```
          10        20        30        40        50        60        70        80        90
1   ATGATGAGGAAAAAGAGTTTTTGGCTTGGGATGCTGACGGCCTTAATGCTCGTGTTCACGATGGCCTTCAGCGATTCCGCGTCTGCTGCT
1    M  M  R  K  K  S  F  W  L  G  M  L  T  A  L  M  L  V  F  T  M  A  F  S  D  S  A  S  A  A

         100       110       120       130       140       150       160       170       180
91  CAGCCGGCGAAAAATGTTGAAAAGGATTATATTGTCGGATTTAAGTCGGGAGTGAAAACCGCATCCGTCAAAAAGGACATCATCAAAGAG
31   Q  P  A  K  N  V  E  K  D  Y  I  V  G  F  K  S  G  V  K  T  A  S  V  K  K  D  I  I  K  E

         190       200       210       220       230       240       250       260       270
181 AGCGGCGGAAAAGTGGACAAGCAGTTTAGAATCATCAACGCGGCAAAAGCGAAGCTAGACAAAGAAGCGCTTGAGGAAGTCAAAAATGAT
61   S  G  G  K  V  D  K  Q  F  R  I  I  N  A  A  K  A  K  L  D  K  E  A  L  E  E  V  K  N  D

         280       290       300       310       320       330       340       350       360
271 CCGGATGTCGCTTATGTGGAAGAGGATCACGTAGCTCATGCTTTGGCGCAAACCGTTCCTTACGGCATTCCTCTCATTAAAGCGGACAAA
91   P  D  V  A  Y  V  E  E  D  H  V  A  H  A  L  A  Q  T  V  P  Y  G  I  P  L  I  K  A  D  K

         370       380       390       400       410       420       430       440       450
361 GTGCAGGCTCAAGGCTACAAGGGAGCGAACGTAAAAGTCGCCGTCCTGGATACAGGAATCCAAGCTTCTCATCCGGACTTGAACGTAGTC
121  V  Q  A  Q  G  Y  K  G  A  N  V  K  V  A  V  L  D  T  G  I  Q  A  S  H  P  D  L  N  V  V

         460       470       480       490       500       510       520       530       540
451 GGCGGAGCAAGCTTTGTGGCTGGCGAAGCTTATAACACCGACGGCAACGGACACGGCACACATGTTGCCGGTACAGTAGCTGCGCTTGAC
151  G  G  A  S  F  V  A  G  E  A  Y  N  T  D  G  N  G  H  G  T  H  V  A  G  T  V  A  A  L  D

         550       560       570       580       590       600       610       620       630
541 AATACAACGGGTGTATTAGGCGTTGCGCCAAGCGTATCCTTGTACGCGGTTAAAGTACTGAATTCAAGCGGAAGCGGATCATACAGCGGC
181  N  T  T  G  V  L  G  V  A  P  S  V  S  L  Y  A  V  K  V  L  N  S  S  G  S  G  S  Y  S  G

         640       650       660       670       680       690       700       710       720
631 ATTGTAAGCGGAATCGAGTGGGCGACAACAAACGGCATGGATGTTATCAATATGAGCCTTGGGGGAGCATCAGGCTCGACAGCGATGAAA
211  I  V  S  G  I  E  W  A  T  T  N  G  M  D  V  I  N  M  S  L  G  G  A  S  G  S  T  A  M  K

         730       740       750       760       770       780       790       800       810
721 CAGGCAGTCGACAATGCATATGCAAGAGGGGTTGTCGTTGTAGCTGCAGCAGGGAACAGCGGATCTTCAGGAAACACGAATACAATTGGC
241  Q  A  V  D  N  A  Y  A  R  G  V  V  V  V  A  A  A  G  N  S  G  S  S  G  N  T  N  T  I  G

         820       830       840       850       860       870       880       890       900
811 TATCCTGCGAAATACGATTCTGTCATCGCTGTTGGCGCGGTAGACTCTAACAGCAACAGAGCTTCATTTTCCAGTGTGGGAGCAGAGCTT
271  Y  P  A  K  Y  D  S  V  I  A  V  G  A  V  D  S  N  S  N  R  A  S  F  S  S  V  G  A  E  L

         910       920       930       940       950       960       970       980       990
901 GAAGTCATGGCTCCTGGCGCAGGCGTATACAGCACTTACCCAACGAACACTTATGCAACATTGAACGGAACGTCAATGGCTTCTCCTCAT
301  E  V  M  A  P  G  A  G  V  Y  S  T  Y  P  T  N  T  Y  A  T  L  N  G  T  S  M  A  S  P  H

        1000      1010      1020      1030      1040      1050      1060      1070      1080
991 GTAGCGGGAGCAGCAGCTTTGATCTTGTCAAAACATCCGAACCTTTCAGCTTCACAAGTCCGCAACCGTCTCTCCAGCACGGCGACTTAT
331  V  A  G  A  A  A  L  I  L  S  K  H  P  N  L  S  A  S  Q  V  R  N  R  L  S  S  T  A  T  Y

        1090      1100      1110      1120      1130      1140
1081 TTGGGAAGCTCCTTCTACTATGGGAAAGGTCTGATCAATGTCGAAGCTGCCGCTCAATAA
361  L  G  S  S  F  Y  Y  G  K  G  L  I  N  V  E  A  A  A  Q  *
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Fig. S1 Nucleotide sequence and amino acid sequence of keratinase gene from *Bacillus* sp. LCB12.

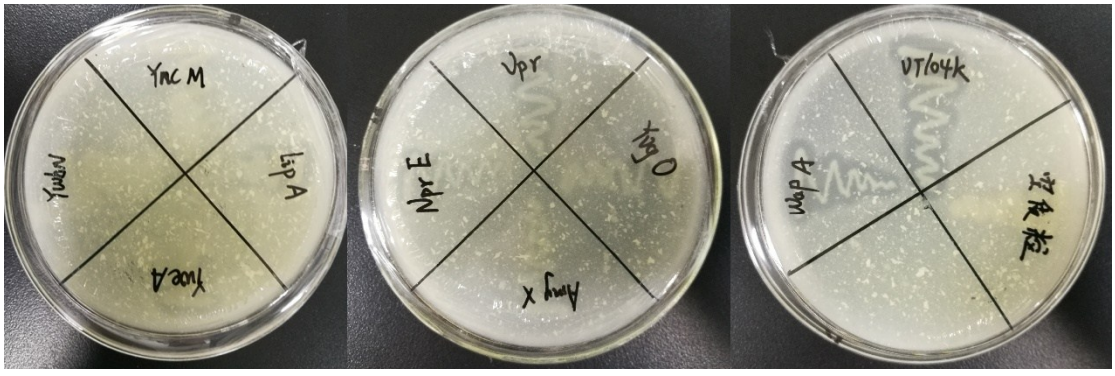

Fig. S2 Function analysis of recombinant *B. subtilis* SCK6 with different SPs.