Supplementary Table 1 Primers used in this study

Primer	Sequence (5'-3')^{a}	Paired with	Intention
SCFV-F	CCC**AAGCTT**CTGGTTGAGACCAAAAAATTTTTT**GGTCTC**AATGCAGATCCAGCTGGTGC	SCFV-R	Amplifying scFv with two *Bsa* I
OR-SCFV-F	CCC**AAGCTT**CTGGTTGAGACCAAAAAATTTTTT**GGTCTC**AATGCAAATTCAGCTGGTGC	OR-SCFV-R	Amplifying OR-scFv with two *Bsa* I
POS-SCFV-F	CC**AAGCTT**AAAGGAGGACAACTAATGCAGATCCAGCTGGTGC	SCFV-R	Amplifying scFv for pXMJ19-CSCFV
SCFV-R	CC**GGATCC**TTACTTGATCTCCAGCTTAGTGC		
POS-OR-SCFV-F	CC**AAGCTT**AAAGGAGGACAACTAATGCAAATTCAGCTGGTGC	OR-SCFV-R	Amplifying OR-scFv for pXMJ19-COR-SCFV
OR-SCFV-R	CC**GGATCC**TTATTTGATCTCCAGTTTGGTACC		
T1-F	TTT**GGTCTC**ATGGTTTAGGTAGCTTAAGTAGCCCTG		
BT1-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTGGACGGATCGTGGAGATC	T1-F	Amplifying T-BEP1
MT1-R	TTT**GGTCTC**ACCATTGTCGTGTTCCTTTCTGTTTC	T1-F	Amplifying T-MEP1
T2-F	TTT**GGTCTC**ATGGTTCTGAATTCATGACCCGCA		
BT2-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTGAAAGGATGGACTTCTTCTGC	T2-F	Amplifying T-BEP2
MT2-R	TTT**GGTCTC**ACCATGGTGTCTCCTAAAAGTTATTTCAG	T2-F	Amplifying T-MEP2
T3-F	TTT**GGTCTC**ATGGTTTTCAACAGCATTGATTTCGA		
BT3-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTACGTGGGGCTTGGTACG	T3-F	Amplifying T-BEP3
MT3-R	TTT**GGTCTC**ACCATTGTATGTCCTCCTGGACTTCG	T3-F	Amplifying T-MEP3
T4-F	TTT**GGTCTC**ATGGTTCTGACATCGAAGTCACCAAAG		
BT4-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTAGCTCTGCCAGAGCTGCT	T4-F	Amplifying T-BEP4
MT4-R	TTT**GGTCTC**ACCATTACTTCGCCTCCTTCCTCTTAT	T4-F	Amplifying T-MEP4
T5-F	TTT**GGTCTC**ATGGTTCGTCACTCGCATCATTCTAC		
BT5-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTCCGGTGTGCGCGTC	T5-F	Amplifying T-BEP5
MT5-R	TTT**GGTCTC**ACCATTGGTGTCACCTCCTGCTTG	T5-F	Amplifying T-MEP5
T6-F	TTT**GGTCTC**ATGGTTGGGACACAGGGTGTCCT		
BT6-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTTTGGTGGTTCCAAGGTCAA	T6-F	Amplifying T-BEP6
MT6-R	TTT**GGTCTC**ACCATAATGGTGCCTCCTGTTTTAG	T6-F	Amplifying T-MEP6

T7-F	TTT**GGTCTC**ATGGTTAAATTCATAAACTTTTGCCGTAA		
BT7-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTCGGGTCCGGGTTGG	T7-F	Amplifying T-BEP7
MT7-R	TTT**GGTCTC**ACCATGTTCGGTTTCCTTCGGC	T7-F	Amplifying T-MEP7
T8-F	TTT**GGTCTC**ATGGTACCAACCCAGGCCGC		
BT8-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTTTGTACTGCTTTCCGCCG	T8-F	Amplifying T-BEP8
MT8-R	TTT**GGTCTC**ACCATAGAGGGCTACCCCTTATCTG	T8-F	Amplifying T-MEP8
T9-F	TTT**GGTCTC**ATGGTAGTGTGTTAGTATTCGATGGGTC		
BT9-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTGAACGGGTGTCGCTCAGC	T9-F	Amplifying T-BEP9
MT9-R	TTT**GGTCTC**ACCATGAGTAAATCTCCTGGATGATCG	T9-F	Amplifying T-MEP9
T10-F	TTT**GGTCTC**ATGGTCCATTTGGGGCAATCCA		
BT10-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTTAGATCTCAGGCTCAATCGTG	T10-F	Amplifying T-BEP10
MT10-R	TTT**GGTCTC**ACCATGTTTTACTCCTTTATTCGCAAGT	T10-F	Amplifying T-MEP10
T11-F	TTT**GGTCTC**ATGGTGCATTGCATCTAACAAGGTCG		
BT11-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTTGGCCATCCTGCTCACC	T11-F	Amplifying T-BEP11
MT11-R	TTT**GGTCTC**ACCATTACTTGTTCTCCTGCTGCTCA	T11-F	Amplifying T-MEP11
T12-F	TTT**GGTCTC**ATGGTCGGGCGCCTAGAGGG		
BT12-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTTTCGCGCAGTGCGC	T12-F	Amplifying T-BEP12
MT12-R	TTT**GGTCTC**ACCATGATGTCCTCCCGGTGGTT	T12-F	Amplifying T-MEP12
HP1-F	TTT**GGTCTC**ATGGT ACGGTGAACATGCAGTAAATG		
BHP1-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT TTTTCAGAGTTGAACCATTTTACT	HP1-F	Amplifying HP-BEP1
MHP1-R	TTT**GGTCTC**ACCAT GAAATTTCCTCCTAAAGCGATC	HP1-F	Amplifying HP-MEP1
HP2-F	TTT**GGTCTC**ATGGT CGATTCAAATAGGTGCTGATATT		
BHP2-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT AGTGTGTTAAGCGCTGCAAT	HP2-F	Amplifying HP-BEP2
MHP2-R	TTT**GGTCTC**ACCAT TGTTTTGTTCCTCCCTGAATATG	HP2-F	Amplifying HP-MEP2
HP3-F	TTT**GGTCTC**ATGGT GAAATCGTAAAAGTTGATGCAG		

BHP3-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT GTAGAACCGTTTTGGTTGTATAATG	HP3-F	Amplifying HP-BEP3
MHP3-R	TTT**GGTCTC**ACCAT AATCAATTTCCTCCTTTCCTAAG	HP3-F	Amplifying HP-MEP3
HP4-F	TTT**GGTCTC**ATGGT TACCACCATGTCGTATAACCC		
BHP4-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT ATGAATAATGAAGATACGAATGAAG	HP4-F	Amplifying HP-BEP4
MHP4-R	TTT**GGTCTC**ACCAT GACATTTCCCCCTAATTGATTG	HP4-F	Amplifying HP-MEP4
HP5-F	TTT**GGTCTC**ATGGT TTTTCGGACCGTAGTGCA		
BHP5-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT GCAATACGGACTGTTCTTGC	HP5-F	Amplifying HP-BEP5
MHP5-R	TTT**GGTCTC**ACCAT TTAAAAGCCTCCTCTCTTAGCG	HP5-F	Amplifying HP-MEP5
HP6-F	TTT**GGTCTC**ATGGT GGGAAAGAATATGTGGTCCAA		
BHP6-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT TTTGGGCGGATAATGTACAT	HP6-F	Amplifying HP-BEP6
MHP6-R	TTT**GGTCTC**ACCAT CTGTTTGCACCTCCTTTTGG	HP6-F	Amplifying HP-MEP6
HP7-F	TTT**GGTCTC**ATGGT AAAGGGTTTAAGCTACCTTTTATG		
BHP7-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT TTTGCTCCCATACGTTTTAAAC	HP7-F	Amplifying HP-BEP7
MHP7-R	TTT**GGTCTC**ACCAT TTTACTAGCACCTCCGAAAATAT	HP7-F	Amplifying HP-MEP7
HP8-F	TTT**GGTCTC**ATGGT GAAAAGGATCAAGGAATAGGATG		
BHP8-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT GCTTCTGCAACCGCATTG	HP8-F	Amplifying HP-BEP8
MHP8-R	TTT**GGTCTC**ACCAT GCCTTTCACCTCCTCCCA	HP8-F	Amplifying HP-MEP8
HP9-F	TTT**GGTCTC**ATGGT TACGAAGAAGTGCCGAAGAG		
BHP9-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT GCATGTGATTTGGAACGGTC	HP9-F	Amplifying HP-BEP9
MHP9-R	TTT**GGTCTC**ACCAT TCTAAAATCCTCCTTAAGAGCTTT	HP9-F	Amplifying HP-MEP9
HP10-F	TTT**GGTCTC**ATGGT AGGTTCTAACACACCGATCAAC		
BHP10-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT CGTGAACCTTCTGAAGGTTTTA	HP10-F	Amplifying HP-BEP10
MHP10-R	TTT**GGTCTC**ACCAT TAGGACACCTCCTTATCCGATC	HP10-F	Amplifying HP-MEP10

HP11-F	TTT**GGTCTC**ATGGT CAATCTGCAGAGAAGATTGTTG		
BHP11-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT GTCATACCAATTTTTCTTCCTAAGAT	HP11-F	Amplifying HP-BEP11
MHP11-R	TTT**GGTCTC**ACCAT TCGTCACACCTCCTATTAAGATC	HP11-F	Amplifying HP-MEP11
HP12-F	TTT**GGTCTC**ATGGT AAGAGGTATATGGAGCCGCTATA		
BHP12-R	TTT**GGTCTC**ACCATTAGTTGTCCTCCTTT TTGATGAGTTGGTTTTTACGCTC	HP12-F	Amplifying HP-BEP12
MHP12-R	TTT**GGTCTC**ACCAT CCTGTTTCACCTCCAAATCATAT	HP12-F	Amplifying HP-MEP12

[a] The sites for the restriction enzymes are in boldface

Supplementary Table 2 Information about gene resources

C. glutamicum transcriptomic data (T-Set)

Source gene name	GeneID	Promoter predicted score[a]	Original relative Abundance[b]	Number (n)
rpsO	NCgl1901	1, 0.86, 0.83	145501.21	1
NCgl2252	NCgl2252	0.96	103193.55	2
tuf	NCgl0480	1	82146.61	3
rplJ	NCgl0468	0.98, 0.84	54100.16	4
NCgl1504	NCgl1504	0.82, 0.97, 0.92, 0.81	48226.93	5
dnaK	NCgl2702	0.87, 0.93	41129.44	6
NCgl2177	NCgl2177	0.93, 0.97	37574.99	7
rplU	NCgl2280	0.89	37186.55	8
tig	NCgl2329	0.87	36838.62	9
NCgl1941	NCgl1941	0.96, 0.99	30018.77	10
NCgl0576	NCgl0576	0.85, 0.98	26576.12	11
NCgl2088	NCgl2088	0.88, 0.98	26092.99	12

[a] the promoter prediction score threshold was set to 0.8 as default in program. Previously reported tests showed that above this threshold, the rate of false predictions was lower than 0.2%. (Reese MG, Application of a time-delay neural network to promoter annotation in the Drosophila melanogaster genome. Comput Chem. 2001, 26,51-56). Due to the possibility of tandem promoters, a prediction may found several possible promoters.

[b] Transcriptional performance (average FPKM of two sets of data obtained from two conditions with 30% or 50% dissolved oxygen levels in transcriptomic analysis (GEO accession number: GSE77502))

B. subtilis proteomic data (HP-Set)

Source gene name	GeneID	Promoter predicted score[a]	Original relative Abundance[b]	Number (n)
cspB	BSU09100	0.99, 0.96	27185	1
flagellin	BSU35360	0.90, 0.93, 0.99	18102	2
rplD	BSU01170	0.96	14481	3

yweA	BSU37800	0.99, 0.91	12297	4
rplV	BSU01210	0.92, 0.81, 0.89	11979	5
rpsF	BSU40910	0.98, 0.95	11325	6
rpsP	BSU15990	0.96, 0.98	9646	7
hbs	BSU22790	0.91, 0.96, 0.85, 0.96	9070	8
tuf	BSU01130	0.98, 0.87	8788	9
rplO	BSU01350	0.95, 0.97, 0.97, 0.96	8097	10
rplC	BSU01160	0.86, 0.99, 0.88, 0.95	7636	11
rpsO	BSU16680	0.96, 0.92, 0.99, 0.96	7461	12

[a] As described in the prior table in Table 2.

[b] According to the data provided by PaxDb: Protein Abundance Database (http://pax-db.org/about).

Supplementary Sequence 1

Original scFv (OR-scFv)

Heavy chain (FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4)-linker-light-chain (FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4)

ATGCAGATCCAGTTGGTGCAGTCTGGACCTGAGCTGAAGAAGCCTGGAGAGACAGTCAAGATCTCCTGCAAGGCTTCTGGGTATACCTTCACATATTATGGAATGAACTGGGTGAAGCAGGCTCCAGGAAAGGGTTTAAAGTGGATGGGCTGGATAAACACCTACACTGGAGAGCCAACATATGCTGATGACTTCAAGGGACGGTTTGCCTTCTCTTTGGAAACCTCTGCCAGCACTGCCTATTTGCAGATCAGCAACCTCAAAAATGAGGACACGGCTACATATTTCTGTTCAAGTCAAAATTACTACGGTAATAATAACAGATACTTCGATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCCTCAGGCGGTGGTAGTGGTGGTGGTAGTGGCGGCGGTAGCCAAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGTAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCACATCCATCCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGTATAGTAACCCACGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAATAA

Codon-optimized scFv

ATGCAGATCCAGCTGGTGCAGTCTGGCCCAGAACTGAAGAAGCCAGGCGAAACCGTGAAAATCTCCTGCAAGGCCTCCGGCTATACCTTTACCTACTACGGTATGAACTGGGTCAAGCAGGCCCCAGGCAAGGGCCTCAAGTGGATGGGCTGGATCAACACCTACACCGGCGAGCCAACCTACGCAGACGATTTCAAGGGCCGCTTCGCCTTCTCCCTGGAAACCTCCGCATCCACCGCATACCTGCAGATCTCCAACCTCAAGAATGAGGACACCGCCACCTACTTCTGCTCCTCCCAGAACTACTACGGCAACAACAACCGCTACTTCGACGTCTGGGGCGCAGGCACTACCGTGACCGTCTCCTCCGGTGGTGGTTCCGGTGGTGGTTCCGGTGGCGGCTCCCAGATCGTGCTGTCCCAGTCCCCTGCAATCCTGTCCGCATCCCCAGGCGAGAAGGTCACCATGACCTGCCGCGCCTCCTCCTCCGTCAACTACATGCACTGGTACCAGCAGAAGCCAGGCTCCTCCCCAAAGCCATGGATCTACGCCACCTCCATCCTGGCATCCGGCGTGCCAGCCCGTTTTTCCGGCTCCGGTTCCGGCACCTCTTACTCCCTGACCATCTCCCGCGTCGAAGCAGAGGACGCAGCAACCTACTACTGCCAGCAGTGGTACTCCAACCCACGCACCTTCGGCGGCGGCACTAAGCTGGAGATCAAGTAA

Supplementary Sequence 2

The sequence of HP-BEP4 which can be directly connected to target gene to control its expression in *C. glutamicum*

TACCACCATGTCGTATAACCCGGATCAGCCTGATGAAAAAAGAATTCCGTGGGATGATGAGACGATCGGTTTTAACTGGAACACTGAATTCAGATAAAAATAGGAACGTGATCAATCGAAGAGCAGAGGCATCTTCGACTTTTTTTGCCCTTTTTTAAAATAGGATAAAAGATATAAAATGTCAGGCAGATGTTACTAGAAAAAGAGAGGGAAATCGTCCATTTGAACCTTGTATAAACAGGAAGGAATTCTCATTGAATTCCAAGTGTTAATATTCCTTAAAAAACATTTACTTCCATGGAAAATGATGATAGATTAATTTTTAAGAAAAAGAACTGGTAATTCGCGAATTATGAAAAAGCGCTTTTTCTGCAGAGGACGCTCTGGCCAAATTTCAACAATCAATTAGGGGGAAATGTCATGCTAAAAAGAACTTCATTCGTATCTTCATTATTCAT**AAAGGAGGACAACTA**

Underlined sequence: the 38-bp N-terminal sequences of yweA gene in *B. subtilis.*

Bold sequence: the imbedded SD2 sequence.