Supplementary Materials for

A DNA Nanoscope that identifies and precisely localizes over a hundred unique molecular features with nanometer accuracy

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Supplementary Materials and Methods

DNA origami design, manufacture and purification

Design: The rectangular DNA origami nanostructure used in all experiments was designed using the cadnano software (*27*), according to principles laid out in (*28*). The origami is 18 helices tall and 376 base pairs wide, and is 'twist corrected' (*28*) to promote flatness and minimize stress. Assuming a helix width of 2 nm and a helix to helix spacing of 1 nm, the structure's height is calculated to be 18*2 nm + 17*1 nm = 53 nm. Assuming a rise of 0.34 nm per base pair, the structure's width is calculated to be 376*0.34 nm = 127.84 nm. The origami is composed of a scaffold strand (M13mp18 single-stranded DNA, New England Biolabs (NEB), catalog no. N4040S) and 216 'blunt' staple oligos (Integrated DNA Technologies (IDT). See Supplementary Fig. 6 for the scaffold routing and Supplementary Table 2 for 'blunt' staple oligo sequences. Extended staple oligos (IDT) composed of a 'blunt' staple followed by a barcoded handle domain are used to recruit barcoded molecular ruler primers (IDT) via hybridization. The sequences for extended staple oligos are listed in Supplementary Table 3 and the sequences for barcoded molecular ruler primers are listed in Supplementary Table 4.

Manufacture of randomly tagged DNA origami patterns: Random sparse tagging was achieved by setting up a winner take all competition for staple incorporation at every target site, by supplying both the barcoded 'handle' staple and the corresponding barcode-less 'blunt' staple. At every target site, either the handle staple or the corresponding blunt staple can incorporate into the DNA origami, but not both. In any particular copy of the DNA origami, a site was successfully tagged when the handle staple won the competition, allowing recording primer recruitment at that site. Conversely, the site was not tagged when the blunt staple won the competition. The average density of tagged points on a DNA origami depends on the relative propensity of incorporation of these competing staples. The relative propensity, and hence the average density of tagged points on a DNA origami, was tuned by varying the relative concentrations of competing staples. The locations of the barcoded handle staples for each pattern are presented in Supplementary Fig. 7, 8 and 9.

The scaffold strand (5 nM final concentration) was combined with: (i) all 216 'blunt' staple oligos (50 nM final concentration of each oligo, see Table S2 for sequences), (ii) the appropriate subset (depending of the pattern being tagged, see Supplementary Fig. 7, 8 and 9 and Supplementary Table 3) of barcoded 'handle' staple oligos (5 nM final concentration of each

oligo) and (iii) corresponding appropriate subset of barcoded primers of type a and a* (5 nM final concentration of each oligo, see Supplementary Table 4 for sequences) in 1X TE Mg buffer (pH 7.4, 10 mM Tris-HCl, 0.1 mM EDTA, 10 mM $MgSO_4$). The mixture was then cooled from 90 °C to 60 °C at the rate of 1 min/°C and then from 60 °C to 50 °C at the rate 10 min/°C and finally from 50 °C to 25 °C at the rate of 1 min/°C. Folded origami was stored at 4 °C for up to one week prior to purification.

Purification: DNA origami patterns were purified by agarose gel electrophoresis to eliminate aggregated structures and unbound oligos. 20 µL of folded DNA origami was mixed with 4 µL of 6X loading dye and loaded per lane in a 8 cm tall and 6 cm wide 1 % agarose gel (UltraPure agarose, Thermo Fisher Scientific, catalog no. 16500100) pre-stained with 1X SYBR Gold. The gel was run at 80 V for 2 hours on an Amersham instrument to separate well-folded DNA origami from excess oligos and aggregates. The band corresponding to well-folded DNA origami was visualized under a blue-light transilluminator (Safe Imager, Thermo Fisher Scientific) and excised with a clean razor blade. The gel slice was transferred to a freeze-n-squeeze DNA gel-extraction spin column (Bio-Rad, catalog no. 7326165), crushed with a clean pestle, kept at -20 °C for 10 min and then centrifuged at 2,000 g for 4 min. The flow through containing purified DNA origami was diluted 10-fold in 1X TE Mg buffer and 50 µL aliquots were stored at -20 °C for recording experiments.

DNA nanoscope recording experiment

1. Prepare fluid-exchange reaction chamber: A thin layer of mica of dimensions 25 mm X 75 mm is peeled from a mica sheet (Muscovite Mica V-1 Quality, Electron Microscopy Sciences, catalog no. 71855-05-10) using sticky tape (3M Scotch Clear Magic Tape, 25 mm wide). The mica sheet stuck to the tape is then affixed to a sticky bottomless six-channel slide (sticky-slide VI 0.4, ibidi, catalog no. 80608) to assemble fluid-exchange reaction chambers for recording experiments. Each channel is used to perform an independent DNA nanoscope recording experiment.

2. Deposit origami on surface: 50 µL of frozen DNA origami aliquot is thawed and heated to 42 °C for 2 min, to dissociate any aggregates. It is then added to a reaction chamber and allowed to bind to the mica surface for 10 min. The chamber is then washed twice with 50 µL of 1X TE Mg to remove unbound origami. The exposed, unbound mica surface is then passivated with a BSA solution (50 µg/mL, NEB) for 5 min and further washed with 1X TE Mg and a magnesium-

supplemented 1X Thermopol buffer (20 mM Tris-HCl, 10 mM $(NH_4)_2SO_4$, 10 mM KCl, 7 mM $MgSO_4$, 0.1% Triton®-X-100, pH 8.8 @ 25 °C, NEB, catalog no. B9004S).

3. Perform molecular ruler reaction: 50 µL of the recording mix, consisting of 100 nM extension hairpin type 'a', 100 nM extension hairpin type 'a*', 0.08 U/µL Bsm DNA polymerase LF (*ThermoFisher Scientific,* catalog no. EP0691), 100 µM dNTP solution mix (NEB, catalog no. N0447S), 1X Thermopol buffer and 5 mM $MgSO_4$, is added to the reaction chamber and the slide kept at 37 ºC for 3 hours. After 3 hours, the supernatant containing distance records is collected for further processing.

PCR amplification of distance records

Distance records were amplified by PCR. For PAGE analysis, the PCR reaction mix contained distance records (1 µL per 20 µL reaction mix), fluorescent PCR primer 1 (0.3 µM, IDT. See Supplementary Table 1 for sequence), fluorescent PCR primer 2 (0.3 µM, IDT. See Supplementary Table 1 for sequence), AccuPrime *Pfx* Reaction Mix (1X), AccuPrime *Pfx* DNA polymerase (0.025 U/µL, *ThermoFisher Scientific*, catalog no. 12344024) and EvaGreen fluorescent nucleic acid dye (1X, Biotium, catalog no. 31000-T). For next-gen sequencing analysis, the PCR mix contained inner primers (10 nM each, IDT), outer primers (0.3 µM each, IDT) and the other PCR mix components listed above. The outer primers are sequencing barcodes used to multiplex multiple libraries (i.e. distinct DNA nanoscope experiments) on the same sequencing chip. The inner primers contain sequences common to the ends of all barcoded recording primers. The sequence information for these can be found in table S5.

Temperature cycling for the PCR mix had (i) an initial denaturation step of 95 °C for 2 min, followed by (ii) 25 to 35 cycles of denaturation at 95 °C for 15s and primer binding and extension at 60 °C for 45s and (iii) a final extension at 65 °C for 2 min. The progress of the PCR amplification was monitored on a real time PCR machine. The number of temperature cycles was chosen to allow the signal to plateau, indicating completion of the PCR reaction.

PAGE characterization of distance records for calibration experiments

The length distribution of the distance records for each calibration distance was characterized using PAGE. 10 µL of PCR-amplified distance records were mixed with 10 µL of 2X denaturing loading dye (95 % formamide, 10 mM NaOH, 0.025 % bromophenol blue, 1 mM EDTA), heated to 95 °C for 2 min and then loaded into individual lanes of an 8 cm X 8 cm 4 % denaturing polyacrylamide gel (4 % v/v acrylamide/bis-acrylamide (19:1), 7.4 M Urea, 0.5X TBE). The gel

was electrophoresed at a voltage of 180 V for 30 min at 50 °C. The gel was then stained with a SYBR Gold (1:10,000 v/v) solution for 10 min and then imaged on a Typhoon FLA 9500 gel scanner (General Electric) in the red (635 nm emission laser and 665 nm low-pass red filter) and blue channels (473 nm emission laser and 510 nm low-pass blue filter). Gel images were analyzed with the Fiji image processing software package.

Purification of distance records for next-gen sequencing

Distance records were purified to remove short-length spurious distance records prior to sample preparation for next-gen sequencing. The purification steps were as follows:

1. **Column concentration**: The post-PCR distance records were cleaned and concentrated using a bind-wash-elute procedure on a silica membrane column using the MinElute PCR purification kit (Qiagen, catalog no. 28004) and it's associated standard protocol. The input was 100 µL of post-PCR mix and the elution volume was 10 µL in buffer EB (10 mM Tris-Cl, pH 8.5).

2. **PAGE purification:** Concentrated samples were mixed with 10 µL of 2X denaturing loading dye (95 % formamide, 10 mM NaOH, 0.025% bromophenol blue, 1 mM EDTA), heated to 95 °C for 2 min and then loaded into individual lanes of an 8 cm X 8 cm 4 % denaturing polyacrylamide gel (4 % v/v acrylamide/bis-acrylamide (19:1), 7.4 M Urea, 0.5X TBE). The gel was electrophoresed at a voltage of 180 V for 60 min to 80 min at 50 °C to allow the short-length spurious distance records to diffuse out of the gel into the surrounding running buffer. The appropriate time to run the gel to allow this to happen was determined by monitoring, in adjacent lanes, the migration of fluorescent fiduciary bands that co-migrate with short-length spurious distance records.

3. **PAGE concentration:** After the short-length spurious distance records were discharged into the surrounding running buffer, the desired distance records, which range in size from ~150 b to ~1 kb and were distributed over a large gel volume, were concentrated by reversing the current flow, as follows. First, the running buffer was replaced to prevent the spurious records from re-entering the gel. Next, 50 µL of a dense 15 % denaturing polyacrylamide gel (15 % v/v acrylamide/bis-acrylamide (19:1), 7.4 M Urea, 0.5X TBE) was pipetted into each lane of the gel and allowed to polymerize. The voltage across the gel terminals was now reversed and the gel run at 180 V for 60 min to 80 min at 50 °C to allow the desired distance records to collect in the dense gel, concentrating them. The dense gel was excised with a razor blade. A clean 0.5 mL tube was pierced at the bottom with a 20-gauge syringe needle and placed into a 1.5 mL tube,

setting up a gel-shredder tube-in-tube widget. The excised gel from each lane was placed in the gel-shredder tube-in-tube widget and centrifuged at 14,000 g for 2 min. The disintegrated gel collects in the 1.5 mL tube, and the 0.5 mL tube is discarded. 50 µL of buffer EB is added to the 1.5 mL tube, which is then heated to 65 °C for 5 min followed by freezing at –20 °C for 10 min. The frozen pellet is transferred to a Freeze 'N Squeeze gel extraction spin column (Biorad, catalog no. 7326165) and centrifuged at 14,000 g for 3 min to collect ~ 50 µL of solution containing desired distance records. The solution is finally cleaned and concentrated using a bind-wash-elute procedure on a silica membrane column using the MinElute PCR purification kit (Qiagen, catalog no. 28004) and it's associated standard protocol. The final elution volume is 10 µL in buffer EB (10 mM Tris-Cl, pH 8.5). The concentration is measured on a NanoDrop 2000 (ThermoFisher) using OD260 absorption.

Library preparation for next-gen sequencing

Purified distance records were prepared for next-gen sequencing using the Oxford Nanopore SQK-LSK109 ligation sequencing kit. The protocol titled '*1D Genomic DNA by Ligation'* (see Oxford nanopore website) was used to prepare samples. A total of 0.5 pmole of purified distance records were used in the library preparation. Sometimes samples from two different experiments (i.e. distinct patterns) were combined, in which case we used 0.25 pmole of sample from each experiment. Briefly, the protocol involves a combined step of DNA repair and end-prep with the NEBNext FFPE DNA Repair Mix (New England Biolabs, catalog no. M6630S) and the NEBNext Ultra II End Repair / dA-Tailing Module (New England Biolabs, catalog no. E7546) respectively. This is followed by cleanup with the Agencourt AMPure XP beads (2X bead to sample ratio). Then, sequencing adaptors are ligated using the NEBNext Quick T4 DNA Ligase (New England Biolabs, catalog no. E6056) followed by a final round of bead clean-up. The sample is then mixed with loading beads, added to a 'primed' flow cell (FLO-MIN106) (see protocol for details) and sequenced for between 12 hours to 24 hours, producing around 10 million to 15 million raw reads. The sample can be split across multiple flow cells if more reads are required.

Data analysis workflow

We use Oxford Nanopore's Guppy basecalling software (v3.2.1) to (1) read sequence information from raw sequencing data and then use MATLAB scripts to (2) demultiplex reads from different experiments, (3) extract the lengths of the distance records and assign them to

their appropriate target-pair, (4) infer the distance for each target-pair from all assigned distance records, and finally (5) reconstruct the underlying geometry from pairwise distance measurements. The MATLAB scripts referenced below can be found at github.com/nikhil314/DNA-Nanoscope. Details of the process are as follows:

1. **Basecalling using Guppy (v3.2.1):** Guppy is a base-calling software provided by Oxford Nanopore that can be downloaded and run on local machines. It takes raw sequencing data in the FAST5 file format and produces sequences in the FASTQ file format. Guppy was run on Windows Server 2008 machines with either 12 or 16 CPU cores. The process took about 40min to base-call 1 million reads on our computing setup. The command used to perform base-calling was:

```
guppy_basecaller.exe --input_path <input_path_fast5> --save_path
<output_path_fastq> --num_callers 12 --cpu_threads_per_caller 4 --
qscore_filtering -q 50000 -c dna_r9.4.1_450bps_fast.cfg
```

where:

`<input_path_fast5>` is the path of the raw reads in FAST5 format,

`<output_path_fastq>` is the path where base-called reads are stored in FASTQ format,

`--num_callers` specifies the number of parallel base-calling instances to run,

`--cpu_threads_per_caller` specifies the number of threads used by each instance of the base-calling software,

`--qscore_filtering` specifies that the reads be filtered by quality (default is to pass all reads with q_score above 7),

`-q` specifies number of reads to write per fastq file, and

`-c` specifies the configuration file.

2. **Demultiplex reads from different experiments:** The ends of the reads are scanned for sequencing barcodes (using local sequence alignment) and sorted into subdirectories based on barcodes identified. The MATLAB command used was:

```
sort_barcoded_reads(fastq_dir,ONT_barcodes)
```

where:

`fastq_dir` is the path of the fastq sequence files and

`ONT_barcodes` specifies the sequencing barcodes and their reverse complements.

The output is written into fastq files with reads that are sorted into sub-directories corresponding to the identity of the sequencing barcodes.

3. **Extract record lengths and assign to correct target pair:** Reads are scanned to identify the unique staple barcode sequences associated with each distance record. The length of the repeat region between the barcode sequences is extracted and assigned to the appropriate target pair. The following MATLAB command was executed for each directory containing reads from the same experiment:

```
pairwise_record_list = extract_pairwise_record_lengths(target_barcodes,path,
library_size, color_length)
```

where:

`target_barcodes` specifies the staple barcode sequences,

`path` specifies the path of the fastq reads,

`library_size` specifies the number of sequencing libraries that were combined for a single run,

`color_length` specifies the length of the auxiliary tag sequence, and

`pairwise_record_list` is the output, a matrix of size (n, n, 2001) where n is the number of target points and cell (i, j, k) holds the number of distance records of length k bases (only counting the repeat region) between points i and j. All distance records of length > 2000 are stored in the slice (:, :, 2001).

`pairwise_record_list` variables from different sequencing runs of the same experiment were combined by simply adding them.

4. **Infer the measured distance between every target pair:** The distribution of distance record lengths between every pair of points was examined to identify the major peak (in base pairs), which was then converted into a distance (in nanometers) by applying the calibration function. The MATLAB function used was:

```
[pairwise_distances, pairwise_peak_heights] =
finddist_geometry(pairwise_records_list,calibration_fun)
```

where:

`pairwise_records_list` is the output of extract_pairwise_record_lengths (see previous step),

`calibration_fun` is a cfit object that holds the calibration function of the ruler, which maps bases to nanometers,

`pairwise_distances` is one output, an array of measured distances for each pair of points, and

`pairwise_peak_heights` is the peak height (in bases) corresponding to the distances measured. It is a measure of the confidence in the measurement.

5. **Reconstruct geometry from pairwise distance measurements:** The distance measurements are integrated into a coherent embedding of the targets in the 2D Euclidean plane, using the following MATLAB function:

```
[theta, prune, score] = solveDGP(pairwise_distances, pairwise_peak_heights, opt_threshold)
```

where:

`pairwise_distances` and `pairwise_peak_heights` are the outputs from `finddist_geometry` (see previous step),

`opt_threshold` is a parameter used to prune unreliable measurements and to generate weights for measurements reflecting their reliability (see supplementary text for details on how `opt_threshold` is auto-set),

`theta` is a list of coordinates, specifying the final embedding,

`prune` is a logical-valued array indicating which target points were dropped from the final reconstruction, and

score is a measure of the internal consistency of the embedding. See supplementary text S2D.

The final embedding is compared to the designed pattern by superimposing them to minimize the RMSD (root-mean-square deviation). The MATLAB script used is:

```
[theta_translated, lrms] = superimpose(theta, theta_designed, prune)
```

where:

`theta` and `prune` are the outputs from `solveDGP`,

`theta_designed` contains a list of coordinates specifying the designed pattern,

`theta_translated` is the superimposition of the final embedding that minimizes the RMSD between the designed and reconstructed pattern, and

`lrms` is the corresponding RMSD.

Supplementary Notes

1. Design of molecular ruler primers and extension hairpins

Two main considerations went into the design of molecular ruler primers and extension hairpins. First, we reasoned that even weak secondary structure in the growing primers ('a a …a' and 'a* a* … a*') would result in a high propensity intra-molecular reaction where the primer folds back on itself. Normally such a state is transient and would resolve itself. However, in the presence of DNA polymerase in the molecular ruler reaction mixture, the primer could extend back on itself, proving fatal to the ruler reaction. This led us towards adopting a two letter code for the sequence domains 'a' and 'a*'. The second consideration was the number of bases added to the primer at every growth step. Here, we reasoned that the fewer the number of bases added at each step, the more gradual the growth of the primer and consequently more precise the ruler. These two considerations, unfortunately, are in tension with each other. A two-letter code results in a relatively weak binding interaction between a primer and an extension hairpin. Experiments showed that a toehold binding interaction of at least 12 bases (of an {A, T} alphabet) is necessary for the extension reaction to proceed with reasonable efficiency, under standard reaction conditions. In conventional PER repeat extension reactions, the extension sequence at each step is identical to the toehold sequence (for example, 's' is extended to 's s'). Thus, a conventional PER implementation would result in the addition of 12 bases at every step. However, we engineered a system where a 12 base toehold only adds a 4 base repeat at every step (Supplementary Fig. 2), by making the toehold sequence itself a repeat. In particular we chose 'a' = 'r r r' where 'r' = 'AAAT'. Thus, a toehold sequence of a (= 'r r r') was extended by the sequence 'r' at every step of the extension reaction. Correspondingly, we chose 'a*' = 'r* r* r*' and extended it by 'r*' at every step. The complete sequences for the primers and extension hairpins are listed in Supplementary Table 1.

2. Inferring geometry from pairwise distance measurements

The question of inferring geometry from pairwise distance measurements is modeled as an embedding problem in two-dimensional Euclidean space. Each target point i of the pattern is parameterized with X and Y co-ordinates as (x_i, y_i). We look for an embedding that minimizes the error between the experimentally measured distances and the Euclidean embedded distances. Not every measurement made by the ruler is equally reliable. We observed a clear positive correlation between the height of the major peak (in units of number of reads) and the accuracy

of the measurement. Therefore, we developed an algorithm that assigns weights to the various measurements according to the height of the corresponding major peak. The embedding algorithm proceeds in three stages – pruning, producing an initial embedding and finally, refining the embedding.

A. Pruning: A threshold parameter (auto-tuned, as explained below) was used to filter measurements. All measurements corresponding to peak heights less than the threshold were marked unreliable and pruned. All measurements corresponding to peak heights greater than the threshold were marked equally reliable and retained. In rare cases, some points were left with very few (less than three) associated reliable distance measurements as a result of this pruning. Such points were dropped from the reconstruction by deleting all associated distance measurements.

B. Initial embedding: We used a robust facial reduction algorithm (*18*) to obtain an initial embedding. This initial embedding has been shown to work well as an initial solution for generating embeddings using nonlinear optimization approaches, making it less likely that the optimization process is trapped in local minima or at saddle points.

C. Refining the embedding: In refining the embedding, we assigned each measurement a weight in the range $[0,1]$ to denote its reliability. Measurements with corresponding peak heights less than the threshold parameter are assigned a weight of zero (i.e. pruned). Measurements with corresponding peak heights greater than the threshold parameter were assigned a positive weight w_{ij} as described in the below equations. In particular the objective function J, which we seek to minimize, is defined as:

$$J = \sum_{i=1}^{n} \sum_{j=1}^{i-1} \frac{w_{ij}}{W} \left(d_{ij}^{measured} - d_{ij}^{embedded} \right)^2$$

where:

$\{1,2,\cdots,n\}$ are the uniquely identified points that make up the pattern,

$w_{ij} = \max\left(\frac{2}{1 - e^{-k\left(p_{ij} - t\right)}} - 1, 0 \right)$ is the weight assigned to the measured distance between points i and j. The smoothness parameter $k = 0.8$, p_{ij} is the peak height and t is the threshold parameter. Note that $w_{ij} \in [0,1]$,

$W = \sum_{i=1}^{n} \sum_{j=1}^{i-1} w_{ij}$ is the sum of all weights, used to normalize the weights,

$d_{ij}^{measured}$ is the experimentally measured distance between points i and j and,

$d_{ij}^{embedded} = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2}$ is the embedded Euclidean distance.

The optimization is performed using the fminunc MATLAB function, which implements a quasi-Newton algorithm to find the minimum of an unconstrained multivariable function.

D. Choosing the threshold parameter: The threshold parameter was auto-set, without any *a priori* knowledge of the geometry of the designed pattern, as follows. The embedding was performed for all integer values of the threshold parameter t from 0 to 100 and an embedding score was calculated as $score = J + \alpha r$

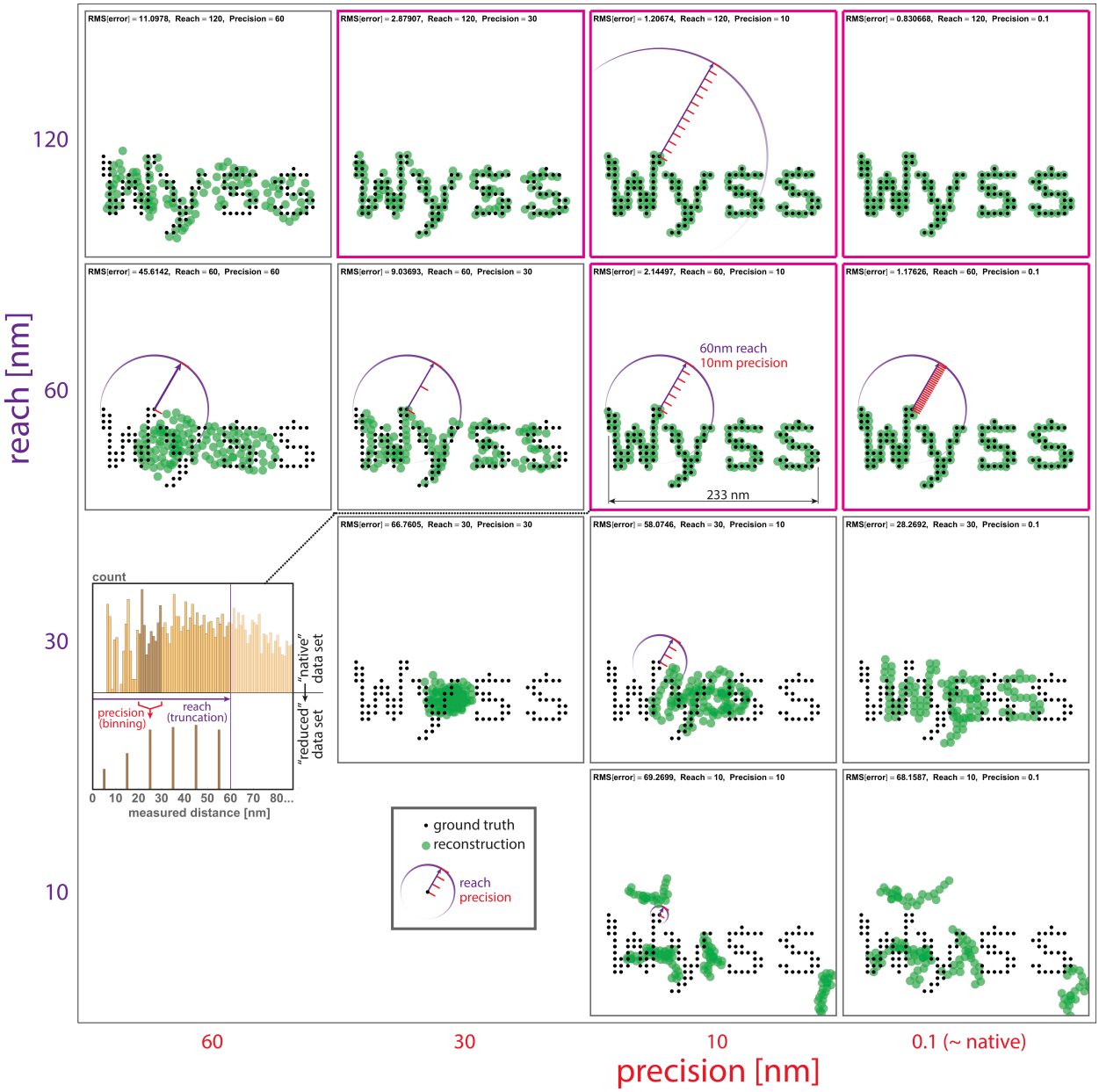
where:

J is the objective function, defined above,

α is the penalty applied for pruning points. We empirically set $\alpha = 0.5$ for all patterns except for the Wyss pattern, for which $\alpha = 0.25$ and,

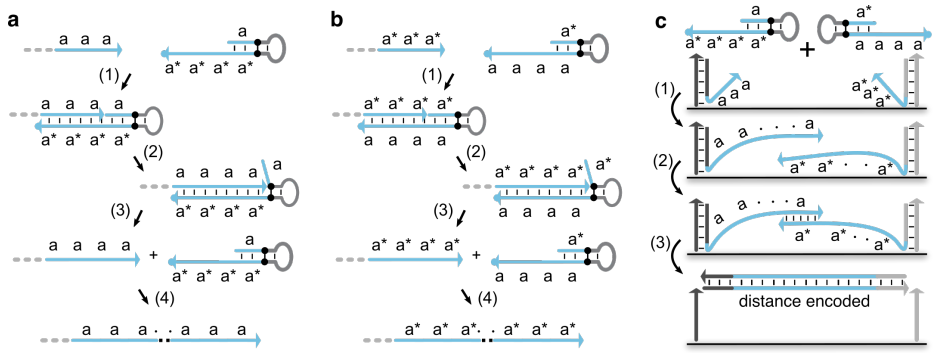
r is the number of points pruned.

The optimum threshold was chosen to be the one that minimized $score$, reflecting the best agreement between the measured and embedded distances. Note that the embedding score cannot take negative values. The term J captures the agreement between the measured distances and the embedded distances for all non-pruned points. The penalty term for pruned points, αr, is necessary to prevent the algorithm from trivially achieving $J = 0$ by setting the threshold to a very high value that prunes all points because all weights w_{ij} are set to zero.

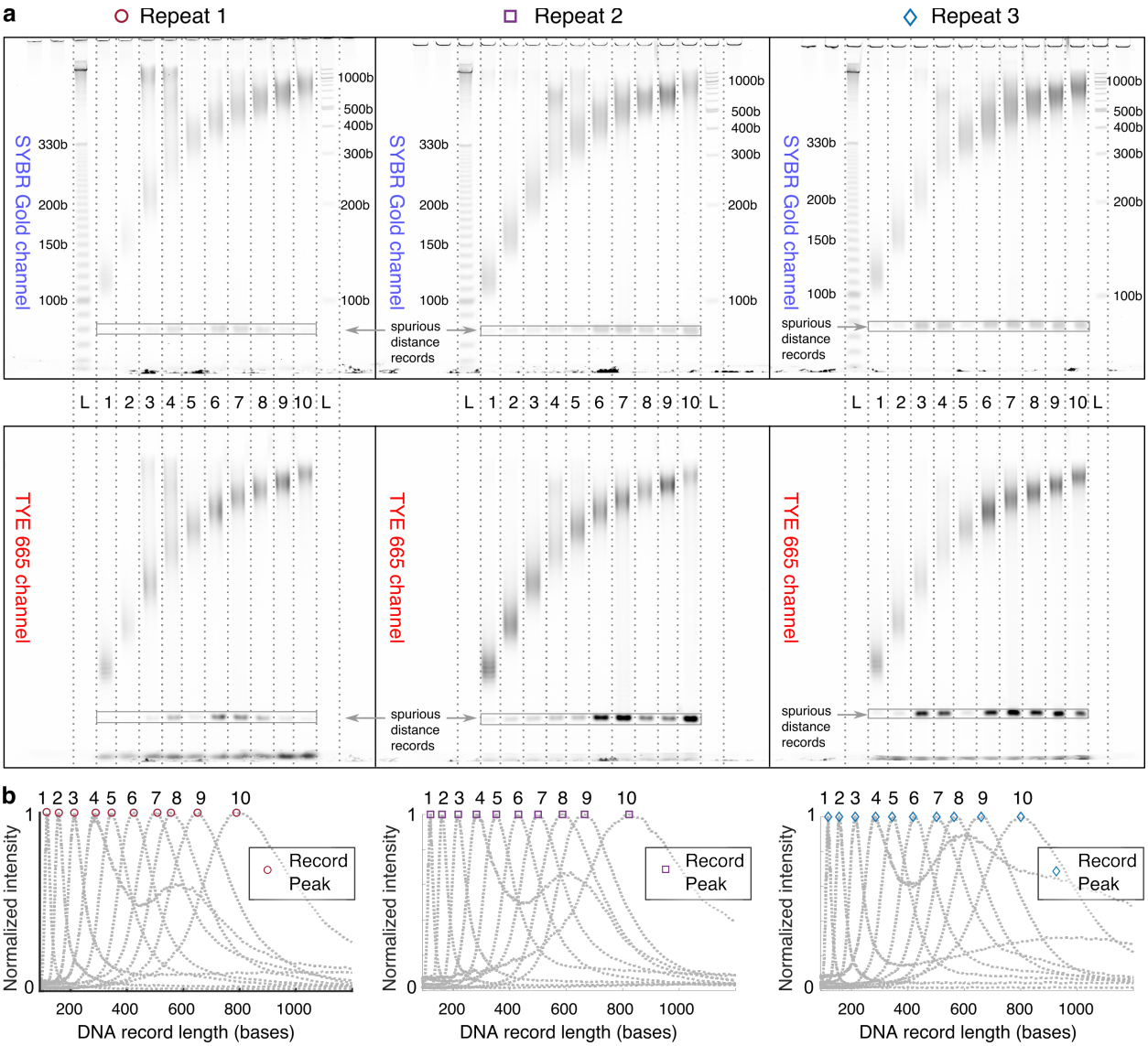


Supplementary Fig. 1. Effect of ruler precision and reach in reconstruction. Shown are results of a completely *in silico* study simulating diminished ruler precision and reach. A base "ground truth" geometry ("Wyss") comprising 121 points and spanning 233 nm was designed. Distance measurements for each pair (i.e., post sequencing and processing) were generated by modifying known (ground truth) values about a normal distribution of error with a fixed coefficient of variation (CV) of 5%. Measurements were then degraded by deteriorating precision and/or limiting reach. "Precision" is effectively the width of bins used to group similar measurements (histogram inset), while "reach" is the length of the farthest distance that results in a measurement. Reconstructions follow the same computational process (a reconstruction minimizing total discrepancy^2 between reads) as in the main text. Results show that limiting precision (60 nm), even at high (120 nm) reach, results in high RMSD. Similarly, high precision (0.1 nm, virtually without binning) yielded poor results if reach was limited to nearest neighbors

(10 nm). Only with reasonable precision of 10 nm and reach of 60 nm (1/4 of total pattern span, enough to cross gaps within and between letter components) did reconstructions fall near RMSD = 2 nm. Further precision or reach improvements helped, but minimally. Pink outlines denote reconstructions near or below RMSD = 2nm.

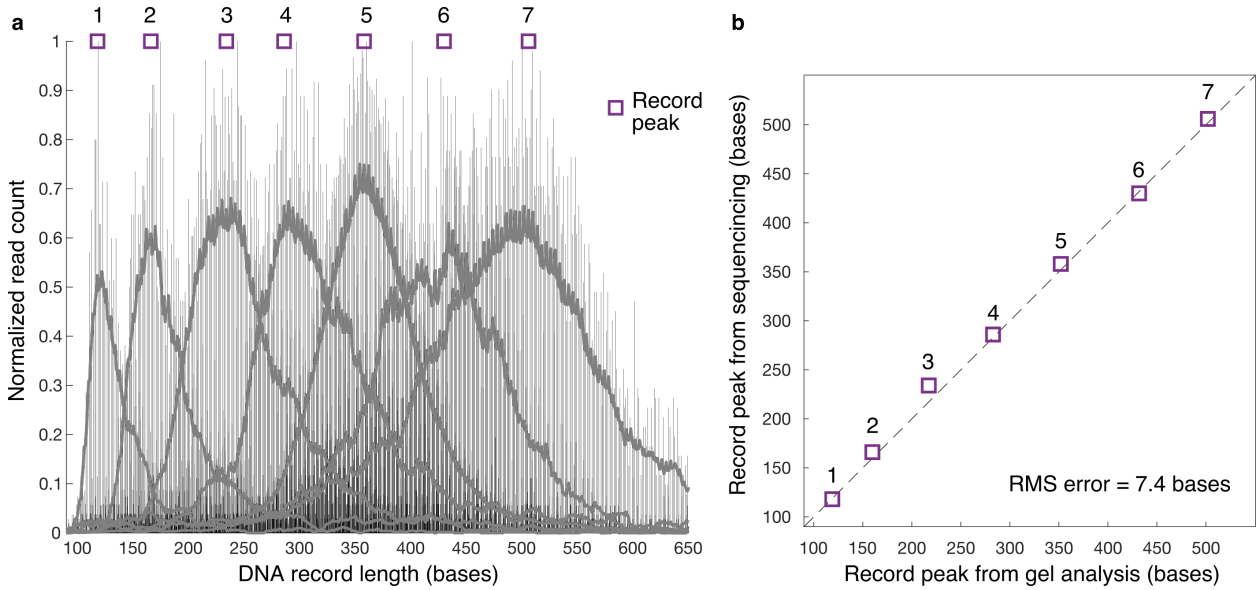


Supplementary Fig. 2. The full molecular ruler mechanism. Note that unlike the simplified version depicted in Fig. 2, the primer actually binds to the hairpin using a 12 base domain 'a a a'. The rest of the details of the mechanism are identical. **a.** A primer exchange reaction (PER) cascade repeatedly adds the four base sequence domain 'a', as follows. (1) The recording primer hybridizes to a PER hairpin, (2) a strand displacing DNA polymerase (Bsm large fragment) extends the primer into the stem of the hairpin and in the process copies domain 'a'. A 'stopper', a non-canonical base pair modification (isoG-isoC) on the template that is not recognized by the DNA polymerase, blocks further extension. The polymerase dissociates from the hairpin. (3) The recording primer is only weakly bound to the hairpin and also dissociates. (4) The above sequence of reactions repeat, adding domain 'a' every time. **b.** In the same manner, a complementary PER cascade repeatedly adds the four base sequence domain 'a*'. **c.** A double-stranded DNA 'distance record' is generated as follows. Consider two DNA labeled targets with recording primers hybridized to them. (1) The primers take part in PER reaction cascades, as described in parts A and B, adding sequence repeats of 'a' and 'a*' respectively. (2) The extended primers hybridize, (3) copy each other with the aid of the polymerase, are displaced from the targets and released into solution, making a distance record. The whole process is isothermal and autonomous.

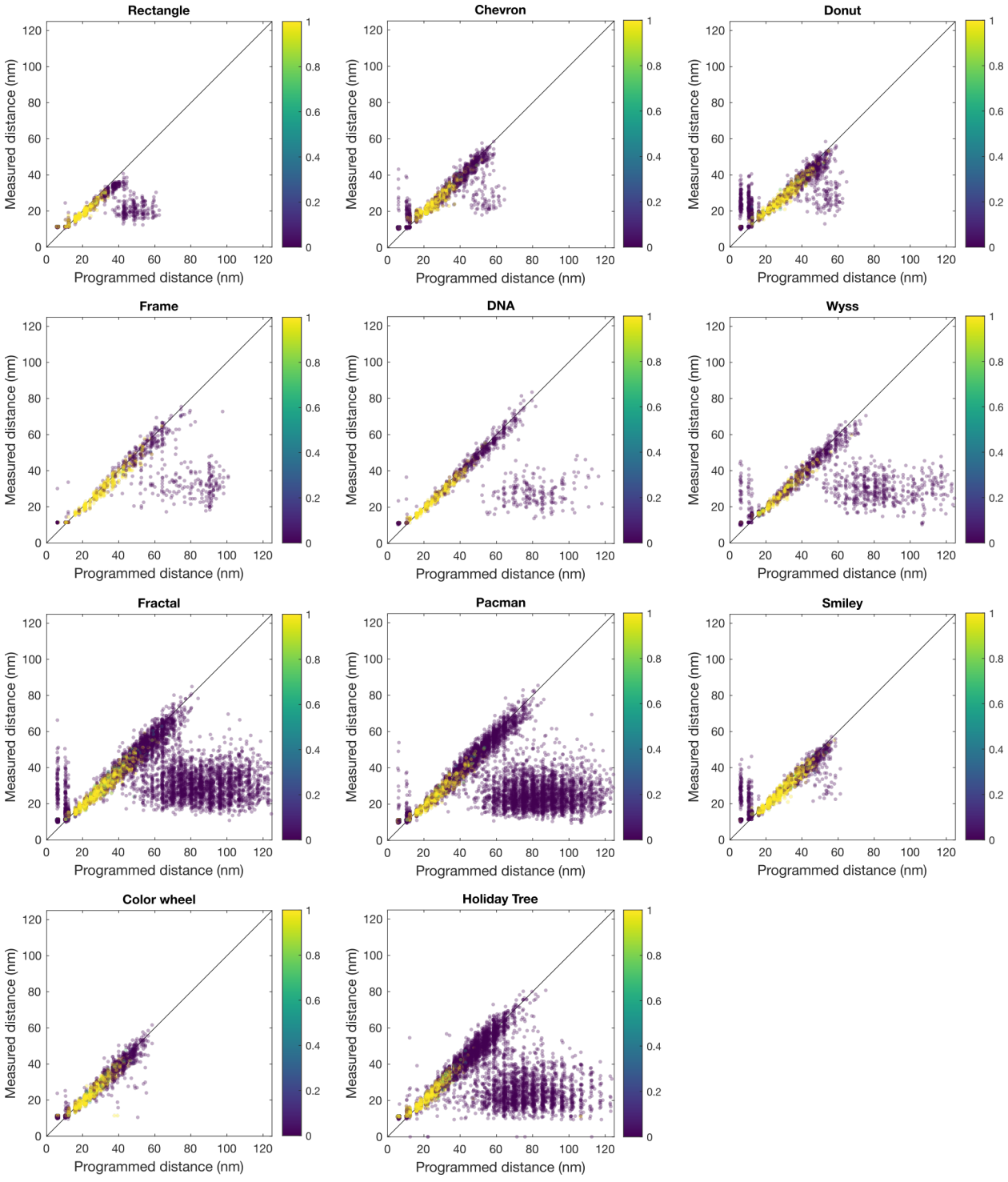


Supplementary Fig. 3. Molecular ruler calibration experiment. The experimental setup is described in Fig. 3. **a.** PAGE characterization of distance records. After PCR, distance records were size separated on a denaturing PAGE (see Materials and Methods section for details). The gels were imaged in two non-overlapping optical channels. Solid lines indicate gel boundaries and dotted lines are lane guides. SYBR Gold is known to stain DNA in a sequence and length dependent manner, confounding estimation of relative quantities of distance records of various lengths. Instead, the relative molar ratio of distance records of various lengths was estimated using the TYE665 channel. The TYE665 intensity should be proportional to the molar amount of the distance record, since it is introduced in an equimolar ratio by conjugation of the dye to the PCR primers. The SYBR Gold channel is used to track the ladder and hence estimate the absolute length of the distance records. **b. L**ength distribution of distance records for various calibration distances. Each distance measurement reveals a distinct length distribution of distance records. The distance records are skew-normal distributed, with longer distances resulting in longer records that are more broadly distributed. The peak of the distribution was used an archetype to generate a calibration curve. Gel profiles corresponding to lane 4 show a minor

peak, which we believe is due to either a defect in manufacturing DNA origami or contamination. This peak is ignored.

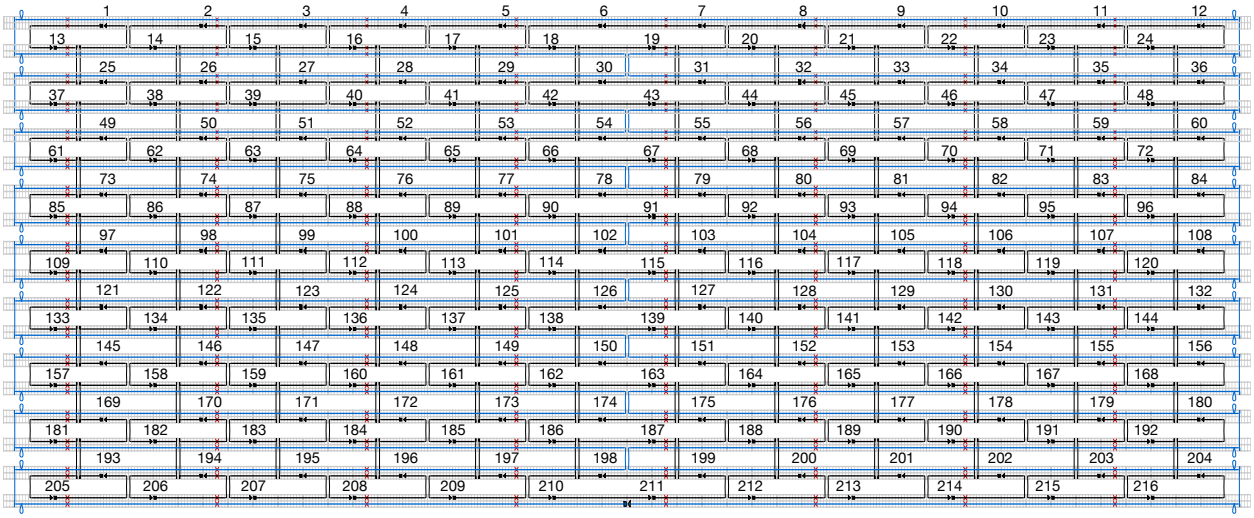


Supplementary Fig. 4. Characterization of the lengths of distance records by sequencing. Records from ruler experiments corresponding to seven different calibration distances were barcoded using barcoded PCR primers, pooled and then read using next-generation DNA sequencing. The programmed calibration distances are 1 = 21.4 nm, 2 = 32.0 nm, 3 = 42.8 nm, 4 = 53.4 nm, 5 = 63.9 nm, 6 = 74.8 nm and 7 = 85.3 nm **a.** The height of the bars equals the number of reads, normalized relative to the count of the most read record. The length includes primer regions, 32 bases each, flanking the variable length repeat region. The gray 'outline' curves are the moving average traces (span = 8) of the record lengths, shown here to allow the reader to discern records belonging to different calibration distances and their corresponding peaks. Next-gen sequencing sampled a few thousand reads for every pair of distances, while gel electrophoresis looks at billions of records in aggregate and hence results in smoother profiles (Fig. S3). **b.** A comparison of the peak locations characterized by gel electrophoresis (X-axis) versus peak locations obtained from next-generation DNA sequencing shows no significant systematic biases in sampling distance records with next-gen sequencing. The typical sequencing depth used in this work (about a few hundred sequences per pairwise distance) is inadequate to accurately sample record distributions corresponding to longer calibration distances (8, 9 and 10 in Fig. 3) and hence these are not included in this figure. The absence of accurate measurements of these longer distances from our sequencing data did not preclude us from successfully reconstructing patterns with points that span longer distances.

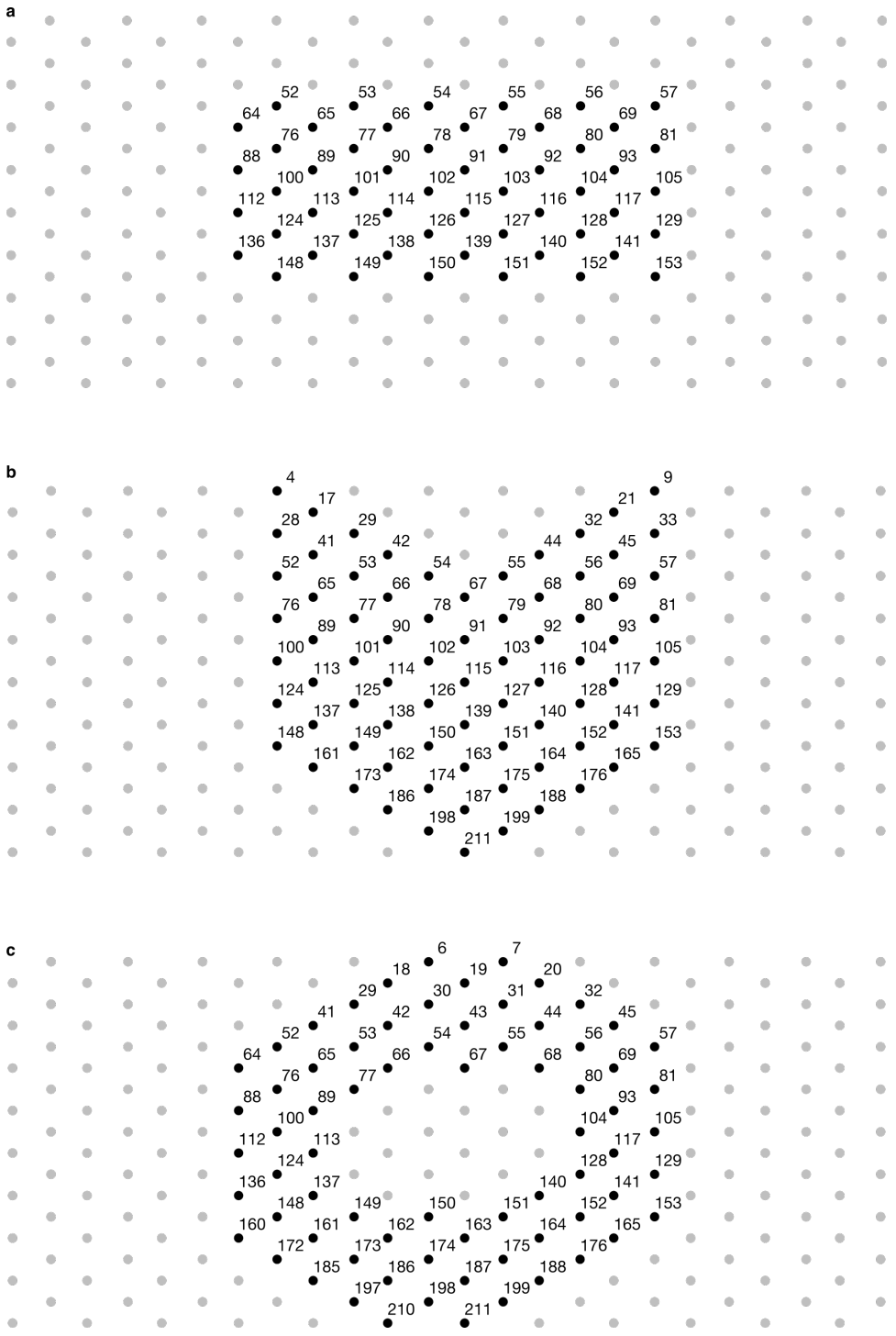


Supplementary Fig. 5. Programmed distances versus measured distance for each pattern from Fig. 4. Each dot within one plot corresponds to a unique pair of points. The color of the dot indicates the weight assigned to that measurement by the reconstruction algorithm (see Supplementary Note 2 for details). The overall quality of the reconstructions exceeds the average accuracy of the measurements made because of network effects. The plots indicate that points that are farther apart from each other are more likely to have an unreliable ruler measurement.

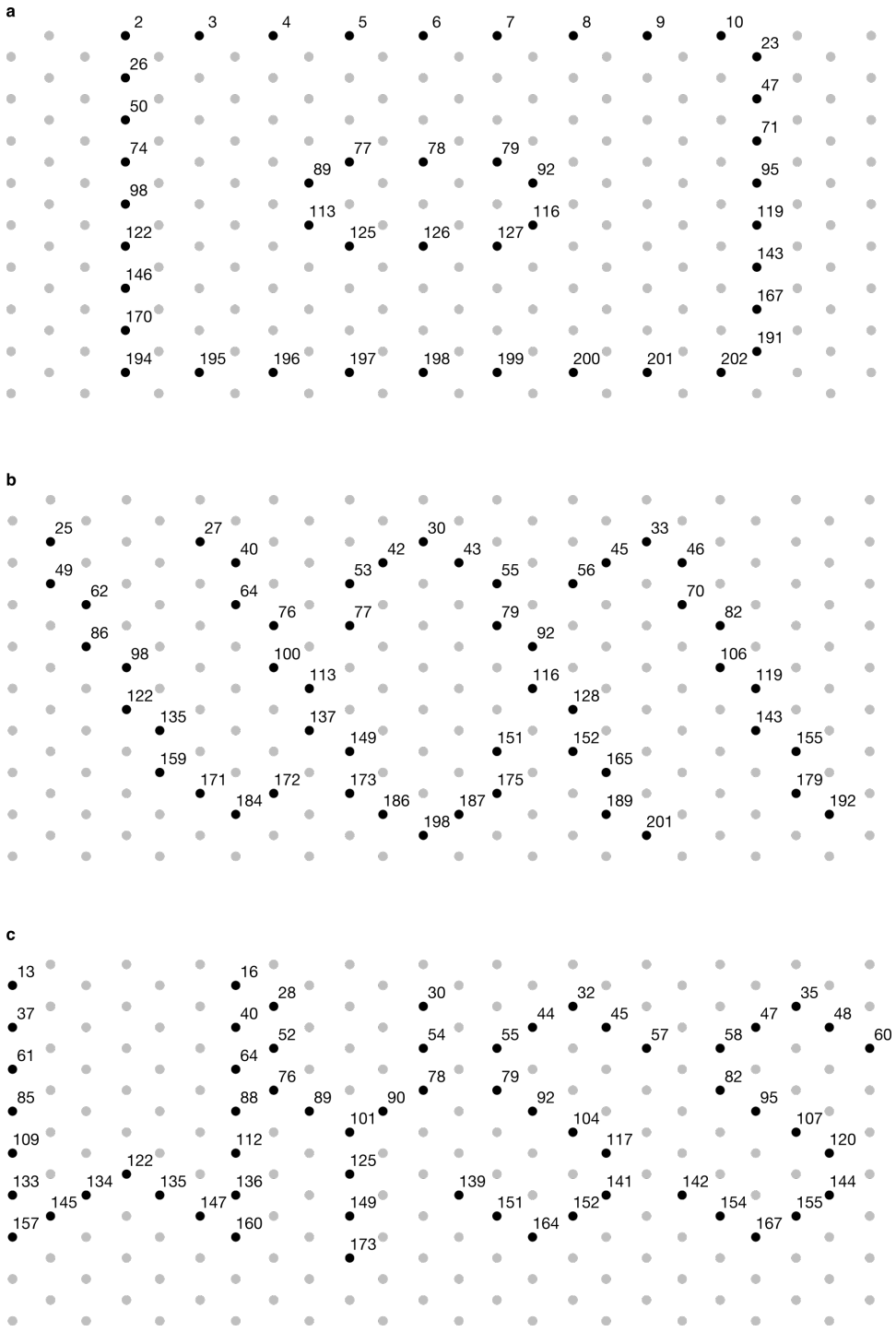
This is a result of two factors. One, fewer records are generated for longer distances because the efficiency of successfully creating records drops with increasing distance, likely limited by insufficient primer extensions due to either deleterious reactions and/or insufficient reaction time. Two, the longer the distance being measured, the more the number of sequence reads required to accurately sample the distribution of distance records. This is because the lengths of distance records are more broadly distributed as the distance being measured increases. We expect deeper sequencing to yield accurate distance measurements over longer distances.



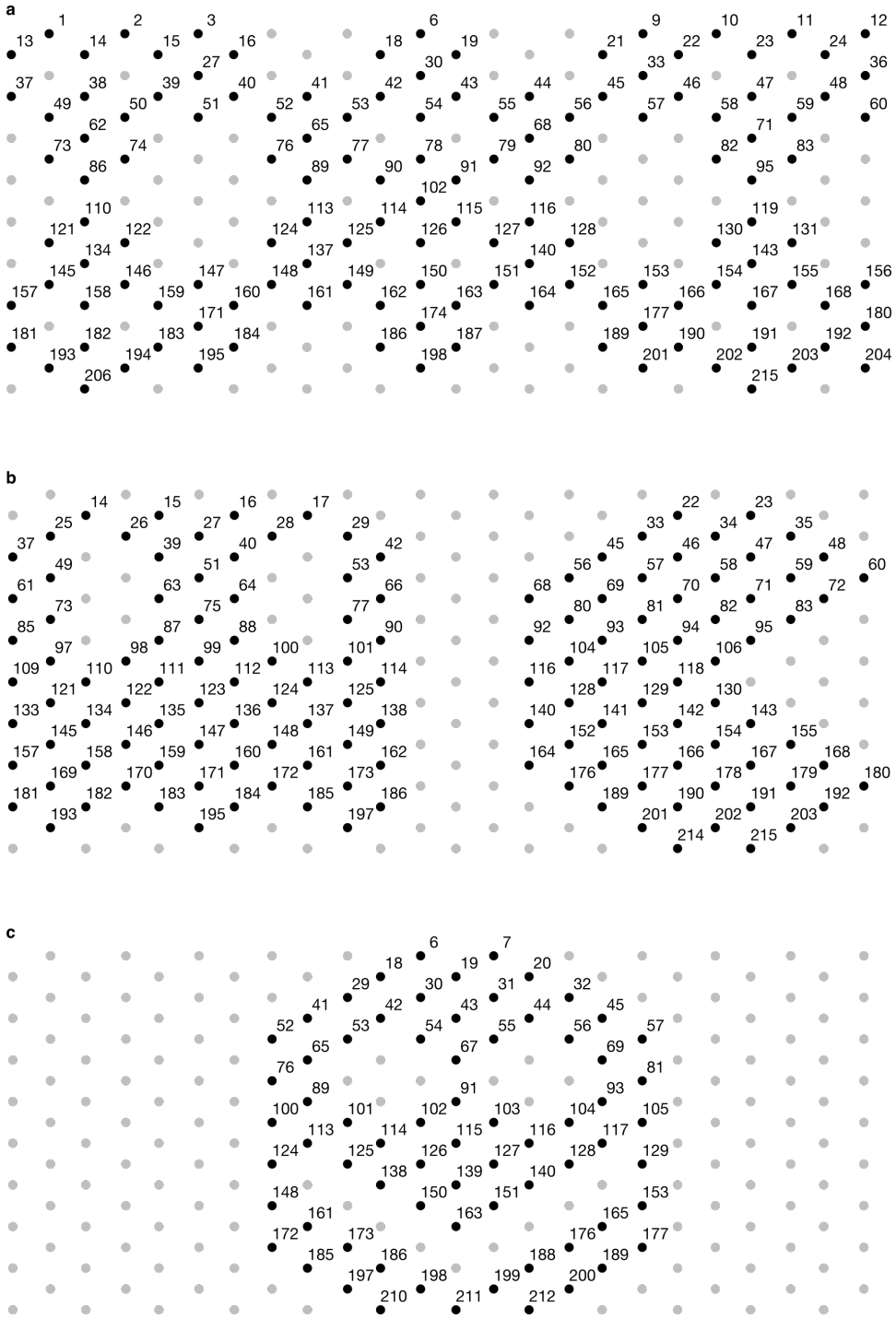
Supplementary Fig. 6. Scaffold and staple diagram for the DNA origami used in this work. The scaffold strand (M13mp18) is depicted in blue and the staple strands in black. Arrows at the end of strands represent 3 prime ends and the blocks at the other end represent 5 prime ends. The red crosses represent 'skipped' bases in the cadnano design software, corresponding to twist corrections (see Materials and Methods) made to minimize strain and promote flatness. The numeric labels correspond to the three prime ends of the staple strands. They are also the sequence IDs for blunt staples, extended staples and recording primers in the corresponding supplementary tables. The 'blunt' staple sequences are listed in Table S2, extended staple sequences in Table S3 and recording primer sequences in Table S4.



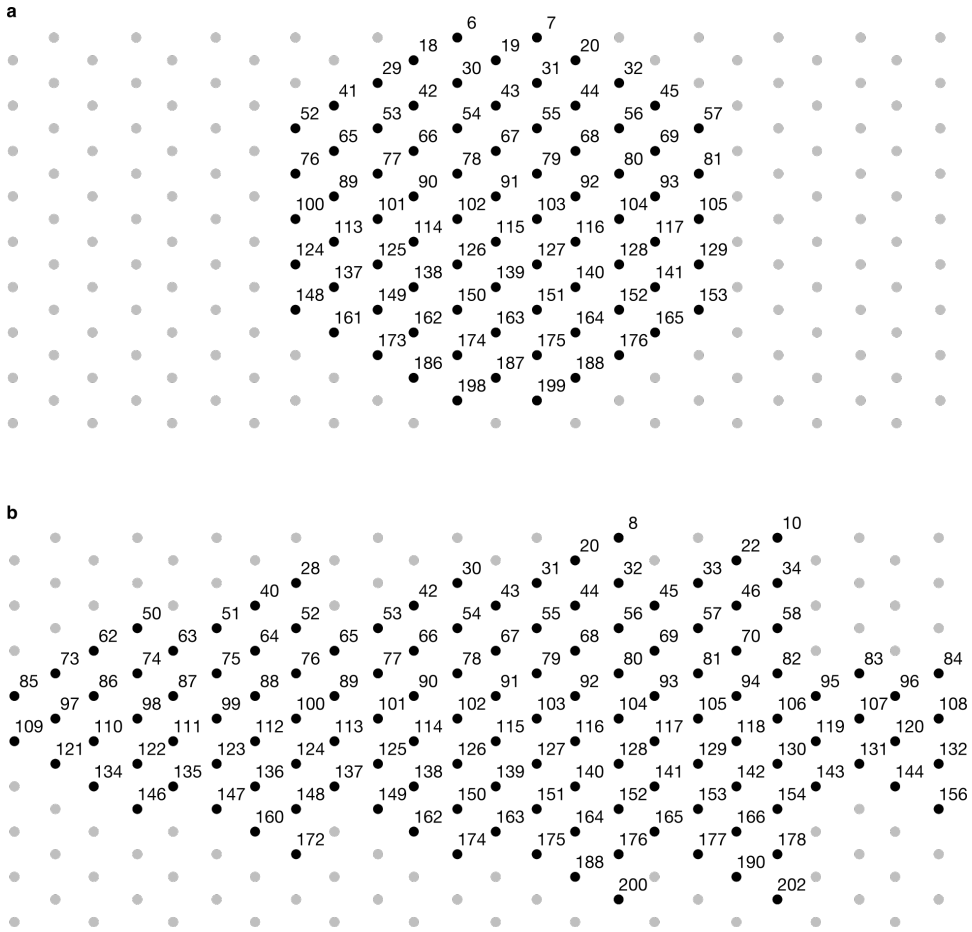
Supplementary Fig. 7. Pattern diagrams. Grey dots are 3' ends of blunt staples and black dots are 3' ends where either a blunt or extended staples may be incorporated. Numeric labels indicate the unique identity of every position in an origami. **a.** Rectangle. **b.** Chevron. **c.** Donut.



Supplementary Figure 8. Pattern diagrams. Grey dots are 3' ends of blunt staples and black dots are 3' ends where either a blunt or extended staples may be incorporated. Numeric labels indicate the unique identity of every position in an origami. **a.** Frame. **b.** DNA. **c.** Wyss.



Supplementary Figure 9. Pattern diagrams. Grey dots are 3' ends of blunt staples and black dots are 3' ends where either a blunt or extended staples may be incorporated. Numeric labels indicate the unique identity of every position in an origami. **a.** Fractal. **b.** Pacman. **c.** Smiley.



Supplementary Figure 10. Pattern diagrams. Grey dots are 3’ ends of blunt staples and black dots are 3’ ends where either a blunt or extended staples may be incorporated. Numeric labels indicate the unique identity of every position in an origami. **a.** Color wheel. **b.** Holiday tree.

Strand	Sequence (5' to 3')
Recording primer 'a'	TCGTGCGAGTATAGAAAGTGAGGGATTAATGGAAATAAATAAAT
Recording primer 'a*'	TCTACCCCATGAAGAGTAAATAGGTTGTGGGAATTTATTTATTT
PER growth hairpin 'a'	AAAT/iisodG/mCGCCCGCCACTAGCGGGCmG/iMe-isodC/ATTTATTTATTTATTT/3InvdT/
PER growth hairpin 'a*'	ATTT/iisodG/mCGCCCGCCACTAGCGGGCmG/iMe-isodC/AAATAAATAAATAAAT/3InvdT/
PCR Primer 1	/TYE665/TCGTGCGAGTATAGAAAGTGAGGGATTAATGG
PCR Primer 2	/TYE665/TCTACCCCATGAAGAGTAAATAGGTTGTGGGA

Supplementary Table 1. Growth hairpins, recording primers and fluorescent PCR primers for the molecular ruler calibration experiments described in Fig. 3 and Fig. S3.

Location ID	Blunt origami staple sequences, 5' to 3'
1	AACCATCGCGTAACACTGAGTTTCGCCACCCT
2	TTGATACCACAACGCCTGTAGCACGCCACC
3	GCTTGCTTCATAGTTAGCGTAACGAGGTGTAT
4	AAAAGGAGGTCTTTCCAGACGTTACGAGAGGG
5	TTCACGTTTATGGGATTTTGCTATTTTGCT
6	CATGAAAGTATTAAGAGGCTGAGACTCCTCA
7	GCGTTTGCAGAGCCACCACCGGAATTCTGAAA
8	CATCGGCACGCCACCCTCAGAACTAATGCC
9	TTGCCTTTACCACCCTCAGAGCCGGTGCCTTG
10	AGCACCGTCCAGAGCCGCCGCCAGAGTGTACT
11	CCGGAAACAGGCAGGTCAGACGAAAGCGTC
12	ATCACCAGCAAACAAATAAATCCTGAAAGCGC
13	CAGAGCCACCACCCTCATTTTCATAGGAACC
14	CTCAGAACCGCCACCCTCAGAACCGTCACCAG
15	CACCGTACTCAGGAGGTTTAGTACTTCCACAG
16	TTGATATAAGTATAGCCCGGAATATCTAAAG
17	CAGTACCAGGCGGATAAGTGCCGTGTAAATGA
18	AGAGAAGGATTAGGATTAGCGGGGAACAACTT
19	AACAACTATTCAGCGGAGTGAGAAAAAATCAC
20	CCCTGCCTATTTCGGAACCTATTACCGCCTCC
21	AGTAACAGTGCCCGTATAAACAGTCGCCACCC
22	GGTAATAAGTTTTAACGGGGTCACCACCAGA
23	ATACATGGCTTTTGATGATACAGGCATTGACA
24	AGTCTCTGAATTTACCGTTCCAGTTTGGCCTT
25	ACCGAACTAAAGGCCGCTTTTGCGATGACAAC
26	GGAACGAGCAGCGAAAGACAGCAAAACAGC
27	AAATCCGCAACGGCTACAGAGGCTGTTTATCA
28	GATTTGTATTTTTCATGAGGAAGTAAGGCTCC
29	ATTATACCAAATACGTAATGCCATAATTTT
30	CGGAACCCATCTTTTCATAATCTAGAAAGG
31	ACGTAGAAAGAAACGCAAAGACACCCTTATTA
32	TTAAGACTTTTGTCACAATCAATGCGTTTT
33	AATAACGGTTACCAGCGCCAAAGAAATCAAGT
34	AGTTACCACAACCGATTGAGGGAGTCGATAGC
35	TTTTTAAGCGGAAATTATTCATTAGCAAGG
36	TGAAATAGCGTCACCGACTTGAGCCCAGCAAA
37	CATGTACCCCACGCATAACCGAGGCTTGCA
38	TACAAACTGATAGTTGCGCCGACAGGATCGTC

Location ID	Blunt origami staple sequences, 5' to 3'
39	ACAGCCCTTCGAGGTGAATTTCTTTCGGAACG
40	TTTTGTCCCTTTAATTGTATCGTTGAGGAC
41	ATTTTCTGGAAAATCTCCAAAAAATTCCATTA
42	TCAACAGTAAGGAATTGCGAATAACTACGAAG
43	ACACTAAACTAAAACGAAAGAGGCGTGGCAAC
44	CTCAGAGCTTTTCGGTCATAGCCCCACGGAAT
45	TCAGAGCCAGCGTCAGACTGTAGCAGAAAATT
46	ACCACCAAATCAGTAGCGACAGCAAAAGGG
47	GGAGGTTGGTCACCAATGAAACCAGGAAGGTA
48	GATATTCATAGCACCATTACCATTAAAGGTGA
49	CCAAAAGGATAGGCTGGCTGACCTATAAGGGA
50	ATACCACATGACAAGAACCGGATCTTAGCC
51	GGTAGAAAAACGTAACAAAGCTGCTTGTGTCG
52	TAAAACGAGGCTTGCCCTGACGAGACAACGGA
53	GTCAGGACAGTAAATTGGGCTTGCCCAGCG
54	ATATAAAAATACATACATAAAGAAAAGAAT
55	TACAAAATTAAGAAACGATTTTTTGTTAGCAA
56	ACGAGCGTGAAAATAGCAGCCTTGGCATGA
57	TACAATTTTAAAAACAGGGAAGCGAACGCAAT
58	AATCAAGATTAACTGAACACCCTGCCGAACAA
59	CCTCCCGAAATTGAGCGCTAATAGAAGCCC
60	GTATTCTACAAGAATTGAGTTAAGAGAAACAA
61	GGGAGTTGACCAACTTTGAAAGGTACAGAC
62	ACCCTCAGGCGCAGACGGTCAATCTCATCAAG
63	AGGGTAGCGACCTGCTCCATGTTAATTCATTA
64	TAAAGACTCATCGCCTGATAAATCATTCAG
65	AACGGGTAAAGCGCGAAACAAAGTAAACACCA
66	GCACCAACACACTCATCTTTGACCAGATGGTT
67	ATGCGATTACTTTAATCATTGTGATTATCCCA
68	AAGTTTATCCTTATTACGCAGTATGTTTAACG
69	CATATGGTAATACCCAAAAGAACTTACAGAGA
70	CGACATTGAAGGAAACCGAGGACATTAGAC
71	AATATTGAAAAAGTAAGCAGATAGAACAAAGT
72	ATTATCACCAATAGCTATCTTACCTCAGAGAG
73	CCTTTAATCAGACGACGATAAAAAACATAACG
74	AGCAAACTCTTTTGCAAAAGAAGTTTAGGA
75	TAATTCGAAATAGTAAAATGTTTATTATTACA
76	GGAAGCCCAATACTGCGGAATCGTTACGTTAA

Location ID	Blunt origami staple sequences, 5' to 3'
77	AAGCAAAGATCCCCCTCAAATGCTATACCA
78	ATCCAAAAAACAGCCATATTATATTACCTT
79	ACAATAAAGTTTATCAACAATAGATTGCCAGT
80	ACAAAAGGAAAATAATATCCCATAACGCTA
81	CGAGCCAGGTAGAAACCAATCAATCACCCAGC
82	CGCCAACACTTATCATTCCAAGAAAAGCCTTA
83	AGGGCTTATACCGCACTCATCGATAGCGAA
84	TCTTACCATTTATTTTCATCGTAGCTTATCCG
85	CAGGCGCAATTACGAGGCATAGATAACCCT
86	AGTAATCTTTCAACTAATGCAGATCCAAAATA
87	CCCAAATCGATTCATCAGTTGAGATTTTGCCA
88	TGAATAAACTAACGGAACAACAGACTGGAT
89	GAACGAGTGTTGGGAAGAAAAATCCATAAATA
90	TAATTTCATTAAGAACTGGCTCATTTTAAACA
91	ATCAGGTCAACGAGAATGACCATAATGCAGAA
92	TCAAAAATCTTTCCAGAGCCTAATTAAGTCCT
93	GAATAACATATCCTGAATCTTACCCCTAATTT
94	GGGAGAATTAGTTGCTATTTTGAATCGGCT
95	CAGAGGGTCTTGCGGGAGGTTTTGCGGGTATT
96	ATAACCCAAGAACGCGAGGCGTTTGAACAAGC
97	TTTGCGGGATTGCTGAATATAATGAGAGAGTA
98	TTGTACCATTTAAATATGCAACTGACCGGA
99	AATAAAGCAAGTTTCATTCCATATTCGCGTTT
100	CAGGCAAGATTCTGCGAACGAGTAGATTAAGA
101	ATAGTAGTTAGATACATTTCGCATAGTCAG
102	CGCGCCTCAACATGTTCAGCTAAATCAAAA
103	ACCTCCGGTGCTGATGCAAATCCAAGACGACG
104	CAAAATCACGCGAGAAAACTTTTAGTACCG
105	AGACGCTGTAATTTCATCTTCTGAGGCATTTT
106	ATCCTTGATTGAAATACCGACCGTTTTAACAA
107	AAATCGTCTAAATAAGAATAAACCAACAGT
108	AATATATGCTAGAAAAAGCCTGTTATACAAAT
109	CGTTTACTGCTCCTTTTGATAAATGGCTTA
110	GCGAGAGGCCAACAGGTCAGGATTCTGTAGCT
111	GAGGGGGTGCTTCAAAGCGAACCAAAAGTACG
112	AGCGTCCGAAAGACTTCAAATAAACAGTTG
113	TTCATTGACGGATTGCATCAAAAAGATTTAGT
114	GTTCAGAATTTACCCTGACTATTAAATGGTCA

Location ID	Blunt origami staple sequences, 5' to 3'
115	GCGAGCTGTTTAGCTATATTTTCAATAACTAT
116	GAACAAGATAAAGTAATTCTGTCCATCGCAAG
117	ACGAGCATTAATAAGAGAATATAATCAAATAT
118	GTCTTTCTGTAATTTAGGCAGACCTAAATT
119	AAACCAAGATTGAGAATCGCCATAGTGATAAA
120	AAGCCGTTGTATAAAGCCAACGCTACCGGAAT
121	TTTTTGTTTATATTTTAAATGCAAGTAATACT
122	AACGTTAAAGGTAAAGATTCAAAAAATCGG
123	GAAGATTGGAGACAGTCAAATCACAATTAAGC
124	CGGTTGATCAACCGTTCTAGCTGAAAATCATA
125	TCGTAAAAAGGGTAGCTATTTTTTCTACTA
126	ATGTAAACTTAGGTTGGGTTATTTTGGGGC
127	TTCAGGTTCTTTTACATCGGGAGACCTTTTTA
128	CGTAAAACCCTGATTGCTTTGAAAATTTAT
129	GTTAGAACCGCGCAGAGGCGAATTTTAGATTA
130	TGTTTGGACTGAGCAAAAGAAGATCCCTTAGA
131	AGATGATGAGAAAACAAAATTAACTTCTGT
132	GAGCGGAACATTTGAATTACCTTTCATAAATC
133	GAGCTTAAGAAGCCTTTATTTCTTTTTAGA
134	CAACATGTAAAACATTATGACCCTTGCCTGAG
135	GTGTCTGGCTCAGAGCATAAAGCTAGGGTGAG
136	ATTCCCAGCAAAGAATTAGCAACATCAATA
137	TTGACCATAGCATTAACATCCAATTAAATTAA
138	ATAACCTGAAAAGGTGGCATCAATGAGAGATC
139	TGGAGCAACTATCAGGTCATTGCCATACAGTA
140	ACAAAGAATAGGTCTGAGAGACTAAACAATAA
141	ATTTTAGTAGAAGAGTCAATAGTGTACCAAGT
142	TAATGGTAAACATAGCGATAGCATTCATTT
143	TAAGGCGTGCTATTAATTAATTTTGATGAAAC
144	CATAATTATGAGTGAATAACCTTGTTACATTT
145	AAGGCGATCGCGTCTGGCCTTCCTGCATTAAA
146	TTACGCCAAACATTAAATGTGAGAATTGTA
147	GGAAGGGCGGATTCTCCGTGGGAAAAAAACAG
148	GCCATTCGCCGTAATGGGATAGGTATGTACCC
149	CACCGCTTGGCGCATCGTAACCGACGGTAA
150	ACAGTACTAACGTCAGATGAATTGAGAGTC
151	TGGTCAGTAAGGTTATCTAAAATACGTAGATT
152	GAACCTCACAACTAATAGATTAGATTTGCA

Location ID	Blunt origami staple sequences, 5' to 3'
153	GCAAATGATACATTTGAGGATTTAATGGAAGG
154	GCCTGCAAACAAACAATTCGACAAATCCTGAT
155	AAAACAGATGCCCGAACGTTATTGATTATC
156	AAAAATACGTAACATTATCATTTTACCAGAAG
157	ACCCTCAAAATCAGCTCATTTTCCATCAAA
158	TAATGTGTTATTTTGTTAAAATTCGTAGCCAG
159	AAAGGCCGTATAAGCAAATATTTACGAGTAAC
160	TGATATTAATCAGAAAAGCCCCCAAACGGC
161	TGCCGGAGCTAGCATGTCAATCATCACGTTGG
162	TACAAAGGACAAGAGAATCGATGATGCATCTG
163	CAGGAAGAAGGGGACGACGACAGTTGAAAGGA
164	CGGATTCGAGAAATAAAGAAATTGTCTTTAGG
165	TACAAAATCTACCATATCAAAATTAGCCGTCA
166	CAATTACTTATACTTCTGAATAGAAGTATT
167	AAACATCAGCAATTCATCAATATACTCGTATT
168	AACAATTTTTATCATCATATTCCTAATTTTAA
169	CTGATTGCGACGGCCAGTGCCAAGTGTGCTGC
170	GTTTTTCTTCGACTCTAGAGGATTTCGCTA
171	AGAGGCGGCGAATTCGTAATCATGAACTGTTG
172	GCTGCATTTGTGTGAAATTGTTATGGCAAAGC
173	CCCGCTTTACAACATACGAGCCGTTTCCGG
174	ATTGAGGTGGCAAATCAACAGTATCGGCCT
175	TTGCAACATGACGCTCAATCGTCTTCAATATC
176	GGTAATATATTGGCAGATTCACCCCTTGCT
177	GAGTAGAAATAAAAGGGACATTCTAGCCAGCA
178	CTTCTTTGAACCCTTCTGACCTGATTAACACC
179	GTCCATCAGGCACAGACAATATTAGAAGAT
180	TAATCAGTTCTTTAATGCGCGAACTCGCCATT
181	AATAATTTAAGTTGGGTAACGCACGACGTT
182	CTTTCATCGCTGGCGAAAGGGGGACTTGCATG
183	AACCCGTCGATCGGTGCGGGCCTCCCCCGGGT
184	GGATTGACCATTCAGGCTGCGCGTCATAGC
185	TGTAGATGCTGGTGCCGGAAACCACCGCTCAC
186	CCAGTTTGTCGCACTCCAGCCAGCGAAGCATA
187	CTAACTCAAGCCTGGGGTGCCTAAGAAATACC
188	AGCACTAAAATATCAAACCCTCAAGAAATGGA
189	ATAGATAAAAAATCTAAAGCATCAAGTCACAC
190	AGACTTTCAGTGCCACGCTGAGGGCCAACA

Location ID	Blunt origami staple sequences, 5’ to 3’
191	AAATCCTTGGTGAGGCGGTCAGTAAAGCGTAA
192	AAGTTTGACGAACGAACCACCAGCTTTGAATG
193	CCACGCTGGTTTGCCCCAGCAGGGGCAACAG
194	CTGTTTGATGGTGGTTCCGAAATCAGGGTG
195	TCCCTTATAAATCAAAAGAATAGCGCGCGGGG
196	GGGTTGAGTGTTGTTCCAGTTTGTCGTGCCA
197	GTCCACTATTAAAGAACGTGGACCTCACTG
198	TACATTTGGAAAAACGCTCATGTGAGTGAG
199	CGCTGGCAAGTGTAGCGGTCACGGCCAGCCA
200	AACCACCACACCCGCCGCGCTTACCTTGCT
201	CTACAGGGCGCGTACTATGGTTGCACTTGCCT
202	GCACGTATAACGTGCTTTCCTCGTAGCAATA
203	AGAGCGGGAGCTAAACAGGAGGCAGAGTCT
204	GGGATTTTAGACAGGAACGGTACGTGTTTTTA
205	GTAAAACCCTTCACCGCCTGGCCAAGCGGT
206	CCTGCAGGTTTCACCAGTGAGACGCGAAAATC
207	ACCGAGCTTTTGCGTATTGGGCGCCGGCAAAA
208	TGTTTCCAATGAATCGGCCAACCCGAGATA
209	AATTCCACCCAGTCGGGAAACCTGGAACAAGA
210	AAGTGTAACATTAATTGCGTTGCGTCCAACGT
211	CAAAGGGCGAAAAACCGTCTATCACGCTAGGG
212	TTATTTACCCAGAACAATATTACCCTGCGCGT
213	GACCAGTAGAACTCAAACTATCGGATGCGCCG
214	GAGATAGATTAGTAATAACATCTTTGACGA
215	GAATACGTCGCAAATTAACCGTTGTTAGAATC
216	GCTATTAGGAGGCCACCGAGTAAACGATTAAA

Supplementary Table 2. Blunt staple sequences for DNA origami used in all the experiments.

Location ID	Extended staple sequence with barcoded handle, 5' to 3'
1	AACCATCGCGTAACACTGAGTTTCGCCACCCTCTCCTACGCTGGTATAGACT
2	TTGATACCACAACGCCTGTAGCACGCCACCCTATTGCACTCCTCCAGTAA
3	GCTTGCTTCATAGTTAGCGTAACGAGGTGTATTTAGACCACTAGCGTTAGAC
4	AAAAGGAGGTCTTTCCAGACGTTACGAGAGGGAGCTACAAGAATGACTGACT
5	TTCACGTTTATGGGATTTTGCTATTTTGCTAGGCTTATTGACGATGGATA
6	CATGAAAGTATTAAGAGGCTGAGACTCCTCACGCAAGGTTACGTGTAATGA
7	GCGTTTGCAGAGCCACCACCGGAATTCTGAAACTCTTAGGTGGACAACTACC
8	CATCGGCACGCCACCCTCAGAACTAATGCCCTCATCTCATCCTGCATTGT
9	TTGCCTTTACCACCCTCAGAGCCGGTGCCTTGATCCAGAGGTATATCAGTCC
10	AGCACCGTCCAGAGCCGCCGCCAGAGTGTACTCTCTCTTCGTAGGTGACATC
11	CCGGAAACAGGCAGGTCAGACGAAAGCGTCCGATAGCGTTCGAACAAGAA
12	ATCACCAGCAAACAAATAAATCCTGAAAGCGCGGTACTTCTGCAGGATCATA
13	CAGAGCCACCACCCTCATTTTCATAGGAACCGGCTTGAATTCGCTTGATAG
14	CTCAGAACCGCCACCCTCAGAACCGTCACCAGGAATTAGCGTATTCCGCTTA
15	CACCGTACTCAGGAGGTTTAGTACTTCCACAGTGAGACTAACAAGATGAGGT
16	TTGATATAAGTATAGCCCGGAATATCTAAAGCCAGATATTGTTCTCCGGTT
17	CAGTACCAGGCGGATAAGTGCCGTGTAAATGACCTAGTTGCATAATGTCCTC
18	AGAGAAGGATTAGGATTAGCGGGGAACAACTTGTTACACCGTTAGAGGTTCA
19	AACAACTATTCAGCGGAGTGAGAAAAAATCACCACAATCCTATCAGTTGGTT
20	CCCTGCCTATTTCGGAACCTATTACCGCCTCCAACTAATGGCATTCAGTTCG
21	AGTAACAGTGCCCGTATAAACAGTCGCCACCCGAATAGAGACTTACGTGGCA
22	GGTAATAAGTTTTAACGGGGTCACCACCAGAAGGTGAAGTTTGTGCATAGT
23	ATACATGGCTTTTGATGATACAGGCATTGACATAGTCTCGGAGCGTATAGTG
24	AGTCTCTGAATTTACCGTTCCAGTTTGGCCTTAATGGTTCACAAGGTAGTTC
25	ACCGAACTAAAGGCCGCTTTTGCGATGACAACGAGTCTAGGTAGACCATTGT
26	GGAACGAGCAGCGAAAGACAGCAAAACAGCTTCAACCTGTTACGAAGCAA
27	AAATCCGCAACGGCTACAGAGGCTGTTTATCAGAACTCTGTCGTTCCAATTC
28	GATTTGTATTTTTCATGAGGAAGTAAGGCTCCGTAGTGCATTTTGAAGCTGC
29	ATTATACCAAATACGTAATGCCATAATTTTATAACCTCACGACTCACTAA
30	CGGAACCCATCTTTTCATAATCTAGAAAGGACAACCGGATAACAAGGATG
31	ACGTAGAAAGAAACGCAAAGACACCCTTATTAGGACCGTAAGTAACCATTCG
32	TTAAGACTTTTGTCACAATCAATGCGTTTTGTGTGACGAGTACCATCTAG
33	AATAACGGTTACCAGCGCCAAAGAAATCAAGTGTAGAGTCATTGCACGTACC
34	AGTTACCACAACCGATTGAGGGAGTCGATAGCTACGTGTTACTTCTTGCGAT
35	TTTTTAAGCGGAAATTATTCATTAGCAAGGCAGGCGGATAGTACAGTTAG
36	TGAAATAGCGTCACCGACTTGAGCCCAGCAAAAATAAGGCACTCCTCTTACT
37	CATGTACCCCACGCATAACCGAGGCTTGCAATATCCTCCAGGTCACTTAA
38	TACAAACTGATAGTTGCGCCGACAGGATCGTCTGAGACACTTTACAATCCGG

Location ID	Extended staple sequence with barcoded handle, 5' to 3'
39	ACAGCCCTTCGAGGTGAATTTCTTTCGGAACGAGAGGCATATGAGGTAATCG
40	TTTTGTCCCTTTAATTGTATCGTTGAGGACTAGATCACCACTAGCAACTT
41	ATTTTCTGGAAAATCTCCAAAAAATTCCATTACCTCTCGGATCAATAGGAAG
42	TCAACAGTAAGGAATTGCGAATAACTACGAAGGAAGTGTGTTGGCAAGTATT
43	ACACTAAACTAAAACGAAAGAGGCGTGGCAACTTAACGGTGTGTTGATAGGT
44	CTCAGAGCTTTTCGGTCATAGCCCCACGGAATCTCATTGTCTGGACACTAGG
45	TCAGAGCCAGCGTCAGACTGTAGCAGAAAATTAATTCATCGCATCCACTGAG
46	ACCACCAAATCAGTAGCGACAGCAAAAGGGTTGGCATCTTAAGAGACTGG
47	GGAGGTTGGTCACCAATGAAACCAGGAAGGTAGGTTCCATGTTGATACTCGA
48	GATATTCATAGCACCATTACCATTAAAGGTGACGCACATAAGTCCTTATCCT
49	CCAAAAGGATAGGCTGGCTGACCTATAAGGGAGTCGTCATTAACCTGGATGA
50	ATACCACATGACAAGAACCGGATCTTAGCCTTCCACAGTAGCGATAACTA
51	GGTAGAAAAACGTAACAAAGCTGCTTGTGTCGCTTACAGCACGTTGGTGTAA
52	TAAAACGAGGCTTGCCCTGACGAGACAACGGACTTATGATCGTAGACCGTGG
53	GTCAGGACAGTAAATTGGGCTTGCCCAGCGGAGTATTCCACACGATTGTT
54	ATATAAAAATACATACATAAAGAAAAGAATTAGGAACGACTCTCTTCTCG
55	TACAAAATTAAGAAACGATTTTTTGTTAGCAACATGCAATAGAGTTGTCGAT
56	ACGAGCGTGAAAATAGCAGCCTTGGCATGAACTACCTTGTGTAATTGGCT
57	TACAATTTTAAAAACAGGGAAGCGAACGCAATCTAATGTCGACAACGACGAC
58	AATCAAGATTAACTGAACACCCTGCCGAACAATCCTAACCTACTCCTAGTCG
59	CCTCCCGAAATTGAGCGCTAATAGAAGCCCTGAGTCGATTTGCGATTCAA
60	GTATTCTACAAGAATTGAGTTAAGAGAAACAAACGAATACCATACTGGTTGT
61	GGGAGTTGACCAACTTTGAAAGGTACAGACTGTACTATGCCTTGAATCCA
62	ACCCTCAGGCGCAGACGGTCAATCTCATCAAGGGTAACTAAGCCGTGAGATG
63	AGGGTAGCGACCTGCTCCATGTTAATTCATTATTCCTTGGCTCATTCCTAAC
64	TAAAGACTCATCGCCTGATAAATCATTCAGGCTCTATCTTACATCCGACG
65	AACGGGTAAAGCGCGAAACAAAGTAAACACCACACAGTTCACGTTATTGGTG
66	GCACCAACACACTCATCTTTGACCAGATGGTTGAGAGAATGTTCTGAACGTG
67	ATGCGATTACTTTAATCATTGTGATTATCCCAGGTTCACAATAGAGCGACTA
68	AAGTTTATCCTTATTACGCAGTATGTTTAACGTGTCGAGGTATCTCAACAAG
69	CATATGGTAATACCCAAAAGAACTTACAGAGAGCTTGTTGAACATACCAGAA
70	CGACATTGAAGGAAACCGAGGACATTAGACCCTCTGAACAAACTGAGCTT
71	AATATTGAAAAAGTAAGCAGATAGAACAAAGTAACAGGTAGGTAATAACCGG
72	ATTATCACCAATAGCTATCTTACCTCAGAGAGGGCAATGACTCAATAAGTCG
73	CCTTTAATCAGACGACGATAAAAAACATAACGCGGTGTTCAATAGACGTATC
74	AGCAAACTCTTTTGCAAAAGAAGTTTAGGAGGACTATTCGGTACTCAGAT
75	TAATTCGAAATAGTAAAATGTTTATTATTACATCAACTACGTCCATCAACAC
76	GGAAGCCCAATACTGCGGAATCGTTACGTTAAGAACTGACAATCACTCTGTT

Location ID	Extended staple sequence with barcoded handle, 5' to 3'
77	AAGCAAAGATCCCCCTCAAATGCTATACCAGAGAGCAACCCCTCATATAG
78	ATCCAAAAAACAGCCATATTATATTACCTTGCATAAGCAGGGTTCTAGTG
79	ACAATAAAGTTTATCAACAATAGATTGCCAGTGAAGACCATCTAGAACCTGA
80	ACAAAAGGAAAATAATATCCCATAACGCTAGAACTAGGCGATAGTCTTGC
81	CGAGCCAGGTAGAAACCAATCAATCACCCAGCTGGCTAATGTAATCACCACT
82	CGCCAACACTTATCATTCCAAGAAAAGCCTTATAACAGCTTCGTTCAATCCT
83	AGGGCTTATACCGCACTCATCGATAGCGAATATCGTACTCGCAACACAAT
84	TCTTACCATTTATTTTCATCGTAGCTTATCCGCAGCGAGTGTCTATTCGTAC
85	CAGGCGCAATTACGAGGCATAGATAACCCTTCAATCCGAACCAATGTTCT
86	AGTAATCTTTCAACTAATGCAGATCCAAAATACACAACGTAAAGCGTACAAC
87	CCCAAATCGATTCATCAGTTGAGATTTTGCCAATTCCGATCTAATCGTGCTA
88	TGAATAAACTAACGGAACAACAGACTGGATTCAGGTACTATGAGCTTGAG
89	GAACGAGTGTTGGGAAGAAAAATCCATAAATACACGTAAGTCGTCTTACATG
90	TAATTTCATTAAGAACTGGCTCATTTTAAACAGGAGACTTATCCATTGCGAA
91	ATCAGGTCAACGAGAATGACCATAATGCAGAATGAGTGGTGTGTATTGTGTC
92	TCAAAAATCTTTCCAGAGCCTAATTAAGTCCTAGGCGTACTTTTCTCGATAG
93	GAATAACATATCCTGAATCTTACCCCTAATTTTGATTGAAGGTAACCAGTGA
94	GGGAGAATTAGTTGCTATTTTGAATCGGCTTAGTGAATCCACATGCAACT
95	CAGAGGGTCTTGCGGGAGGTTTTGCGGGTATTTGTACTGGAGCAATCTAGTG
96	ATAACCCAAGAACGCGAGGCGTTTGAACAAGCCTCAAGCTATCCACATAACC
97	TTTGCGGGATTGCTGAATATAATGAGAGAGTAACTTACGTCTTTCGAGACAA
98	TTGTACCATTTAAATATGCAACTGACCGGACTCAATCATCAATTGGTGGT
99	AATAAAGCAAGTTTCATTCCATATTCGCGTTTTTACTTGGACGGAGTGTAAT
100	CAGGCAAGATTCTGCGAACGAGTAGATTAAGAGCAATCTTAGACAGTACCGT
101	ATAGTAGTTAGATACATTTCGCATAGTCAGCCATCAGAATTGTGAGTTCT
102	CGCGCCTCAACATGTTCAGCTAAATCAAAATAGTCCTCATGGTGCTTATA
103	ACCTCCGGTGCTGATGCAAATCCAAGACGACGTGGAGGTATAGGACGTAGTG
104	CAAAATCACGCGAGAAAACTTTTAGTACCGCTTCGGCTTCTAGTGTAAGC
105	AGACGCTGTAATTTCATCTTCTGAGGCATTTTTGGTACAATGCTCTCAATGT
106	ATCCTTGATTGAAATACCGACCGTTTTAACAACTATAACGCACTACGAGGTG
107	AAATCGTCTAAATAAGAATAAACCAACAGTGATGATTCGTTGCTACATCG
108	AATATATGCTAGAAAAAGCCTGTTATACAAATTGCGAACTTATTACACCTCG
109	CGTTTACTGCTCCTTTTGATAAATGGCTTACCGATAACCGTCTTGATGAC
110	GCGAGAGGCCAACAGGTCAGGATTCTGTAGCTCCTACGTTATCTGCAAGGAT
111	GAGGGGGTGCTTCAAAGCGAACCAAAAGTACGTTCATTAGCGCAGATCAGTT
112	AGCGTCCGAAAGACTTCAAATAAACAGTTGGAAGGTTACTTCCAGACCTC
113	TTCATTGACGGATTGCATCAAAAAGATTTAGTTATGTCAGTGGATACTTGGT
114	GTTCAGAATTTACCCTGACTATTAAATGGTCATTAACACGCTTTAGGTTCGT

Location ID	Extended staple sequence with barcoded handle, 5' to 3'
115	GCGAGCTGTTTAGCTATATTTTCAATAACTATCTCGGAAGTTCTCGTAGTAT
116	GAACAAGATAAAGTAATTCTGTCCATCGCAAGAGTCAGAACATTCGATCCAC
117	ACGAGCATTAATAAGAGAATATAATCAAATATCGAGTCACATCAAGGACATT
118	GTCTTTCTGTAATTTAGGCAGACCTAAATTGTACAAGTTCGAACCTACCG
119	AAACCAAGATTGAGAATCGCCATAGTGATAAAGCTACGATACTGCTGAACTC
120	AAGCCGTTGTATAAAGCCAACGCTACCGGAATCGACACGTATAGTCTGTCTA
121	TTTTTGTTTATATTTTAAATGCAAGTAATACTGACATCCGTTTTGAGGTCTT
122	AACGTTAAAGGTAAAGATTCAAAAAATCGGAGCGTATTAGGGATCTTACT
123	GAAGATTGGAGACAGTCAAATCACAATTAAGCTCTAAGCGTACTTGGCTAGA
124	CGGTTGATCAACCGTTCTAGCTGAAAATCATAGACTGTTCCTGGACTGATAT
125	TCGTAAAAAGGGTAGCTATTTTTTCTACTACGGATAGAAGGAACACTACA
126	ATGTAAACTTAGGTTGGGTTATTTTGGGGCGAGCTAGTCCTAGTGGTTAG
127	TTCAGGTTCTTTTACATCGGGAGACCTTTTTATGTAGCGGATTATCAATGCG
128	CGTAAAACCCTGATTGCTTTGAAAATTTATTTAGCTGTTCGTCGATGATT
129	GTTAGAACCGCGCAGAGGCGAATTTTAGATTAACCATTCTTCGTAGTATCCT
130	TGTTTGGACTGAGCAAAAGAAGATCCCTTAGATTCAGTCTACTTCCTTACGA
131	AGATGATGAGAAAACAAAATTAACTTCTGTCTGTCACCATCTAGTACGTT
132	GAGCGGAACATTTGAATTACCTTTCATAAATCTTGTAACCTGGAATACGGTT
133	GAGCTTAAGAAGCCTTTATTTCTTTTTAGATGCGTATTCTCTCTTGTGTT
134	CAACATGTAAAACATTATGACCCTTGCCTGAGTGTATCACCGGATATACCTC
135	GTGTCTGGCTCAGAGCATAAAGCTAGGGTGAGAATGGACCGTCATTAGAAGC
136	ATTCCCAGCAAAGAATTAGCAACATCAATAGAATAGTTGGCCTGAATCTT
137	TTGACCATAGCATTAACATCCAATTAAATTAAACGCTTACTAGCGATGTTAT
138	ATAACCTGAAAAGGTGGCATCAATGAGAGATCCCGAGGTTAGGTATTAGAGG
139	TGGAGCAACTATCAGGTCATTGCCATACAGTATAAGATCCGATACCATAGCG
140	ACAAAGAATAGGTCTGAGAGACTAAACAATAAGCTGGAACAAGTCTGTTATG
141	ATTTTAGTAGAAGAGTCAATAGTGTACCAAGTCCATATAAGGAAGCAGAGGC
142	TAATGGTAAACATAGCGATAGCATTCATTTCCATGACTTACGATGAGTGG
143	TAAGGCGTGCTATTAATTAATTTTGATGAAACAGGTATTCACTGTGGTGTTC
144	CATAATTATGAGTGAATAACCTTGTTACATTTCTCAGTAGACAATCTTCGCT
145	AAGGCGATCGCGTCTGGCCTTCCTGCATTAAACATACTACAGTCCATGTGCG
146	TTACGCCAAACATTAAATGTGAGAATTGTAAACTCACTTCCGTCAATTCG
147	GGAAGGGCGGATTCTCCGTGGGAAAAAAACAGGGCTATCAATAGACTCCTCG
148	GCCATTCGCCGTAATGGGATAGGTATGTACCCTATACCTGTGTCACTCGTAG
149	CACCGCTTGGCGCATCGTAACCGACGGTAAGATCCGCTATTCTATTCCGA
150	ACAGTACTAACGTCAGATGAATTGAGAGTCTCATACGTTCCGGAGATGTA
151	TGGTCAGTAAGGTTATCTAAAATACGTAGATTGGTGAATAGGGGTGATTGAT
152	GAACCTCACAACTAATAGATTAGATTTGCAACGCTTAGATGTAACACAGA

Location ID	Extended staple sequence with barcoded handle, 5' to 3'
153	GCAAATGATACATTTGAGGATTTAATGGAAGGCTTCGGTATTTGGTCATCGA
154	GCCTGCAAACAAACAATTCGACAAATCCTGATATTGACCTACCACATGAGTA
155	AAAACAGATGCCCGAACGTTATTGATTATCCATTGTAGGCCTTGGAGAAT
156	AAAAATACGTAACATTATCATTTTACCAGAAGGCGTACCTAAACATAGGCTC
157	ACCCTCAAAATCAGCTCATTTTCCATCAAACATGTGATACCTTGACACAT
158	TAATGTGTTATTTTGTTAAAATTCGTAGCCAGTTGCATCACTTCATCAGGTA
159	AAAGGCCGTATAAGCAAATATTTACGAGTAACTTCAAGCACATGACCTTATG
160	TGATATTAATCAGAAAAGCCCCCAAACGGCCGTATTGTCATCCGTCACAG
161	TGCCGGAGCTAGCATGTCAATCATCACGTTGGTGCTACTGTTTCCTTCATGG
162	TACAAAGGACAAGAGAATCGATGATGCATCTGGAGTTACCTTTTCGAGTGTC
163	CAGGAAGAAGGGGACGACGACAGTTGAAAGGATAGGTCTGTTGTAGCAACAA
164	CGGATTCGAGAAATAAAGAAATTGTCTTTAGGTATAGAGGAGCCAACCACTA
165	TACAAAATCTACCATATCAAAATTAGCCGTCAGATGGTATTGGGAATGGATG
166	CAATTACTTATACTTCTGAATAGAAGTATTCGGTTGAGAAATACCGTCTT
167	AAACATCAGCAATTCATCAATATACTCGTATTTCACAACAGTGTTGAGCTAT
168	AACAATTTTTATCATCATATTCCTAATTTTAATCACCTAGAGTCTTGGATGT
169	CTGATTGCGACGGCCAGTGCCAAGTGTGCTGCGGTTCATATCTCGACCTCTT
170	GTTTTTCTTCGACTCTAGAGGATTTCGCTACTCATGGAATTACGTCGATC
171	AGAGGCGGCGAATTCGTAATCATGAACTGTTGATATGGTGCAGGAGTATTGT
172	GCTGCATTTGTGTGAAATTGTTATGGCAAAGCGCATTACATCATGGTCCTAG
173	CCCGCTTTACAACATACGAGCCGTTTCCGGCAACTTCGAGGAGAATCCAT
174	ATTGAGGTGGCAAATCAACAGTATCGGCCTGGTCGGTCTTATTCGACATG
175	TTGCAACATGACGCTCAATCGTCTTCAATATCGGTTGTTGTTGTACACACAC
176	GGTAATATATTGGCAGATTCACCCCTTGCTAACGTGGAGTTCCGTATATC
177	GAGTAGAAATAAAAGGGACATTCTAGCCAGCATAGGACCATGGTATCTTAGG
178	CTTCTTTGAACCCTTCTGACCTGATTAACACCGGATTGTTACTCCGAGTAGG
179	GTCCATCAGGCACAGACAATATTAGAAGATGAATCAAGCTGCAATAGTGT
180	TAATCAGTTCTTTAATGCGCGAACTCGCCATTCACAATTACGACGCATTAGG
181	AATAATTTAAGTTGGGTAACGCACGACGTTTAGAACTGCTGTTGTGTTGT
182	CTTTCATCGCTGGCGAAAGGGGGACTTGCATGCAATTCCAGTAACGGCATAG
183	AACCCGTCGATCGGTGCGGGCCTCCCCCGGGTTCTGATGTTGGACTTGTGTA
184	GGATTGACCATTCAGGCTGCGCGTCATAGCGTATCCACTTACACGGTTCT
185	TGTAGATGCTGGTGCCGGAAACCACCGCTCACAACTATCACCTTCTGTGTGA
186	CCAGTTTGTCGCACTCCAGCCAGCGAAGCATAGATAAGAGCGCCACTTATGT
187	CTAACTCAAGCCTGGGGTGCCTAAGAAATACCGGTCTACTATCATGTGGCTT
188	AGCACTAAAATATCAAACCCTCAAGAAATGGATATTGGACACTAAGCTCGTT
189	ATAGATAAAAAATCTAAAGCATCAAGTCACACCCTTCTCAATTTGCTTGTCA
190	AGACTTTCAGTGCCACGCTGAGGGCCAACATCTGTATTCCAACACTGGAG

Location ID	Extended staple sequence with barcoded handle, 5' to 3'
191	AAATCCTTGGTGAGGCGGTCAGTAAAGCGTAACCAACTTCTCTTAGTGTGCT
192	AAGTTTGACGAACGAACCACCAGCTTTGAATGGAGGACTAGAAAGTCGTTGT
193	CCACGCTGGTTTGCCCCAGCAGGGGCAACAGTCTCGGTGAATAAGTCACAC
194	CTGTTTGATGGTGGTTCCGAAATCAGGGTGGTGAACCTATTCGGCTGTAG
195	TCCCTTATAAATCAAAAGAATAGCGCGCGGGGAAGGATTGGTACCGGATAAT
196	GGGTTGAGTGTTGTTCCAGTTTGTCGTGCCAGTACGTGGTTCACTAACCAT
197	GTCCACTATTAAAGAACGTGGACCTCACTGTGACGGTAGAGTACATTCGT
198	TACATTTGGAAAAACGCTCATGTGAGTGAGTAGTGTCTTGTAGGTCATCC
199	CGCTGGCAAGTGTAGCGGTCACGGCCAGCCACTGACCTGTATTGTCCACTG
200	AACCACCACACCCGCCGCGCTTACCTTGCTCATCTAGCAATCTACGCACG
201	CTACAGGGCGCGTACTATGGTTGCACTTGCCTTGGATCTGAAAAGAATGTGC
202	GCACGTATAACGTGCTTTCCTCGTAGCAATACAATACGCGACTCTGCTATT
203	AGAGCGGGAGCTAAACAGGAGGCAGAGTCTTCTGAGGATCTTCCTACCAG
204	GGGATTTTAGACAGGAACGGTACGTGTTTTTAAACTCGCACATGTGTCTAAG
205	GTAAAACCCTTCACCGCCTGGCCAAGCGGTGTGACCGACAGTTACTCATG
206	CCTGCAGGTTTCACCAGTGAGACGCGAAAATCGATACATTGCGTACGACATT
207	ACCGAGCTTTTGCGTATTGGGCGCCGGCAAAAGTATGACACCGAGCAATTCT
208	TGTTTCCAATGAATCGGCCAACCCGAGATACAGCTCTAATATCGAACGGT
209	AATTCCACCCAGTCGGGAAACCTGGAACAAGAGCTATGACAACCGCAGTATA
210	AAGTGTAACATTAATTGCGTTGCGTCCAACGTGCATTGTTGTGTAGACAAGT
211	CAAAGGGCGAAAAACCGTCTATCACGCTAGGGGAACTGATTGAACAACGGTC
212	TTATTTACCCAGAACAATATTACCCTGCGCGTGTGGAACATTCAATGACAGG
213	GACCAGTAGAACTCAAACTATCGGATGCGCCGCGAATCAATGTTCAAGTGGT
214	GAGATAGATTAGTAATAACATCTTTGACGAGATCTGTTCACGAAGTCTCC
215	GAATACGTCGCAAATTAACCGTTGTTAGAATCTTGCATGGTAGATCTTCTCC
216	GCTATTAGGAGGCCACCGAGTAAACGATTAAACCAGATACAACACGTTCAAT

Supplementary Table 3. Staples extended with barcoded handles for recruiting barcoded recording primers. These are used in experiments described in Fig. 4. The location IDs correspond to the numeric position labels in Fig. S6.

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
1	GTCTTGAGCAAATAGCAGGTGACAAGTC TATACCAGCGTAGGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGTC TATACCAGCGTAGGAGATTTATTTATTT
2	GTCTTGAGCAAATAGCAGGTGACATTAC TGGAGGAGTGCAATAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTAC TGGAGGAGTGCAATAGATTTATTTATTT
3	GTCTTGAGCAAATAGCAGGTGACAGTCT AACGCTAGTGGTCTAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTCT AACGCTAGTGGTCTAAATTTATTTATTT
4	GTCTTGAGCAAATAGCAGGTGACAAGTC AGTCATTCTTGTAGCTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGTC AGTCATTCTTGTAGCTATTTATTTATTT
5	GTCTTGAGCAAATAGCAGGTGACATATC CATCGTCAATAAGCCTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTATC CATCGTCAATAAGCCTATTTATTTATTT
6	GTCTTGAGCAAATAGCAGGTGACATCAT TACACGTAACCTTGCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCAT TACACGTAACCTTGCGATTTATTTATTT
7	GTCTTGAGCAAATAGCAGGTGACAGGTA GTTGTCCACCTAAGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGGTA GTTGTCCACCTAAGAGATTTATTTATTT
8	GTCTTGAGCAAATAGCAGGTGACAACAA TGCAGGATGAGATGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAA TGCAGGATGAGATGAGATTTATTTATTT
9	GTCTTGAGCAAATAGCAGGTGACAGGAC TGATATACCTCTGGATAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGGAC TGATATACCTCTGGATATTTATTTATTT
10	GTCTTGAGCAAATAGCAGGTGACAGATG TCACCTACGAAGAGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGATG TCACCTACGAAGAGAGATTTATTTATTT
11	GTCTTGAGCAAATAGCAGGTGACATTCT TGTTCGAACGCTATCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTCT TGTTCGAACGCTATCGATTTATTTATTT
12	GTCTTGAGCAAATAGCAGGTGACATATG ATCCTGCAGAAGTACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTATG ATCCTGCAGAAGTACCATTTATTTATTT
13	GTCTTGAGCAAATAGCAGGTGACACTAT CAAGCGAATTCAAGCCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAT CAAGCGAATTCAAGCCATTTATTTATTT
14	GTCTTGAGCAAATAGCAGGTGACATAAG CGGAATACGCTAATTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTAAG CGGAATACGCTAATTCATTTATTTATTT
15	GTCTTGAGCAAATAGCAGGTGACAACCT CATCTTGTTAGTCTCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACCT CATCTTGTTAGTCTCAATTTATTTATTT
16	GTCTTGAGCAAATAGCAGGTGACAAACC GGAGAACAATATCTGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACC GGAGAACAATATCTGGATTTATTTATTT
17	GTCTTGAGCAAATAGCAGGTGACAGAGG ACATTATGCAACTAGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAGG ACATTATGCAACTAGGATTTATTTATTT
18	GTCTTGAGCAAATAGCAGGTGACATGAA CCTCTAACGGTGTAACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTGAA CCTCTAACGGTGTAACATTTATTTATTT
19	GTCTTGAGCAAATAGCAGGTGACAAACC AACTGATAGGATTGTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACC AACTGATAGGATTGTGATTTATTTATTT
20	GTCTTGAGCAAATAGCAGGTGACACGAA CTGAATGCCATTAGTTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAA CTGAATGCCATTAGTTATTTATTTATTT
21	GTCTTGAGCAAATAGCAGGTGACATGCC ACGTAAGTCTCTATTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTGCC ACGTAAGTCTCTATTCATTTATTTATTT
22	GTCTTGAGCAAATAGCAGGTGACAACTA TGCACAAACTTCACCTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACTA TGCACAAACTTCACCTATTTATTTATTT
23	GTCTTGAGCAAATAGCAGGTGACACACT ATACGCTCCGAGACTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCACT ATACGCTCCGAGACTAATTTATTTATTT
24	GTCTTGAGCAAATAGCAGGTGACAGAAC TACCTTGTGAACCATTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAAC TACCTTGTGAACCATTATTTATTTATTT
25	GTCTTGAGCAAATAGCAGGTGACAACAA TGGTCTACCTAGACTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAA TGGTCTACCTAGACTCATTTATTTATTT
26	GTCTTGAGCAAATAGCAGGTGACATTGC TTCGTAACAGGTTGAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTGC TTCGTAACAGGTTGAAATTTATTTATTT
27	GTCTTGAGCAAATAGCAGGTGACAGAAT TGGAACGACAGAGTTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAAT TGGAACGACAGAGTTCATTTATTTATTT
28	GTCTTGAGCAAATAGCAGGTGACAGCAG CTTCAAAATGCACTACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGCAG CTTCAAAATGCACTACATTTATTTATTT
29	GTCTTGAGCAAATAGCAGGTGACATTAG TGAGTCGTGAGGTTATAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTAG TGAGTCGTGAGGTTATATTTATTTATTT

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
30	GTCTTGAGCAAATAGCAGGTGACACATC CTTGTTATCCGGTTGTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATC CTTGTTATCCGGTTGTATTTATTTATTT
31	GTCTTGAGCAAATAGCAGGTGACACGAA TGGTTACTTACGGTCCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAA TGGTTACTTACGGTCCATTTATTTATTT
32	GTCTTGAGCAAATAGCAGGTGACACTAG ATGGTACTCGTCACACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAG ATGGTACTCGTCACACATTTATTTATTT
33	GTCTTGAGCAAATAGCAGGTGACAGGTA CGTGCAATGACTCTACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGGTA CGTGCAATGACTCTACATTTATTTATTT
34	GTCTTGAGCAAATAGCAGGTGACAATCG CAAGAAGTAACACGTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATCG CAAGAAGTAACACGTAATTTATTTATTT
35	GTCTTGAGCAAATAGCAGGTGACACTAA CTGTACTATCCGCCTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAA CTGTACTATCCGCCTGATTTATTTATTT
36	GTCTTGAGCAAATAGCAGGTGACAAGTA AGAGGAGTGCCTTATTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGTA AGAGGAGTGCCTTATTATTTATTTATTT
37	GTCTTGAGCAAATAGCAGGTGACATTAA GTGACCTGGAGGATATAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTAA GTGACCTGGAGGATATATTTATTTATTT
38	GTCTTGAGCAAATAGCAGGTGACACCGG ATTGTAAAGTGTCTCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCGG ATTGTAAAGTGTCTCAATTTATTTATTT
39	GTCTTGAGCAAATAGCAGGTGACACGAT TACCTCATATGCCTCTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAT TACCTCATATGCCTCTATTTATTTATTT
40	GTCTTGAGCAAATAGCAGGTGACAAAGT TGCTAGTGGTGATCTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAAGT TGCTAGTGGTGATCTAATTTATTTATTT
41	GTCTTGAGCAAATAGCAGGTGACACTTC CTATTGATCCGAGAGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTTC CTATTGATCCGAGAGGATTTATTTATTT
42	GTCTTGAGCAAATAGCAGGTGACAAATA CTTGCCAACACACTTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAATA CTTGCCAACACACTTCATTTATTTATTT
43	GTCTTGAGCAAATAGCAGGTGACAACCT ATCAACACACCGTTAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACCT ATCAACACACCGTTAAATTTATTTATTT
44	GTCTTGAGCAAATAGCAGGTGACACCTA GTGTCCAGACAATGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCTA GTGTCCAGACAATGAGATTTATTTATTT
45	GTCTTGAGCAAATAGCAGGTGACACTCA GTGGATGCGATGAATTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTCA GTGGATGCGATGAATTATTTATTTATTT
46	GTCTTGAGCAAATAGCAGGTGACACCAG TCTCTTAAGATGCCAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCAG TCTCTTAAGATGCCAAATTTATTTATTT
47	GTCTTGAGCAAATAGCAGGTGACATCGA GTATCAACATGGAACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCGA GTATCAACATGGAACCATTTATTTATTT
48	GTCTTGAGCAAATAGCAGGTGACAAGGA TAAGGACTTATGTGCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGGA TAAGGACTTATGTGCGATTTATTTATTT
49	GTCTTGAGCAAATAGCAGGTGACATCAT CCAGGTTAATGACGACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCAT CCAGGTTAATGACGACATTTATTTATTT
50	GTCTTGAGCAAATAGCAGGTGACATAGT TATCGCTACTGTGGAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTAGT TATCGCTACTGTGGAAATTTATTTATTT
51	GTCTTGAGCAAATAGCAGGTGACATTAC ACCAACGTGCTGTAAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTAC ACCAACGTGCTGTAAGATTTATTTATTT
52	GTCTTGAGCAAATAGCAGGTGACACCAC GGTCTACGATCATAAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCAC GGTCTACGATCATAAGATTTATTTATTT
53	GTCTTGAGCAAATAGCAGGTGACAAACA ATCGTGTGGAATACTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACA ATCGTGTGGAATACTCATTTATTTATTT
54	GTCTTGAGCAAATAGCAGGTGACACGAG AAGAGAGTCGTTCCTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAG AAGAGAGTCGTTCCTAATTTATTTATTT
55	GTCTTGAGCAAATAGCAGGTGACAATCG ACAACTCTATTGCATGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATCG ACAACTCTATTGCATGATTTATTTATTT
56	GTCTTGAGCAAATAGCAGGTGACAAGCC AATTACACAAGGTAGTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGCC AATTACACAAGGTAGTATTTATTTATTT
57	GTCTTGAGCAAATAGCAGGTGACAGTCG TCGTTGTCGACATTAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTCG TCGTTGTCGACATTAGATTTATTTATTT
58	GTCTTGAGCAAATAGCAGGTGACACGAC TAGGAGTAGGTTAGGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAC TAGGAGTAGGTTAGGAATTTATTTATTT

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
59	GTCTTGAGCAAATAGCAGGTGACATTGA ATCGCAAATCGACTCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTGA ATCGCAAATCGACTCAATTTATTTATTT
60	GTCTTGAGCAAATAGCAGGTGACAACAA CCAGTATGGTATTCGTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAA CCAGTATGGTATTCGTATTTATTTATTT
61	GTCTTGAGCAAATAGCAGGTGACATGGA TTCAAGGCATAGTACAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTGGA TTCAAGGCATAGTACAATTTATTTATTT
62	GTCTTGAGCAAATAGCAGGTGACACATC TCACGGCTTAGTTACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATC TCACGGCTTAGTTACCATTTATTTATTT
63	GTCTTGAGCAAATAGCAGGTGACAGTTA GGAATGAGCCAAGGAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTTA GGAATGAGCCAAGGAAATTTATTTATTT
64	GTCTTGAGCAAATAGCAGGTGACACGTC GGATGTAAGATAGAGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGTC GGATGTAAGATAGAGCATTTATTTATTT
65	GTCTTGAGCAAATAGCAGGTGACACACC AATAACGTGAACTGTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCACC AATAACGTGAACTGTGATTTATTTATTT
66	GTCTTGAGCAAATAGCAGGTGACACACG TTCAGAACATTCTCTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCACG TTCAGAACATTCTCTCATTTATTTATTT
67	GTCTTGAGCAAATAGCAGGTGACATAGT CGCTCTATTGTGAACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTAGT CGCTCTATTGTGAACCATTTATTTATTT
68	GTCTTGAGCAAATAGCAGGTGACACTTG TTGAGATACCTCGACAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTTG TTGAGATACCTCGACAATTTATTTATTT
69	GTCTTGAGCAAATAGCAGGTGACATTCT GGTATGTTCAACAAGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTCT GGTATGTTCAACAAGCATTTATTTATTT
70	GTCTTGAGCAAATAGCAGGTGACAAAGC TCAGTTTGTTCAGAGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAAGC TCAGTTTGTTCAGAGGATTTATTTATTT
71	GTCTTGAGCAAATAGCAGGTGACACCGG TTATTACCTACCTGTTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCGG TTATTACCTACCTGTTATTTATTTATTT
72	GTCTTGAGCAAATAGCAGGTGACACGAC TTATTGAGTCATTGCCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAC TTATTGAGTCATTGCCATTTATTTATTT
73	GTCTTGAGCAAATAGCAGGTGACAGATA CGTCTATTGAACACCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGATA CGTCTATTGAACACCGATTTATTTATTT
74	GTCTTGAGCAAATAGCAGGTGACAATCT GAGTACCGAATAGTCCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATCT GAGTACCGAATAGTCCATTTATTTATTT
75	GTCTTGAGCAAATAGCAGGTGACAGTGT TGATGGACGTAGTTGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTGT TGATGGACGTAGTTGAATTTATTTATTT
76	GTCTTGAGCAAATAGCAGGTGACAAACA GAGTGATTGTCAGTTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACA GAGTGATTGTCAGTTCATTTATTTATTT
77	GTCTTGAGCAAATAGCAGGTGACACTAT ATGAGGGGTTGCTCTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAT ATGAGGGGTTGCTCTCATTTATTTATTT
78	GTCTTGAGCAAATAGCAGGTGACACACT AGAACCCTGCTTATGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCACT AGAACCCTGCTTATGCATTTATTTATTT
79	GTCTTGAGCAAATAGCAGGTGACATCAG GTTCTAGATGGTCTTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCAG GTTCTAGATGGTCTTCATTTATTTATTT
80	GTCTTGAGCAAATAGCAGGTGACAGCAA GACTATCGCCTAGTTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGCAA GACTATCGCCTAGTTCATTTATTTATTT
81	GTCTTGAGCAAATAGCAGGTGACAAGTG GTGATTACATTAGCCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGTG GTGATTACATTAGCCAATTTATTTATTT
82	GTCTTGAGCAAATAGCAGGTGACAAGGA TTGAACGAAGCTGTTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGGA TTGAACGAAGCTGTTAATTTATTTATTT
83	GTCTTGAGCAAATAGCAGGTGACAATTG TGTTGCGAGTACGATAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATTG TGTTGCGAGTACGATAATTTATTTATTT
84	GTCTTGAGCAAATAGCAGGTGACAGTAC GAATAGACACTCGCTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTAC GAATAGACACTCGCTGATTTATTTATTT
85	GTCTTGAGCAAATAGCAGGTGACAAGAA CATTGGTTCGGATTGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGAA CATTGGTTCGGATTGAATTTATTTATTT
86	GTCTTGAGCAAATAGCAGGTGACAGTTG TACGCTTTACGTTGTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTTG TACGCTTTACGTTGTGATTTATTTATTT
87	GTCTTGAGCAAATAGCAGGTGACATAGC ACGATTAGATCGGAATAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTAGC ACGATTAGATCGGAATATTTATTTATTT

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
88	GTCTTGAGCAAATAGCAGGTGACACTCA AGCTCATAGTACCTGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTCA AGCTCATAGTACCTGAATTTATTTATTT
89	GTCTTGAGCAAATAGCAGGTGACACATG TAAGACGACTTACGTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATG TAAGACGACTTACGTGATTTATTTATTT
90	GTCTTGAGCAAATAGCAGGTGACATTCG CAATGGATAAGTCTCCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTCG CAATGGATAAGTCTCCATTTATTTATTT
91	GTCTTGAGCAAATAGCAGGTGACAGACA CAATACACACCACTCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGACA CAATACACACCACTCAATTTATTTATTT
92	GTCTTGAGCAAATAGCAGGTGACACTAT CGAGAAAAGTACGCCTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAT CGAGAAAAGTACGCCTATTTATTTATTT
93	GTCTTGAGCAAATAGCAGGTGACATCAC TGGTTACCTTCAATCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCAC TGGTTACCTTCAATCAATTTATTTATTT
94	GTCTTGAGCAAATAGCAGGTGACAAGTT GCATGTGGATTCACTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGTT GCATGTGGATTCACTAATTTATTTATTT
95	GTCTTGAGCAAATAGCAGGTGACACACT AGATTGCTCCAGTACAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCACT AGATTGCTCCAGTACAATTTATTTATTT
96	GTCTTGAGCAAATAGCAGGTGACAGGTT ATGTGGATAGCTTGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGGTT ATGTGGATAGCTTGAGATTTATTTATTT
97	GTCTTGAGCAAATAGCAGGTGACATTGT CTCGAAAGACGTAAGTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTGT CTCGAAAGACGTAAGTATTTATTTATTT
98	GTCTTGAGCAAATAGCAGGTGACAACCA CCAATTGATGATTGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACCA CCAATTGATGATTGAGATTTATTTATTT
99	GTCTTGAGCAAATAGCAGGTGACAATTA CACTCCGTCCAAGTAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATTA CACTCCGTCCAAGTAAATTTATTTATTT
100	GTCTTGAGCAAATAGCAGGTGACAACGG TACTGTCTAAGATTGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACGG TACTGTCTAAGATTGCATTTATTTATTT
101	GTCTTGAGCAAATAGCAGGTGACAAGAA CTCACAATTCTGATGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGAA CTCACAATTCTGATGGATTTATTTATTT
102	GTCTTGAGCAAATAGCAGGTGACATATA AGCACCATGAGGACTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTATA AGCACCATGAGGACTAATTTATTTATTT
103	GTCTTGAGCAAATAGCAGGTGACACACT ACGTCCTATACCTCCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCACT ACGTCCTATACCTCCAATTTATTTATTT
104	GTCTTGAGCAAATAGCAGGTGACAGCTT ACACTAGAAGCCGAAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGCTT ACACTAGAAGCCGAAGATTTATTTATTT
105	GTCTTGAGCAAATAGCAGGTGACAACAT TGAGAGCATTGTACCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAT TGAGAGCATTGTACCAATTTATTTATTT
106	GTCTTGAGCAAATAGCAGGTGACACACC TCGTAGTGCGTTATAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCACC TCGTAGTGCGTTATAGATTTATTTATTT
107	GTCTTGAGCAAATAGCAGGTGACACGAT GTAGCAACGAATCATCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAT GTAGCAACGAATCATCATTTATTTATTT
108	GTCTTGAGCAAATAGCAGGTGACACGAG GTGTAATAAGTTCGCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAG GTGTAATAAGTTCGCAATTTATTTATTT
109	GTCTTGAGCAAATAGCAGGTGACAGTCA TCAAGACGGTTATCGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTCA TCAAGACGGTTATCGGATTTATTTATTT
110	GTCTTGAGCAAATAGCAGGTGACAATCC TTGCAGATAACGTAGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATCC TTGCAGATAACGTAGGATTTATTTATTT
111	GTCTTGAGCAAATAGCAGGTGACAAACT GATCTGCGCTAATGAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACT GATCTGCGCTAATGAAATTTATTTATTT
112	GTCTTGAGCAAATAGCAGGTGACAGAGG TCTGGAAGTAACCTTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAGG TCTGGAAGTAACCTTCATTTATTTATTT
113	GTCTTGAGCAAATAGCAGGTGACAACCA AGTATCCACTGACATAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACCA AGTATCCACTGACATAATTTATTTATTT
114	GTCTTGAGCAAATAGCAGGTGACAACGA ACCTAAAGCGTGTTAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACGA ACCTAAAGCGTGTTAAATTTATTTATTT
115	GTCTTGAGCAAATAGCAGGTGACAATAC TACGAGAACTTCCGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATAC TACGAGAACTTCCGAGATTTATTTATTT
116	GTCTTGAGCAAATAGCAGGTGACAGTGG ATCGAATGTTCTGACTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTGG ATCGAATGTTCTGACTATTTATTTATTT

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
117	GTCTTGAGCAAATAGCAGGTGACAAATG TCCTTGATGTGACTCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAATG TCCTTGATGTGACTCGATTTATTTATTT
118	GTCTTGAGCAAATAGCAGGTGACACGGT AGGTTCGAACTTGTACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGGT AGGTTCGAACTTGTACATTTATTTATTT
119	GTCTTGAGCAAATAGCAGGTGACAGAGT TCAGCAGTATCGTAGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAGT TCAGCAGTATCGTAGCATTTATTTATTT
120	GTCTTGAGCAAATAGCAGGTGACATAGA CAGACTATACGTGTCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTAGA CAGACTATACGTGTCGATTTATTTATTT
121	GTCTTGAGCAAATAGCAGGTGACAAAGA CCTCAAAACGGATGTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAAGA CCTCAAAACGGATGTCATTTATTTATTT
122	GTCTTGAGCAAATAGCAGGTGACAAGTA AGATCCCTAATACGCTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGTA AGATCCCTAATACGCTATTTATTTATTT
123	GTCTTGAGCAAATAGCAGGTGACATCTA GCCAAGTACGCTTAGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCTA GCCAAGTACGCTTAGAATTTATTTATTT
124	GTCTTGAGCAAATAGCAGGTGACAATAT CAGTCCAGGAACAGTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATAT CAGTCCAGGAACAGTCATTTATTTATTT
125	GTCTTGAGCAAATAGCAGGTGACATGTA GTGTTCCTTCTATCCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTGTA GTGTTCCTTCTATCCGATTTATTTATTT
126	GTCTTGAGCAAATAGCAGGTGACACTAA CCACTAGGACTAGCTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAA CCACTAGGACTAGCTCATTTATTTATTT
127	GTCTTGAGCAAATAGCAGGTGACACGCA TTGATAATCCGCTACAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGCA TTGATAATCCGCTACAATTTATTTATTT
128	GTCTTGAGCAAATAGCAGGTGACAAATC ATCGACGAACAGCTAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAATC ATCGACGAACAGCTAAATTTATTTATTT
129	GTCTTGAGCAAATAGCAGGTGACAAGGA TACTACGAAGAATGGTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGGA TACTACGAAGAATGGTATTTATTTATTT
130	GTCTTGAGCAAATAGCAGGTGACATCGT AAGGAAGTAGACTGAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCGT AAGGAAGTAGACTGAAATTTATTTATTT
131	GTCTTGAGCAAATAGCAGGTGACAAACG TACTAGATGGTGACAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACG TACTAGATGGTGACAGATTTATTTATTT
132	GTCTTGAGCAAATAGCAGGTGACAAACC GTATTCCAGGTTACAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACC GTATTCCAGGTTACAAATTTATTTATTT
133	GTCTTGAGCAAATAGCAGGTGACAAACA CAAGAGAGAATACGCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACA CAAGAGAGAATACGCAATTTATTTATTT
134	GTCTTGAGCAAATAGCAGGTGACAGAGG TATATCCGGTGATACAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAGG TATATCCGGTGATACAATTTATTTATTT
135	GTCTTGAGCAAATAGCAGGTGACAGCTT CTAATGACGGTCCATTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGCTT CTAATGACGGTCCATTATTTATTTATTT
136	GTCTTGAGCAAATAGCAGGTGACAAAGA TTCAGGCCAACTATTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAAGA TTCAGGCCAACTATTCATTTATTTATTT
137	GTCTTGAGCAAATAGCAGGTGACAATAA CATCGCTAGTAAGCGTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATAA CATCGCTAGTAAGCGTATTTATTTATTT
138	GTCTTGAGCAAATAGCAGGTGACACCTC TAATACCTAACCTCGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCTC TAATACCTAACCTCGGATTTATTTATTT
139	GTCTTGAGCAAATAGCAGGTGACACGCT ATGGTATCGGATCTTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGCT ATGGTATCGGATCTTAATTTATTTATTT
140	GTCTTGAGCAAATAGCAGGTGACACATA ACAGACTTGTTCCAGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATA ACAGACTTGTTCCAGCATTTATTTATTT
141	GTCTTGAGCAAATAGCAGGTGACAGCCT CTGCTTCCTTATATGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGCCT CTGCTTCCTTATATGGATTTATTTATTT
142	GTCTTGAGCAAATAGCAGGTGACACCAC TCATCGTAAGTCATGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCAC TCATCGTAAGTCATGGATTTATTTATTT
143	GTCTTGAGCAAATAGCAGGTGACAGAAC ACCACAGTGAATACCTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAAC ACCACAGTGAATACCTATTTATTTATTT
144	GTCTTGAGCAAATAGCAGGTGACAAGCG AAGATTGTCTACTGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGCG AAGATTGTCTACTGAGATTTATTTATTT
145	GTCTTGAGCAAATAGCAGGTGACACGCA CATGGACTGTAGTATGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGCA CATGGACTGTAGTATGATTTATTTATTT

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
146	GTCTTGAGCAAATAGCAGGTGACACGAA TTGACGGAAGTGAGTTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAA TTGACGGAAGTGAGTTATTTATTTATTT
147	GTCTTGAGCAAATAGCAGGTGACACGAG GAGTCTATTGATAGCCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGAG GAGTCTATTGATAGCCATTTATTTATTT
148	GTCTTGAGCAAATAGCAGGTGACACTAC GAGTGACACAGGTATAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAC GAGTGACACAGGTATAATTTATTTATTT
149	GTCTTGAGCAAATAGCAGGTGACATCGG AATAGAATAGCGGATCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCGG AATAGAATAGCGGATCATTTATTTATTT
150	GTCTTGAGCAAATAGCAGGTGACATACA TCTCCGGAACGTATGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTACA TCTCCGGAACGTATGAATTTATTTATTT
151	GTCTTGAGCAAATAGCAGGTGACAATCA ATCACCCCTATTCACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATCA ATCACCCCTATTCACCATTTATTTATTT
152	GTCTTGAGCAAATAGCAGGTGACATCTG TGTTACATCTAAGCGTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCTG TGTTACATCTAAGCGTATTTATTTATTT
153	GTCTTGAGCAAATAGCAGGTGACATCGA TGACCAAATACCGAAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCGA TGACCAAATACCGAAGATTTATTTATTT
154	GTCTTGAGCAAATAGCAGGTGACATACT CATGTGGTAGGTCAATAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTACT CATGTGGTAGGTCAATATTTATTTATTT
155	GTCTTGAGCAAATAGCAGGTGACAATTC TCCAAGGCCTACAATGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATTC TCCAAGGCCTACAATGATTTATTTATTT
156	GTCTTGAGCAAATAGCAGGTGACAGAGC CTATGTTTAGGTACGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGAGC CTATGTTTAGGTACGCATTTATTTATTT
157	GTCTTGAGCAAATAGCAGGTGACAATGT GTCAAGGTATCACATGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATGT GTCAAGGTATCACATGATTTATTTATTT
158	GTCTTGAGCAAATAGCAGGTGACATACC TGATGAAGTGATGCAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTACC TGATGAAGTGATGCAAATTTATTTATTT
159	GTCTTGAGCAAATAGCAGGTGACACATA AGGTCATGTGCTTGAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATA AGGTCATGTGCTTGAAATTTATTTATTT
160	GTCTTGAGCAAATAGCAGGTGACACTGT GACGGATGACAATACGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTGT GACGGATGACAATACGATTTATTTATTT
161	GTCTTGAGCAAATAGCAGGTGACACCAT GAAGGAAACAGTAGCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCAT GAAGGAAACAGTAGCAATTTATTTATTT
162	GTCTTGAGCAAATAGCAGGTGACAGACA CTCGAAAAGGTAACTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGACA CTCGAAAAGGTAACTCATTTATTTATTT
163	GTCTTGAGCAAATAGCAGGTGACATTGT TGCTACAACAGACCTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTTGT TGCTACAACAGACCTAATTTATTTATTT
164	GTCTTGAGCAAATAGCAGGTGACATAGT GGTTGGCTCCTCTATAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTAGT GGTTGGCTCCTCTATAATTTATTTATTT
165	GTCTTGAGCAAATAGCAGGTGACACATC CATTCCCAATACCATCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATC CATTCCCAATACCATCATTTATTTATTT
166	GTCTTGAGCAAATAGCAGGTGACAAAGA CGGTATTTCTCAACCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAAGA CGGTATTTCTCAACCGATTTATTTATTT
167	GTCTTGAGCAAATAGCAGGTGACAATAG CTCAACACTGTTGTGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATAG CTCAACACTGTTGTGAATTTATTTATTT
168	GTCTTGAGCAAATAGCAGGTGACAACAT CCAAGACTCTAGGTGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAT CCAAGACTCTAGGTGAATTTATTTATTT
169	GTCTTGAGCAAATAGCAGGTGACAAAGA GGTCGAGATATGAACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAAGA GGTCGAGATATGAACCATTTATTTATTT
170	GTCTTGAGCAAATAGCAGGTGACAGATC GACGTAATTCCATGAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGATC GACGTAATTCCATGAGATTTATTTATTT
171	GTCTTGAGCAAATAGCAGGTGACAACAA TACTCCTGCACCATATAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAA TACTCCTGCACCATATATTTATTTATTT
172	GTCTTGAGCAAATAGCAGGTGACACTAG GACCATGATGTAATGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAG GACCATGATGTAATGCATTTATTTATTT
173	GTCTTGAGCAAATAGCAGGTGACAATGG ATTCTCCTCGAAGTTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATGG ATTCTCCTCGAAGTTGATTTATTTATTT
174	GTCTTGAGCAAATAGCAGGTGACACATG TCGAATAAGACCGACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATG TCGAATAAGACCGACCATTTATTTATTT

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
175	GTCTTGAGCAAATAGCAGGTGACAGTGT GTGTACAACAACAACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTGT GTGTACAACAACAACCATTTATTTATTT
176	GTCTTGAGCAAATAGCAGGTGACAGATA TACGGAACTCCACGTTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGATA TACGGAACTCCACGTTATTTATTTATTT
177	GTCTTGAGCAAATAGCAGGTGACACCTA AGATACCATGGTCCTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCTA AGATACCATGGTCCTAATTTATTTATTT
178	GTCTTGAGCAAATAGCAGGTGACACCTA CTCGGAGTAACAATCCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCTA CTCGGAGTAACAATCCATTTATTTATTT
179	GTCTTGAGCAAATAGCAGGTGACAACAC TATTGCAGCTTGATTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAC TATTGCAGCTTGATTCATTTATTTATTT
180	GTCTTGAGCAAATAGCAGGTGACACCTA ATGCGTCGTAATTGTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCTA ATGCGTCGTAATTGTGATTTATTTATTT
181	GTCTTGAGCAAATAGCAGGTGACAACAA CACAACAGCAGTTCTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAA CACAACAGCAGTTCTAATTTATTTATTT
182	GTCTTGAGCAAATAGCAGGTGACACTAT GCCGTTACTGGAATTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAT GCCGTTACTGGAATTGATTTATTTATTT
183	GTCTTGAGCAAATAGCAGGTGACATACA CAAGTCCAACATCAGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTACA CAAGTCCAACATCAGAATTTATTTATTT
184	GTCTTGAGCAAATAGCAGGTGACAAGAA CCGTGTAAGTGGATACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGAA CCGTGTAAGTGGATACATTTATTTATTT
185	GTCTTGAGCAAATAGCAGGTGACATCAC ACAGAAGGTGATAGTTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTCAC ACAGAAGGTGATAGTTATTTATTTATTT
186	GTCTTGAGCAAATAGCAGGTGACAACAT AAGTGGCGCTCTTATCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAT AAGTGGCGCTCTTATCATTTATTTATTT
187	GTCTTGAGCAAATAGCAGGTGACAAAGC CACATGATAGTAGACCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAAGC CACATGATAGTAGACCATTTATTTATTT
188	GTCTTGAGCAAATAGCAGGTGACAAACG AGCTTAGTGTCCAATAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAACG AGCTTAGTGTCCAATAATTTATTTATTT
189	GTCTTGAGCAAATAGCAGGTGACATGAC AAGCAAATTGAGAAGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTGAC AAGCAAATTGAGAAGGATTTATTTATTT
190	GTCTTGAGCAAATAGCAGGTGACACTCC AGTGTTGGAATACAGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTCC AGTGTTGGAATACAGAATTTATTTATTT
191	GTCTTGAGCAAATAGCAGGTGACAAGCA CACTAAGAGAAGTTGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGCA CACTAAGAGAAGTTGGATTTATTTATTT
192	GTCTTGAGCAAATAGCAGGTGACAACAA CGACTTTCTAGTCCTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACAA CGACTTTCTAGTCCTCATTTATTTATTT
193	GTCTTGAGCAAATAGCAGGTGACAGTGT GACTTATTCACCGAGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGTGT GACTTATTCACCGAGAATTTATTTATTT
194	GTCTTGAGCAAATAGCAGGTGACACTAC AGCCGAATAGGTTCACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTAC AGCCGAATAGGTTCACATTTATTTATTT
195	GTCTTGAGCAAATAGCAGGTGACAATTA TCCGGTACCAATCCTTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATTA TCCGGTACCAATCCTTATTTATTTATTT
196	GTCTTGAGCAAATAGCAGGTGACAATGG TTAGTGAACCACGTACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATGG TTAGTGAACCACGTACATTTATTTATTT
197	GTCTTGAGCAAATAGCAGGTGACAACGA ATGTACTCTACCGTCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACGA ATGTACTCTACCGTCAATTTATTTATTT
198	GTCTTGAGCAAATAGCAGGTGACAGGAT GACCTACAAGACACTAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGGAT GACCTACAAGACACTAATTTATTTATTT
199	GTCTTGAGCAAATAGCAGGTGACACAGT GGACAATACAGGTCAGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCAGT GGACAATACAGGTCAGATTTATTTATTT
200	GTCTTGAGCAAATAGCAGGTGACACGTG CGTAGATTGCTAGATGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCGTG CGTAGATTGCTAGATGATTTATTTATTT
201	GTCTTGAGCAAATAGCAGGTGACAGCAC ATTCTTTTCAGATCCAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGCAC ATTCTTTTCAGATCCAATTTATTTATTT
202	GTCTTGAGCAAATAGCAGGTGACAAATA GCAGAGTCGCGTATTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAATA GCAGAGTCGCGTATTGATTTATTTATTT
203	GTCTTGAGCAAATAGCAGGTGACACTGG TAGGAAGATCCTCAGAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTGG TAGGAAGATCCTCAGAATTTATTTATTT

Location ID	Barcoded recording primer type 'a'	Barcoded recording primer type 'a*'
204	GTCTTGAGCAAATAGCAGGTGACACTTA GACACATGTGCGAGTTAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCTTA GACACATGTGCGAGTTATTTATTTATTT
205	GTCTTGAGCAAATAGCAGGTGACACATG AGTAACTGTCGGTCACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCATG AGTAACTGTCGGTCACATTTATTTATTT
206	GTCTTGAGCAAATAGCAGGTGACAAATG TCGTACGCAATGTATCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAATG TCGTACGCAATGTATCATTTATTTATTT
207	GTCTTGAGCAAATAGCAGGTGACAAGAA TTGCTCGGTGTCATACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGAGAA TTGCTCGGTGTCATACATTTATTTATTT
208	GTCTTGAGCAAATAGCAGGTGACAACCG TTCGATATTAGAGCTGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACCG TTCGATATTAGAGCTGATTTATTTATTT
209	GTCTTGAGCAAATAGCAGGTGACATATA CTGCGGTTGTCATAGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGTATA CTGCGGTTGTCATAGCATTTATTTATTT
210	GTCTTGAGCAAATAGCAGGTGACAACTT GTCTACACAACAATGCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACTT GTCTACACAACAATGCATTTATTTATTT
211	GTCTTGAGCAAATAGCAGGTGACAGACC GTTGTTCAATCAGTTCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGACC GTTGTTCAATCAGTTCATTTATTTATTT
212	GTCTTGAGCAAATAGCAGGTGACACCTG TCATTGAATGTTCCACAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGCCTG TCATTGAATGTTCCACATTTATTTATTT
213	GTCTTGAGCAAATAGCAGGTGACAACCA CTTGAACATTGATTCGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGACCA CTTGAACATTGATTCGATTTATTTATTT
214	GTCTTGAGCAAATAGCAGGTGACAGGAG ACTTCGTGAACAGATCAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGGAG ACTTCGTGAACAGATCATTTATTTATTT
215	GTCTTGAGCAAATAGCAGGTGACAGGAG AAGATCTACCATGCAAAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGGGAG AAGATCTACCATGCAAATTTATTTATTT
216	GTCTTGAGCAAATAGCAGGTGACAATTG AACGTGTTGTATCTGGAAATAAATAAAT	TCCATCTTGTCTGTTAGCAAGCTGATTG AACGTGTTGTATCTGGATTTATTTATTT

Supplementary Table 4. Barcoded recording primers for pattern reconstruction experiments in Fig. 4.

Direction	Barcode ID	Inner Primers (5' to 3')	Outer Primers (5' to 3')
Forward	1	AAGAAAGTTGTCGGTGTCTTTGTG GTCTTGAGCAAATAGCAGGTGACA	AAGAAAGTTGTCGGTGTCTTTGTG
Forward	2	TCGATTCCGTTTGTAGTCGTCTGT GTCTTGAGCAAATAGCAGGTGACA	TCGATTCCGTTTGTAGTCGTCTGT
Forward	3	GAGTCTTGTGTCCCAGTTACCAGG GTCTTGAGCAAATAGCAGGTGACA	GAGTCTTGTGTCCCAGTTACCAGG
Forward	4	TTCGGATTCTATCGTGTTTCCCTA GTCTTGAGCAAATAGCAGGTGACA	TTCGGATTCTATCGTGTTTCCCTA
Forward	5	CTTGTCCAGGGTTTGTGTAACCTT GTCTTGAGCAAATAGCAGGTGACA	CTTGTCCAGGGTTTGTGTAACCTT
Forward	6	TTCTCGCAAAGGCAGAAAGTAGTC GTCTTGAGCAAATAGCAGGTGACA	TTCTCGCAAAGGCAGAAAGTAGTC
Forward	7	GTGTTACCGTGGGAATGAATCCTT GTCTTGAGCAAATAGCAGGTGACA	GTGTTACCGTGGGAATGAATCCTT
Forward	8	TTCAGGGAACAAACCAAGTTACGT GTCTTGAGCAAATAGCAGGTGACA	TTCAGGGAACAAACCAAGTTACGT
Forward	9	AACTAGGCACAGCGAGTCTTGGTT GTCTTGAGCAAATAGCAGGTGACA	AACTAGGCACAGCGAGTCTTGGTT
Forward	10	AAGCGTTGAAACCTTTGTCCTCTC GTCTTGAGCAAATAGCAGGTGACA	AAGCGTTGAAACCTTTGTCCTCTC
Forward	11	GTTTCATCTATCGGAGGGAATGGA GTCTTGAGCAAATAGCAGGTGACA	GTTTCATCTATCGGAGGGAATGGA
Forward	12	CAGGTAGAAAGAAGCAGAATCGGA GTCTTGAGCAAATAGCAGGTGACA	CAGGTAGAAAGAAGCAGAATCGGA
Forward	13	AGAACGACTTCCATACTCGTGTGA GTCTTGAGCAAATAGCAGGTGACA	AGAACGACTTCCATACTCGTGTGA
Forward	14	AACGAGTCTCTTGGGACCCATAGA GTCTTGAGCAAATAGCAGGTGACA	AACGAGTCTCTTGGGACCCATAGA
Forward	15	AGGTCTACCTCGCTAACACCACTG GTCTTGAGCAAATAGCAGGTGACA	AGGTCTACCTCGCTAACACCACTG
Forward	16	CGTCAACTGACAGTGGTTCGTACT GTCTTGAGCAAATAGCAGGTGACA	CGTCAACTGACAGTGGTTCGTACT
Forward	17	ACCCTCCAGGAAAGTACCTCTGAT GTCTTGAGCAAATAGCAGGTGACA	ACCCTCCAGGAAAGTACCTCTGAT
Forward	18	CCAAACCCAACAACCTAGATAGGC GTCTTGAGCAAATAGCAGGTGACA	CCAAACCCAACAACCTAGATAGGC
Forward	19	GTTCCTCGTGCAGTGTCAAGAGAT GTCTTGAGCAAATAGCAGGTGACA	GTTCCTCGTGCAGTGTCAAGAGAT
Forward	20	TTGCGTCCTGTTACGAGAACTCAT GTCTTGAGCAAATAGCAGGTGACA	TTGCGTCCTGTTACGAGAACTCAT
Forward	21	GAGCCTCTCATTGTCCGTTCTCTA GTCTTGAGCAAATAGCAGGTGACA	GAGCCTCTCATTGTCCGTTCTCTA
Forward	22	ACCACTGCCATGTATCAAAGTACG GTCTTGAGCAAATAGCAGGTGACA	ACCACTGCCATGTATCAAAGTACG
Forward	23	CTTACTACCCAGTGAACCTCCTCG GTCTTGAGCAAATAGCAGGTGACA	CTTACTACCCAGTGAACCTCCTCG
Forward	24	GCATAGTTCTGCATGATGGGTTAG GTCTTGAGCAAATAGCAGGTGACA	GCATAGTTCTGCATGATGGGTTAG
Reverse	25	GTAAGTTGGGTATGCAACGCAATG TCCATCTTGTCTGTTAGCAAGCTG	GTAAGTTGGGTATGCAACGCAATG
Reverse	26	CATACAGCGACTACGCATTCTCAT TCCATCTTGTCTGTTAGCAAGCTG	CATACAGCGACTACGCATTCTCAT
Reverse	27	CGACGGTTAGATTCACCTCTTACA TCCATCTTGTCTGTTAGCAAGCTG	CGACGGTTAGATTCACCTCTTACA
Reverse	28	TGAAACCTAAGAAGGCACCGTATC TCCATCTTGTCTGTTAGCAAGCTG	TGAAACCTAAGAAGGCACCGTATC
Reverse	29	CTAGACACCTTGGGTTGACAGACC TCCATCTTGTCTGTTAGCAAGCTG	CTAGACACCTTGGGTTGACAGACC

Direction	Barcode ID	Inner Primers (5' to 3')	Outer Primers (5' to 3')
Reverse	30	TCAGTGAGGATCTACTTCGACCCA TCCATCTTGTCTGTTAGCAAGCTG	TCAGTGAGGATCTACTTCGACCCA
Reverse	31	TGCGTACAGCAATCAGTTACATTG TCCATCTTGTCTGTTAGCAAGCTG	TGCGTACAGCAATCAGTTACATTG
Reverse	32	CCAGTAGAAGTCCGACAACGTCAT TCCATCTTGTCTGTTAGCAAGCTG	CCAGTAGAAGTCCGACAACGTCAT
Reverse	33	CAGACTTGGTACGGTTGGGTAACT TCCATCTTGTCTGTTAGCAAGCTG	CAGACTTGGTACGGTTGGGTAACT
Reverse	34	GGACGAAGAACTCAAGTCAAAGGC TCCATCTTGTCTGTTAGCAAGCTG	GGACGAAGAACTCAAGTCAAAGGC
Reverse	35	CTACTTACGAAGCTGAGGGACTGC TCCATCTTGTCTGTTAGCAAGCTG	CTACTTACGAAGCTGAGGGACTGC
Reverse	36	ATGTCCCAGTTAGAGGAGGAAACA TCCATCTTGTCTGTTAGCAAGCTG	ATGTCCCAGTTAGAGGAGGAAACA
Reverse	37	GCTTGCGATTGATGCTTAGTATCA TCCATCTTGTCTGTTAGCAAGCTG	GCTTGCGATTGATGCTTAGTATCA
Reverse	38	ACCACAGGAGGACGATACAGAGAA TCCATCTTGTCTGTTAGCAAGCTG	ACCACAGGAGGACGATACAGAGAA
Reverse	39	CCACAGTGTCAACTAGAGCCTCTC TCCATCTTGTCTGTTAGCAAGCTG	CCACAGTGTCAACTAGAGCCTCTC
Reverse	40	TAGTTTGGATGACCAAGGATAGCC TCCATCTTGTCTGTTAGCAAGCTG	TAGTTTGGATGACCAAGGATAGCC
Reverse	41	GGAGTTCGTCCAGAGAAGTACACG TCCATCTTGTCTGTTAGCAAGCTG	GGAGTTCGTCCAGAGAAGTACACG
Reverse	42	CTACGTGTAAGGCATACCTGCCAG TCCATCTTGTCTGTTAGCAAGCTG	CTACGTGTAAGGCATACCTGCCAG
Reverse	43	CTTTCGTTGTTGACTCGACGGTAG TCCATCTTGTCTGTTAGCAAGCTG	CTTTCGTTGTTGACTCGACGGTAG
Reverse	44	AGTAGAAAGGGTTCCTTCCCACTC TCCATCTTGTCTGTTAGCAAGCTG	AGTAGAAAGGGTTCCTTCCCACTC
Reverse	45	GATCCAACAGAGATGCCTTCAGTG TCCATCTTGTCTGTTAGCAAGCTG	GATCCAACAGAGATGCCTTCAGTG
Reverse	46	GCTGTGTTCCACTTCATTCTCCTG TCCATCTTGTCTGTTAGCAAGCTG	GCTGTGTTCCACTTCATTCTCCTG
Reverse	47	GTGCAACTTTCCCACAGGTAGTTC TCCATCTTGTCTGTTAGCAAGCTG	GTGCAACTTTCCCACAGGTAGTTC
Reverse	48	CATCTGGAACGTGGTACACCTGTA TCCATCTTGTCTGTTAGCAAGCTG	CATCTGGAACGTGGTACACCTGTA

Supplementary Table 5. Inner and outer PCR primers for DNA nanoscope experiments in Fig. 4 and Fig. S4. Inner and outer primers in the same row are designed to be used together to PCR barcoded recording primers. Any 'forward' inner and outer primer pair can be used with any 'reverse' inner and outer primer pair to generate a unique sequencing library. Multiple such distinct libraries can be combined and run on the same sequencing chip. The sequence of the outer primer is used to demultiplex libraries.

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