Supplementary materials

Alignment and translation

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Wild_type:    1  ATG AAT AAA TAT CAT TTT CCA AAG GAT TTT ATT TGG GGA GTA GCT ACT TCA TCA TAT CAG
Optimized:    1  ATG AAC AAA TAC CAC TTC CCG AAA GAC TTC ATT TGG GGC GTT GCA ACC AGC AGC TAT CAA
                  M   N   K   Y   H   F   P   K   D   F   I   W   G   V   A   T   S   S   Y   Q

Wild_type:   61  ATT GAA GGT GCT TAC AAT GAA GAT GGA AAA GGA GAA AAT ATA TGG GAT AGA TTT ACT TCT
Optimized:   61  ATC GAA GGC GCG TAT AAC GAA GAC GGC AAA GGC GAA AAC ATC TGG GAT CGT TTT ACC AGC
                  I   E   G   A   Y   N   E   D   G   K   G   E   N   I   W   D   R   F   T   S

Wild_type:  121  ATA CCA GGT AAC ATA TAT AAA AAT CAT AAT GGT AAT GTA GCG TGT GAC CAT TAT CAT TTA
Optimized:  121  ATC CCG GGC AAC ATC TAC AAA AAC CAC AAC GGC AAC GTT GCT TGC GAT CAT TAC CAT CTG
                  I   P   G   N   I   Y   K   N   H   G   N   V   A   C   D   H   Y   H   L

Wild_type:  181  TAT GAA AAG GAT ATA GAG ATA TTA GAA GAA CTA GGT ATT AAA AAC TAC AGA CTT TCA ATA
Optimized:  181  TAC GAG AAA GAC ATC GAG ATC CTG GAA GAA CTG GGC ATC AAA AAC TAC CGT CTG AGC ATC
                  Y   E   K   D   I   E   I   L   E   E   L   G   I   K   N   Y   R   L   S   I

Wild_type:  241  TCA TGG GCA AGA ATA TTT CCA AAG GGA TAC GGA GAG GTA AAT CAA AAG GGA CTA GAG TTT
Optimized:  241  AGC TGG GCA CGT ATT TTT CCG AAA GGC TAC GGC GAA GTT AAT CAG AAA GGC CTG GAG TTC
                  S   W   A   R   I   F   P   K   G   Y   G   E   V   N   Q   K   G   L   E   F

Wild_type:  301  TAT AAA AAA TTA ATA AAT AAA TTG GTA AGC AAG GGT ATT CAA CCT GCA GTA ACG CTA TAT
Optimized:  301  TAC AAA AAA CTG ATC AAC AAA CTG GTC TCC AAA GGC ATT CAG CCG GCA GTT ACC CTG TAT
                  Y   K   K   L   I   N   K   L   V   S   K   G   I   Q   P   A   V   T   L   Y

Wild_type:  361  CAC TGG GAT TTG CCA CAA CAC CTT CAA GAC ATT GGG GGA TGG GCA AAT AGA AAG GTA GTA
Optimized:  361  CAT TGG GAT CTG CCG CAA CAT CTG CAA GAT ATT GGC GGT TGG GCG AAT CGC AAA GTT GTT
                  H   W   D   L   P   Q   H   L   Q   D   I   G   G   W   A   N   R   K   V   V

Wild_type:  421  GAT TAT TTT GTT GAA TAT GCA GAG CTA ATG TTT AAG GAG TTT GGA GAT TTA GTT CCT ATA
Optimized:  421  GAT TAC TTC GTC GAG TAC GCC GAA CTG ATG TTC AAA GAG TTC GGC GAC CTG GTT CCG ATT
                  D   Y   F   V   E   Y   A   E   L   M   F   K   E   F   G   D   L   V   P   I

Wild_type:  481  TGG ATT ACT CAT AAT GAA CCA TGG GTT GTT TCA ATG TTA GGT TAT GCT TGG GGA GTA CAT
Optimized:  481  TGG ATT ACC CAC AAC GAA CCG TGG GTT GTT AGT ATG CTG GGT TAC GCT TGG GGC GTT CAC
                  W   I   T   H   N   E   P   W   V   V   S   M   L   G   Y   A   W   G   V   H

Wild_type:  541  GCA CCT GGC ATT AAG GAC TAT AAG ATG GCA GTA CAA GTT GCA CAC AAC GTA CTT TTA TCA
Optimized:  541  GCA CCG GGC ATT AAA GAC TAC AAA ATG GCG GTT CAG GTT GCA CAT AAC GTT CTG CTG AGC
                  A   P   G   I   K   D   Y   K   M   A   V   Q   V   A   H   N   V   L   L   S

Wild_type:  601  CAT GGA AAA GTT GTA AGG CTT TAT AGA AGC ATG AAT TTA AAG GGT AAA ATA GGT ATA ACT
Optimized:  601  CAC GGC AAA GTT GTT CGT CTG TAT CGT AGC ATG AAC CTG AAA GGC AAA ATC GGC ATC ACC
                  H   G   K   V   V   R   L   Y   R   S   M   N   L   K   G   K   I   G   I   T

Wild_type:  661  TTA AAC CTA ATA ACT TCA TAC CCA AAT TCA ACT GAT GAA AAG GAT GTA TTA GCA GCA AAA
Optimized:  661  CTG AAC CTG ATT ACC AGC TAT CCG AAC AGC ACC GAC GAA AAA GAC GTT CTG GCA GCG AAA
                  L   N   L   I   T   S   Y   P   N   S   T   D   E   K   D   V   L   A   A   K

Wild_type:  721  ATA TAT GAT GGG TTT GTA AAT AGA TGG TAC TTA GAC CCA GTA TTA AAG GGA AAG TAT CCT
Optimized:  721  ATC TAC GAC GGC TTC GTT AAC CGT TGG TAC CTG GAC CCG GTT CTG AAA GGC AAA TAC CCG
                  I   Y   D   G   F   V   N   R   W   Y   L   D   P   V   L   K   G   K   Y   P

Wild_type:  781  GAT GAT ATG GTT AAG TTA TAT AAA GAA CAA AAT ATC CTT CCT GAG CTT AAC GAA GAG GAT
Optimized:  781  GAC GAC ATG GTC AAA CTG TAC AAA GAG CAG AAC ATC CTG CCG GAA CTG AAC GAA GAA GAC
                  D   D   M   V   K   L   Y   K   E   Q   N   I   L   P   E   L   N   E   E   D

Wild_type:  841  ATG GAG ATA ATA AGC GAA AAA ATA GAC TTC CTA GGT ATA AAT TAT TAT ACA AGA GCA GTT
Optimized:  841  ATG GAG ATC ATC AGC GAG AAA ATC GAC TTC CTG GGC ATT AAC TAT TAT ACC CGC GCG GTT
                  M   E   I   I   S   E   K   I   D   F   L   G   I   N   Y   Y   T   R   A   V

Wild_type:  901  GTA AAG TAT GAT GAA ACA TCT TAT CCA TTA AAG GCA ACA ACT ATA GAC TTA GAT AAT CCA
Optimized:  901  GTC AAA TAC GAC GAA ACC AGC TAT CCG CTG AAA GCA ACC ACC ATC GAT CTG GAT AAC CCG
                  V   K   Y   D   E   T   S   Y   P   L   K   A   T   T   I   D   L   D   N   P

Wild_type:  961  AAA ACT CAA ATG GGA TGG GAA ATA TAT CCT CAA GGT TTA TAT GAT ATG CTT ACT TAT CTT
Optimized:  961  AAA ACC CAG ATG GGC TGG GAA ATC TAT CCG CAA GGT CTG TAC GAC ATG CTG ACC TAT CTG
                  K   T   Q   M   G   W   E   I   Y   P   Q   G   L   Y   D   M   L   T   Y   L

Wild_type: 1021  CAT GAA ACT TAT GAT GGC ATA GAC ATA ATG ATT ACA GAA AAT GGA GCT GCA TTT AAC GAT
Optimized: 1021  CAC GAA ACC TAC GAC GGC ATC GAT ATC ATG ATC ACC GAA AAC GGC GCA GCG TTT AAC GAT
                  H   E   T   Y   D   G   I   D   I   M   I   T   E   N   G   A   A   F   N   D

Wild_type: 1081  ATA GTA AAT TCA AAT GGT AAG GTT GTA GAT GAT GCT AGA ATC TAT CTT TAT GAA CAT
Optimized: 1081  ATC GTC AAC AGC AAC GGC AAA GTC GTT GAC GAC GCG CGT ATC CAT TAT CTG TAC GAA CAC
                  I   V   N   S   N   G   K   V   V   D   D   A   R   I   H   Y   L   Y   E   H

Wild_type: 1141  CTA AAA GTA GTT CAT AGA GCA ATT TCA GAG GGA GTT AAT CTT AAG GCA TAT TAC TTA TGG
Optimized: 1141  CTG AAA GTC GTT CAT CGC GCG ATT AGC GAA GGC GTT AAC CTG AAA GCC TAC TAT CTG TGG
                  L   K   V   V   H   R   A   I   S   E   G   V   N   L   K   A   Y   Y   L   W

Wild_type: 1201  TCA TTC TTA GAT AAC TTT GAA TGG GCT GAA GGA TAT GAA AAA AGG TTT GGT ATT GTT TTT
Optimized: 1201  AGC TTC CTG GAT AAC TTC GAG TGG GCA GAA GGT TAC GAA AAA CGC TTC GGC ATC GTC TTC
                  S   F   L   D   N   F   E   W   A   E   G   Y   E   K   R   F   G   I   V   F

Wild_type: 1261  GTA GAT TAC ACA AAC CAA AAC AGA ATA ATA AAG AAT AGC GGA TAT TGG TAT AGA GAT GTT
Optimized: 1261  GTC GAT TAC ACC AAC CAG AAC CGC ATC ATC AAA AAC AGC GGC TAC TGG TAT CGC GAC GTT
                  V   D   Y   T   N   Q   N   R   I   I   K   N   S   G   Y   W   Y   R   D   V

Wild_type: 1321  ATT AAA AAT AAT GGA TTA AAT GAA TAA
Optimized: 1321  ATC AAA AAC AAC GGC CTG AAC GAG TGA
                  I   K   N   N   G   L   N   E   *
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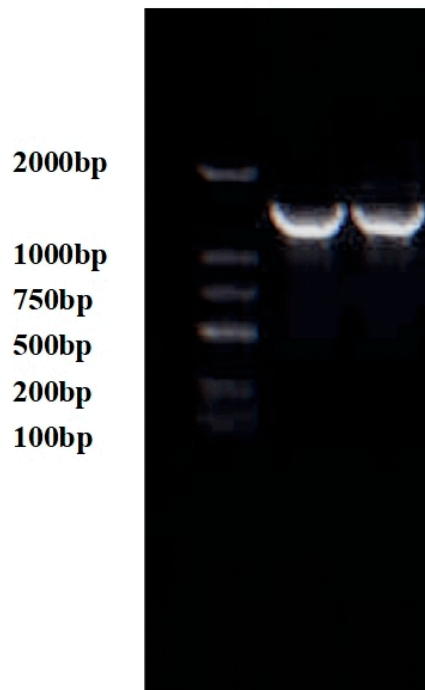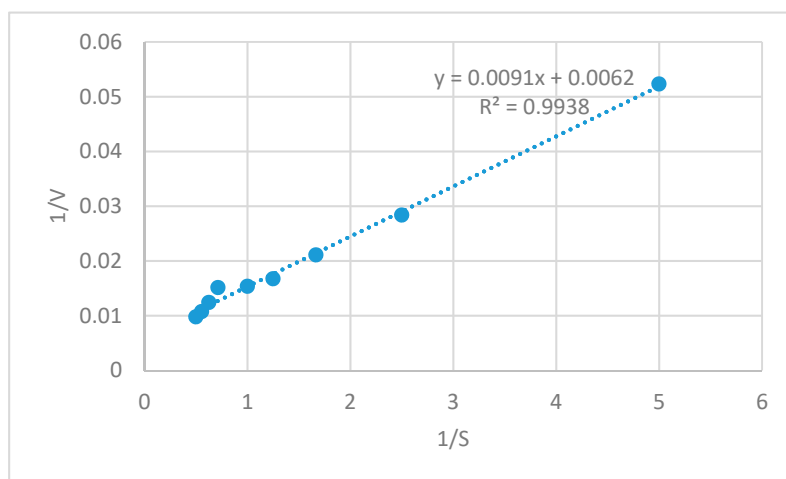
Supplementary Figure S1 Gene Optimization of thbg2. Wild_type represents t
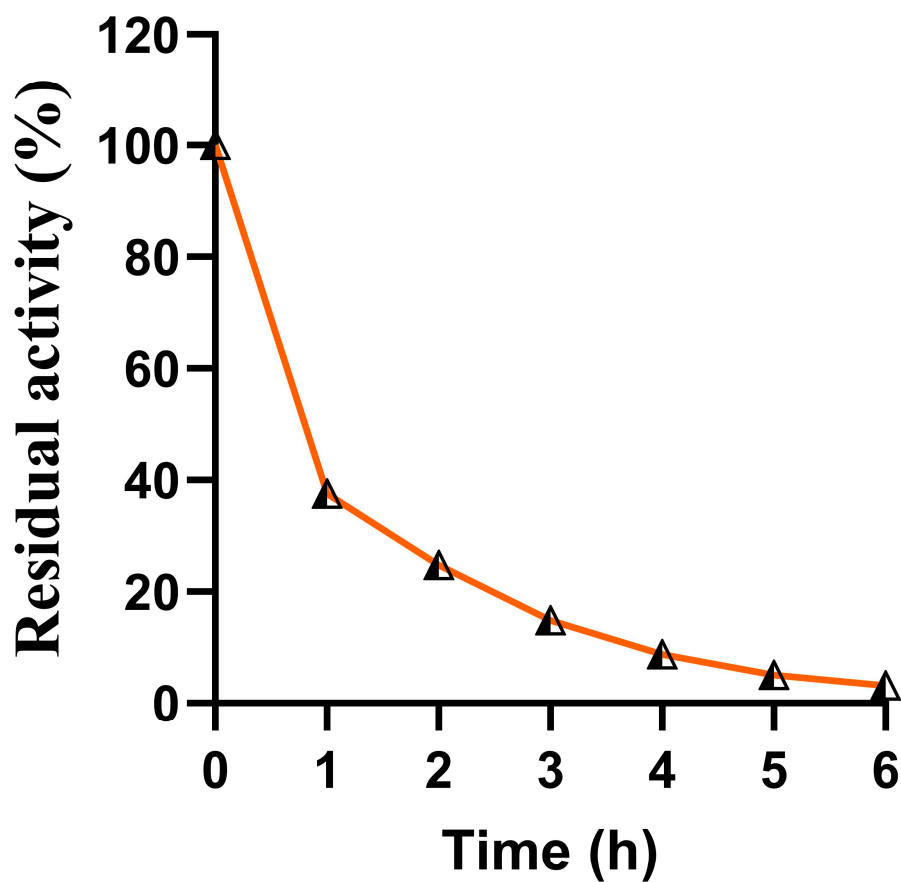
he original gene sequence of the thbg2 from the metagenomic database. Optimi
zed represents the optimized sequence of the thbg2 based on the codon of *E.
coli*.

Supplementary Figure S2 PCR amplification products

Supplementary Figure S3 Lineweaver-Burk plot of ThBg2 β-glucosidase

Supplementary Figure S4 The effect of temperature on stability of the commercial cellulase at 50 °C for 0, 1, 2, 3, 4, 5, and 6 h. The residual activity of the commercial cellulase was determined at 50 °C and pH5.6 using 1% sodium carboxymethyl cellulose as substrate. Cellulase activity was determined by DNS method.