

**Table S2.** Sequences of probes

To clearly describe the what we have in this supplementary file, the following is a brief introduction of the construction of LASSOs. Two precursors sequences, the pre-LASSO and the long adapter sequences, are separately synthesized before assembled to form LASSO probes. Pre-LASSO could be either dsDNA oligos or ssDNA gained through oligo synthesis. It is combined by five parts, namely ligation arm, extension arm, two primer annealing sites that are going to function in the following producing procedures and one piece of sequence used for fusing the two predecessors. The long adapter is obtained from a plasmid template. It consists of one primer annealing site, the conserved linker region as well as a corresponding complementary sequence for the fusion site. After the preparation of pre-LASSO and the adapter, these two predecessors will be fused together by overlap-extension PCR. In the next step, the complex then goes through intramolecular ligation after being processed with EcoRI. Finally, the DNA circle will be transformed into a linear one with the desired sequence through inverted PCR and removal of the inversion PCR primers. For more details of construction of LASSOs, you may go through the previous publication (Tosi. et al., Nature Biomedical Engineering, 2017)

The sequences of pre-LASSOs, the long adapters as well as the final LASSO probes from inversed PCR are provided in this files. Here is a chart showing what different colors represent in the text.

GAGT...	Fusion PCR primer annealing site (Forward Primer)
GCCCTCAGTTCCAGTACGGAAGCGAATTCCAGCTT	RFP200 (Reverse Fusion PCR Primer for 200 LA)
CCCCTCCGATGGCCCTGTCATGAATTCCAGCTT	RFP400 (Reverse Fusion PCR Primer for 400 LA)
CAAGCCCACGGTGCGCCTCGAATTCCAGCTT	RFP400 (Reverse Fusion PCR Primer for 800 LA)
TTGG...	Ligation arm (Sequences are inverted in the final LASSO obtained from inverted PCR)
AACA...	Inverted PCR primer annealing site (TioINew & SapINew)
GATT...	Extension arm (Sequences are inverted in the final LASSO obtained from inverted PCR)
AGAG...	Fusion overlapping sequence
ATCG...	Removed inversed PCR primer annealing sites (marked by dark green in the pre-LASSOs, corresponding to the third row of the table)
CTCC.. AAAC...	Primers for post-capture PCR

## Individual Sequences

### Pre-LASSO 0.6 kb

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCCGGTCTGGTTCGCAACACTTCTTGCGGCGATAGAAGGTTCTGGCTCTT  
CGATC GATTGGGTAATGAATATCCGGTCTTGTC AAGAGAGAAGTCCTAGCACGGTAACC

### Pre-LASSO 1.0 kb

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCCGGTCTGGTTCGCAACACTTCTTGCGGCGATAGAAGGTTCTGGCTCTT  
CGATC GCCGTTGCTACCTCGTTCCGATGC AAGAGAAGTCCTAGCACGGTAACC

### Pre-LASSO 1.5 & 2.0 kb

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCCGGTCTGGTTCGCAACACTTCTTGCGGCGATAGAAGGTTCTGGCTCTT  
CGATC GGCTCTGAGGGTGGCGTTCTGAGG AAGAGAAGTCCTAGCACGGTAACC

### Pre-LASSO 4.0 kb

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCCGGTCTGGTTCGCAACACTTCTTGCGGCGATGGTTCTGGCTCTTCGAT  
CGGCCAATCCGTTATTGTTTCTCCGATGTA AAGAGAAGTCCTAGCACGGTAACC

### LA-242

AAGAGAAGTCCTAGCACGGTAACCTCCGAGGATGTCATCAAAGAGTTTAAAGAGTTTATGAGATTTAAGGTCAAGATGGAGGG  
AAGCGTCAACGGACACGAGTTCGAGATTGAGGGAGAAGGAGAAGGCCGGCCTTACGAGGGCACACAAACCGCTAAGCTCAA  
GGTCACAAAAGGAGGACTAACTATAACGGTCTAAGGTAGCGAACCCTCCCTTCTCTGGGATATTCTGAGGCCCTCAGTTCCA  
GTACGGAAGCGAATTCCAGCTT

### LA-442

AAGAGAAGTCCTAGCACGGTAACCTCCGAGGATGTCATCAAAGAGTTTAAAGAGTTTATGAGATTTAAGGTCAAGATGGAGGG  
AAGCGTCAACGGACACGAGTTCGAGATTGAGGGAGAAGGAGAAGGCCGGCCTTACGAGGGCACACAAACCGCTAAGCTCAA  
GGTCACAAAAGGAGGACTAACTATAACGGTCTAAGGTAGCGAACCCTCCCTTCTCTGGGATATTCTGAGGCCCTCAGTTCCA  
GTACGGAAGCAAAGCCTATGTTAAACACCCTGCCGACATCCCTGACTATCTGAAGCTCTCCTTCCCTGAAGGCTTCAAGTGGGA  
GAGATTCATGAACTTCGAGGACGGAGGCGTGGTGACAGTCACACAAGATAGCACCTCCAGGACGGAGAGTTTATTATAAG  
GTGAAACTCAGAGGAACCAACTTCCCTTGATGGCCCTGTCATGAATTCCAGCTT

### LA-750

AAGAGAAGTCCTAGCACGGTAACCTCCGAGGATGTCATCAAAGAGTTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAA  
CGGACACGAGTTCGAGATTGAGGGAGAAGGAGAAGGCCGGCCTTACGAGGGCACACAAACCGCTAAGCTCAAGGTCACAAA  
AGGAGGACTAACTATAACGGTCTAAGGTAGCGAACCCTCCCTTCTCTGGGATATTCTGAGGCCCTCAGTTCCAGTACGGAA  
GCAAAGCCTATGTTAAACACCCTGCCGACATCCCTGACTATCTGAAGCTCTCCTTCCCTGAAGGCTTCAAGTGGGAGAGATTCA  
TGAATTCGAGGACGGAGGCGTGGTGACAGTCACACAAGATAGCACCTCCAGGACGGAGAGTTTATTATAAGGTGAAACT  
CAGAGGAACCAACTTCCCTCGATGGCCCTGTCATGCAAAAAAACAATGGGATGGGAAGCCTCCACCGAGAGAATGTATC  
CTGAGGATGGCGCTCTGAAAGGCGAAATTTAAATGAGACTGAAACTCAAAGACGGAGGACACTACGATGCCGAGGTCAAAA  
CAACCTACAAGGCCAAGAAACAAGTGCAGTGCCTGGCGCCTACATGACTGATATTAACTCGACATTATCAGCCATAATGGG  
GACTACACCATCGTGAACAATATGAGAGAGCTGAGGGCAGACATAGCACAGGCGCTGGA CAAGCCCACGGTGCCTCGA  
ATTCCAGCTT

## Fusion Sequences

M13\_0.6-LA\_0.2

### Fusion

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCCGGTCTGGTTCGC AACACTTCTTGCGGCGATAGAAGGTTCTGGCTCTT  
CGATC GATTGGGTAATGAATATCCGGTCTTGTC AAGAGAGAAGTCCTAGCACGGTAACCTCCGAGGATGTCATCAAAGAGT  
TTAAAGAGTTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAACGGACACGAGTTTCGAGATTGAGGGAGAAGGAGAAG  
GCCGGCCTTACGAGGGCACACAAACCGCTAAGCTCAAGGTCACAAAAGGAGGACTAATAACGGTCCTAAGGTAGCGAAC  
CCTCCCTTCTCCTGGGATATTCTGAGCCCTCAGTTCAGTACGGAAGCGAATTCCAGCTT

Inv\_M13\_0.6-LA\_0.2

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCGTTCCGTACTGGAAGTGAAGGCTCAGAATAT  
CCCAGGAGAAGGGGAGGGTTCGCTACCTTAGGACCGTTATAGTTAGTCTCTTTTGACCTTGAGCTTAGCGGTTTGTTGTGC  
CCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTAAATCTCATA  
AACTCTTAAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTCTCT CTTGACAAGAACCGGATATTCATTACCCAA  
ATC GATCGAAGAGCCAGGAACC

GGTTCCTGGCTCTTCGATCGATTTGGGTAATGAATATCCGGTCTTGTC AAGAGAGAAGTCCTAGCACGGTAACCTCCGAGGAT  
GTCATCAAAGAGTTTAAAGAGTTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAACGGACACGAGTTTCGAGATTGAGG  
GAGAAGGAGAAGGCCGGCCTTACGAGGGCACACAAACCGCTAAGCTCAAGGTCACAAAAGGAGGACTAATAACGGTCC  
TAAGGTAGCGAACCTCCCTTCTCCTGGGATATTCTGAGCCCTCAGTTCAGTACGGAAGCGAATTCTTGAGTTTGCTCCG  
GTCTGGTTCGCAACACTTCTTGCGGCGAT(reverse complement of the sequence above)

Inv\_M13\_0.6-LA\_0.4

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCATGACAGGGCCATCGGAGGGGAAGTTGGTTC  
CTCTGAGTTTACCTTATAAATAAACTCTCCGTCCTGGAGGGTGCTATCTTGTTGACTGTCACACGCCTCCGTCCTCGAAGTT  
CATGAATCTCTCCACTTGAAGCCTTCAGGGAAGGAGAGCTTCAGATAGTCAGGGATGTCGGCAGGGTGTTTAACATAGGCTT  
TGCTTCCGTAAGTGAAGTGAAGGCTCAGAATATCCAGGAGAAGGGGAGGGTTCGCTACCTTAGGACCGTTATAGTTAGTCCT  
CCTTTTGACCTTGAGCTTAGCGTTTGTTGTCCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTT  
GACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTC  
TCT CTTGACAAGAACCGGATATTCATTACCCAAATC GATCGAAGAGCCAGGAACC

Inv\_M13\_0.6-LA\_0.8

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCGAGGCGCACCGTGGGCTTGTCAGCGCCTGT  
GCTATGTCTGCCCTCAGCTCTCTCATATTGTTCCACGATGGTGTAGTCCCCATTATGGCTGATAATGTCGAGTTTAATATCAGTC  
ATGTAGGCGCCAGGCAGCTGCACTTGTTTCTTGGCCTTGAGGTTGTTTTGACCTCGGCATCGTAGTGTCTCCGCTTTGAGTT  
TCAGTCTCATTTAATTTGCCTTTAGAGCGCCATCCTCAGGATACATTCTCTCGGTGGAGGCTTCCCATCCATTGTTTTTTTTT  
GCATGACAGGGCCATCGGAGGGGAAGTTGGTTCTCTGAGTTTACCTTATAAATAAACTCTCCGTCCTGGAGGGTGCTATCTT  
GTGTGACTGTCACACGCCTCCGTCCTCGAAGTTCATGAATCTCTCCACTTGAAGCCTCAGGGAAGGAGAGCTTCAGATAGT  
CAGGGATGTCGGCAGGGTGTTTAACATAGGCTTTGCTTCCGTAAGTGAAGTGAAGGCTCAGAATATCCAGGAGAAGGGGAG  
GGTTCGCTACCTTAGGACCGTTATAGTTAGTCTCTTTTGACCTTGAGCTTAGCGTTTGTTGTCCTCGTAAGGCCGGCCT  
TCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCC  
TCGGAGGTTACCGTGCTAGGACTTCTCT CTTGACAAGAACCGGATATTCATTACCCAAATC GATCGAAGAGCCAGGAACC

M13\_1.0-LA\_0.2

Fusion

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCGGTCTGGTTGCAACACTTCTTGCGGCGATAGAAGGTTCTGGCTCTT  
CGATC GCCGTTGCTACCCTCGTTCCGATGC AGAGAAGTCCTAGCACGGTAACCTCCGAGGATGTCATCAAAGAGTTTAAAGAG  
TTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAACGGACACGAGTTCGAGATTGAGGGAGAAGGAGAAGGCCGGCCT  
TACGAGGGCACACAAACCGCTAAGCTCAAGGTCACAAAAGGAGGACTAACTATAACGGTCCTAAGGTAGCGAACCCCTCCCCTT  
CTCCTGGGATATTCTGAGCCCTCAGTTCCAGTACGGAAGCGAATTCCAGCTT

Inv\_M13\_1.0-LA\_0.2

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCGCTTCCGTA CTGGA ACTGAGGGCTCAGAATAT  
CCCAGGAGAAGGGGAGGGTTGCTACCTTAGGACCGTTATAGTTAGTCTCCTTTTGTGACCTTGAGCTTAGCGGTTTGTGTGC  
CCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTTAAATCTCATA  
AACTCTTTAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTCTCT GCATCGGAACGAGGGTAGCAACGGC GATC  
GAAGAGCCAGGAACC

Inv\_M13\_1.0-LA\_0.4

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCATGACAGGGCCATCGGAGGGGAAGTTGGTTC  
CTCTGAGTTTACCTTATAAATAAACTCTCCGTCCTGGAGGGTGCTATCTTGTTGACTGTCACCACGCCTCCGTCCTCGAAGTT  
CATGAATCTCTCCACTTGAAGCCTTCAGGGAAGGAGAGCTTCAGATAGTCAGGGATGTCGGCAGGGTGTTTAACATAGGCTT  
TGCTTCCGTA CTGGA ACTGAGGGCTCAGAATATCCAGGAGAAGGGGAGGGTTCGCTACCTTAGGACCGTTATAGTTAGTCCT  
CCTTTTGTGACCTTGAGCTTAGCGTTTGTGTGCCCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTT  
GACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTC  
TCT GCATCGGAACGAGGGTAGCAACGGC GATCGAAGAGCCAGGAACC

Inv\_M13\_1.0-LA\_0.8

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCGAGGCGCACCGTGGGCTTGTCAGCGCCTGT  
GCTATGTCTGCCCTCAGCTCTCTCATATTGTTCCACGATGGTG TAGTCCCCATTATGGCTGATAATGTCGAGTTTAAATCAGTC  
ATGTAGGCGCCAGGCAGCTGCACTTGTTTCTTGGCCTTG TAGGTTGTTTTGACCTCGGCATCGTAGTGTCTCCGTCCTTGAGTT  
TCAGTCTCATTTTAATTTGCGCTTTCAGAGCGCCATCCTCAGGATACATTCTCTCGGTGGAGGCTTCCCATCCATTGTTTTTTTTT  
GCATGACAGGGCCATCGGAGGGGAAGTTGGTTCCTCTGAGTTTACCTTATAAATAAACTCTCCGTCCTGGAGGGTGCTATCTT  
GTGTGACTGTCACCACGCCTCCGTCCTCGAAGTTCATGAATCTCTCCACTTGAAGCCTTCAGGGAAGGAGAGCTTCAGATAGT  
CAGGGATGTCGGCAGGGTGTTTAACATAGGCTTTGCTCCGTA CTGGA ACTGAGGGCTCAGAATATCCAGGAGAAGGGGAG  
GGTTCGTA CTAGGACCGTTATAGTTAGTCCTCTTTTGTGACCTTGAGCTTAGCGGTTTGTGTGCCCTCGTAAGGCCGGCCT  
TCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCC  
TCGGAGGTTACCGTGCTAGGACTTCTCT GCATCGGAACGAGGGTAGCAACGGC GATCGAAGAGCCAGGAACC

M13\_2.0-LA\_0.2

Fusion-LA\_0.2

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCGGTCTGGTTCGC AACACTTCTTGCGGCGATAGAAGGTTCTGGCTCTT  
CGATC GGCTCTGAGGGTGGCGTTCTGAGG AGAGAAGTCCTAGCACGGTAACC TCCGAGGATGTCATCAAAGAGTTTAAAGA  
GTTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAACGGACACGAGTTCGAGATTGAGGGAGAAGGAGAAGGCCGGCC  
TTACGAGGGCACACAAACCGCTAAGCTCAAGGTCACAAAAGGAGGACTAACTATAACGGTCTTAAGGTAGCGAACCCCTCCCT  
TCTCCTGGGATATTCTGAGCCCTCAGTCCAGTACGGAAGCGAATTCCAGCTT

Inv\_ M13\_2.0-LA\_0.2

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCAA GAATTCGCTTCCGTACTGGAAGTGAAGGCTCAGAATAT  
CCCAGGAGAAGGGGAGGGTTCGCTACCTTAGGACCGTTATAGTTAGTCCCTCTTTGTGACCTTGAGCTTAGCGGTTTGTGTGC  
CCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTTAAATCTCATA  
AACTCTTAAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTCTCT CCTCAGAACCGCCACCCTCAGAGCC GATCG  
AAGAGCCAGGAACC

Inv\_ M13\_2.0-LA\_0.4

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCAA GAATTCATGACAGGGCCATCGGAGGGGAAGTTGGTTC  
CTCTGAGTTTACCTTATAAACTCTCCGTCCTGGAGGGTGCTATCTTGTGTGACTGTACCACGCCTCCGTCCTCGAAGTT  
CATGAATCTCTCCACTTGAAGCCTTCAGGGAAGGAGAGCTTCAGATAGTCAGGGATGTCGGCAGGGTGTTAACATAGGCTT  
TGCTTCCGTAAGTGAAGTGAAGGCTCAGAATATCCAGGAGAAGGGGAGGGTTCGCTACCTTAGGACCGTTATAGTTAGTCCT  
CCTTTGTGACCTTGAGCTTAGCGGTTTGTGTGCCCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTT  
GACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTAAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTC  
TCT CCTCAGAACCGCCACCCTCAGAGCC GATCGAAGAGCCAGGAACC

Inv\_ M13\_2.0-LA\_0.8

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCAA GAATTCGAGGCGCACCGTGGGCTTGTCAGCGCCTGT  
GCTATGTCTGCCCTCAGCTCTCTCATATTGTTCCACGATGGTGTAGTCCCCATTATGGCTGATAATGTCGAGTTTAATATCAGTC  
ATGTAGGCGCCAGGCAGCTGCACTTGTTTCTTGGCCTTGAGGTTGTTTGACCTCGGCATCGTAGTGCCTCCGTCTTTGAGTT  
TCAGTCTCATTTTAATTTGCCTTTTCAAGCGCCATCCTCAGGATACATTCTCTCGGTGGAGGCTTCCCATCCATTGTTTTTTTTT  
GCATGACAGGGCCATCGGAGGGGAAGTTGGTTCTCTGAGTTTACCTTATAAAATAAACTCTCCGTCCTGGAGGGTGCTATCTT  
GTGTGACTGTACCACGCCTCCGTCCTCGAAGTTCATGAATCTCTCCACTTGAAGCCTTCAGGGAAGGAGAGCTTCAGATAGT  
CAGGGATGTCGGCAGGGTGTTAACATAGGCTTTGCTTCCGTAAGTGAAGTGAAGGCTCAGAATATCCAGGAGAAGGGGAG  
GGTTCGCTACCTTAGGACCGTTATAGTTAGTCTCCTTTGTGACCTTGAGCTTAGCGGTTTGTGTGCCCTCGTAAGGCCGGCCT  
TCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCC  
TCGGAGGTTACCGTGCTAGGACTTCTCT CCTCAGAACCGCCACCCTCAGAGCC GATCGAAGAGCCAGGAACC

M13\_4.0-LA\_0.2

Fusion

GAGTATTACCGCGGCGAATTC TTGGAGTTTGCTTCCGGTCTGGTTCGC AACACTTCTTGC GGCGATAGAAGGTTCTGGCTCTT  
CGATC GGCGAATCCGTTATTGTTTCTCCCGATGTA AGAGAAGTCCTAGCACGGTAACC TCCGAGGATGTCATCAAAGAGTTTAA  
AGAGTTTATGAGATTTAAGGTCAAGATGGAGGGAAGCGTCAACGGACACGAGTTTCGAGATTGAGGGAGAAGGAGAAGGCC  
GGCCTTACGAGGGCACACAAACCGCTAAGTCAAGGTCACAAAAGGAGGACTAACTATAACGGTCCTAAGGTAGCGAACCT  
CCCCTTCTCCTGGGATATTCTGAGCCCTCAGTTCCAGTACGGAAGCGAATTCCAGCTT

Inv\_ M13\_4.0-LA\_0.2

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCGCTTCCGTACTGGAAGTGAAGGCTCAGAATAT  
CCCAGGAGAAGGGGAGGGTTCGCTACCTTAGGACCGTTATAGTTAGTCCCTCTTTGTGACCTTGAGCTTAGCGGTTTGTGTGC  
CCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTAAATCTCATA  
AACTCTTTAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTCTCT TACATCGGGAGAAACAATAACGGATTTCGC  
CGATCGAAGAGCCAGGAACC

Inv\_ M13\_4.0-LA\_0.4

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCATGACAGGGCCATCGGAGGGGAAGTTGGTTC  
CTCTGAGTTTACCTTATAAACTCTCCGTCCTGGAGGGTGCTATCTTGTGTGACTGTACCACGCCTCCGTCCTCGAAGTT  
CATGAATCTCTCCACTTGAAGCCTTCAGGGAAGGAGAGCTTCAGATAGTCAGGGATGTCGGCAGGGTGTTAACATAGGCTT  
TGCTTCCGTACTGGAAGTGAAGGCTCAGAATATCCAGGAGAAGGGGAGGGTTCGCTACCTTAGGACCGTTATAGTTAGTCCT  
CCTTTGTGACCTTGAGCTTAGCGGTTTGTGTGCCCTCGTAAGGCCGGCCTTCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTT  
GACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTAACTCTTTGATGACATCCTCGGAGGTTACCGTGCTAGGACTTC  
TCT TACATCGGGAGAAACAATAACGGATTTCGCC GATCGAAGAGCCAGGAACC

Inv\_ M13\_4.0-LA\_0.8

ATCGCCGCAAGAAGTGTT GCGAACCAGACCGGAAGCAAACCTCCAA GAATTCGAGGCGCACCGTGGGCTTGTCAGCGCCTGT  
GCTATGTCTGCCCTCAGCTCTCTCATATTGTTCCACGATGGTGTAGTCCCCATTATGGCTGATAATGTCGAGTTTAATATCAGTC  
ATGTAGGCGCCAGGCAGCTGCACTTGTTTCTTGGCCTTGAGGTTGTTTGACCTCGGCATCGTAGTGCCTCCGTCTTTGAGTT  
TCAGTCTCATTTTAATTTGCCTTTTCAAGCGCCATCCTCAGGATACATTCTCTCGGTGGAGGCTTCCCATCCATTGTTTTTTTTT  
GCATGACAGGGCCATCGGAGGGGAAGTTGGTTCCTCTGAGTTTACCTTATAAATAAACTCTCCGTCCTGGAGGGTGCTATCTT  
GTGTGACTGTCACCACGCCTCCGTCCTCGAAGTTCATGAATCTCTCCACTTGAAGCCTTCAGGGAAGGAGAGCTTCAGATAGT  
CAGGGATGTCGGCAGGGTGTTAACATAGGCTTTGCTCCGTAAGTTCGAACTGAGGGCTCAGAATATCCAGGAGAAGGGGAG  
GGTTCGCTACCTTAGGACCGTTATAGTTAGTCTCCTTTGTGACCTTGAGCTTAGCGGTTTGTGTGCCCTCGTAAGGCCGGCCT  
TCTCCTTCTCCCTCAATCTCGAACTCGTGCCGTTGACGCTTCCCTCCATCTTGACCTTAAATCTCATAAACTCTTTGATGACATCC  
TCGGAGGTTACCGTGCTAGGACTTCTCT TACATCGGGAGAAACAATAACGGATTTCGCC GATCGAAGAGCCAGGAACC