

Supporting Information

Hierarchical assembly of DNA nanostructures based on four-way toehold mediated strand displacement

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S1 Designs	2
S1.1 SST units	2
S1.2 Higher-order structure from preformed units	4
S2 Methods	5
S2.1 Sample preparation.....	5
S2.2 AFM imaging	5
S2.3 Yield quantification by agarose gel electrophoresis and AFM	5
S2.4 Time course assay with fluorescent labeling.....	5
S3 Results.....	6
S3.1 Construction of SST units.....	6
S3.2 Construction of multi-unit strips	7
S3.2.1 Optimization of SST multimerization.....	7
S3.2.2 AFM imaging results	10
S3.2.3 Yield and cost comparison.....	16
S3.3 Verification and qualification of the toehold-mediated strand displacement	17
S3.3.1 Agarose gel electrophoresis results.....	17
S3.3.2 AFM imaging results	18
S4 Sequence information.....	19
S5 References.....	54

S1 Designs

S1.1 SST units

SST design used in this study is adopted from an earlier study¹. For a rectangular unit with protection tiles and connection tiles (Figure S1a), it consists of 424 component DNA strands. Based on the locations, those component DNA strands can be divided into three groups: core tiles (25 rows and 14 columns) including 322 center core tiles (in black) and 28 boundary core tiles on top and bottom rows (in green), connection tiles (12 or 13 on each side of an individual unit, in cyan) and protection tiles (24 on each side, in magenta). On the other hand, for a rectangular unit with terminal tiles (Figure S1b), it consists of 375 component DNA strands and can be divided into two groups: core tiles including 322 center core tiles (in black) and 28 boundary core tiles (in green) and terminal tiles (12 or 13 on each side, in red). A typical terminal unit of the multi-unit strip has terminal tiles on the terminal side and connection tiles and protection tiles on the connecting side.

A standard Z-shape center core tile is composed of four consecutive binding domains (10, 11, 10 and 11 nt), each of which pairs with the desired domain in one of the four neighboring tiles, while a boundary core tile at top or bottom boundary is composed of two domains (10 and 11 nt). A standard Z-shape terminal tile (10, 11, 10 and 11 nt) is also composed of four consecutive binding domains, with 10-nt ones complementary to domains in the core tiles while the unpaired two are eleven consecutive thymine nucleotides (T11). Similarly, a standard Z-shape connection tile (10, 11, 10 and 11 nt) is composed of four consecutive binding domains, with two domains complementary to those in the core tiles and the other two complementary to the domains in the respective protection tiles (or ultimately complementary to specific domains in the connection tiles of a matching unit). A protection tile has a binding domain (11 nt) to be complementary to that in a specific connection tile, followed by seven consecutive nucleotides with thymine (T7) or seven consecutive nucleotides with adenine (A7).

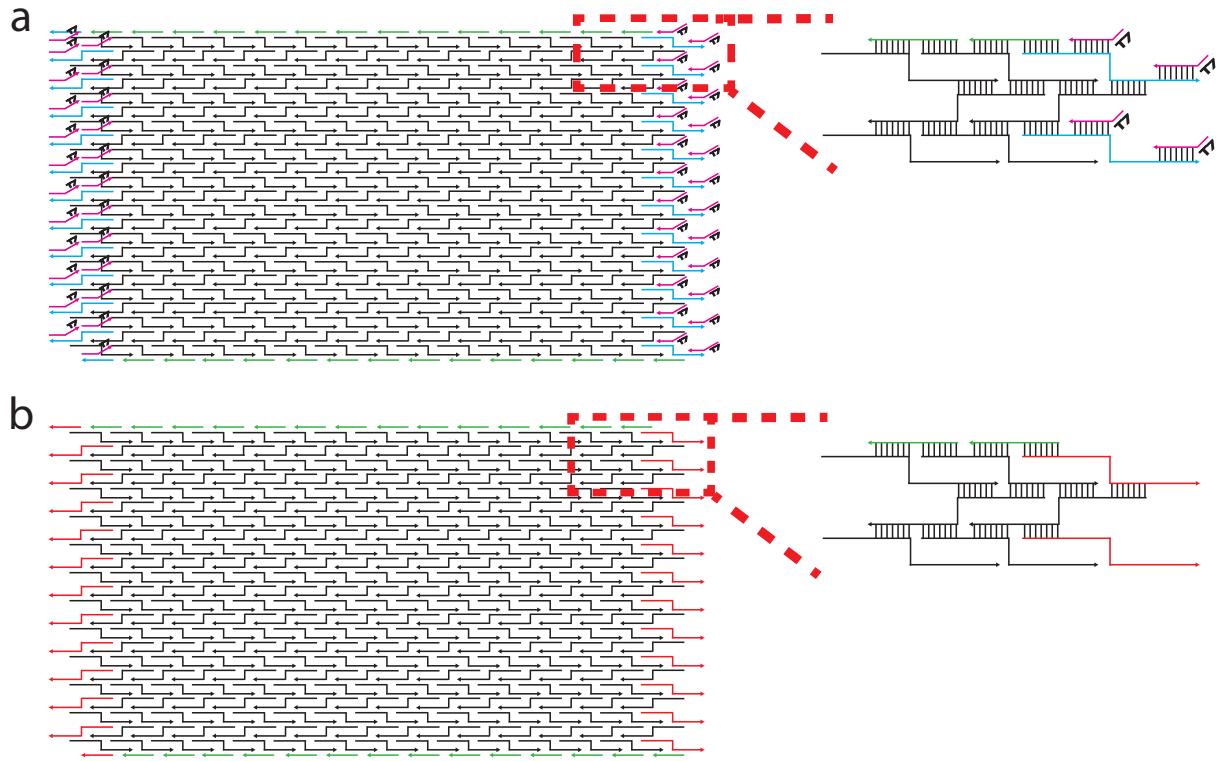


Figure S1. Schematic diagrams illustrating tile composition of SST units. (a) A rectangular unit with connection tiles and protection tiles. The center core tiles are in black, the boundary core tiles are in green, the connection tiles are in cyan, and the protection tiles are in magenta. (b) A rectangular unit with terminal tiles. The center core tiles are in black, the boundary tiles are in green and the terminal tiles are in red. Zoom-in views show the strand-level details (black bars depict domains of base pairs).

S1.2 Higher-order structure from preformed units

The core tiles were shared among preformed SST units while the connection tiles were specifically designed for individual units. Individual units were preformed in the first step with their sticky domains in the connection tiles covered by the protection tiles (Figure S2a), and in the successive step, T7 or A7 served as toe hold to mediate a four-way strand displacement event, gradually displacing the protection tiles and exposing the complementary connection tiles to combine matching units (Figure S2b).

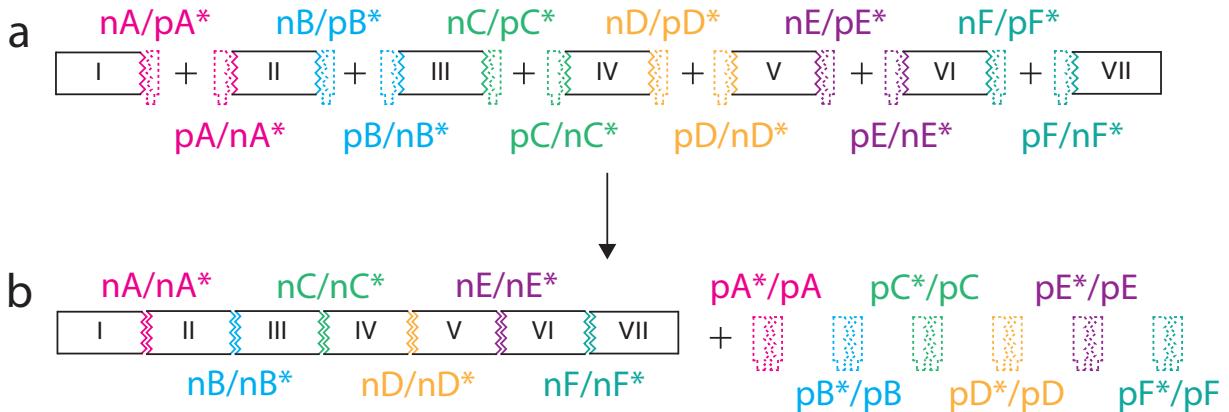


Figure S2. Schematic diagram of a seven-unit hierarchical assembly. When seven preformed units (a) are mixed together, they can form a seven-unit strip with displaced protection tiles as byproducts (b). Individual units are marked as I to VII. nX/nX^* depict the complementary connection tiles (solid lines) and pX/pX^* depict the complementary protection tiles (dash boxes with overhangs indicating T7 or A7 toe holds). The complementary connection/protection tiles are shown in the same colors and letters (A/A* in magenta, B/B* in cyan, C/C* in green, D/D* in orange, E/E* in purple, F/F* in turquoise).

S2 Methods

S2.1 Sample preparation

To assemble individual units, the component DNA strands were mixed in a roughly equimolar concentration of 300nM in 0.5× TBE buffer supplemented with 15mM MgCl₂. The mixtures were then subjected to an annealing from 90°C to 25°C over 17 hour or from 90°C to 10°C over 24 hour using a thermal cycler. The annealed products were subjected to 2% native agarose gel electrophoresis (gel prepared in 0.5× TBE buffer supplemented with 10mM MgCl₂ and pre-stained with SYBR safe) at 100 V in an ice water bath for analysis and purification. To purify the desired product from the gel, the resulted single dominant band containing the DNA construct was excised, crushed and centrifuged in Freeze N' Squeeze Extraction Spin column (Biorad) at 438 g for 4 min for collection. The purified samples were then imaged under AFM.

To assemble higher-order structures, the purified preformed units were mixed in a roughly equimolar concentration in 0.5× TBE buffer supplemented with 15 mM MgCl₂, and then subjected to an isothermal condition for 17 hr using a thermal cycler (e.g. 40°C for 17 hr). The annealed products were subjected to 1% native agarose gel electrophoresis (gel prepared in 0.5× TBE buffer supplemented with 10mM MgCl₂ and pre-stained with SYBR safe) at 100 V in an ice water bath. The resulted bands containing the desired higher-order structures were excised, collected and the purified samples were imaged under AFM.

S2.2 AFM imaging

The annealed samples were imaged using an SPM Multimode with Digital Instruments Nanoscope V controller (Vecco). A 5 μ l droplet of purified samples (or unpurified samples after dilution) and 50 μ l drop of 0.5× TBE supplemented with 15 mM Mg²⁺ were applied to a freshly cleaved mica surface. A general concentration around 10 nM would be preferred for AFM imaging. The images were captured under liquid tapping mode, with C-type triangular tips (resonant frequency, $f_0 = 40\text{-}75\text{kHz}$; spring constant, $k = 0.24\text{Nm}$) from the SNL-10 silicon nitride cantilever chip (Bruker Corporation).

S2.3 Yield quantification by agarose gel electrophoresis and AFM

The yield of a specific unit was estimated by using native agarose gel electrophoresis, pre-stained with SYBR Safe DNA stain, and the intensity of the target band was measured against the overall intensity of the entire lane. For example, the yield of seven-unit multimerization was estimated under AFM with the number of complete seven-unit strips ($\times 7$) divided by the total number of all identifiable units (11%).

S2.4 Time course assay with fluorescent labeling

To monitor the toehold-mediated strand displacement events during assembly, a time course experiment was performed in a trimeric system (trimer assembled from units 1, 2 and 3). One of the protection tiles of unit 1 was modified with FAM fluorophore. Samples from different time points were collected and subjected to agarose gel electrophoresis (post-stained with SYBR Gold). Fluorescent signal from FAM (before staining) or SYBR Gold (after staining) was recorded by a typhoon scanner.

S3 Results

S3.1 Construction of SST units

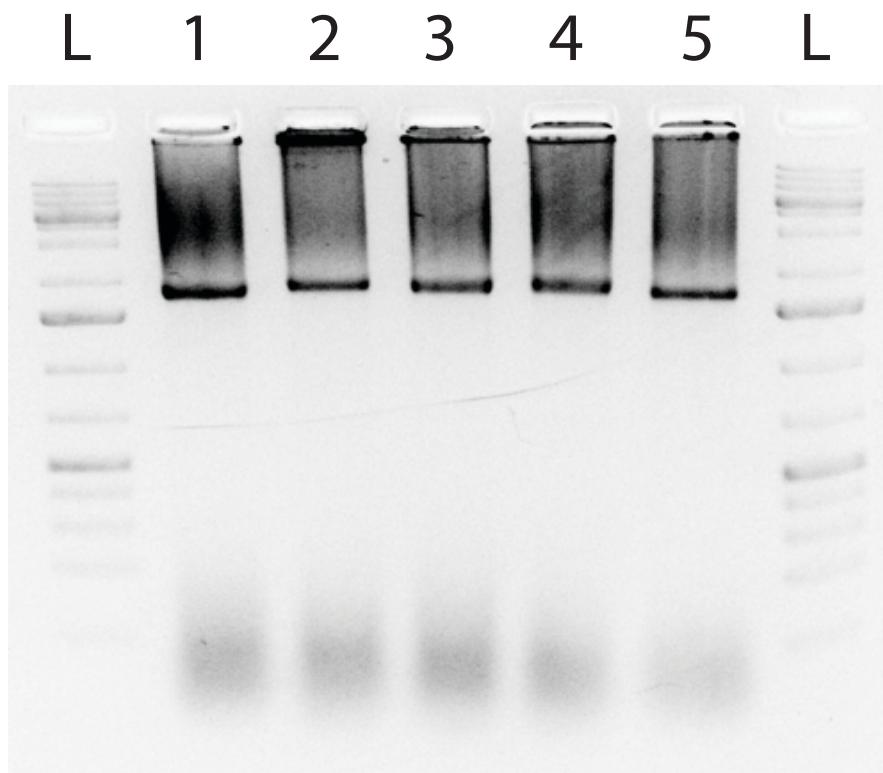


Figure S3. Native agarose gel electrophoresis results of individual SST units for five-unit strip (lane L: 1kb DNA ladder, lane 1: unit I, lane 2: unit II, lane 3: unit III, lane 4: unit IV, lane five: unit V). By comparing the intensity of the target band containing each SST unit against the overall amount of DNA loaded in each well, the yields of individual units were estimated to be 9%, 6%, 7%, 7% and 8% respectively (refer to S2.3).

S3.2 Construction of multi-unit strips

S3.2.1 Optimization of SST multimerization

In order to obtain optimal condition to assemble the preformed units into higher-order structures, isothermal temperatures ranging from 36°C to 48°C (36°C, 37°C, 40°C, 44°C, 45°C, 48°C) were tested (Figure S4), and according to five-unit multimerization, the formation of the desired product was encouraged under isothermal annealing temperatures ranging from 36 °C to 44 °C. Preformed units (after purification) with different number of connection tiles (Figure S5), different concentrations and different concentration ratio were also tested for trimerization (Figure S6).

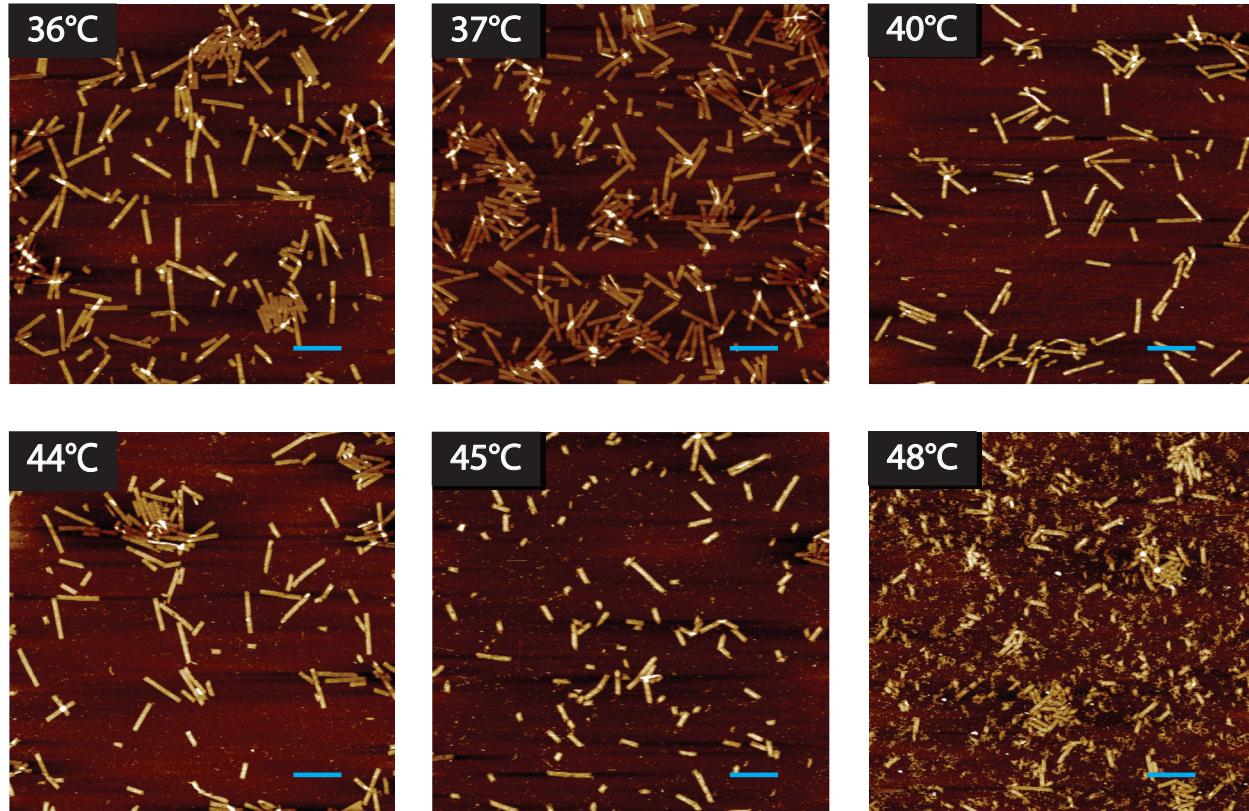


Figure S4. AFM results of five-unit strip under different isothermal annealing conditions. AFM results of six temperature points (36°C-48°C) showed different combination efficiency, and the formation of the desired product was encouraged under isothermal annealing temperatures ranging from 36 °C to 44 °C. Scar bars: 500 nm.

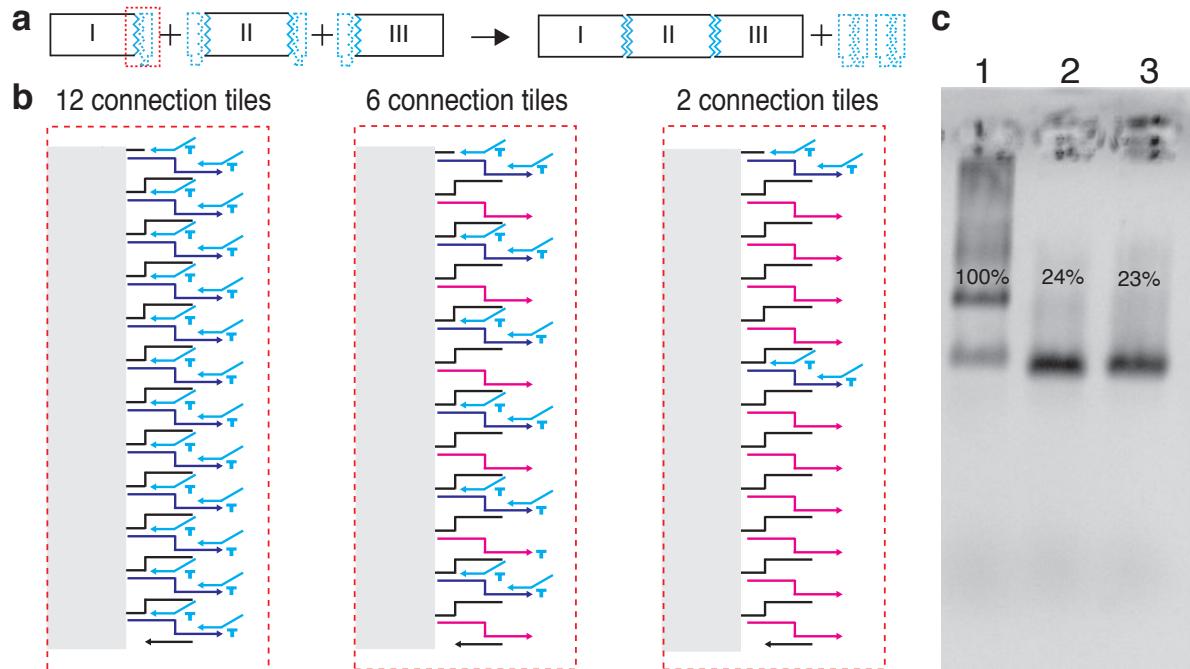


Figure S5. Trimerization from preformed units with different numbers of connection tiles in between matching units. (a) Schematic diagrams of trimerization from preformed units. (b) Red boxes in dashed line depict strand details of connection tiles and protection tiles. The connection tiles are in black, the protection tiles are in cyan, and the terminal tiles to replace the corresponding connection tiles are in magenta. Diagrams of 12, 6 and 2 connection tiles are shown in left, middle and right panels respectively. (c) Native agarose gel results of trimerization from preformed units with different numbers of connection tiles. Lane 1: trimerization with 12 pairs of connection tiles; lane 2: trimerization with 6 pairs of connection tiles; lane 3: trimerization with 2 pairs of connection tiles. When the yield with all 12 connection tiles in between matching units is benchmarked as 100%, the yields with 6 and 2 connection tiles are 24% and 23% respectively.

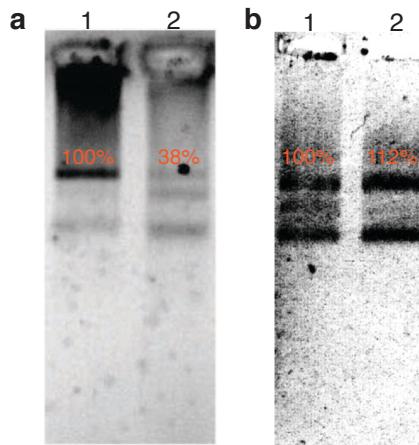


Figure S6. Native agarose gel results of trimerization from preformed units of different concentration or concentration ratio. (a) Trimerization from preformed units of different concentrations. Lane 1: purified units of original concentration; lane 2: purified units of diluted concentration (2.7 folds). When the yield of sample in lane 1 is benchmarked as 100%, the yield of sample in lane 2 is calculated as 38%. (b) Trimerization from preformed units of different concentration ratio. Lane 1: concentration ratio of three units as 1:1:1; lane 2: concentration ratio of three units as 1:3:1. When the yield of sample in lane 1 is benchmarked as 100%, the yield of sample in lane 2 is calculated as 112%.

S3.2.2 AFM imaging results

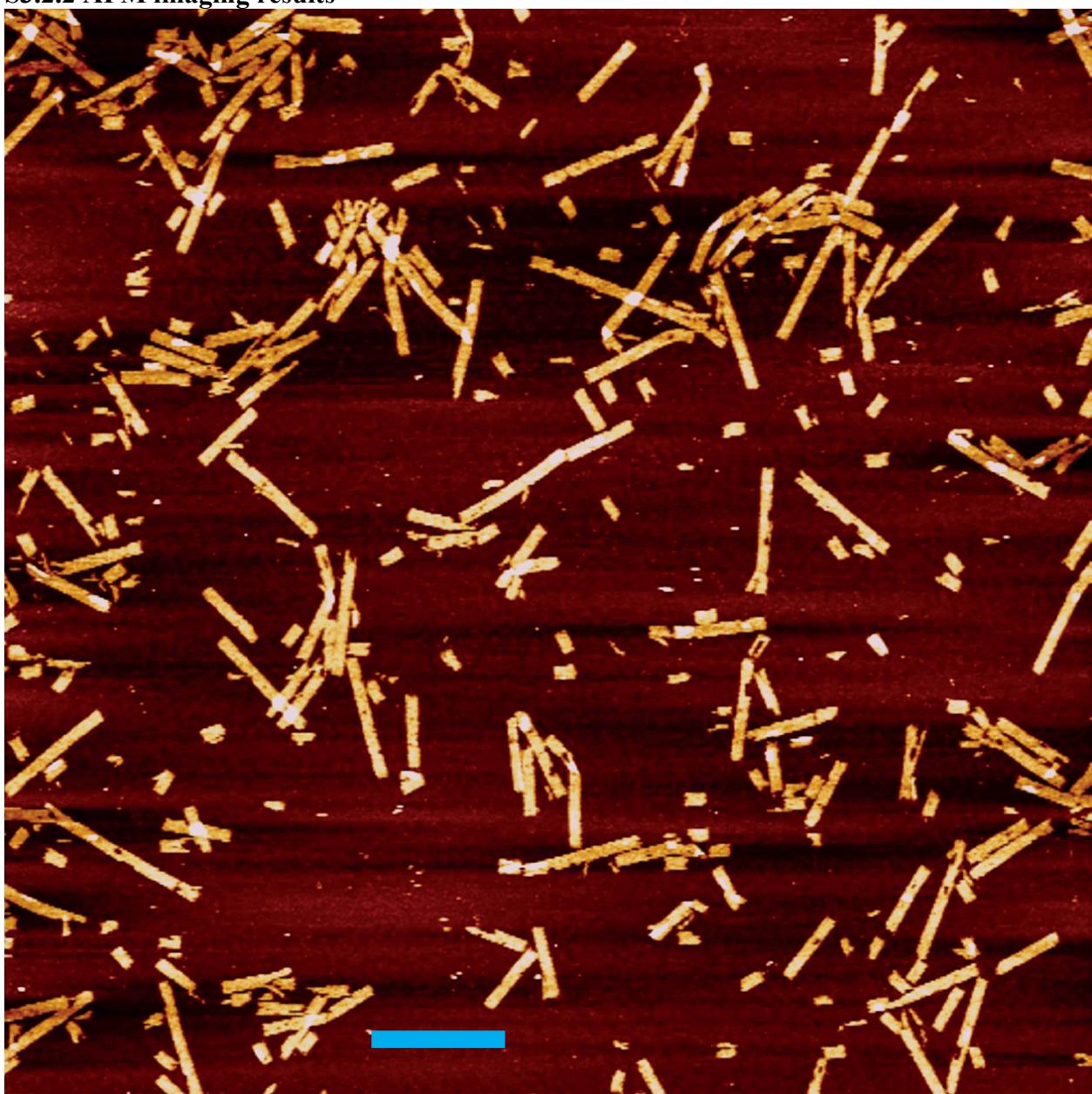


Figure S7. AFM image of five-unit strip. Scale bar: 500 nm.

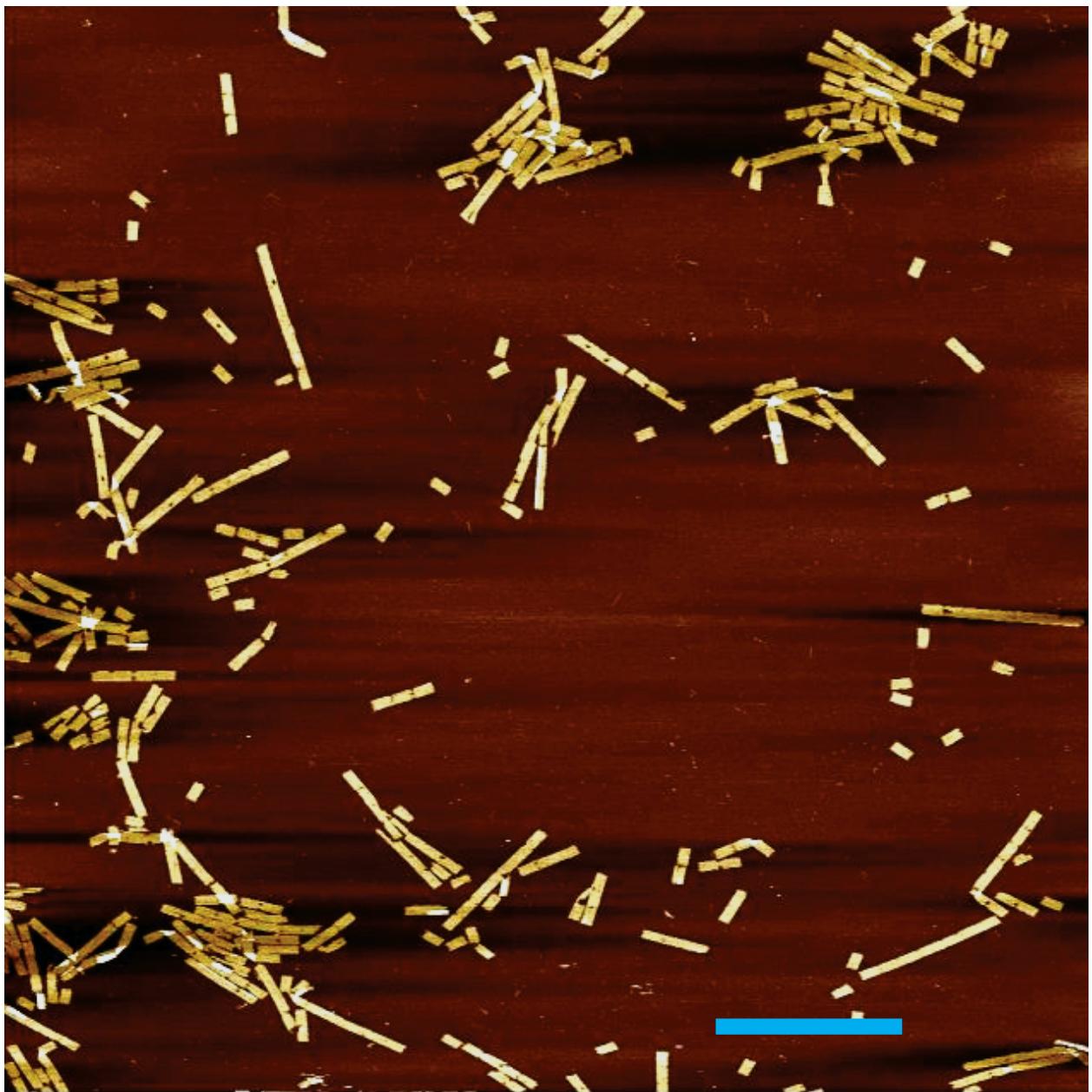


Figure S8. AFM image of seven-unit strip. Scale bar: 700 nm.

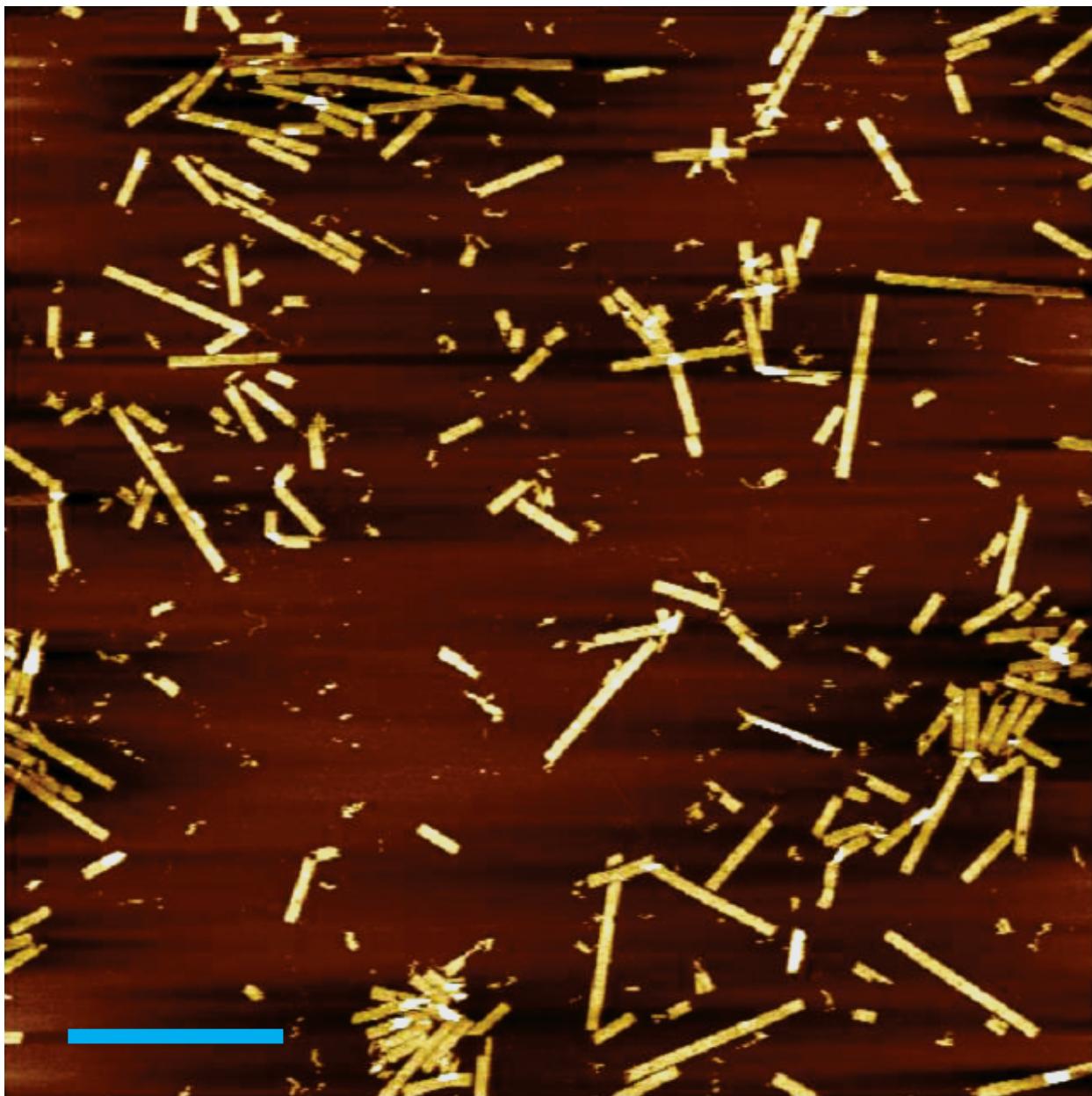


Figure S9. AFM image of nine-unit strip. Scale bar: 900 nm.

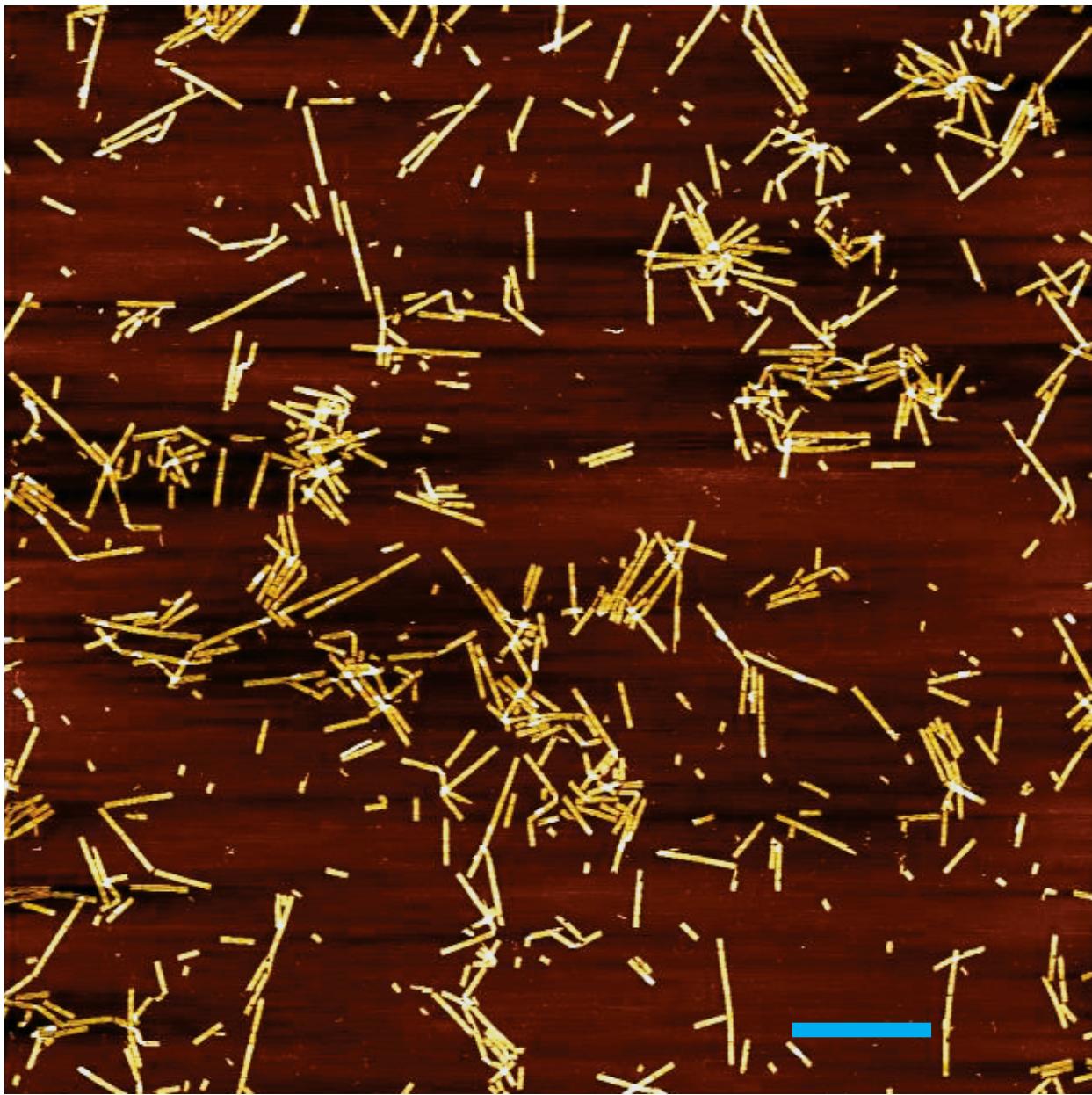


Figure S10. AFM image of eleven-unit strip. Scale bar: 1 μ m.

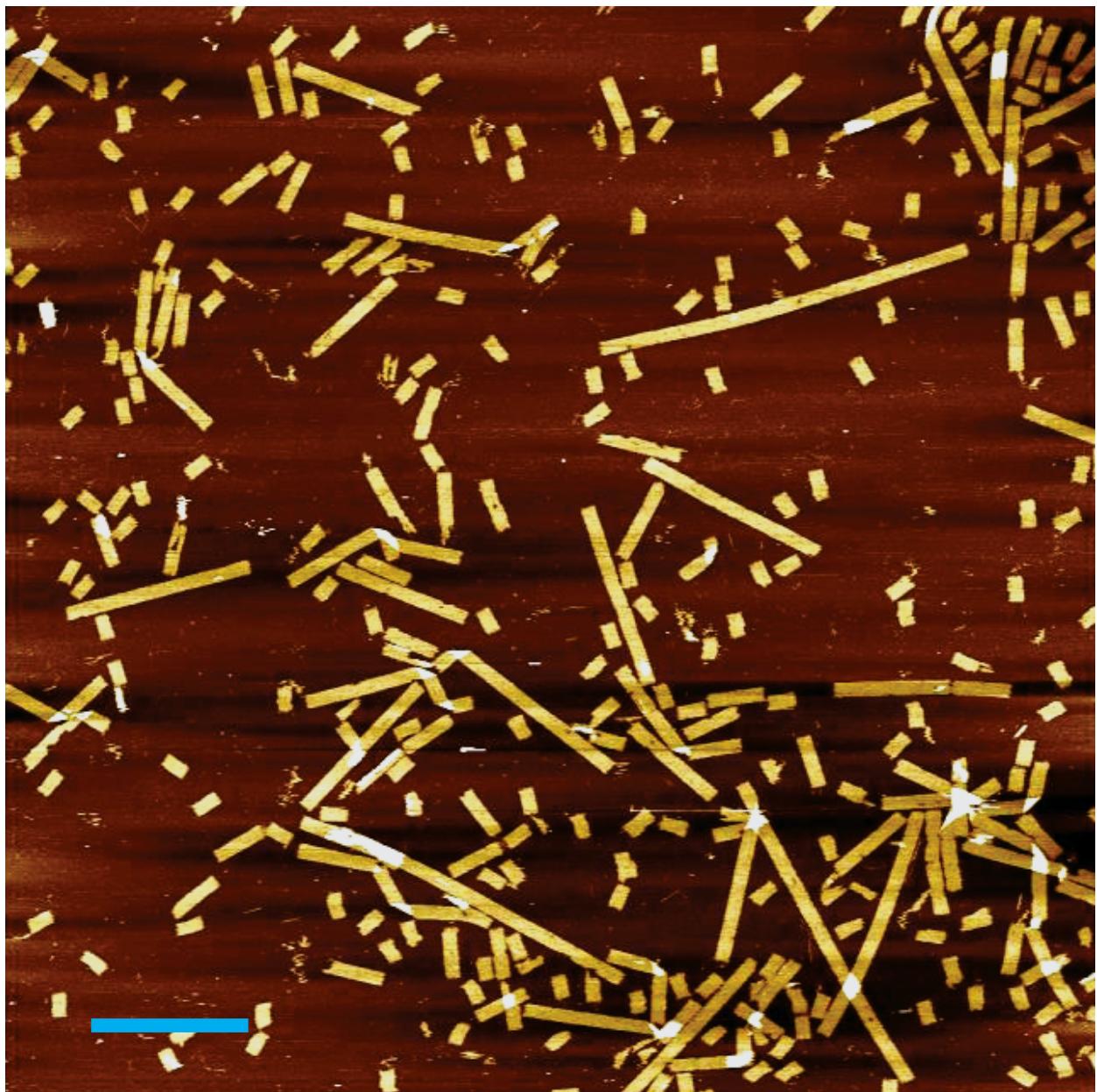


Figure S11. AFM image of thirteen-unit strip. Scale bar: 500 nm.

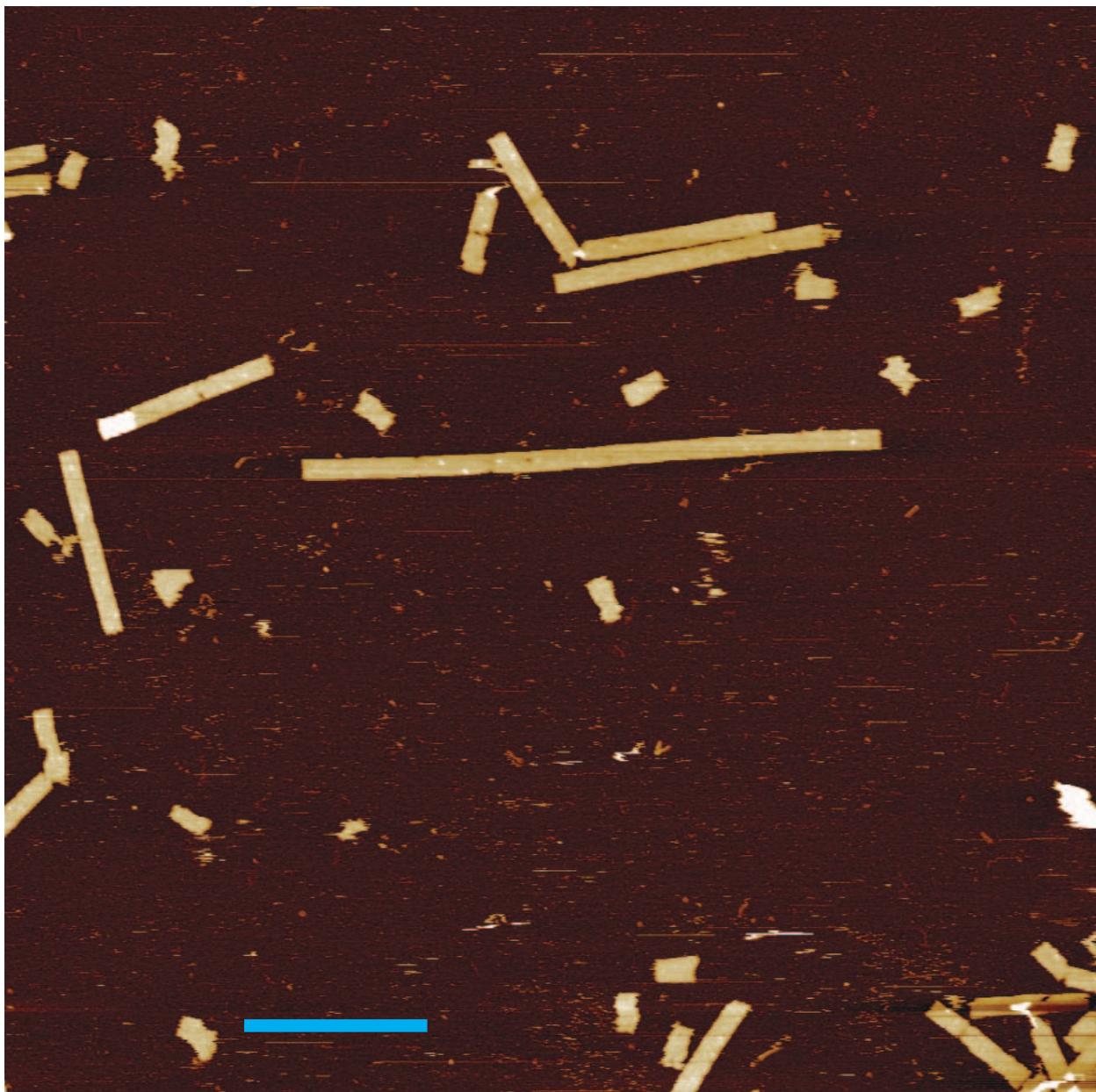


Figure S12. AFM image of fifteen-unit strip. Scale bar: 500 nm.

S3.2.3 Yield and cost comparison

Yield and cost comparison between one-pot assembly and hierarchical assembly are shown in Table S1 and Table S2. According to an earlier study², a yield drop was observed for increasingly larger 2D SST nanostructures from one-pot assembly. For example, the yield of origami-sized 2D SST structure (similar to the unit size in this study) was ~20% and the yield of a structure twice as large was less than 5%. According to our unpublished results, the yield of a 2D SST structure five times as large was less than 1% and structures of even larger sizes failed to self-assemble. The overall yield of hierarchical assembly in this study is superior than that from one-pot assembly especially for larger structures.

	Yield	Units counted
5-unit strip	29%	300
7-unit strip	11%	354
9-unit strip	16%	446
11-unit strip	17%	582
13-unit strip	4%	632
15-unit strip	4%	839

Table S1. Yields of higher-order structures with different numbers of preformed units.

	Total number of nt	Total number of shared nt	Synthesis cost by one-pot assembly (US\$)	Synthesis cost by hierarchical assembly (US\$)
5-unit strip	79128	70560	7560	2268
7-unit strip	111132	98784	10584	2646
9-unit strip	143136	127008	13608	3024
11-unit strip	175140	155232	16632	3402
13-unit strip	207144	183456	19656	3780
15-unit strip	239148	211680	22680	4158

Table S2. Cost comparison between one-pot assembly and hierarchically assembly. Cost estimation is based on DNA synthesis price of US\$ 0.1/nt.

S3.3 Verification and qualification of the toehold-mediated strand displacement

S3.3.1 Agarose gel electrophoresis results

To monitor an assembly based on toehold mediated strand displacement, a trimeric system of SST units 1, 2 and 3, was applied and a time course assay was performed (S11-S12). One of the protection tiles of unit 1 was modified with a FAM fluorophore. When this modified protection tile gradually displaced by its partner from the neighboring unit 2, the disappearance of such fluorescent signal served as an indicator of successful assembly based on a four-way toehold mediated strand displacement. The normalized FAM fluorescent intensity of unit 1 and the ratio of the SYBR Gold fluorescent intensity of the trimer band to that of the monomer band at each time point are plotted to demonstrate reaction kinetics.

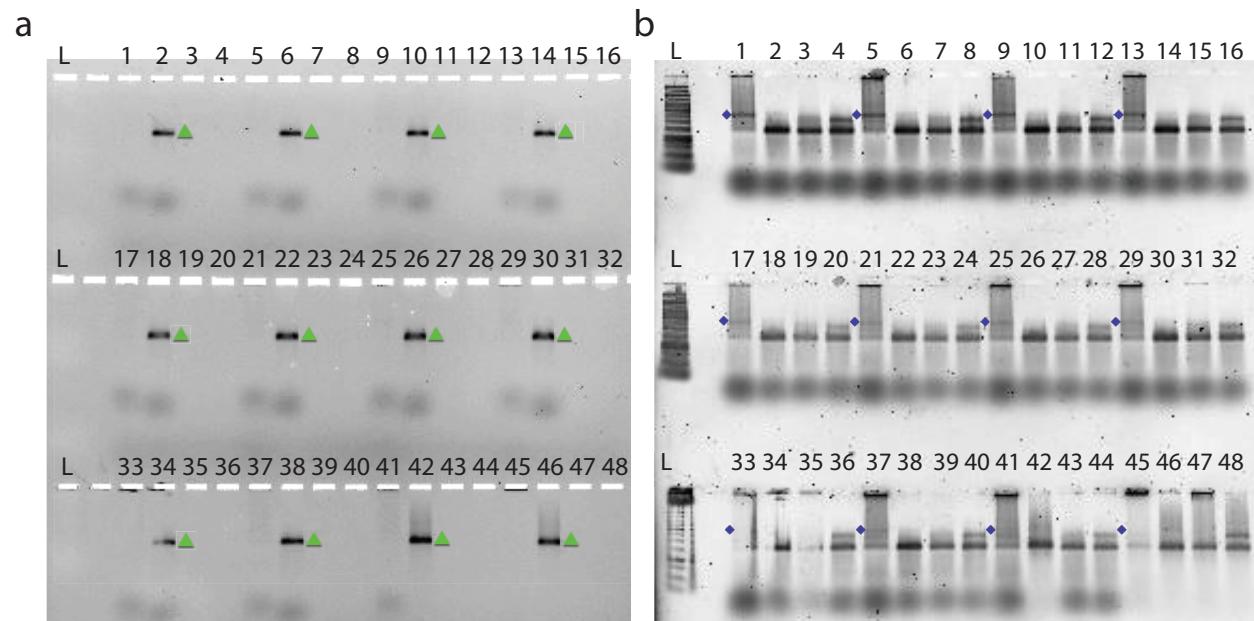


Figure S13. Native agarose gel electrophoresis results of a 20-hr time course experiment of trimerization from three units. (a) Before SYBR Gold staining, the gel loaded with samples of different time points was scanned in FAM channel. Green triangles point at bands with FAM labeling (negative control with unit 1 only). (b) After SYBR Gold staining, the same gel was scanned in SYBR Gold channel. Blue diamonds point at trimer bands. All samples at each time point were loaded in the following order: trimer, unit 1, unit 2, and unit 3. (lane L: 1kb DNA ladder, lanes 1-4: 20 hours, lanes 5-8: 12 hours, lanes 9-12: 10 hours, lanes 13-16: 8 hours, lanes 17-20: 7 hours, lanes 21-24: 6 hours, lanes 25-28: 5 hours, lanes 29-32: 4 hours, lanes 33-36: 3 hours, lanes 37-40: 2 hours, lanes 41-44: 1 hour, lanes 45-48: 0 hour).

S3.3.2 AFM imaging results

To verify the complete trimer strip from units 1, 2 and 3 of the time course experiment, the purified samples were imaged under AFM (Figure S12).

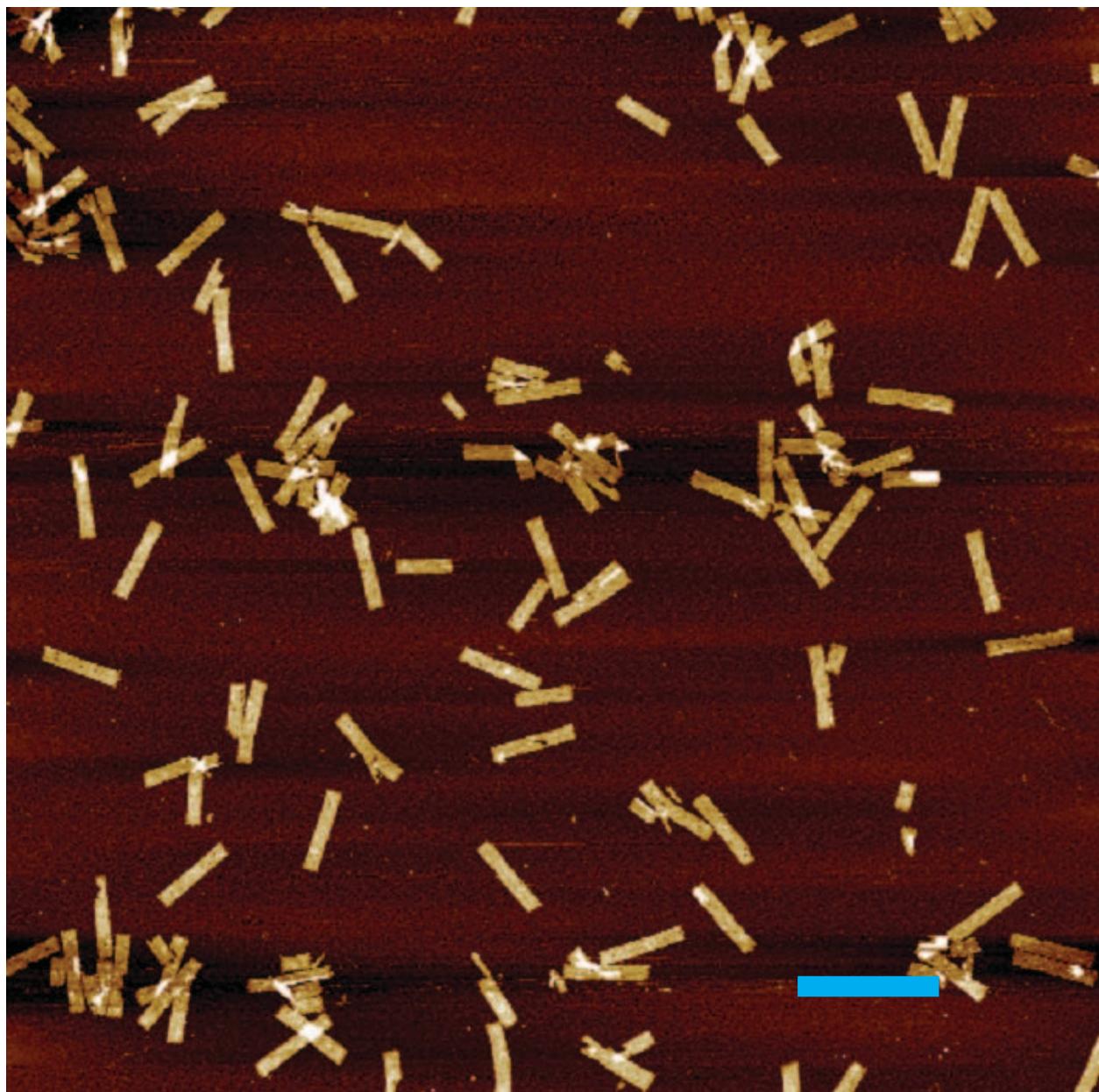


Figure S14. AFM image of trimer strip formed after the 20-hr time course. Scale bar: 300 nm.

S4 Sequence information

The listed DNA sequences for the center core tiles and the boundary core tiles are named according to their positions as ‘x-y’ (x: row number, y: column number). For example, the component DNA strand named as 1-2 in ‘boundary core tiles’ is located at row 1 and column 2. A terminal tile with T11 or A6 unpaired domains is named with a suffix ‘_11T’ or ‘_6A’. A connection or protection tiles, on the other hand, is named according to the matching scheme (a-a*, b-b*, c-c*, d-d*, e-e*, f-f*, g-g*, h-h*, i-i*, j-j*, k-k*, l-l*, m-m*, n-n* and o-o*) and row number. For examples, connection tile a*_4 is at row 4 of group a* and it has two corresponding protection tiles a_4_1 and a_4_2.

ID	Sequence	Description
1-2	TGTATAGTATCCAGCAGCTTA	Boundary Core Tiles
1-3	CATCGTTACCGAGATTGATGG	
1-4	GGACTAGACCGTTAACAGTT	
1-5	AATTCAAGCGTAGCCATCCCTC	
1-6	TGGAGTTTCACCTGATGTTCG	
1-7	TCGTGGTCAGAAAGACACCG	
1-8	TGTGGAAGTCTCTCAAAGGC	
1-9	CTGCGGCATGGTCACTGCCCG	
1-10	GACCGCAGACGTGCATTGCCG	
1-11	AATGGTCCCTCAGCCGGTGCT	
1-12	AATTCGTTGGTATTGTTGAGG	
1-13	GAGCTGATCTGCAGAGTACGC	
1-14	GGGTCCCAGGATATTGATGCA	
1-15	TACGTTGCTGAGCTCTATTAA	
25-2	CAGCATGCCAAGCGTCGACT	
25-3	TTCCAATTCAGGGAAATATG	
25-4	CCCATGTTAGCGTTAGCCCACA	
25-5	GGAAGTTTCGTTACAAGAGT	
25-6	CGGCACGAAGCGTATAACGGTG	
25-7	AGCGAGGGAATCGTTCTAAAG	
25-8	ATTGACTTACCAAGGGCCCTT	
25-9	ATCATACGGCTAGTTGCAACG	
25-10	GAATCACGTTAGTCACACCA	
25-11	AAGCATCTCACGGACTCAATA	
25-12	CGCTCATTCAAATTCGTCG	
25-13	CACATAAATTCTTAAGGTAA	
25-14	TTACTATGTGACAGGGTAAAG	
25-15	GACCGCCTGATTAAGAGCAGC	
2-1	AGTGCTTAGTTAACGCTGGCTGGATCGGCATGTAG	Center Core Tiles
2-2	ATACTATACACCATCAATCTCAGAAAGACTTTGACGATACTC	
2-3	GGTAACGATGAACACTGGTTAACTCGCGCGAGCGACCCTCAGTG	
2-4	GGTCTAGTCGAGGATGGCTAACTATTATTGACCGAAA	
2-5	CGCTTGAATTCAACATCAGGGTATGCTCCCTACTGAAATAG	
2-6	TGAAACTCCACGGTGTCTTCCCTCAGCTTATAGGAGTAAG	
2-7	TGACCGACGAGCCTTGAAGACACAAAGTGTCTAGAGCCGAC	
2-8	GACTTCCACACAGGCACTGACGCACGGTTAGATCGAGGCTAC	
2-9	CATGCCGAGCGCAATGCACCATATTCAACTCAATCCGAC	
2-10	GTCTCGGTTCAGCACCGGCTGAGGACTAAGGGCCCTGCCGG	
2-11	AGGGACCATTCTCAACAAACAATCACCATAGATTGTATGT	
2-12	CCAACGAATTGCGTACTCTGCGTGTGCTTACTATCTTACA	
2-13	AGATCAGCTCTGCATCAATATTATCATGTGGACGCTGGGAC	
2-14	CCCGGGACCTAAATAGAGCTATGACATACAGATCCTGGAGA	

3-2	AAGTCTTCTACTACATGCCACTTAACCTAGATGCTCATTC
3-3	GCTCGCGAGAGTATCGTCATGCTTAATACGAATCCTGACT
3-4	AAATAATAGTCACTGAGGGCTTCCCCTCAAGTGGTTGCCA
3-5	GGGAGCATACTTCGGTCCATTCCCCTACAGAGGTACGAGGT
3-6	AAAGCTGAGGCTATTCAGTATAGCCATACTCGAAGGTCTA
3-7	GACACTTGTGCTACTCCTATACTGAGGCTACAATATACGCC
3-8	CTAACCGTGCCTCGCTCTAACATGTGCAAGAGCTTAAAGT
3-9	TGTGAATATGGTAGCCTCGATAGATTAAAGGGCCAAGCCGAG
3-10	CCTTAGTCCTGCGATTGAGCAAACCCGCGCAAGGAGTAAG
3-11	ATGGTGATTGCCGGCAGGGCAATTATCAGGAGCGTCCAGTT
3-12	TAAAGCACACACATACAATCTGGTCAACTCATCCGACCCCTGG
3-13	CACATGATAATGTAAGATAGTGTCCGTGCTGCCAGGGACCC
3-14	TGTATGTCATGTCCCAGCGTCAGCAGATCGTATGGTCAAATT
3-15	GTTGGGCCGGTCTCCAGGATCGACCTCAGGCAACCAGCCACG
4-1	ACAAACGGTAGAATGAGCATCCAGGGCGTGAGCCCTTGAGTT
4-2	TAGGTTAAAGAGTCAGGATTCAAGACATAGCGTCCCGATCAG
4-3	GTATTAAGCATGGCAAACCAACGCCAGTATGTAATCCCGGGC
4-4	TTGATGGAAACCTCGTACCTCGGCTGGCCCAGTGGTCAAG
4-5	CTGTACGGGATAAGACCTTCGGTGGTAGCCCACCACTCGCCT
4-6	AGTATGGCTAGGGTATATTGCCGACCACTTTGTTGGGATT
4-7	TAGCCTCAGTACTTTAAGCTCGTATCCACCACGGGAAAGAAA
4-8	TTGCACATTGCTCGGCTTGGCGAAGTAAGAGCTGCTCCCATC
4-9	CCTTAATCTTACTCCTTGAGTCATTAATCGTTAGGTG
4-10	CGCGGGTTGAACTGGACGCTGTTGTAAGCCCGAACATAAG
4-11	CCTGATAATTCCAGGGTCGACCAGCCTAACGGTGGCGGTAC
4-12	TGAGTTGACCGGGTCCCTGGCAGATGATCAGACAGATCCCTA
4-13	AGCAGCGACAAATTGACCATGAGGAGCTGATCGACCGAGG
4-14	ACGATCTGCTCGTGGCTGGTCCCTGAATACGCATACTCGATC
5-2	CGCTATGTCTAACTCAAGGGCCAGTTACGTAATCCCGCGCAA
5-3	ACATACTGGCCTGATCGCGGACCATAGACCATCGGACCCGCA
5-4	GGCCGAGCCGGCCGGGATTATTCCCTGCTGCTCAGATCAGA
5-5	GGGCTACCACCTGACCACCTGCTTAGATTATGTTGTCGTAC
5-6	AGTGGTCGGGAGGCGAGTGGTATGAGTGGCACATCGCATTAA
5-7	TGGTGGATAACATCCAAACAAACTGTAGTCATTGGCGAG
5-8	CTCTTACTTCTTCTTCCCGGGTGCCACCGAACCTAACG
5-9	TTAATGCACTGATGGGAGCAGAACGGCGTCCGGCGTGCCTAA
5-10	GGCTTACAACGACCTAACGATGATATCTCGTTGAAAGTGG
5-11	CTTAGGCTGGCTATGTTCCGGGAAGTAGCTTCGTGATTCTC
5-12	CTGATCATCTGTACCGCCCAACCTGTGTCAGTCACCTGATTC
5-13	CGAGCTCCTCTAGGGATCTGTATAGAACCTATCGTAAGGAG
5-14	CGTATTCAAGGCTGGTCAGATAACTGATATCAACATAGCCAC
5-15	AAGTCAACGTGATCGAGTATGACAGGGTAAGAGCTCAGCT
6-1	TGAGTGAGGTTGCGCGGATTGACCCATGTGCGCACGACTCC
6-2	TACGTAACTGTGGGTCCGATCCCGTCTGAGTCATTACATC
6-3	TGGTCTATGGTCTGATCTGAGAGTGCACTTCAAGCAAAGTTG
6-4	CAGCAGGAATGTACGAACACATAGTGACACGGTGGAGCGT
6-5	TAAATCTAAGTAAATGCGATGGGCACAAACCCCTCCACAATGAA
6-6	TGCCACTCATCTCGGCCAATATTGCACTTCTGATTCAATA
6-7	TGACTACAGTCGTTAGGATTCGACGACATGCTCGAGGACTTG
6-8	GGTGGCACCGTGGCACGCCCTCAGCCTCAAGGCCAGAGCG
6-9	GGACGCCCTTCAACTTCAACGTTGATTGACACATTCAAGGAA
6-10	GAAGATATCAGAGAATCAGGATGAGGCCAGCATCGTACTGGG
6-11	AGCTACTCCGAATCAGGTGAATCGTCACGATCGTACGGTAG

6-12	CTGACACAGGCTCCTTACGATATGGGCTCGAGTGAGAGACTA
6-13	AGGGTTCTATGTGGCTATGTTAACGCAATTTCGATCACGGG
6-14	GATATCAGTTAGCTGAGGACTTGTACACGTTGCATGAATT
7-2	TCAGACGGGAGGAGTCGTGCGGTTGCATTACGAGGTAAGTA
7-3	GAAGTGCACTGATGAATAGACAAACTGTTAGGCTAGGATAT
7-4	CGTGTCACTACAACCTTGCTTATAGGCTGGGCCGCCTCCT
7-5	GGGTTGTGCCACGCTCCGCACGATACTTATTCTAGAACTAGC
7-6	AAAGTCAATTTCATTGTGAATCCGGTTCCATTGTTCTA
7-7	GCATGTGCTATTGAATCAGAACATCGCTCGAAGTGTGACT
7-8	TTGAGGCTGACAAGTCCTCGAAGATGTACGCAATGTATGCCG
7-9	TCAATCAAACCGCTCTGGCGCTACTGTTACCTCATGCCCTG
7-10	GCTGCGCTCATTCTGAATGTCAAGATCTCCACATCTCGAGG
7-11	TCGTGACGATCCCAGTACGATGGTGCACGCTATTCTCGCG
7-12	TCGAGCCCATCTACCGTAGGACATATCCTTAGTGTGAGTTGTAC
7-13	ATATTGCGTTAGTCTCTCACGTGCGCTTAGTGGGACCGG
7-14	ACGTGTAACACCCGTGATCGAGTCAGTATCAATAACCCCTAGG
7-15	AGCGGATCTAAATTCTATGCCACGAGAACATCGCTACACCGAA
8-1	CTATCGGAGGTACTTACCTCGAGAAAGGGCGATTCCGATCGC
8-2	TAATGCGAACATATCCTAGGCCACCTTCAGCATGCAAAGTC
8-3	TAAACAGTTAGGAGGCGGCCAGAACCTCACGCCACGTGA
8-4	CAGGACCTATGCTAGTTCTAGTAGCTAGTCGAGAACATCTACT
8-5	AATAAGTATCTAGAACAAATGGTGGCTGTACCCGAATGTG
8-6	GAAACCGGATAGTCACACTGTCGACCGTGTAAAGAAGATGC
8-7	CGAAGCGATTCCGCATACATTCTACCCGTTAACACCGAAA
8-8	GCGTACATCTCAGGGCGATGACTCCCAGCATATGTATAGGG
8-9	GGTAACAGTACCTCGAGATGTTGCTCCGGCTTGAAGTCGAAT
8-10	GGAGATCTTGCAGGAATAGTATGAAACCATGTGACATAAT
8-11	CGTGGCAACCGTACAACTCACCGACTGCACAAAGCGTGCAAA
8-12	TAAGGATATGCCGTCCCACGGCACCTAATCGCACAGACCC
8-13	AAGACGACACCCCTAGGGTTATTACCCCTGGTGGTATGCCA
8-14	TGATACTGACTTCGGTGTAGCGCAAGACAGGACCCGACGCCA
9-2	GCTGAAAGGTGGATCGGAATGACGTAACGACAAAGTAAGG
9-3	GTGGAGTTCTGAACTTTGCATAGTGAATGTTGAAACATTGG
9-4	CGACTAGCTATCACGTGGCAGGTGCACAGAACATGAGCGGAAAT
9-5	TACAAGCCACAGTAGATTCTATTGATCATCGATGCCGCA
9-6	ACACGGTCGACACATTCCGGAACCAAGTCTGTTAAAGTAC
9-7	AACCGGGTAGGCATTCTTCTTGGTAGTACAGCATCCC
9-8	ATGCTGGGAGTTCGGTGTTCGTATCGCAGGGTGTAGT
9-9	AGCCGGAGCACCACATACATCGAACCTTTGCCCTACCAAT
9-10	TGGTCCATAATTGCACTTCACTGACGATCCCTAGACCTT
9-11	TGTGCAGTCGATTATGTCACAATGTGACGTCCTGTAACGACC
9-12	ATTAGGTGCCTTGCACGCTTCACTTACCTGGTACGGAAG
9-13	CCAAGGGTAAGGGTCTGTGCGGTACCGAACGGCTGGCGAC
9-14	CCTGTCCTGCTGGCATAACCGAACATTACGTCGTTATCGA
9-15	ATATCGTCTTGGCTCGGGTAGTGTGCGTTAAAGTT
10-1	TGAATTCTATCCTTACTTTGTTCGAAAGTAATCCATTGTC
10-2	CGTTTACGTCCAATGTTCACGACTGTGACGACAATTGTCG
10-3	ACATTCACTATTCCGCTCAGGCTATGGCATGCAACGATAAC
10-4	TTCTGTCACCTCGGGCATCCATCCAGTGCCTATGATACT
10-5	GATGATCAAAGTACTTTAAACTCATCCCTGTTCAACTCTGCA
10-6	AGACTTGGTGGGATGCTGTAGCAAGACATCAGCATCCTCGT
10-7	CTACCCACCAACTAACGACCTGTATGATACATTGAGTGATC
10-8	CGACGATACGATTGGTAGGGCGCTCGTCCATCTATTGTCG

10-9	AAAGAGTTCGAAAGGTCTAAGTCTGCGAGTGCCTCCCAGGAT
10-10	GGATCGTCAGGGTCGTTACAGTCGAGTAGAGCCCTACAAT
10-11	GACGTCACATCTCCGTACCACCTGACTACATGAGGTAGGAT
10-12	AGGTAAAGTGGTCGCCAAGCCCACTCGAGTTGACTGTGA
10-13	CGTCGTGACTCGATAACGAGAAGGTGTTCACCTCTCAGTG
10-14	ACGTGAATCTAAACTTTAACCAATCGTCTGCGATGTATGA
11-2	GTCACAGTCGGACAATGGGATTAGAGGTCTGGACCCGCGCAT
11-3	TGCCATAGCCCCACAATTGCCCTTATATTCCATTACGGCC
11-4	GCACTGGATGGTATCGTTGCATAGCCACGCTGGACGGAAGTA
11-5	ACAGGGATGAAGTATCATAACGGTAGGCCTACCTGCCGGTTAC
11-6	GATGTCCTGCTGCAGAGTTGACTCACGCAAAGAGAAAGGGCA
11-7	GTATCATGACACGAGGATGCTATAGGCCCTCTAAATACCTT
11-8	TGGAACGAGGGATCACTCAATAATGGCGGGCAATTAGATGA
11-9	CACTCGCAGAGCGACAATAGAGGTTGATCGATTAATTAGCAG
11-10	CTCTACTCGAACCTGGGAGGAATGTCGGTGCCTCGCAGC
11-11	TGTAGTCAGGATTGTTAGGCGGTATCACCTCGTCACGCTATGA
11-12	AACTCGAGTGTACCTACCTCACGAGATAACACAAATGTACCG
11-13	GAAACACCTTACACAGTCAGCTAAAGTCAGTGTATCAAAC
11-14	CAGACGATTGCACTGAGAAGTCTAAGTTGTCACGTTCATGC
11-15	CCCTGTAGACTCATACATCGAAAGAGACATCAGAATGTTCCA
12-1	ATTGGACGTAATGCGCGGGTCGATTGAAATCTGCTAATGGTC
12-2	CAGACCTCTAGGCCGTATGGGATGGTGGAAACGTCGCAAT
12-3	AATATAAAGGTACTCCGTCCGTAAAGAGTGGGTATTACGC
12-4	AGCGTGGCTAGTAACCGGCAGCGTTACCAAGTCAGTAGTTTC
12-5	GTAGGCCTACTGCCCTTCTCCCAGGTCAGTCCTCACAAAC
12-6	TTTGCCTGAGAAGGTATTAGGCTACTACTCTCCGCTCCGA
12-7	AGGGCGCTATTCATCTAATTGGAGTTCTGCGTGGCTACGC
12-8	CCCGCCCATTCTGCTAATTAAACATTACACATCTACGCTCCCT
12-9	TCGATCAACCGCTGCGCAGCAGCAGCGATGTTGTACATAC
12-10	CACCGACATTCATAGCGTGAGACGGGACAGCCACGTCCTGG
12-11	CGAGGTGATACGGTACATTGTTAGAAAGCAAGCAGTATTCA
12-12	TGTTATCTCGTTGATACACTCGAAAGCGCATCTCTTAAAG
12-13	GAACTTAGCGCATGAACGTGCGCTCTAGTACTGGCTAAC
12-14	ACAAACTTAGTGAACATTCTGATAGATTGTCAGTCAATCG
13-2	TCCACCATTGCGACCATAGCACATTTACTTCAGTCACATGC
13-3	CACTCTTACATTGCGACGTTGTCGTGGTGCCACGTTGA
13-4	CTGGTGAACGGCGTAATAGCCGTGCGTAGCCAGTCTGAGTG
13-5	GACCTGCCGGAAACTACGAAATCAATTAGCTAGTATAGAA
13-6	GAGTAGCGTTGGTGAAGGACGCATGCCATGAGGGCGT
13-7	GCAGAAACTCTCGGAGCGGAACACACCATCTTAAAGGCCGG
13-8	ATGTGTAATGGCGTAGGCCACTATGACCCGTCCATGAGC
13-9	ATCGCTGCGTAGGGAGCGTAGATTAAACATTCAAGCGACGCT
13-10	CTGCTCCGTCGTATGACAAACGGTTAGAACTATTACGCGGC
13-11	TTGCTTCTACCAGACGTGGGAGATGCGGTCTTCCGCCCT
13-12	TGCGCTTCTCGCTGAATACTGCGATTTAGCTCAAATGCACGAG
13-13	TACTAGAGCGTTAAAGAGACCGCGACGACTGGGTTAAAC
13-14	ACAATCTATCGGTTCAGCCAGGCGGACTGGGTGTTGGGCCAT
13-15	AACCTTATGGCGATTGACTGGATGGCTCGTCTGACACAAAG
14-1	TCTGGCATAGGCATTGTGACTGTCTAGTCTTAATCAGGCAA
14-2	AAAGTAAATGTCAACGTGGCAGAAGGGCAAAGATGTTGTTG
14-3	CCACGACAACCACTCAGACTGGGTTCTGCCGACTTCGCGAT
14-4	GCTAGCGCACTTCTATAACTAGTCGACACAGACATGTGCTATG
14-5	CTAATTGATTACGCCCTCATGCGTCAACGCCAGGGCAAAT

14-6	GCGATGCGTCCCCGCCTTAAGCTATTGACAGCGGTGCGCA
14-7	AGATGGTGTGGCTAACATGGTGGACAGCCCTGACTAACCCA
14-8	ACGGGTCTATAAGCGTCGTTAGTTCTACCATCATGAAT
14-9	AATGTTAAATGCCGCTGAATAGCAATTGACGCTGGTTGCT
14-10	GTTCTAAACCAGGGCGGAAAGCGCGCACACCTGTGGACCCAT
14-11	ACCGCATTCTCTCGTGCATTTACTTATAATGGATTACTAACG
14-12	GAGCTAAATCGTAAACCCAACACTCCGGTCTGGATCCTT
14-13	GTCGTCGCGGATGGCCAACAGCAATCGGGCTTAAGCAGCT
14-14	CCCAGTCCGCCTTGTGTCAGACCTACTGCGACCCGGTTGAG
15-2	TTTGCCCTTCTTGCCTGATTATAGCCCGTAGGTAGTTACCAT
15-3	CGGCAGAACCCAACGAACATCACATTGAGTTCCGCTAATT
15-4	TCTGTGTCGAATGCCAAAGTGCCTAGTGTAGCCGACCTTAGA
15-5	GCGGTTGACGCATAGCACATGAGCCGTATTCGGTTCAATCT
15-6	GTCAAATAGCATTGCCCTGGCGCATAAAGCCGGAATGGCAC
15-7	GGGCTGTCCATGCGCACCGCTGATTACTCGGAATTAGGGAAA
15-8	TAGAAACTAATGGGTTAGTCAATGAGACCCGGATGGGAGAG
15-9	GTCAAATTGCATTCAATGATGGCGACGCCACGTGATGCTTGC
15-10	GGTGTGCGCGAGCAAACCAACAGCGTGTAGACTTACATTGTCTG
15-11	CATTATAAGTATGGTCCACAGAACCTGAACGCTATTAGCCG
15-12	ACCGGAGTAGCGTTAGTAATCACAGTGTATCGCAATGTACA
15-13	GCCCCGATTGCAAGGATCCAGACTCTAAACCGTAGAACAAATGT
15-14	CGCAGTAGGTAGCTGCTTAAGCAAACACTCATTGGCCTGAG
15-15	TACAGAACCACTAACCGGGTGACCAGGCCAGGTACCGCTAT
16-1	GGGCTAGGTATGTAACTACTATCTCCGCCAACCTAA
16-2	CTACGGGCTAGAATTAGCGGAGCCCATCCTAGACCTCGACCC
16-3	ACTACAAATGTTCTAAGGTGGGCATGTATCATGTTGTAAG
16-4	CTACACTAGGAGATTGAACCGCTTACGGAGCAACCGCGTCAA
16-5	AAATAACGGCTGTGCCATTCCCGGCCCTAACGGACGCGGAA
16-6	GCTTATGCGTTCCCTAATTATCAAGAAAGGCAAGCCACGT
16-7	CCGAGTAATCCTCTGCCATCTACGAATGAGGGCATCACCG
16-8	CGGGCTCATGGCAAGCATCAGGATAATATTCCCTGTTAGCA
16-9	CGTGGCGTCGACAGACAATGTGTCTGAAATTATCGTAAAGTG
16-10	AACTACACCGGCTAATAGCAGAAACCGACACCCCTCCGGAT
16-11	GTTCAGGTTCTGTACATTGCGATTAACGGAGCCATCTAAGAC
16-12	ATGACACTGTACATTGTTCTAACAGAGTTATGCTCTGTT
16-13	CGGTTAGAGCTGCAGGCCAACCGGTATAAACACTGCTAGT
16-14	TGAGTGTGATAGCGGTACCTGAACATATAGGACTCCAAT
17-2	TAGGATGGGCTTAGGGTTCGGTTAGAAGTCTCGAAGCCG
17-3	GATGACATGCGGGTCGAGGTCACTACGCGAGACTAATGCCA
17-4	GCTCCTAAAGCTACAAACATGTACAGGCGTTACGTGAAG
17-5	TTGAAGGGCGTTACGCGGTTCTCATTGTTAGAGAAACTA
17-6	CTTCTTGATTTCCCGCGTCCGGTAGCTTTCTAGGTGATA
17-7	CTCATCGTAACGTGGCTTGCACATGTTAGTTAATTCTCTG
17-8	AATATTATCCCGGTATGGCGTACTATATGACGCTGCTT
17-9	AATTCCAGACTGTAACAGGGCGGGACGCAACCAAAGGA
17-10	GTCGGTTCTCACTTACGATCTAAAGGAACGAATCAAGGC
17-11	CTCCGTTAATATCCGGAGGGTAGTTAGCGGGCGCGTACCCCA
17-12	AAACTCTGTGCTTAGATGGCTTATGCGATTAAGCCGACCC
17-13	TTATAGCCGGAACAGAGCATGGTTGCACCAGATCAATCTC
17-14	ATATAGTTCAACTAGCAGTGTGCTACAGGTTGGTGCAAAC
17-15	GGCCGGGTCTGGAGTCCTAGTAGTGTCTTATCGGATGTC
18-1	GATAAATGCCCGCTTCGGAGAGCTTCTTGCTTAAATCG
18-2	ACTTCTAAACTGCCATTAGTTCAACCGCGACGAGCGAATGG

18-3	CTGCGTAGCTCTCACGTAAC T GCGTAGGTCAACGATTGGCT
18-4	GACCTGTGACTAGTTCTCTAATAGCTCCCACCGCTCGCAAG
18-5	ACGAATGAAGTATCACCTAACGTTCATGATTCCATGGTCAA
18-6	AAAGAGCTACCAGAGAATTAAATGCCCTCCTTGAAGGCCCT
18-7	CTAACATAGTAAGACGACGGTGAAGTGGCGCATGTAGCTGTAGC
18-8	CATATAGTACTCCTTGTTGGTAGCGGTTGTTCAACGGTC
18-9	CGTCGCCGGGCCTGATTGGAGTTCACTCTTCTTGACCG
18-10	TTCCTTAAGTAGGGTACCGGTGAAATCCAGGATACTGAA
18-11	CCCGCTAACTGGGTCGGCTTAAGACTGGGTCAGCCATGCCA
18-12	ATCGCATAAGGAGATTGATCTATGGAATCTGATGGCGGCCAT
18-13	GGTGCAAACCGTTGCACCAAAGCGGTTGACGGGTTCATG
18-14	ACCTGTAGCGGACATCCGATATTGACGATGCCAACCGGGT
19-2	TCGCGGTTGACGATTAAAGCATGAACCTCGCTGATCGTCACT
19-3	GACCTACGCACCATTGCTCGTTAACCTTATTATCATGTGA
19-4	TGGGAGCTATAGCAATCGTTGAGTCACATTGAACTGAGA
19-5	AATCATGAAACTTGCAGCGTTTCAGTGACTTCATGCCCTCT
19-6	AGGAGGGCGATTGACCATGGGTACGGCGGTGCCAGAAGG
19-7	ATGCGCCACTAGGGCCTTCAGTTGGCACGACCATACGGCAG
19-8	AACCGCTACCGCTACAGCTACAGTCTAACATCTCCATGAGC
19-9	GAGTGAAC TCGACCGTTGAACGTGCTTAAGATGTTAGTTGA
19-10	TGGATTACACGGTCAAGAAACCTTCCACGGTACCCCTAGAA
19-11	CACCCAGTCTTACTGTATCCGTACAACGTAGGTTTCGACG
19-12	CAGATCCATTGGCATGGCTGCAGCTAGCAATCTACAGCATG
19-13	TACAACCGCTATGGCCCATGCTCCGTCATGGCTGATTC
19-14	GATCGTCAACATGAAACCGTTAGGCCAAGCAAATATAAG
19-15	TAGTGATGAAACCCGGTTGCCACACCATATGTGATTTAGA
20-1	TGTCTGAATTATCGACGATCAATGGGCTCCACATTGTTGA
20-2	GCGAGGTTCATCACATGATAACCTAGTTAAAGAGGGCGATGG
20-3	TAGGGTTAATCTCAGTTCAAACAAGGGTAGTCACGGTGAAG
20-4	TGTGCACTACAGAGGGCATGAACGGGTAGCCACTACCAACCC
20-5	AGTCACTGAACCTTCTGGCGTGTACCGACGGAGGCCGAAAGT
20-6	ACCGCCCGTACTGCCGTATGGTTAGAGATCCGAACTCTC
20-7	TCGTGCCAACGCTCATGGAGACTAATCGTCACTGGTACGC
20-8	TGTTAGACTCAAACATTACAGATGCAGGCACCGTA
20-9	TCTTAAGCACTCTAGGGTACGACTGAGATGAGCATAACTCC
20-10	CGTGAAGGGCGTCGAAACCTTGTGGTAGCCCTTAGGATGA
20-11	ACGTTGTAACCAGCTGTAGACTCCCTGACGCACATTATG
20-12	TTGCTAGCTGGAATCGACGCATAGAATAAAATTATTGTTCGTT
20-13	TTGACGGAGCCTATATTGCACTACAACGTGATGGTGGTGG
20-14	TTGGGCTAATCTAAAGATCAGGCGAGTGCCTGCTACTCGA
21-2	TTTAAC TAGGTCCAACAATGTAGCAATTGGTGGAGCCCTGG
21-3	CTACCCCTGTCCATGGCCTCTGACGGTTATCTTCCGGGCC
21-4	GGCTACCCGTCTCACCGTGAGTATCTCACGATGTCTACTG
21-5	CCGCGTACAGGGTGGTAGTCAATTAAAGGTATCAGCTCGA
21-6	ATCTCTAAACACTTGGCTAGGCTGCAAAGTAGGAGCCAT
21-7	ACACGATTAGGAGAGTTCCGGATTAGACCGAGGCATAGCCGTC
21-8	CATCTGATAAGCGTACCGAGTGTCACTGGCAGGGAGTACCTGA
21-9	CATCTCAGTCTACGGTGCTGATGCCCTTACTGTTCACTG
21-10	GCTACCAAGGGAGTTATGCTGGAGAAAGCGTCAGGCTACC
21-11	GTCAAGGGAGTCATCTAACGAGTGTGGAATCTCCTTGAAC
21-12	ATTATTCTACATAATGTGCTTCGGCTAACGTTATACCG
21-13	CACGTTGTATAACGAACAATAGGGCGCGCGTCCGTTAAGGG
21-14	GGCACTCGCCGGCACCACTCAAACCGGCCACGGTATTCTC

21-15	TGAGGGCGGCTCGAGTAGCAGCGTGGACAGTACTCAGGAGGT	
22-1	ATACGATATCCCAGGGCTGCCATTCACTCGGGACTGTCACCT	
22-2	ACCAATTGCTGGCCCGGAAAGCCGTAGATGCTTAGATTAG	
22-3	ATAACCGTCACAGTAGACATCAAATGTGCGAGACGAACCTTC	
22-4	GTGGAGATACTCGAGCTGATAATAACGTTATTAGCTATCAAG	
22-5	CCTTAAATTGATGGCTCCTACGCCATGAAGACCATGGGCTG	
22-6	TTTGCAGCCTGACGGCTATGCCATGAATCTCCACGAATTG	
22-7	CTGGTCTAATTCAAGGTACTCGCACCGTACTATCCTGCTTG	
22-8	CGTGCCTGAGGCCTGAAACAGAACATTGCAAGGGCACGGCAA	
22-9	TAAAGGCATGGTAGCCTGACGTCCGGACATAGTCTCAGATA	
22-10	GCTTTCTCCCGTCAAGGAAGATTACAAGACCGGAGGCCTCA	
22-11	ATTCCACACTCGGTATAACGTAAGATATAACGGATCTCTTCAG	
22-12	TTAGGCCGAACCTTAACGGAATCATCCACTAAGACGGCAGG	
22-13	ACGCGCGCCCGAGAATACCGTTATTATGTAAGACCGTGGCCAC	
22-14	GGCGGTTGAACCTCCTGAGTAAATTGAGTAAAGAAGTTAC	
23-2	ATCTAGACGGAGGTGACAGCTAACAGTATTACCTATGATCGTA	
23-3	TCGCACATTTCTAATCTAAGCTACTGCTCGTCCCTGCGGTG	
23-4	ATAACGTTATGAAAGTTGTCCTAGTATGTTCTAGTATAA	
23-5	CTTCATGGCCCTGATAGCTAATCGCTCATAGACCTCCCTAA	
23-6	GAGATTCAATGCCGATGGTGCACCTTCCATCGTCCGAC	
23-7	AGTACGGTGCCGAATTGTCGGGCGATGCGCTGGATCATAGGT	
23-8	CTTGCATTAAAGCAGGATTGCACCCCTATGCATGCCAT	
23-9	ATGTCCGGACTTGCCTGGCCATGACAAGTCTGGGTACCAAC	
23-10	GTCTTGTAAATTATCTGAGACTTATGCTATTAGTATTCTACTC	
23-11	CGTATATCTTGAGGCCTCCGCAGTCTCATATTGCATTGC	
23-12	AGTGGATGATCTGAAGAGATCGACTCATCTGGTACGTACA	
23-13	TTACATAATACCTGCCGTCTGCGGGTTACTGCCCTTCG	
23-14	TACTCAATTGTCGGCAGGCCGCTGCGAGTCATTGTT	
23-15	CCACCGCGCAGTAAACTTCTTGCTTTGCACTTCAGGAAAGTG	
24-1	TCCTTCGATTACGATCATAGTAAAGACGCAAGTCGACGCTT	
24-2	GTAATACTTACCGCAGGGAGGGCATGCTGCATATTCCCT	
24-3	ACGAGCAGTATTATACTAGGAGAAATTGGAATGTGGGCTAAC	
24-4	AACATACTAGTGTAGGAGGTGCTACATGGGACTCTGTGAA	
24-5	TATGAGCGATGTCGGACGATGCGAAACTTCCCACCGTATAcg	
24-6	GAAAGGTGCGACCTATGATCCCTCGTGCCTGAGTAAACGA	
24-7	AGCGCATCGCATGGCATGCATTCCCTCGCTAAGGGCCCTGG	
24-8	AGAGGGTGCAGTTGGTACCCATAAAGTCATCGTCAACTA	
24-9	GACTTGTATGAGTAAATACGCCGTATGATTGGTGTGACTA	
24-10	TAATAGCATAGCAATGCAATGAACGTGATTCTATTGAGTCCG	
24-11	ATGAAGACTGTGTACGTACCTGAGATGCTCGACGAAATT	
24-12	AAGATGAGTCCGAAGGAGGCAGGAATGAGCGTTACCTAAGA	
24-13	GTAAACCGCAACAAATGACTAATTATGTCCTTACCTGT	
24-14	CGGCAGACCGCACTTCCTGACACATAGTAAGCTGCTTTAA	
1-1	ACTAAGCACTTTTTTTTTTT	
3-1	TCCAGCAGGCTTTTTTTTTTACCGTTGTTTTTTTTTT	
5-1	TCACGCCCTGTTTTTTTTCCACTACATTTTTTTTT	
7-1	CACATGGGTCTTTTTTTCTCCGTAGTTTTTTTT	
9-1	CGCCCTTCTTTTTTTTATAGAATTCAATTTTTTTT	
11-1	TACTTCGAATTTTTTTTACGTCATTTTTTTTT	
13-1	GATTTCAATTTTTTTCTATGCCAGATTTTTTTT	
15-1	AAGACTAGACTTTTTTTGACCTAGCCCTTTTTTT	
17-1	GCGGGAGATATTTTTTGGCATTATCTTTTTTT	
19-1	CAAAGAAGCTTTTTTTTAATTGACACATTTTTTTT	

Terminal Tiles

21-1	GGAGACCCATTTTTTTTTGATATCGTATTTTTTTTT	
23-1	CCGAGTGAATTTTTTTTTATCGAAAGGATTTTTTTT	
25-1	TGCCTCTTATTTTTTTT	
2-15	CAGCAACGTATTTTTTTCCGGCCAACTTTTTTTT	
4-15	GCCTGAGGTCTTTTTTTACGTTGACTTTTTTTTT	
6-15	CTTACCCCTGTTTTTTTTAGATCCGCTTTTTTTTT	
8-15	GATCTTCTCGTTTTTTTAAGACGATATTTTTTTTT	
10-15	GCACGACACTTTTTTTGTCTACAGGGTTTTTTTT	
12-15	GATGTCCTTTTTTTCCATAAGGTTTTTTTTTT	
14-15	GACGCCGATCTTTTTTTGGTTCTGTATTTTTTTTT	
16-15	TGGCCTGGTCTTTTTTGACCCGGCCTTTTTTTTT	
18-15	AGACACTACTTTTTTTTCACTACTATTTTTTTTT	
20-15	CATATGGTGTTTTTTTGCGCCCTCATTTTTTTTT	
22-15	ACTGTCCACGTTTTTTTGCGCGGTGGTTTTTTTT	
24-15	AGTGCAAAGCTTTTTTCAGGCGTCTTTTTTT	
1-1 6A	ACTAAGCACTAAAAAA	
3-1 6A	TCCAGCAGGCAAAAATACCGTTGTAAGAAAAAA	
5-1 6A	TCACGCCCTGAAAAAACCTACACTCAAAAAAA	
7-1 6A	CACATGGTCAAAAACCTCGATAGAAAAAA	
9-1 6A	CGCCCTTCTAAAAAAATAGAATTCAAAAAAA	
11-1 6A	TACTTCGAAAAAAATACGTCCAATAAAAAAA	
13-1 6A	GATTCATCAAAAACTATGCCAGAAAAAA	
15-1 6A	AAGACTAGACAAAAAGACCTAGCCAAAAAA	
17-1 6A	GCAGGAGATAAAAAAGGCATTATCAAAAAAA	
19-1 6A	CAAAGAAGCTAAAAAAATCAGACAAAAAA	
21-1 6A	GGAGACCCATAAAAAGATATCGTATAAAAAAA	
23-1 6A	CCGAGTGAATAAAAATCGAAAGGAAAAAA	
25-1 6A	TGCCTCTTAAAAAA	
2-15 6A	CAGCAACGTAAAAAACCGGCCAACAAAAAA	
4-15 6A	GCCTGAGGTCAAAAACGTTGACTAAAAAA	
6-15 6A	CTTACCCCTGTAAAAATAGATCCGCTAAAAAA	
8-15 6A	GATCTTCTCGAAAAAAAGACGATATAAAAAAA	
10-15 6A	GCACGACACTAAAAGTCTACAGGGAAAAAA	
12-15 6A	GATGTCCTTAAAAACCATAAGGTTAAAAAA	
14-15 6A	GACGCCGATCAAAAATGGTTCTGTAAAAAA	
16-15 6A	TGGCCTGGTCAAAAAGACCCGGCAAAAAA	
18-15 6A	AGACACTACTAAAATTCACTACTAAAAAA	
20-15 6A	CATATGGTGTAAAAAGCGCCCTAAAAAA	
22-15 6A	ACTGTCCACGAAAAATGCGCGGTGGAAAAAA	
24-15 6A	AGTGCAAAGCAAAAATCAGGCGGTCAAAAAA	
a_1	GCACACCTCTAGCTCTATT	
a_2	AGAGGTGTGCGTAACTAAAGGCCTTACACGAGTTAGCAC	
a_3	TGTAAGAGCGTCTCCAGGATCCGAGATCACTAACCGCCACG	
a_4	AGTGATCTCGCAGGCATTAGTCATTCTGTCTGGAGA	
a_5	GACAGGAATGGATCGAGTATGTACATTGACGAGTCCTCAGCT	
a_6	CGTCAATGTACTGCGCTCACAGTAAAGTAAGCAGCTACTGGC	
a_7	CTTACTTTACAATTATCGCAGTAGACACCCGCTACACCGAA	
a_8	GGGTGTCTACGTTCAATTGTTAGCAGTTGGCGCGATAGGCA	
a_9	CCAACGTGTGGCGTCGGGTGGAAGATCGCTTAAAGTT	
a_10	GCGATCTCCTGCCCTAATTAGCATGCACTAGTCACCG	
a_11	ACTGCATGCTTCATACATCGATCGCAATCAAAGAATGTTCCA	
a_12	TTGATTGCGAAAGCTTAAATACGTCCCAGCGAATTCCAA	
a_13	CTATGGGACGCGATTGACTTGGCTGTCACTGACACAAAG	

Connection Tiles

a_14	TGATGACAGCTGCTACATAACAATGAGCGGGATTCTGGCGTAG
a_15	TCCCCGCTCATCTCAACCGGGTAGGACGAACGGGTACCGCTAT
a_16	CGTTCGTCCTCGAGTCCAGAAAGCAGCACAGCCCTCTAAT
a_17	TGTGCTGCTTATTGGAGTCTGTAAATCGTTATCGGATGTC
a_18	AACGATTACGACCACCTACAGCAGAGCCCATTAAATCTATA
a_19	TGGGCCTCTGCACCCGGTTGCCAAGCGCGCGGTGATCTTAGA
a_20	CCGCGCGCTCAGGGCGGCCATCAGACTGACTCCACCCTTA
a_21	TCAAGTCTGATCGAGTAGCAGCCTTCGTTAAACTCAGGAGGT
a_22	TTTACGAAGGCAGAACATCGTGGGGCTCCACTTCAGCCAC
a_23	GGAGGCCAAGTAAACTTCTTATTAAATAGTTTCAGGAAAGTG
a_24	AACTATTAATTCTTCACTTCTGCACCCCTACCAAGCTCCATAT
a_25	GTTAGGGTGCATTAAGAGCAGC
a*_1	AACGACTGTCCCCTTAGTTAC
a*_2	GACAGTCGTTAACGCTGCTGGATTCTATCATTGGCATGTAG
a*_3	ATGATAGAACATGTGCTAACTCGGCCTTACGGGACTAATGCCTG
a*_4	CCCGTAAGGCGAATGAGCATCCAGACACATGGCCTTGAGTT
a*_5	CATGTGTCGTCTCCAGCACACAGACACGGATGTGAGCGCAG
a*_6	TCCGTGTCGTGCGCGGATTGGTACTGATCGCACGACTCC
a*_7	ATCAGTACCAAGCAGTAGCTGGCATACAAATAACAATTGGAC
a*_8	ATTTGTATGCTACTTACCTCGTGTGACATGCATTCCGATCGC
a*_9	GCATGTCACATGCCATTGCGTTAGGACTGTTAATTAGGGCA
a*_10	ACAGTCCTAACCTTACTTTGCTGTTACGATCCCATTGTC
a*_11	CGTAGAACAGCGGTGACCTATGCTTAGACAATATTAAGCTT
a*_12	TTGTCTAACGATGCGCGGTCGCGGTTCTGTAATGGTC
a*_13	GAAAGCCGCGTGGAAATTGTTGAACCGTGTATGTAGCA
a*_14	CACGGTTAACGATTGTGACTCAGCTTGACTAATCAGGCAA
a*_15	GTCAAAGCTGCTACGCCAGAACATCGTCCGCCTCGGACTCGA
a*_16	GGCGGACTGAATGGTAACTTACCGCGCTGCGCAACCCCTAAA
a*_17	CGCAGCGCTGATTAGAAGGCCGACCCCTAGGTGTAGGTGGTC
a*_18	CCTAGGGTCGCGCTTCGGAGACCGTTATCTGTTAACG
a*_19	GATAAACGGTTATAGATTAACTCCATCTTGTGGCCGCCG
a*_20	CAAGATGGGAATCGACGATCAAAGGCCCTGACATTGTTGGA
a*_21	CAGGGCCCTTAACGGTGGAGCACTACACTCGATTCTGGCG
a*_22	AAGTGTAGTGCAGGGCTGCCGATCTGCCAGACTGTCACCT
a*_23	TGGCCAGATCGTGGCTGAAGTATATATTGAGAAGTGGAAAGA
a*_24	TGCAATATATTACGATCATAGTTAACGGTGCAGTCGACGCTT
a*_25	GCACCTAACATATGGAGCTG
b_1	TGGGCACACGAGCTATTAA
b_2	CGTGTGCCACGAACCGGCTGGTAGGTTGCCTTAATTGGTG
b_3	GGCAACCTACTCTCCAGGATCAGCATGAACCAACCAGCCACG
b_4	GGTCATGCTTGGAAAGAGCGCGCAATTATGAGTTCACCC
b_5	TAATTGCCGCGATCGAGTATCGTAGCGGAAAGTCTCAGCT
b_6	TTCCGCTACGTCCAGAGCGTGTGCTGAGTCTGCCATTAGGG
b_7	GACTCAGCGAAATTACATCGCAGAGATGTACAGCTACACCGAA
b_8	TGTACATCTCTGTTGACTGGAGCTGTGGCACCTGTTACCA
b_9	GCCACAGCTCTGGCGTGGCTGATATTGCTTAAAGTT
b_10	GCAATATCAGCCATATTTATACGTGAAATCCGTTACTCCCT
b_11	GATTCACGTTACATACATCGACATCCCTTCAGAATGTTCCA
b_12	GAAAGGGATGAGGAGTTCTATGTAAGTGTCTAAGC
b_13	TATTCACTACCGATTGACTTGGCTGCTTACACTGACACAAAG
b_14	TGTAAGCAGCCCGCTTACATGACGCTAGACCCCTG
b_15	CGTTATGCATCTAACCGGGTTCTGGTCTGGTACCGCTAT
b_16	AAGACCAAGACTTATTACCGGAGATTCTGAGTTGGC

b_17	GAGAATCTCCATTGGAGTCCTGAAAGTTGGTTATCGGATGTC
b_18	ACCAACTTCAATAAACCGCGTTGCCAACCTCGGTGACCATT
b_19	GTGTCGAAACACCCGGTTGCCAACCTCGGTGACCATT
b_20	TGGCGAGTTGGTTAGCGCCCAGGAAACGGACTCGTCAGTCAA
b_21	GTCCGTTCTCGAGTAGCAGATAACCTAGTACTCAGGAGGT
b_22	ACTAGGGTATTCAAGGTATCGCTGAGTCCAGTAAAGGTATTAT
b_23	ACTGGACTCAGTAAACTTCTTATGTAATACTTCAGGAAAGTG
b_24	AGTATTACATCCAAGTCGGCAACCTCCGTTAACCGCTGCTC
b_25	AACGGAGGTTTAAGAGCAGC
b*_1	GTGAAATTGTCAGCCGGTTCG
b*_2	ACAATTTCACTAAGCTGCTGGATTAACCAGTCGGCATGTAG
b*_3	ACTGGTTAACCAATTAAACCGTAGCAGCGCTTCCAAG
b*_4	GCTGCTACGGGAATGAGCATCTCCTACTCACGCCCTGAGTT
b*_5	GTGAGTAGGAGGGTGAACTCAGGTGCGGACACACGCTCTGGA
b*_6	TGTCCGCACCTTGCACGGATTAGATGCCATCGCACGACTCC
b*_7	ATGGCCATCTCCCTAACCGCAATGACTTACACAAGTCAAACA
b*_8	TGTAAGTCATTACTTACCTCGGGCAATCCAATTCCGATCGC
b*_9	TGGATTGCCTGGTAACAGGTTGATGAGACATAAATATGGG
b*_10	GTCTCATCAACCTTACTTTGTCATTGTAATATCCCATTGTC
b*_11	ATTACAATGCAGGGAGTAACGAGCATAGCTTATAGAAACTCCT
b*_12	AAGCTATGCTATGCGCGGGTCGCCATGCAGGTGCTAATGGTC
b*_13	CCTGCATGGCGCTTAGAACACAGTCCTCATTATGAAACGCGG
b*_14	AATGGAGACTGCATTGTGACTGCCATGCATTAATCAGGCAA
b*_15	ATGCATCGGCCAAGGGTCTAGGATAATTGTGGTGAATAAAG
b*_16	ACGAATTATCATGGTAACTACGATGGCGACACGAACCCCTAAA
b*_17	TGTCGCCATCGCCTAACACTCATATGGGATATGCGTATTTATT
b*_18	ATATCCCATACGGCTTCGGAGCAGCGCTGCTGCTTAAATCG
b*_19	GCAGACGCTGAATGGTCACCGGAACGGTCCTTGGCGCTAAC
b*_20	AGGACCGTTATCGACGATCATCGGCTACTACATTGTTGGA
b*_21	AGTAGGCCGATTGACTGACCGACTATACTCCAGCGATACCTGA
b*_22	TGGAGTATGCCAGGGCTGCCCTGCTAGGTGACTGTCACCT
b*_23	ACCTAGCAGGATAATACTTCAGCATACCAGGGCAGTTGG
b*_24	TGGTATGCTGTACGATCATAGATCTGCACAAAGTCACGCTT
b*_25	TTGTGCAGATGAGCAGCGCTT
c_1	TCATGGAGCCAGCTCTATTAA
c_2	GGCTCCATGATGATGCATCCCGTCGGACAGTGGCATTCCC
c_3	ACTGTCGACTCTCCAGGATCTAAAGACCCAACCAGGCCACG
c_4	GGGTCTTAATATCTGCTGTCTATTGTATGTGATCTACGGCC
c_5	ACATACAATAGATCGAGTATGCTGCATGCGAAGTCCTCAGCT
c_6	TCGCATGCAGGGCACTGAAAGTCATGCGCGCTGTGTCTTGGG
c_7	GCGCGCATGAAATTATCGCACCTCATCGTGTACACCGAA
c_8	AACGATGAGGTTATACATATATCCTTGAATCCTATCTAAA
c_9	TTCAAGAGGATGGCGTCGGTCTCGTACTAAGTTAAAGTT
c_10	TTAGTACGAGAAGATTGCCGGCCCAATATACATTCTG
c_11	ATTGCCGGCCTACATCGAGGTCTATGCAAGAATGTTCCA
c_12	TGCATAGACCAACAAAGGCCCTCGTATAGTGCATGTCACCGA
c_13	CACTATACGGCGATTGACTGGGCCAAGCTCTGACACAAAG
c_14	AGCTTGGCCAAGCTTTCTATTCTGAACTTCTACAGAGT
c_15	GTTCGAGAATCTAACCGGGTCGGCTCTGGCGGTACCGCTAT
c_16	GCCAGAGCCGCTGTTAGTGCACAGTCAGCGGAACGTTG
c_17	CGTCTACTATATTGGAGTCCTCGAGGTGCTATCGGATGTC
c_18	GCGACCTCGGAGCATCAACAAATGCAGTGACTGTGAAACAAC
c_19	AGTCACTGCAACCCGGTTGCCGCAGGTGCCGTGATTTAGA

c_20	CGGCACCTGCCTCCCAC T T C C A C A G A G G C T C T G G A G T G T C
c_21	AGCCTCTGTGTCAGTAGCAGGCTATGACAAACTCAGGAGGT
c_22	TTGTCATAGCATGGTGCTCAACGTCTGCTTCTGTACACC
c_23	AGCAGGACGTAAACTTCTTGCTCTGGACTCAGGAAAGTG
c_24	GTCCAGAGCACACGCCCTTGAGTTCCATAACGAGAGTGTAGG
c_25	GTTATGGAACCTAAGAGCAGC
c*_1	TAACCAGAAAGGGATGCATCA
c*_2	TTTCTGGTTATAAGCTGCTGGAGCCCTACGGTCGGCATGTAG
c*_3	CCGTAGGGCTGGAAATGCCCGCTGCCCTGACAGCAGATA
c*_4	AAGGCCGAGCGAATGAGCATCTGACACTATGCCCTTGAGTT
c*_5	GATAGTGTCAAGGCCGTAGATCGAGATTGCTCTTCAGTGCC
c*_6	AGACAATCTTGGCGGATTCTGCTGGCCGCCACGACTCC
c*_7	GGCCGAGCAGCCAAGACACACATTTAAGGCTATATGTATAA
c*_8	GCCTTAAATGTACTTACCTCGGTCAACGAGAATTCCGATCGC
c*_9	TCTCGTTGACTTAGATAGGAGTTACCGTCCGGCAAATCTT
c*_10	GAACGTAACCCCTACTTGTGTCATAGATCCCATTGTC
c*_11	CTATGGAGACCAAGAACATGTATTAAGCTATCGAGGCCTTGTT
c*_12	CGATAGCTTAATGCGCGGGTCTGCTGTTCATGCTAATGGTC
c*_13	TGAAACGACATCGTACATCGGAATCTCCAGAAAGAGTT
c*_14	GGAGAGATTGCGATTGTGACTCGCACGAAAGTAATCAGGCAA
c*_15	CTTCGGTGCAGCTCTGTAGAAAGCTTCACCGATGCACTAACAG
c*_16	TCGGTGAAGCATGGTAACACTACGTGTTAGCCTCGAACCTAAA
c*_17	AGGCTAACACCAAACGTTCCCGAATTGCGGTTGTGATGCT
c*_18	CCGCAATTGCGGGCTTCGGAGCGGGTCCGTTGTTAACATCG
c*_19	AACGGACCCGGAGTTGTTCACTCATCTGCCTGGAAGTGGAG
c*_20	AGGCAGATGAATCGACGATCAGATAACGTGGACATTGTTGGA
c*_21	CCACGTTATCGACACTCCAGGTTATCTCAGTTGAGCACCCAT
c*_22	ACTGAGATAACCAGGGCTGCCCTATGATGGAGACTGTCACCT
c*_23	TCCATCATAGGGTGTACAGGAGCATATCAAATCAAGGGCGTG
c*_24	TTTGATATGCTACGATCATAGAGGCCTGTACAGTCGACGCTT
c*_25	GTACAGGCCTCTACACTCTC
d_1	CCTTCCCCTTAGCTCTATTAA
d_2	AACGGGAAGGTACCAATCATTACTGGCACACATAGGAAATA
d_3	GTGTGCCAGTTCTCCAGGATCGTATCCGACGAACCAGCCACG
d_4	CGTCGGATACGTCGGCTTCTACGGCGAAGCCTGTCCAAG
d_5	TTCGGCGTAGATCGAGTATGGTGGCCTCGAGTCCTCAGCT
d_6	CGGAGGCCACCCAGCCACTTATTGGGTGCGTCTGGACTCA
d_7	CGCACCCAATAATTATCGCACACAGCTCGCCTACACCGAA
d_8	GCGAGCTGTGGCCCAGGGCTATAAACCCGTAAAGCAGGCAAG
d_9	TACGGGTTATGGCGTCGGGTATCTGATTGTTAAAGTT
d_10	GAATCAGATGTGCGTCTGCTGACCTATCTCACGTACCCCAA
d_11	GAGATAGGTCTCATACATCGATAATAGTGCCAGAATGTTCCA
d_12	GGCACTATTATAACATTGTATGCGAACTGCCCTCCGGTCG
d_13	GCAAGTTGCCGATTGACTGGCTCCCTAAGTACGACACAAAG
d_14	TTAGGGAGCCTATTGCGGGATTGAACCTCCCTCCTCGTC
d_15	GAGTTCAATCCTCAACCGGGCTCCTCGTTGGGTACCGCTAT
d_16	CAACGAGGAGGTCTGAGGCACCATCCGAATGGTGTGGTGGC
d_17	ATTGCGGATGATTGGAGTCCTTCGCTGAATTATCGGATGTC
d_18	ATTCAAGCGAACGCCAAGGTGACCATGCTTATCTTGCAGGG
d_19	TAAGCATGGTACCGGGTGGCCAGAGTTCGTGATCTTCTAGA
d_20	CGAACTCTGGTCTATGACTTCGCAAGCTAAACCCCTCGTAGAT
d_21	TTTAGGCTGCTCGAGTAGCAGGCCAAGGATTACTCAGGAGGT
d_22	AATCCTTGGCAGATGAAACTCCTCGTGTGACTTTACTGGCTT

d_23	GTCACACGAGGTAAACTCTTAAGTGGCGTGTCAAGGAAAGTG
d_24	CACGCCACTCACTGCCCATTAATTACATACGCTGATCGG
d_25	ATGTAATTATTAAAGAGCAGC
d*_1	TAAGCGTCAGAATGATTGGTA
d*_2	CTGACGCTTATAAGCTGGCCCTCCCTAGTCGGCATGTAG
d*_3	CTAGGGAAGGTATTCCTAATCACTGACAAGGAAACGCCGAC
d*_4	CTTGTCACTGGAATGAGCATCAGGCAGGAAAGCCCTGAGTT
d*_5	TTCCGCGCCTCTGGACAGGCGCAATCGCCAAGTGGCTGG
d*_6	GGACGATTGCTTGCAGGATTAGGGCTGCCGACAGACTCC
d*_7	GGCAGGCCCTTGAGTCCAAGAATAAGTCTTAGGCCCTGGC
d*_8	AAGGACTTATTACTTACCTCGGGCGTTAACGATTCCGATCGC
d*_9	CTTAAACGCCCTGCCTGCCTCAATAAGCGAGCACGCA
d*_10	GCTTTATTGACCTTACTTGTGAGAGGCCACATCCCATTGTC
d*_11	GTGGCCTCTCTAGGTACCGTGTATGTTAACATGTTA
d*_12	AACATACAGCATGCGCGGGTCCCGTTATCCTGTAATGGTC
d*_13	GGATAAACGGCGACCGGAGCGCGTTAACACACGCAAATA
d*_14	TAGTTAACGCGCATTGTGACTTGAGAATATCTAACAGGCAA
d*_15	GATATTCTCAGACGAGGAAGGCTGCCGAGCGTGCCTCAGAC
d*_16	GCTCCCGCAGATGGTAACTACATACCAAAACACGAACCCTAAA
d*_17	TGTTGGTATGGCACCACACCGAGAGACCTCCACCTGGCG
d*_18	GAGGTCTCTCCGGCTTCGGAGGTTGAAAGAGTGTCTTAATCG
d*_19	CTCTTCAACCCCGCAAAGAACGCGCCAGAACAGTCAAGA
d*_20	TGGCGCGCTATCGACGATCACTATCGCCTACATTGTTGA
d*_21	AGGACGATAGATCTACGAGGGCGATACAGAGGAGTTTACATCT
d*_22	CTCTGTATGCCAGGGCTGCCGTGGAATCAGACTGTCACT
d*_23	TGATTCCACGAAGCCAGTAAACTGGAGTTAACGCGCAGTG
d*_24	TAACTCCCAGTACGATCATAGAGAGCATAGTCGACGCTT
d*_25	ATGATGCTCTCCGATCAGCGT
e_1	ATAACAATATAGCTTATTAA
e_2	ATATTGTTATGCATCTGTAGTAGGGTTATTCTAGATGGTC
e_3	AATAAACCTCTCCAGGATCTGGTAGACTAAACCAGCCACG
e_4	TAGTCTACCAGTGCAATATCGTACGTTAACGACGGCTAT
e_5	TAAACGTACGGATCGAGTATGCTATTCAACAGTCCCTAGCT
e_6	GGTAAATAGCGGAACCAGGTTCCAGATAACAGGTTAATTGT
e_7	GTATCTGAAAATTCTATGCCAGGGCTCTGGTACACCGAA
e_8	CAGAGACGCCATGCCCGCATATAATCATCTTGTAAAGCCG
e_9	AGATGATTATTGGCGTCGGTAGATGTGGAGGTTAAAGTT
e_10	CTCCACATCTCTGTACGCATAATTATTGATTGATTACATT
e_11	TCAATAATTATCATACATCGATTGGAACCTTAGAATGTTCCA
e_12	AAGGTCCAACCGGCTTGGTAGTACTCATTGGCAAGGGCC
e_13	AATGAGTACTCGATTGACTTGCCTGCGATGTCGACACAAAG
e_14	ACATGGACGCTCTGTGAGATCTAGGGCACCATGGAATGAT
e_15	GGTGCCTAGCTAACCGGGTCTCTCTAGGTACCGCTAT
e_16	TAAGGAAGGACTGTCGGCGCTGAGGCATCCACGACAGCAC
e_17	GATGCCCTCAATTGGAGTCCTCAGTCAGATATCGGATGTC
e_18	TCTTGACTGAGGTTCCCTTGTGACTGATGCGACTTATAAT
e_19	GCATCACTACACCCGGTTGCCATGATTGGCTGATCTTAA
e_20	GCCCCAATCATACAGCCGGAGGACGCTAACAGTTAACGTT
e_21	TGTTAACGCGTGGAGTAGCAGAACAGCTTATAACTCAGGAGGT
e_22	TATAAAGCTTGGAGTCTGATGCTAGTCGAAAGGTAAGATAGA
e_23	CTTTCGACTAGTAAACTCTTAACATGCCATTCAAGGAAAGTG
e_24	ATGGCATGTTATGGAGGGATCCGTCGGACCGATCGCCTC
e_25	GTCCGAACGGTTAACGAGCAGC

e* _1	GAACCCGCAGACTACAGATGC
e* _2	CTGCGGGTTCTAAGCTGCTGGAATAACTCGATCGGCATGTAG
e* _3	TCGAGTATTAGACCCATCTAGTGCCTGAGCTATATTGGCAAC
e* _4	AGCTACCGCAGAATGAGCATCTGGTCCTACGCCCTGAGTT
e* _5	GTAAGGACCAATAGCCGTGCTGGAGTCGTATCCGGTCCCG
e* _6	ATACGACTCCTTGCGCGGATTGTGGACGGCGCACGACTCC
e* _7	CCCGTCCACAACAATTAACTATCTAACACATGCGGCGCAT
e* _8	GTGTTAGATTACTTACCTCGGTTCGATAAGATTCGATCGC
e* _9	CTTATCGAACCGGCTTAGCATACACACCGATGCGTACAGAG
e* _10	TCGGTGTGTACCTTACTTTGTAGAAAGTGGGATCCCATTGTC
e* _11	CCCACCTTCTAATGTAATCAAGGCCGACCCACCAAGCCGGT
e* _12	GGGTGGGCCATGCCGGGCGTAGGAGTTCTGCTAATGGTC
e* _13	GAACCTCTACGGCCCTGCCCCGTTGGTCCCATCTCACAGAG
e* _14	GGGACCAACAGCATTGTGACTCCGCCACTCTAACATCAGGCAA
e* _15	GAGTGGCGGATCATTGCAACCACCTGAGCCGCGACAG
e* _16	TCAGGGTGGTATGGTAACACTACGCTTCCCTACGAACCCCTAAA
e* _17	TAGGAAAGCGTGTGTCGTGGCCTTAGTGGACAAAGGAACC
e* _18	CCACTAAGGCCGCTTCGGAGACATCGCTTGTAAATCG
e* _19	AAAGCGATGTATTATAAGTCCGAGGGTAACCCCTCCGGCTGT
e* _20	GTTACCCCTCGATCGACGATCACTGGCTGGCACATTGTTGA
e* _21	GCCAAGCCAGCAACTTACAACAAGTTCGCGAGCATCAGACTC
e* _22	TCGCGAACCTCAGGGCTGCCTGCGTCGCCGACTGTCACCT
e* _23	GGCGACGCAATCTATCTTACGACATGGCGATCCCTCCCAT
e* _24	CGCCCAGTCTACGATCATAGATTAGGATCTAGTCGACGCTT
e* _25	AGATCCTAATGAGGACGATCG
f_1	GCAGAATCTCAGCTCTATTAA
f_2	GAGATTCTGCTGCCAGTTGTGACATATCCGCCTACAGTATA
f_3	CGGATATGTCTCTCCAGGATCGGCCTGACTTAACCAGCCACG
f_4	AAGTCAGGCCATGCAATTGGTAGGTGTCGGACACGCCAAC
f_5	CCGACACCTAGATCGAGTATGATCGACATGAAGTCCTCAGCT
f_6	TCATGTCGATGCCCTGCACAGTGAACCTCACTTCTGGTTCGCG
f_7	AGTGAGGTTCAATTGATGCCGAGAACGAAAGCAGCTACACCGAA
f_8	TGCTTCGTTCATAGTAGCATGCCCTAGGCGGACTCCACAAT
f_9	CGCCTAGGCCTGGCTGGGTTTGATAGAGGTTAAAGTT
f_10	CTCTATCAAATCAAGATGTCGGTTGTCCTGCCATACCGGC
f_11	AGGAGACAACATCACATCGAGTCGACGTTAGAATGTTCCA
f_12	AAACGTCGACAGTGATTGACCCCTATAATGGGATCAATAAGA
f_13	CCATTATAGGCAGTGACTTGAGTTGTTCTGACACAAAG
f_14	AAACACAACCTCTGTGAGAAGTGTGACGAAAGGATTGACCT
f_15	TTCGTCAACACTCAACCGGGTCGCCCTAGGCGGTACCGCTAT
f_16	GCCTAAGGCGGATACGCTGGATACGTCATCGCTAACGCTGAC
f_17	GATTGACGTAATTGGAGTCCTCAACCTGTCGATCGGATGTC
f_18	CGACAGGTTGCGAACGCTCCCTCGTGGCAGACTCGCAAAGT
f_19	CTGCCACGAGACCCGGTGCCTACACATTGATCTTACA
f_20	AATTGATGAGTAACGTCAGCTAATCGGGTACGTTCT
f_21	CCGATTAGCTTCGAGTAGCAGAAAGTATAGGACTCAGGAGGT
f_22	CCTATACTTTGAGATCTTAGCAAATTGTATGGATGCCGCAA
f_23	ATACAATTGGTAAACTTCTTGTGCCAGCATCAGGAAAGTG
f_24	TGCTGGCAACAGATTCAAGCAGACTCAATTCTCTGAGGCGTG
f_25	GGAATTGAGTTAACGAGCAGC
f* _1	TCTAGTGTCTACAACTGGCAA
f* _2	AGACACTAGATAAGCTGCTGGAGTCCGGGATCGGCATGTAG
f* _3	TCCCGGGACTTAACTGTAGGCGCAGGTACTCAAATTGCA

f* 4	AGTACCTGCGGAATGAGCATCTGTCAAATGCCCTGAGTT
f* 5	GATTGACAGTGGCGTGTGTTAGACCTGACTGTGCAGGC
f* 6	CAGGTCTAACCGCAGGATTAGTAAGAACCGCACGACTCC
f* 7	GTTCTTACTCGAACCAAGATCGAGTCACATGCTACTAAT
f* 8	GTTGACTCGATACTTACCTCGCTAAACGACCATTCCGATCGC
f* 9	GGTCGTTAGATTGTGGAGTCACAGGGTGCACATCTTGAC
f* 10	CGCACCCGTGCTTACTTTGTCTGATTGCGCATCCCATTGTC
f* 11	GCGCAATCAGGCCGGTATGCCGGCATTCTGTCAATCACT
f* 12	GAGAACATAGGTCAATCCTTCTTGCAGTCAGCGTATC
f* 13	ATGGATAAACTCTTATTGATCGTGAGCTGCTTCTCACAGA
f* 14	AGCAGCTCACGCATTGTGACTATATGTTCATAATCAGGCAA
f* 15	TGAAACATATAGGTCAATCCTTCTTGCAGTCAGCGTATC
f* 16	CTCGCAAGAAATGGTAACTACCTCTGGCCAAACCTAAA
f* 17	GCCAGAAGAGGTCAAGCTTAGCGTATCCACTGGGAGCGTTGCG
f* 18	CAGTGGATACCGCTTCGGAGGCTCTGAATGTTAATCG
f* 19	TTCAGAGAGCACTTGCAGTGGTCGCAGGGCAGACGTTAC
f* 20	CCTCGGACCATCGACGATCATGCACCTCTCCACATTGTTGGA
f* 21	GGAGAGTGCAGAAACGTCAGCTAACAGGCTAACAGGCTAAC
f* 22	CCTGTTGAGCCCAGGGCTGCCGACCCGATAAGACTGTCACCT
f* 23	TTATCGGGTCTTGCACATCCTGGTAGGCGTCTGCTGAATCT
f* 24	ACGCCTACCATACGATCATAGGGAGGTTCAGAGTCGACGCTT
f* 25	CTGAACCTCCCACGCCTCAGA
g 1	TTTCTCAATAGCTTATTAA
g 2	ATTGAAGAAATTGCTGCTTCTCACTAGTTAATTCTCTCCAC
g 3	TTAACTAGTGTCTCCAGGATCGCCGCCACCAACCAGCCACG
g 4	GGTGC CGCGTCTGGTCATGGACGCGTGTATATGCT
g 5	CGACCGTCCGATCGAGTATGTACAAACGTCAGCCTCAGCT
g 6	GACGTTGACTGGCGCGAATAACGGCCCTATGGTTCGA
g 7	GGGCGCGTAAATTATCGCGAAGTGGTCACTACACCGAA
g 8	GTGACGCACTAGGTGATCAGGAGAATAATGACATAGGTGGCT
g 9	TCATTATTCTTGGCGTGGGTCCACGGGTTAAAGTTT
g 10	CCGGTGGACCTTAGCAGGACGTTACCGTCCGGCCCTCTGTT
g 11	CGGACGGTAATCATACATCGAGAACGGTCTCAGAATGTTCA
g 12	GAGACCGTCCCGCGAAGATCAGCAAAGAGTGTGAGGGCG
g 13	CTCTTGCTGCATTGACTTGCAGGGTATGCTGACACAAAG
g 14	CATACCTCGACCTAACGACTCCTGAAGGGCGTCAACCCGT
g 15	GCCCTTCAGGCTAACCGGGTGTATAAGGCCGTACCGCTAT
g 16	GGCCTATACTTAATGACCAAAGATGCCCTACGACAGGTCCGA
g 17	GTAGGCATCTATTGGAGTCCTTAGCGCTACTATCGGATGTC
g 18	GTAGCGCTAACGAGTGGTATGAGGTGACTATGAAAGTGGT
g 19	TAGTCACCTACCGGTTGCCCTCAATTCTGATCTTACA
g 20	AGAATTGAAGATAGCGTCAACGATCTAGCACAGGAGTATC
g 21	GCTAGATCGTCCAGTAGCAGTGAAGCAATCACTCAGGAGGT
g 22	GATTGCTTACAAGCTAACAGTTAGGTGTTACTACCGA
g 23	CACACCTAACGTAACCTCTTAGTTCGTCAGGAAAGTG
g 24	CGAAACTAACGATATGTCTGGACGCTACTGAAAGACTT
g 25	TATAGCGTCCTAACGAGCAGC
g* 1	AGTACACCTGAGAACGAGCAA
g* 2	CAGGTGTACTTAAGCTGCTGGAACAGACATGTGGCATGTAG
g* 3	CATGTCTGTTGGAGAGAAACTGAGAACGATGACCAAGAC
g* 4	GCGTTCTCAGGAATGAGCATCATTAAACTGCCCTGAGTT
g* 5	CAGTTAAATAGCATATAAAGAGGCCACAACCTCGCGCCAG
g* 6	GTTGTGGCTTGCACGGATTTCGTCTGCCGCACGACTCC

g* 7	GCAGACGAAATCGAACCGATAACGAAGTTAACCTGATCACCT
g* 8	TTAACCTCGTTACTTACCTCGACAAGTCCCGATTCGATCGC
g* 9	CGGGACTTGTAGCCACCTATGATATATGGATCGCTCTGCTAA
g* 10	ATCCATATATCCTTACTTTGACTCGCCTTATCCCATTGTC
g* 11	AAGGCCGAGTGAACAGAGGGCTGAATCATGGATTCGCGCG
g* 12	CCATGATTCAATGCGCGGGTGGTATGTTGCTAATGGTC
g* 13	ACATACCACCCGCCTGCATCATTCTGAAAGTAGCTTAGGT
g* 14	TTCCACAGAAGCATTGTGACTTCCTGAAATTAAATCAGGCAA
g* 15	ATTTCCAGGAACGGGTTAGACGCGAATTCAATTGGTCATTAA
g* 16	ATGAATTGCGATGGTAACTACAGATCGACAACGAACCCCTAAA
g* 17	TTGTCGATCTTGGACCTGTCGGATATGAGTCATACCTGTC
g* 18	ACTCATATCCCGCTTCGGAGCTGTTGATGCTTAATCG
g* 19	TCAACAAACAGACCACTTCATCAATCACTGTTGACGGCTAT
g* 20	ACAGTGATTGATCGACGATCAAGGAGGGTATACATTGTTGGA
g* 21	ATACCCTCCTGATACTCCTGTTCAAGGTTGTTAGGCTTG
g* 22	ACCTTGAACCCCAGGGCTGCCGGTCACGGCAGTGTACCT
g* 23	GCCGTGAACCTCCGTAAGTAATAAGCAGGTGCAAGACATATG
g* 24	CACCTGCTTATACGATCATAGTCTAGACTCAAGTCGACGCTT
g* 25	TGAGTCTAGAAAGCTTTCAAG
h 1	GGTCGAGGGAAAGCTCTATTAA
h 2	TCCCTCGACCGCTCGATATCGTTACTCTGAGCTTAAAGGCC
h 3	TCAGAGTAAATCTCCAGGATCCGGCATTCAAACCAAGGCCACG
h 4	TGAAATGCCGGTCCCTGATTCCTGAAGCGGCTCCCTAGATA
h 5	CCGCTTCAGGGATCGAGTATGACGACATTGAGTCCTCAGCT
h 6	CAATGTGCGTCTAGGATCCAATCCCTATCATAAAGCCCAC
h 7	GATAGGGATTAATTATCGACAACTCCATGCTACACCGAA
h 8	ATGGGAGTTGCTCCGATTACGGAGGTAACACTGCAAGCG
h 9	TTTACCTCCGTGGCGTCGGGTACCGAAGGAAGTTAAAGTT
h 10	TTCCCTCGGTGCGCAGCCACCGTAGACCGCTGTTCTCGGT
h 11	AGCGGTCTACTCATACATCGATTGCGATCTCAGAAATGTTCCA
h 12	GAGATGCGAATCCACACCTAGTTGAGTCGTTATGAGCTCT
h 13	AACGACTCAACGATTGACTTGTAAAGTCCACTGACACAAAG
h 14	TGGACCTAACAGTAAAGCATTAGGAGTCCAGGTAAATCATAA
h 15	TGGACTCCTACTCAACCGGTATCTGCCCTGGTACCGCTAT
h 16	AGGGCAAGATTACATAAACAGAGACTGCGCCGACCGACTC
h 17	GCGCAACTCTATTGGAGTCTAGTGTATGAGTATCGGATGTC
h 18	CTCATACACTATTATGTGCTTATTGCCGGTCTGCTCT
h 19	ACCCGGAATACCCGGTGGCAGTGAGCGGATGATCTTAA
h 20	TCCGCTCACTCTTACAATCACTATTACGTGAATGTACAAT
h 21	ACGTAATAGTCGAGTAGCAGTCTTCTATGAACTCAGGAGT
h 22	TCATAGAAGACGATGGGAAAGCCGTCTCGATGATGTACAACG
h 23	ATCGAGACGGTAAACTCTTTAGAGTAACTCAGGAAAGTG
h 24	GTATACTCTAACTAGGTAGACCCGTGGTCGAGTCCGGAAAGT
h 25	TCGACCACGGTTAAGAGCAGC
h* 1	TGCCGCTCGACGATATCGAGC
h* 2	TCGAGCGGCATAAGCTGCTGGAGAAAGCAATTGGCATGTAG
h* 3	ATTGCTTCTGGCTTTAACGCTATCCTAGCCGAATCAGGAAC
h* 4	GGCTAGGATAGAATGAGCATCGCTAGGGAGTGCCTTGAGTT
h* 5	ACTCCCTAGCTATCTAGGGAGACGAGACTACGGATCTAAG
h* 6	GTAGTCTCGTTGCGCGGATTTAACGGCTAGCGCACGACTCC
h* 7	CTAGCCGTTAGTGGCTTTATCGCTGGCAGCTGAATCGGGAG
h* 8	GCTGCCAGCGTACTTACCTCGGGCTTGACTAATCCGATCGC
h* 9	TAGTCAAGCCCGCTTGCAGTGTCCAGAAGAAGCGTGGCTGCG

h* 10	TTCTTCTGGACCTTACTTGTATCACAGACGATCCCATTGTC
h* 11	CGTCTGTGATACCGAAGAAACTCGCGAGCCGCTAGGTGTGGA
h* 12	CGGCTCGCGAATCGCGGGTGCAGACCGTGTGTAATGGTC
h* 13	ACCGTCTGCAGAGGCTACATACAAGCTATATGCTTACTG
h* 14	ATAGGCTTGTGCATTGTGACTGTGAGAATTAAATCAGGCAA
h* 15	AATTCTGCACTTATGATTACCCATACCCATGCTGTTATGTA
h* 16	CATGGGTATGATGGTAACTACCCAATATCACCGAACCTAAA
h* 17	GTGATATTGGGAGTCGGTCCGATGCACGGTAAGCACATAAT
h* 18	ACCCGTGCATCGGCTTCGGAGCGAAATCATTGCTTAATCG
h* 19	AATGATTCGAAGAGCAACAGATAGAACTATTGATTGTAAG
h* 20	ATAGTTCTATATCGACGATCAAACGTACCGCACATTGTTGGA
h* 21	GCGGTACGTTATTGTACATCGGTGCCACTCTTCCCATCG
h* 22	AGTCGGCACCCCAGGGCTGCCCTGCCAGCCAGACTGTCACCT
h* 23	TGGCTGGCAACGGTGTACATCGTTGGACC CGCTACCTAGT
h* 24	GCGGTCCA ACTACGATCATAGATTATGCCCTAGTCGACGCTT
h* 25	AGGGCATAATACTCCGGAC
i 1	CACTTAGTTAGCTCTATTAA
i 2	AAACTAAGTGGATACGCTTATCAGAACGCTGCCATGTTT
i 3	AGCGTCTGATCTCCAGGATCCAGAGGCAATAACCCAGCCACG
i 4	ATTGCCCTGCGACTTTAATGCCCTACGTCGTTGCAACCTG
i 5	ACGACGTAGGGATCGAGTATGGGCAAAGACCAGTCCTCAGCT
i 6	GGTCTTGCCGTCGCTCGATCAGAACTGTATAAAGCATCA
i 7	ACAGTTCTGAAATTATCGCAGACAACTCGAGCTACACCGAA
i 8	TCGAGTTGCGGAGTCGGGAAACGACGGTCTTAAGAAACA
i 9	GACCGTGC GTTGGCGTCGGGTGTTGATAGGTGTTAAAGTT
i 10	ACCTATCAACGCTAGTGGATTACCCCTCAGGGCTCAGCCC
i 11	CTGAGGGTAATCATACTCGAAGTCTCAGAGAGAAATGTTCCA
i 12	CTCTGAGACTGGACACGTACATGACGACAATCTGTTATGC
i 13	ATTGTCGTCACGATTGACTGTGTCACCTCAGTCTGACACAAAG
i 14	ACTGAGGTGACTTGGTAGGCCGATTGAGTACAATTAGAAA
i 15	ACTCGAACATCGCTAACCGGGCTTACCTCTAGGTACCGCTAT
i 16	TAGAGGTAGGTCTCCAGGCCATACTATGACTAGCCCCAAACA
i 17	GTCATAGTATATTGGAGTCCTATCACCGCGATATCGGATGTC
i 18	TCGCGGTGATGGTAAATGCCCTCATCAATCAATATAAGCTT
i 19	GATTGATGAGACCCGGTGCATGGACGTCGATCTT TAGA
i 20	CGACGCCATAAGGCTAGAGCGTTACGTCTAGGTGAGGACCA
i 21	TAGACGTAACTCGAGTAGCAGCAGATCTAAACTCAGGAGGT
i 22	ATTAGATCTGGTGGTTACTGTGTA CGAACGGTAGCTCGGGCC
i 23	CCGTCGTCAGTAAACTTCTGTTATCTATTCAAGGAAAGTG
i 24	ATAGATAAACCGGGCTTGT CATTACCTCGGTGACGGAATAG
i 25	CCGAGGTAATTAAAGAGCAGC
i* 1	TGAAGCATCTAAAGCGTATC
i* 2	GGATGCTTCATAAGCTGCTGGCCTCCAGCTCTGGCATGTAG
i* 3	GAGCTGGAGGAACATGCCGAGAACACTACTCATTAAAGTCG
i* 4	AAGTAGTTCTGAATGAGCATCGTACAACATGCCCTGAGTT
i* 5	ATAGTTGTACCGAGGTTGCACAAGGCTCTGTGCGAACGCGAC
i* 6	CACAGGACCTTGC CGGGATTGCCCGTTACCGCACGACTCC
i* 7	GTAACGGGCCTGATGTTATGTCCTTCTCCACTCC
i* 8	GGAAAGAGACTACTACCTCGTTGCACCTCCATCCGATCGC
i* 9	GGAGGTGCAATGTTCTTAAAGGTCAATCCCTCCACTAGGC
i* 10	GGGATTGACCCCTTACTTTGTTATACCGAAATATCCCATGTC
i* 11	ATTCTGGTATGGGCTGAGGCCCTGGTATGTATGACGTGTCC
i* 12	TACATACCAGATGCCGGTCCCTAGCGGAGTGCTAATGGTC

i* 13	CTCCGCTAAGGCATAAACAAAGCCGTCTGGCGCTACCAAG
i* 14	CCAGACACGGGCATTGTGACTCTTCCTGTTAATCAGGCAA
i* 15	ACAGAGAAAGTTCTAATTGTGCTTGGAAACGCCCTGGAGA
i* 16	TTTCCAAGCATGTAACATAAAAGATTCCGAACCTAA
i* 17	GAATCTTATTGTTGGCTAAGGGCTCCTCGCATTACCG
i* 18	AGGAAGCCCTCGGCTTCGGAGAACTAAGTGCTTAGCCT
i* 19	CCAGTTAGTTAACGTTATTCGATAACGCTCTAGCCT
i* 20	GTTATCGTAGATCGACGATCAGGCAGTCATCACATTGTTGGA
i* 21	GATGACTGCCTGGCCTCACCTAACCCGGGCACAGTAACCAC
i* 22	GCCCCGGTTACCAGGGCTGCCTAGCGCCTGCGACTGTCACCT
i* 23	GCAGGCCTAGGCCGAGCTAACCTGACGAGACAAGCCG
i* 24	TCGTCAAGGTTACGATCATAGAGTCCGAGTAGTCGACGCTT
i* 25	ACTCGGGACTCTATTCCGTCA
j 1	GGGAATATCCAGCTATTAA
j 2	GGATATTCCGTTATTGGCCTGTATTTCGCGGACTGA
j 3	AAATATGACATCTCCAGGATCGTCCGTACAGAACCGCCACG
j 4	CTGTACGGACTTACACCCGACATAGTGGTGGTACAGGGCCGA
j 5	CCACCACTATGATCGAGTATGAGATAAGCGTAGTCCTCAGCT
j 6	ACGTTATCTGACTTCACACCGTGCATTGGTCGTCCACG
j 7	CAATGGCACGAATTCATCGCATCAAGTTACGGTACACCGAA
j 8	CGTAACCTGACCTTCCATTGCTCTAGGGCAAATGCAAAG
j 9	CCCTAGAGACTGGCGTGGTCTTATAATTAGTTAAAGTT
j 10	TAATTATAAGGAAAGTAGATCTGCATTTCAGCGCACCTCCT
j 11	CTGAAATGCATCATACTACATCGATCTGAAAGGGAGATGTTCCA
j 12	CCCTTCAGAGCCTGTTCAGTTAGCGTATTGTCGCTTC
j 13	TACGGCTAACCGATTGACTGGTATTGAGGTCTGACACAAAG
j 14	ACCTCAATACCAATGCCGCGAAAGACGAATAGAAATTGAC
j 15	TTCGCTTTCTCAACCGGGTGTCTATATAGGTACCGCTAT
j 16	TATATAGACGCTTGGCGTGGCTCTGTCTATTAAACCTAGAT
j 17	TAGACAGAGCATGGAGTCCTACTGCAAACATACGGATGTC
j 18	GTTTGCAGTACGGTACTCGCCAGGTACAGAATAATGTGCG
j 19	CGTATGACCTACCCGGTTGCCGTGACTTACGTGATCTTAA
j 20	CGTAAGTCACAAGAACTACCGAACCGACAAGGACGAAACGA
j 21	CTTGTGGTTCGAGTAGCAGCAAGGCCAGTACTCAGGAGGT
j 22	ACTGGCCTTGGCGACTATTCTAGCACTCAATGGAGTTGGTT
j 23	TTGAGTGCTAGTAAACTCTTAAGAGGGCGTTCAGGAAAGTG
j 24	ACGCCCTTCGTTGGAGAATTGGCTATGTGCACAATCTG
j 25	CATAGCCAATTAAAGAGCAGC
j* 1	GATATGCTTAGGCAATAAAC
j* 2	TAAGCATATCTAAGCTGGAGAGGATTAATCGGCATGTAG
j* 3	TTAACCTCTCAGTCCCGGTATCGTACGAGTCGGGTGAA
j* 4	TCGTACGATAGAATGAGCATCTTAAATGCCCTGAGTT
j* 5	ATTAATAAATCGGCCCTGAGAAGGGGAGCGTGTAAAGTC
j* 6	GCTGCCCTTCGCGCGATTCTAATCGTCGACGACTCC
j* 7	ACCGATTAGGCGTGGACGACCTAACTGACAGGAATGGAAAGG
j* 8	CTGTCAGTTAACTTACCTCGATCGATTAAATCCGATCGC
j* 9	TTAAATCGATTTGCATTGTGAGCTGGCGATCTACTTCC
j* 10	GGCCAGCTCACCTTACTTTGTGCGTACCCATCCATTGTC
j* 11	GGGTCAGCGCAGGAGGTGCCGTAGGACCGTCTGAAACAGGC
j* 12	ACGGTCCTACATGCGCGGGTCGCTTATTACTGCTAATGGTC
j* 13	AGTAATAAGCTGAAGCGACAACGACCCCTAGGACGGCATTG
j* 14	CTAAGGGTCGGCATTGTGACTTCTCTAAATAATCAGGCAA
j* 15	TTTAGAGGAAGTCAATTCTATTCCATGGCCAGCCAAAGAG

j* 16	GCCATGGAAAATGGTAACTACTGATGTGTGCCGAACCCCTAAA
j* 17	GCACACATCAATCTAGGTTAACCTGTGAGACGGCGAGTACCG
j* 18	GTCTCACAAAGCGGCTTCGGAGCAAAGAGAGGTGCTTAATCG
j* 19	CCTCTTTGCGCACATTATTCTAAACAGGCGTAGTTCTT
j* 20	CCTGTTAAGATCGACGATCAGTACTGTACAACATTGTTGGA
j* 21	TGTACAGTACTCGTTCTGCGCCGGCTAAGAAATAGTCGG
j* 22	TTACCGGGCGCCAGGGCTGCCAATATGCCTAGACTGTACCT
j* 23	TAGGCATATTAAACCAACTCGAGTATAACACGTCTCCAACCG
j* 24	CGTTGTATACTACGATCATAGTGGTGAGAGAGTCGACGCTT
j* 25	CTCTCAACCACAGATTGTGCA
k 1	CCCTTAGGCTAGCTATTAA
k 2	AGCCTAAAGGGAGTGAGTGC AAATATATGAATTAGGTATCGTA
k 3	ATTCA TATATTCTCCAGGATCAGTGCCTGAACCAGCCACG
k 4	CAGGGCAGCTAATCGGCCACGGCGCAGTGC ACCATGTGCCATT
k 5	GTC ACTGCGCAGTGCAGTATGTTATTGTTATTAGTCCTCAGCT
k 6	AATA ACAATAACGCCGAAAGC ATCGGCCTCGGGTGCAGA
k 7	GAGGACCGATAATT CATGCGATTGTTAAGGGGCTACACCGAA
k 8	CCCTTAACAAT GTGTCGAGGGCTCGGG GATACCTGTGGTCT
k 9	ATCC CGGAGCTGGCTCGGGT CCACCATGCAGTTAAAGTT
k 10	TGC ATGGTGGAGACTAGGC CTAGAGAATTAGCTTACATCTC
k 11	TAAAT TCTCTTCATA CATCGACAACCATGC AGAAATGTTCCA
k 12	GTC ATGGTGGTGCAGAAGCT GAGTTATCTCGCGGACCGCT
k 13	GAGATA AACTCCGATTGACT TGACCTCCAACCT GACACAAAG
k 14	GGTTGGAGGTCGATT CAGTTGACCTTATAGC CGTGC GTGGC
k 15	GCTATAAGGTCT CAACCGGTTAATAG GGCGGTACCGCTAT
k 16	GCC CTTATAATACGT CAAAGGATGATA GGTCAGTGGTCAA
k 17	GACCTAT CATATTGGAGT CCTGCATGTGATA ATCGGATGTC
k 18	TATC CACATGCTCT CCACACTCGGG TACACGTC GTTAAATG
k 19	GTGGT GACCCACCGG TTGCCTGGA ATAATATGAT CTT AGA
k 20	TATTATT CCAGAGC AAATGCT CGACAGGT GTAAGCC GCCCTC
k 21	ACAC CTGTC GAGTAGC AGCCC GATAATT ACTCAG GAGGT
k 22	AATTAT CGGAA ACTAAC AGAGG AGATAG GACC ACCA ACTCTT
k 23	GTC CTTATCT CGTAAACT CTTGC ACCG TTATT CAGGAA AGTG
k 24	ATAAC CCGTC CTCTT ATT CATGG TATAT GTT CCTG TTT AT
k 25	CATAT ACCATT AAGAGC AGC
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k* 2	TCAT AGC ACGTA AGCT GCTGGGG GATACT CTTC GGCAT GTAG
k* 3	AGAGT ATCC CTACG ATA CCTATT CTCG TGGCG TGGCC GATT
k* 4	CCAC GGAGA AGAA ATGAG C CATCC CAGGA ATGAG GCC CTTG GAGTT
k* 5	CTC ATT CCT GAA ATGG C ACAT GAA AGAG GAT CG CTT CG CCG
k* 6	GAT CCT CTT TGC CG GGATT AC GTAC AG GTC GAC ACT CC
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k* 8	GCTT ACT CT ATA CT AC CTCG CG GATA AC GC ATT CCG AT CGC
k* 9	GCGT AT CCGA AG ACCAC AG GT CC TA AC GAC AG GC CT AG GT
k* 10	GTC GTT AGGG CCT ACT TTG TC CTG TCT TA AT CC ATT GTC
k* 11	TAAAG AC AGGG GAG AT GTA AG CG GAG CC CT CG AG GTT CT GCA C
k* 12	CGA AGGG CT CAT GCG GGGT CT CGGG TAGT AT GCT A AT GG TC
k* 13	TACT ACCC GA AG CGG TCC CG GT CAC GA ACT GCA ACT GA AT CG
k* 14	CAG TTC CGT GAG CATT GT GACT ATA TAC GTT AA CAG GCA A
k* 15	ACGT GT TAT GCC CAC CG GAC GTT CC ACT TT CC TT GAC GTA
k* 16	GAA AGT GG AA AT GG TA ACT ACC GA AG CT TAT CGA AA CC CT AAA
k* 17	ATA AG CT CG TT GC ACC ACT CC CAG AAG T CT GAG T GT GG GAG A
k* 18	AAG ACT T CT GCG GTT CG GAG T CT CATT GG CT GCT TTA AT CG

k* 19	GCCAATGAGACATTAAACGACCACTCTACAGAGCATTGCTC
k* 20	CTGTAGAGTGTGACGATCAAACCCACCGTACATTGTTGGA
k* 21	ACGGTGGGTTGAGGGCGGCTTGACGAGCCTCTGTAGTT
k* 22	GAGGCTCGTCCCAGGGCTGCCAACCTAGGTGACTGTACCT
k* 23	GACCTAGGTGAAAGAGTGGTGTCCATTGTAGAATAAGAAG
k* 24	TACAATGGAATACGATCATAGACACTAAGCTAGTCGACGCTT
k* 25	AGCTTAGTGTATAAACAGGAA
1_1	CTATTAGGAAAGCTCTATTAA
1_2	TTCCTTAATAGAACCTCTAAGGGCATCAACACGCGCGATGATG
1_3	GTGTTGATGCTCTCCAGGATCTTGAAGCCAAAACCAGCCACG
1_4	TTGGCTTCAATCCTTAGATTATTATGACGTGCTCTGGCT
1_5	GTCATATGAAGATCGAGTATGTGTGAACCTGAGTCCTCAGCT
1_6	CAAGTTCACATAAGGGCGATACTCCGCCGACCGACAGGAGTA
1_7	GTCGGCGGAGAATTATCGCAAACGAAAGTCGCTACACCGAA
1_8	GACTTCGTTATATAGAGAGCGTCAAAGTTACCGCGACCCAT
1_9	TAACTTGACTGGCGTCGGGTATTGTCAAGACGTTAAAGTTT
1_10	GTCTGACAATGTGTCGCAATCAAGGAGCCCTGCCCTAACGAC
1_11	AGGGCTCCTTCATACATCGATGCGAGTAGGAGAAATGTTCCA
1_12	CCTACCTGCAATGACCGGTAAGAGAAACACATATAGTCAGG
1_13	GTGTTCTCTCGATTGACTGGATGGTCACGCTGACACAAAG
1_14	CGTGACCATCTAACGGCGATAGCCGCACGTTAGTAACGTG
1_15	ACGTGGGCTCTAACCGGGTGCATAAACCGGTACCGCTAT
1_16	GGTTGTATGCGGGACACTCACACCCGGTAGAGAGTGGTCAA
1_17	TCTACCGGTATTGGAGTCCTCACCGTGCACATACGGATGTC
1_18	GTGCACGGTGGCTAACACCTCCCACGTCTACCGATGCA
1_19	GACGTGATGGACCCGGTTGCCCTACCTTACTTGATTTAGA
1_20	AGTAGGGTGATTCAAATCTCGAGGTTAAGTTCCGGGACTG
1_21	ACTTAAACCTTCGAGTAGCAGCGCACCTGACTCAGGAGGT
1_22	CAAGGTGCGCAAGTCTATTATAACAAAGAGGAATCAGTAATT
1_23	CCTCTTGTAGTAAACTTCTGTGACACGCATCAGGAAAGTG
1_24	TGCGTGTCACTGGTCTTAGTGCACGCCAAGTAAGGATTAA
1_25	TTGGCGTGCTTAAGAGCAGC
I* 1	AACATACAGGCCTTAGGAGTT
I* 2	CCTGTATGTTAAGCTGCTGGAGCATCATATTGGCATGTAG
I* 3	ATATGATGCTCATCGCCACGTCCAAATAATCTAAGGA
I* 4	TTTGGGACGTGAATGAGCATCTCGCTGGTCGCCCTGAGTT
I* 5	GACCGAGCGAAGCCAGAGCACAGTAGAGCCCTATGCCCTTA
I* 6	GGGCTCTACTTTCGCGGGATTGGTTCTCCTCGCACGACTCC
I* 7	AGGAGAACCATACTCCTGTCGTCCTTAATAGCTCTATAT
I* 8	TATTAAGGGATACTTACCTCGCCGGCTTTATTCCGATCGC
I* 9	AAAGAGCCGGATGGTCGGTAGTAATGTGGATTGCGACAC
I* 10	CACATTACTACCTTACTTGTCGACAGAAGATCCCATTGTC
I* 11	CTTCGTGTACGTGCTTAGGGCCTGTACAATTACCGGTCA
I* 12	ATTGTACAAGATGCGCGGGTCCCCTGAAAGCTGTAATGGTC
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I* 18	ATGGAGGGCCCGGCTCGGAGCCATTACCGATGCTTAATCG
I* 19	TCGGTAATGGATGCATCGTAGCGTGAGATCGAGATTGAA
I* 20	ATCTCCACGCATCGACGATCAGACACGGTCGACATTGTTGGA
I* 21	CGACCGTGTCCAGTCCCGGAATCCTTATTGCTAATAGACTTG

I* 22	GCAATAAGGACCAGGGCTGCC TAGTGGATAAGACTGTCACCT
I* 23	TTATCCACTAAATTACTGATTCAACGTGCGCACTAACAGACCA
I* 24	GCGCACGTTGTACGATCATAGTCGAGAGATAGTCGACGCTT
I* 25	ATCTCTCGAATAAATCCTTAC
m 1	CTCCGGTCGGAGCTCTATTAA
m 2	CCGACCGGAGGAAATCCCTACACAGCAGACCCAATCCTCCTG
m 3	GGTCTGCTGTTCTCCAGGATCCAAACTTGATAACCAGGCCACG
m 4	ATCAAGTTGGGCCATCTACTGGCTGATGGCGTGCTACGCA
m 5	CCATCAAGCCGATCGAGTATGAAGTGCTTAGTCCTCAGCT
m 6	ACAAGCACTTCACGC GGTCGAGTATTAGGTAAATCGAATCG
m 7	CCTAATACTCAATTATCGCAGGCGCGTTGGCTACACCGAA
m 8	CAAACGCCCGCTGATGAACCGATA CGCAGGAGTCGATGACG
m 9	CCTGCGTATCTGGCGTCGGGTGGAGGCTACCGTTAAAGTT
m 10	GGTAGCCTCCGCACTTTAAGGATAGATAGGGAAAGACTGGCT
m 11	CCCTATCTATTACATACATCGACTCACTGACAGAAATGTTCCA
m 12	GTCAGTGAAGTACAGTGGCGTTACGGTTGGCGCGAGGGCAT
m 13	CCCAACCGTACGATTGACTTGCTGCAGCGTCTGACACAAAG
m 14	GACGCTGCAGCCTGAACGTCTGGCTGGCTGGAATGGTAAA
m 15	AGGCCAGCCACTCAACCGGGCTAGTACAAAGGTACCGCTAT
m 16	TTTGTACTAGTCCTTGGCATGTAAGTTGTTCTCGGTCTG
m 17	CAAACTTACATGGAGTCCTTATCAATAATATCGGATGTC
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m 24	GGATTATGAGT GACAGCCCTGATCCAGCAAGCAAGCGCTAA
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n_1	TGATAACCTAACGCTCTATTAA
n_2	TAGGTTATCATCGCTTGCACCGCGTTGCGCCCATGCGGTTG
n_3	GCGAAACGCTCTCCAGGATCTGCGAAGAAACCAGCCACG
n_4	TCTTCGCAGAGCAGCAAGAAGAAAGCATGTATGTCGATTCT
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n_7	GTTCTAATTAAATTATGCGACCTCCTACCAGCTACACCGAA
n_8	TGGTAGGAGGTAGATGAATGCCAATCCGAGCTGCGCAGAA
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n_16	GACCGTGTGACACACCATGTTGGAGATCGTTATTCAAGC
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n_19	ATTGGAGCACACCCGGTTGCCCTACACGATTGATTTAGA
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n_22	GTGCTTATTCCCGCTATTGACTATAAGGATGTGATGCC
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n_25	AATCAAACATTTAAGAGCAGC
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n* 2	TACGGACGTCTAACGCTGGCAACTCTACTTCGGCATGTAG
n* 3	AGTAGAGTTGCAACCGCATGGCGTGGGACTTCTGCTGC
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n* 6	TTCCGGCGGTTTGCACGGATTGTTAGGAATCGCACGACTCC
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n* 12	TCCGTTCTAAATGCGCGGGTCGACCATCCATTGCTATGGTC
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n* 22	GGTGCCAACCCAGGGCTGCCAGACCGTTGACTGTCACCT
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o_1	CCCTATTCCAGCTATTAA
o_2	GGAAATAGGGACTTCCCTCTTCCGTGGAGCATGCCTCTGAC

o_3	GCTCCACGGATCTCCAGGATCTCCCTAGACCAACCAGCCACG	
o_4	GGTCTAGGGAGACTAGCAATATCCAAACCTGCCAGGTTGATA	
o_5	CAGGTTGGAGATCGAGTATGCCTTACAGCCAGTCCTCAGCT	
o_6	GGCTGTAAAGGTAGAATCGGGTGCCTGGCCGCTATTGTCAG	
o_7	GGCCCAGGGCAATTATGCGAATGACCAATGCTACACCGAA	
o_8	ATTTGGTCATGCGTGCTTCCTCAATGCCGCCAGGTTCTCCA	
o_9	CGGGCATTGATGGCGTGGGGATTACAGAGTTAAAGTT	
o_10	TCTGTAAATCCAAGTGCAGTCGTCACTCTGACAACCGGTATA	
o_11	TCAAGAGTGATCATACATCGATCTATTGAACAGAAATGTTCCA	
o_12	GTTCAATAGAACGAGGCCAAGTGTGTTACTGAGTAATCTAAC	
o_13	TCAGTAAACACGATTGACTTGTGAGAGCATGCTGACACAAAG	
o_14	CATGCTCTCAGGTGGGGGTCTGGTCTCATCACAGACCGCA	
o_15	ATGAGACAGCTCAACCGGGTAACCCGGCCAGGTACCGCTAT	
o_16	TGGCCGGGTTCTGAAAGCTGACGGACATCTATTGTCCACGTC	
o_17	TAGATGTCCGATTGGAGTCCTTGTCTGGCCTATCGGATGTC	
o_18	GGCCCAGACAGAGCCTTAGCCGGGATTACAGTCTCACGGG	
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o_20	GAGTACCACTGAGAACCCCTCAGCAGTAACTAGTTCCATGCA	
o_21	AGTTACTGCTTCAGTAGCAGTAAAGGATCCACTCAGGAGGT	
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o_23	CAATTGCCGTGAAACTTCTTGCCGTGCCCATCAGGAAAGTG	
o_24	TGGGCACGGCTACCGAATGGACACTCATACTTATCTCGCAA	
o_25	AGTATGAGTGTAAAGAGCAGC	
o*_1	TCCTACCGATAGAGAGGAAGT	
o*_2	ATCGGTAGGATAAGCTGCTGGCTGGCGTTGGCATGTAG	
o*_3	AACGCCAGAGTCAGAGCATTGAAGGCCTATATTGCTAGTC	
o*_4	TAGGCCCTCAGAATGAGCATCGACCGACCCGCCCTGAGTT	
o*_5	AGGGTCGGTCTATCAACCTGGTGTACAGCAAACCCGATTCTA	
o*_6	TTGCTGTACATTGCGCGGATTACGTAAGAGCGCACGACTCC	
o*_7	CTCTTACGTGCTGACAATAGCCTTGCTCTCGGAAGCACGC	
o*_8	GAGAGCAAAGTACTTACCTCGCGCGGTTGAATCCGATCGC	
o*_9	TCAACCGCGCTGGAGAACGTGATGTACCAACTCGACTGCAC	
o*_10	AGTGGTACATCCTTACTTTGTATTTAGTGTATCCATTGTC	
o*_11	AGCACTAAATTATACCGGTGAGGTTAGTTGCTGGCGTCT	
o*_12	CAACTAACCTATGCGCGGGTCCGTTATATTGCTAATGGTC	
o*_13	AATATAAACGGTAGATTACGAGTGTACGATTACGCCGACC	
o*_14	AAATCACTGCGCATTGTGACTCTCTGGAAAGTAATCAGGCAA	
o*_15	CTTCCAGAAGTGCAGGCTGTGGCATGAGCTCTCAGCTCAAG	
o*_16	GAGCTCATGCATGGTAACCTACCCGGGAGTAGCGAACCCCTAA	
o*_17	CTACTCCCGGGACGTGGACAAATCTCTAAGGCTAAGGCTC	
o*_18	TTAGAGAGATCGCTTCGGAGCTCGGTATGTGCTTAATCG	
o*_19	CATGACCGAGCCCGTGAGACTGAGGATGTGAGGGTTCTCA	
o*_20	ACATCCTCAATCGACGATCATGCATGCTGGACATTGTTGGA	
o*_21	CCAGCATGCATGCATGGAACCTCGCACCCGGGGTAATGACG	
o*_22	CCGGGTGCCGCCAGGGCTGCCGCTGCACAAGACTGTCACCT	
o*_23	TTGTGCAGCGTATTATCATGACTAACCTCCATTGGTA	
o*_24	AGGAAGTTAGTACGATCATAGGAAGAGGTACAGTCGACGCTT	
o*_25	GTACCTCTTCTTGTGAGATAA	
a_2_1	TTTTTTCCCTTAGTTAC	
a_2_2	TTTTTTGTGCTAACCTCG	
a_4_1	TTTTTTTACTAATGCCTG	
a_4_2	TTTTTTTCTCCAGCACA	
a_6_1	TTTTTTTGTGAGCGCAG	

Protection Tiles

a_6_2	TTTTTTTGCCAGTAGCTG
a_8_1	TTTTTTAACAAATTGGAC
a_8_2	TTTTTTTGCCTATCGCG
a_10_1	TTTTTTTAATTAGGGCA
a_10_2	TTTTTTTCGGTGACCTAT
a_12_1	TTTTTTTATTAAAGCTT
a_12_2	TTTTTTTTGGAAATTGCG
a_14_1	TTTTTTTGTATGTAGCA
a_14_2	TTTTTTCTACGCCAGAA
a_16_1	TTTTTTTCTGGACTCGA
a_16_2	TTTTTTTATTAGAAGGGC
a_18_1	TTTTTTTGTAGGTGGTC
a_18_2	TTTTTTTATAGATTAA
a_20_1	TTTTTTTGGGCCGCCG
a_20_2	TTTTTTTAACGGTGGAG
a_22_1	TTTTTTTCGATTCTGGCG
a_22_2	TTTTTTTGTGGCTGAAGT
a_24_1	TTTTTTTGAAGTGGAAAGA
a_24_2	TTTTTTTATATGGAGCTG
a* 1	GTAAC TAAAGGAAAAAAA
a* 3_1	CGAGTTAGCACAAAAAAA
a* 3_2	CAGGCATTAGTAAAAAAA
a* 5_1	TGTGCTGGAGAAAAAAA
a* 5_2	CTGC GCTCACAAAAAAA
a* 7_1	CAGCTACTGGCAAAAAAA
a* 7_2	GTCCAATTGTTAAAAAAA
a* 9_1	CGCGATAGGCAAAAAAA
a* 9_2	TGCCCTAATTAAAAAAA
a* 11_1	ATAGGT CACCGAAAAAAA
a* 11_2	AAGCTTAAATAAAAAAAA
a* 13_1	CGAATT TCCAAAAAAA
a* 13_2	TGCTACATACAAAAAAA
a* 15_1	TTCTGGCGTAGAAAAAAA
a* 15_2	TCGAGTCCAGAAAAAAA
a* 17_1	GCCCTTCTAATAAAAAAA
a* 17_2	GACCACCTACAAAAAAA
a* 19_1	TTAAATCTATAAAAAAAA
a* 19_2	CGGGCGGCCAAAAAAA
a* 21_1	CTCCACCGTTAAAAAAA
a* 21_2	CGCCAGAATCGAAAAAAA
a* 23_1	ACTTCAGCCACAAAAAAA
a* 23_2	TCTTCCACTTCAAAAAAA
a* 25	CAGCTCCATATAAAAAAA
b_2_1	AAAAAAACAGCCGGTCG
b_2_2	AAAAAAACACCAATTAAA
b_4_1	AAAAAAAGCTCTTCCAAG
b_4_2	AAAAAAAGGGTGAACCTCA
b_6_1	AAAAAAACACGCTCTGGA
b_6_2	AAAAAAACCCCTTAAGGCA
b_8_1	AAAAAAACAAGTCAAACA
b_8_2	AAAAAAATGGTAACAGGT
b_10_1	AAAAAAAATAAATATGGG
b_10_2	AAAAAAAAGGGAGTAACG

b_12_1	AAAAAAAAATAGAACTCCT
b_12_2	AAAAAAAAGCTTAGAACAC
b_14_1	AAAAAAAATATGAACGCGG
b_14_2	AAAAAAAACAAGGGTCTAG
b_16_1	AAAAAAAAGGTGAATAAG
b_16_2	AAAAAAAAGCGAAACTCA
b_18_1	AAAAAAAAGCGTATTATTATT
b_18_2	AAAAAAAATGGTCACCG
b_20_1	AAAAAAAATGGGCGCTAAC
b_20_2	AAAAAAAATTGACTGACGA
b_22_1	AAAAAAAAGCGATACCTGA
b_22_2	AAAAAAAATAATAACCTTT
b_24_1	AAAAAAAAGGCCGACTTGG
b_24_2	AAAAAAAAGCTGCTCTTAA
b*_1	CGAACCGGCTGTTTTTTTT
b*_3_1	TTTAATTGGTGTTTTTTTTT
b*_3_2	CTTGGAAAGAGCTTTTTTTTT
b*_5_1	TGAGTCACCCTTTTTTTTT
b*_5_2	TCCAGAGCGTGTTTTTTTTT
b*_7_1	TGCCTTAAGGGTTTTTTTTTT
b*_7_2	TGTTTGACTTGTTTTTTTTTT
b*_9_1	ACCTGTTACCATTTTTTTTT
b*_9_2	CCCATATTATTTTTTTTTT
b*_11_1	CGTTACTCCCTTTTTTTTT
b*_11_2	AGGAGTTCTATTTTTTTTTT
b*_13_1	GTGTTCTAACGTTTTTTTT
b*_13_2	CCGCCTTCATATTTTTTTT
b*_15_1	CTAGACCCTGTTTTTTTT
b*_15_2	CTTTATTACCTTTTTTTTT
b*_17_1	TGAGTTGCGTTTTTTTT
b*_17_2	AATAAATACGTTTTTTTT
b*_19_1	CGGTGACCATTTTTTTTTT
b*_19_2	GTTAGCGCCCATTTTTTTT
b*_21_1	TCGTCAGTCAATTTTTTTT
b*_21_2	TCAGGTATCGCTTTTTTT
b*_23_1	AAAGGTATTATTTTTTTT
b*_23_2	CCAAGTCGGCCTTTTTTT
b*_25	AAGCGCTGCTTTTTTT
c_2_1	TTTTTTGGGATGCATCA
c_2_2	TTTTTTGGGAAATGCC
c_4_1	TTTTTTGACAGCAGATA
c_4_2	TTTTTTGGCCGTAGATC
c_6_1	TTTTTTCTTCAGTGCC
c_6_2	TTTTTTCCCAAGACACA
c_8_1	TTTTTTTATATGTATAA
c_8_2	TTTTTTTTAGATAGGA
c_10_1	TTTTTTCGGCAAATCTT
c_10_2	TTTTTTCAAGAATGTAT
c_12_1	TTTTTTAGGCCTTGTT
c_12_2	TTTTTTTCGTGACATCG
c_14_1	TTTTTTAGAAAGAGTTT
c_14_2	TTTTTTTACTCTGTAGAA
c_16_1	TTTTTTTGCACTAACAG

c_16_2	TTTTTTTCAAACGTTCCG
c_18_1	TTTTTTTTGTTGATGCT
c_18_2	TTTTTTTGAGTTGTCAC
c_20_1	TTTTTTGGAAGTGGGAG
c_20_2	TTTTTTGACACTCCAGG
c_22_1	TTTTTTTGAGCACCCAT
c_22_2	TTTTTTGGTGTACAGGA
c_24_1	TTTTTTTCAAGGGCGTG
c_24_2	TTTTTTCTACACTCTC
c*_1	TGATGCATCCCCAAAAAA
c*_3_1	GGGCATTCCCCAAAAAA
c*_3_2	TATCTGCTGTCAAAAAAA
c*_5_1	GATCTACGCCAAAAAA
c*_5_2	GGCACTGAAAGAAAAAA
c*_7_1	TGTGTCTGGGAAAAAA
c*_7_2	TTATACATATAAAAAAA
c*_9_1	TCCTATCTAAAAAAA
c*_9_2	AAGATTGCCGAAAAAA
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c*_11_2	AACAAAGCCTAAAAAA
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c*_15_1	TTCTACAGAGTAAAAAA
c*_15_2	CTGTTAGTGCBBBBBBB
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c*_19_2	CTCCCACCTCCAAAAAA
c*_21_1	CCTGGAGTGTCAAAAAA
c*_21_2	ATGGGTGCTCAAAAAAA
c*_23_1	TCCTGTACACCAAAAAAA
c*_23_2	CACGCCCTTGAAAAAA
c*_25	GAGAGTGTAGGAAAAAA
d_2_1	AAAAAAAAATGATTGGTA
d_2_2	AAAAAAATATTCCTAAT
d_4_1	AAAAAAAGAAACGCCGAC
d_4_2	AAAAAAACTGGACAGGC
d_6_1	AAAAAAAAGTGGCTGG
d_6_2	AAAAAAATGAGTCCAAGA
d_8_1	AAAAAAATAGCCCTGGGC
d_8_2	AAAAAAACTGCCTGCCT
d_10_1	AAAAAAAGAGCAGACGCA
d_10_2	AAAAAAATTAGGGTACGT
d_12_1	AAAAAAAATACAATGTTA
d_12_2	AAAAAAACGACGGGAGCG
d_14_1	AAAAAAACACCGCAAATA
d_14_2	AAAAAAAGACGAGGAAGG
d_16_1	AAAAAAAGTGCCTCAGAC
d_16_2	AAAAAAAGGCACACACC
d_18_1	AAAAAAACACCTGGCCG
d_18_2	AAAAAAACCGCGCAAAGA
d_20_1	AAAAAAAGAAGTCATAGA
d_20_2	AAAAAAATCTACGAGGG

d_22_1	AAAAAAAAGAGTTTCATCT
d_22_2	AAAAAAAAAGCCAGTAAA
d_24_1	AAAAAAAATGCGGCAGTG
d_24_2	AAAAAAAGCTGCTCTTAA
d*_1	TACCAATCATTTTTTTT
d*_3_1	ATTAGGAAATATTTTTT
d*_3_2	GTCGGCGTTCTTTTTT
d*_5_1	GCCTGTCCAAGTTTTTT
d*_5_2	CCAGGCCACTTTTTTTT
d*_7_1	TCTTGACTCATTTTTT
d*_7_2	GCCCAGGGCTATTTTTT
d*_9_1	AGGCAGGGCAAGTTTTTT
d*_9_2	TGCGTCTGCTCTTTTTT
d*_11_1	ACGTACCCTAATTTTTT
d*_11_2	TAACATTGTATTTTTTT
d*_13_1	CGCTCCGGTCGTTTTTT
d*_13_2	TATTTGCGGTGTTTTTT
d*_15_1	CCTTCCTCGTCTTTTTT
d*_15_2	GTCTGAGGCACTTTTTT
d*_17_1	GGTGTGGTGCCTTTTTT
d*_17_2	CGGCCAAGGTGTTTTTT
d*_19_1	TCTTGCGCGGTTTTTT
d*_19_2	TCTATGACTCTTTTTT
d*_21_1	CCCTCGTAGATTTTTTT
d*_21_2	AGATGAAACTCTTTTTT
d*_23_1	TTTACTGGCTTTTTTTT
d*_23_2	CACTGCCGCATTTTTTT
d*_25	TTAAGAGCAGCTTTTTT
e_2_1	TTTTTTTACTACAGATGC
e_2_2	TTTTTTTGACCCATCTAG
e_4_1	TTTTTTTATATTGGCAAC
e_4_2	TTTTTTTATAGCCGTGCT
e_6_1	TTTTTTTCCTGGTCCCC
e_6_2	TTTTTTTACAATTAACCT
e_8_1	TTTTTTTATGCGGCGCAT
e_8_2	TTTTTTTCGGCTTAGCA
e_10_1	TTTTTTTGCGTACAGAG
e_10_2	TTTTTTTAATGTAATCAA
e_12_1	TTTTTTTACCAAGCCGGT
e_12_2	TTTTTTTGGCCCTTGCCTC
e_14_1	TTTTTTTATCTCACAGAG
e_14_2	TTTTTTTATCATCGCAT
e_16_1	TTTTTTTGCCGCCGACAG
e_16_2	TTTTTTTGCGTGTGCGTG
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e_18_2	TTTTTTTATTATAAAAGTC
e_20_1	TTTTTTTCCCTCCGGCTGT
e_20_2	TTTTTTTCAACTACAAC
e_22_1	TTTTTTTGCGATCAGACTC
e_22_2	TTTTTTTCTATCTTAC
e_24_1	TTTTTTTATCCCTCCCAT
e_24_2	TTTTTTTGAGGGACGATCG
e*_1	GCATCTGTAGTAAAAAAA

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e* 3 2	GTTGCCAATATAAAAAAA
e* 5 1	AGCACGGCTATAAAAAAA
e* 5 2	CGGGAACCAGGAAAAAA
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e* 7 2	ATGCGCCGCATAAAAAAA
e* 9 1	TGCTAAAGCCGAAAAAA
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f 24 1	AAAAAAACTGCTGAATCT
f 24 2	AAAAAAAGCTGCTCTTAA
f* 1	TTGCCAGTTGTTTTTTT
f* 3 1	CCTACAGTATATTTTTT
f* 3 2	ATGCAATTGGTTTTTTT
f* 5 1	GACACGCCAACTTTTTT
f* 5 2	GCCTGCACAGTTTTTTT
f* 7 1	TCTTGGTTGCGTTTTTT

f* 7 2	ATTAGTAGCATTTTTTT
f* 9 1	GACTCCACAATTTTTTT
f* 9 2	TCAAGATGTCGTTTTTT
f* 11 1	GCCATACCGGCTTTTTT
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f* 25	TTAACAGCAGCTTTTTT
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g 4 2	TTTTTTAGCATATAAAG
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g 6 2	TTTTTTTCGAACCGATA
g 8 1	TTTTTTCTGATCACCT
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g 12 2	TTTTTTTCGCCTGCATCA
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g 14 2	TTTTTTTACGGGTTAGAC
g 16 1	TTTTTTTTGGTCATTAA
g 16 2	TTTTTTTCGGACCTGTC
g 18 1	TTTTTTTCATACCTGTTC
g 18 2	TTTTTTTACCACTTTCAT
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g 20 2	TTTTTTTGATACTCCTGT
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g 24 2	TTTTTTAAGTCTTCAG
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g* 9 2	TTAGCAGGACGAAAAAAA
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g* 13_1	TGATGCAGGC GAAAAAAA
g* 13_2	ACCTAAGCACTAAAAAAA
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g* 15_2	TTAATGACCAAAAAAAA
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g* 21_2	CAAGCCTAACAAAAAAA
g* 23_1	TTACTTACGGAAAAAAA
g* 23_2	CATATGTCTTGAAGAAA
g* 25	CTGAAAGACTTAAAGAAA
h_2_1	TTTTTTTCGATATCGAGC
h_2_2	TTTTTTTGGCCTTAAGC
h_4_1	TTTTTTTGAATCAGGAAC
h_4_2	TTTTTTTATCTAGGGAG
h_6_1	TTTTTTTGGGATCCTAAG
h_6_2	TTTTTTTGTGGGCTTTAT
h_8_1	TTTTTTTGAATCGGGAG
h_8_2	TTTTTTTCGCTTGCAGTG
h_10_1	TTTTTTTGCCTGGCTGCG
h_10_2	TTTTTTTACCGAAGAAC
h_12_1	TTTTTTTCTAGGTGTGGA
h_12_2	TTTTTTTAGAGGCTACAT
h_14_1	TTTTTTTATGCTTTACTG
h_14_2	TTTTTTTTATGATTACC
h_16_1	TTTTTTCTGTTATGTA
h_16_2	TTTTTTTGAGTCGGTCCG
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h_24_2	TTTTTTTACTTCCGGAC
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h* 13_2	CAGTAAAGCATAAAAAAA
h* 15_1	GGTAATCATAAAAAAA
h* 15_2	TACATAAACAGAAAAAAA
h* 17_1	CGGACCGACTAAAAAAA

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h* 19 2	CTTTACAATCAAAAAAAA
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h* 21 2	CGATGGGAAAGAAAAAAA
h* 23 1	GATGTACAACGAAAAAAA
h* 23 2	ACTAGGTAGACAAAAAAA
h* 25	GTCCGGGAAGTAAAAAAA
i 2 1	AAAAAAAATAAAGCGTATC
i 2 2	AAAAAAAAAACATGCCG
i 4 1	AAAAAAACATTAAGTCG
i 4 2	AAAAAAACAGGTGACACA
i 6 1	AAAAAAATCCGAAGCGAC
i 6 2	AAAAAAATGATGCTTAT
i 8 1	AAAAAAATTCCGACTCC
i 8 2	AAAAAAATGTTCTTAAA
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i 14 2	AAAAAAATTCTAATTGT
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i 16 2	AAAAAAATGTTGGGCTA
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i 18 2	AAAAAAAAGCTTATATT
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i 20 2	AAAAAAATGGTCCTCACC
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i 22 2	AAAAAAAGGCCGAGCTA
i 24 1	AAAAAAAGACAAAGCCG
i 24 2	AAAAAAACTATCCGTCA
i* 1	GATACGCTTATTTTTT
i* 3 1	CGGCCATGTTTTTTTT
i* 3 2	CGACTTAATGTTTTTT
i* 5 1	TGTGCAACCTGTTTTTT
i* 5 2	GTCGCTCGGATTTTTT
i* 7 1	ATAAAGCATCATTTTTT
i* 7 2	GGAGTCGGGAATTTTTT
i* 9 1	TTTAAGAACATTTTTT
i* 9 2	GCCTAGTGGGATTTTTT
i* 11 1	GGCCTCAGCCCTTTTTT
i* 11 2	GGACACGTACATTTTTT
i* 13 1	CTTGTATGCTTTTTT
i* 13 2	CTTGGTAGCGCTTTTTT
i* 15 1	ACAATTAGAAATTTTTT
i* 15 2	TCTCCAGGCCGTTTTTT
i* 17 1	TAGCCAAACATTTTTT
i* 17 2	GGTAAATGCCGTTTTTT
i* 19 1	AATATAAGCTTTTTTT
i* 19 2	AAGGCTAGAGCTTTTTT
i* 21 1	GGTGAGGACCATTTTTT
i* 21 2	GTGGTTACTGTTTTTT

i* 23_1	TAGCTCGGCCTTTTTT
i* 23_2	CGGGCTTGTCTTTTTT
i* 25	TGACGGAATAGTTTTT
j 2_1	TTTTTTGGCCAATAAAC
j 2_2	TTTTTTTCAGTCCCGCG
j 4_1	TTTTTTGTCGGGTGTAA
j 4_2	TTTTTTTCGGCCCTGTA
j 6_1	TTTTTTGTGTGAAAGTC
j 6_2	TTTTTTCGTGGACGACC
j 8_1	TTTTTTGAATGGAAAGG
j 8_2	TTTTTTCTTGATTTG
j 10_1	TTTTTTGATCTACTTCC
j 10_2	TTTTTTAGGAGGTGCCG
j 12_1	TTTTTTCTGAAACAGGC
j 12_2	TTTTTTTGAAAGCGACAA
j 14_1	TTTTTTGACGGCATTG
j 14_2	TTTTTTGTCAATTCTA
j 16_1	TTTTTTCAGCCAAGAG
j 16_2	TTTTTTTATCTAGGTTAA
j 18_1	TTTTTTGGCGAGTACCG
j 18_2	TTTTTTTCGACATTATT
j 20_1	TTTTTTTCGGTAGTTCTT
j 20_2	TTTTTTTCGTTCGTGC
j 22_1	TTTTTTGAAATAGTCGG
j 22_2	TTTTTTAACCAACTCGA
j 24_1	TTTTTTTCTCCAACCG
j 24_2	TTTTTTCAGATGTGCA
j* 1	GTTTATTGGCCAAAAAAA
j* 3_1	CGCGGGACTGAAAAAAA
j* 3_2	TTACACCCGACAAAAAAA
j* 5_1	TACAGGGCCGAAAAAAA
j* 5_2	GACTTCACACAAAAAAA
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j* 21_1	GCACGAAACGAAAAAAA
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j* 25	TGCACAATCTGAAAAAAA
k 2_1	AAAAAAATTGCACTCACT
k 2_2	AAAAAAATACGATACCTA

k_4_1	AAAAAAAACGTGGCCGATT
k_4_2	AAAAAAAAATGGCACATG
k_6_1	AAAAAAAGCTTCGGCCG
k_6_2	AAAAAAATCTGAGCACCC
k_8_1	AAAAAAACCTCGACGACA
k_8_2	AAAAAAAAGACCACAGGT
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k_10_2	AAAAAAAGAGATGTAAGC
k_12_1	AAAAAAAAGCTCTGCAC
k_12_2	AAAAAAAAGCGGTCCGCG
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k_20_1	AAAAAAAAGCATTTGCTC
k_20_2	AAAAAAAGAGGGCGGCTT
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k_22_2	AAAAAAAAGAGGTGGTG
k_24_1	AAAAAAAGAATAAAGAAG
k_24_2	AAAAAAAATAAACAGGAA
k*_1	AGTGAGTGCATTTTTT
k*_3_1	TAGGTATCGTATTTTTT
k*_3_2	AATCGGCCACGTTTTTT
k*_5_1	CATGTGCCATTTTTTTT
k*_5_2	CGGCCGAAAGCTTTTTT
k*_7_1	GGGTGCTCAGATTTTTT
k*_7_2	TGTCGTCGAGGTTTTTT
k*_9_1	ACCTGTGGCTTTTTTT
k*_9_2	AGACTAGGCCTTTTTTT
k*_11_1	GCTTACATCTCTTTTTT
k*_11_2	GTGCAGAACGCTTTTTT
k*_13_1	CGCGGACCGCTTTTTT
k*_13_2	CGATTCAAGTGTCTTTT
k*_15_1	CGTCGCGTGGCTTTTTT
k*_15_2	TACGTCAAAGGTTTTTT
k*_17_1	GAGTGGTGCATTTTTT
k*_17_2	TCTCCACACTCTTTTTT
k*_19_1	GTCGTTAAATGTTTTTT
k*_19_2	GAGCAAATGCTTTTTT
k*_21_1	AAGCCGCCCTTTTTTT
k*_21_2	AACTAACAGAGTTTTTT
k*_23_1	CAACACTCTTTTTTTT
k*_23_2	CTTCTTATTCTTTTTT
k*_25	TTCCCTGTTATTCTTTTT
1_2_1	TTTTTTCCCTAGGAGTT
1_2_2	TTTTTTCATCATCGCGC
1_4_1	TTTTTTTAATCTAAGGA
1_4_2	TTTTTTAGCCAGAGCAC
1_6_1	TTTTTTTATCGCCCTTA
1_6_2	TTTTTTTACTCCTGTCG
1_8_1	TTTTTTGCTCTATAT

1_8_2	TTTTTTTATGGGTCGCGG
1_10_1	TTTTTTGATTGCGACAC
1_10_2	TTTTTTGTGCTAGGGC
1_12_1	TTTTTTTTACCGGTCA
1_12_2	TTTTTTCTGACTATAT
1_14_1	TTTTTTTATGCCGTTAG
1_14_2	TTTTTTCACAGTTACTA
1_16_1	TTTTTTGTGAGTGTCCC
1_16_2	TTTTTTTGGAACCACTC
1_18_1	TTTTTTGAGGGTTAGC
1_18_2	TTTTTTATGCATCGGTA
1_20_1	TTTTTTCGAGATTGAA
1_20_2	TTTTTTCAGTCCGGAA
1_22_1	TTTTTTTAATAGACTTG
1_22_2	TTTTTTTAATTACTGATT
1_24_1	TTTTTTACTAACGACCCA
1_24_2	TTTTTTAAATCCTTAC
1* 1	AACTCCTAACGGAAAAAA
1* 3_1	GCGCGATGATGAAAAAAA
1* 3_2	TCCTTAGATTAAAAAAAA
1* 5_1	GTGCTCTGGCTAAAAAAA
1* 5_2	TAAGGGCGATAAAAAAAA
1* 7_1	CGACAGGAGTAAAAAAA
1* 7_2	ATATAGAGAGCAAAAAAA
1* 9_1	CCCGCACCCATAAAAAAA
1* 9_2	GTGTCGCAATCAAAAAAA
1* 11_1	GCCCTAACGACAAAAAAA
1* 11_2	ATGACCGTAAAAAAA
1* 13_1	ATATAGTCAGGAAAAAAA
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1* 15_1	TAGTAACTGTGAAAAAAA
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1* 19_2	TTCAAATCTCGAAAAAAA
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1* 21_2	CAAGTCTATTAAAAAAA
1* 23_1	AATCAGTAATTAAAAAAA
1* 23_2	TGGGTCTTAGTAAAAAAA
1* 25	GTAAGGATTTAAAAAAA
m_2_1	AAAAAAAGTAGGGATTTC
m_2_2	AAAAAAACAGGAGGATTG
m_4_1	AAAAAAAAGTAGATGCC
m_4_2	AAAAAAATGCGTAGCACG
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m_8_1	AAAAAAAGGTTCATCAGC
m_8_2	AAAAAAACGTCACTGACT
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m_10_2	AAAAAAAAGGCCAGTCTT
m_12_1	AAAAAAAACGCCACTGTA
m_12_2	AAAAAAAATGCCCTCGCG

m_14_1	AAAAAAAAAGACGTTCAAGG
m_14_2	AAAAAAAATTTACCATTCC
m_16_1	AAAAAAAATGCCAAAGGA
m_16_2	AAAAAAACAGACCGAGAA
m_18_1	AAAAAAATCCATCTCTCT
m_18_2	AAAAAAATAGCAGATGGT
m_20_1	AAAAAAACGAGACTCCTA
m_20_2	AAAAAAATCACCTCCAAA
m_22_1	AAAAAAATAGGAAGCGCC
m_22_2	AAAAAAAGTAAATACATT
m_24_1	AAAAAAAAGGGCTGTCA
m_24_2	AAAAAAATTAGCGCTTGC
m*_1	GAAATCCCTACTTTTTT
m*_3_1	CAATCCTCCTGTTTTTT
m*_3_2	GGCCATCTACTTTTTTT
m*_5_1	CGTGCTACGCATTTTTT
m*_5_2	TCACCGGGTCTTTTTT
m*_7_1	TAATCGAACGTTTTTT
m*_7_2	GCTGATGAACCTTTTTT
m*_9_1	AGTCGATGACGTTTTTT
m*_9_2	GCACTTAACGTTTTTT
m*_11_1	AAAGACTGGCTTTTTTT
m*_11_2	TACAGTGGCGTTTTTTT
m*_13_1	CGCGAGGGCATTTTTTT
m*_13_2	CCTGAACGTCTTTTTT
m*_15_1	GGAATGGTAAATTTTTT
m*_15_2	TCCTTGGCATTTTTTT
m*_17_1	TTCTCGGTCTGTTTTTT
m*_17_2	AGAGAGATGGATTTTTT
m*_19_1	ACCATCTGCTATTTTTT
m*_19_2	TAGGAGTCTCGTTTTTT
m*_21_1	TTTGGAGGTGATTTTTT
m*_21_2	GGCGCTTCCTATTTTTT
m*_23_1	AATGTATTTACTTTTTT
m*_23_2	TGACAGCCCTTTTTTT
m*_25	GCAAGCGCTAATTTTTT
n_2_1	TTTTTTGGTCAAAGCGA
n_2_2	TTTTTTCAACCGCATGG
n_4_1	TTTTTTCTCTGCTGC
n_4_2	TTTTTTAGGAATCGACA
n_6_1	TTTTTTGTAATACGCAC
n_6_2	TTTTTTAGAAAGTTAGG
n_8_1	TTTTTTGCATTCATCTA
n_8_2	TTTTTTCTGCGCAGC
n_10_1	TTTTTTTATTGGTTGAC
n_10_2	TTTTTTAGCACTGTTAT
n_12_1	TTTTTTCAGAATAAATA
n_12_2	TTTTTTGTGGATGCTAA
n_14_1	TTTTTTCAAGGTATGGA
n_14_2	TTTTTTGCTAAATATGC
n_16_1	TTTTTTCATGGTGTGTC
n_16_2	TTTTTTGCTGAATAAAC
n_18_1	TTTTTTGCGACCGGACC

n_18_2	TTTTTTTCAACAGCGGCA
n_20_1	TTTTTTTCAGAACGAAT
n_20_2	TTTTTTTATAAAGATGCT
n_22_1	TTTTTTTAATAGGCGGGA
n_22_2	TTTTTTTGGCATCACATC
n_24_1	TTTTTTTTAAACCCACG
n_24_2	TTTTTTTGACGCAAATGA
n*_1	TCGTTTGACCAAAAAAA
n*_3_1	CCATGCGGTTGAAAAAAA
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o_12_2	AAAAAAAGTTAGATTAC
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o_14_2	AAAAAAATGCGGTCTGTG
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o_20_2	AAAAAAATGCATGGAAC
o_22_1	AAAAAAAGGTGAATGACG
o_22_2	AAAAAAATATTATCATGA

o_24_1	AAAAAAAATCCATT CGGTA
o_24_2	AAAAAAAATT GCGAGATAA
o*_1	ACTTCCTCTCTTTTTTT
o*_3_1	ATGCCTCTGACTTTTTT
o*_3_2	GACTAGCAATATTTTTT
o*_5_1	CCAGGGTGATATTTTTT
o*_5_2	TAGAATCGGGTTTTTTT
o*_7_1	GCTATTGTCAGTTTTTT
o*_7_2	GCGTGCTCCCTTTTTT
o*_9_1	CACGTTCTCCATTTTTT
o*_9_2	AAGTGCAGTCGTTTTTT
o*_11_1	CAACCGGTATATTTTTT
o*_11_2	AGACGGCCAAGTTTTTT
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o*_13_2	GGTCGGCGGGTTTTTTT
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o*_17_1	TTGTCCACGTCTTTTTT
o*_17_2	GAGCCTTAGCCTTTTTT
o*_19_1	AGTCTCACGGTTTTTTT
o*_19_2	TGAGAACCCCTCTTTTTT
o*_21_1	AGTTCCATGCATTTTTT
o*_21_2	CGTCATTACACCTTTTTT
o*_23_1	TCATGATAATATTTTTT
o*_23_2	TACCGAATGGATTTTTT
o*_25	TTATCTCGCAATTTTTT

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