

73H-ParE_1448A
19H-ParE_1448A
11H-ParE_1448A
11H-ParE_DC3000
38H-ParE_1448A
32H-ParE_B728a
12H-ParE_1448A
12H-ParE_DC3000
4H-ParE_DC3000
4H-ParE_1448A
4H-ParE_B728a

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1      10      20      30      40      50      60      70      80      90      100      110      116
MKIIFWTPFAVGRDRRIYDYIE--ADNPSSAALAUDELFEERSGRIVDHEGIGK-PCRIVGTCEL-VAHRN---YILVYDVVD---NAVRLRLVLAHARHWPPS
MPQIEELSEKADSDLEAIEHYAAGLMGHQRADEVSTILE-SIEDIATFTGMGR-PSGAPDVRELALTRYPP--ELVSVVRS---QVVFLVRVLHERNERLNTSKI PDQFS
MCVFWLKTALINLDEEAAYIA--QDNPAATAAFVKAIQSSVTDIASFAMGR-ECRIAGTREWPLPDLP--YILVYRIIRS---GRILVLRIFHTIRQSPVW
MCVFWLKTALINLDEEAAYIA--LENPAATAAFVKAIQI SVKDIASFALGR-ECRIAGTREWPLPDLP--YILVYRIIRS---GRILVLRIFHTIRQSPVW
MLPVWLSPALDDIREIATYIA--WENPSAARRIKSLIQEAEIETMAEHYLYR-SCBAPGTREL-VAHPN---YILVYRVTL---KRIEYVVIHARQYPS
MTTFKLEELPSALIEWEKLGHTIR--VQLKKKLLERLGLPRI PGDAIHGMEDHYKI-LRSG-----YILVYRVIE---DRVYIVYVAVGIRERGNIDYSAKGRLGP
MTYNLEFDARALIEWHKLGDTIR--QQLKKKLLATILVAPRVEANLHALIDCYKIKLRSG-----YILVYQVID---QEVYFVYVAVDGREREEVYRKATDRLGR
MTYSLEFDARALIEWRKLGDTIR--QQLKKKLLATILVAPRVEANLHALIDCYKIKLRSG-----YILVYQVID---QEVYFVYVAVDGREREEVYRKATDRLGR
MNMFAIRRTDVAACGSILEDQVEHIAVYQGFSPAAQRIDTLIDA IQDKLSTLGLYPVSFRLSELGVLHYRELNADGTRIFMEVRIETDDINVMIVLVLGGQSVEQALIRYCLLQPI
MNTFATIRTEVAACGSILEDQVEHIAITQGFSLAAQRINTLIDV IQDKLSTLGLYPVSFRLSELGVLHYRELNADGTRIFMEVMDAGVTVMIVLVLGGQSVEQALIRYCLLQPI
MNTFATIRRTDVAACGSILEDQVEHIAVYQGFSSAAQRIDTLIDA IQDKLSTLGLYPVSFRLSELGVLHYRELNADGTRIFMEVMDAGDINVMIVLVLGGQSVEQALIRYCLLQAI

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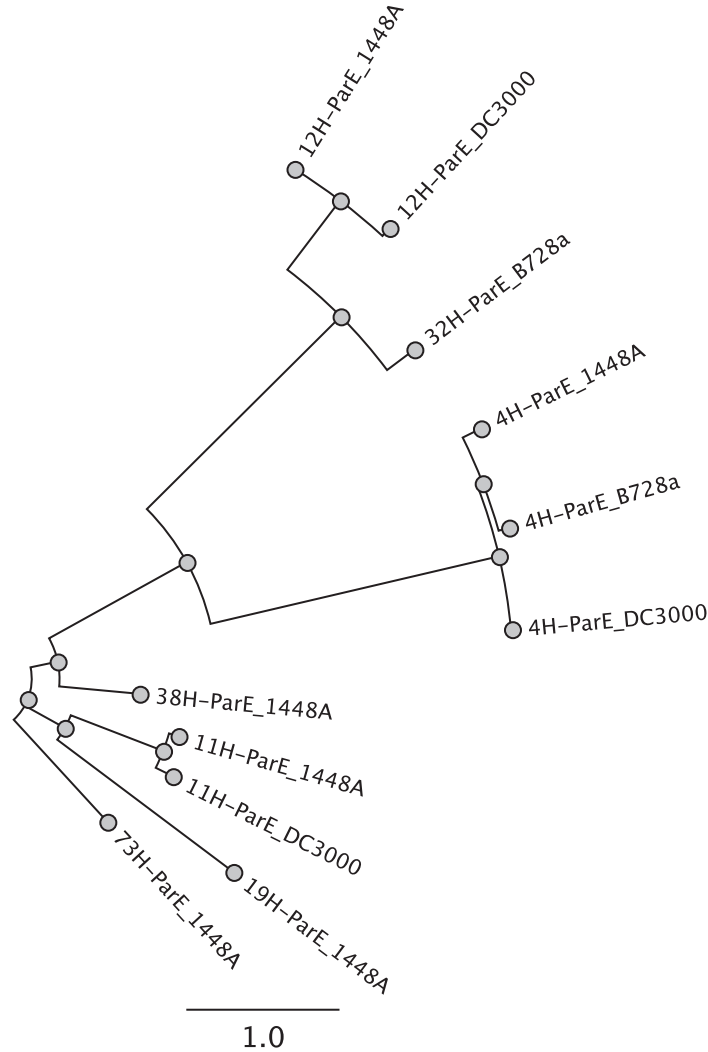


Fig. S2. Alignment (up) and clustering (down) of different parE homologs in the three model strains B728a, 1448A, and DC3000. Orthologs with same hit names were conserved (eg. 4H-parE), but paralogs with different hit names were not conserved (eg. parE of 1448A).