

Supplementary Information

Long oligos: direct chemical synthesis of genes with up to 1,728 nucleotides

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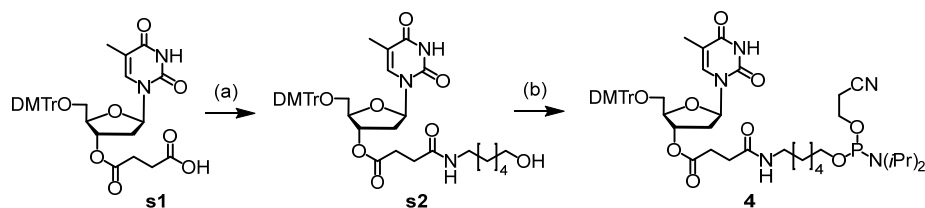
Experimental Procedures

General information:

Glass wool (cat# G0034) was purchased from Flinn Scientific, Inc. Glass beads (Borosilicate Solid Glass Microspheres, 2.2 g/cc, 53-63 μm , cat#BSGMS-2.2) were purchased from Cospheric LLC. 2-[(Acetoxy(polyethyleneoxy)propyl)triethoxysilane (cat# SIA0078.0) was purchased from Gelest. Other small molecule chemicals for organic synthesis, oligo deprotection and cleavage, and catching-by-polymerization such as DBU, saturated NH_4OH , *N,N*-dimethylacrylamide, *N,N'*-methylenebis(acrylamide), ammonium persulfate, and *N,N,N',N'*-tetramethylethylenediamine (TMEDA) were purchased from Aldrich or other companies. Reagents for oligo synthesis were purchased from Glen Research and Hongene Biotech. Oligos were synthesized on an ABI 394 DNA/RNA synthesizer. Some steps for the functionalization of glass wool and glass beads were performed on a MerMade 6 synthesizer.

Polymerase chain reactions (PCR) were performed using an Applied Biosystems 2720 Thermal Cycler. Gel images were obtained on a UVP GelDoc-IT Imaging System 2UV Transilluminator at 302 nm. Oligo primers were purchased from IDT. GelRed® (cat# 41003) was purchased from Biotium. Solid phase reversible immobilization (SPRI) bead (cat# CNGS005) was purchased from BullDog Bio. QIAprep® Spin Miniprep Kit (cat# 27106) and QIAquick® Gel Extraction Kit (cat# 28704) were purchased from Qiagen. dNTPs, Phusion Hot Start II High Fidelity DNA polymerase (cat# F549S), DreamTaq™ Hot Start Green PCR Master Mix (cat# K9021), TopVision agarose (cat# R0491), GeneRuler 1 KB+ ladder (cat# SM1334) Luria Broth powder (cat# 12795-027) and Zero Blunt™ TOPO™ PCR Cloning Kit (cat# 450031) were purchased from ThermoFisher. SOC medium (cat# B8020S), and NEB® 5-alpha cells (cat# C2987H) were purchased from New England Biolab. Sanger sequencing was carried out at MCLAB (<https://mclab.com/>).

No unexpected or unusually high safety hazards were encountered in the following experiments.



Scheme S1. Synthesis of linker phosphoramidite **4**. Conditions: (a) $\text{H}_2\text{N}(\text{CH}_2)_6\text{OH}$ (1.1 eq), HBTU (1 eq), DIEA (3 eq), DMF, rt, 8 h, 91%. (b) Diisopropylammonium tetrazolide (1.5 eq), N,N,N',N' -tetraisopropylphosphorodiamidite (1.5 eq), rt, 12 h, 87%.

To a solution of compound **s1** (2 g, 3.1 mmol, 1 eq) in dry DMF (20 mL) was added DIEA (1.2 g, 9.3 mmol, 3 eq) and HBTU (1.17 g, 3.1 mmol, 1 eq). The mixture was stirred under nitrogen at rt for 15 min. The content was transferred dropwise to flask containing the solution of 6-amino-1-hexanol (0.25 g, 3.41 mmol, 1.1 eq) in dry DMF (5 mL) via a cannula with its inlet terminus wrapped with cotton to prevent transfer of insoluble materials formed. After stirring at rt for 8 h, the mixture was concentrated to ~30 mL under vacuum from an oil pump. The residue was purified by dissolving the sample in the solvent mixture of acetone/hexane 3:1 with 5% Et_3N , loading onto a column (SiO_2), and eluting with the same solvent mixture. Compound **s2** was given as a pale yellow foam upon drying under high vacuum: 2.1 g, 91%; ^1H NMR (500 MHz, CDCl_3) δ 1.27-1.50 (m, 8H), 2.40-2.62 (m, 9H), 2.82 (s, 2H), 2.94 (s, 2H), 3.14-3.18 (m, 2H), 3.41 (s, 3H), 3.53-3.55 (t, $J = 5.0$ Hz, 1H), 4.11 (s, 1H), 5.43 (s, 1H), 6.33-6.37 (m, 1H), 6.78-6.80 (d, $J = 10.0$ Hz, 4H), 7.18-7.35 (m, 9H), 7.58 (s, 1H), 7.95 (s, 1H), 9.82 (s, 1H); ^{13}C NMR (126 MHz, CDCl_3) δ 8.7, 25.2, 26.2, 29.1, 30.5, 31.3, 32.2, 36.7, 47.2, 55.2, 62.4, 63.6, 75.4, 83.9, 84.3, 87.0, 111.4, 113.3, 127.1, 128.0, 130.0, 135.1, 135.7, 144.1, 150.6, 158.7, 163.1, 164.1, 171.4, 172.3. The compound is known.¹

To a solution of compound **s2** (2 g, 2.6 mmol, 1 eq) in dry ACN was added diisopropylammonium tetrazolide (0.69 g, 4.0 mmol, 1.5 eq) and 2-cyanoethyl N,N,N',N' -tetraisopropylphosphorodiamidite (1.2 g, 4.0 mmol, 1.5 eq) at rt under nitrogen. After stirring overnight, the mixture was concentrated to dryness. The product was purified by dissolving in the solvent mixture of acetone/hexane 3:1 with 5% Et_3N , loading onto a column (SiO_2), and eluting with the same solvent mixture. The product was given as a white foam upon drying under high vacuum: 2.2 g, 87%; ^1H NMR (500 MHz, CDCl_3) δ 1.10-1.12 (t, $J = 5.0$ Hz, 12H), 1.18-1.54 (m, 8H), 2.40-2.68 (m, 8H), 3.12-3.16 (m, 1H), 3.40-4.08 (m, 14H), 5.43 (s, 1H), 6.25 (s, 1H), 6.32-6.39 (m, 1H), 6.76-6.78 (d, $J = 10.0$ Hz, 4H), 7.14-7.34 (m, 9H), 7.55 (s, 1H); ^{13}C NMR (126 MHz, CDCl_3) δ 11.5, 20.3, 22.8, 24.5, 25.5, 26.4, 29.3, 30.4, 31.0, 37.8, 39.4, 42.8, 45.2, 55.1, 58.2, 63.5, 75.4, 83.8, 84.2, 86.9, 111.4, 113.2, 117.8, 127.0, 128.0, 129.9, 135.1, 135.4, 144.1, 150.7, 158.6, 164.0, 171.0, 172.3; ^{31}P NMR (202 MHz, CDCl_3) δ 146.97, 147.01. The compound is known.²

Glass surface functionalization

Glass wool (2 g) from commercial source was soaked in a piranha solution ($\text{H}_2\text{SO}_4/\text{H}_2\text{O}_2$ 3:1, v/v, ~20 mL) with occasional shaking at rt. Caution, piranha solution is highly reactive and corrosive; appropriate safety procedure must be followed. After 1 h, the supernatant was removed. The glass wool was washed sequentially with water and ACN each for 5 times, and then allowed to dry in the air.

The activated glass wool (**5**, 2 g, see Scheme 2 for the surface functionalization procedure) in the solution of 1% 2-[(acetoxypoly(ethyleneoxy)propyl)triethoxysilane (**2**) in freshly distilled toluene (20 mL) was incubated at rt for 20 min. The supernatant was removed, and the glass wool was washed with toluene

5 times and then incubated in an oven at 100 °C for 4 h. After cooling to rt, the glass wool was washed with chloroform to give the functionalized glass wool **6**.

To remove the acetyl group, the glass wool **6** (1 g) was incubated in NH₄OH (30%, 10 mL) at 55 °C for 2 h. The supernatant was removed, and the glass wool was washed sequentially with water and ACN each for 5 times, and then allowed to dry in the air. This converted **6** to **7**.

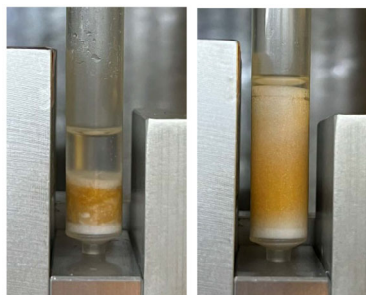


Figure S1. The trityl color on glass wool (left) and glass beads (right) during the detritylation steps for the conversion of **8** to **1**.

The glass wool (**7**, 1 g) was packed in a DNA synthesis column. On a MerMade 6 synthesizer, the following steps were carried out. Between the steps, the glass wool was washed with dry ACN. Coupling: **3** (0.5 mL, 0.1 M in ACN), DCI (0.5 mL, 0.25 M in ACN), 10 min waiting; repeat 4 times. Oxidation: I₂ (1 mL, 0.02 M in THF/pyridine/H₂O), 1 min waiting; repeat 2 times. Deblocking: DCA (1 mL, 2% in DCM), 90 sec waiting; repeat 3 times. The coupling and oxidation steps were repeated 1 time. This converted **7** to **8**. The deblocking (see Figure S1 for color), coupling (**4** instead of **3**), and oxidation steps were repeated. This converted **8** to **1**. The loading was determined to be 981 nmol/g using a method involving treating the glass wool with an acid and measuring the UV absorption of trityl cations.³

Glass beads (5 g) were functionalized using the same conditions as described above. The loading was determined to be 256 nmol/g. The functionalized glass beads are also represented by **1** in this paper.

Oligo synthesis: The synthesis of the 800-mer GFP gene on glass wool is used for the description (the sequences of the 800-mer GFP and 1,728-mer Φ 29 DNA polymerase genes are given in the sequence alignment documents in the supporting information). The glass wool **1** (30 mg, 29.4 nmol) was packed in an empty 0.2 μ mol synthesis column, and loaded onto an ABI 394 DNA/RNA synthesizer. The synthesizer manufacturer recommended 1 μ mol synthetic cycle with slight modifications was used. The specific conditions were the following. Deblocking: DCA (2% in DCM), 98 sec. Coupling: Bz-dA, Ac-dC, *i*Bu-dG or dT phosphoramidite (0.1 M in ACN); DCI (0.25 M in ACN), 2.5 sec $\times$ 2 reagent delivery, 35 sec waiting. Capping: Cap A, THF/pyridine/Ac₂O; cap B, 1-methylimidazole (16% in THF), 10 sec delivery, 10 sec waiting. Oxidation: I₂ (0.02 M in THF/pyridine/H₂O), 8 sec delivery, 15 sec waiting. Washing conditions between the steps were the same as recommended by the synthesizer manufacturer except for an additional wash with ACN after the oxidation step to ensure complete washing. For purposes such as refilling reagents, the synthesis was set up as several shorter ones such as 200-mer. The average stepwise yields as indicated by the trityl assay of the synthesizer were consistently 99.6%, 99.7% or 99.8% after the syntheses reached over 100 synthetic cycles. The last nucleotide was incorporated with the polymerizable tagging phosphoramidite PTP, where B is thymine, on a MerMade 6 synthesizer (0.1 M in ACN, 0.25 M DCI in ACN, 5 min; repeat 3 times; followed by capping and oxidation as usual; no detritylation). The detritylation

of the 799th nucleotide before the coupling step involving PTP was also performed on the MerMade 6 synthesizer. The trityl color was visible (Figure S2).

Using glass beads as the solid support, the 800-mer GFP gene (50 mg glass beads, theoretically 12.8 nmol) and the 1,728-mer Φ 29 DNA polymerase gene (130 mg glass beads, 33.28 nmol) were synthesized under the same conditions described above.

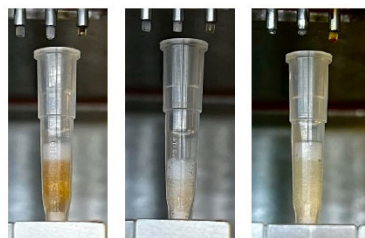


Figure S2. Images showing trityl color of last detritylation before coupling with PTP. The oligo synthesis was carried out on an ABI synthesizer, while the last detritylation and PTP tagging was carried out on a MerMade 6 synthesizer. Left: glass wool/800-mer synthesis. Middle: glass beads/800-mer synthesis. Right: glass beads/1,728-mer synthesis. The trityl color as well as the trityl assay data from the ABI synthesizer are useful for estimating the probability of success of the long oligo syntheses.

Oligo deprotection and cleavage: The deprotection and cleavage of the 800-mer GFP gene on glass wool is used for the description. To the glass wool (~30 mg, theoretically 29.4 nmol oligo) in a 1.5 mL centrifuge tube was added DBU (10% in ACN). The tube was gently shaken at rt for 10 min. The supernatant was removed, and the DBU treatment was repeated 1 time. After the supernatant was removed, the glass wool was washed with ACN for 5 times. Saturated NH₄OH (0.5 mL) was added. The tube was sealed and heated at 55 °C for 16 h. After cooling to rt, the supernatant was transferred to a clean centrifuge tube. The glass wool was washed with water (200 μ L $\times$ 3). The supernatant and washes were combined, and the volume was adjusted to 50 μ L by evaporation and dilution.

The 800-mer GFP (theoretically 5.12 nmol, corresponding to ~20 mg glass beads) and 1,728-mer Φ 29 DNA polymerase (theoretically 33.28 nmol, corresponding to ~130 mg glass beads) genes synthesized on glass beads were cleaved and deprotected under the same conditions described above except that only a portion of glass beads was subjected to the procedure for the case of GFP gene.

Oligo purification using catching-by-polymerization (CBP): The purification of the 800-mer GFP gene synthesized on glass wool is used for the description. Polymerization: To the 50 μ L solution of crude oligo containing tagged full-length oligo and failure oligos (Scheme 1) as well as other materials (theoretically 29.4 nmol oligo) in a 1.5 mL centrifuge tube was added 12 μ L polymerization solution (*N,N*-dimethylacrylamide, 340.5 μ L, 3.32 mmol; *N,N'*-methylenebis(acrylamide), 17 mg, 0.11 mmol; sodium acrylate, 3 mg, 0.032 mmol; water, 170.5 μ L). After mixing, ammonium persulfate (0.23 M, 5 μ L) and *N,N,N',N'*-tetramethylethylenediamine (TMEDA, 0.69 M, 5 μ L) were added. The tube was closed, and the content was quickly mixed with a short vortex and spin. The polymerization reaction was allowed to proceed at rt for 1 h. Washing: The gel (~100 μ L in size) was transferred into a 50 mL centrifuge tube. NaOAc solution (20%, pH unadjusted, 20 mL) was added. The mixture was gently shaken at rt overnight. The gel was taken to another 50 mL centrifuge tube, and Et₃N solution (5%, 20 mL) was added. The tube was shaken at rt overnight. The gel was taken out, placed into a 2 mL centrifugal filter unit over the filter, and cut into small pieces using a spatula. The gel was washed with water (0.5 mL $\times$ 5). Cleavage: To half

volume of the gel, minimum AcOH (80%, ~200 μ L) that could cover the gel was added. The mixture was incubated at rt for 5 min with occasional shaking. The liquid and gel were separated by centrifugation. The liquid was diluted with water (800 μ L) to minimize the possibility of oligo damage by acid. The treatment of the gel with acid was repeated two times. The gel was washed with water (0.3 mL $\times$ 3). The bottom of the filtering unit holding the gel was stopped with parafilm, and to the gel was added water (500 μ L). The mixture was shaken at rt overnight. The solution and gel was separated by centrifugation, and the gel was washed with water (250 μ L $\times$ 2). These gave the oligo solutions in five tubes (~1 mL each). The solutions were concentrated, combined and evaporated to dryness. The residue acid is suggested to be removed by precipitation of the oligo from NH_4OH solution by $n\text{BuOH}^4$ if the oligo needs to be stored for more than two days. The oligo (theoretically 14.7 nmol) was dissolved in water (10 μ L). Quantification using Qubit 4 Fluorometer indicated that 13.7 μ g (55.56 pmol) oligo was obtained. The overall yield for the 800-mer synthesis and purification was 0.38% (Entry 8, Table 1).

The 800-mer GFP and 1,728-mer Φ 29 DNA polymerase genes synthesized on glass beads were purified using the same CBP procedure described above. For the 800-mer, all the crude oligo (theoretically 5.12 nmol) was subjected to the polymerization for CBP. Half of the polyacrylamide gel was subjected for cleavage. Quantification of the purified oligo (theoretically 2.56 nmol) with Qubit 4 Fluorometer indicated that 84 ng (0.34 pmol) oligo was obtained. The overall yield for the 800-mer synthesis and purification was 0.013% (Entry 8, Table 1). For the 1,728-mer, all the crude oligo (theoretically 33.28 nmol) was subjected to the polymerization. Half of the gel was subjected to cleavage. Quantification of the purified oligo (theoretically 16.64 nmol) with Qubit 4 Fluorometer indicated that 1.416 μ g (2.64 pmol) oligo was obtained. The overall yield for the 1,728-mer synthesis and purification was 0.016 % (Entry 10, Table 1).

PCR amplification: The 800-mer GFP gene synthesized on glass wool is used for the description. The mixture of CBP-purified oligo (~30 ng as quantified with Qubit 4 Fluorometer), Thermo Scientific™ Phusion™ High-Fidelity DNA Polymerase (0.4 U), forward and reverse primers (**p1a-b**, 0.5 μ M each), HF buffer (1 $\times$), dNTPs (0.2 mM each), and nuclease-free water (20 μ L total mixture volume, concentrations were final) was subjected to the following PCR cycles: 98 $^\circ\text{C}$ for 30 sec for initial denaturing; 98 $^\circ\text{C}$ for 7 sec, 58 $^\circ\text{C}$ for 15 sec, and 72 $^\circ\text{C}$ for 25 sec for 32 cycles; and 72 $^\circ\text{C}$ for 7 min. The PCR product was analyzed with agarose gel (1%) electrophoresis (GelRed® staining). Gel images are given in Figure 1.

The same PCR conditions were applied to the 800-mer GFP gene synthesized on glass beads. For the 1,728-mer Φ 29 DNA polymerase gene, the PCR was conducted similarly except for the following modifications: primers were **p2a-b**; template quantity was ~7 ng; and the PCR cycles were modified so that the annealing step was 60.6 $^\circ\text{C}$ for 10 seconds and the following elongation step was 72 $^\circ\text{C}$ for 30 sec. Gel images of the PCR products are given in Figure 1.

Cloning and sequencing: The 800-mer GFP gene synthesized on glass wool is used for the description. The PCR product (3 μ L out of 20 μ L) was ligated into the pCR™4Blunt-TOPO™ vector following manufacturer's protocol. The resulting recombinant DNA was then transformed into One Shot Mach1 T1 Phage-Resistant Chemically Competent *E. coli* following manufacturer's protocol. The transformed cells (50 μ L) were spread over kanamycin containing agar plates, which was incubated in a 37 $^\circ\text{C}$ incubator overnight. A portion of selected colonies was harvested using a sterile pipette tip and transferred into 50 μ L of lysis buffer (1% triton X-100, 20 mM Tris, pH 8.0, 2 mM EDTA, pH 8.0). The lysis solutions were then heated at 95 $^\circ\text{C}$ for 10 min. Colony PCR reactions were set up using the recipe: DreamTaq PCR Mater Mix (1 $\times$), 2 μ L colony lysis solution, primers **p1a-p1b** (0.5 μ M each), and water to 20 μ L (all concentrations are final). The samples were then subjected to the following PCR conditions: 95 $^\circ\text{C}$ for 2 min for initial denaturing; 95 $^\circ\text{C}$ for 30 sec for denaturing, 57 $^\circ\text{C}$ for 30 sec for annealing, and 72 $^\circ\text{C}$ for

extension for 1 min for 32 cycles; 72 °C for extension for 7 min. The PCR products were analyzed with electrophoresis on a 1% agarose gel (Figures 2A-C). Plasmid DNA from additional portions of the colonies that showed expected band in the colony PCR analysis were sent to MCLAB for Sanger sequencing. Both forward (**p4a**) and reverse (**p4b**) reads were obtained, which were assembled into a single contig using the Cap3 program (<https://doua.prabi.fr/software/cap3>). Several colonies that were unable to generate contigs due to poor sequencing quality were not included here. The contigs that were generated successfully were aligned to the reference sequence using the BLAST alignment software to trim off vector sequence and were then aligned with the reference sequence using CLUSTAL Omega. The data are included in the supporting information.

The cloning and sequencing procedures for the 800-mer GFP gene synthesized on glass beads were exactly the same. Gel images of colony PCR products are given in Figures 2D-F. For the 1,728-mer Φ 29 DNA polymerase gene synthesized on glass beads, the following adjustments were applied. For colony PCR, the primers **p3a-b**, which covered a 600-mer region within the 1,728-mer gene, were used with an annealing temperature of 57.5 °C. Gel image of PCR products is given in Figure 2G. For Sanger sequencing and data analysis, four sequencing reads were generated for each plasmid, which was from the colonies giving bands in Figure 2G, using primers **p3a-b** and **p4a-b**. All four reads were used to generate the contig. Detailed sequence data are provided in the supporting information. The results are summarized in Table 2. Colony PCR was also carried out using primers **p2a-b**, which covered the entire 1,728-mer gene. The annealing temperature was 55.3 °C. The gel images of the PCR products are given in Figures 2H-I.

Table S1. Primers used in this study.

Primer	Sequence	Purpose
p1a	GCGAATTAATACGACTCACT	Primer for 800-mer GFP gene amplification
p1b	AAACCCCTCCGTTTGTAGAGA	Primer for 800-mer GFP gene amplification
p2a	ATGAAGCATATGCCGAGAAA	Primer for 1,728-mer Φ 29 DNA polymerase gene amplification
p2b	TTATTTGATTGTGAATGTGTCATCA	Primer for 1,728-mer Φ 29 DNA polymerase gene amplification
p3a	ATGACAGCAGGCAGTGACA	Primer for 1,728-mer Φ 29 DNA polymerase gene sequencing
p3b	GCTAGTTGCTTGATCGCTCC	Primer for 1,728-mer Φ 29 DNA polymerase gene sequencing
p4a	GTAAAACGACGGCCAG	Primer for 800-mer GFP gene sequencing [M13 forward (-20)]
p4b	CAGGAAACAGCTATGAC	Primer for 800-mer GFP gene sequencing [M13 reverse]

Loading Calculation for Glass Wool and Glass Beads

Glass wool

Assumptions: mass, 1 g; density, d g/mL; diameter, $2r$ μ m; radius, r μ m; length, L μ m

$$\text{Volume of 1 g of solid glass: } 1 \text{ g} \div d \text{ g/cm}^3 = \frac{1}{d} \text{ cm}^3 = \frac{1}{d} \times 10^{12} \mu\text{m}^3$$

$$\text{Volume of 1 glass fiber: } r^2\pi L \mu\text{m}^3$$

$$\text{Number of glass fiber: } \left(\frac{1}{d} \times 10^{12} \mu\text{m}^3 \right) \div (r^2\pi L \mu\text{m}^3) = \frac{10^{12}}{dr^2\pi L}$$

$$\text{Surface area of one glass fiber: } (2r^2\pi) + (2r\pi L) \approx 2r\pi L \mu\text{m}^2 \text{ (L is } \sim 1,000 \text{ times of } r)$$

Total surface area of 1 g glass wool: $[2r\pi L \mu\text{m}^2] \times \frac{10^{12}}{dr^2\pi L} = \frac{2}{dr} \times 10^{12} \mu\text{m}^2 = \frac{2}{dr} \times 10^{18} \text{nm}^2$

Area needed for one DNA molecule on surface: 3.2 molecules/nm² according to reference.⁵

Number of molecules: $[\frac{2}{dr} \times 10^{18} \text{nm}^2] \times [3.2 \text{ molecule/nm}^2] = \frac{6.4}{dr} \times 10^{18} \text{ molecules}$

Mole of molecules: $10.403 \times 10^{17} \text{ molecules} = [\frac{6.4}{dr} \times 10^{18}] \div [6.02 \times 10^{23}] \text{ mole} = \frac{1.063}{dr} \times 10^{-5} \text{ mol} = \frac{10.63}{dr} \mu\text{mol}$ ($\mu\text{mol/g}$, where the units of d and r are g/mL and μm , respectively)

Example: when d = 2.2 g/mL and r = 4 μm , loading = $10.63 \div (2.2 \times 4) = 1.208 (\mu\text{mol/g})$

Glass beads

Assumptions: mass, 1 g; density, d g/mL; diameter, 2r μm

Volume of 1 g of solid glass: $1 \text{ g} \div d \text{ g/cm}^3 = \frac{1}{d} \text{ cm}^3 = \frac{1}{d} \times 10^{12} \mu\text{m}^3$

Volume of one glass bead: $\frac{4}{3}r^3\pi \mu\text{m}^3$

Number of glass beads: $(\frac{1}{d} \times 10^{12} \mu\text{m}^3) \div [\frac{4}{3}r^3\pi \mu\text{m}^3] = \frac{3}{4dr^3\pi} \times 10^{12}$

Surface area of one glass bead: $4r^2\pi \mu\text{m}^2$

Total surface area of 1 g glass bead: $[4r^2\pi \mu\text{m}^2] \times [\frac{3}{4dr^3\pi} \times 10^{12}] = \frac{3}{dr} \times 10^{12} \mu\text{m}^2 = \frac{3}{dr} \times 10^{18} \text{nm}^2$

Area needed for one DNA molecule on surface: 3.2 molecules/nm² according to reference.⁵

Number of molecules: $[\frac{3}{dr} \times 10^{18} \text{nm}^2] \times [3.2 \text{ molecule/nm}^2] = \frac{9.6}{dr} \times 10^{18} \text{ molecules}$

Mole of molecules: $\frac{9.6}{dr} \times 10^{18} \text{ molecules} = [\frac{9.6}{dr} \times 10^{18}] \div [6.02 \times 10^{23}] \text{ mole} = \frac{1.59}{dr} \times 10^{-5} \text{ mol} = \frac{15.9}{dr} \mu\text{mol}$ ($\mu\text{mol/g}$, where the units of d and r are g/mL and μm , respectively).

Example: when d = 2.2 g/mL and r = 29 μm , loading = $15.9 \div (2.2 \times 29) = 0.249 (\mu\text{mol/g})$

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Sequencing results for the 800-mer GFP gene synthesized on glass wool (GW).
 "800mer_Ref" is the reference sequence. The numbers in the names of the sequences
 correspond to the lane numbers in Figures 3A-C.

800mer_Ref	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-1	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-2	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-3	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-4	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-5	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-6	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-8	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-9	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-11	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-12	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-13	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-14	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-15	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTCATTTGTAGAGCTCATCCATGCCATG	60
GW-16	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-17	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-18	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-20	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-21	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-23	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-24	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-25	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-26	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-27	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-28	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-29	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-30	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-32	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-33	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-34	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-35	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-36	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-38	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-39	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-40	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-42	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-45	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GW-48	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60

800mer_Ref	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GW-1	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GW-2	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GW-3	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GW-4	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120

GW-29	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-30	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-32	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-33	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-34	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-35	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-36	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-38	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-39	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-40	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-42	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-45	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GW-48	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240

[illegible]

GW-42	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTGTCTGCCGTGATGTA	300
GW-45	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTGTCTGCCGTGATGTA	300
GW-48	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTGTCTGCCGTGATGTA	300

800mer_Ref	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-1	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-2	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-3	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-4	TA-ATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	359
GW-5	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-6	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-8	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-9	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-11	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-12	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-13	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-14	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-15	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-16	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-17	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-18	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-20	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-21	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-23	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-24	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-25	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-26	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-27	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-28	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-29	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-30	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-32	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-33	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-34	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-35	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-36	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCAT-----	353
GW-38	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-39	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-40	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-42	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-45	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GW-48	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360

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800mer_Ref	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAAC TTGACTTC	420
GW-1	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAAC TTGACTTC	420
GW-2	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAAC TTGACTTC	420
GW-3	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAAC TTGACTTC	420
GW-4	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAAC TTGACTTC	419

GW-29	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-30	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-32	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-33	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-34	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-35	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-36	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	530
GW-38	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-39	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-40	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-42	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-45	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GW-48	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540

[illegible]

GW-42	GCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTGGCCATGGAACAGGTAGTTTTCC	600
GW-45	GCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTGGCCATGGAACAGGTAGTTTTCC	600
GW-48	GCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTGGCCATGGAACAGGTAGTTTTCC	600

800mer_Ref	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-1	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-2	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-3	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-4	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	659
GW-5	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-6	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-8	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-9	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-11	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	659
GW-12	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-13	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-14	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-15	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-16	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-17	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-18	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-20	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-21	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-23	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-24	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-25	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-26	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-27	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-28	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-29	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-30	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-32	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-33	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-34	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-35	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-36	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	650
GW-38	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-39	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-40	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-42	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-45	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GW-48	AGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660

800mer_Ref	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GW-1	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GW-2	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GW-3	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GW-4	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	719

GW-17	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-18	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTT-TCCTCCTTATACTTAAGCCCTATA	779
GW-20	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-21	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-23	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-24	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-25	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-26	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-27	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTT-TCCTCCTTATACTTAAGCCCTATA	779
GW-28	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-29	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-30	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-32	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-33	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-34	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-35	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-36	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	770
GW-38	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-39	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-40	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-42	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-45	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780
GW-48	TCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTCCTCCTTATACTTAAGCCCTATA	780

800mer_Ref	GTGAGTCGTATTAATTCGC	799
GW-1	GTGAGTCGTATTAATTCGC	799
GW-2	GTGAGTCGTATTAATTCGC	799
GW-3	GTGAGTCGTATTAATTCGC	799
GW-4	GTGAGTCGTATTAATTCGC	798
GW-5	GTGAGTCGTATTAATTCGC	799
GW-6	GTGAGTCGTATTAATTCGC	799
GW-8	GTGAGTCGTATTAATTCGC	799
GW-9	GTGAGTCGTATTAATTCGC	799
GW-11	GTGAGTCGTATTAATTCGC	798
GW-12	GTGAGTCGTATTAATTCGC	799
GW-13	GTGAGTCGTATTAATTCGC	799
GW-14	GTGAGTCGTATTAATTCGC	799
GW-15	GTGAGTCGTATTAATTCGC	799
GW-16	GTGAGTCGTATTAATTCGC	799
GW-17	GTGAGTCGTATTAATTCGC	799
GW-18	GTGAGTCGTATTAATTCGC	798
GW-20	GTGAGTCGTATTAATTCGC	799
GW-21	GTGAGTCGTATTAATTCGC	799
GW-23	GTGAGTCGTATTAATTCGC	799
GW-24	GTGAGTCGTATTAATTCGC	799
GW-25	GTGAGTCGTATTAATTCGC	799
GW-26	GTGAGTCGTATTAATTCGC	799
GW-27	GTGAGTCGTATTAATTCGC	798
GW-28	GTGAGTCGTATTAATTCGC	799

GW-29	GTGAGTCGTATTAATTCGC	799
GW-30	GTGAGTCGTATTAATTCGC	799
GW-32	GTGAGTCGTATTAATTCGC	799
GW-33	GTGAGTCGTATTAATTCGC	799
GW-34	GTGAGTCGTATTAATTCGC	799
GW-35	GTGAGTCGTATTAATTCGC	799
GW-36	GTGAGTCGTATTAATTCGC	789
GW-38	GTGAGTCGTATTAATTCGC	799
GW-39	GTGAGTCGTATTAATTCGC	799
GW-40	GTGAGTCGTATTAATTCGC	799
GW-42	GTGAGTCGTATTAATTCGC	799
GW-45	GTGAGTCGTATTAATTCGC	799
GW-48	GTGAGTCGTATTAATTCGC	799

Sequencing results for the 800-mer GFP gene synthesized on glass beads (GB).
 "800mer_Ref" is the reference sequence. The numbers in the names of the sequences
 correspond to the lane numbers in Figures 3D-F.

800mer_Ref	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-1	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-2	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-3	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-4	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-5	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-7	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-10	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-12	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-15	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-16	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-17	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-18	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-19	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-20	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-21	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-22	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-23	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-24	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-25	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-27	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-29	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-30	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-31	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-33	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-34	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-36	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-38	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-40	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-41	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-42	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-43	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-44	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-45	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-46	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60
GB-47	AAACCCCTCCGTTTTAGAGAGGGGTTATGCTAGTTATTTGTAGAGCTCATCCATGCCATG	60

800mer_Ref	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GB-1	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GB-2	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GB-3	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GB-4	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GB-5	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120
GB-7	TGTAATCCCAGCAGCAGTTACAAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGGG	120

GB-43	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GB-44	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GB-45	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GB-46	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240
GB-47	ATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAAT	240

800mer_Ref	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-1	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-2	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-3	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-4	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-5	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-7	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-10	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-12	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-15	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-16	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-17	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-18	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-19	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-20	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-21	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-22	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-23	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-24	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-25	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-27	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-29	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-30	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-31	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-33	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-34	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-36	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-38	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-40	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-41	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-42	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-43	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-44	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-45	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-46	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300
GB-47	GTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGTA	300

800mer_Ref	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GB-1	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GB-2	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GB-3	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360
GB-4	TACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTTT	360

[illegible]

800mer_Ref		
GB-1	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-2	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-3	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-4	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-5	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-7	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-10	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-12	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-15	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-16	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-17	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-18	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-19	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-20	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-21	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420
GB-22	AAAATCAATACCTTTTAACTCGATACGATTAACAAGGGTATCACCTTCAAACCTTGACTTC	420

GB-41	AGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAACC	480
GB-42	AGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAACC	480
GB-43	AGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAACC	480
GB-44	AGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAACC	480
GB-45	AGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAACC	480
GB-46	AGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAACC	480
GB-47	AGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATATAGTGCGTTCCTGTACATAACC	480

800mer_Ref	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-1	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-2	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-3	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-4	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-5	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-7	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-10	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-12	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-15	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-16	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-17	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-18	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-19	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-20	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-21	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-22	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-23	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-24	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-25	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-27	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-29	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-30	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-31	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-33	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-34	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-36	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-38	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-40	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-41	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-42	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-43	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-44	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-45	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-46	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540
GB-47	TTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCATATGATCCGGATAACGGGAAAA	540

800mer_Ref	GCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTGGCCATGGAACAGGTAGTTTTCC	600
GB-1	GCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTGGCCATGGAACAGGTAGTTTTCC	600
GB-2	GCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTGGCCATGGAACAGGTAGTTTTCC	600

[illegible]

GB-21	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-22	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-23	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-24	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-25	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-27	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-29	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-30	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-31	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-33	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-34	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-36	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-38	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-40	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-41	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-42	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-43	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-44	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-45	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-46	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660
GB-47	AGTAGTGCAAATAAAATTTAAGGGTAAGTTTTCCGTATGTTGCATCACCTTCACCCTCTCC	660

GB-38	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-40	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-41	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-42	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-43	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-44	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-45	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-46	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
GB-47	ACTGACAGAAAATTTGTGCCCATTAACATCACCATCTAATTCAACAAGAATTGGGACAAC	720
	*****	**

[illegible]

800mer_Ref GTGAGTCGTATTAATTCGC 799

GB-1	GTGAGTCGTATTAATTCGC	798
GB-2	GTGAGTCGTATTAATTCGC	799
GB-3	GTGAGTCGTATTAATTCGC	799
GB-4	GTGAGTCGTATTAATTCGC	799
GB-5	GTGAGTCGTATTAATTCGC	799
GB-7	GTGAGTCGTATTAATTCGC	799
GB-10	GTGAGTCGTATTAATTCGC	799
GB-12	GTGAGTCGTATTAATTCGC	799
GB-15	GTGAGTCGTATTAATTCGC	799
GB-16	GTGAGTCGTATTAATTCGC	799
GB-17	GTGAGTCGTATTAATTCGC	799
GB-18	GTGAGTCGTATTAATTCGC	799
GB-19	GTGAGTCGTATTAATTCGC	799
GB-20	GTGAGTCGTATTAATTCGC	799
GB-21	GTGAGTCGTATTAATTCGC	799
GB-22	GTGAGTCGTATTAATTCGC	799
GB-23	GTGAGTCGTATTAATTCGC	799
GB-24	GTGAGTCGTATTAATTCGC	799
GB-25	GTGAGTCGTATTAATTCGC	799
GB-27	GTGAGTCGTATTAATTCGC	799
GB-29	GTGAGTCGTATTAATTCGC	799
GB-30	GTGAGTCGTATTAATTCGC	799
GB-31	GTGAGTCGTATTAATTCGC	799
GB-33	GTGAGTCGTATTAATTCGC	799
GB-34	GTGAGTCGTATTAATTCGC	799
GB-36	GTGAGTCGTATTAATTCGC	799
GB-38	GTGAGTCGTATTAATTC--	797
GB-40	GTGAGTCGTATTAATTCGC	799
GB-41	GTGAGTCGTATTAATTCGC	799
GB-42	GTGAGTCGTATTAATTCGC	799
GB-43	GTGAGTCGTATTAATTCGC	799
GB-44	GTGAGTCGTATTAATTCGC	799
GB-45	GTGAGTCGTATTAATTCGC	799
GB-46	GTGAGTCGTATTAATTCGC	799
GB-47	GTGAGTCGTATTAATTCGC	799

Sequencing results for the 1,728-mer Phi29 DNA polymerase gene synthesized on glass beads (GB). "1728mer_Reference" is the reference sequence. The numbers in the names of the sequences correspond to the lane numbers in Figure 3G.

1728mer_Reference	atgaagcatatgccgagaaagatgtatagttgtgactttgagacaactactaaagtggaa	60
1728mer_1	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_2	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_3	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_4	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_5	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_6	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_7	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGCGGAA	60
1728mer_9	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_8	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_10	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_11	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_12	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_13	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_14	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_15	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60
1728mer_16	ATGAAGCATATGCCGAGAAAGATGTATAGTTGTGACTTTGAGACAACACTAAAGTGGAA	60

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1728mer_Reference	gactgtagggatatgggcgtatgggttatatgaatatagaagatcacagtgagtacaaaata	120
1728mer_1	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_2	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	118
1728mer_3	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_4	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_5	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_6	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_7	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_9	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_8	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_10	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_11	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_12	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_13	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_14	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_15	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120
1728mer_16	GACTGTAGGGTATGGGCGTATGGTTATATGAATATAGAAGATCACAGTGAGTACAAAATA	120

1728mer_Reference	ggtaatagcctggatgagtttatggcgtgggtgttgaaggtacaagctgatctatatatttc	180
1728mer_1	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTT	180
1728mer_2	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTT	178
1728mer_3	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTT	180
1728mer_4	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTT	180
1728mer_5	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTT	180
1728mer_6	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTT	180

1728mer_7	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_9	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_8	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_10	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_11	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_12	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTTATCTATATTTTC	180
1728mer_13	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_14	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_15	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180
1728mer_16	GGTAATAGCCTGGATGAGTTTATGGCGTGGGTGTTGAAGGTACAAGCTGATCTATATTTTC	180

1728mer_Reference	cataacctcaaatttgacggagctttttatcattaactgggttggaacgtaatgggttttaag	240
1728mer_1	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_2	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	238
1728mer_3	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_4	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_5	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_6	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_7	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_9	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_8	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_10	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_11	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_12	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_13	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_14	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_15	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240
1728mer_16	CATAACCTCAAATTTGACGGAGCTTTTATCATTAACCTGGTTGGAACGTAATGGTTTTAAG	240

1728mer_Reference	tggtcggctgacggattgccaaacacatataatacgcatacatctcgcacatgggacaatgg	300
1728mer_1	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_2	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	298
1728mer_3	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_4	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_5	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_6	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCAGG-GACAATGG	299
1728mer_7	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_9	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_8	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_10	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_11	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_12	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_13	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_14	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300
1728mer_15	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCAT--GACAATGG	298
1728mer_16	TGGTCGGCTGACGGATTGCCAAACACATATAATACGATCATATCTCGCATGGGACAATGG	300

1728mer_Reference	tacatgattgatatatgttttaggctacaaagggaaacgtaagatacatacagtgatatat	360
1728mer_1	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_2	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	358
1728mer_3	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_4	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_5	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_6	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	359
1728mer_7	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_9	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_8	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_10	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_11	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_12	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_13	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_14	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360
1728mer_15	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	358
1728mer_16	TACATGATTGATATATGTTTAGGCTACAAAGGGAAACGTAAGATACATACAGTGATATAT	360

1728mer_Reference	gacagcttaaagaactaccgtttcctgttaagaagatagctaaagactttaactaact	420
1728mer_1	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_2	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	418
1728mer_3	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_4	GACAGCTTAAAGAACTACCGTTTCCTGTTAAG-AGATAGCTAAAGACTTTAACTAACT	419
1728mer_5	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_6	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	419
1728mer_7	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_9	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_8	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_10	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_11	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_12	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_13	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_14	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420
1728mer_15	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	418
1728mer_16	GACAGCTTAAAGAACTACCGTTTCCTGTTAAGAAGATAGCTAAAGACTTTAACTAACT	420

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1728mer_Reference	gttccttaaaggatgattgattaccacaaagaaagaccagtcggctataagataacaccc	480
1728mer_1	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_2	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	478
1728mer_3	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_4	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	479
1728mer_5	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_6	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	479
1728mer_7	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_9	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_8	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_10	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_11	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480

1728mer_12	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_13	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_14	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480
1728mer_15	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	478
1728mer_16	GTTCTTAAAGGTGATATTGATTACCACAAAGAAAGACCAGTCGGCTATAAGATAACACCC	480

1728mer_Reference	gaagaatacgctatattaaaaacgatattcagattattgcggaacgtctgttaattcag	540
1728mer_1	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_2	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	538
1728mer_3	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_4	GAAGAATACGCCTATATTA AAAACGATATTCAGATTGTTGCGGAACGTCTGTTAATT CAG	539
1728mer_5	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_6	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	539
1728mer_7	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_9	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_8	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_10	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_11	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_12	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_13	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_14	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540
1728mer_15	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	538
1728mer_16	GAAGAATACGCCTATATTA AAAACGATATTCAGATTATTGCGGAACGTCTGTTAATT CAG	540

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1728mer_Reference	tttaagcaag-gtttagaccggatgacagcaggcagtgacagtctaaaagggtttcaagga	599
1728mer_1	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_2	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	597
1728mer_3	TTTAAGCAAGGGTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	600
1728mer_4	TTTAAGCAAG-GTTTAGACCTGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	598
1728mer_5	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_6	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	598
1728mer_7	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_9	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_8	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_10	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_11	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_12	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_13	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_14	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599
1728mer_15	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	597
1728mer_16	TTTAAGCAAG-GTTTAGACCGGATGACAGCAGGCAGTGACAGTCTAAAAGGTTTCAAGGA	599

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1728mer_Reference	tattataaccactaagaaattcaaaaagggtgtttcctacattgagtccttgactcgataa	659
1728mer_1	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGACTCGATAA	659
1728mer_2	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGACTCGATAA	657
1728mer_3	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGACTCGATAA	660
1728mer_4	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGACTCGATAA	658

1728mer_5	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_6	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	658
1728mer_7	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_9	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_8	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_10	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_11	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_12	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_13	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_14	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659
1728mer_15	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	657
1728mer_16	TATTATAACCACTAAGAAATTCAAAAAGGTGTTTCCTACATTGAGTCTTGGACTCGATAA	659

1728mer_Reference	ggaagtgagatacgctatagagg-tggttttacatggttaaatgataggttcaaagaaa	718
1728mer_1	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_2	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	716
1728mer_3	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	719
1728mer_4	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	717
1728mer_5	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_6	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	717
1728mer_7	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_9	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_8	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_10	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_11	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_12	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_13	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_14	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	718
1728mer_15	GGAAGTGAGATACGCCTATAGAGG-TGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	716
1728mer_16	GGAAGTGAGATACGCCTATAGAGGGTGGTTTTACATGGTTAAATGATAGGTTCAAAGAAA	719

1728mer_Reference	aagaaatcggagaaggcatggtccttcgatgttaaatagtctatatcctgcacagatgtata	778
1728mer_1	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_2	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	776
1728mer_3	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	779
1728mer_4	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	777
1728mer_5	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_6	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	777
1728mer_7	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_9	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_8	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_10	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_11	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_12	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_13	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_14	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	778
1728mer_15	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	776
1728mer_16	AAGAAATCGGAGAAGGCATGGTCTTCGATGTTAATAGTCTATATCCTGCACAGATGTATA	779

1728mer_Reference	gccgtctccttccatatggtgaacctatagtattcgagggtaaatacgtttgggacgaag	838
1728mer_1	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_2	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	836
1728mer_3	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	839
1728mer_4	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	837
1728mer_5	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_6	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	837
1728mer_7	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_9	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_8	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_10	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_11	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_12	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_13	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_14	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	838
1728mer_15	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	836
1728mer_16	GCCGTCTCCTTCCATATGGTGAACCTATAGTATTCGAGGGTAAATACGTTTGGGACGAAG	839

1728mer_Reference	attaccactacacatacagcatatcagatgtgagttcgaattgaaagagggtatatac	898
1728mer_1	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_2	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	896
1728mer_3	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	899
1728mer_4	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	897
1728mer_5	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_6	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	897
1728mer_7	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_9	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_8	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_10	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_11	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_12	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_13	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_14	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	898
1728mer_15	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	896
1728mer_16	ATTACCCACTACACATACAGCATATCAGATGTGAGTTCGAATTGAAAGAGGGCTATATAC	899

1728mer_Reference	ccactatacagataaaaagaagtaggttttataaaggtaatgagtagcctaaaaagtagcg	958
1728mer_1	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_2	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	956
1728mer_3	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	959
1728mer_4	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	957
1728mer_5	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_6	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	957
1728mer_7	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_9	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_8	CCACTATACAGATAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958

1728mer_10	CCACTATACAGATAAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_11	CCACTATACAGATAAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_12	CCACTATACAGATAAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_13	CCACTATACAGATAAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_14	CCACTATACAGATAAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	958
1728mer_15	CCACTATACAGATAAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	956
1728mer_16	CCACTATACAGATAAAAAAGAAGTAGGTTTTATAAAGGTAATGAGTACCTAAAAAGTAGCG	959

1728mer_Reference	gcggggagatagccgacctctggttgtcaaatgtagacctagaattaatgaaagaacact	1018
1728mer_1	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_2	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1016
1728mer_3	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1019
1728mer_4	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1017
1728mer_5	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_6	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1017
1728mer_7	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_9	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_8	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_10	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_11	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_12	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_13	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_14	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1018
1728mer_15	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1016
1728mer_16	GCGGGGAGATAGCCGACCTCTGGTTGTCAAATGTAGACCTAGAATTAATGAAAGAACACT	1019

1728mer_Reference	acgatttatataacgttgaatatatcagcggcttaaaatttaaagtaactacaggtttgt	1078
1728mer_1	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_2	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1076
1728mer_3	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1079
1728mer_4	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1077
1728mer_5	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_6	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1077
1728mer_7	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_9	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_8	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_10	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_11	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_12	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_13	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_14	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1078
1728mer_15	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1076
1728mer_16	ACGATTTATATAACGTTGAATATATCAGCGGCTTAAATTTAAAGTAACTACAGGTTTGT	1079

1728mer_Reference	ttaaagattttatagataaatggacgtacatcaagacgacatcagaaggagcgatcaagc	1138
1728mer_1	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_2	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1136

1728mer_3	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1139
1728mer_4	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1137
1728mer_5	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_6	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1137
1728mer_7	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_9	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_8	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACTACATCAGAAGGAGCGATCAAGC	1138
1728mer_10	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_11	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_12	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_13	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_14	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1138
1728mer_15	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1136
1728mer_16	TTAAAGATTTTATAGATAAATGGACGTACATCAAGACGACATCAGAAGGAGCGATCAAGC	1139

1728mer_Reference	aactagcaaaactgatgttaaacagtcctatacggtaaattcgctagtaaccctgatgtta	1198
1728mer_1	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_2	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1196
1728mer_3	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1199
1728mer_4	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1197
1728mer_5	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_6	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1197
1728mer_7	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_9	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_8	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_10	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_11	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_12	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_13	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_14	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1198
1728mer_15	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1196
1728mer_16	AACTAGCAAAACTGATGTTAAACAGTCTATACGGTAAATTCGCTAGTAACCCTGATGTTA	1199

1728mer_Reference	cagggaaagtccttattttaaaagagaatggggcgctaggtttcagacttggagaagagg	1258
1728mer_1	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_2	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1256
1728mer_3	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1259
1728mer_4	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1257
1728mer_5	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_6	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1257
1728mer_7	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_9	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_8	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_10	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_11	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_12	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_13	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258
1728mer_14	CAGGGAAAGTCCCTTATTTAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1258

1728mer_15	CAGGGAAAGTCCCTTATTTAAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1256
1728mer_16	CAGGGAAAGTCCCTTATTTAAAAGAGAATGGGGCGCTAGGTTTCAGACTTGGAGAAGAGG	1259

1728mer_Reference	aaacaaaagaccctgtttatacacctatgggcggttttcatcactgcatgggctagataca	1318
1728mer_1	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_2	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAG-TACA	1315
1728mer_3	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1319
1728mer_4	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1317
1728mer_5	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_6	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1317
1728mer_7	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_9	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_8	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_10	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_11	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_12	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_13	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_14	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1318
1728mer_15	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1316
1728mer_16	AAACAAAAGACCCTGTTTATACACCTATGGGCGTTTTCATCACTGCATGGGCTAGATACA	1319

1728mer_Reference	cgacaattacagcggcacaggcttggtatgatcggataatatactgtgatactgacagca	1378
1728mer_1	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_2	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1375
1728mer_3	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1379
1728mer_4	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1377
1728mer_5	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_6	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1377
1728mer_7	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_9	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_8	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_10	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_11	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_12	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_13	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_14	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1378
1728mer_15	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1376
1728mer_16	CGACAATTACAGCGGCACAGGCTTGTTATGATCGGATAATATACTGTGATACTGACAGCA	1379

1728mer_Reference	tacatttaacgggtacagagatacctgatgtaataaaagatatagttgaccctaagaaat	1438
1728mer_1	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_2	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAGATATAGTTGACCCTAAGAAAT	1435
1728mer_3	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAGATATAGTTGACCCTAAGAAAT	1439
1728mer_4	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAGATATAGTTGACCCTAAGAAAT	1437
1728mer_5	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_6	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAGATATAGTTGACCCTAAGAAAT	1437
1728mer_7	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAGATATAGTTGACCCTAAGAAAT	1438

1728mer_9	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_8	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_10	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_11	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_12	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_13	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_14	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1438
1728mer_15	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1436
1728mer_16	TACATTTAACGGGTACAGAGATACCTGATGTAATAAAAAGATATAGTTGACCCTAAGAAAT	1439

1728mer_Reference	tgggatactgggcacatgaaagtacattcaaaagagctaaatatctgagacagaagacct	1498
1728mer_1	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_2	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1495
1728mer_3	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1499
1728mer_4	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1497
1728mer_5	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_6	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1497
1728mer_7	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_9	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_8	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_10	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_11	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_12	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_13	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_14	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1498
1728mer_15	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1496
1728mer_16	TGGGATACTGGGCACATGAAAGTACATTCAAAAAGAGCTAAATATCTGAGACAGAAGACCT	1499

1728mer_Reference	atatacaagacatctatatgaaagaagtagatggtaagttagtagaaggtagtccagatg	1558
1728mer_1	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_2	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1555
1728mer_3	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1559
1728mer_4	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1557
1728mer_5	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_6	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1557
1728mer_7	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_9	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_8	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_10	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_11	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_12	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_13	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_14	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1558
1728mer_15	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1556
1728mer_16	ATATACAAGACATCTATATGAAAGAAGTAGATGGTAAGTTAGTAGAAGGTAGTCCAGATG	1559

1728mer_Reference	attacactgatataaaatttagtggttaaattgtgcgggaatgactgacaagattaagaaag	1618
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1728mer_1	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_2	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1615
1728mer_3	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1619
1728mer_4	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1617
1728mer_5	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_6	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1617
1728mer_7	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_9	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_8	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_10	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_11	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_12	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_13	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_14	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1618
1728mer_15	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1616
1728mer_16	ATTACACTGATATAAAATTTAGTGTTAAATGTGCGGGAATGACTGACAAGATTAAGAAAG	1619

1728mer_Reference	aggttacgtttgagaatttcaaagtcggattcagtcggaaaatgaagcctaagcctgtgc	1678
1728mer_1	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_2	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1675
1728mer_3	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1679
1728mer_4	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1677
1728mer_5	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_6	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1677
1728mer_7	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_9	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_8	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_10	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_11	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_12	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_13	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_14	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1678
1728mer_15	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1676
1728mer_16	AGGTTACGTTTGAGAATTTCAAAGTCGGATTCAGTCGGAAAATGAAGCCTAAGCCTGTGC	1679

1728mer_Reference	aagtgccgggCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_1	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_2	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1725
1728mer_3	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1729
1728mer_4	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1727
1728mer_5	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_6	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1727
1728mer_7	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_9	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_8	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_10	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_11	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_12	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728

1728mer_13	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_14	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1728
1728mer_15	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1726
1728mer_16	AAGTGCCGGGCGGGGTGGTTCTGGTTGATGACACATTCACAATCAAATAA	1729

Sequencing results of 399-mer and 401-mer synthesized on CPG with reduced loading

The work has been reported in the paper *Beilstein Journal of Organic Chemistry*, **2023**, *19*, 1957-1965. <https://doi.org/10.3762/bjoc.19.146>. However, only 6 out of 20 sequencing results were reported in that paper. All the 20 sequencing results are now presented below for comparison with those of the present work. The number in the name of the sequences corresponds to the number of lanes in Figure 3 of the above referenced paper. For the 399-mer, sequence “contig_399-26” is correct. For the 401-mer, sequence “contig_401-10” is correct.

399-mer

399-reference	TAAACCCCTCCGTTTTAGAGAGGGGTATGCTAGTTATTTGTAGAGCTCATCCATGCCAT
contig_399-1	-----
contig_399-5	TAAACCCCTCCGTTTTAGAGAGGGGTATGCTAGTTATTTGTAGAGCTCATCCATGCCAT
contig_399-7	-----
contig_399-12	-----
contig_399-13	TAAACCCCTCCGTTTTAGAGAGGGGTATGCTAGTTATTTGTAGAGCTCATCCATGCCAT
contig_399-15	TAAACCCCTCCGTTTTAGAGAGGGGTATGCTAGTTATTTGTAGAGCTCATCCATGCCAT
contig_399-19	-----
contig_399-22	TAAACCCCTCCGTTTTAGAGAGGGGTATGCTAGTTATTTGTA-AGCTCATCCATGCCAT
contig_399-26	TAAACCCCTCCGTTTTAGAGAGGGGTATGCTAGTTATTTGTAGAGCTCATCCATGCCAT
contig_399-30	-----

399-reference	GTGTAATCCCAGCAGCAGTTACAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGG
contig_399-1	-----TTTCGTTGG
contig_399-5	GTGTAATCCCAGCAGCAGTTACAACTCAAGAAGGACCATGT-GTCACGCTTTTCGTTGG
contig_399-7	-----TTACAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGG
contig_399-12	-----CGCTTTTCGTTGG
contig_399-13	GTGTAATCCCAGCAGCAGTTACAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGG
contig_399-15	GTGTAATCCCAGCAGCAGTTACAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGG
contig_399-19	-----CATGTGGTCACGCTTTTCGTTGG
contig_399-22	GTGTAATCCCAGCAGCAGTTACAACTCAAGAAGGACCATGTGGTCACGC-----
contig_399-26	GTGTAATCCCAGCAGCAGTTACAACTCAAGAAGGACCATGTGGTCACGCTTTTCGTTGG
contig_399-30	-----

399-reference	GATCTTTTCGAAAGGGCAGATTGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-1	GATCTTTTCGAAAGGGCAGATTGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-5	GATCTTTTCGAAAGGGCAGA-TGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-7	GATCTTTTCGAAAGGGCAGATTGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-12	GATCTTTTCGAAAGGGCAGATTGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-13	GATCTTTTCGAAAGGGCAGATTGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-15	GATCTTTTCGAAAGGGCAGATTGTGTCGAC-GGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-19	GATCTTTTCGAAAGGGCAGATTGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-22	-----
contig_399-26	GATCTTTTCGAAAGGGCAGATTGTGTCGACAGGTAATGGTTGTCTGGTAAAAGGACAGGGC
contig_399-30	-----

399-reference	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-1	CATCG-CAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-5	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-7	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-12	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-13	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-15	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-19	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-22	-----
contig_399-26	CATCGCCAATTGGAGTATTTTGTGATAATGGTCTGCTAGTTGAACGGATCCATCTTCAA
contig_399-30	-----ATCCATCTTCAA

399-reference	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-1	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-5	T-----GTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-7	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-12	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-13	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-15	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-19	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-22	-----ATGT
contig_399-26	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT
contig_399-30	TGTTGTGGCGAATTTTGAAGTTAGCTTTGATTCCATTCTTTTGTCTGCCGTGATGT

399-reference	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-1	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-5	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-7	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-12	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-13	ATACATTGTGTAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-15	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-19	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-22	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-26	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT
contig_399-30	ATACATTGTGTGAGTTATAGTTGTACTCGAGTTTGTGTCCGAGAATGTTTCCATCTTCTT

399-reference	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-1	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-5	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-7	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-12	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-13	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-15	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-19	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-22	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-26	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG
contig_399-30	TAAAATCAATACCTTTTAACTCGATACGATTAACAAGGG

401-mer

401-reference	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-1	-----
contig_401-3	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-6	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-8	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTG-AGTTCCCGTC-TCTTTGAAAGATA
contig_401-10	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-14	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-16	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-20	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-25	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTTTGAAAGATA
contig_401-31	TATCACCTTCAAACCTTGACTTCAGCACGCGTCTTGTAGTTCCCGTCATCTT-----

401-reference	TAGTGCGTTCCTGTACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-1	-----TTGAAAAAGTCATGCCGTTTCA
contig_401-3	TAGTGCGTTCCTGTACATAACCTT-GGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-6	TAGTACGTTTCCTGTACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-8	TAGTGCGTTCCTGTACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-10	TAGTGCGTTCCTGTACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-14	TAGTGCGTTCCTGTACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-16	TAGTGCG-TCCTGTACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-20	TAGTGCGTTCCTGTACATAACCTTCGGGCATGGCACTCTTGAAAAAGTCATGCCGTTTCA
contig_401-25	TAGTGCGTTCCTGTACATAACCTTCGGGCATGGCACTCTTG-AAAAGTCATGCCGTTTCA
contig_401-31	-----

401-reference	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTG
contig_401-1	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTG
contig_401-3	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAG-----
contig_401-6	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTG
contig_401-8	TATGATCCGG-----
contig_401-10	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTG
contig_401-14	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAGTGACAAGTGTTG
contig_401-16	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAGAGAAAGTAGTGAC-AGTGTTG
contig_401-20	TATGATCCGGATAACGGGAAAAGCATTGAACACCATAAAGAGAAAGTAGTGACAAGTGTTG
contig_401-25	TAT-----
contig_401-31	-----

401-reference	GCCATGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATG
contig_401-1	GCCATGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATG
contig_401-3	-----
contig_401-6	GCCATGGAACAGGTAGTTTCCAGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATG
contig_401-8	-----
contig_401-10	GCCATGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATG
contig_401-14	GCCATGGAACAGGTAGTTTTCCAGTAGTGCAAATAAA-----
contig_401-16	GCCATGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATG
contig_401-20	GCCATGGAACAGGTAGTTTTCCAGTAGTGCAAATAAATTTAAGGGTAAGTTTTCCGTATG
contig_401-25	-----
contig_401-31	-----

401-reference	TTGCATCACCTTCACCCTCTCCACTGACAGAAAATTTGTGCCCATTAACATCACCATCTA
contig_401-1	TTGCATCACCTTCACCCTCTCCACTGACAGAAAATTTGTGCCCATTAACATCACCATCTA
contig_401-3	-----
contig_401-6	TTGCATCACCTTCACCCTCTCCACTGACAGAAAATTTGTGCCCATTAACATCA-CATCTA
contig_401-8	-----
contig_401-10	TTGCATCACCTTCACCCTCTCCACTGACAGAAAATTTGTGCCCATTAACATCACCATCTA
contig_401-14	-----
contig_401-16	TTGCATCACCTTCACCCTCTCCACTGACAGAAAATTTGTGCCCATTAACATCACCATCTA
contig_401-20	TTGCATCACCTTCACCCTCTCCACTGACAGAAAATTTGTGCCCATTAACATCACCATCTA
contig_401-25	-----
contig_401-31	-----

401-reference	ATTCAACAAGAATTGGGACAACCTCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTC
contig_401-1	ATTCAACAAGAATTGG-----CAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTC
contig_401-3	-----CTCCTTTACTCATATTTTTTC
contig_401-6	ATTCAACAAGAATTGGGACAACCTCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTC
contig_401-8	-----GTGAAAAGTTCTTCTCCTTTACTCATATTTTTTC
contig_401-10	ATTCAACAAGAATTGGGACAACCTCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTC
contig_401-14	-----TTTTTC
contig_401-16	ATTCAACAAGAATTGGGACAACCTCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTC
contig_401-20	ATTCAACAAGAATTGGGACAACCTCCAGTGAAAAGTTCTTCTCCTTTACTCATATTTTTTC
contig_401-25	-----ATATTTTTTC
contig_401-31	-----CTTCTCCTTTACTCATATTTTTTC

401-reference	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-1	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-3	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-6	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-8	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-10	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-14	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-16	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-20	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-25	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC
contig_401-31	CTCCTTATACTTAAGCCCTATAGTGAGTCGTATTAATTTCGC