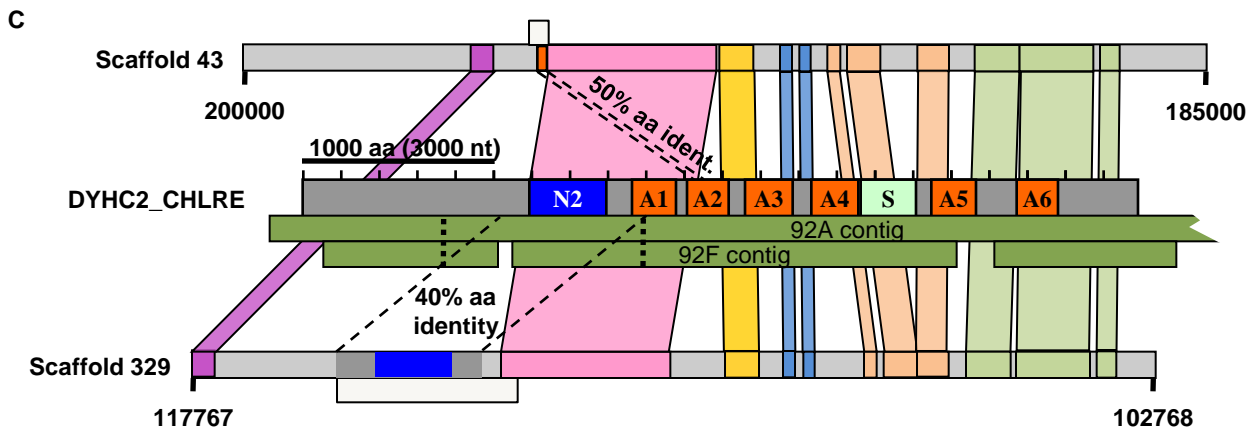
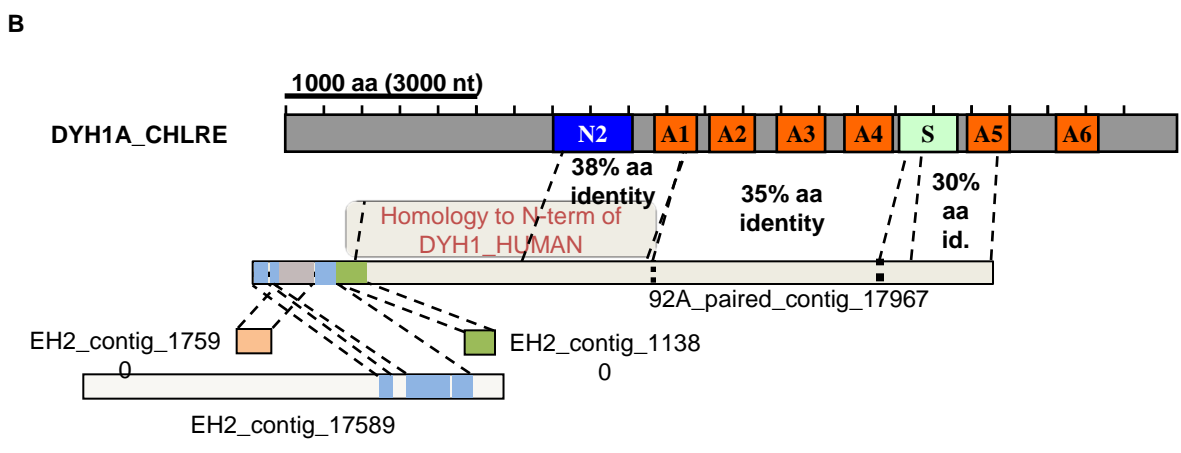
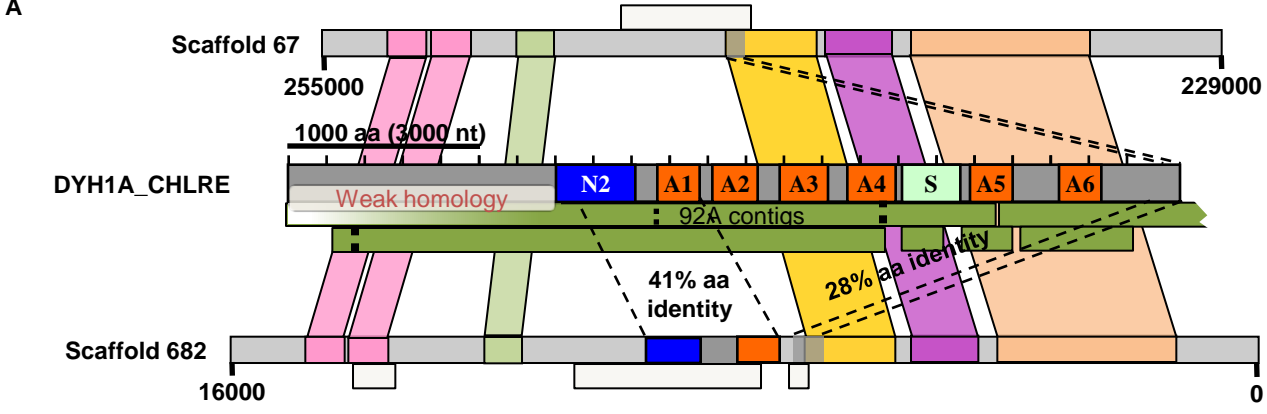


Figure S9

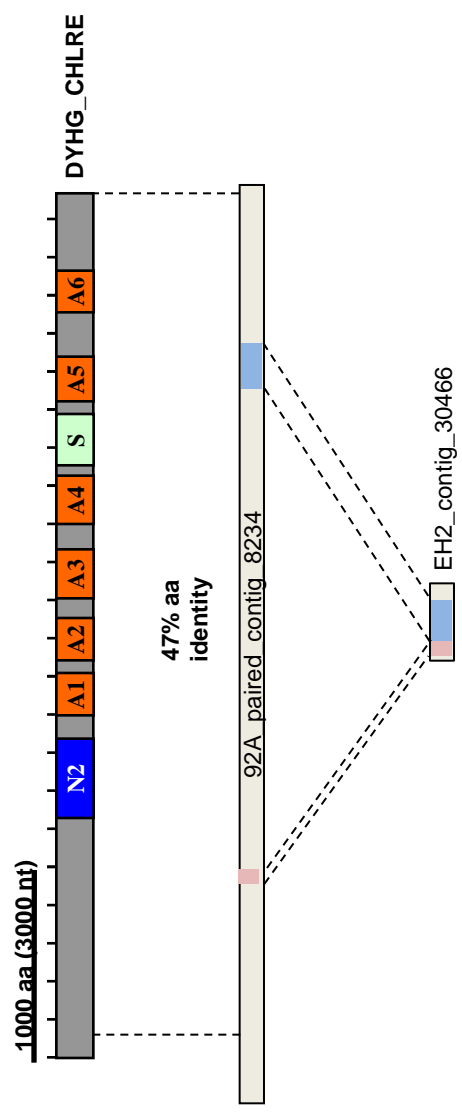
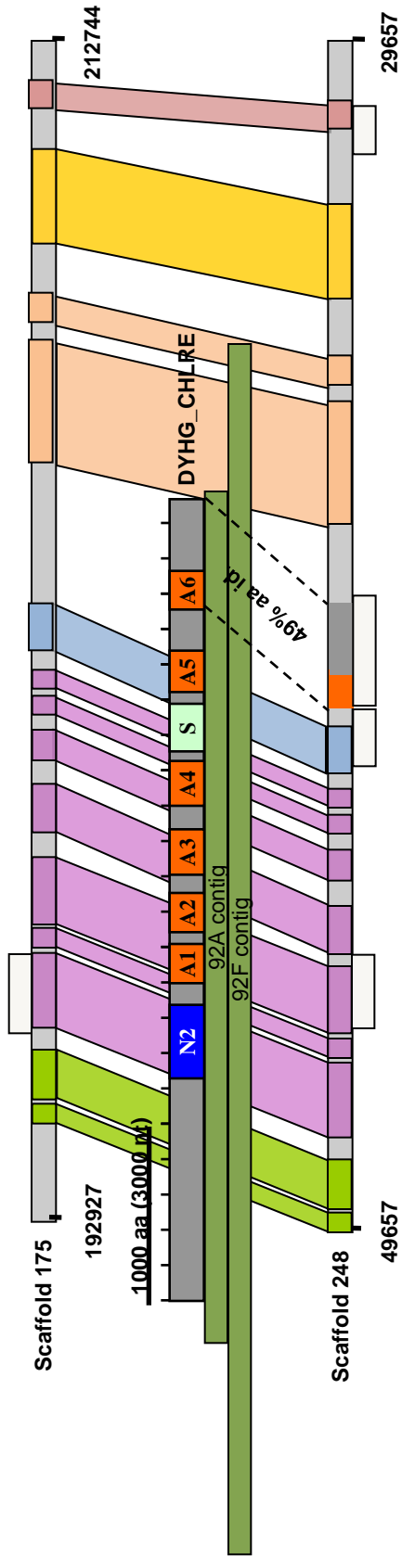


Figure S10

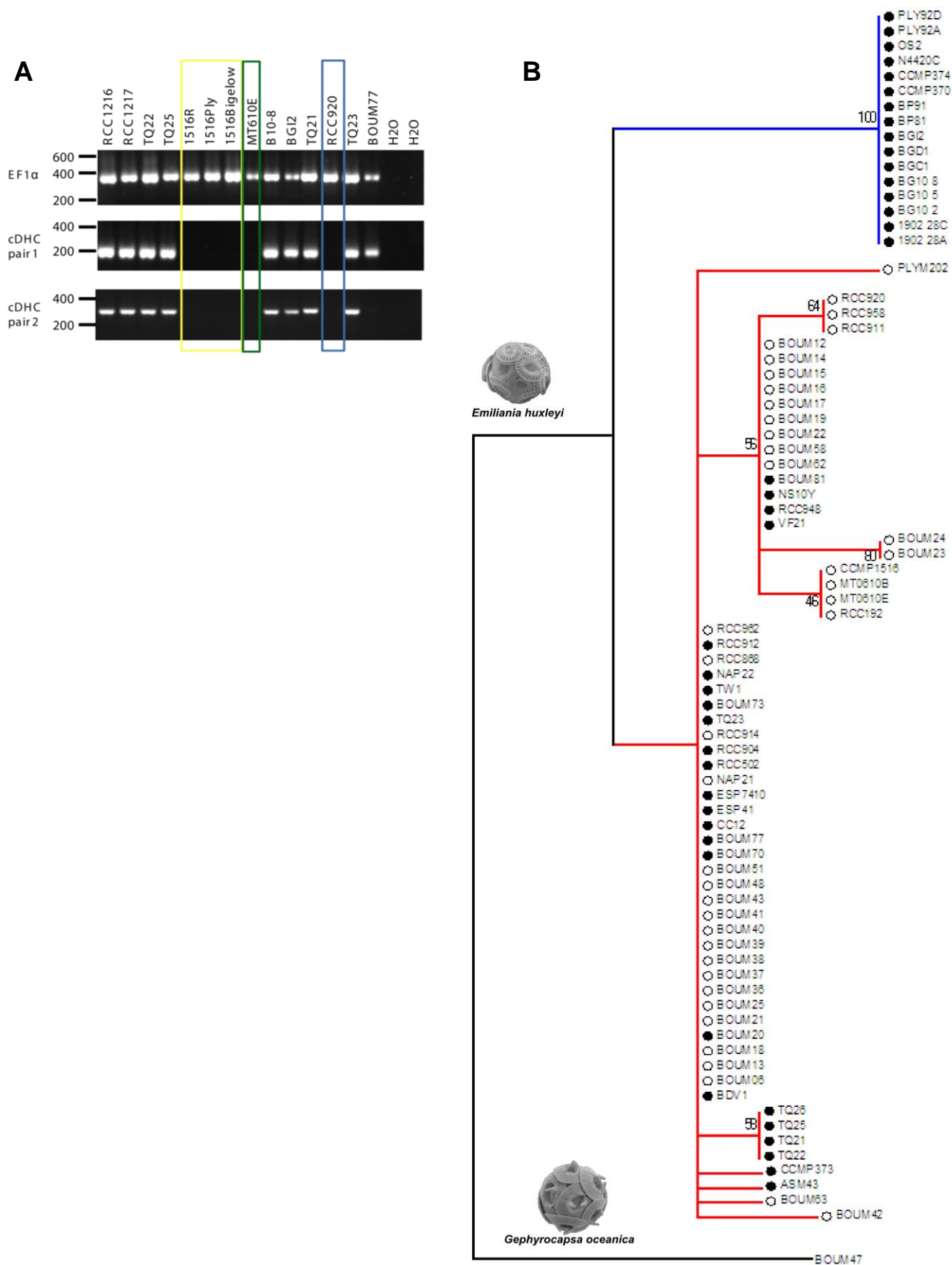
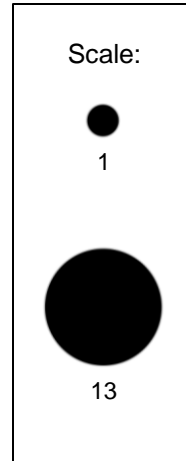
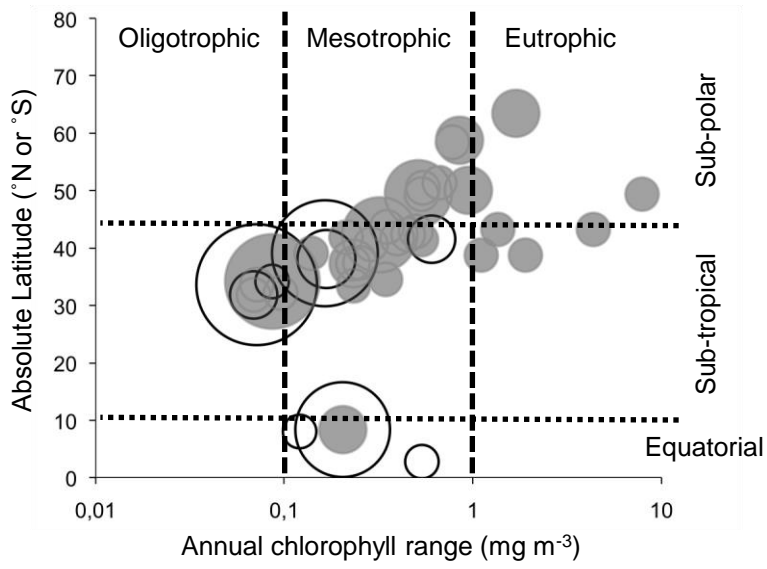
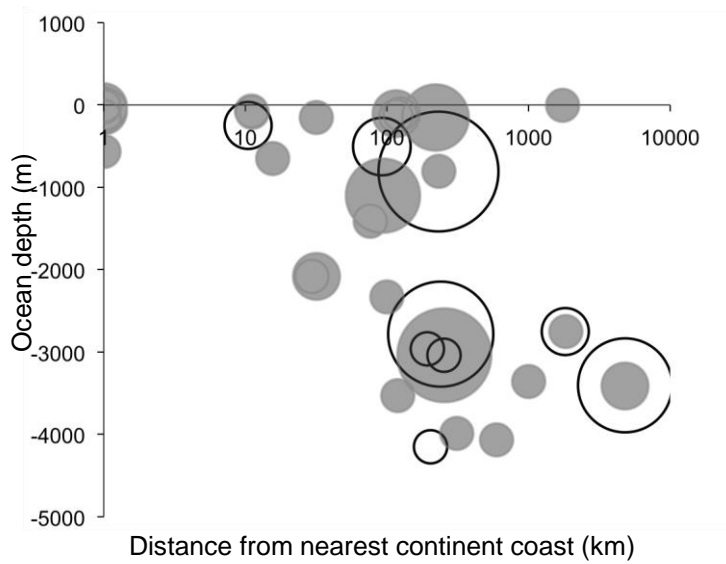


Figure S11

A**B**

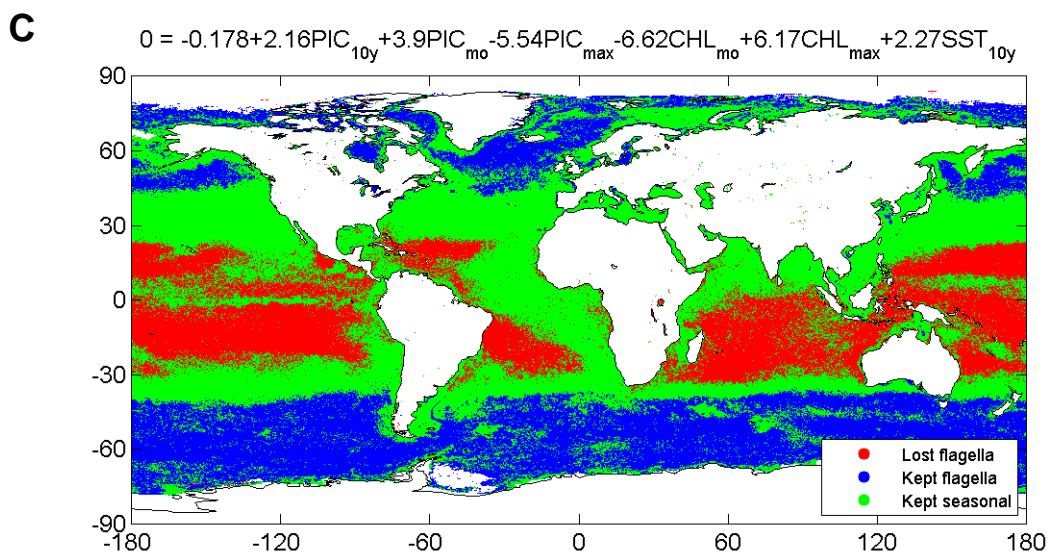
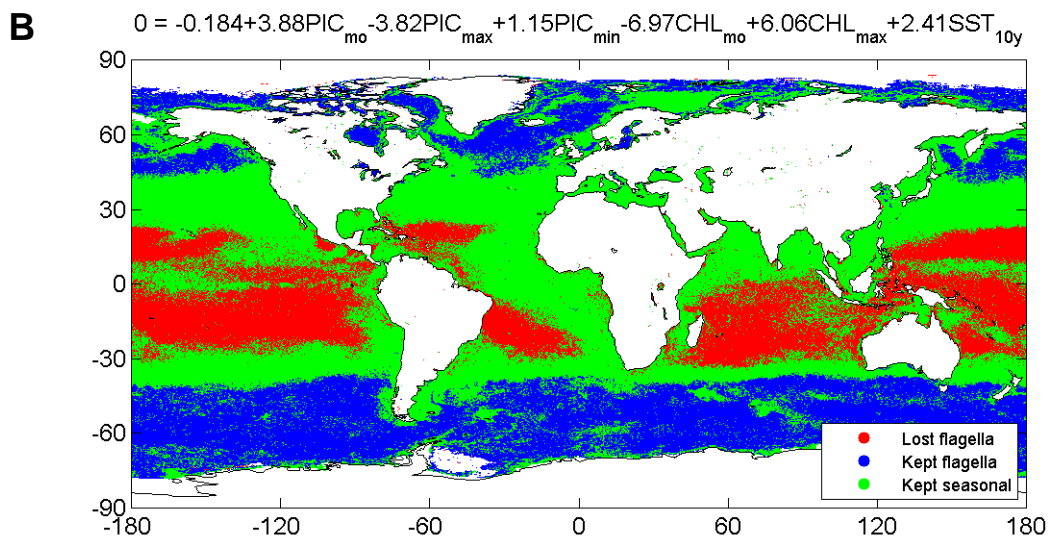
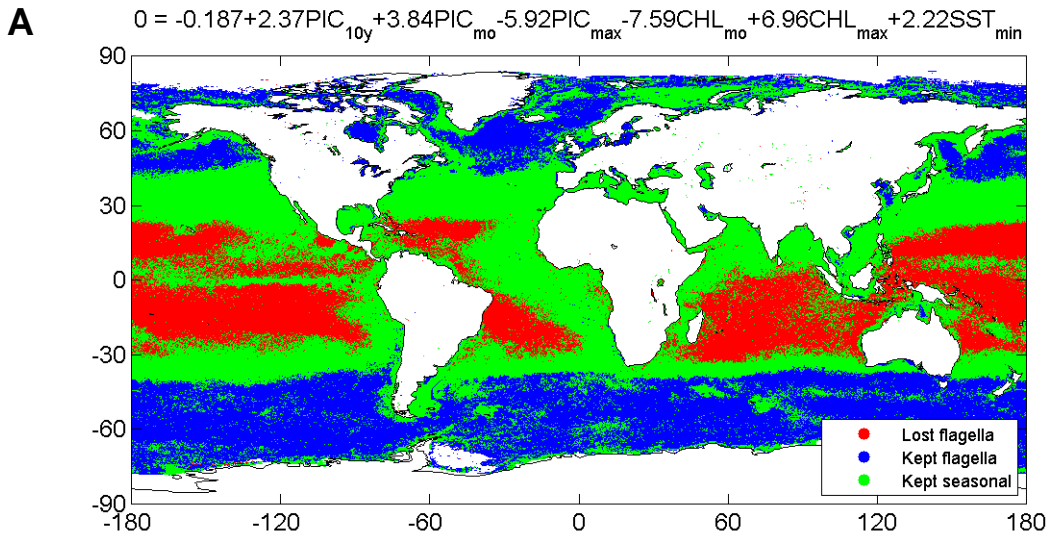


Figure S13

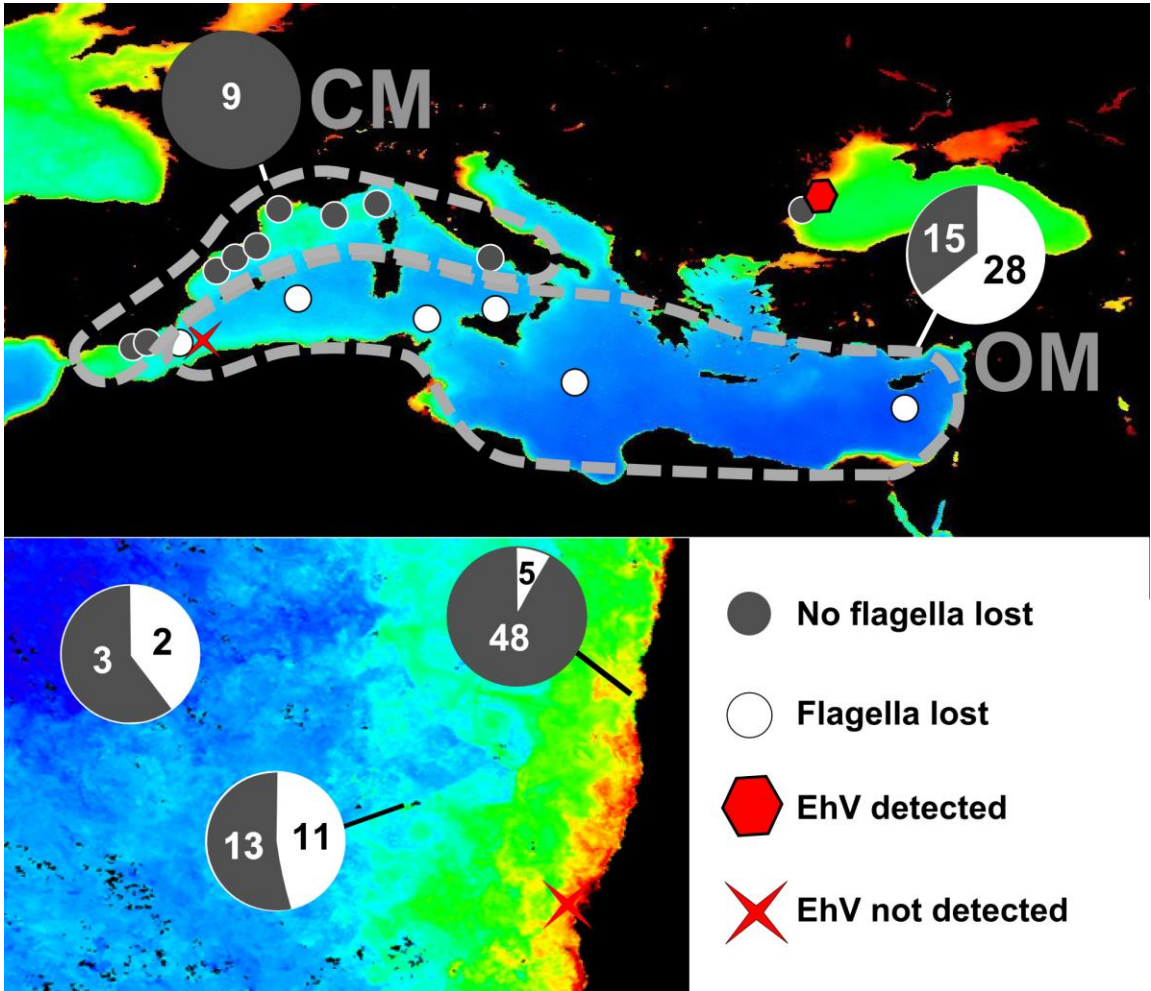


Figure S14