

```

SjPpt1      1:      M I W R G F C V F R F S R Q F L L R N N A Y K V L I G . . . I I H : 30
SpPpt1     1:      M I I K P I A S P . . A R Y F L R T P S W S A V A I F Q A V A K I K : 31
ScryoPpt1  1:      M I K T A P R I H . . H P F I P I Q C W T N I L V N K I N T F : 31
SoPpt1     1:      M F L T T P R I Y . . S S I P S R C S I Y V L N K R S L T Y : 31
HsPpt1     1: M T P I S Q V R M R K G S A H T A A Q P G R L G L H P A G A T A H A C R G M T S I R A R P G L T S A M I C S R A A G F A R G I R A L A L A A : 70
ScCoq2     1:      M F I W O R K S I I L L G R S I L G S G R V T V A G T I G S S R R R R : 34

SjPpt1     31: T S Y R A Y S S . . . . S E S D Q C N G V R S K T K E . . . . . K R A I F E I K T Y C S L S R V H A P V G T I L L Y : 84
SpPpt1     32: P L O I R T N S . . . . . S N S V T P L I S P S K K S . . . . . K D L F S K R W O Y Y A E I S R A G S P T G T I L L Y : 82
ScryoPpt1  32: S V S I R O T F G Y S S L S E S K Q N T O P P P A V K K S . . . . . W E S R L E E W T A Y A H L S R A Y N P T G T I L L Y : 89
SoPpt1     32: S F I V R O T S A Y S S F S E S N Q D N I K O L P T V K K P . . . . . L F S O L S Q I N A Y A H L S R A F N P T G T I L L Y : 89
HsPpt1     71: L P G W R G R S F A L A R A A G A P H G G D L Q P A C P F P R G R Q L S L S A A A V D S A F P L O P V L R L M R L K P I C T I L L Y : 140
EcUbiA     1:      M E I S L T Q N L L A H H L M R T K P T C A L L I L : 29
ScCoq2     35: I S S S S S S P S S K E S A P V F T S K E L E V A R K E R L D . . . . G L G P V S R L P K W I P Y A E L M R L K P V G T I L L Y : 99

SjPpt1     85: C P C T W S I L M A A Y S I K V P I E S T V K I L T I F A L G S F V M R S A G C V I N D L W D R K L D A K V R R S S N R P L A N G V G V P : 154
SpPpt1     83: S P C T W S I L M A A Y A Y D S I L V N V T K M L A L F G V G S F L M R S A G C V I N D L W D R E L D A K V E R S K S R P L A S G K I S V R : 152
ScryoPpt1  90: S P C T W S I L M G A Y S I N S L F D V S K M L A L F G V G S F L M R S A G C V I N D L W D R K L D A K V E R S K S R P L A S R L V S V R : 159
SoPpt1     90: S P C T W S I L M G A Y S I N S L F D V F K I L A L F G A G S F L M R S A G C V I N D L W D R N L D A K V E R S K S R P L A N K L V S V R : 159
HsPpt1     141: L P C T W S I G I A A E P G . . . C E P D W Y M L S L F C H G A L M R G A G C T I N D W D O D Y K K V T R I A N R P I A A G D I S T F : 207
EcUbiA     30: W P T L W A I W A T P G V P . . . Q L W I L A I F V A G V W L M R A A G C V I N D Y A D R K E D G H V K R I A N R P L E S G A V I E R : 94
ScCoq2     100: L P C S W S I L M G A M M Q G A I L S A T A G M L G I F G V G A L V M R G A G C T I N D F L D R K L D Q V I R S V E R P I A S G R V S P R : 169

SjPpt1     155: E A I G L L G V O L S T A L I I I C S L N S Y T V K L G V I S L L E P V S I Y P S F K R F T Y Y P Q A F L G L T F S Y G A I M G W P A L V G A : 224
SpPpt1     153: Q A I S L L S V O L T A S L G I L L Q L N P Y T I K L G V A S L I P V C I Y P A M K R I T Y Y P Q V V L G L T F G Y G A M G W P A L A G E : 222
ScryoPpt1  160: E V S I L G V O L T A S L G I L L Q L N P Y T I K L G V A S L I P V C I Y P A M K R I T Y Y P Q V V L G L T F G Y G A M G W P A L V G E : 229
SoPpt1     160: E A I S L L G V O L T A S L G I L L Q L N P Y T I K L G I A S L L P V C I Y P A M K R I T Y Y P Q V V L G L T F G Y G A M G W P A L V G E : 229
HsPpt1     208: Q S F V F L G G O L T L A L G I L L C L N Y S I A L G A S L L I V T I Y P I M K R I S Y W P Q I A L G L T F N W G A I G W S A I K C : 276
EcUbiA     95: E A R A L F V V L W L I S F L L V L T L N T M T I L S I A A L A L A W I Y P F M K R Y T H L P O V V L G A A F C W S I P M F A A S . . : 162
ScCoq2     170: R A I V F L G A Q T L V G I G I S L I P A Q C W W L G I A S L P I V F T Y P L F K R F T Y Y P Q A A L S A C F N W G A I I G P P A G . . : 237

SjPpt1     225: D A M F W P V V A P L Y L S V E W V I M Y D T I Y A H Q D K L D D V I A G I Y S T A L I F C K R T K P V I F L A S T I Q Y V F L S E A G : 294
SpPpt1     223: A C M N W S V V A P L Y L S I T S W I V L Y D T I Y A H Q D K R D D V K A N I Y S T A L R F G D N T K P V I C G L A A T O L A T L A T A G I : 292
ScryoPpt1  230: A C M N W S V V A P L Y L S A V S W I V L Y D T I Y A H Q D K R D D V K A N I Y S M A L R Y G D N T K P V I T G L A I F O L S I L T T A G I : 299
SoPpt1     230: A I M N W S V V A P L Y L S I V S W I V L Y D T I Y A H Q D K R D D V K A N I Y S M A L R Y G D N T K P I T G L A I F O L S I L T T A G I : 299
HsPpt1     276: . S C D P S V C L P L Y F S G V M W T I Y D T I Y A H Q D K R D D V L I G I K S T A L R F G E N T K P V L S G F S A M L A L S L V G V : 345
EcUbiA     162: . E S V P L S C W L M I A N I L W A V A Y D T Q Y A M V D R D D D V R I G I R S T A L I F C Q O Y D K L I T G I Q I G V L A M A I I C E : 231
ScCoq2     237: . V M S W P T I E P L Y L S S Y L M C I T Y D T I Y A H Q D K R F D I K A G I R S T A L A W G P R T K S I M K A N S A S O A I L A V A G : 306

SjPpt1     295: A N . . H Q G P I F Y L L G V C G S Y I S T L L M I I N V N I N S P K N C M I W F K O N S K M G A I T L A I T L D W I S F L K : 357
SpPpt1     293: M N . . G O G P I F Y T L G V A G A A Y R L S M I Y K V D L D I P K D C F R F E K R N S N T G I L V A A A I A L D W L A K S I Y D S : 358
ScryoPpt1  300: C N . . S Q G P I F Y T L G V A G A A Y R I F S M I Y K V D L S P K D C F S W F K R N S N T G I L V T A A I A L D W L A K A I T S : 363
SoPpt1     300: F N . . N O G P I F Y T L G V A G T A Y R I F S M I Y K V D L S P K D C F S W F K R N S N T G I L V T A A I A L D W L A K A I T S : 363
HsPpt1     346: N S G . Q T P Y A A L G A V G A H . . L T H O I Y T I D I H R F E D C W N R F I S N R T L C L I V F L I V L G N L W E K K I D K T K : 412
EcUbiA     232: L N G L G W G Y W S I L V A G A L F V Y Q O K I I A N R R . . . E A C F A F M N N N Y V C L V I F L G L A I S Y W H F : 290
ScCoq2     307: N S G L L W C P C F I G . G L C V F A Y R L F S M I K K V D L D N P K N C W I Y F N A N I N T G L Y F T A L A D Y I L R L I G F L : 372

HsPpt1     413: K G I E N K I E N : 421

```

Fig. S1. Alignment of the amino acid sequences of PHB:polyprenyl diphosphate transferase.

SjPpt1: PHB:decaprenyl diphosphate transferase encoded by *Sjpt1* from *S. japonicus* (NCBI accession number: XP_011049027); SpPpt1: PHB:decaprenyl diphosphate transferase encoded by *ppt1* from *S. pombe* (Z69728); ScryoPpt1: SPOG_00640 from *S. cryophilus* (XP_013024269); SoPpt1: SOCG_02185 from *S. octosporus* (XP_013016133); HsPPT1: PHB:decaprenyl diphosphate transferase encoded by *PPT1* from *H. sapiens* (NP_056512); EcUbiA: PHB:octaprenyl diphosphate transferase encoded by *ubiA* from *E. coli* (NP_418464); and ScCoq2: PHB:hexaprenyl diphosphate transferase encoded by *COQ2* from *S. cerevisiae* (CAA96321). Identical and similar amino acid residues in more than three sequences are indicated by black and gray boxes, respectively. Numbers on the left and right sides indicate the positions of amino acid residues. Dots indicate the absence of the corresponding amino acid residues at those positions. The amino acid sequences were aligned by the ClustalW program.

```

SjDps1      1:  M L R G R N S V W R : 11
SpDps1      1:  M L Q V V Y L K : 8
ScryoDps1   1:  M L K : 2
SoDps1      1:  M L H N G I L K : 8
ScCoq1      1:  M F Q R S G A A H H I K I L S S R R C : 20
HsDPS1      1: M A S R W W R R R G C S W K P A A R S P G P S P G R A G L P G S A A A E V R A Q V H R R K G L D L S Q I P Y I N L V R H T S A C P N : 70

SjDps1      12: R S T I F S V C H I N T N N S P C V Q E K T E T A L I R D L L R R V S P G I R R M L G C N L E L D A S T Y Y T I A O G K Q R P S L : 81
SpDps1      9: H M R L W S L G K V R S T V L R F S T T N R N A S H L I K N E L E O S P G I R O L A S N S E L E E C S Y Y T I A O G K O M R P S L : 78
ScryoDps1   3: C F T M S I W N P L V V F S R S M S K T A N P T G L I E N E L Q V S P G I R L L S R F E E L S K C S Y Y T I A O G K O M R P S L : 72
SoDps1      9: Q S L S I W R K G C R V F S R S N K T A N P A G L I E N E L Q V S P G I R E L L S R C E E L S K C S Y Y T I A O G K O M R P S L : 78
ScCoq1      21: F K S S F A V A L N A A S K L V T P K I L W N N P I S L S K E N T A K N I V A L G S G H P V L K V S Y Y P E T E G K K R P L I : 90
HsDPS1      71: V C R I S R F H H T T P D S K L S E K Y T D P F K G W R L K G Y E D I R E L L I S T S E L K E M S E Y Y F D C K G A P R F I : 140
EcIspB      1: M N L E K I N E L T A D D A G V N A I L E Q L N S D V Q L I Q L G Y I V S C G K R I R E M I : 51

SjDps1      82: V L L S R A V S L N G I N R S V A S . . . . . E R Y L D C N E A L L D G . . . . . : 116
SpDps1      79: V L L M S A T S L C H G I D R S V V G . . . . . D K Y I D D D L R S F S T C . . . . . : 113
ScryoDps1   73: V L L M S A T S L C S S I D G S I V G . . . . . S S L L E D D A E V Y I S T C . . . . . : 107
SoDps1      79: V L L M S A T S L C S S I D G S V V G . . . . . S S L L E D D A E D H P T C . . . . . : 113
ScCoq1      91: V L L S R A L S E I P M T E R N H K I D K S D V P E D P I Y S K P S Q N L F Q P A S S I S E L H L L H C I K P L N P L T K G P E P L : 160
HsDPS1      141: V A L M A R A C N I H H N N S R H V O . . . . . : 160
EcIspB      52: A L L A A R A V G Y E G N . . . . . : 64

SjDps1      116: . . . . . D V L P S Q L R L A Q I T E M I H V A S L L H D D V I D L A I H R R G Q V S C N I A F G N Q O A V A G D F I L R A S T : 177
SpDps1      113: . . . . . Q V L P S Q L R L A Q I T E M I H A S L L H D D V I D H A N V R R G S P S N I A F G N R S I L A G N F I L R A S T : 174
ScryoDps1   107: . . . . . Q V L P S Q L R L A Q I T E M I H T A S L L H D D V I D H A S V R R G P S S N I A F G N R S V L T G N F I L G R A S T : 168
SoDps1      113: . . . . . Q V L P S Q L R L A Q I T E M I H T A S L L H D D V I D H A S S R R G P S S N I A F G N R S V L T G N F I L G R A S T : 174
ScCoq1      161: P E E T F D K Q R G L L K O R R L A E I V E M I H T A S L L H D D V I D H S D T R R G P S C N A A T N I M A V L A G D F I L G R A I V : 230
HsDPS1      160: . . . . . S Q R A I L A E M I H T A S L L H D D V I D H S S R R G H V N K I W E E I M A V L A G L I L S A A S I : 217
EcIspB      64: . . . . . A H T P A A T E F I H T A L L H D D V D E S D M R R C A A A N A A F G N A A S V L V G D F I Y T R A F Q : 121

SjDps1      178: A M A R L R N P V T E L L A T V I A D L R G E F I Q L K N T . . . . . V D E K G G A L Q A S . . . . . : 220
SpDps1      175: A M A R L R N P V T E L L A T V I A D L V R G E P I Q L K N T . . . . . V D P S S E E K Q S N . . . . . : 218
ScryoDps1   169: A M A R L R N P V T E L F A T V A D L V R G E P I Q L K N T . . . . . V N T N L B A Q A F H . . . . . : 212
SoDps1      175: A M A R L R N P V T E L F A T V A D L V R G E P I Q L K N T . . . . . A D T N S L E I Q P F H . . . . . : 218
ScCoq1      231: S I S R L I N E P E V E L S N S I A N L V G E F I Q L K N T S I D A D I T I E N G H K L P V P S K K E V K E H F R V P S R Q Q G : 300
HsDPS1      218: A L A R L G N T V I S I T C V I D L V R G E P I Q L K S K . . . . . E N E N E R . . . . . : 255
EcIspB      122: M M T S L G S L V L E I S E A V N V A E G E V L O L M N . . . . . V N D P D I T E E N . . . . . : 162

SjDps1      220: . . . . . F D Y Y E K Y L K T A S L I S K S C M A A A L G K A V P S T V O A I G E T G R C G I A F O L M D D A L D K : 278
SpDps1      218: . . . . . F D Y Y E K Y L K T A S L I S K S C K A S T L G O C S P T V A T A A E Y G R C G T A F O L M D D V L D Y T : 276
ScryoDps1   212: . . . . . F D Y Y E K Y L K T A S L I S K S C S A A I L G O C S P T V I O A A S D G R V G T A F O L M D D V L D Y T : 270
SoDps1      218: . . . . . F D Y Y E K Y L K T A S L I S K S C S A A I L G O C S P T V I A A N V G R V G T A F O L M D D V L D Y T : 276
ScCoq1      301: L Q L S H D Q I I E T A F Y Y I E K Y L K T A A L I S K S C R C A A I S G A S P A V I E C Y D G R N G I C F O L M D D L D T : 370
HsDPS1      255: . . . . . R A H V E K T I K K T A S L I A N S C R A V S L G C P D P V H I T A Y Q Y G N G I A F O L M D D V L D Y T : 313
EcIspB      162: . . . . . V R V I Y S K T A R L F E A A A C S I L L G C I P E E K L O D Y G R V G T A F O L M D D L D Y N : 217

SjDps1      279: S I D G D L G R P A N A D L K G L A T A P V L F A W K O P E L E S A R S N F S K S E A . . . . . E O A R Q V R E A D G R K T E A W : 344
SpDps1      277: S K D E T L G R A A G A D L K G L A T A P V L F A W K Y P E L G A M I N R F N P S D . . . . . I O A R S L V E C T D I E O H T W : 342
ScryoDps1   271: S K D E T L G R A A N A D L N L G L A T A P V L F A W K Y P E L G A M I N R F N P S D . . . . . V K K A R E L V S T D G I E A T K W : 336
SoDps1      277: S K D E T L G R A A N A D L N L G L A T A P V L F A W K Y P E L G A M I N R F N P S D . . . . . V K K A R E L V S T D G I E A T K W : 342
ScCoq1      371: V S G K D L G R P S G A D L K G L A T A P V L F A W K E D P S L G P L S R N S E R G D . . . . . V E K T I S V R L H N G I A K T K I L : 436
HsDPS1      314: S C S Q G R P T S A D L K G L A T A P V L F A C Q Q P E N A M I R R F S L P G D . . . . . V D R A R Q V V L Q D G Q O T T Y L : 379
EcIspB      218: A D C E Q L G N V G D D L N E K P L E L L H A M H G T P E Q A Q I R T A I E C N G R H L E P V L E A N A C G S E W R Q R : 289

SjDps1      345: A G O I W K A G L I S S H P D S P P L O A L D I C R N V I T R K : 381
SpDps1      343: A K E Y I K A K T S L L C L P D S P A R K A L F A L A K V I T R K : 378
ScryoDps1   337: A K I Y I K A H V Q C I P D S P A R O A L H A A E K V V E R N Y : 372
SoDps1      343: A K E Y I K A H A L O C I P D S P S R O A L H A A E K V V E R N Y : 378
ScCoq1      437: A E Y R D K A L O N R D S D P S A N S A L E F L T N S I T R K : 473
HsDPS1      380: A O C H E A I R E S N R P S P E R D A L Q L S E I V I T R K : 415
EcIspB      288: A E E P A D K A I A A L Q V L P D I E M R E A L I G L A H I A V Q R D : 323

```

Fig. S2. Alignment of the amino acid sequences of polyprenyl diphosphate synthase.

SjDps1: decaprenyl diphosphate synthase encoded by *dps1* from *S. japonicus* (NCBI accession number: XP_002175659.1); SpDps1: decaprenyl diphosphate synthase encoded by *dps1* from *S. pombe* (CAB66154); ScryoDps1: SPOG_01333 from *S. cryophilus* (XP_013025475.1); SoDps1: SOCG_05355 from *S. octosporus* (XP_013017639); ScCoq1: hexaprenyl diphosphate synthase encoded by *COQ1* from *S. cerevisiae* (NP_009557.1); HsDPS1: decaprenyl diphosphate synthase encoded by *DPS1* (*PDSS1*) from *H. sapiens* (NP_055132.2); and EcIspB: octaprenyl diphosphate synthase encoded by *ispB* from *E. coli* (CUU95387.1). Identical and similar amino acid residues in more than three sequences are indicated by black and gray boxes, respectively.

```

SjDlp1      1:      M.....TYVRFARIMPRFGRN...SSWSSVLLKAVGVVSEKSTYHSD: 41
SpDlp1      1:      MSFFFAS.....LLRPSAIISSLLSLKK..PSWSSVLLKAVGVVSRDSRWHS: 47
ScryoDlp1   1:      MGLPLH.....ILRNPSLISSVFSVVK...SSWASVLLKAVGVVSRDSRWHD: 46
SoDlp1      1:      MGLPLH.....ILRNPSLISSVFSASK..SSWASVLLKAVGVVSRDSRWHD: 46
HsDLP1      1: MNFRQLLHLERYLGASGSPRRLWWSPLDITSSVGSWRGRSSKSPAHWNQVSEAEKLVGYPSFMS.: 68
MmDLP1      1: MSLRQLLRISGYLGASGPPSRHWYFRSLDSTISAGSWRGRSSRSPAHWNQVSEAEKLVGYPASFMS.: 69

SjDlp1      42: LIATLSEEMNLRSQLVQWTNS.EPLLDTVIQPYTTS.HARFFHPLLVLMSRASLDA T P S K Q O . . . . . : 104
SpDlp1      48: LLKMLSEEMSLNGQINTWTDN.NPLLDEITKPYRKS.STRFFHPLLVLMSRASVNGDPPSQOL . . . . . : 110
ScryoDlp1   47: LLNVLSEEMSLNKQLNAWTGN.NPLLDRIETPYRRS.NTOFFHPLLVLMSRASRIEGDTSQOM . . . . . : 109
SoDlp1      47: LLSVLSEEMQSLNKQLNSWTGN.NPLLDRIETPYRKS.DTOFFHPLLVLMSRASRVEGDTSQOM . . . . . : 109
HsDLP1      69: LRCLLSDELSNIAMQARKLVGTQHPLLTARGLVHDSWNSLQLGLVLLISKAGPSSVNTSCQNYDMV: 138
MmDLP1      70: LRCLLSDELSNIAMQARKLVGTGHPLLTARALVHDSRHNQLGLVLLISKAGPSTRNASQNYDMV: 139

SjDlp1      104: ...VORYKQLSRVTELIHAANLIHKSQO.....EHAKEAHSITKLVKLVGDYLLGKASVDLASELKD: 162
SpDlp1      110: ...VORYKQLARVTELIHAANLIHINIG.....EQSNEQ...IKLATLVGDYLLGKASVDLAHLEN: 166
ScryoDlp1   109: ...VORYKQLSRVTELIHAANLIHINIR.....EQSTEE...IKLATLVGDYLLGKASVDLASHLES: 165
SoDlp1      109: ...VORYKQLSRVTELIHAANLIHINIR.....EQSTEE...IKLATLVGDYLLGKASVDLASHLES: 165
HsDLP1      139: SGI VSCQRSLAEITELIHTALLVHRGIVNLSLQSSDGPLKDMQFGNKAILSGDFLLANACNGLALLQN: 208
MmDLP1      140: SGV VSCQRSLAEITELIHTALLVHRGIVNLSLQSSDGPLKDMQFGNKAILSGDFLLANACNGLALLQN: 209

SjDlp1      163: NSITELMASATANLIEGNFPQTRD.....TMSIEERRRRLQSAFLPAKACLCASTLNRASEHTS: 223
SpDlp1      167: NATTELMAVIANLVEGHFGSRQNG.....SVGLSN.ERTILLOSAFPAPAKACLCASTLNNSQOYIN: 227
ScryoDlp1   166: SAVTELMAVIANLVEGHFMKP.KS.....HANSQS.ERMLLQSAFLPAKACLSASTLNNSAYIN: 225
SoDlp1      166: NAVTELMAVIANLVEGHFMKAGSS.....PADQANERMLLQSAFLPAKACLSASTLNNSAHTN: 227
HsDLP1      209: TKVVELLSSALMDLVGCVYHENSTSKESYITDDIGISTWKEQTFLSHCALLAKSCQAAMELAKHDAEVO: 277
MmDLP1      210: TKVVELLSSALMDLVGCVYQENSASTKENSIPDDIGISTWKEQTFLSHCALLAKSCQAAMELAKHDAAVO: 279

SjDlp1      224: QACFHYGLHLGTAMQVRSN.PDKTELR.....: 250
SpDlp1      228: DACFHYGKFLGLSLQAHKVPSPDAQLQKN.....: 258
ScryoDlp1   226: KACFHYGRYLGLSMHVAHEDSESIDKTKK.....: 256
SoDlp1      228: KACFHYGRFLGLSMHVAHEDPEKMDLKMKK.....: 258
HsDLP1      278: NMAFYGKHMAMSHKINSDVQFFIKKTSDSMTFNLNSAPVVLHQEFLGRDLWIKQIGEAQEKGRLDYAK: 347
MmDLP1      280: DMAFYGKHMAMSHKINADLQFFIKKASDSKTFNLNSAPVVLHQEFLGRDLWIKQIGEAQEKGLSNYSK: 349

SjDlp1      250: .....LDDEVNRAKRVLSVLPDVEVKQTLYEIADA AANDG: 286
SpDlp1      258: .....NDLKYVENAKSSLSVFPDIEAKQALMEIANSVSK : 294
ScryoDlp1   256: .....KILLNGYRKNAKALITVFPDVEAKQALREIARISIA : 293
SoDlp1      258: .....LEVLNDYQKKAKDALITVFPDVEAKQALIEIADRVSIA : 295
HsDLP1      348: LRERIKAGKGVTSAILDCRYHGNKALHALESFPPSEASALENTVFAVTRFS : 399
MmDLP1      350: LRETIKAGKGVTSAILDCRYHGNKALHALESFPPSEASALENTVFAVTRFS : 401

```

Fig. S3. Alignment of the amino acid sequences of solanesyl or decaprenyl diphosphate synthase subunit 2.

SjDlp1: decaprenyl diphosphate synthase subunit 2 encoded by *Sjdlp1* from *S. japonicus* (NCBI accession number: XP_002173102); SpDlp1: decaprenyl diphosphate synthase subunit 2 encoded by *dlp1* from *S. pombe* (CAB10123.1); ScryoDlp1: SPOG_02630 from *S. cryophilus* (XP_013024026); SoDlp1: SOCG_05034 from *S. octosporus* (XP_013016971); HsDLP1: decaprenyl diphosphate synthase subunit 2 encoded by *DLP1* (*PDSS2*) from *H. sapiens* (NP_065114); and MmDLP1: solanesyl diphosphate synthase subunit 2 encoded by *mDLP1* from *M. musculus* (AAI47695). Identical and similar amino acid residues in more than three sequences are indicated by black and gray boxes, respectively.

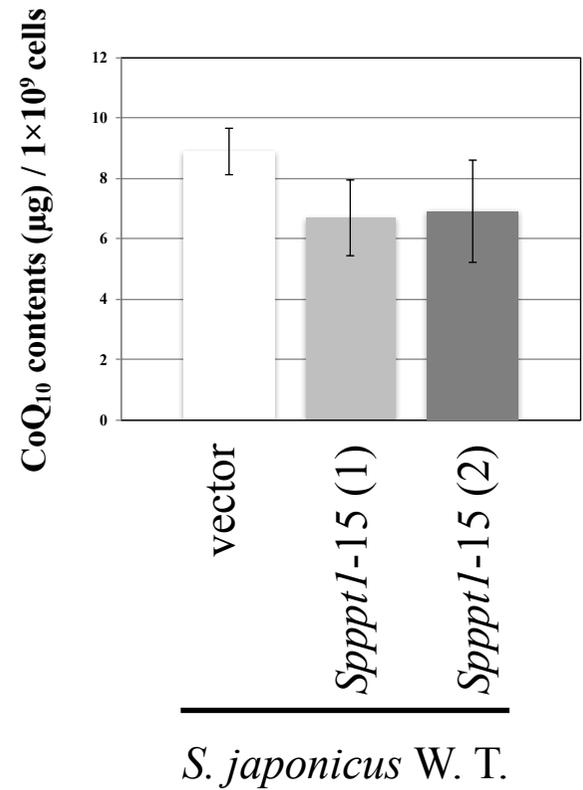


Fig. S4. Production of CoQ₁₀ in *S. japonicus* harboring *S. pombe ppt1* gene

CoQ₁₀ contents per cell were measured by HPLC in *S. japonicus* NIG5091 harboring vector (pSJU11) or plasmid expressing *S. pombe ppt1* (pSJU11-Spppt1-15). *Spppt1-15* (1) and *Spppt1-15* (2) were two independent transformants. Error bars represent the standard deviation of two measurements.

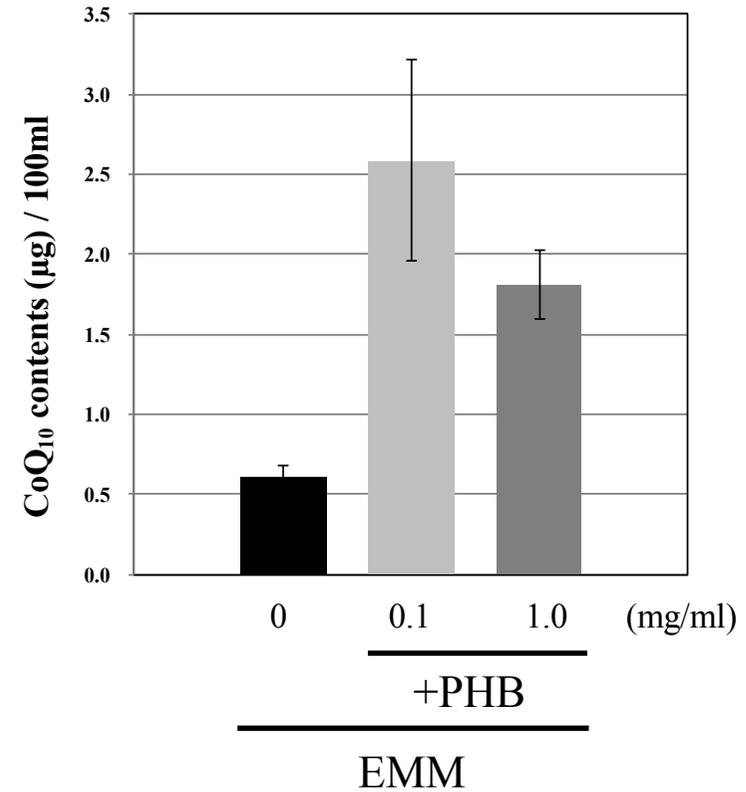
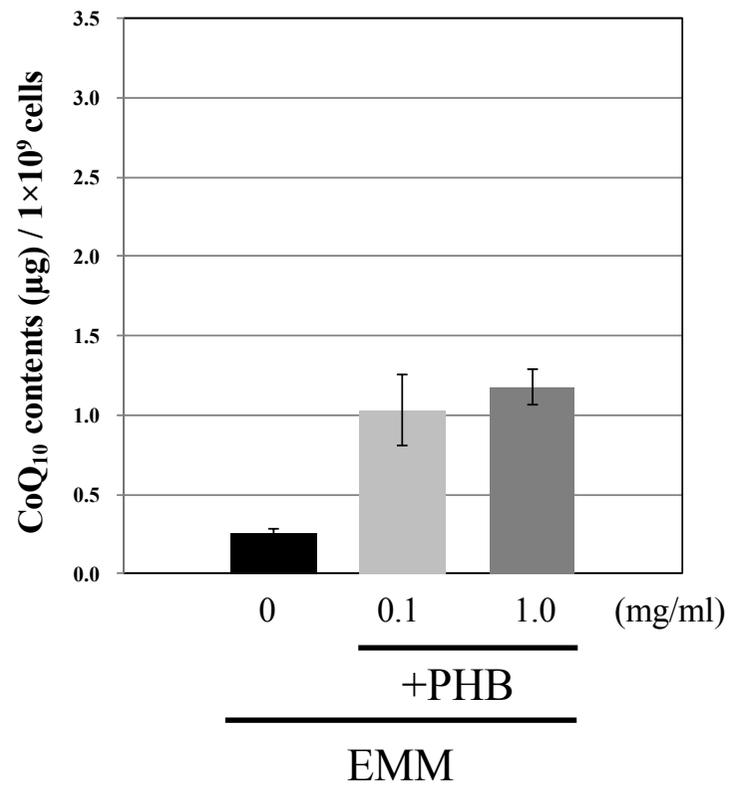


Fig. S5. Increased CoQ₁₀ production by supplementation of PHB.

S. japonicus NIG2028 was cultured in EMM medium with or without 0.1 or 1.0 mg/ml PHB for 48 hours at 30°C. CoQ₁₀ contents per cell (A) and per culture (B) were measured by HPLC. Error bars represent the standard deviation of three measurements of total CoQ₁₀.

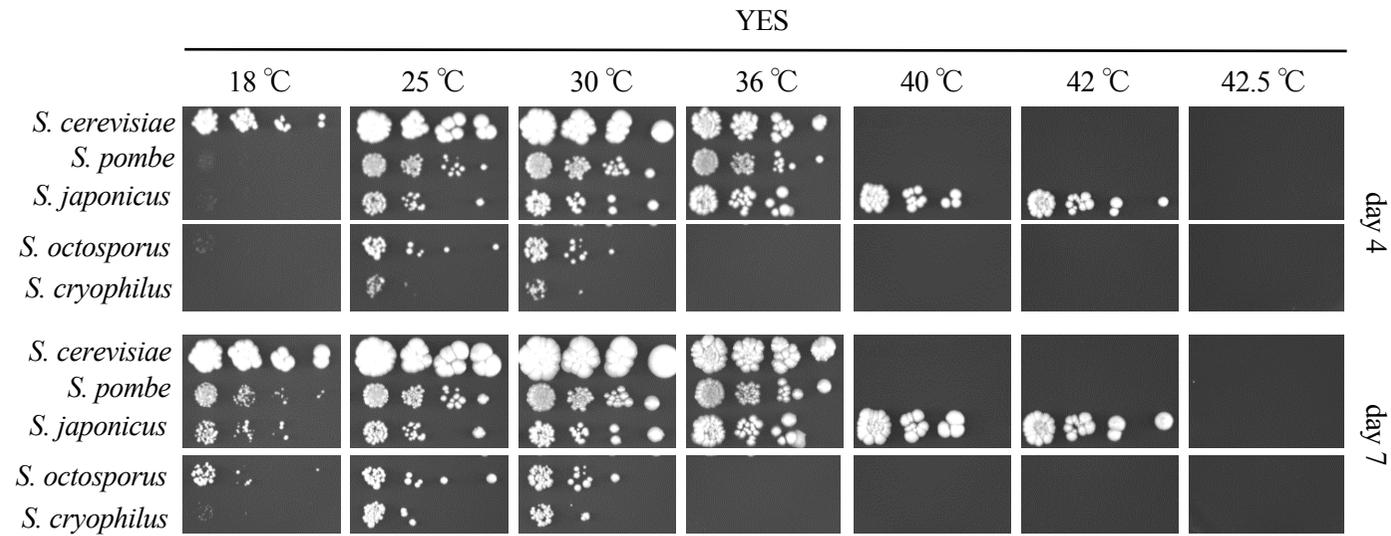


Fig. S6. Growth of *S. cerevisiae*, *S. pombe*, *S. japonicus*, *S. octosporus*, and *S. cryophilus* in different temperatures. *S. cerevisiae* kyokai No. 9, *S. pombe* L972, *S. japonicus* NIG2028, *S. octosporus* yFS286, and *S. cryophilus* OY26 strains were grown, serially diluted, and spotted on YES for 4 or 7 days at the indicated temperatures.

Table S1. PCR primers used in this study

Primer name	Sequence
Sjppt1(ORF)-Sall-F	5'-CGCgtcgacAATGATTTGGAGGGGGTTC -3'
Sjppt1-BamHI-R	5'-GCGggatccTACTTAAGAAATGATATAATCC -3'
Sjdps1-Sall-F	5'-TAgtcgacAATGTTACGGGGAGTACGA-3'
Sjdps1-BamHI-R	5'-TAggatccCTACTTTTTACGAGTGAT-3'
Sjdlp1-Sall-F	5'-AGTgtcgacAATGCTTACATATGTTTCGA-3'
Sjdlp1-BamHI-R	5'-TAggatccTTAGCCATCATTGCTGC-3'
Sjnm1-897-F	5'-GCggtaccGAAGTTTTATTGGTAACTTA-3'
Sjnm1-24-R	5'-AAGTAATCGCGAACTTGATG-3'
Spppt1-Sjnm1-24-F-New	5'-CATCAAGTTCGCGATTACTTTTCAGATTAC AATATGATAATTAAGCCTATAGC-3'
Spppt1-BamHI-R	5'-ATggatccTTAAGAATCGTAAATAAAGG-3'