

Supplementary data for

Developing a Transformation-Independent and Unbiased qPCR Assay to Rapidly Evaluate the Determinants of DNA Assembly Efficiency

Xiaoyan Ma ^{a,#}, Xinxin Liang ^{a,#}, Yi-Xin Huo ^{a,b,*}

^a Key Laboratory of Molecular Medicine and Biotherapy, School of Life Science, Beijing Institute of Technology, Beijing 100081, China

^b UCLA Institute of Advancement (Suzhou), Suzhou 215123, China

These authors contributed equally to this work.

* Corresponding author.

E-mail: huoyixin@bit.edu.cn

Table S1

Primers used for quantification.

Primers ^a	Sequence 5'→3'
q-RL1-F	acggcgctcttggtggtcagag
q-RL1-R	gcatgttaacggcggttgctcgg
q-RL23-F	aacgggcaactgctgtagtgga
q-RL23-R	tggtggtggcggaacgggtactt
q-RL45-F	ccgcagctacgagccgttaaca
q-RL45-R	accgccgtcaccagagacagaa
q-RL67-F	agccgaatagcctctccacca
q-RL67-R	ggctttcttgccgccaaggatc
q-GG-F	tacctgtccgcctttctcccttcg
q-GG-R	cctcgctctgctaactcgtttacca
q-GA1-F	cggttatggtgttcaatgctttgcg
q-GA1-R	acgtgtcttgtagttcccgctcatct
q-GA2-F	atgccgtcggttggaactgctttgat
q-GA2-R	ggcggttggaatctctccatttgc
q-GA3-F	ggctggcttaactatgcggcatca
q-GA3-R	accctggcggttacccaacttaatcg
q-GA4-F	actttctgacgccgatgctgtttcc
q-GA4-R	tgccagtgcgatgcttcaatgac
q-GA5-F	gcgggatttcagcagcaactcagt
q-GA5-R	attaagcacgtcaacctccggcatc
q-GA6-F	ctgatgccaacgaagcgatgtag
q-GA6-R	tcactgtgtgctccaccagatc
q-Joint-F	acaatacgaatcggtgtgcgcag
q-Joint-R	ttcaccctcgccaacgcacttaag
q-P1-F	tgccggaggcggtgatcaatgtc
q-P1-R	ccatgcggtctgctgcgagata
q-BP1-F	cagcaggacgcactgaccgaatt
q-BP1-R	tcttccgaagcgtaagtccacatgc
q-B-F	tcgacgccgcttcgttctacca
q-B-R	gcacaacaactggcgggcaaac
q-purple-F	acggcgctcttggtggtcagag
q-purple-R	gcatgttaacggcggttgctcgg

^a Primers q-RL1-F to q-RL67-R were used to quantify the DNA fragments in restriction ligation. Primers q-GG-F and q-GG-R were used to quantify the DNA fragments in Golden Gate assembly. Primers q-GA1-F to q-GA6-R were used to quantify the DNA fragments in Gibson assembly. Primers q-Joint-F, q-Joint-R,

q-purple-F, and q-purple-R were used for the measurement of the fidelity of Gibson assembly. Primers q-P1-F to q-B-R were used to quantify the DNA fragments in multi-part assembly. Primers q-purple-F and q-purple-R were used to study the effects of terminal secondary structures on Gibson assembly. Primers q-RL1-F and q-purple-F were identical, and primers q-RL1-R and q-purple-R were also identical.

Table S2

Primers for the amplification of DNA fragments with secondary structures in the overlap regions.

Primers ^a	Sequence 5'→3'
OL-I-F1	gtctgatggctggtctctgaGTCGCCCTTAATTGTGAGCG
OL-I-F2	gtatgatgctgcattatacGTCGCCCTTAATTGTGAGCG
OL-I-F3	ggaagctgctgcagccactGTCGCCCTTAATTGTGAGCG
OL-I-F4	gtctgatgctggaatcagatGTCGCCCTTAATTGTGAGCG
OL-I-F5	gtctgatgctgcatcaggcGTCGCCCTTAATTGTGAGCG
OL-I-F6	ggtggctgagtgacgcctcgGTCGCCCTTAATTGTGAGCG
OL-I-F7	gcctgatgctgcatcaggGTCGCCCTTAATTGTGAGCG
OL-I-F8	gtcggatgctgcatccgatGTCGCCCTTAATTGTGAGCG
OL-I-F9	gtctgatgctgcatcagacGTCGCCCTTAATTGTGAGCG
OL-I-F10	gtcggatgctgcatccgacGTCGCCCTTAATTGTGAGCG
OL-b-R1	tcagagaccagccatcagacGGAAGAGCGCCCAATACGC
OL-b-R2	gtataatgcacgcatacGGAAGAGCGCCCAATACGC
OL-b-R3	agtggctgcacgcagcttccGGAAGAGCGCCCAATACGC
OL-b-R4	atctgattcacgcacagacGGAAGAGCGCCCAATACGC
OL-b-R5	gcctgatgcacgcacagacGGAAGAGCGCCCAATACGC
OL-b-R6	cgaggctgactcagccaccGGAAGAGCGCCCAATACGC
OL-b-R7	acctgatgcacgcacagcGGAAGAGCGCCCAATACGC
OL-b-R8	atcggatgcacgcacccgacGGAAGAGCGCCCAATACGC
OL-b-R9	gtctgatgcacgcacagacGGAAGAGCGCCCAATACGC
OL-b-R10	gtcggatgcacgcacccgacGGAAGAGCGCCCAATACGC
OL-I-R1	aagccagcgaccaccagccCATGCCGAAGCTCAGAAGTG
OL-I-R11	gttcacgattcatcgtggacCATGCCGAAGCTCAGAAGTG
OL-I-R12	gttcgcgattcatcgcggacCATGCCGAAGCTCAGAAGTG
OL-b-F1	ggctgggtggtcgtgcttGCTTCCTCGCTCACTGACTCG
OL-b-F11	gtccacgatgaatcgtgaacGCTTCCTCGCTCACTGACTCG
OL-b-F12	gtccgcgatgaatcgcgaacGCTTCCTCGCTCACTGACTCG

^a Small letters indicate overlap sequences. Primers OL-I-F4 and OL-b-R4 were also used for the amplification of the fragments used in the assembly OL11 and OL12. Primers OL-I-R1 and OL-b-F1 were used for the amplification of the fragments used in the assembly OL1–OL10.

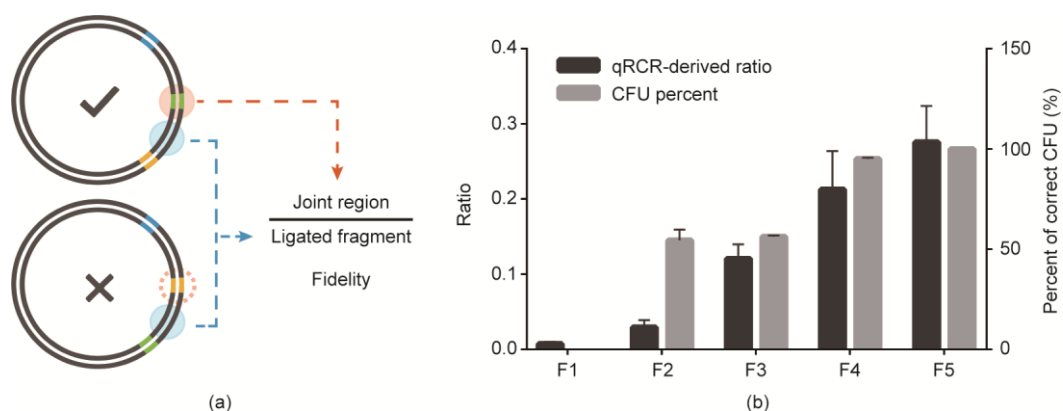


Fig. S1. (a) A modified qPCR assay for the measurement of the fidelity of DNA assembly. (b) The fidelity of five sets of Gibson assembly determined by both the CFU-based measurement and the alternative qPCR assay.