

**YB334 BSH sequence and other strains' BSH sequence used in Figure S1**

>131-B

MCTGVRFSDDDEGNTYFGRNLDWSFSYGETILVTPRGYHYDTVFGAGGKAKPNAVIGVGVMMADRP  
MYFDCANEHGLAIAGLNFPGYASFVHEPVEGTENVATFEFPLWVARNFDSVDEVEEALRNVTLVSQI  
VPGQQESLLHWFIFDGGKRSIVVEQMADGMHVHDDVDVLTNQPTFDHFMENLRNYM CVS NEMA  
EPTSWGKASLTAWGAGVGMHGIPGDVSSPSRFVRVAYTNAHYPQQNDEAANVSRLFHTLGSVQM  
VDGMAKMGDGGQFERTLFTSGYSSKTNTYYMNTYDDLAI RSYAMADYDMDSSELISVAR

>195-B

MCTGVRFSDDDEGNTYFGRNLDWSFSYGETILVTPRGYHYDTVFGAGGKAKPNAVIGVGVMMADRP  
MYFDCANEHGLAIAGLNFPGYASFAHEPVEGTENVATFEFPLWVARNFDSVDEVEEALRNVTLVSQI  
VPGQQESLLHWFIFDGGKRSIVVEQMADGMHVHDDVDVLTNQPTFDHFMENLRNYM CVS NEMA  
EPTSWGKASLTAWGAGVGMHGIPGDVSSPSRFVRVAYTNAHYPQQNDEAANVSRLFHTLGSVQM  
VDGMAKMGDGGQFERTLFTSGYSSKTNTYYMNTYDDPAIRSYAMADYDMDSSELISVAR

>YB334-L

MCTGLRFTDDQGNLYFGRNLDVGDYGEQVIITPRNYPLPYKFLDNTTTT KAVIGMGIVVDGYPSYF  
DCYNEDGLGIAGLNFPHF A KFS DGPIDGKINLASYEIMLWVTQNFTHVSEVKEALKNVNLVNEAINTS  
FAVAPLHWIISDSDEAIIVEVSKQYGMKVFDDKVGVL TN SPDFNWHLTNLGN Y TGLNPHDATAQSW  
NGQKVAPWGVGTGSLGLPGDSIPADRFVKAAYLNVNYPTAKGEKANVAKFFNILKSVAMIKGSVN  
DQ GKDEYTVYTACYSSGSKTY YCNFEDDFELKTYKLDDHTMNSTSLVTY

>004-L

MCTGLRFTDDQGNLYFGRNLDVGDYGEQVIITPRNYPLPYKFLDNTTTT KAVIGMGIVVDGYPSYF  
DCYNEDGLGIAGLNFPHF A KFS DGPIDGKINLASYEIMLWVTQNFTHVSEVKEALKNVNLVNEAINTS  
FAVAPLHWIISDSDEAIIVEVSKQYGMKVFDDKVGVL TN SPDFNWHLTNLGN Y TGLNPHDATAQSW  
NGQKVAPWGVGTGSLGLPGDSIPADRFVKAAYLNVNYPTAKGEKANVAKFFNILKSVAMIKGSVN  
DQ GKDEYTVYTACYSSGSKTY YCNFEDDFELKTYKLDDHTMNSTSLVTY

>094-L

MCTGLRFTDEQGNLYFGRNLDVGDYGEQVIITPRNYPLPYKFLDNTTTT KAVIGMGIVVDGYPSYFD  
CYNEDGLGIAGLNFPHF A KFS DGPIDGKINLASYEIMLWVTQNFTHVSEVKEALKNVNLVNEAINTSF  
AVAPLHWIISDSDEAIIVEVSKQYGMKVFDDKVGVL TN SPDFNWHLTNLGN Y TGLNPHDATAQSW  
NGQKVAPWGVGTGSLGLPGDSIPADRFVKAAYLNVNYPTAKGEKANVAKFFNILKSVAMIKGSVN  
DQ GKDEYTVYTACYSSGSKTY YCNFEDDFELKTYKLDDHTMNSTSLVTY

>135-L

MCTGLRFTDDQGNLYFGRNLDVGDYGEQVIITPRNYPLPYKFLDNTTTT KAVIGMGIVVDGYPSYF  
DCYNEDGLGIAGLNFPHF A KFS DGPIDGKINLASYEIMLWVTQNFTHVSEVKEALKNVNLVNEAINTS  
FAVAPLHWIISDSDEAIIVEVSKQYGMKVFDDKVGVL TN SPDFNWHLTNLGN Y TGLNPHDATAQSW  
NGQKVAPWGVGTGSLGLPGDSIPADRFVKAAYLNVNYPTAKGEKANVAKFFNILKSVAMIKGSVN  
DQ GKDEYTVYTACYSSGSKTY YCNFEDDFELKTYKLDDHTMNSTSLVTY

>HJG-L

MCTAITLNGNSNYFGRNLDLDFSYGEQVIITPAEYEFKFRKEKAIKNHKS LIGV GIVADDYPLYFDAINE  
DGLGMAGLNFPGNAYYSDFLENDKDNITPFEFILWILGQCSDVNEARNLVERINLINLSFSEQPLAGL  
HWLIADREKSIVVEVTKSGVHIYDNPIGVLTNNPEFN Y QMYNLNKYRNLSISTPQNTFSDSVDLKV D G  
TGFGGIGLPGDASPESRFVRAAFSKLNSKGT TLEEDITQFFHILGTVEQIKGVNKTESGKEYTVYSNCY  
DLDNKTLYYTTYENRQIVSVTLNKDKNGNKL VVYPFERKQIINKLN

>193-L

MCTAITLNGNSNYFGRNLDLDFSYGEQVIITPAEYEFKFRKEKAIKNHKSLIGVGIVADDYPLYFDAINE  
DGLGMAGLNFPGNAYYSDFLENDKDNITPFEFILWILGQCSDVNEARNLVERINLINFSFSEQLPLAGL  
HWLIADREKSIVVEVTKSGVHIYDNPIGVLNPEFNQMYNLNKYRNLSISTPQNTFSDSVDLKVDG  
TGFGGIGLPGDASPESRFVRAAFSKLNSSKGTVEEDITQFFHILGTVEQIKGVNKTESGKEEYTVYSNC  
YDLDNKTLTYTTYENRQIVAVTLNEDKNGNRLIAYPFERKQVINKLN