Supplementary Information 1 for Isothermal self-assembly of complex DNA structures under diverse and biocompatible conditions

Cameron Myhrvold[1,2], Mingjie Dai[2,3], Pamela A. Silver[1,2], Peng Yin[1,2]

[1]Department of Systems Biology, Harvard Medical School, Boston, Massachusetts 02115, USA.

[2]Wyss Institute for Biologically Inspired Engineering, Harvard University, Boston, Massachusetts 02115, USA.

[3]Program in Biophysics, Harvard University, Boston, Massachusetts, 02115, USA.

Supplementary Methods

Sequence design

Sequences were designed using custom MATLAB software. First, the sequences of individual domains were generated randomly using an equal proportion of each nucleotide. A list of orthogonal domains was generated by comparing newly generated domain sequences with each previously generated domain in the list, and its reverse complement. A pair of domains was considered orthogonal if and only if consecutive 8 nucleotide repeats were avoided. For structures with domains shorter than 9 nucleotides, orthogonality was defined as having an edit distance ≥ 2.

A list of orthogonal tile sequences was generated based on the prescribed interactions between neighboring tiles. A tile is generated by concatenating domains from the orthogonal domain list with specified linker sequences. After each domain was added to a tile (and its reverse complement added to the neighboring tile), all pairs of non-neighboring tiles were checked for orthogonality as defined for domains. Finally, polyT linkers of specified lengths were added between domains, and all pairs of non-neighboring tiles were checked for orthogonality again. Standard domains had a 50% GC content. In some cases, we changed the domain GC content to 30% (low GC) or 70% (high GC); for these structures, orthogonality was checked between domains but not between tiles. See Supplementary Data for sequence information for all of the structures used in this study.

Structure assembly

DNA oligonucleotides were synthesized by Integrated DNA Technologies (IDT) in 96-well plates using standard desalting without additional purification and were stored at -20 °C. Subsequently, the strands were mixed together to create a 1 µM (5×) master mix. A standard assembly reaction contained 200 nM of each strand in 0.5× TE buffer (5 mM Tris-base, 1 mM EDTA) supplemented with 10 mM $MgCl_2$ in a 10 µl or 20 µl volume. 5 mM HEPES buffer was used for assembly at pH 7. Structures were assembled isothermally in a thermocycler (Bio-Rad DNA Engine) by rapidly ramping to a specific temperature, holding at that temperature for a specified period of time, and then rapidly cooling to 4 °C. When necessary, the gradient feature of the thermocycler was used to test a range of assembly temperatures simultaneously. According to the manufacturer, the temperature gradient on these thermocyclers is reproducible to within ±0.2 °C (see Supplementary Text S2 for details). For structures with very low assembly temperatures, strands were mixed in a 4 °C cold room and kept on ice until they were placed in a thermocycler.

Gel electrophoresis

Structures were routinely analyzed by electrophoresis in a 2% native agarose gel containing 0.5× TBE buffer (45 mM Tris-borate, 1 mM EDTA) and 10 mM $MgCl_2$ and pre-stained with 0.5× SYBR Safe (Invitrogen). 5 µl of each assembly reaction was mixed with 1 µl of 6× bromophenol blue loading dye and loaded into the gel. 2 µl of a DNA ladder (Fermentas 1 kb plus) was used as a molecular size standard. Electrophoresis was performed for 90 minutes at 90 V in 0.5× TBE buffer supplemented with 10 mM $MgCl_2$. An ice-water bath was used to prevent additional assembly or degradation of the structures during electrophoresis. Structures with very low assembly temperatures were analyzed by electrophoresis in a 4 °C cold room to ensure that a consistently low temperature was maintained. Afterwards, gels were scanned with a Typhoon FLA 9000 (General Electric) using the SYBR Safe channel (excitation at 473 nm, emission ≥ 510 nm). Gel images were quantified with TotalLab Quant (TotalLab

Ltd.) using rubber band background correction. The yield was calculated as the integrated intensity of the product band divided by the integrated intensity of the entire lane.

Gel purification

Gel bands were visualized using a Safe Imager 2.0 Blue-Light Transilluminator (Invitrogen) and excised from the gel using a fresh razor blade. The excised piece was then placed into a Freeze 'N Squeeze column (Bio-Rad) and crushed using a plastic pestle. The column was centrifuged at 400× *g* for 8 minutes, yielding a purified sample.

Atomic force microscopy imaging

Images of folded structures were obtained with a Veeco Multimode V atomic force microscope. C-type Bruker SNL-10 tips were used under tapping mode in fluid. Folded (purified or unpurified) samples were deposited onto mica surfaces and incubated at 4 °C for 10 min in folding buffer supplemented with 5 mM $NiCl_2$ (structures without linkers) or 10 mM $NiCl_2$ (structures with linkers) to enhance surface binding. Structures with linkers were complemented with concentrated (>25× access, measured against linker concentration, rather than structure concentration) polyA strands in folding buffer, and incubated for 1 hour at 21 °C before mica deposition.

Modeling of molecular crowding

Theoretical modeling of molecular crowding was done to explain the measured formation and predict folding quality at non-experimented conditions. A rough model was derived based on the estimated effective ion concentration (Mg^{2+}) and effective strand concentration in a crowded environment. See Supplementary Text S3 for details.

Text S1: Structure naming conventions

Structures are named as follows: when relevant, the motif number (Wei *et al.*, 2013) is indicated, followed by an underscore, the domain length, and the linker length. In some cases, additional modifications (e.g. split domains, altered GC content) are appended to the end of the name. Otherwise, the notation is the same as in Wei *et al.*, 2013.

Text S2: Notes about experiments

As mentioned in the main text, we observed that structures assembling at extreme temperatures generally had lower and more variable yield. The m1_21mer structure was particularly variable; this was eventually tracked down to temperature variations between different individual thermocyclers. Thus, it is important to calibrate thermocyclers relative to one another (or to an absolute thermometer) in order to ensure reproducible assembly of the m1_21mer structure. The other structures we tested were not significantly affected by this variability. We also observed substantial variability in the high Mg^{2+}, high PEG experiments (Fig. 5c), especially at intermediate PEG concentrations of around 14 mM. This may

reflect inherent stochasticity in the aggregation process if this is near a "critical" PEG concentration for aggregation to occur.

Text S3: Modeling

Theoretical modeling of molecular crowding was done to explain the measured formation and predict folding quality at non-experimented conditions. A rough model is derived where effective ion concentration ([Mg^{2+}]) and effective strand concentration in a crowded space is considered as the absolute concentration divided by the fraction of effective empty space in which these ions are dispersed, as in

$$\left[\mathrm{Mg}^{2+}\right]_{eff} = \left[\mathrm{Mg}^{2+}\right]_{abs} / F_{eff\_spc}$$
$$[\mathrm{strands}]_{eff} = [\mathrm{strands}]_{abs} / F_{eff\_spc}$$

Afterwards, we used a model by which we consider the degree of assembly at a certain magnesium and strand concentration as a simple function of both concentrations

$$\mu = \left[\mathrm{Mg}^{2+}\right]_{eff} \cdot [\mathrm{strands}]_{eff}^{\alpha}$$

The exponent α is to be empirically determined based on data from Fig. 5 b,c,d and data at very high Mg^{2+} concentrations (not shown). Blue dots in the plots show transition points from formation to non-formation, or vice versa. Four transition points are used for generating and validating each plot, namely the transition from formation to non-formation at high [Mg^{2+}] and varying [PEG-8000] (Fig. 5c), non-formation to formation at low [Mg^{2+}] and varying [PEG-8000] (Fig. 5d), formation to non-formation and non-formation to formation at varying [Mg^{2+}] and zero [PEG-8000] (Fig. 5b and data not shown). These data points determined the value of α to be 3.

To convert PEG-8000 concentration to effective empty space, we considered two crowding effects, which we termed here "dry volume" and "wet volume". Dry volume takes into account the space taken by a certain molecule in its closest packing form in solution, whereas wet volume considers the extra space taken by unpacked polymer molecules in a dilute solution. We hypothesize that, on top of occupying a certain dry volume, each unit concentration of molecules also occupies a certain fraction of the remaining empty space[1,2]. Therefore, the fraction of effective empty space is determined by the following formula:

$$F_{eff\_spc} = \left(1 - c \cdot V_{dry}\right) \cdot \exp(-c \cdot V_{wet})$$

where V_{dry} and V_{wet} describe the dry and wet volume components in unit of per M concentration. Or, equivalently, one could write:

$$F_{eff\_spc} = \left(1 - c/c_{dry\_sat}\right) \cdot \exp\left(-c/c_{wet\_sat}\right)$$

where $c_{dry\_sat} = 1/V_{dry}$ and $c_{wet\_sat} = 1/V_{wet}$ express dry and wet volumes in terms of saturation concentration. In a dilute solution, each molecule occupies both dry and wet volume as can be seen in the approximation:

$$F_{eff\_spc\_dilute} \cong 1 - c_{dilute} \cdot \left(V_{dry} + V_{wet}\right)$$

where $V_{dry} + V_{wet} = V_{wet\_total}$ gives the effective occupied space as measured by the hydrodynamic radius.

For PEG-8000, $\left[\text{PEG-8000}\right]_{dry\_sat} = 79\ \text{mM}$, as calculated from solubility at 20 °C, $\left[\text{PEG-8000}\right]_{wet\_total\_sat} = 17\ \text{mM}$, as calculated from hydrodynamic radius of 2.9 nm. This gives $\left[\text{PEG-8000}\right]_{wet\_sat} = 22\ \text{mM}$ for PEG-8000.

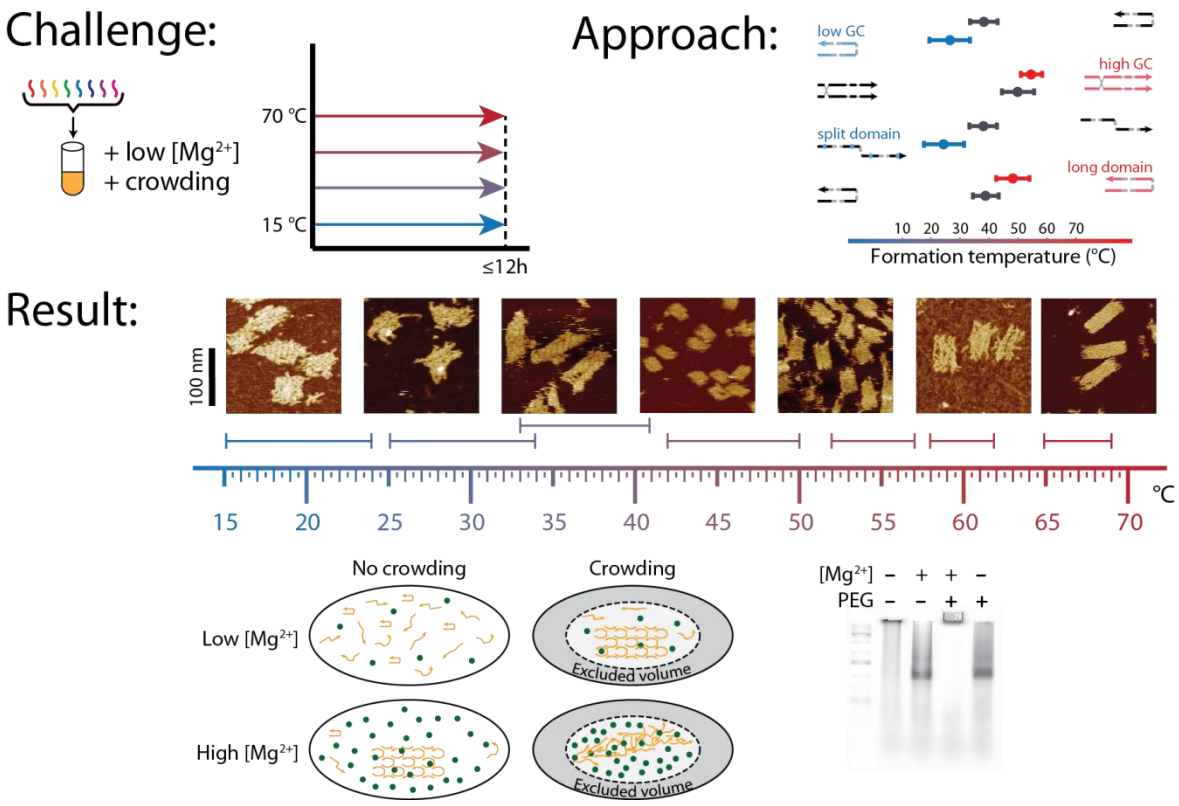

Figure S1. Summary of the study. Single-stranded tile (SST) structures are engineered to self-assemble isothermally across a diverse range of temperatures and conditions. We achieved this by varying several structural parameters, including domain length and linker length; as a result, we achieved isothermal assembly of SST across a 15-69°C range. Atomic force microscopy images of structures are shown, as well as their respective assembly temperature ranges. We also achieved structure assembly under biocompatible conditions (e.g., physiological pH and temperature, low salinity and high crowding) after just one hour of assembly.

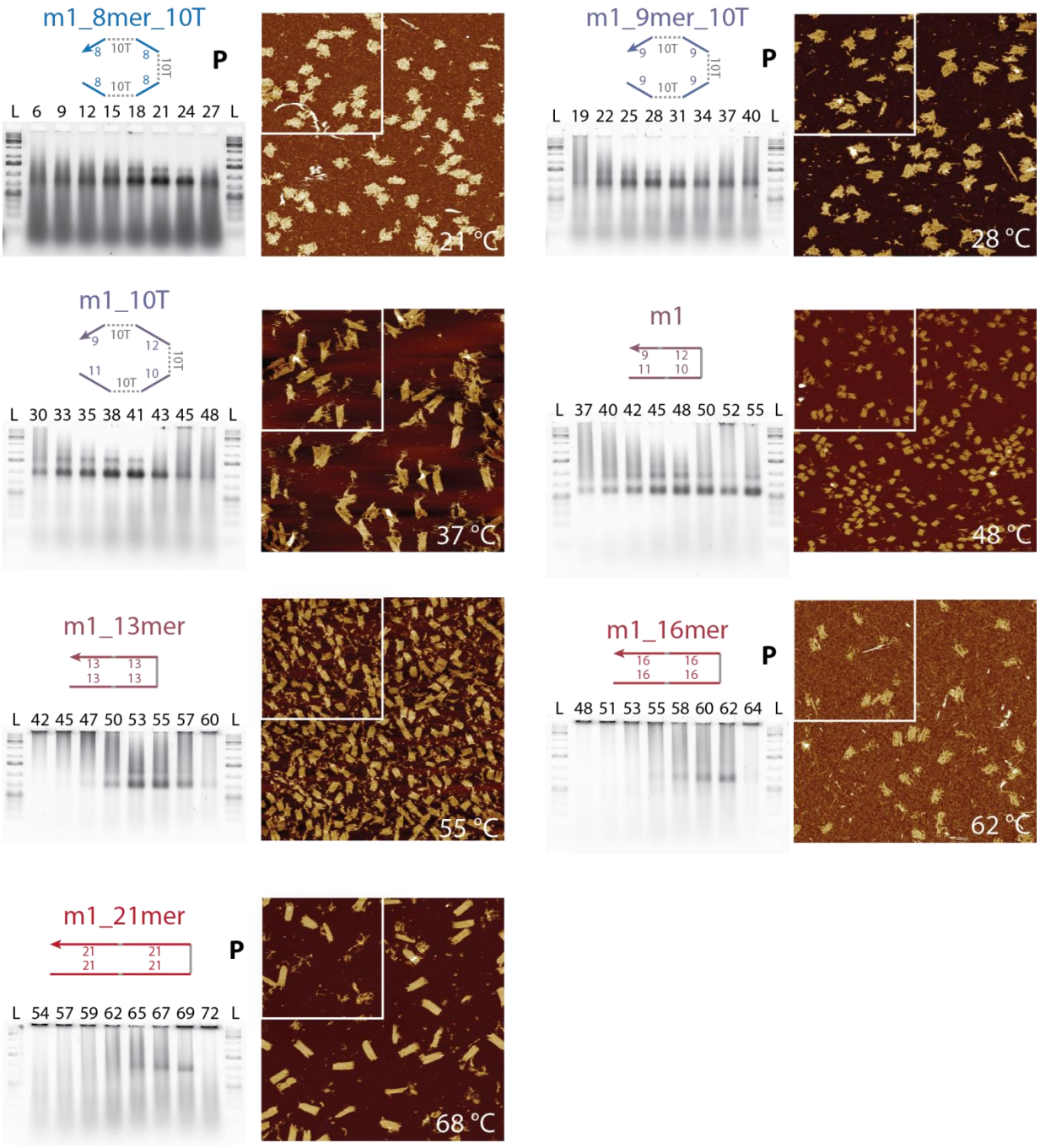

Figure S2. Raw gel data for Fig. 2. Assembly temperatures are indicated above each lane. An "L" indicates the use of 1 kb+ double-stranded DNA ladder (Fermentas). Strand diagrams and atomic force microscopy (AFM) images are also shown for each structure in Fig. 2. Assembly temperatures for the AFM images are indicated. Structures that were gel-purified are indicated using a bold P.

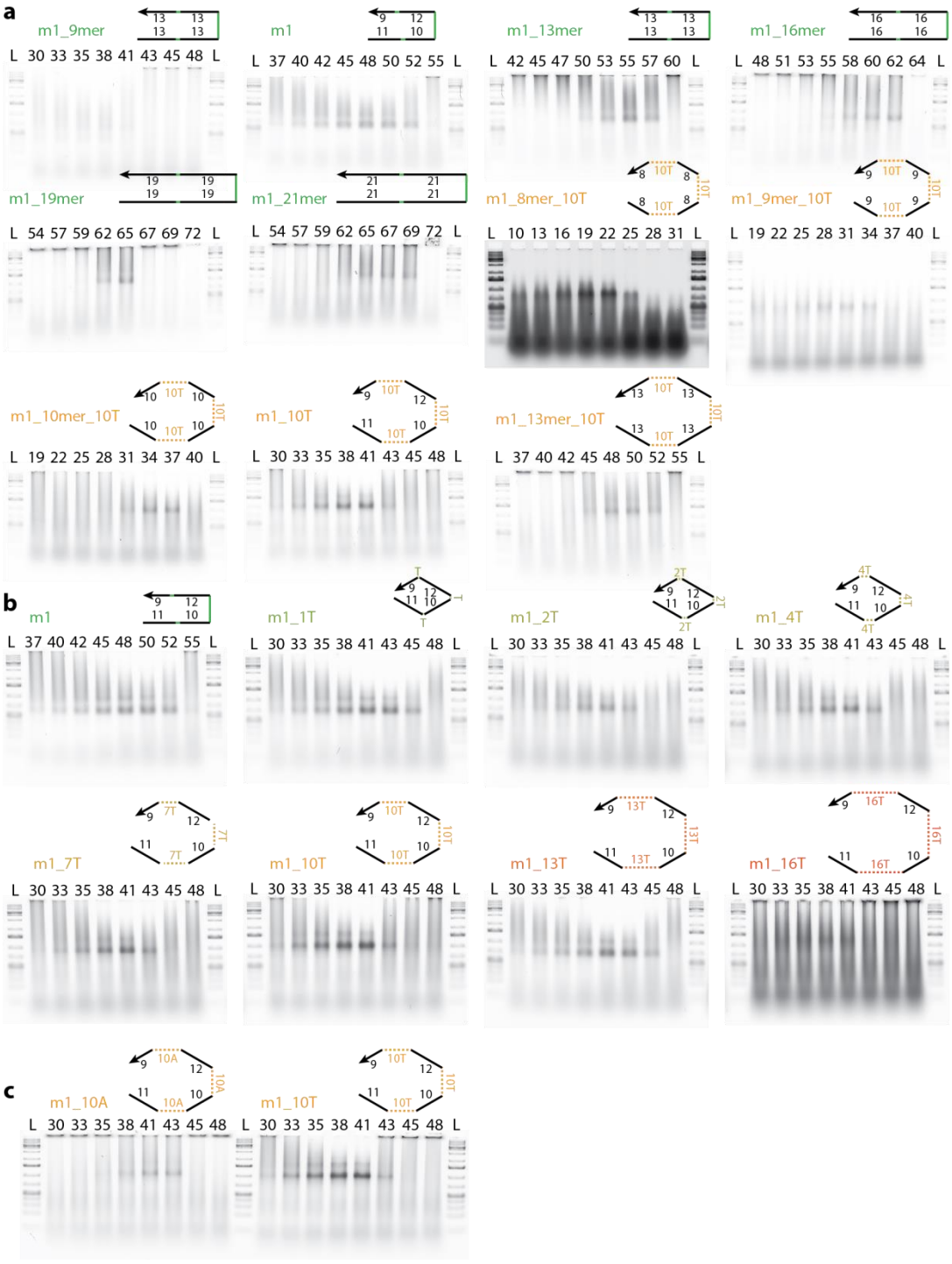

Figure S3. Raw gel data for Fig. 3. (**a**) Raw gels used to generate the data in Fig. 3c. (**b**) Raw gels used to generate the data in Fig. 3d. (**c**) Gel data indicate that structures with a 10A and 10T linker form at similar temperatures after 1 hour of assembly. Assembly temperatures are indicated above each lane. An "L" indicates the use of 1 kb+ double-stranded DNA ladder (Fermentas). Unless otherwise indicated, 200 nM of each strand was assembled in 0.5× TE buffer supplemented with 10 mM Mg^{2+}. Structures with domain length < 16 nt were assembled isothermally for 1 hour; otherwise they were assembled isothermally for 12 hours.

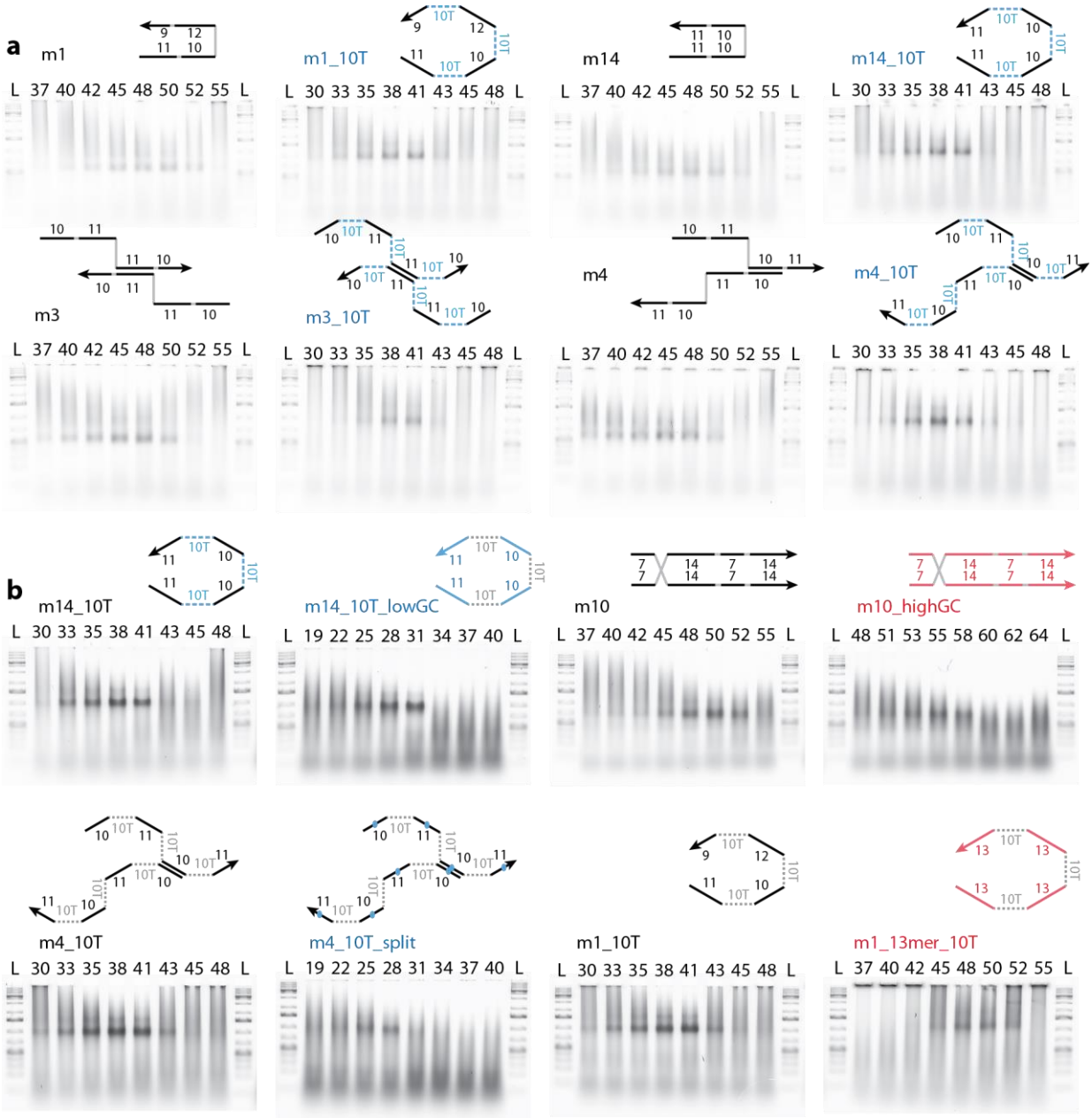

Figure S4. Raw gel data for Fig. 4. (**a**) and (**b**) respectively describe raw gels used to generate the data in Fig. 4a and Fig. 4b. Structure names and assembly temperatures are indicated. An "L" indicates the use of 1 kb+ double-stranded DNA ladder (Fermentas). 200 nM of each strand was assembled isothermally for 1 hour in 0.5× TE buffer supplemented with 10 mM Mg^{2+} at the indicated temperatures.

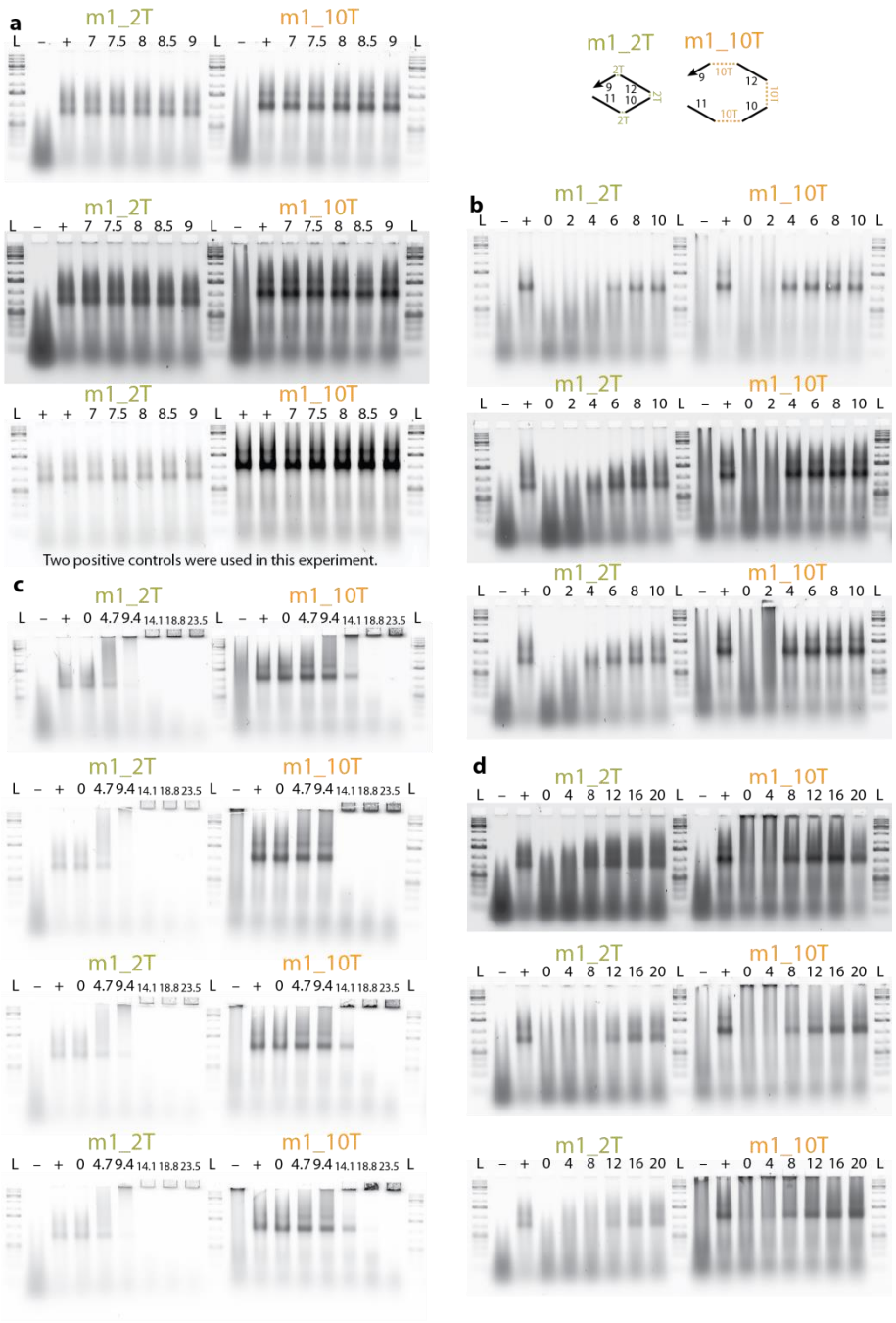

Figure S5. Raw gel data for Fig. 5. (**a**) Raw gel data for pH variation experiments. Structures and pH values are shown above each lane. "–" and "+" indicate negative (no magnesium) and positive (standard reaction conditions) controls, respectively. (**b**) Raw gel data for Mg^{2+} experiments. Structures and Mg^{2+} concentrations in mM are shown above each lane. "–" and "+" are used as in (a). (**c**) Raw gel data for high salinity, PEG experiments. Structures and PEG concentrations in mM are shown above each lane. "–" and "+" are used as in (a). (**d**) Raw gel data for low salinity, PEG experiments. Structures and PEG concentrations in mM are shown above each lane. "–" and "+" are used as in (a). Unless otherwise indicated, 200 nM of each strand was assembled isothermally at 37 °C for 1 hour in 0.5× TE buffer supplemented with 10 mM Mg^{2+}.

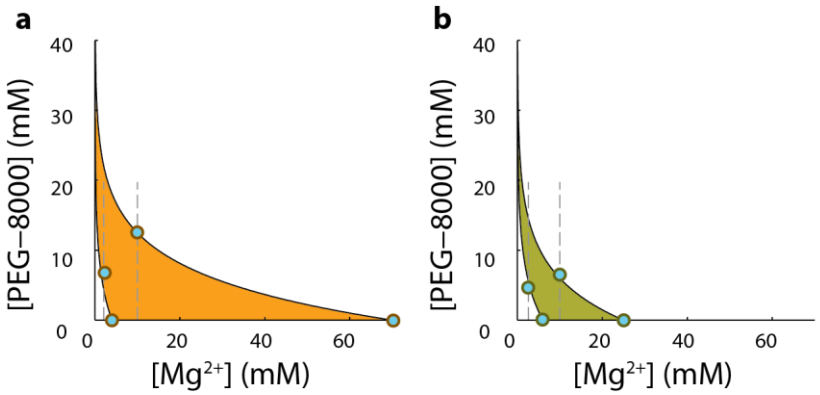

Figure S6. Detailed plots of crowding model. We show the predicted assembly ranges for the structure with 10T linkers **(a)**, and the structure with 2T linkers **(b)**. Raw data points which influenced the fitting of the model are shown as blue dots, and dotted grey lines indicate the experimental data (a subset shown in Fig. 5b-d) upon which the model is based. Shaded regions are as in Fig. 5g (orange: 10T linker, olive: 2T linker).

Supplementary References

1. Ogston, A. G. The spaces in a uniform random suspension of fibres. *Transactions of the Faraday Society* **54**, 1754 (1958).

2. Smithies, O. Why the kidney glomerulus does not clog: a gel permeation/diffusion hypothesis of renal function. *Proceedings of the National Academy of Sciences of the United States of America* **100**, 4108–13 (2003).

Structure name	Avg. domain length (nt)	Linker length (nt)	Number of strands	Strand type 1	Strand type 2 (if different)	Optimal assembly temperature (mean ± FWHM/2, °C)
m1_8mer_10T	8	10	66	8-8-8-8		18.42 ± 6.49
m1_9mer_10T	9	10	66	9-9-9-9		26.81 ± 12.71
m1_10mer_10T	10	10	66	10-10-10-10		34.98 ± 4.47
m1_10T	10.5	10	66	11-10-12-9	12-9-11-10	38.51 ± 4.87
m1_13mer_10T	13	10	66	13-13-13-13		48.66 ± 5.51
m1_9mer	9	0	66	9-9-9-9		35.90 ± 6.42
m1	10.5	0	66	11-10-12-9	12-9-11-10	47.38 ± 6.09
m1_13mer	13	0	66	13-13-13-13		54.77 ± 3.69
m1_16mer	16	0	66	16-16-16-16		60.07 ± 4.60
m1_19mer	19	0	66	19-19-19-19	19-19-19-19	63.80 ± 2.70
m1_21mer	21	0	66	21-21-21-21	21-21-21-21	64.80 ± 6.09
m1_1T	10.5	1	66	11-10-12-9	12-9-11-10	40.66 ± 5.56
m1_2T	10.5	2	66	11-10-12-9	12-9-11-10	39.37 ± 4.79
m1_4T	10.5	4	66	11-10-12-9	12-9-11-10	39.14 ± 4.81
m1_7T	10.5	7	66	11-10-12-9	12-9-11-10	39.73 ± 4.73
m1_13T	10.5	13	66	11-10-12-9	12-9-11-10	40.31 ± 5.41
m1_16T	10.5	16	66	11-10-12-9	12-9-11-10	37.01 ± 7.46
m14	10.5	0	66	10-11-11-10	11-10-10-11	46.83 ± 5.95
m14_10T	10.5	10	66	10-11-11-10	11-10-10-11	37.92 ± 5.37
m3.1	10.5	0	66	10-11-11-10	11-10-10-11	45.63 ± 5.63
m3.1_10T	10.5	10	66	10-11-11-10	11-10-10-11	39.34 ± 4.36
m4.1	10.5	0	66	10-11-11-10	11-10-10-11	44.39 ± 7.90
m4.1_10T	10.5	10	66	10-11-11-10	11-10-10-11	37.84 ± 4.57
m14_10T_lowGC	10.5	10	66	10-11-11-10	11-10-10-11	26.66 ± 7.06
m10	10.5	0	64	7-14-7-14		50.03 ± 5.43
m10_highGC	10.5	0	64	7-14-7-14		54.46 ± 3.64
m4.1_10T_split	10.5	10	66	10-11-11-10	11-10-10-11	24.44 ± 7.04
m1_10A	10.5	10	66	11-10-12-9	12-9-11-10	N/A

		m1_8mer_10T	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	ATAGATGGTTTTTTTTTTCGCCCACA	
B1	1-2	CTCCGGGCTTTTTTTTTTAACCGACC	
C1	1-3	ACGCTTTATTTTTTTTTTCTACCACG	
D1	1-4	CGTTTCTGTTTTTTTTTTCCCAGAAA	
E1	1-5	AGGCCACCTTTTTTTTTTGCCCTCGG	
F1	1-6	CCCTGGCCTTTTTTTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTTTTTTGGAAATAGTTTTTTTTTTCCATCTATTTTTTTTTTTTTTTTT	
H1	2-2	CGGTATGATTTTTTTTTTCGGCCAAATTTTTTTTTTGCCCGGAGTTTTTTTTTTTGTGGGCG	
A2	2-3	GGCAGGCATTTTTTTTTTTGGTGGGTTTTTTTTTTTTAAAGCGTTTTTTTTTTTGGTCGGTT	
B2	2-4	GATGCAGGTTTTTTTTTTGTGCCGTATTTTTTTTTTCAGAAACGTTTTTTTTTTCGTGGTAG	
C2	2-5	CCTAAGGTTTTTTTTTTTCCATAAAGTTTTTTTTTTGGTGGCCTTTTTTTTTTTTTTCTGGG	
D2	2-6	CTAGCTCCTTTTTTTTTTCGCCGGTGTTTTTTTTTTGGCCAGGGTTTTTTTTTCCGAGGGC	
E2	3-1	GACTCTCCTTTTTTTTTTGAACCCTATTTTTTTTTTTCATACCGTTTTTTTTTTCTATTTCC	
F2	3-2	AGTGCAGGTTTTTTTTTTACAATCCTTTTTTTTTTGCCTGCCTTTTTTTTTTTTGGCCG	
G2	3-3	CGTTCTGTTTTTTTTTTAATGCGGGTTTTTTTTTCCTGCATCTTTTTTTTTACCCACCA	
H2	3-4	ATAGGAATTTTTTTTTTGCGAAGGTTTTTTTTTTACCTTAGGTTTTTTTTTACGGCAC	
A3	3-5	CCCGAAGGTTTTTTTTTGAACGGAATTTTTTTTTGGAGCTAGTTTTTTTTTCTTTATGG	
B3	3-6	CCTCATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCGGCG	
C3	4-1	TTTTTTTTTTTTTTTTTGTCAGACTTTTTTTTTTGGAGAGTCTTTTTTTTTTTTTTTTT	
D3	4-2	CTGTCCGGTTTTTTTTTCGGCCTGTTTTTTTTTTCCTGCACTTTTTTTTTTTAGGGTTC	
E3	4-3	CCTGTCGATTTTTTTTTGTACTGAATTTTTTTTTACAGAACGTTTTTTTTTGGATTGTA	
F3	4-4	GTCCTGGATTTTTTTTTGTCGCGCCTTTTTTTTTATTCCTATTTTTTTTTCCCGCATT	
G3	4-5	GGTGGAGCTTTTTTTTTAACACCAATTTTTTTTCCTTCGGGTTTTTTTTTACCTTCGC	
H3	4-6	CGTTCTAGTTTTTTTTTGGTTATCTTTTTTTTTGGATGAGGTTTTTTTTTCCGTTC	
A4	5-1	TATCGACGTTTTTTTTTGTACTAACTTTTTTTTCCGGACAGTTTTTTTTTAGTCTGAC	
B4	5-2	CGTTCATATTTTTTTTTCATGTGTTTTTTTTTCGACAGGTTTTTTTTTACAGGCCG	
C4	5-3	GAGCCTCCTTTTTTTTTATATGGTCTTTTTTTTTCCAGGACTTTTTTTTTCAGTAC	
D4	5-4	TCATAATCTTTTTTTTTAAAGTCATTTTTTTTTGCTCCACCTTTTTTTTGGCGCGAC	
E4	5-5	GAATGTGTTTTTTTTTATCTGCGGTTTTTTTTCTAGAACGTTTTTTTTTGGTGTT	
F4	5-6	GTGTGGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGATAACC	
G4	6-1	TTTTTTTTTTTTTTTTTCGAGATGTTTTTTTTTCGTCGATATTTTTTTTTTTTTTTT	
H4	6-2	AGCTGTGTTTTTTTTTTCGCCTATCTTTTTTTTTTATGAACGTTTTTTTTTGTTAGTAC	
A5	6-3	ATCTGTAGTTTTTTTTTCGACTCCTTTTTTTTTGGAGGCTCTTTTTTTTTACACATGA	
B5	6-4	GGGACTTATTTTTTTTTAGAACTAATTTTTTTTGATTATGATTTTTTTTTGACCATAT	
C5	6-5	GCGGCGTATTTTTTTTTCCTTATGCTTTTTTTTTACACATTCTTTTTTTTTGACTTTA	
D5	6-6	AGCTACAGTTTTTTTTTAGTTCCTATTTTTTTTCACCACACTTTTTTTTCCGCAGAT	
E5	7-1	ACCTCATGTTTTTTTTTCGAATAGATTTTTTTTTACACAGCTTTTTTTTTACATCTCG	
F5	7-2	CAGATGCTTTTTTTTTTCAACTCTTTTTTTTTTCTACAGATTTTTTTTTGATAGGCG	
G5	7-3	ACCGTACGTTTTTTTTTCTGCCCTTTTTTTTTTAAGTCCCTTTTTTTTTAGGAGTCG	
H5	7-4	TCATAGTATTTTTTTTTTGCATTTCTTTTTTTTTACGCCGCTTTTTTTTTAGTTCT	
A6	7-5	TAGCCATGTTTTTTTTTGGCAAGTATTTTTTTTTCTGTAGCTTTTTTTTTGCATAAGG	
B6	7-6	TATTATCGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGAACT	
C6	8-1	TTTTTTTTTTTTTTTTTACGCGATCTTTTTTTTTTCATGAGGTTTTTTTTTTTTTTTT	
D6	8-2	CTCAGCCTTTTTTTTTTTCGCCTCTTTTTTTTTTAGCATCTGTTTTTTTTTTCTATTCG	
E6	8-3	CTCCACAGTTTTTTTTTGAAGTCAATTTTTTTTTCGTACGGTTTTTTTTTAAGAGTTG	
F6	8-4	CGGGAAACTTTTTTTTTGAGTTCGCTTTTTTTTTACTATGATTTTTTTTTAAGGGCAG	
G6	8-5	GCCCAGCTTTTTTTTTTGGTGAGAGTTTTTTTTTCATGGCTATTTTTTTTTGAAATGCA	
H6	8-6	CTTCCGGCTTTTTTTTTTCATGAGTTTTTTTTTCGATAATATTTTTTTTTACTTGCC	
A7	9-1	TTAAAGGGTTTTTTTTTCCTTTGGTTTTTTTTAGGCTGAGTTTTTTTTGATCGCGT	
B7	9-2	TCGCATCGTTTTTTTTTGTCCGAACTTTTTTTTTCTGTGGAGTTTTTTTTAGAGGCGA	
C7	9-3	TAACATGATTTTTTTTTACTAGCCCTTTTTTTTTGTTTCCCGTTTTTTTTTGACTTC	
D7	9-4	TGTCCACATTTTTTTTTCTCACTCATTTTTTTTAGCTGGGCTTTTTTTTGCGAACTC	
E7	9-5	ACGGGTCTTTTTTTTTGTGGTCTCTTTTTTTTGCCGGAAGTTTTTTTTCTCTCACC	

F7	9-6	TTCGGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCATGAA
G7	10-1	TTTTTTTTTTTTTTTTTTCATAACGGTTTTTTTTTCCCTTTAATTTTTTTTTTTTTTTTTT
H7	10-2	AGAACCATTTTTTTTTTTGCGAAAGGTTTTTTTTTTCGATGCGATTTTTTTTTTCCAAAGGA
A8	10-3	GTCTAACATTTTTTTTTTCCTTAGAATTTTTTTTTTTCATGTTATTTTTTTTTTGTTCGGAC
B8	10-4	CGTCTCGTTTTTTTTTTTACCAGTTTTTTTTTTTTTTGTGGACATTTTTTTTTTGGGCTAGT
C8	10-5	AAACCTCCTTTTTTTTTTACGGTTAGTTTTTTTTTTAGACCCGTTTTTTTTTTTGAGTGAG
D8	10-6	TCCTATCATTTTTTTTTTGGATGCTTTTTTTTTTTTTAGTCCGAATTTTTTTTTGAGACCAC
E8	11-1	ATGGTTCTTTTTTTTTTCCGTTATG
F8	11-2	TGTTAGACTTTTTTTTTCCTTTCGC
G8	11-3	ACGAGACGTTTTTTTTTTTTCTAAGG
H8	11-4	GGAGGTTTTTTTTTTTTAAACTGGT
A9	11-5	TGATAGGATTTTTTTTTTCTAACCGT
B9	11-6	TTTTTTTTTTTTTTTTTTAAGCATCC
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_9mer_10T

Well	Name	Sequence
A1	1-1	AGAGCAATGTTTTTTTTTTAAGCTTGGA
B1	1-2	CCCTGCGGATTTTTTTTTTGTTAATTCA
C1	1-3	TCCATAACCTTTTTTTTTTCACGCCGCA
D1	1-4	GAACTGTCCTTTTTTTTTTCTAACCGGT
E1	1-5	TTGAGCTCGTTTTTTTTTTAACATGGCC
F1	1-6	GTCCCAGACTTTTTTTTTTTTTTTTTTT
G1	2-1	TTTTTTTTTTTTTTTTTTTGCGTAGCATTTTTTTTTTTCATTGCTCTTTTTTTTTTTTTTTTTTT
H1	2-2	ACCTCAAGCTTTTTTTTTTGAAATTTTTTTTTTTTTTTTCCGCAGGGTTTTTTTTTTTCCAAGCTT
A2	2-3	AGTCCTAGATTTTTTTTTTCCTTGGGCCTTTTTTTTTTGGTTATGGATTTTTTTTTTTGAATTAAC
B2	2-4	TCTAGGAATTTTTTTTTTTCAGTCACCTTTTTTTTTTTGGACAGTTCTTTTTTTTTTTGCGGCGTG
C2	2-5	TTCCCTTAATTTTTTTTTTGCACATTGGTTTTTTTTTTCGAGCTCAATTTTTTTTTTACCGGTTAG
D2	2-6	GCATTGTATTTTTTTTTTTAAGCTTCGTTTTTTTTTTGTCTGGGACTTTTTTTTTGGCCATGTT
E2	3-1	AGTTCGGGATTTTTTTTTTCGCTGGGTATTTTTTTTTTGCTTGAGGTTTTTTTTTTATGCTACGC
F2	3-2	CTGATTTCTTTTTTTTTTTCCCTCGCGTTTTTTTTTTCTAGGACTTTTTTTTTTAAAAATTTC
G2	3-3	GTGAATGACTTTTTTTTTGACCGCGCGTTTTTTTTTATTCCTAGATTTTTTTTGGCCCAAGG
H2	3-4	AGACTTAACTTTTTTTTTGAGCTGGACTTTTTTTTTTAAGGGAATTTTTTTTTAGGTGACTG
A3	3-5	TCTCCAGGCTTTTTTTTTTCGGGTCTTTTTTTTTTATACAATGCTTTTTTTTTCCAATGTGC
B3	3-6	TCTAGGGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGAAGCTT
C3	4-1	TTTTTTTTTTTTTTTTTTTGTCGAGTGTTTTTTTTTTCCCGAACTTTTTTTTTTTTTTTTTT
D3	4-2	CGTACGTGCTTTTTTTTTTTTCACGCGTTTTTTTTTAGAAATCAGTTTTTTTTTTACCCAGCG
E3	4-3	CCATACTTTTTTTTTTTTAGGAGCGGATTTTTTTTTGTCATTCACTTTTTTTTTCGCGAGGGA
F3	4-4	CGAGGGTTATTTTTTTTTCTGCAGTTCTTTTTTTTTGTTAAGTCTTTTTTTTTCGCGCGGTC
G3	4-5	ACCGAGATGTTTTTTTTTGACCAGCTGTTTTTTTTTGCCTGGAGATTTTTTTTTGTCCAGCTC
H3	4-6	CGCTCCTCCTTTTTTTTTGGACTGTTTTTTTTTTTTGGCCCTAGATTTTTTTTTAGACCCGAA
A4	5-1	GCAATTAGTTTTTTTTTTGATACCCGATTTTTTTTTGCACGTACGTTTTTTTTTCACTCGACA
B4	5-2	TCATCACACTTTTTTTTTAATGTCTCCTTTTTTTTTAAAGTATGGTTTTTTTTTCGCGTGAAA
C4	5-3	CCCCACATTTTTTTTTTTCATCTGGATTTTTTTTTAACCCTCGTTTTTTTTTCCGCTCCT
D4	5-4	AGGGCTATTTTTTTTTTTGTGAAGCCTTTTTTTTTCATCTCGGTTTTTTTTTGAACTGCAG
E4	5-5	AGATCAGCGTTTTTTTTTCGCCGATTATTTTTTTTGGAGGAGCGTTTTTTTTTCAGCTGGTC
F4	5-6	ATAGTATCGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAACAGTCC
G4	6-1	TTTTTTTTTTTTTTTTTTTGCAGTGCTTTTTTTTTTACTAATTGCTTTTTTTTTTTTTTTTT
H4	6-2	GGTGCACGGTTTTTTTTTCTTAGCCGATTTTTTTTTGTGTGATGATTTTTTTTTCGGGTATC
A5	6-3	CCTTTGCTATTTTTTTTTGTATTAGGTTTTTTTTTAATGTGGGGTTTTTTTTGGAGACATT
B5	6-4	AGTTCTTCGTTTTTTTTTCTAACCTGATTTTTTTTTAATAGCCCTTTTTTTTTCCAGATGA
C5	6-5	TGTGCCCCTTTTTTTTTGCCATCGCGTTTTTTTTTCGCTGATCTTTTTTTTTGGCTTCACA
D5	6-6	CATGTCCAATTTTTTTTTCAAGGGGACTTTTTTTTTCGATACTATTTTTTTTTAATCGGCG
E5	7-1	TGCTTAGCATTTTTTTTTAGCTGTTGATTTTTTTTTCCGTGCACCTTTTTTTTAGCACTGCA
F5	7-2	CGTTTTTTTTTTTTTTTATCTGGCAGTTTTTTTTTAGCAAAGGTTTTTTTTTCGGCTAAG
G5	7-3	GCGGGGAAATTTTTTTTTGCTCTTATATTTTTTTTCGAAGAACTTTTTTTTTACCTAATAC
H5	7-4	ACAGTTGGCTTTTTTTTTAGATTCTTCTTTTTTTTAGGGGCACATTTTTTTTTCAGGTTAG
A6	7-5	CGCAACTCTTTTTTTTTTGTAGTCAGTTTTTTTTTTGGACATGTTTTTTTTTCGCGATGGC
B6	7-6	TCTGTGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCCCCTTG
C6	8-1	TTTTTTTTTTTTTTTTTTTGTCCTAAATTTTTTTTTTGCTAAGCATTTTTTTTTTTTTTTTT
D6	8-2	AAATGGCCATTTTTTTTTTAGTTGTGTTTTTTTTTTAAAAAAACGTTTTTTTTTTCAACAGCT
E6	8-3	CTCAGTCAATTTTTTTTTCTTGGCTGGTTTTTTTTTTTTCCCCGCTTTTTTTTTCTGCCAGAT
F6	8-4	CTGCACTGTTTTTTTTTTTGCTATGTCTTTTTTTTTGCCAACTGTTTTTTTTTTTATAAGAGC
G6	8-5	AGGCTCATGTTTTTTTTTTATAGCTAATTTTTTTTTTAGAGTTGCGTTTTTTTTTGAAGAATCT
H6	8-6	AACAGAAAATTTTTTTTTCGCTATATGTTTTTTTTTAGTCACAGATTTTTTTTTACTGACTAC
A7	9-1	TGGCCACAATTTTTTTTTTCTGAATTCTTTTTTTTTTGGCCATTTTTTTTTTTTTTAGGACA
B7	9-2	GATTCCAAATTTTTTTTTGGCGTATTTTTTTTTTTTTTGACTGAGTTTTTTTTTACACAACTA
C7	9-3	CCGAGTTTCTTTTTTTTTTTTCGTTCGTTTTTTTTTACAGTGCAGTTTTTTTTTCCAGCCAAG
D7	9-4	CAGCGTTGATTTTTTTTTCGCAACTTGTTTTTTTTTCATGAGCCTTTTTTTTTTGACATAGCA
E7	9-5	CTGATGTAGTTTTTTTTTTCTCCGCTATTTTTTTTTTTTTCTGTTTTTTTTTTTATTAGCTAT

Back to overview

F7	9-6	AGCGCGGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATATAGCG
G7	10-1	TTTTTTTTTTTTTTTTTTTAGGCGCATGTTTTTTTTTTTTTGTGGCCATTTTTTTTTTTTTTTTTTT
H7	10-2	ATTGCCATGTTTTTTTTTTATACCGTCCTTTTTTTTTTTTTTGGAATCTTTTTTTTTTGAATTCAGA
A8	10-3	GAGGAGGGCTTTTTTTTTTCTGTATTGTTTTTTTTTTTTGAAACTCGGTTTTTTTTTTAAATACGCC
B8	10-4	TTTATATCGTTTTTTTTTTACGGGGCCATTTTTTTTTTTCAACGCTGTTTTTTTTTTCGAACGAAA
C8	10-5	TAATATTTCTTTTTTTTTTTATGCGTAGTTTTTTTTTTCTACATCAGTTTTTTTTTTCAAGTTGCG
D8	10-6	ATTCCCAAATTTTTTTTTTGGCTCGCTTTTTTTTTTTTCCCGCGCTTTTTTTTTTTAGCGGAGA
E8	11-1	CATGGCAATTTTTTTTTTCATGCGCCT
F8	11-2	GCCCTCCTCTTTTTTTTTGGACGGTAT
G8	11-3	CGATATAAATTTTTTTTTACAATACAG
H8	11-4	GAAATATTATTTTTTTTTTGGCCCCGT
A9	11-5	TTTGGGAATTTTTTTTTTCTACGCATA
B9	11-6	TTTTTTTTTTTTTTTTTTAGCGAGCCA
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_10mer_10T

Well	Name	Sequence
A1	1-1	GTTCATAGTGTTTTTTTTTTCTCTGTGAGA
B1	1-2	GCATGGGAAATTTTTTTTTTACTGCAAGCT
C1	1-3	GCTCGGCATTTTTTTTTTTTGCTGCGTTGT
D1	1-4	CTCGGTACCATTTTTTTTTTCTCTGGTACT
E1	1-5	GAGCCACCATTTTTTTTTTTCTGTCTCAAA
F1	1-6	ACTTAGGAAGTTTTTTTTTTTTTTTTTTT
G1	2-1	TTTTTTTTTTTTTTTTTTTTCGTGGTGGCATTTTTTTTTTCACTATGAACTTTTTTTTTTTTTTTTTTT
H1	2-2	GCTTAAATTATTTTTTTTTTGGCGCTTGGCTTTTTTTTTTTTTCCCATGCTTTTTTTTTTTCTCACAGAG
A2	2-3	CGTGTCTAGTTTTTTTTTTTGTTCTACGGCTTTTTTTTTTAATGCCGAGCTTTTTTTTTTAGCTTGCAGT
B2	2-4	AAGTGGATCTTTTTTTTTTTTAATTTTAGTTTTTTTTTTTGGTACCGAGTTTTTTTTTACAACGCAGC
C2	2-5	GCGACTCACCTTTTTTTTTTGCTTATACCTTTTTTTTTTTATGGTGGCTCTTTTTTTTTAGTACCAGAG
D2	2-6	GAACTTTTCGTTTTTTTTTTAAGCTTGTCATTTTTTTTTTCTTCCTAAGTTTTTTTTTTTTTGAGACAG
E2	3-1	GCAGATTTTCTTTTTTTTTTCCAGTGCTTATTTTTTTTTTTAATTTAAGCTTTTTTTTTTGCCACCACG
F2	3-2	TAGGGTGTTGTTTTTTTTTTCACTAGGTTATTTTTTTTTTACTAGACACGTTTTTTTTTTGCCAAGCGCC
G2	3-3	ATCGGACGGTTTTTTTTTTTTCATAATGGATTTTTTTTTTAGATCCACTTTTTTTTTTTGCCGTAGAAC
H2	3-4	AAAAGGATAATTTTTTTTTTGATGCGCCAATTTTTTTTTTGGTGAGTCGCTTTTTTTTTCTAAAAATTA
A3	3-5	CGAGAGTCCTTTTTTTTTTTGGGCGATGCATTTTTTTTTTCGAAAAGTTCTTTTTTTTTTAGGTATAAGC
B3	3-6	ATGGGGCACCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGACAAGCTT
C3	4-1	TTTTTTTTTTTTTTTTTTTTCTTCATCTGTTTTTTTTTTGAAAATCTGCTTTTTTTTTTTTTTTTTTT
D3	4-2	AGCTGCGCTTTTTTTTTTTTATTGCCCACCTTTTTTTTTTCAACACCCTATTTTTTTTTTTAAGCACTGG
E3	4-3	GGAGCCATCATTTTTTTTTTGCAGTTGGATTTTTTTTTTTACCGTCCGATTTTTTTTTTTTAACCTAGTG
F3	4-4	GTGTGGTTTTTTTTTTTTTTTATGTGCAGCTTTTTTTTTTTTATCCTTTTTTTTTTTTTTTCCATTATGA
G3	4-5	TACGCGCCCCTTTTTTTTTTGCACCACTGTTTTTTTTTTTTAGGACTCTCGTTTTTTTTTTTTGGCGCATC
H3	4-6	CATAACTGCATTTTTTTTTTTAGATCAACATTTTTTTTTTGGTGCCCCATTTTTTTTTTTTGCATCGCCC
A4	5-1	CCAAGATGATTTTTTTTTTTCGCTGGTTAATTTTTTTTTTAAGCGCAGCTTTTTTTTTTCAGATGAAGA
B4	5-2	CGACAGAGACTTTTTTTTTTACTCATATTGTTTTTTTTTTGATGGCTCCTTTTTTTTTGGTGGGCAAT
C4	5-3	CTTGTCCCAATTTTTTTTTTACAGTTTTTTTTTTTTTTTTAAAACCACACTTTTTTTTTATCCAACTGC
D4	5-4	GGTTTGCCCCTTTTTTTTTAGCTTTAGATTTTTTTTTTGGGGCGCGTATTTTTTTTTGCTGCACATA
E4	5-5	TAGACGACCGTTTTTTTTTTATTCCCGAGTTTTTTTTTTGCAGTTATGTTTTTTTTTACAGTGGTGC
F4	5-6	TCGCACAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTTGATCTA
G4	6-1	TTTTTTTTTTTTTTTTTTTAAAATTTCGTTTTTTTTTTTATCATCTTGGTTTTTTTTTTTTTTTTTT
H4	6-2	TAGAGGGCCTTTTTTTTTTGAAGGTAAGGTTTTTTTTTGTCTCTGTCGTTTTTTTTTTTTAACCAGCG
A5	6-3	CAAAATAGGATTTTTTTTTCATGATACTGTTTTTTTTTTTGGGACAAGTTTTTTTTTCAATATGAGT
B5	6-4	CTTTTTTCTGTTTTTTTTTTCGAATATCAGTTTTTTTTTTGGGGCAAACCTTTTTTTTTAAAAAACTGT
C5	6-5	CTCACTGACATTTTTTTTTTTCCGATCGTGTTTTTTTTTTCGGTCGTCTATTTTTTTTTTATCTAAAGCT
D5	6-6	CAACCTCGCGTTTTTTTTTTCTGCTCGTGCTTTTTTTTTTAACTGTGCGATTTTTTTTTCTCGGGAATA
E5	7-1	TAGCAGAATCTTTTTTTTTTACTCTCCCACTTTTTTTTTTAGGCCCTCTATTTTTTTTTACGAAATTTT
F5	7-2	AAACATAGGGTTTTTTTTTGTAGACCCCTTTTTTTTTTTCCTATTTTGTTTTTTTTTCCTTACCTTC
G5	7-3	TTTGTGACGTTTTTTTTTTGTAGGTACGATTTTTTTTTTCAGAAAAAAGTTTTTTTTTCAGTATCATG
H5	7-4	ACATACCGCCTTTTTTTTTTCTGATCGGCGTTTTTTTTTTGTCAGTGAGTTTTTTTTTCTGATATTCG
A6	7-5	GCTGCGTGCCTTTTTTTTTTGTGCCCGCGATTTTTTTTTTCGCGAGGTTGTTTTTTTTTCACGATCGGA
B6	7-6	TCCTACGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCACGAGCAG
C6	8-1	TTTTTTTTTTTTTTTTTTTTCTAAATATCCTTTTTTTTTTGATTCTGCTATTTTTTTTTTTTTTTTTT
D6	8-2	TGCCGCTCGCTTTTTTTTTTATAGCTCATTTTTTTTTTTCCCTATGTTTTTTTTTTTTGTGGGAGAGT
E6	8-3	GTTATGGGTCTTTTTTTTTTAAACAACACATTTTTTTTTTACGTCACAAATTTTTTTTTAGGGGTCTAC
F6	8-4	TGAGACTGGCTTTTTTTTTTTAAACAAATGTTTTTTTTTTGGCGGTATGTTTTTTTTTTTCGTACCTAC
G6	8-5	CCGCATAACATTTTTTTTTTGTCCAGACGTTTTTTTTTTTGGCACGCAGCTTTTTTTTTCGCCGATCAG
H6	8-6	ACTCTAACAGTTTTTTTTTCGCATTCAGGTTTTTTTTTTGTACGTAGGATTTTTTTTTTCGCGGGCAC
A7	9-1	CTTTTCTGATTTTTTTTTTCGACATCTCTTTTTTTTTTGCGAGCGGCATTTTTTTTTGGATATTTAG
B7	9-2	AGGCTAATCCTTTTTTTTTTGCTCGGACGTTTTTTTTTTGACCCATAACTTTTTTTTTAATGAGCTAT
C7	9-3	TAGGTACATGTTTTTTTTTCACCGCATACTTTTTTTTTTGCCAGTCTCATTTTTTTTTTGTGTTGTTT
D7	9-4	GGCACTAACATTTTTTTTTTTATTGCCTACTTTTTTTTTTGTTATGCGGTTTTTTTTTCATTTGTTTA
E7	9-5	TGCGAGGGACTTTTTTTTTTTATCTGGTCATTTTTTTTTTCTGTTAGAGTTTTTTTTTTACGTCTGGAC

Back to overview

F7	9-6	CCCTCAGATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTGAATGCG
G7	10-1	TTTTTTTTTTTTTTTTTTTTTCCGCGAGCTTTTTTTTTTTTATCAGAAAAGTTTTTTTTTTTTTTTTTTT
H7	10-2	CACGGTGAACTTTTTTTTTTGCTGGTCGAGTTTTTTTTTTGGATTAGCCTTTTTTTTTTTAGAGATGTCG
A8	10-3	TGCGTCCGAATTTTTTTTTTCTCTCAAGGGTTTTTTTTTTCATGTACCTATTTTTTTTTTACGTCCGAGC
B8	10-4	TTTGACGCATTTTTTTTTTTAAACGAAGAATTTTTTTTTTTGTTAGTGCCTTTTTTTTTTGTATGCGGTG
C8	10-5	GCTGTAAACTTTTTTTTTTTAAAGATTCTGTTTTTTTTTTGTCCCTCGCATTTTTTTTTTGTAGGCAATA
D8	10-6	GGTCGGCATCTTTTTTTTTTGCTACCGTTGTTTTTTTTTTTATCTGAGGGTTTTTTTTTTTGACCAGATA
E8	11-1	GTTCACCGTGTTTTTTTTTTAGCTCGCGGA
F8	11-2	TTCGGACGCATTTTTTTTTTCTCGACCAGC
G8	11-3	ATGCGTCAAATTTTTTTTTTCCCTTGAGAG
H8	11-4	AGTTTACAGCTTTTTTTTTTTTCTTCGTTT
A9	11-5	GATGCCGACCTTTTTTTTTTCAGAATCTTT
B9	11-6	TTTTTTTTTTTTTTTTTTTTCAACGGTAGC
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_10T	
WellPosition	**Name**	**Sequence**	Back to overview
A1	1-1	GCCGGTGTCATATTTTTTTTTTGGACCAGAG	
B1	1-2	GCCTCAACGGCTTTTTTTTTTTTTAGCACGT	
C1	1-3	AACAGAGAGGTATTTTTTTTTTCTCCAAAGA	
D1	1-4	ACTTAGTTACCGTTTTTTTTTTGCTCGTTGA	
E1	1-5	GTGTAAAGCTGGTTTTTTTTTTCGGTGACGC	
F1	1-6	GGTTACAGATACTTTTTTTTTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTTTTTTTTTGCCATTGAGCTTTTTTTTTTTTATGACACCGGCTTTTTTTTTTTTTTTTTT	
H1	2-2	GAGACGGCGTCTTTTTTTTTTGTCGGCGAACTTTTTTTTTTAGCCGTTGAGGCTTTTTTTTTTCTCTGGTCC	
A2	2-3	CTGGGCGGATGTTTTTTTTTTTTTACAGTGCGTTTTTTTTTTTACCTCTCTGTTTTTTTTTTTTACGTGCTAA	
B2	2-4	TCCGATTGCTATTTTTTTTTTGACGCATTGTTTTTTTTTTTCGGTAACTAAGTTTTTTTTTTTCTTTGGAG	
C2	2-5	CAACATCTGCATTTTTTTTTTGCAGCTGTAGTTTTTTTTTTCCAGCTTTACACTTTTTTTTTTCAACGAGC	
D2	2-6	ATCTGCCGCGGTTTTTTTTTTAGTTGCTGCTTTTTTTTTTGTATCTGTAACCTTTTTTTTTGCGTCACCG	
E2	3-1	CACGGAACGGCATTTTTTTTTTCGAACGTGTTTTTTTTTTGACGCCGTCTCTTTTTTTTTGCTCAATGGC	
F2	3-2	TCGTCCTAGGCCTTTTTTTTTCTGGACTTCTTTTTTTTTTCATCCGCCCAGTTTTTTTTTGTTCGCCGAC	
G2	3-3	TTCCGGATCGACTTTTTTTTTCCTCGCCATTTTTTTTTTTAGCAATCGGATTTTTTTTTCGCACTGTAA	
H2	3-4	TTACCTAGAAATTTTTTTTTTACCCGATGATTTTTTTTTTGCAGATGTTGTTTTTTTTTACAATGCGTC	
A3	3-5	GAAGCTGGCAAGTTTTTTTTTGTTGCTATATTTTTTTTTCCGCGGCAGATTTTTTTTTCTACAGCTGC	
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAGCAACTA	
C3	4-1	TTTTTTTTTTTTTTTTTTTTGGTTTCGAGATTTTTTTTTTGCCGTTCCGTGTTTTTTTTTTTTTTTTT	
D3	4-2	GATTAGAGCATTTTTTTTTTAATCTCTTTCTTTTTTTTTGGCCTAGGACGATTTTTTTTTCACGTTCGA	
E3	4-3	GCTGAGGTGTGTTTTTTTTTCCGAGAAACATTTTTTTTTTGTCGATCCGGAATTTTTTTTTGAAGTCCAG	
F3	4-4	TCTAGGAAACCTTTTTTTTTTCGGATATGTGTTTTTTTTTTATTTCTAGGTAATTTTTTTTTTATGGCGAGG	
G3	4-5	CGGCAGTTTAATTTTTTTTTTGACCTGCTCTTTTTTTTTTTCTTGCCAGCTTCTTTTTTTTTTCATCGGGT	
H3	4-6	GAACAAATATCTTTTTTTTTTTACACCCTATTTTTTTTTTTTCCATCTTCCCGTTTTTTTTTTATAGCAAC	
A4	5-1	GGTCGGATCACTTTTTTTTTTCCCGCCAACTTTTTTTTTTATGCTCTAATCTTTTTTTTTTCTCGAAACC	
B4	5-2	GAACTCGTCTCCTTTTTTTTTGCTCAGGGTTTTTTTTTTCACACCTCAGCTTTTTTTTTGAAAGAGATT	
C4	5-3	CTAATAATAAGCTTTTTTTTTGTGCCTAGCTTTTTTTTTGGTTTCCTAGATTTTTTTTTTGTTTCTCGG	
D4	5-4	TGAGCAAAGCAGTTTTTTTTTACACAAAGGTTTTTTTTTTTAAACTGCCGTTTTTTTTTCACATATCCG	
E4	5-5	ACCATCACCCTATTTTTTTTTCGATTCTCATTTTTTTTTGATATTTGTTCTTTTTTTTTAGAGCAGGTC	
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGGTGTA	
G4	6-1	TTTTTTTTTTTTTTTTTTTTCTAGCTCACCTTTTTTTTTTAGTGATCCGACCTTTTTTTTTTTTTTTTT	
H4	6-2	ACTTCACTATTTTTTTTTTTTAAGGTGTTGTTTTTTTTTGGAGACGAGTTCTTTTTTTTTGTTGGCGGG	
A5	6-3	ATTTAGACTAGTTTTTTTTTTCGCCTGGATTTTTTTTTTGCTTATTATTAGTTTTTTTTTACCCTGAGC	
B5	6-4	CAGAAAGTGAGTTTTTTTTTGGCCTCAGGTTTTTTTTTTCTGCTTTGCTCATTTTTTTTTGCTAGGCAC	
C5	6-5	GGTCAGGTCAATTTTTTTTTCGGTCATCTCTTTTTTTTTTAGGGTGATGGTTTTTTTTTCCTTTGTGT	
D5	6-6	AAAGCTCGGATTTTTTTTTTAGCGCCCGGTTTTTTTTTCTGAGTTTGCTATTTTTTTTTGAGAATCG	
E5	7-1	TTGCACGACCGTTTTTTTTTTATCGTCTCTTTTTTTTTTAATAGTGAAGTTTTTTTTTGGTGAGCTAG	
F5	7-2	ACTTACAACGCCTTTTTTTTTTGAAATAAGTTTTTTTTTCTAGTCTAAATTTTTTTTTCAACACCTTA	
G5	7-3	AATAATTACCTCTTTTTTTTTACATACGCTTTTTTTTTCTCACTTTCTGTTTTTTTTTATCCAGGCGA	
H5	7-4	CTGGTCATCTCATTTTTTTTTGAATGAGAATTTTTTTTTTGACCTGACCTTTTTTTTACCTGAGGCC	
A6	7-5	TAGCGTGAATGGTTTTTTTTTATGAGACGCTTTTTTTTTATCCGAGCTTTTTTTTTTGAGATGACCG	
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCGGGCGCTA	
C6	8-1	TTTTTTTTTTTTTTTTTTTTGGACATTCCTTTTTTTTTTTACGGTCGTGCAATTTTTTTTTTTTTTTTT	
D6	8-2	TGCGAAGGCCGTTTTTTTTTAAGCTGGCAGTTTTTTTTTGGCGTTGTAAGTTTTTTTTTTAGAGACGAT	
E6	8-3	TGCAGGCGGGCTTTTTTTTTCAAAGGATAATTTTTTTTTGAGGTAATTATTTTTTTTTTTCTTATTTCA	
F6	8-4	GCTTCCGTTGCTTTTTTTTTTGATGCCATTTTTTTTTTTTGAGATGACCAGTTTTTTTTTAGCGTATGT	
G6	8-5	CAGGCGAAATCTTTTTTTTTTAGCGTTGGCTTTTTTTTTTCCATTCACGCTATTTTTTTTTTTCTCATTC	
H6	8-6	AGCGCTGGAGGTTTTTTTTTGCTCAATGTTTTTTTTTTTGACTTGAGTGACTTTTTTTTTGCGTCTCAT	
A7	9-1	AATCTCCCACGCTTTTTTTTTTATTGGACCTTTTTTTTTTCGGCCTTCGCATTTTTTTTTAGGAATGTCC	
B7	9-2	TCAGTGTATACCTTTTTTTTTGACTGTAAATTTTTTTTTGCCCGCCTGCATTTTTTTTTCTGCCAGCTT	
C7	9-3	GCCTTCGCACAGTTTTTTTTTGGTCTGACTTTTTTTTTGCAACGGAAGCTTTTTTTTTTATCCTTTG	
D7	9-4	GTCTAGGTATCCTTTTTTTTTCTGCTGGGATTTTTTTTTGATTTCGCCTGTTTTTTTTAATGGCATCA	
E7	9-5	GCCGGAATTTGCTTTTTTTTTTAGCATTTATTTTTTTTTCCTCCAGCGCTTTTTTTTTAGCCAACGCT	

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTTTTTTTTTTTCTGTCTCGTATTTTTTTTTTGCGTGGGAGATTTTTTTTTTTTTTTTTTTTT
H7	10-2	TAGTAAACTCCTTTTTTTTTTAAGGCTACCCTTTTTTTTTTGGTATACACTGATTTTTTTTTTAGGTCCAAT
A8	10-3	TGTAAGTCGATTTTTTTTTTTTAAACCACTGTTTTTTTTTTCTGTGCGAAGGCTTTTTTTTTTTTTACAGTC
B8	10-4	CAGAAATATTGTTTTTTTTTTAACTGTGATTTTTTTTTTTTGGATACCTAGACTTTTTTTTTTGTCAGACCA
C8	10-5	TGAGAGCTCTGTTTTTTTTTTATGAATTCGCTTTTTTTTTTGCAAATTCCGGCTTTTTTTTTTTCCCAGCAG
D8	10-6	TTTCCTAGTTGTTTTTTTTTTAATATCCACGTTTTTTTTTTAATAAAGGTAATTTTTTTTTTTTAAATGCTA
E8	11-1	GGAGTTTACTATTTTTTTTTTTACGAGACAG
F8	11-2	ATCGACTTACATTTTTTTTTTGGGTAGCCTT
G8	11-3	CAATATTTCTGTTTTTTTTTTCAGTGGTTTA
H8	11-4	CAGAGCTCTCATTTTTTTTTTAATCACAGTT
A9	11-5	CAACTAGGAAATTTTTTTTTTGCGAATTCAT
B9	11-6	TTTTTTTTTTTTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_13mer_10T

Back to overview

Well	Name	Sequence
A1	1-1	TGAGATGACTCTTTTTTTTTTTTTAATGGGCATATC
B1	1-2	GACGACCAGGCCGTTTTTTTTTTAGTGTTGCCACTC
C1	1-3	CGGTCCCAGCGCGTTTTTTTTTTCGCAGCTGATGTG
D1	1-4	ATGGGCTGAGTTTTTTTTTTTTTTGTTTTGCATTGA
E1	1-5	CCAGGGTCGGACATTTTTTTTTTGTGTAATTTCGAG
F1	1-6	CAATTCCTGATATTTTTTTTTTTTTTTTTTTTTTT
G1	2-1	TTTTTTTTTTTTTTTTTTTTTTTTATTAGCTAGGCCTTTTTTTTTTTAAGAGTCATCTCATTTTTTTTTTTTTTTTTTTTT
H1	2-2	CCGATTTATTGGGTTTTTTTTTTATTGCAGACCACCTTTTTTTTTTCGGCCTGGTCGTCTTTTTTTTTTGATATGCCCATTA
A2	2-3	GCACGAGTACGCTTTTTTTTTTTTTATGCCCTGATTCTTTTTTTTTTCGCGCTGGGACCGTTTTTTTTTTGAGTGGCAACACT
B2	2-4	AGCTCCGGGGTTCTTTTTTTTTTTTAATACTCGGTTGTTTTTTTTTTAAACTCAGCCCATTTTTTTTTTTCACATCAGCTGCG
C2	2-5	GGTGGAGACCAGATTTTTTTTTTGGAACTTGGGTACTTTTTTTTTTTGTCCGACCCTGGTTTTTTTTTTTCAATGCAAAACA
D2	2-6	GTTGAACGCGACTTTTTTTTTTTCATTAGTGGCTTATTTTTTTTTTATATCAGGAATTGTTTTTTTTTTCTCGAAATTACAC
E2	3-1	ATCTCAACGTGCCTTTTTTTTTTATAGTTCTCCAAATTTTTTTTTCCCAATAAATCGGTTTTTTTTTTAGGCCTAGCTAAT
F2	3-2	GTTTGTGCTAGGATTTTTTTTTTAAGCACGCTTCGTTTTTTTTTTAGCGTACTCGTGCTTTTTTTTTGGTGGTCTGCAAT
G2	3-3	GCGCGCTCCGTCATTTTTTTTTCGACCTGCCGATGTTTTTTTTTTGAACCCCGGAGCTTTTTTTTTTGAATCAGGGCATA
H2	3-4	CTGTATGACCGTATTTTTTTTTAGTTGAATGACTGTTTTTTTTTTCTGGTCTCCACCTTTTTTTTTCAACCGAGTATTA
A3	3-5	TAAGGCAGCGACCTTTTTTTTTTGTAACGCTAGAGTTTTTTTTTAGTCGCGTTCAACTTTTTTTTTGTACCCAAGTTCC
B3	3-6	GTATTTGGAATTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGCCACTAATG
C3	4-1	TTTTTTTTTTTTTTTTTTTTTTTATCGGAGAATGCTTTTTTTTTTTGGCACGTTGAGATTTTTTTTTTTTTTTTTTTT
D3	4-2	GAAATCATAGTAGTTTTTTTTTAGCACCAATGTCTTTTTTTTTTTCCTAGCACAAACTTTTTTTTTTTTGGAGAACTAT
E3	4-3	CGTGACAGACGGATTTTTTTTTCTTCAGTGCGTATTTTTTTTTTTGACGGAGCGCGCTTTTTTTTTCGAAGCGTGCTTA
F3	4-4	GGAATAATGTGGTTTTTTTTTTTCAATTTCTCGCCTTTTTTTTTTACGGTCATACAGTTTTTTTTTCATCGGCAGGTCG
G3	4-5	AGCCACCTCCGTTTTTTTTTTTAGCGTCGTAACATTTTTTTTTTGGTCGCTGCCTTATTTTTTTTTCAGTCATTCAACT
H3	4-6	CCTTTCACACGTTTTTTTTTTGGCGAAGTGACCTTTTTTTTTTAATTCCAAATACTTTTTTTTTCTCTAGCGTTACA
A4	5-1	CACATCTGTGCGTTTTTTTTTGGCCTCATTACATTTTTTTTTCTACTATGATTTCTTTTTTTTTAGCATTCTCCGAT
B4	5-2	AGGTATTGGACACTTTTTTTTTCGTCACAAGCCGTTTTTTTTTCCGTCTGTCACGTTTTTTTTTAGACATTGGTGCT
C4	5-3	CCTCACGGGACTCTTTTTTTTTGAAACTAGGTTCCTTTTTTTTTACCACATTATTCCTTTTTTTTTATACGCACTGAAG
D4	5-4	GTCAGCGCATGTATTTTTTTTTAGGTAATTAATGGTTTTTTTTTAACGGAGGTGGCTTTTTTTTTGGCGAGAAATTGA
E4	5-5	TTATTACCTCAGTTTTTTTTTTTTTGGTTGGTACATTTTTTTTTAACGTGTGAAAGGTTTTTTTTTATGTTACGACGCT
F4	5-6	GAACGTCCCGCGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGTCACTTCGCC
G4	6-1	TTTTTTTTTTTTTTTTTTTTTTTAGTTGAACCGGGTTTTTTTTTTACGCACAGATGTGTTTTTTTTTTTTTTTTTTTT
H4	6-2	CACCGGAAACATGTTTTTTTTTAAATCACTGATTCTTTTTTTTTGTGTCCAATACCTTTTTTTTTTATGTAATGAGGCC
A5	6-3	CGGCATCAAGCGGTTTTTTTTTGTCGTAGTCCTATTTTTTTTTTGAGTCCCGTGAGGTTTTTTTTTCGGCTTGTGACGA
B5	6-4	TCGGTTAACTTGCTTTTTTTTTGGCGAAACGAACATTTTTTTTTTACATGCGCTGACTTTTTTTTTGGAACCTAGTTTC
C5	6-5	GTCCAGTAAACGTTTTTTTTTTAAGAGACCACGATTTTTTTTTACTGAGGTAATAATTTTTTTTTCCATTAATTACCT
D5	6-6	TCCAAGGCTCGAGTTTTTTTTTACCCGATTACCTGTTTTTTTTTCGCGGGACGTTCTTTTTTTTTGTACCAACCAAA
E5	7-1	TTGTTCTCGGATCTTTTTTTTTCTACTGAATTATATTTTTTTTTCATGTTTCCGGTGTTTTTTTTTACCCGGTTCAACT
F5	7-2	TATCGCGCCCCTCTTTTTTTTTGCGCAAGCTCACGTTTTTTTTTCCGCTTGATGCCGTTTTTTTTTGAATCAGTGATTT
G5	7-3	TTGGGGCCAAGCGTTTTTTTTTGTGCGCGGTGTCCTTTTTTTTTGCAAGTTAACCGATTTTTTTTTATAGGACTACGAC
H5	7-4	CGGTTATGAACCTTTTTTTTTTGCGATCTTGTCATTTTTTTTTACGTTTACTGGACTTTTTTTTTGTTCGTTTCGCC
A6	7-5	AAAGGCGTACGACTTTTTTTTTATGAACGTCGATTTTTTTTTTCTCGAGCCTTGGATTTTTTTTTCGTGGTCTCTTA
B6	7-6	CTACTCGAGCGGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGGTAATCGGGT
C6	8-1	TTTTTTTTTTTTTTTTTTTTTTTCCTGTACTTCGGATTTTTTTTTGATCCGAGAACAATTTTTTTTTTTTTTTTTTT
D6	8-2	CTCCCTGTATTTGTTTTTTTTTTAGCTTTCTTCAGTTTTTTTTTGAGGGGCGCGATATTTTTTTTTTATAATTCAGTAG
E6	8-3	CTGTCAGAACGGGTTTTTTTTTGTACCGTCTGCGTTTTTTTTTTCGCTTGGCCCCAATTTTTTTTTCGTGAGCTTGCGC
F6	8-4	CAGCCGACTGAAATTTTTTTTTACGCATGCTTTATTTTTTTTTTAGGTTCATAACCGTTTTTTTTTGGACACCGCGCAC
G6	8-5	ATCACTGTTCCTCTTTTTTTTTTGACACCTCGGACTTTTTTTTTGTCGTACGCCTTTTTTTTTTTTGACAAGATCGCA
H6	8-6	CGCGCGAATTTGTTTTTTTTTTTAGAATATCATTGTTTTTTTTTCCCGCTCGAGTAGTTTTTTTTTAATCGACGTTCAT
A7	9-1	GGCGAATGGCGAATTTTTTTTTCTGTTCAACCCTTTTTTTTTTCAAATACAGGGAGTTTTTTTTTCCGAAGTACAGG
B7	9-2	AGATCACGCTCGCTTTTTTTTTCTTTCGATGCAAATTTTTTTTTCCCGTTCTGACAGTTTTTTTTTCTGAAGAAAGCTA
C7	9-3	CCTTCACGGGCGCTTTTTTTTTCCCACAAGGACGGTTTTTTTTTTCAGTCGGCTGTTTTTTTTTACGCAGACGGTAC
D7	9-4	TGCGGACCCCCATTTTTTTTTTGACGGTCGAGTGTTTTTTTTTTGAGGAACAGTGATTTTTTTTTTATAAAGCATGCGT
E7	9-5	TTGCTGCAGTGATTTTTTTTTTGCAACTCCCCTAATTTTTTTTTACAAATTCGCGCGTTTTTTTTTGTCCGAGGTGTCA

F7	9-6	AAGCTGTAGTGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAATGATATTCTA
G7	10-1	TTTTTTTTTTTTTTTTTTTTTTTTAAATACGTCAGATTTTTTTTTTTTCGCCATTCGCCTTTTTTTTTTTTTTTTTTTTTTT
H7	10-2	ATGGATGGTATTGTTTTTTTTTTCTACTTTCGGACGTTTTTTTTTTGCGAGCGTGATCTTTTTTTTTTTAAGGGTTGAACAG
A8	10-3	ATGTAAATTATGTTTTTTTTTTTTAAAATTCACAAGTTTTTTTTTTGCGCCCGTGAAGGTTTTTTTTTTTTTGCATCGAAAG
B8	10-4	TTTTCGTAAATAGTTTTTTTTTTCCCATGTTGATTCTTTTTTTTTTATGGGGGTCCGCATTTTTTTTTTCCGTCCTTGTGGG
C8	10-5	CTTAATGTATCCATTTTTTTTTTTCGTACATGATATTTTTTTTTTTATCACTGCAGCAATTTTTTTTTTACACTCGACCGTC
D8	10-6	GTCTCTTCGATCGTTTTTTTTTTCCATCCCAGATGGTTTTTTTTTTACCACTACAGCTTTTTTTTTTTTTTAGGGGAGTTGC
E8	11-1	CAATACCATCCATTTTTTTTTTTTCTGACGTATTTA
F8	11-2	ACATAATTTACATTTTTTTTTTTCGTCCGAAAGTAG
G8	11-3	CTATTTACGAAAATTTTTTTTTTCTTGTGAATTTTA
H8	11-4	TGGATACATTAAGTTTTTTTTTTGAATCAACATGGG
A9	11-5	CGATCGAAGAGACTTTTTTTTTTATATCATGTACGA
B9	11-6	TTTTTTTTTTTTTTTTTTTTTTTCCATCTGGGATGG
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_9mer

Well	Name	Sequence
A1	1-1	AGAGCAATGAAGCTTGGA
B1	1-2	CCCTGCGGAGTTAATTCA
C1	1-3	TCCATAACCCACGCCGCA
D1	1-4	GAACTGTCCCTAACCGGT
E1	1-5	TTGAGCTCGAACATGGCC
F1	1-6	GTCCCAGACTTTTTTTTT
G1	2-1	TTTTTTTTTGCGTAGCATCATTGCTCTTTTTTTTTT
H1	2-2	ACCTCAAGCGAAATTTTTTCCGCAGGGTCCAAGCTT
A2	2-3	AGTCCTAGACCTTGGGCCGGTTATGGATGAATTAAC
B2	2-4	TCTAGGAATCAGTCACCTGGACAGTTCTGCGGCGTG
C2	2-5	TTCCCTTAAGCACATTGGCGAGCTCAAACCGGTTAG
D2	2-6	GCATTGTATAAGCTTCGTGTCTGGGACGGCCATGTT
E2	3-1	AGTTCGGGACGCTGGGTAGCTTGAGGTATGCTACGC
F2	3-2	CTGATTTCTTCCCTCGCGTCTAGGACTAAAAATTTC
G2	3-3	GTGAATGACGACCGCGCGATTCCTAGAGGCCCAAGG
H2	3-4	AGACTTAACGAGCTGGACTTAAGGGAAAGGTGACTG
A3	3-5	TCTCCAGGCTTCGGGTCTATACAATGCCCAATGTGC
B3	3-6	TCTAGGGCCTTTTTTTTTTTTTTTTTTACGAAGCTT
C3	4-1	TTTTTTTTTTGTCGAGTGTCCCGAACTTTTTTTTTT
D3	4-2	CGTACGTGCTTTCACGCGAGAAATCAGTACCCAGCG
E3	4-3	CCATACTTTAGGAGCGGAGTCATTCACCGCGAGGGA
F3	4-4	CGAGGGTTACTGCAGTTCGTTAAGTCTCGCGCGGTC
G3	4-5	ACCGAGATGGACCAGCTGGCCTGGAGAGTCCAGCTC
H3	4-6	CGCTCCTCCGGACTGTTTGGCCCTAGAAGACCCGAA
A4	5-1	GCAATTAGTGATACCCGAGCACGTACGCACTCGACA
B4	5-2	TCATCACACAATGTCTCCAAAGTATGGCGCGTGAAA
C4	5-3	CCCCACATTTCATCTGGATAACCCTCGTCCGCTCCT
D4	5-4	AGGGCTATTTGTGAAGCCCATCTCGGTGAACTGCAG
E4	5-5	AGATCAGCGCGCCGATTAGGAGGAGCGCAGCTGGTC
F4	5-6	ATAGTATCGTTTTTTTTTTTTTTTTTTAAACAGTCC
G4	6-1	TTTTTTTTTTGCAGTGCTACTAATTGCTTTTTTTTT
H4	6-2	GGTGCACGGCTTAGCCGAGTGTGATGATCGGGTATC
A5	6-3	CCTTTGCTAGTATTAGGTAATGTGGGGGGAGACATT
B5	6-4	AGTTCTTCGCTAACCTGAAATAGCCCTTCCAGATGA
C5	6-5	TGTGCCCCTGCCATCGCGCGCTGATCTGGCTTCACA
D5	6-6	CATGTCCAACAAGGGGACCGATACTATTAATCGGCG
E5	7-1	TGCTTAGCAAGCTGTTGACCGTGCACCAGCACTGCA
F5	7-2	CGTTTTTTTATCTGGCAGTAGCAAAGGTCGGCTAAG
G5	7-3	GCGGGGAAAGCTCTTATACGAAGAACTACCTAATAC
H5	7-4	ACAGTTGGCAGATTCTTCAGGGGCACATCAGGTTAG
A6	7-5	CGCAACTCTGTAGTCAGTTTGGACATGCGCGATGGC
B6	7-6	TCTGTGACTTTTTTTTTTTTTTTTTTTGTCCCCTTG
C6	8-1	TTTTTTTTTTGTCCTAAATGCTAAGCATTTTTTTTT
D6	8-2	AAATGGCCATAGTTGTGTAAAAAAACGTCAACAGCT
E6	8-3	CTCAGTCAACTTGGCTGGTTTCCCCGCCTGCCAGAT
F6	8-4	CTGCACTGTTGCTATGTCGCCAACTGTTATAAGAGC
G6	8-5	AGGCTCATGATAGCTAATAGAGTTGCGGAAGAATCT
H6	8-6	AACAGAAAACGCTATATGAGTCACAGAACTGACTAC
A7	9-1	TGGCCACAATCTGAATTCTGGCCATTTTTTAGGACA
B7	9-2	GATTCCAAAGGCGTATTTTTGACTGAGACACAACTA
C7	9-3	CCGAGTTTCTTTCGTTCGACAGTGCAGCCAGCCAAG
D7	9-4	CAGCGTTGACGCAACTTGCATGAGCCTGACATAGCA
E7	9-5	CTGATGTAGTCTCCGCTATTTTCTGTTATTAGCTAT

Back to overview

F7	9-6	AGCGCGGGATTTTTTTTTTTTTTTTTTCATATAGCG
G7	10-1	TTTTTTTTTAGGCGCATGTTGTGGCCATTTTTTTTT
H7	10-2	ATTGCCATGATACCGTCCTTTGGAATCGAATTCAGA
A8	10-3	GAGGAGGGCCTGTATTGTGAAACTCGGAAATACGCC
B8	10-4	TTTATATCGACGGGGCCATCAACGCTGCGAACGAAA
C8	10-5	TAATATTTCTATGCGTAGCTACATCAGCAAGTTGCG
D8	10-6	ATTCCCAAATGGCTCGCTTCCCGCGCTTAGCGGAGA
E8	11-1	CATGGCAATCATGCGCCT
F8	11-2	GCCCTCCTCGGACGGTAT
G8	11-3	CGATATAAAACAATACAG
H8	11-4	GAAATATTATGGCCCCGT
A9	11-5	TTTGGGAATCTACGCATA
B9	11-6	TTTTTTTTTAGCGAGCCA
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	GCCGGTGTCATAGGACCAGAG	
B1	1-2	GCCTCAACGGCTTTAGCACGT	
C1	1-3	AACAGAGAGGTACTCCAAAGA	
D1	1-4	ACTTAGTTACCGGCTCGTTGA	
E1	1-5	GTGTAAAGCTGGCGGTGACGC	
F1	1-6	GGTTACAGATACTTTTTTTTT	
G1	2-1	TTTTTTTTTTTGCCATTGAGCTATGACACCGGCTTTTTTTTT	
H1	2-2	GAGACGGCGTCGTCGGCGAACAGCCGTTGAGGCCTCTGGTCC	
A2	2-3	CTGGGCGGATGTTACAGTGCGTACCTCTCTGTTACGTGCTAA	
B2	2-4	TCCGATTGCTAGACGCATTGTCGGTAACTAAGTTCTTTGGAG	
C2	2-5	CAACATCTGCAGCAGCTGTAGCCAGCTTTACACTCAACGAGC	
D2	2-6	ATCTGCCGCGGTAGTTGCTGCGTATCTGTAACCGCGTCACCG	
E2	3-1	CACGGAACGGCATCGAACGTGGACGCCGTCTCGCTCAATGGC	
F2	3-2	TCGTCCTAGGCCCTGGACTTCCATCCGCCCAGGTTCGCCGAC	
G2	3-3	TTCCGGATCGACCCTCGCCATTAGCAATCGGACGCACTGTAA	
H2	3-4	TTACCTAGAAATACCCGATGATGCAGATGTTGACAATGCGTC	
A3	3-5	GAAGCTGGCAAGGTTGCTATACCGCGGCAGATCTACAGCTGC	
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTGCAGCAACTA	
C3	4-1	TTTTTTTTTTTGGTTTCGAGATGCCGTTCCGTGTTTTTTTTT	
D3	4-2	GATTAGAGCATAATCTCTTTCGGCCTAGGACGACACGTTCGA	
E3	4-3	GCTGAGGTGTGCCGAGAAACAGTCGATCCGGAAGAAGTCCAG	
F3	4-4	TCTAGGAAACCCGGATATGTGATTTCTAGGTAAATGGCGAGG	
G3	4-5	CGGCAGTTTAAGACCTGCTCTCTTGCCAGCTTCTCATCGGGT	
H3	4-6	GAACAAATATCTACACCCTATTCCATCTTCCCGTATAGCAAC	
A4	5-1	GGTCGGATCACTCCCGCCAACATGCTCTAATCTCTCGAAACC	
B4	5-2	GAACTCGTCTCCGCTCAGGGTCACACCTCAGCGAAAGAGATT	
C4	5-3	CTAATAATAAGCGTGCCTAGCGGTTTCCTAGATGTTTCTCGG	
D4	5-4	TGAGCAAAGCAGACACAAAGGTTAAACTGCCGCACATATCCG	
E4	5-5	ACCATCACCCTACGATTCTCAGATATTTGTTCAGAGCAGGTC	
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTATAGGGTGTA	
G4	6-1	TTTTTTTTTTTCTAGCTCACCAGTGATCCGACCTTTTTTTTT	
H4	6-2	ACTTCACTATTTAAGGTGTTGGGAGACGAGTTCGTTGGCGGG	
A5	6-3	ATTTAGACTAGTCGCCTGGATGCTTATTATTAGACCCTGAGC	
B5	6-4	CAGAAAGTGAGGGCCTCAGGTCTGCTTTGCTCAGCTAGGCAC	
C5	6-5	GGTCAGGTCAACGGTCATCTCTAGGGTGATGGTCCTTTGTGT	
D5	6-6	AAAGCTCGGATTAGCGCCCGGCTGAGTTTGCTATGAGAATCG	
E5	7-1	TTGCACGACCGTATCGTCTCTAATAGTGAAGTGGTGAGCTAG	
F5	7-2	ACTTACAACGCCTGAAATAAGCTAGTCTAAATCAACACCTTA	
G5	7-3	AATAATTACCTCACATACGCTCTCACTTTCTGATCCAGGCGA	
H5	7-4	CTGGTCATCTCAGAATGAGAATTGACCTGACCACCTGAGGCC	
A6	7-5	TAGCGTGAATGGATGAGACGCATCCGAGCTTTGAGATGACCG	
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTCCGGGCGCTA	
C6	8-1	TTTTTTTTTTTGGACATTCCTACGGTCGTGCAATTTTTTTTT	
D6	8-2	TGCGAAGGCCGAAGCTGGCAGGGCGTTGTAAGTAGAGACGAT	
E6	8-3	TGCAGGCGGGCCAAAGGATAAGAGGTAATTATTCTTATTTCA	
F6	8-4	GCTTCCGTTGCTGATGCCATTTGAGATGACCAGAGCGTATGT	
G6	8-5	CAGGCGAAATCAGCGTTGGCTCCATTCACGCTATTCTCATTC	
H6	8-6	AGCGCTGGAGGGCTCAATGTTGACTTGAGTGACGCGTCTCAT	
A7	9-1	AATCTCCCACGCATTGGACCTCGGCCTTCGCAAGGAATGTCC	
B7	9-2	TCAGTGTATACCGACTGTAAAGCCCGCCTGCACTGCCAGCTT	
C7	9-3	GCCTTCGCACAGTGGTCTGACGCAACGGAAGCTTATCCTTTG	
D7	9-4	GTCTAGGTATCCCTGCTGGGAGATTTCGCCTGAATGGCATCA	
E7	9-5	GCCGGAATTTGCTAGCATTTACCTCCAGCGCTAGCCAACGCT	

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTCTGTCTCGTAGCGTGGGAGATTTTTTTTTTT
H7	10-2	TAGTAAACTCCAAGGCTACCCGGTATACACTGAAGGTCCAAT
A8	10-3	TGTAAGTCGATTAAACCACTGCTGTGCGAAGGCTTTACAGTC
B8	10-4	CAGAAATATTGAACTGTGATTGGATACCTAGACGTCAGACCA
C8	10-5	TGAGAGCTCTGATGAATTCGCGCAAATTCCGGCTCCCAGCAG
D8	10-6	TTTCCTAGTTGAATATCCACGAATAAAGGTAATTAAATGCTA
E8	11-1	GGAGTTTACTATACGAGACAG
F8	11-2	ATCGACTTACAGGGTAGCCTT
G8	11-3	CAATATTTCTGCAGTGGTTTA
H8	11-4	CAGAGCTCTCAAATCACAGTT
A9	11-5	CAACTAGGAAAGCGAATTCAT
B9	11-6	TTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_13mer

Well	Name	Sequence
A1	1-1	TGAGATGACTCTTTAATGGGCATATC
B1	1-2	GACGACCAGGCCGAGTGTTGCCACTC
C1	1-3	CGGTCCCAGCGCGCGCAGCTGATGTG
D1	1-4	ATGGGCTGAGTTTTGTTTTGCATTGA
E1	1-5	CCAGGGTCGGACAGTGTAATTTCGAG
F1	1-6	CAATTCCTGATATTTTTTTTTTTTTT
G1	2-1	TTTTTTTTTTTTTATTAGCTAGGCCTAAGAGTCATCTCATTTTTTTTTTTTT
H1	2-2	CCGATTTATTGGGATTGCAGACCACCCGGCCTGGTCGTCGATATGCCCATTA
A2	2-3	GCACGAGTACGCTTATGCCCTGATTCCGCGCTGGGACCGGAGTGGCAACACT
B2	2-4	AGCTCCGGGGTTCTAATACTCGGTTGAAACTCAGCCCATCACATCAGCTGCG
C2	2-5	GGTGGAGACCAGAGGAACTTGGGTACTGTCCGACCCTGGTCAATGCAAAACA
D2	2-6	GTTGAACGCGACTCATTAGTGGCTTAATATCAGGAATTGCTCGAAATTACAC
E2	3-1	ATCTCAACGTGCCATAGTTCTCCAAACCCAATAAATCGGAGGCCTAGCTAAT
F2	3-2	GTTTGTGCTAGGATAAGCACGCTTCGAGCGTACTCGTGCGGTGGTCTGCAAT
G2	3-3	GCGCGCTCCGTCACGACCTGCCGATGGAACCCCGGAGCTGAATCAGGGCATA
H2	3-4	CTGTATGACCGTAAGTTGAATGACTGTCTGGTCTCCACCCAACCGAGTATTA
A3	3-5	TAAGGCAGCGACCTGTAACGCTAGAGAGTCGCGTTCAACGTACCCAAGTTCC
B3	3-6	GTATTTGGAATTATTTTTTTTTTTTTTTTTTTTTTTTTTAAGCCACTAATG
C3	4-1	TTTTTTTTTTTTTATCGGAGAATGCTGGCACGTTGAGATTTTTTTTTTTTTT
D3	4-2	GAAATCATAGTAGAGCACCAATGTCTTCCTAGCACAAACTTTGGAGAACTAT
E3	4-3	CGTGACAGACGGACTTCAGTGCGTATTGACGGAGCGCGCCGAAGCGTGCTTA
F3	4-4	GGAATAATGTGGTTCAATTTCTCGCCTACGGTCATACAGCATCGGCAGGTCG
G3	4-5	AGCCACCTCCGTTAGCGTCGTAACATGGTCGCTGCCTTACAGTCATTCAACT
H3	4-6	CCTTTCACACGTTGGCGAAGTGACCTTAATTCCAAATACCTCTAGCGTTACA
A4	5-1	CACATCTGTGCGTGGCCTCATTACATCTACTATGATTTCAGCATTCTCCGAT
B4	5-2	AGGTATTGGACACTCGTCACAAGCCGTCCGTCTGTCACGAGACATTGGTGCT
C4	5-3	CCTCACGGGACTCGAAACTAGGTTCCACCACATTATTCCATACGCACTGAAG
D4	5-4	GTCAGCGCATGTAAGGTAATTAATGGAACGGAGGTGGCTGGCGAGAAATTGA
E4	5-5	TTATTACCTCAGTTTTGGTTGGTACAAACGTGTGAAAGGATGTTACGACGCT
F4	5-6	GAACGTCCCGCGATTTTTTTTTTTTTTTTTTTTTTTTTTAGGTCACTTCGCC
G4	6-1	TTTTTTTTTTTTTAGTTGAACCGGGTACGCACAGATGTGTTTTTTTTTTTTT
H4	6-2	CACCGGAAACATGAAATCACTGATTCGTGTCCAATACCTATGTAATGAGGCC
A5	6-3	CGGCATCAAGCGGGTCGTAGTCCTATGAGTCCCGTGAGGCGGCTTGTGACGA
B5	6-4	TCGGTTAACTTGCGGCGAAACGAACATACATGCGCTGACGGAACCTAGTTTC
C5	6-5	GTCCAGTAAACGTTAAGAGACCACGAACTGAGGTAATAACCATTAATTACCT
D5	6-6	TCCAAGGCTCGAGACCCGATTACCTGTCGCGGGACGTTCTGTACCAACCAAA
E5	7-1	TTGTTCTCGGATCCTACTGAATTATACATGTTTCCGGTGACCCGGTTCAACT
F5	7-2	TATCGCGCCCCTCGCGCAAGCTCACGCCGCTTGATGCCGGAATCAGTGATTT
G5	7-3	TTGGGGCCAAGCGGTGCGCGGTGTCCGCAAGTTAACCGAATAGGACTACGAC
H5	7-4	CGGTTATGAACCTTGCGATCTTGTCAACGTTTACTGGACTGTTCGTTTCGCC
A6	7-5	AAAGGCGTACGACATGAACGTCGATTCTCGAGCCTTGGATCGTGGTCTCTTA
B6	7-6	CTACTCGAGCGGGTTTTTTTTTTTTTTTTTTTTTTTTTCAGGTAATCGGGT
C6	8-1	TTTTTTTTTTTTTCCTGTACTTCGGAGATCCGAGAACAATTTTTTTTTTTTT
D6	8-2	CTCCCTGTATTTGTAGCTTTCTTCAGGAGGGGCGCGATATATAATTCAGTAG
E6	8-3	CTGTCAGAACGGGGTACCGTCTGCGTCGCTTGGCCCCAACGTGAGCTTGCGC
F6	8-4	CAGCCGACTGAAAACGCATGCTTTATAGGTTCATAACCGGGACACCGCGCAC
G6	8-5	ATCACTGTTCCTCTGACACCTCGGACGTCGTACGCCTTTTGACAAGATCGCA
H6	8-6	CGCGCGAATTTGTTAGAATATCATTGCCCGCTCGAGTAGAATCGACGTTCAT
A7	9-1	GGCGAATGGCGAACTGTTCAACCCTTCAAATACAGGGAGTCCGAAGTACAGG
B7	9-2	AGATCACGCTCGCCTTTCGATGCAAACCCGTTCTGACAGCTGAAGAAAGCTA
C7	9-3	CCTTCACGGGCGCCCCACAAGGACGGTTTCAGTCGGCTGACGCAGACGGTAC
D7	9-4	TGCGGACCCCCATGACGGTCGAGTGTGAGGAACAGTGATATAAAGCATGCGT
E7	9-5	TTGCTGCAGTGATGCAACTCCCCTAAACAAATTCGCGCGGTCCGAGGTGTCA

Back to overview

F7	9-6	AAGCTGTAGTGGTTTTTTTTTTTTTTTTTTTTTTTTTTTCAATGATATTCTA
G7	10-1	TTTTTTTTTTTTTTAAATACGTCAGATTCGCCATTCGCCTTTTTTTTTTTTT
H7	10-2	ATGGATGGTATTGCTACTTTCGGACGGCGAGCGTGATCTAAGGGTTGAACAG
A8	10-3	ATGTAAATTATGTTAAAATTCACAAGGCGCCCGTGAAGGTTTGCATCGAAAG
B8	10-4	TTTTCGTAAATAGCCCATGTTGATTCATGGGGGTCCGCACCGTCCTTGTGGG
C8	10-5	CTTAATGTATCCATCGTACATGATATATCACTGCAGCAAACACTCGACCGTC
D8	10-6	GTCTCTTCGATCGCCATCCCAGATGGACCACTACAGCTTTTAGGGGAGTTGC
E8	11-1	CAATACCATCCATTCTGACGTATTTA
F8	11-2	ACATAATTTACATCGTCCGAAAGTAG
G8	11-3	CTATTTACGAAAACTTGTGAATTTTA
H8	11-4	TGGATACATTAAGGAATCAACATGGG
A9	11-5	CGATCGAAGAGACATATCATGTACGA
B9	11-6	TTTTTTTTTTTTTCCATCTGGGATGG
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_16mer	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	CGGAAAACACGAACACTTAAAAGGCAGCTTCG	
B1	1-2	TTGTGACTACAGCGTCCTGGTAAAATGACTCC	
C1	1-3	TCTCGAATTGTATTCAAGCATGTCCGACTGAT	
D1	1-4	ACCAGCTAGTTGATGACAGACCGAAGCAAGAA	
E1	1-5	CAACTTAATGCTAGGAACCTTAATTCTTAGTG	
F1	1-6	TCTGCGAGTATTCCTGTTTTTTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTTTTTGAGGCTCCTGATGGCGTGTTCGTGTTTTCCGTTTTTTTTTTTTTTTT	
H1	2-2	ATGTCGGGGGTCCCGCCGTGTCGATTCAATTAGACGCTGTAGTCACAACGAAGCTGCCTTTTAA	
A2	2-3	TTCCCTTCGAGACACCTAGCTCAGTCAATGTGTGAATACAATTCGAGAGGAGTCATTTTACCAG	
B2	2-4	TGATACCCATAATGATAGTACTTACTTCAGCATCATCAACTAGCTGGTATCAGTCGGACATGCT	
C2	2-5	TAACAGAGGAGCCATCGAAGCCTCCCTACAGCTCCTAGCATTAAGTTGTTCTTGCTTCGGTCTG	
D2	2-6	TCGGGTCTATGCAGTGTGCCCGCTGATCGTGACAGGAATACTCGCAGACACTAAGAATTAAGGT	
E2	3-1	GCCAAGCCGCATTTTCTCTCCCCATAAGTTTCGCGGGACCCCCGACATGCCATCAGGAGCCTCA	
F2	3-2	TCTCTCGTCGGTCTTGTCAGGCGCCATAGAGTGGTGTCTCGAAGGGAATAATTGAATCGACACG	
G2	3-3	CCCAGGGTGATTACTCGGATGCCACATTCTCCATCATTATGGGTATCACACATTGACTGAGCTA	
H2	3-4	TGACATCAAAGCGAGGCTCAGGAGGCGTGACGGATGGCTCCTCTGTTATGCTGAAGTAAGTACT	
A3	3-5	ATGCACGACTTCAATGCGCTCGTCTTAAAGGCCACTGCATAGACCCGAGCTGTAGGGAGGCTTC	
B3	3-6	CTTTCACATACAGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACGATCAGCGGGCA	
C3	4-1	TTTTTTTTTTTTTTTTATCTAGTATAACAAGGGAAAATGCGGCTTGGCTTTTTTTTTTTTTTTT	
D3	4-2	ATCTGAGTACAACGTGTGAAGGCTTGCAGAATCAAGACCGACGAGAGAGAAACTTATGGGGAGA	
E3	4-3	AGTGGGGTTTGCATGATTATATTCCTATGCCCGAGTAATCACCCTGGGACTCTATGGCGCCTGA	
F3	4-4	CCTACGAACTTGTCGATGAGACTCTCGAGCAACCTCGCTTTGATGTCAGGAGAATGTGGCATCC	
G3	4-5	GTCTGCAGCGAGTGCAATTAATCGAACCGGAGCATTGAAGTCGTGCATCGTCACGCCTCCTGAG	
H3	4-6	GAATTGATCGATTTTCTTGTGGTAGAACGACGACACTGTATGTGAAAGGCCTTTAAGACGAGCG	
A4	5-1	CTACTGGGAAGTTGATACGTAACCCCCAATCTCACGTTGTACTCAGATCCTTGTTATACTAGAT	
B4	5-2	GGACGGTAAGATCCTGTTCCTAATTACCTATCTCATGCAAACCCCACTATTCTGCAAGCCTTCA	
C4	5-3	GCTACGAATCAGAGCAGTAACAGGACCCATTCTCGACAAGTTCGTAGGGGGCATAGGAATATAA	
D4	5-4	TGCGCAGGCGTACAGAGGCATAGCCCGTTCATTGCACTCGCTGCAGACTTGCTCGAGAGTCTCA	
E4	5-5	ATGTACAGTGAATTTGGCTCTTACAAGTGTTTGAAAATCGATCAATTCCTCCGGTTCGATTAAT	
F4	5-6	GGCAAGCACGGTTTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGTCGTTCTACCACAA	
G4	6-1	TTTTTTTTTTTTTTTTTGCGAACATTATCTTTATCAACTTCCCAGTAGTTTTTTTTTTTTTTTT	
H4	6-2	CTTCTAGGTCTACTAAACTACGCAAGATGTCCCAGGATCTTACCGTCCAGATTGGGGGTTACGT	
A5	6-3	CGTTAAAGCGCGGCTCTGCTCGTTTGGTCCACTGCTCTGATTCGTAGCGATAGGTAATTAGGAA	
B5	6-4	CCTCACAACAAGCTGTGTCTAAGCTACCAGTATCTGTACGCCTGCGCAGAATGGGTCCTGTTAC	
C5	6-5	TCGCCACACCTATGTCTTTGGGTCGACATTAACAAATTCACTGTACATATGAACGGGCTATGCC	
D5	6-6	ACTCAGGCCTCACAGCTCTTGGCGGCGGGGAGTGAAACCGTGCTTGCCAAACACTTGTAAGAGC	
E5	7-1	GGCTGCTTCGTCGGATAGATATGTCGCCAGCTTTAGTAGACCTAGAAGAAAGATAATGTTCGCA	
F5	7-2	ATGTCTAGTCTGAAGGCCATGGGCGCTCCTGCGAGCCGCGCTTTAACGGGACATCTTGCGTAGT	
G5	7-3	CGAACGATGGGGTACCGATAGCGTTTTTTGCGACAGCTTGTTGTGAGGGTGGACCAAACGAGCA	
H5	7-4	TGAGGTCCCATAACCGCCCAGCAATATAGTTGGACATAGGTGTGGCGATACTGGTAGCTTAGAC	
A6	7-5	AGCCCACACTCAACCACCCGTGCTATAGGTTTGCTGTGAGGCCTGAGTTTAATGTCGACCCAAA	
B6	7-6	AATCTCCCTCCGTGACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCCCCGCCGCCAAGA	
C6	8-1	TTTTTTTTTTTTTTTTTGCCGAAGGCTAGAACAATCCGACGAAGCAGCCTTTTTTTTTTTTTTTT	
D6	8-2	GTAGTCCCCAGCTGAAATTGATGGCCCCTACCCCTTCAGACTAGACATAGCTGGCGACATATCT	
E6	8-3	TTTCAGCGCCCGAAATATCCTCGGCACTTTCAGGTACCCCATCGTTCGGCAGGAGCGCCCATGG	
F6	8-4	AGGACTCGTTGTTACGATCTGCTGCGATTCTGCGGTTATGGGACCTCACGCAAAAAACGCTATC	
G6	8-5	ACTGCCGTTGCACCTCAGCCTTTCGTCCTCGGTGGTTGAGTGTGGGCTCAACTATATTGCTGGG	
H6	8-6	TTTATGGTGTTGATTTACCCCCCCTTATCCTGGTCACGGAGGGAGATTAAACCTATAGCACGGG	
A7	9-1	AGTTGTTTGCAGCGTATAATAATTACGCTGTCTTCAGCTGGGGACTACTGTTCTAGCCTTCGGC	
B7	9-2	CTATCGACTTTTATTTCTAACCTGTCCGTACCATTTCGGGCGCTGAAAGGTAGGGGCCATCAAT	
C7	9-3	CGATTATTAATCACTAGCCTGACCGGGCCAGTCGTAACAACGAGTCCTTGAAAGTGCCGAGGAT	
D7	9-4	TGACATAACCCAGGACTATCACCTTCTACACTGAGGTGCAACGGCAGTCAGAATCGCAGCAGAT	
E7	9-5	ATCTATGTCGTGGCGCGCGGTGATGTATAGCAAAATCAACACCATAAACCGAGGACGAAAGGCT	

F7	9-6	TACTTGACCCTCAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGGATAAGGGGGGGT
G7	10-1	TTTTTTTTTTTTTTTTTACATGGACCTGCAACCTACGCTGCAAACAACTTTTTTTTTTTTTTTTT
H7	10-2	TTGCTCATAGTTTAAGGCTGATTACGAGCATCAAATAAAAGTCGATAGGACAGCGTAATTATTA
A8	10-3	CGCGTCCGCATTAGACAGGGATACATGGTTGGTAGTGATTAATAATCGGGTACGGACAGGTTAG
B8	10-4	TCGAGTAGCGGTAGTGGGTTCTCACGGGAGAGGTCCTGGGTTATGTCAACTGGCCCGGTCAGGC
C8	10-5	CATTGGACTGCCTTGGTATGTGTGTATTAGTCGCGCCACGACATAGATAGTGTAGAAGGTGATA
D8	10-6	CGGATCATCTGAATTAACCGACCTGACGTCCTATTTGAGGGTCAAGTATGCTATACATCACCGC
E8	11-1	CTTAAACTATGAGCAAGGTTGCAGGTCCATGT
F8	11-2	GTCTAATGCGGACGCGGATGCTCGTAATCAGC
G8	11-3	CACTACCGCTACTCGACCAACCATGTATCCCT
H8	11-4	CCAAGGCAGTCCAATGCTCTCCCGTGAGAACC
A9	11-5	TAATTCAGATGATCCGGACTAATACACACATA
B9	11-6	TTTTTTTTTTTTTTTTTAGGACGTCAGGTCGGT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_19mer	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	AAGGCGAAGATGGAGGCTTCTGGTGTCGGAAAGTAAAT	
B1	1-2	TTGTAACGTCGATTTGGACCGGGCGCAAGCGCTATGAG	
C1	1-3	ACTGCCGCCTAAGGGGAGCGCTTATCAAATCTCTCGGG	
D1	1-4	CCACCGTCCTTCTAAGGCTTAAGTGGTCAAACATTGAG	
E1	1-5	AATTAGGCAGTTGACCCGAAACTTCACAGTATTCTTGG	
F1	1-6	TGGCAAGATATAGATCGTATTTTTTTTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTTTTTTTTACGGTTAATGCAAACGGAGAAGCCTCCATCTTCGCCTTTTTTTTTTTTTTTTTTT	
H1	2-2	AACATACCCCATCACATAAACGAACGGTGGACAGCCCTGTCCAAATCGACGTTACAAATTTACTTTCCGACACCAG	
A2	2-3	ACGGTATTGACAAAAGTCCCTGCGGACAAATAGATAGTGCTCCCCTTAGGCGGCAGTCTCATAGCGCTTGCGCCCG	
B2	2-4	CAGATCTTAGGTCAGCGCTAGGCCACGAAGCAGTCCTAAGCCTTAGAAGGACGGTGGCCCGAGAGATTTGATAAGC	
C2	2-5	AAGTTGCCTCACAGAGTACTCTAACGTACTTATGGGTATCGGGTCAACTGCCTAATTCTCAATGTTTGACCACTTA	
D2	2-6	TCAAACGTGCCTTCACATATCAATAGGGGTGAATAAGCTACGATCTATATCTTGCCACCAAGAATACTGTGAAGTT	
E2	3-1	CCTATACCTGAGATTTCTGGCTGGCTGATCTATCACTTTTATGTGATGGGGTATGTTCTCCGTTTGCATTAACCGT	
F2	3-2	CAAAAGCTGGTTTGGCCACGCAACCGAAACGCGGACAGGGACTTTTGTCAATACCGTAGGGCTGTCCACCGTTCGT	
G2	3-3	TACTTAGGGCTCGTTAATAGAACATCAAGAGGAGAACTAGCGCTGACCTAAGATCTGACTATCTATTTGTCCGCAG	
H2	3-4	GGCACAGCACCCGTACTGGGATCGGGATCTATGACGCTGTACTCTGTGAGGCAACTTTAGGACTGCTTCGTGGCCT	
A3	3-5	GGTACGCAGGAAGTAGCAAGTACGCGCGCATCGTGCGGTATGTGAAGGCACGTTTGATACCCATAAGTACGTTAGA	
B3	3-6	GGTTGCGGTACCTTAACCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCTTATTCACCCCTATTGA	
C3	4-1	TTTTTTTTTTTTTTTTTTTAAAGATCCTACTTGACTGTCAGAAATCTCAGGTATAGGTTTTTTTTTTTTTTTTTT	
D3	4-2	AGGCGATGAAAGGAGAAATGCTCAGAACGTTACGGGAGGTGGCCAAACCAGCTTTTGAAGTGATAGATCAGCCAGC	
E3	4-3	GTCCCAAGTGATGAGAGTCCATTATCTCCCCATACGTGTATTAACGAGCCCTAAGTACTGTCCGCGTTTCGGTTGC	
F3	4-4	GTATCTTTTGCTCGGACTCTTGGCAAACCCATGAAAGACCAGTACGGGTGCTGTGCCAGTTCTCCTCTTGATGTTC	
G3	4-5	GACAGACTCTGACTTAGCAGTCATTCCTTTTCGCGCGTTTGCTACTTCCTGCGTACCAGCGTCATAGATCCCGATC	
H3	4-6	CAGGTTTCCGGCCAATAGCGTGGTTCACAAGCAGTGCGGGGTTAAGGTACCGCAACCCCGCACGATGCGCGCGTAC	
A4	5-1	GAGGCCGCAGTCGGGAGACTACACGGGACGTCGCAGTAATTTCTCCTTTCATCGCCTACAGTCAAGTAGGATCTTT	
B4	5-2	GCCGGCACGGTAATATGTAGCCATGTGGCTCCGGAAGTGACTCTCATCACTTGGGACCTCCCGTAACGTTCTGAGC	
C4	5-3	ATGCGATTTTTATCATAACTGCTGATAAATATCAGCGTGAGTCCGAGCAAAAGATACCACGTATGGGGAGATAATG	
D4	5-4	CTTCGGGTATGCGGGCAGGCAGGGAACACAGGAGAGGTTGCTAAGTCAGAGTCTGTCTCTTTCATGGGTTTGCCAA	
E4	5-5	CGGGCCTAGATAGAATGAAGTCGGAGAAACGGGAAAACGCTATTGGCCGGAAACCTGACGCGCGAAAAGGAATGAC	
F4	5-6	ACGCTGGATTCCTACAAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGCACTGCTTGTGAACCAC	
G4	6-1	TTTTTTTTTTTTTTTTTTTTATTGTGCATCGTAGTGGATGTCTCCCGACTGCGGCCTCTTTTTTTTTTTTTTTTT	
H4	6-2	CGCGATAGAAGTGCTTGAGACGTACCCACAAAGGGAATTACATATTACCGTGCCGGCTACTGCGACGTCCCGTGTA	
A5	6-3	TGCACACAATGGATAGTAGGAGACAAAGTTCTCGTGTCGTTATGATAAAAATCGCATACTTCCGGAGCCACATGGC	
B5	6-4	TAGGCACTGGGTTAGTATGTCGCCTAACTAAGCAACGTCCTGCCCGCATACCCGAAGACGCTGATATTTATCAGCA	
C5	6-5	CCAGTTATCTTTGCCGCAACACGCGGGCCCAACGGGCGTTCATTCTATCTAGGCCCGACCTCTCCTGTGTTCCCTG	
D5	6-6	GTAACTGCCGGATCAATTACAAACTCTTCCGCGTGCCTCCTTGTAGGAATCCAGCGTGTTTTCCCGTTTCTCCGAC	
E5	7-1	CCGTCCTCATTTAGTAACCTGCAGGGCCGCCGGATATGCTCAAGCACTTCTATCGCGATCCACTACGATGCACAAT	
F5	7-2	CGTAGCGATAGTTTTGCACCATGTAGGCAATTTTCTACCTACTATCCATTGTGTGCAATTCCCTTTGTGGGTACGT	
G5	7-3	AGCATCGTCAGTAACAGGCCTCCGTCGTACTCCGGCATCATACTAACCCAGTGCCTAGACACGAGAACTTTGTCTC	
H5	7-4	GTTGAGGGCTGACCGCCTTACTCCCGGTTAAGATTCACTTGCGGCAAAGATAACTGGACGTTGCTTAGTTAGGCGA	
A6	7-5	GTAGTGAAAATACTATTACGGTATAAGGCTATATGCCGTAATTGATCCGGCAGTTACCGCCCGTTGGGCCCGCGTG	
B6	7-6	GCGTTCCGTCTACCCAACCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGCACGCGGAAGAGTTTG	
C6	8-1	TTTTTTTTTTTTTTTTTTTTCTAACTTGGTCGCTCGTTGGTTACTAAATGAGGACGGTTTTTTTTTTTTTTTTTT	
D6	8-2	GAGAGCACAACCAAAGGTTATTTACCTTCCCTGAGTACGTGCAAAACTATCGCTACGCATATCCGGCGGCCCTGCA	
E6	8-3	TACCCGTATTATCCGCGTATATGAGTGTCGTGTGCAGAGCCTGTTACTGACGATGCTGTAGAAAATTGCCTACATG	
F6	8-4	CTGCATCACTCGGAAACGACTCTGGCAATGTCGCACGAAAGGCGGTCAGCCCTCAACATGCCGGAGTACGACGGAG	
G6	8-5	GGCGTTGGAATTGACCTCTGAATGTCAAAACTTAACATGTAATAGTATTTTCACTACGTGAATCTTAACCGGGAGT	
H6	8-6	TCGTACGGTGCCGGGATAAATGTCCTGTCAGCGACCCTGGTTGGGTAGACGGAACGCCGGCATATAGCCTTATACC	
A7	9-1	CTGTGCCGCATAGTCGTACAAAAGCCGACTTAGATCACAACCTTTGGTTGTGCTCTCAACGAGCGACCAAGTTAGA	
B7	9-2	TGACCTTCGAACAATCCTATTAAGCACCACCGATCGACTACGCGGATAATACGGGTAGTACTCAGGGAAGGTAAAT	
C7	9-3	CTCGGATACGATAACCCTGGCTATCCACTTGAGTAAAATCGTTTCCGAGTGATGCAGTCTGCACACGACACTCATA	
D7	9-4	GTCGGTGTGCTGACCATGCTTGCCCGACATGCCCTTCTAGAGGTCAATTCCAACGCCTCGTGCGACATTGCCAGAG	
E7	9-5	CTATATGTTTGGGCGATTGCAACTAGAGCTATAACAATTTATCCCGGCACCGTACGAATGTTAAGTTTTGACATTC	

F7	9-6	ATCCCACTGCAGGCTAGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGGGTCGCTGACAGGACAT
G7	10-1	TTTTTTTTTTTTTTTTTTTTTAAGTTATACTTGTTTAGGTACGACTATGCGGCACAGTTTTTTTTTTTTTTTTTT
H7	10-2	GAACATCTCACGTATACACCCGATTAGCTCGGTAATTCTAGGATTGTTCGAAGGTCAGTGATCTAAGTCGGCTTTT
A8	10-3	GCCGCTTCCGCTTTGGATAGGCAACGTACCGGCAACATCAGGGTTATCGTATCCGAGGTCGATCGGTGGTGCTTAA
B8	10-4	GACTAGTGTTCCGTATTTTGATATGGAGCATTCTTGTCGCATGGTCAGCACACCGACTTTTACTCAAGTGGATAGC
C8	10-5	GAGTGAACGATAGGGTGACTGGCCTGCCGTCTGTCGGTCAATCGCCCAAACATATAGAGAAGGGCATGTCGGGCAA
D8	10-6	ATGTAACTTATACTAGGTCGTAATCAATGGTAAAAACAGCCTAGCCTGCAGTGGGATATTGTTATAGCTCTAGTTG
E8	11-1	GTGTATACGTGAGATGTTCCTAAACAAGTATAACTTAA
F8	11-2	TATCCAAAGCGGAAGCGGCGAATTACCGAGCTAATCGG
G8	11-3	AAAATACGGAACACTAGTCATGTTGCCGGTACGTTGCC
H8	11-4	GTCACCCTATCGTTCACTCGACAAGAATGCTCCATATC
A9	11-5	GACCTAGTATAAGTTACATACCGACAGACGGCAGGCCA
B9	11-6	TTTTTTTTTTTTTTTTTTTTGTTTTTACCATTGATTAC
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_21mer	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	GACTCGGATCTCTTCAACTGGTATAAGCTCATGTGCTAGGAT	
B1	1-2	GCGGGAACCGACTTCAAACTTTCTCAAGCCCTGGACCAACGG	
C1	1-3	AAACCGATCTAGCCTCAGGCGACATTTGTATCTCCATCCACA	
D1	1-4	TACCACCGCAGAACCTCGCCGCCTGCGTTCGAAACAATCGGA	
E1	1-5	AGTTTGTTCGGGATGTGCTTCTCCTTCAGGTTTTTCTTTTAC	
F1	1-6	ATTATCATATATCCTATTCATTTTTTTTTTTTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTTTTTTTTTCGCGGTTAAGTCTTCTCAATCCCAGTTGAAGAGATCCGAGTCTTTTTTTTTTTTTTTTTTTT	
H1	2-2	TGAGCGGCCCCTACCCTCAGACCGAGCGCAATGCAAGAGTCTAAGTTTGAAGTCGGTTCCCGCATCCTAGCACATGAGCTTATA	
A2	2-3	CTGGAATCGGACGTCAGCCCCTAGATCTGTTTTGATCTTCGGCGCCTGAGGCTAGATCGGTTTCCGTTGGTCCAGGGCTTGAGA	
B2	2-4	CAAAAAATTGTTGGCTTTACGTACATGTCGTGGCCTCTAACCCGGCGAGGTTCTGCGGTGGTATGTGGATGGAGATACAAATGT	
C2	2-5	CTTTGTTATCGGTACAGATGCGCCTCCGACTACTTACTTCACGAAGCACATCCCGAACAAACTTCCGATTGTTTCGAACGCAGG	
D2	2-6	TGTATGACAGGTGAAAATACTGTAACCTCCTATCATAGAGATATGAATAGGATATATGATAATGTAAAAGAAAAACCTGAAGGA	
E2	3-1	ATGACGAGGCCGGCTCTTGCCGTACAGGTAGGTATATATGTCTCTGAGGGTAGGGGCCGCTCAGATTGAGAAGACTTAACCGCG	
F2	3-2	TCGCGACCTGATGTGGGCTACTTCTAATATGTAGTGTGTCACGGGGCTGACGTCCGATTCCAGAGACTCTTGCATTGCGCTCGG	
G2	3-3	GACGAGCTAGGCGAGTGGAAGTGGCCACCGAGCTGGTATTATCGTAAAGCCAACAATTTTTTGCCGAAGATCAAAACAGATCTA	
H2	3-4	ACTTTAATCGCGCCGTTGTAATACTTGGTGTCTCCGGTCGTAGCATCTGTACCGATAACAAAGGGTTAGAGGCCACGACATGTA	
A3	3-5	GCGACGGGTTACTTCCAGGGTCTCCAAAACACGCGCGGTCACAGTATTTTCACCTGTCATACAGTGAAGTAAGTAGTCGGAGGC	
B3	3-6	GAATTCGCCTTGAGTAATACCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATCTCTATGATAGGAGGTTAC	
C3	4-1	TTTTTTTTTTTTTTTTTTTTTGCTTGTACGGAGAGAATGAATGGCAAGAGCCGGCCTCGTCATTTTTTTTTTTTTTTTTTTTT	
D3	4-2	GCTCAACCCACGGAACAATAAGGCATCCATGGGGCAGAAGCGGTAGCCCACATCAGGTCGCGAGACATATATACCTACCTGTAC	
E3	4-3	ACTGCCAGTCCTGGGCTGATGAAGGGTCGTAAGCAGAAGGCCCTTCCACTCGCCTAGCTCGTCGTGACACACTACATATTAGAA	
F3	4-4	GAATGAAAATCTGTCAACAGTTTATGGTTAACTACGGACACTTTACAACGGCGCGATTAAAGTATAATACCAGCTCGGTGGCCA	
G3	4-5	AGTGTTACCTGTGTCGATTGACACGGAGCTCACGCGGAACCCACCCTGGAAGTAACCCGTCGCTACGACCGGAGACACCAAGTA	
H3	4-6	CCACACAGTGCGTTTTATGCAGTGTGAATTATACGAGGTGTGGGTATTACTCAAGGCGAATTCGTGACCGCGCGTGTTTTGGAG	
A4	5-1	GGGCACACCTACGTGAAATTCAGATACGGGTAATAATTGTAGTTATTGTTCCGTGGGTTGAGCATTCATTCTCTCCGTACAAGC	
B4	5-2	CCGATCCGCTCTGCACGTACACACACGAGTCGTCAAAATTCGCATCAGCCCAGGACTGGCAGTCGCTTCTGCCCCATGGATGCC	
C4	5-3	ATCGTCTGTTTAGTGCAAGGGATGTCCGTGACGTAGATACCGACTGTTGACAGATTTTCATTCGGCCTTCTGCTTACGACCCTT	
D4	5-4	GTACCTTCTGTACGACCAGCTGAAGTTGGAAGCGAGTTGGGCTCAATCGACACAGGTAACACTAGTGTCCGTAGTTAACCATAA	
E4	5-5	TCCGAGGCTTCACGTGGGAGGCCAAAAAGATCACCGCTGCCATGCATAAAACGCACTGTGTGGGGGGTTCCGCGTGAGCTCCGTG	
F4	5-6	TTAGGGCTGCAGACTAATAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACACCTCGTATAATTCACAC	
G4	6-1	TTTTTTTTTTTTTTTTTTTTTTATCGTAGGTTCCGGCCGACGGAATTTCACGTAGGTGTGCCCTTTTTTTTTTTTTTTTTTTT	
H4	6-2	GCATGTCCAGTGTTTGTCCGACTGGATCACTAGATTTGGGCATGTACGTGCAGAGCGGATCGGCTACAATTATTACCCGTATCT	
A5	6-3	ACCACCCCGGATTGACTACGGGATTCCCTCTAAGTCACATACCCCTTGCACTAAACAGACGATCGAATTTTGACGACTCGTGTG	
B5	6-4	TCGATGATTTCCCGAGGAGCGACAGAGCTTCTCGCAATTTCAAGCTGGTCGTACAGAAGGTACCGGTATCTACGTCACGGACAT	
C5	6-5	GGCCGCAGTGCTATCCCTATGGCGAAGGCCATGAAGAAGCCCCCTCCCACGTGAAGCCTCGGAGCCCAACTCGCTTCCAACTTC	
D5	6-6	CCTTCGACTGGCCGGGGGCATGGTCGAGCTGTGGCAACCCTTTCTATTAGTCTGCAGCCCTAATGGCAGCGGTGATCTTTTTGG	
E5	7-1	GAGGGCGATCCCAAGACAATTGATACAATTGGATGCTAAGGCTCGGACAAACACTGGACATGCCGTCGGCCGGAACCTACGATA	
F5	7-2	AAATGTTTGGGGGCCCAGATCCAGGAAAATTAGACCGCATGCCCGTAGTCAATCCGGGGTGGTTGCCCAAATCTAGTGATCCAG	
G5	7-3	GACCCAAAAATGAAATGCAGCAATCACACATTCACTTACAAACGCTCCTCGGGAAATCATCGAGTATGTGACTTAGAGGGAATC	
H5	7-4	ATCCTCCCGTCTAGTTGTAGGATGTCGTCCCGGATGGTCCACCATAGGGATAGCACTGCGGCCTGAAATTGCGAGAAGCTCTGT	
A6	7-5	CACAAGGCGTGGATTAGAAATCTTCAATCCAGCGTCGCACATATGCCCCCGGCCAGTCGAAGGGGGCTTCTTCATGGCCTTCGC	
B6	7-6	AGAGGAATGACTCACCTCAAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGGGTTGCCACAGCTCGACC	
C6	8-1	TTTTTTTTTTTTTTTTTTTTTCTACCCTTGGAATAACTTTGTAATTGTCTTGGGATCGCCCTCTTTTTTTTTTTTTTTTTTTT	
D6	8-2	CCCGGTTGCTAGTCATAAGAGTTTCCATATGCAATGATAAGTGATCTGGGCCCCCAAACATTTGCCTTAGCATCCAATTGTATC	
E6	8-3	TTTGTATGATGCCAGGTTCCTAGTGCCCTGTAGGTACAAGGTGCTGCATTTCATTTTTGGGTCGCATGCGGTCTAATTTTCCTG	
F6	8-4	CGGCTAACATCTGATGCAGTTAATCCAATAGATCATAAGTCGCCTACAACTAGACGGGAGGATTTTGTAAGTGAATGTGTGATT	
G6	8-5	GCTGATATCCGGACCTCAATTACGGTTTAAATAGTATATTACATTTCTAATCCACGCCTTGTGGTGGACCATCCGGGACGACAT	
H6	8-6	ACAGGACGGCTGCATATAGCGCCATGTTGGACGCAGCTCATTCTTGAGGTGAGTCATTCCTCTATGTGCGACGCTGGATTGAAG	
A7	9-1	GCGACAGTTGTCTTAGGGGTCGATGCCCCTCGCTGTATCTATCTCTTATGACTAGCAACCGGGACAAAGTTATTCCAAGGGTAG	
B7	9-2	CGACGTAAGCCATTACGCTGAGGCCCATCCAGCTCCCTTAACAGGAACCTGGCATCATACAAAACTTATCATTGCATATGGAAA	
C7	9-3	TGACGATTAGCATGTATAACCTTCGCACTGCCCAGTTCGAGAAACTGCATCAGATGTTAGCCGACCTTGTACCTACAGGGCACT	
D7	9-4	CGAGCCCGAAGCGGAGGAAGGAGATTGACCGGCATTTACCTTAATTGAGGTCCGGATATCAGCCGACTTATGATCTATTGGATT	
E7	9-5	TAAACGCGGGAGAGGATCACAGTGGGACTGCGGGGCAGGTTTCGCTATATGCAGCCGTCCTGTGTAATATACTATTTAAACCGT	

F7	9-6	CCCTCACAGCTTACCACAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAATGAGCTGCGTCCAACATGG
G7	10-1	TTTTTTTTTTTTTTTTTTTTTAAGCGCGCATGGGAGTAACTGGACCCCTAAGACAACTGTCGCTTTTTTTTTTTTTTTTTTTT
H7	10-2	CGAGACTAGTAGCGCTTACCCATGCTTAAAACGGATTGTCCATCAGCGTAATGGCTTACGTCGATAGATACAGCGAGGGGCATC
A8	10-3	ATGAACTGCCCGACGAACAACCTTACAGCCGTGCTAGCTCAAGGTTATACATGCTAATCGTCAGTTAAGGGAGCTGGATGGGCC
B8	10-4	GCTTTGCACACGGGAGCTATTACGGACGTATGGTGCATTGATCCTTCCTCCGCTTCGGGCTCGTCTCGAACTGGGCAGTGCGAA
C8	10-5	CGTATAGGGGAGTGGGAAACGATCCCGGCAATGCTCTTGACATGTGATCCTCTCCCGCGTTTAAAGGTAAATGCCGGTCAATCT
D8	10-6	CGTATTCAACACGAGATTACAGTGTGGCGCAATAAATAGACAGACTGTGGTAAGCTGTGAGGGAAACCTGCCCCGCAGTCCCAC
E8	11-1	GGGTAAGCGCTACTAGTCTCGCAGTTACTCCCATGCGCGCTT
F8	11-2	GTTGTTCGTCGGGCAGTTCATTGGACAATCCGTTTTAAGCAT
G8	11-3	AATAGCTCCCGTGTGCAAAGCTTGAGCTAGCACGGCTGTAAG
H8	11-4	CGTTTCCCACTCCCCTATACGATCAATGCACCATACGTCCGT
A9	11-5	TGTAATCTCGTGTTGAATACGTGTCAAGAGCATTGCCGGGAT
B9	11-6	TTTTTTTTTTTTTTTTTTTTTTGTCTATTTATTGCGCCACAC
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_1T	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	GCCGGTGTCATATGGACCAGAG	
B1	1-2	GCCTCAACGGCTTTTAGCACGT	
C1	1-3	AACAGAGAGGTATCTCCAAAGA	
D1	1-4	ACTTAGTTACCGTGCTCGTTGA	
E1	1-5	GTGTAAAGCTGGTCGGTGACGC	
F1	1-6	GGTTACAGATACTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTGCCATTGAGCTTATGACACCGGCTTTTTTTTTT	
H1	2-2	GAGACGGCGTCTGTCGGCGAACTAGCCGTTGAGGCTCTCTGGTCC	
A2	2-3	CTGGGCGGATGTTTACAGTGCGTTACCTCTCTGTTTACGTGCTAA	
B2	2-4	TCCGATTGCTATGACGCATTGTTCGGTAACTAAGTTTCTTTGGAG	
C2	2-5	CAACATCTGCATGCAGCTGTAGTCCAGCTTTACACTTCAACGAGC	
D2	2-6	ATCTGCCGCGGTTAGTTGCTGCTGTATCTGTAACCTGCGTCACCG	
E2	3-1	CACGGAACGGCATTCGAACGTGTGACGCCGTCTCTGCTCAATGGC	
F2	3-2	TCGTCCTAGGCCTCTGGACTTCTCATCCGCCCAGTGTTCGCCGAC	
G2	3-3	TTCCGGATCGACTCCTCGCCATTTAGCAATCGGATCGCACTGTAA	
H2	3-4	TTACCTAGAAATTACCCGATGATTGCAGATGTTGTACAATGCGTC	
A3	3-5	GAAGCTGGCAAGTGTTGCTATATCCGCGGCAGATTCTACAGCTGC	
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTTTTGCAGCAACTA	
C3	4-1	TTTTTTTTTTTTGGTTTCGAGATTGCCGTTCCGTGTTTTTTTTTT	
D3	4-2	GATTAGAGCATTAATCTCTTTCTGGCCTAGGACGATCACGTTCGA	
E3	4-3	GCTGAGGTGTGTCCGAGAAACATGTCGATCCGGAATGAAGTCCAG	
F3	4-4	TCTAGGAAACCTCGGATATGTGTATTTCTAGGTAATATGGCGAGG	
G3	4-5	CGGCAGTTTAATGACCTGCTCTTCTTGCCAGCTTCTTCATCGGGT	
H3	4-6	GAACAAATATCTTACACCCTATTTCCATCTTCCCGTTATAGCAAC	
A4	5-1	GGTCGGATCACTTCCCGCCAACTATGCTCTAATCTTCTCGAAACC	
B4	5-2	GAACTCGTCTCCTGCTCAGGGTTCACACCTCAGCTGAAAGAGATT	
C4	5-3	CTAATAATAAGCTGTGCCTAGCTGGTTTCCTAGATTGTTTCTCGG	
D4	5-4	TGAGCAAAGCAGTACACAAAGGTTTAAACTGCCGTCACATATCCG	
E4	5-5	ACCATCACCCTATCGATTCTCATGATATTTGTTCTAGAGCAGGTC	
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTTTTATAGGGTGTA	
G4	6-1	TTTTTTTTTTTTCTAGCTCACCTAGTGATCCGACCTTTTTTTTTT	
H4	6-2	ACTTCACTATTTTAAGGTGTTGTGGAGACGAGTTCTGTTGGCGGG	
A5	6-3	ATTTAGACTAGTTCGCCTGGATTGCTTATTATTAGTACCCTGAGC	
B5	6-4	CAGAAAGTGAGTGGCCTCAGGTTCTGCTTTGCTCATGCTAGGCAC	
C5	6-5	GGTCAGGTCAATCGGTCATCTCTTAGGGTGATGGTTCCTTTGTGT	
D5	6-6	AAAGCTCGGATTTAGCGCCCGGTCTGAGTTTGCTATTGAGAATCG	
E5	7-1	TTGCACGACCGTTATCGTCTCTTAATAGTGAAGTTGGTGAGCTAG	
F5	7-2	ACTTACAACGCCTTGAAATAAGTCTAGTCTAAATTCAACACCTTA	
G5	7-3	AATAATTACCTCTACATACGCTTCTCACTTTCTGTATCCAGGCGA	
H5	7-4	CTGGTCATCTCATGAATGAGAATTTGACCTGACCTACCTGAGGCC	
A6	7-5	TAGCGTGAATGGTATGAGACGCTATCCGAGCTTTTGAGATGACCG	
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTTTTCCGGGCGCTA	
C6	8-1	TTTTTTTTTTTTGGACATTCCTTACGGTCGTGCAATTTTTTTTTT	
D6	8-2	TGCGAAGGCCGTAAGCTGGCAGTGGCGTTGTAAGTTAGAGACGAT	
E6	8-3	TGCAGGCGGGCTCAAAGGATAATGAGGTAATTATTTCTTATTTCA	
F6	8-4	GCTTCCGTTGCTTGATGCCATTTTGAGATGACCAGTAGCGTATGT	
G6	8-5	CAGGCGAAATCTAGCGTTGGCTTCCATTCACGCTATTTCTCATTC	
H6	8-6	AGCGCTGGAGGTGCTCAATGTTTGACTTGAGTGACTGCGTCTCAT	
A7	9-1	AATCTCCCACGCTATTGGACCTTCGGCCTTCGCATAGGAATGTCC	
B7	9-2	TCAGTGTATACCTGACTGTAAATGCCCGCCTGCATCTGCCAGCTT	
C7	9-3	GCCTTCGCACAGTTGGTCTGACTGCAACGGAAGCTTTATCCTTTG	
D7	9-4	GTCTAGGTATCCTCTGCTGGGATGATTTCGCCTGTAATGGCATCA	
E7	9-5	GCCGGAATTTGCTTAGCATTTATCCTCCAGCGCTTAGCCAACGCT	

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTTCTGTCTCGTATGCGTGGGAGATTTTTTTTTTTT
H7	10-2	TAGTAAACTCCTAAGGCTACCCTGGTATACACTGATAGGTCCAAT
A8	10-3	TGTAAGTCGATTTAAACCACTGTCTGTGCGAAGGCTTTTACAGTC
B8	10-4	CAGAAATATTGTAACTGTGATTTGGATACCTAGACTGTCAGACCA
C8	10-5	TGAGAGCTCTGTATGAATTCGCTGCAAATTCCGGCTTCCCAGCAG
D8	10-6	TTTCCTAGTTGTAATATCCACGTAATAAAGGTAATTTAAATGCTA
E8	11-1	GGAGTTTACTATTACGAGACAG
F8	11-2	ATCGACTTACATGGGTAGCCTT
G8	11-3	CAATATTTCTGTCAGTGGTTTA
H8	11-4	CAGAGCTCTCATAATCACAGTT
A9	11-5	CAACTAGGAAATGCGAATTCAT
B9	11-6	TTTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_2T	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	GCCGGTGTCATATTGGACCAGAG	
B1	1-2	GCCTCAACGGCTTTTTAGCACGT	
C1	1-3	AACAGAGAGGTATTCTCCAAAGA	
D1	1-4	ACTTAGTTACCGTTGCTCGTTGA	
E1	1-5	GTGTAAAGCTGGTTCGGTGACGC	
F1	1-6	GGTTACAGATACTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTGCCATTGAGCTTTATGACACCGGCTTTTTTTTTTT	
H1	2-2	GAGACGGCGTCTTGTCGGCGAACTTAGCCGTTGAGGCTTCTCTGGTCC	
A2	2-3	CTGGGCGGATGTTTTACAGTGCGTTTACCTCTCTGTTTTACGTGCTAA	
B2	2-4	TCCGATTGCTATTGACGCATTGTTTCGGTAACTAAGTTTTCTTTGGAG	
C2	2-5	CAACATCTGCATTGCAGCTGTAGTTCCAGCTTTACACTTTCAACGAGC	
D2	2-6	ATCTGCCGCGGTTTAGTTGCTGCTTGTATCTGTAACCTTGCGTCACCG	
E2	3-1	CACGGAACGGCATTTCGAACGTGTTGACGCCGTCTCTTGCTCAATGGC	
F2	3-2	TCGTCCTAGGCCTTCTGGACTTCTTCATCCGCCCAGTTGTTCGCCGAC	
G2	3-3	TTCCGGATCGACTTCCTCGCCATTTTAGCAATCGGATTCGCACTGTAA	
H2	3-4	TTACCTAGAAATTTACCCGATGATTTGCAGATGTTGTTACAATGCGTC	
A3	3-5	GAAGCTGGCAAGTTGTTGCTATATTCCGCGGCAGATTTCTACAGCTGC	
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTTTTTGCAGCAACTA	
C3	4-1	TTTTTTTTTTTTTGGTTTCGAGATTTGCCGTTCCGTGTTTTTTTTTT	
D3	4-2	GATTAGAGCATTTAATCTCTTTCTTGGCCTAGGACGATTCACGTTCGA	
E3	4-3	GCTGAGGTGTGTTCCGAGAAACATTGTCGATCCGGAATTGAAGTCCAG	
F3	4-4	TCTAGGAAACCTTCGGATATGTGTTATTTCTAGGTAATTATGGCGAGG	
G3	4-5	CGGCAGTTTAATTGACCTGCTCTTTCTTGCCAGCTTCTTTCATCGGGT	
H3	4-6	GAACAAATATCTTTACACCCTATTTTCCATCTTCCCGTTTATAGCAAC	
A4	5-1	GGTCGGATCACTTTCCCGCCAACTTATGCTCTAATCTTTCTCGAAACC	
B4	5-2	GAACTCGTCTCCTTGCTCAGGGTTTCACACCTCAGCTTGAAAGAGATT	
C4	5-3	CTAATAATAAGCTTGTGCCTAGCTTGGTTTCCTAGATTTGTTTCTCGG	
D4	5-4	TGAGCAAAGCAGTTACACAAAGGTTTTAAACTGCCGTTCACATATCCG	
E4	5-5	ACCATCACCCTATTCGATTCTCATTGATATTTGTTCTTAGAGCAGGTC	
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTTTTTATAGGGTGTA	
G4	6-1	TTTTTTTTTTTTTCTAGCTCACCTTAGTGATCCGACCTTTTTTTTTT	
H4	6-2	ACTTCACTATTTTTAAGGTGTTGTTGGAGACGAGTTCTTGTTGGCGGG	
A5	6-3	ATTTAGACTAGTTTCGCCTGGATTTGCTTATTATTAGTTACCCTGAGC	
B5	6-4	CAGAAAGTGAGTTGGCCTCAGGTTTCTGCTTTGCTCATTGCTAGGCAC	
C5	6-5	GGTCAGGTCAATTCGGTCATCTCTTTAGGGTGATGGTTTCCTTTGTGT	
D5	6-6	AAAGCTCGGATTTTAGCGCCCGGTTCTGAGTTTGCTATTTGAGAATCG	
E5	7-1	TTGCACGACCGTTTATCGTCTCTTTAATAGTGAAGTTTGGTGAGCTAG	
F5	7-2	ACTTACAACGCCTTTGAAATAAGTTCTAGTCTAAATTTCAACACCTTA	
G5	7-3	AATAATTACCTCTTACATACGCTTTCTCACTTTCTGTTATCCAGGCGA	
H5	7-4	CTGGTCATCTCATTGAATGAGAATTTTGACCTGACCTTACCTGAGGCC	
A6	7-5	TAGCGTGAATGGTTATGAGACGCTTATCCGAGCTTTTTGAGATGACCG	
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTTTTTCCGGGCGCTA	
C6	8-1	TTTTTTTTTTTTTGGACATTCCTTTACGGTCGTGCAATTTTTTTTTT	
D6	8-2	TGCGAAGGCCGTTAAGCTGGCAGTTGGCGTTGTAAGTTTAGAGACGAT	
E6	8-3	TGCAGGCGGGCTTCAAAGGATAATTGAGGTAATTATTTTCTTATTTCA	
F6	8-4	GCTTCCGTTGCTTTGATGCCATTTTTGAGATGACCAGTTAGCGTATGT	
G6	8-5	CAGGCGAAATCTTAGCGTTGGCTTTCCATTCACGCTATTTTCTCATTC	
H6	8-6	AGCGCTGGAGGTTGCTCAATGTTTTGACTTGAGTGACTTGCGTCTCAT	
A7	9-1	AATCTCCCACGCTTATTGGACCTTTCGGCCTTCGCATTAGGAATGTCC	
B7	9-2	TCAGTGTATACCTTGACTGTAAATTGCCCGCCTGCATTCTGCCAGCTT	
C7	9-3	GCCTTCGCACAGTTTGGTCTGACTTGCAACGGAAGCTTTTATCCTTTG	
D7	9-4	GTCTAGGTATCCTTCTGCTGGGATTGATTTCGCCTGTTAATGGCATCA	
E7	9-5	GCCGGAATTTGCTTTAGCATTTATTCCTCCAGCGCTTTAGCCAACGCT	

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTTTCTGTCTCGTATTGCGTGGGAGATTTTTTTTTTTT
H7	10-2	TAGTAAACTCCTTAAGGCTACCCTTGGTATACACTGATTAGGTCCAAT
A8	10-3	TGTAAGTCGATTTTAAACCACTGTTCTGTGCGAAGGCTTTTTACAGTC
B8	10-4	CAGAAATATTGTTAACTGTGATTTTGGATACCTAGACTTGTCAGACCA
C8	10-5	TGAGAGCTCTGTTATGAATTCGCTTGCAAATTCCGGCTTTCCCAGCAG
D8	10-6	TTTCCTAGTTGTTAATATCCACGTTAATAAAGGTAATTTTAAATGCTA
E8	11-1	GGAGTTTACTATTTACGAGACAG
F8	11-2	ATCGACTTACATTGGGTAGCCTT
G8	11-3	CAATATTTCTGTTCAGTGGTTTA
H8	11-4	CAGAGCTCTCATTAATCACAGTT
A9	11-5	CAACTAGGAAATTGCGAATTCAT
B9	11-6	TTTTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_4T

Well	Name	Sequence
A1	1-1	GCCGGTGTCATATTTTGGACCAGAG
B1	1-2	GCCTCAACGGCTTTTTTTAGCACGT
C1	1-3	AACAGAGAGGTATTTTCTCCAAAGA
D1	1-4	ACTTAGTTACCGTTTTGCTCGTTGA
E1	1-5	GTGTAAAGCTGGTTTTCGGTGACGC
F1	1-6	GGTTACAGATACTTTTTTTTTTTTT
G1	2-1	TTTTTTTTTTTTTTTGCCATTGAGCTTTTTATGACACCGGCTTTTTTTTTTTTT
H1	2-2	GAGACGGCGTCTTTTGTCGGCGAACTTTTAGCCGTTGAGGCTTTTCTCTGGTCC
A2	2-3	CTGGGCGGATGTTTTTTACAGTGCGTTTTTACCTCTCTGTTTTTTACGTGCTAA
B2	2-4	TCCGATTGCTATTTTGACGCATTGTTTTTCGGTAACTAAGTTTTTTCTTTGGAG
C2	2-5	CAACATCTGCATTTTGCAGCTGTAGTTTTCCAGCTTTACACTTTTTCAACGAGC
D2	2-6	ATCTGCCGCGGTTTTTAGTTGCTGCTTTTGTATCTGTAACCTTTTGCGTCACCG
E2	3-1	CACGGAACGGCATTTTTCGAACGTGTTTTGACGCCGTCTCTTTTGCTCAATGGC
F2	3-2	TCGTCCTAGGCCTTTTCTGGACTTCTTTTCATCCGCCCAGTTTTGTTCGCCGAC
G2	3-3	TTCCGGATCGACTTTTCCTCGCCATTTTTTAGCAATCGGATTTTCGCACTGTAA
H2	3-4	TTACCTAGAAATTTTTACCCGATGATTTTTGCAGATGTTGTTTTACAATGCGTC
A3	3-5	GAAGCTGGCAAGTTTTGTTGCTATATTTTCCGCGGCAGATTTTTCTACAGCTGC
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAGCAACTA
C3	4-1	TTTTTTTTTTTTTTTGGTTTCGAGATTTTTGCCGTTCCGTGTTTTTTTTTTTT
D3	4-2	GATTAGAGCATTTTTAATCTCTTTCTTTTGGCCTAGGACGATTTTCACGTTCGA
E3	4-3	GCTGAGGTGTGTTTTCCGAGAAACATTTTGTCGATCCGGAATTTTGAAGTCCAG
F3	4-4	TCTAGGAAACCTTTTCGGATATGTGTTTTATTTCTAGGTAATTTTATGGCGAGG
G3	4-5	CGGCAGTTTAATTTTGACCTGCTCTTTTTCTTGCCAGCTTCTTTTTCATCGGGT
H3	4-6	GAACAAATATCTTTTTACACCCTATTTTTTCCATCTTCCCGTTTTTATAGCAAC
A4	5-1	GGTCGGATCACTTTTTCCCGCCAACTTTTATGCTCTAATCTTTTTCTCGAAACC
B4	5-2	GAACTCGTCTCCTTTTGCTCAGGGTTTTTCACACCTCAGCTTTTGAAAGAGATT
C4	5-3	CTAATAATAAGCTTTTGTGCCTAGCTTTTGGTTTCCTAGATTTTTGTTTCTCGG
D4	5-4	TGAGCAAAGCAGTTTTACACAAAGGTTTTTTAAACTGCCGTTTTCACATATCCG
E4	5-5	ACCATCACCCTATTTTCGATTCTCATTTTGATATTTGTTCTTTTAGAGCAGGTC
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGGTGTA
G4	6-1	TTTTTTTTTTTTTTTCTAGCTCACCTTTTAGTGATCCGACCTTTTTTTTTTTTT
H4	6-2	ACTTCACTATTTTTTTAAGGTGTTGTTTTGGAGACGAGTTCTTTTGTTGGCGGG
A5	6-3	ATTTAGACTAGTTTTTCGCCTGGATTTTTGCTTATTATTAGTTTTACCCTGAGC
B5	6-4	CAGAAAGTGAGTTTTGGCCTCAGGTTTTTCTGCTTTGCTCATTTTGCTAGGCAC
C5	6-5	GGTCAGGTCAATTTTCGGTCATCTCTTTTTAGGGTGATGGTTTTTCCTTTGTGT
D5	6-6	AAAGCTCGGATTTTTTAGCGCCCGGTTTTCTGAGTTTGCTATTTTTGAGAATCG
E5	7-1	TTGCACGACCGTTTTTATCGTCTCTTTTTAATAGTGAAGTTTTTGGTGAGCTAG
F5	7-2	ACTTACAACGCCTTTTTGAAATAAGTTTTCTAGTCTAAATTTTTCAACACCTTA
G5	7-3	AATAATTACCTCTTTTACATACGCTTTTTCTCACTTTCTGTTTTATCCAGGCGA
H5	7-4	CTGGTCATCTCATTTTGAATGAGAATTTTTTGACCTGACCTTTTACCTGAGGCC
A6	7-5	TAGCGTGAATGGTTTTATGAGACGCTTTTATCCGAGCTTTTTTTGAGATGACCG
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCGGGCGCTA
C6	8-1	TTTTTTTTTTTTTTTGGACATTCCTTTTTACGGTCGTGCAATTTTTTTTTTTTT
D6	8-2	TGCGAAGGCCGTTTTAAGCTGGCAGTTTTGGCGTTGTAAGTTTTTAGAGACGAT
E6	8-3	TGCAGGCGGGCTTTTCAAAGGATAATTTTGAGGTAATTATTTTTTCTTATTTCA
F6	8-4	GCTTCCGTTGCTTTTTGATGCCATTTTTTTGAGATGACCAGTTTTAGCGTATGT
G6	8-5	CAGGCGAAATCTTTTAGCGTTGGCTTTTTCCATTCACGCTATTTTTTCTCATTC
H6	8-6	AGCGCTGGAGGTTTTGCTCAATGTTTTTTGACTTGAGTGACTTTTGCGTCTCAT
A7	9-1	AATCTCCCACGCTTTTATTGGACCTTTTTCGGCCTTCGCATTTTAGGAATGTCC
B7	9-2	TCAGTGTATACCTTTTGACTGTAAATTTTGCCCGCCTGCATTTTCTGCCAGCTT
C7	9-3	GCCTTCGCACAGTTTTTGGTCTGACTTTTGCAACGGAAGCTTTTTTATCCTTTG
D7	9-4	GTCTAGGTATCCTTTTCTGCTGGGATTTTGATTTCGCCTGTTTTAATGGCATCA
E7	9-5	GCCGGAATTTGCTTTTTAGCATTTATTTTCCTCCAGCGCTTTTTAGCCAACGCT

Back to overview

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTTTTTCTGTCTCGTATTTTGCGTGGGAGATTTTTTTTTTTTTTT
H7	10-2	TAGTAAACTCCTTTTAAGGCTACCCTTTTGGTATACACTGATTTTAGGTCCAAT
A8	10-3	TGTAAGTCGATTTTTTAAACCACTGTTTTCTGTGCGAAGGCTTTTTTTACAGTC
B8	10-4	CAGAAATATTGTTTTAACTGTGATTTTTTGGATACCTAGACTTTTGTCAGACCA
C8	10-5	TGAGAGCTCTGTTTTATGAATTCGCTTTTGCAAATTCCGGCTTTTTCCCAGCAG
D8	10-6	TTTCCTAGTTGTTTTAATATCCACGTTTTAATAAAGGTAATTTTTTAAATGCTA
E8	11-1	GGAGTTTACTATTTTTACGAGACAG
F8	11-2	ATCGACTTACATTTTGGGTAGCCTT
G8	11-3	CAATATTTCTGTTTTCAGTGGTTTA
H8	11-4	CAGAGCTCTCATTTTAATCACAGTT
A9	11-5	CAACTAGGAAATTTTGCGAATTCAT
B9	11-6	TTTTTTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_7T	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	GCCGGTGTCATATTTTTTTGGACCAGAG	
B1	1-2	GCCTCAACGGCTTTTTTTTTTAGCACGT	
C1	1-3	AACAGAGAGGTATTTTTTTCTCCAAAGA	
D1	1-4	ACTTAGTTACCGTTTTTTTGCTCGTTGA	
E1	1-5	GTGTAAAGCTGGTTTTTTTCGGTGACGC	
F1	1-6	GGTTACAGATACTTTTTTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTTTTTTGCCATTGAGCTTTTTTTTATGACACCGGCTTTTTTTTTTTTTTTT	
H1	2-2	GAGACGGCGTCTTTTTTTGTCGGCGAACTTTTTTTAGCCGTTGAGGCTTTTTTTCTCTGGTCC	
A2	2-3	CTGGGCGGATGTTTTTTTTTACAGTGCGTTTTTTTTACCTCTCTGTTTTTTTTTACGTGCTAA	
B2	2-4	TCCGATTGCTATTTTTTTGACGCATTGTTTTTTTTCGGTAACTAAGTTTTTTTTTCTTTGGAG	
C2	2-5	CAACATCTGCATTTTTTTGCAGCTGTAGTTTTTTTCCAGCTTTACACTTTTTTTTCAACGAGC	
D2	2-6	ATCTGCCGCGGTTTTTTTTAGTTGCTGCTTTTTTTGTATCTGTAACCTTTTTTTGCGTCACCG	
E2	3-1	CACGGAACGGCATTTTTTTTCGAACGTGTTTTTTTGACGCCGTCTCTTTTTTTGCTCAATGGC	
F2	3-2	TCGTCCTAGGCCTTTTTTTCTGGACTTCTTTTTTTCATCCGCCCAGTTTTTTTGTTCGCCGAC	
G2	3-3	TTCCGGATCGACTTTTTTTCCTCGCCATTTTTTTTTAGCAATCGGATTTTTTTCGCACTGTAA	
H2	3-4	TTACCTAGAAATTTTTTTTACCCGATGATTTTTTTTGCAGATGTTGTTTTTTTACAATGCGTC	
A3	3-5	GAAGCTGGCAAGTTTTTTTGTTGCTATATTTTTTTCCGCGGCAGATTTTTTTTCTACAGCTGC	
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAGCAACTA	
C3	4-1	TTTTTTTTTTTTTTTTTTGGTTTCGAGATTTTTTTTGCCGTTCCGTGTTTTTTTTTTTTTTTT	
D3	4-2	GATTAGAGCATTTTTTTTAATCTCTTTCTTTTTTTGGCCTAGGACGATTTTTTTCACGTTCGA	
E3	4-3	GCTGAGGTGTGTTTTTTTCCGAGAAACATTTTTTTGTCGATCCGGAATTTTTTTGAAGTCCAG	
F3	4-4	TCTAGGAAACCTTTTTTTCGGATATGTGTTTTTTTATTTCTAGGTAATTTTTTTATGGCGAGG	
G3	4-5	CGGCAGTTTAATTTTTTTGACCTGCTCTTTTTTTTCTTGCCAGCTTCTTTTTTTTCATCGGGT	
H3	4-6	GAACAAATATCTTTTTTTTACACCCTATTTTTTTTTCCATCTTCCCGTTTTTTTTATAGCAAC	
A4	5-1	GGTCGGATCACTTTTTTTTCCCGCCAACTTTTTTTATGCTCTAATCTTTTTTTTCTCGAAACC	
B4	5-2	GAACTCGTCTCCTTTTTTTGCTCAGGGTTTTTTTTCACACCTCAGCTTTTTTTGAAAGAGATT	
C4	5-3	CTAATAATAAGCTTTTTTTGTGCCTAGCTTTTTTTGGTTTCCTAGATTTTTTTTGTTTCTCGG	
D4	5-4	TGAGCAAAGCAGTTTTTTTACACAAAGGTTTTTTTTTAAACTGCCGTTTTTTTCACATATCCG	
E4	5-5	ACCATCACCCTATTTTTTTCGATTCTCATTTTTTTGATATTTGTTCTTTTTTTAGAGCAGGTC	
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGGTGTA	
G4	6-1	TTTTTTTTTTTTTTTTTTCTAGCTCACCTTTTTTTAGTGATCCGACCTTTTTTTTTTTTTTTT	
H4	6-2	ACTTCACTATTTTTTTTTTAAGGTGTTGTTTTTTTGGAGACGAGTTCTTTTTTTGTTGGCGGG	
A5	6-3	ATTTAGACTAGTTTTTTTTCGCCTGGATTTTTTTTGCTTATTATTAGTTTTTTTACCCTGAGC	
B5	6-4	CAGAAAGTGAGTTTTTTTGGCCTCAGGTTTTTTTTCTGCTTTGCTCATTTTTTTGCTAGGCAC	
C5	6-5	GGTCAGGTCAATTTTTTTCGGTCATCTCTTTTTTTTAGGGTGATGGTTTTTTTTCCTTTGTGT	
D5	6-6	AAAGCTCGGATTTTTTTTTAGCGCCCGGTTTTTTTCTGAGTTTGCTATTTTTTTTGAGAATCG	
E5	7-1	TTGCACGACCGTTTTTTTTATCGTCTCTTTTTTTTAATAGTGAAGTTTTTTTTGGTGAGCTAG	
F5	7-2	ACTTACAACGCCTTTTTTTTGAAATAAGTTTTTTTCTAGTCTAAATTTTTTTTCAACACCTTA	
G5	7-3	AATAATTACCTCTTTTTTTACATACGCTTTTTTTTCTCACTTTCTGTTTTTTTATCCAGGCGA	
H5	7-4	CTGGTCATCTCATTTTTTTGAATGAGAATTTTTTTTTGACCTGACCTTTTTTTACCTGAGGCC	
A6	7-5	TAGCGTGAATGGTTTTTTTATGAGACGCTTTTTTTATCCGAGCTTTTTTTTTTGAGATGACCG	
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCGGGCGCTA	
C6	8-1	TTTTTTTTTTTTTTTTTTGGACATTCCTTTTTTTTACGGTCGTGCAATTTTTTTTTTTTTTTT	
D6	8-2	TGCGAAGGCCGTTTTTTTAAGCTGGCAGTTTTTTTGGCGTTGTAAGTTTTTTTTAGAGACGAT	
E6	8-3	TGCAGGCGGGCTTTTTTTCAAAGGATAATTTTTTTGAGGTAATTATTTTTTTTTCTTATTTCA	
F6	8-4	GCTTCCGTTGCTTTTTTTTGATGCCATTTTTTTTTTGAGATGACCAGTTTTTTTAGCGTATGT	
G6	8-5	CAGGCGAAATCTTTTTTTAGCGTTGGCTTTTTTTTCCATTCACGCTATTTTTTTTTCTCATTC	
H6	8-6	AGCGCTGGAGGTTTTTTTGCTCAATGTTTTTTTTTGACTTGAGTGACTTTTTTTGCGTCTCAT	
A7	9-1	AATCTCCCACGCTTTTTTTATTGGACCTTTTTTTTCGGCCTTCGCATTTTTTTAGGAATGTCC	
B7	9-2	TCAGTGTATACCTTTTTTTGACTGTAAATTTTTTTGCCCGCCTGCATTTTTTTCTGCCAGCTT	
C7	9-3	GCCTTCGCACAGTTTTTTTTGGTCTGACTTTTTTTGCAACGGAAGCTTTTTTTTTATCCTTTG	
D7	9-4	GTCTAGGTATCCTTTTTTTCTGCTGGGATTTTTTTGATTTCGCCTGTTTTTTTAATGGCATCA	
E7	9-5	GCCGGAATTTGCTTTTTTTTAGCATTTATTTTTTCCTCCAGCGCTTTTTTTTAGCCAACGCT	

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTTTTTTTTCTGTCTCGTATTTTTTTGCGTGGGAGATTTTTTTTTTTTTTTTTTT
H7	10-2	TAGTAAACTCCTTTTTTTAAGGCTACCCTTTTTTTGGTATACACTGATTTTTTTAGGTCCAAT
A8	10-3	TGTAAGTCGATTTTTTTTTAAACCACTGTTTTTTTCTGTGCGAAGGCTTTTTTTTTTACAGTC
B8	10-4	CAGAAATATTGTTTTTTTAACTGTGATTTTTTTTTGGATACCTAGACTTTTTTTGTCAGACCA
C8	10-5	TGAGAGCTCTGTTTTTTTATGAATTCGCTTTTTTTGCAAATTCCGGCTTTTTTTTCCCAGCAG
D8	10-6	TTTCCTAGTTGTTTTTTTAATATCCACGTTTTTTTAATAAAGGTAATTTTTTTTTAAATGCTA
E8	11-1	GGAGTTTACTATTTTTTTTACGAGACAG
F8	11-2	ATCGACTTACATTTTTTTGGGTAGCCTT
G8	11-3	CAATATTTCTGTTTTTTTCAGTGGTTTA
H8	11-4	CAGAGCTCTCATTTTTTTAATCACAGTT
A9	11-5	CAACTAGGAAATTTTTTTGCGAATTCAT
B9	11-6	TTTTTTTTTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_13T

Well	Name	Sequence
A1	1-1	GCCGGTGTCATATTTTTTTTTTTTTGGACCAGAG
B1	1-2	GCCTCAACGGCTTTTTTTTTTTTTTTTAGCACGT
C1	1-3	AACAGAGAGGTATTTTTTTTTTTTTCTCCAAAGA
D1	1-4	ACTTAGTTACCGTTTTTTTTTTTTTGCTCGTTGA
E1	1-5	GTGTAAAGCTGGTTTTTTTTTTTTTCGGTGACGC
F1	1-6	GGTTACAGATACTTTTTTTTTTTTTTTTTTTTTT
G1	2-1	TTTTTTTTTTTTTTTTTTTTTTTTTTGCCATTGAGCTTTTTTTTTTTTTTTATGACACCGGCTTTTTTTTTTTTTTTTTTTTTTTTTT
H1	2-2	GAGACGGCGTCTTTTTTTTTTTTTTTGTCGGCGAACTTTTTTTTTTTTTTTAGCCGTTGAGGCTTTTTTTTTTTTTTTTCTCTGGTCC
A2	2-3	CTGGGCGGATGTTTTTTTTTTTTTTTTTACAGTGCGTTTTTTTTTTTTTTTTACCTCTCTGTTTTTTTTTTTTTTTTTTACGTGCTAA
B2	2-4	TCCGATTGCTATTTTTTTTTTTTTTTGACGCATTGTTTTTTTTTTTTTTTTCGGTAACTAAGTTTTTTTTTTTTTTTTTTCTTTGGAG
C2	2-5	CAACATCTGCATTTTTTTTTTTTTTTGCAGCTGTAGTTTTTTTTTTTTTTTCCAGCTTTACACTTTTTTTTTTTTTTTTTCAACGAGC
D2	2-6	ATCTGCCGCGGTTTTTTTTTTTTTTTTAGTTGCTGCTTTTTTTTTTTTTTTGTATCTGTAACCTTTTTTTTTTTTTTTTGCGTCACCG
E2	3-1	CACGGAACGGCATTTTTTTTTTTTTTTTCGAACGTGTTTTTTTTTTTTTTTGACGCCGTCTCTTTTTTTTTTTTTTTTGCTCAATGGC
F2	3-2	TCGTCCTAGGCCTTTTTTTTTTTTTTTCTGGACTTCTTTTTTTTTTTTTTTCATCCGCCCAGTTTTTTTTTTTTTTTTGTTCGCCGAC
G2	3-3	TTCCGGATCGACTTTTTTTTTTTTTTTCCTCGCCATTTTTTTTTTTTTTTTAGCAATCGGATTTTTTTTTTTTTTTTTCGCACTGTAA
H2	3-4	TTACCTAGAAATTTTTTTTTTTTTTTTACCCGATGATTTTTTTTTTTTTTTTGCAGATGTTGTTTTTTTTTTTTTTTTACAATGCGTC
A3	3-5	GAAGCTGGCAAGTTTTTTTTTTTTTTTGTTGCTATATTTTTTTTTTTTTTTTCCGCGGCAGATTTTTTTTTTTTTTTTCTACAGCTGC
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAGCAACTA
C3	4-1	TTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTCGAGATTTTTTTTTTTTTTTTGCCGTTCCGTGTTTTTTTTTTTTTTTTTTTTTTTTT
D3	4-2	GATTAGAGCATTTTTTTTTTTTTTTTTTAATCTCTTTCTTTTTTTTTTTTTTGGCCTAGGACGATTTTTTTTTTTTTTTCACGTTCGA
E3	4-3	GCTGAGGTGTGTTTTTTTTTTTTTTTTTCCGAGAAACATTTTTTTTTTTTTGTCGATCCGGAATTTTTTTTTTTTTTTTGAAGTCCAG
F3	4-4	TCTAGGAAACCTTTTTTTTTTTTTTTCGGATATGTGTTTTTTTTTTTTTTTATTTCTAGGTAATTTTTTTTTTTTTTTTATGGCGAGG
G3	4-5	CGGCAGTTTAATTTTTTTTTTTTTTTGACCTGCTCTTTTTTTTTTTTTTTTCTTGCCAGCTTCTTTTTTTTTTTTTTTTTCATCGGGT
H3	4-6	GAACAAATATCTTTTTTTTTTTTTTTTACACCCTATTTTTTTTTTTTTTTTTCCATCTTCCCGTTTTTTTTTTTTTTTTTATAGCAAC
A4	5-1	GGTCGGATCACTTTTTTTTTTTTTTTTCCCGCCAACTTTTTTTTTTTTTTTATGCTCTAATCTTTTTTTTTTTTTTTTTCTCGAAACC
B4	5-2	GAACTCGTCTCCTTTTTTTTTTTTTTGCTCAGGGTTTTTTTTTTTTTTTTTCACACCTCAGCTTTTTTTTTTTTTTTTGAAAGAGATT
C4	5-3	CTAATAATAAGCTTTTTTTTTTTTTTTGTGCCTAGCTTTTTTTTTTTTTTTGGTTTCCTAGATTTTTTTTTTTTTTTTTGTTTCTCGG
D4	5-4	TGAGCAAAGCAGTTTTTTTTTTTTTTTACACAAAGGTTTTTTTTTTTTTTTTAAACTGCCGTTTTTTTTTTTTTTTTTCACATATCCG
E4	5-5	ACCATCACCCTATTTTTTTTTTTTTTTCGATTCTCATTTTTTTTTTTTTTTGATATTTGTTCTTTTTTTTTTTTTTTTAGAGCAGGTC
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGGTGTA
G4	6-1	TTTTTTTTTTTTTTTTTTTTTTTTTTCTAGCTCACCTTTTTTTTTTTTTTTAGTGATCCGACCTTTTTTTTTTTTTTTTTTTTTTTTT
H4	6-2	ACTTCACTATTTTTTTTTTTTTTTTTTAAGGTGTTGTTTTTTTTTTTTTTTGGAGACGAGTTCTTTTTTTTTTTTTTTTGTTGGCGGG
A5	6-3	ATTTAGACTAGTTTTTTTTTTTTTTTTCGCCTGGATTTTTTTTTTTTTTTTGCTTATTATTAGTTTTTTTTTTTTTTTTACCCTGAGC
B5	6-4	CAGAAAGTGAGTTTTTTTTTTTTTTTGGCCTCAGGTTTTTTTTTTTTTTTTCTGCTTTGCTCATTTTTTTTTTTTTTTTGCTAGGCAC
C5	6-5	GGTCAGGTCAATTTTTTTTTTTTTTTCGGTCATCTCTTTTTTTTTTTTTTTAGGGTGATGGTTTTTTTTTTTTTTTTTTCCTTTGTGT
D5	6-6	AAAGCTCGGATTTTTTTTTTTTTTTTTAGCGCCCGGTTTTTTTTTTTTTTTTCTGAGTTTGCTATTTTTTTTTTTTTTTTGAGAATCG
E5	7-1	TTGCACGACCGTTTTTTTTTTTTTTTTATCGTCTCTTTTTTTTTTTTTTTTAATAGTGAAGTTTTTTTTTTTTTTTTTGGTGAGCTAG
F5	7-2	ACTTACAACGCCTTTTTTTTTTTTTTTTGAAATAAGTTTTTTTTTTTTTTTCTAGTCTAAATTTTTTTTTTTTTTTTTCAACACCTTA
G5	7-3	AATAATTACCTCTTTTTTTTTTTTTTTTACATACGCTTTTTTTTTTTTTTTTCTCACTTTCTGTTTTTTTTTTTTTTTATCCAGGCGA
H5	7-4	CTGGTCATCTCATTTTTTTTTTTTTTTGAATGAGAATTTTTTTTTTTTTTTTTGACCTGACCTTTTTTTTTTTTTTTTACCTGAGGCC
A6	7-5	TAGCGTGAATGGTTTTTTTTTTTTTTTTATGAGACGCTTTTTTTTTTTTTTATCCGAGCTTTTTTTTTTTTTTTTTTTGAGATGACCG
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCGGGCGCTA
C6	8-1	TTTTTTTTTTTTTTTTTTTTTTTTTTGGACATTCCTTTTTTTTTTTTTTTTACGGTCGTGCAATTTTTTTTTTTTTTTTTTTTTTTTT
D6	8-2	TGCGAAGGCCGTTTTTTTTTTTTTTTAAGCTGGCAGTTTTTTTTTTTTTTTGGCGTTGTAAGTTTTTTTTTTTTTTTTTAGAGACGAT
E6	8-3	TGCAGGCGGGCTTTTTTTTTTTTTTTCAAAGGATAATTTTTTTTTTTTTTTGAGGTAATTATTTTTTTTTTTTTTTTTTCTTATTTCA
F6	8-4	GCTTCCGTTGCTTTTTTTTTTTTTTTTGATGCCATTTTTTTTTTTTTTTTTTGAGATGACCAGTTTTTTTTTTTTTTTTAGCGTATGT
G6	8-5	CAGGCGAAATCTTTTTTTTTTTTTTTTAGCGTTGGCTTTTTTTTTTTTTTTCCATTCACGCTATTTTTTTTTTTTTTTTTTCTCATTC
H6	8-6	AGCGCTGGAGGTTTTTTTTTTTTTTTGCTCAATGTTTTTTTTTTTTTTTTTGACTTGAGTGACTTTTTTTTTTTTTTTTGCGTCTCAT
A7	9-1	AATCTCCCACGCTTTTTTTTTTTTTTTATTGGACCTTTTTTTTTTTTTTTTCGGCCTTCGCATTTTTTTTTTTTTTTTAGGAATGTCC
B7	9-2	TCAGTGTATACCTTTTTTTTTTTTTTTGACTGTAAATTTTTTTTTTTTTTTGCCCGCCTGCATTTTTTTTTTTTTTTTCTGCCAGCTT
C7	9-3	GCCTTCGCACAGTTTTTTTTTTTTTTTGGTCTGACTTTTTTTTTTTTTTTTGCAACGGAAGCTTTTTTTTTTTTTTTTTTATCCTTTG
D7	9-4	GTCTAGGTATCCTTTTTTTTTTTTTTTCTGCTGGGATTTTTTTTTTTTTTTGATTTCGCCTGTTTTTTTTTTTTTTTTAATGGCATCA
E7	9-5	GCCGGAATTTGCTTTTTTTTTTTTTTTTAGCATTTATTTTTTTTTTTTTTTCCTCCAGCGCTTTTTTTTTTTTTTTTTAGCCAACGCT

Back to overview

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTTTTTTTTTTTTTTCTGTCTCGTATTTTTTTTTTTTTGCGTGGGAGATTTTTTTTTTTTTTTTTTTTTTTT
H7	10-2	TAGTAAACTCCTTTTTTTTTTTTTAAGGCTACCCTTTTTTTTTTTTTGGTATACACTGATTTTTTTTTTTTTAGGTCCAAT
A8	10-3	TGTAAGTCGATTTTTTTTTTTTTTTAAACCACTGTTTTTTTTTTTTTCTGTGCGAAGGCTTTTTTTTTTTTTTTTACAGTC
B8	10-4	CAGAAATATTGTTTTTTTTTTTTTAACTGTGATTTTTTTTTTTTTTTGGATACCTAGACTTTTTTTTTTTTTGTCAGACCA
C8	10-5	TGAGAGCTCTGTTTTTTTTTTTTTATGAATTCGCTTTTTTTTTTTTTGCAAATTCCGGCTTTTTTTTTTTTTTCCCAGCAG
D8	10-6	TTTCCTAGTTGTTTTTTTTTTTTTAATATCCACGTTTTTTTTTTTTTAATAAAGGTAATTTTTTTTTTTTTTTAAATGCTA
E8	11-1	GGAGTTTACTATTTTTTTTTTTTTTACGAGACAG
F8	11-2	ATCGACTTACATTTTTTTTTTTTTGGGTAGCCTT
G8	11-3	CAATATTTCTGTTTTTTTTTTTTTCAGTGGTTTA
H8	11-4	CAGAGCTCTCATTTTTTTTTTTTTAATCACAGTT
A9	11-5	CAACTAGGAAATTTTTTTTTTTTTGCGAATTCAT
B9	11-6	TTTTTTTTTTTTTTTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m1_16T	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	GCCGGTGTCATATTTTTTTTTTTTTTTTTGGACCAGAG	
B1	1-2	GCCTCAACGGCTTTTTTTTTTTTTTTTTTTAGCACGT	
C1	1-3	AACAGAGAGGTATTTTTTTTTTTTTTTTTCTCCAAAGA	
D1	1-4	ACTTAGTTACCGTTTTTTTTTTTTTTTTGCTCGTTGA	
E1	1-5	GTGTAAAGCTGGTTTTTTTTTTTTTTTTCGGTGACGC	
F1	1-6	GGTTACAGATACTTTTTTTTTTTTTTTTTTTTTTTT	
G1	2-1	TTTTTTTTTTTTTTTTTTTTTTTTTTTTGCCATTGAGCTTTTTTTTTTTTTTTTTTTATGACACCGGCTTTTTTTTTTTTTTTTTTTTTTT	
H1	2-2	GAGACGGCGTCTTTTTTTTTTTTTTTTTGTCGGCGAACTTTTTTTTTTTTTTTTTTAGCCGTTGAGGCTTTTTTTTTTTTTTTTCTCTGGTCC	
A2	2-3	CTGGGCGGATGTTTTTTTTTTTTTTTTTTTTACAGTGCGTTTTTTTTTTTTTTTTTTACCTCTCTGTTTTTTTTTTTTTTTTTTACGTGCTAA	
B2	2-4	TCCGATTGCTATTTTTTTTTTTTTTTTTGACGCATTGTTTTTTTTTTTTTTTTTTCGGTAACTAAGTTTTTTTTTTTTTTTTTCTTTGGAG	
C2	2-5	CAACATCTGCATTTTTTTTTTTTTTTTTGCAGCTGTAGTTTTTTTTTTTTTTTTTTCCAGCTTTACACTTTTTTTTTTTTTTTTTCAACGAGC	
D2	2-6	ATCTGCCGCGGTTTTTTTTTTTTTTTTTTAGTTGCTGCTTTTTTTTTTTTTTTTTGTATCTGTAACCTTTTTTTTTTTTTTTTTGCGTCACCG	
E2	3-1	CACGGAACGGCATTTTTTTTTTTTTTTTTTCGAACGTGTTTTTTTTTTTTTTTTTGACGCCGTCTCTTTTTTTTTTTTTTTTTGCTCAATGGC	
F2	3-2	TCGTCCTAGGCCTTTTTTTTTTTTTTTTTCTGGACTTCTTTTTTTTTTTTTTTTTCATCCGCCCAGTTTTTTTTTTTTTTTTTGTTCGCCGAC	
G2	3-3	TTCCGGATCGACTTTTTTTTTTTTTTTTTCCTCGCCATTTTTTTTTTTTTTTTTTAGCAATCGGATTTTTTTTTTTTTTTTCGCACTGTAA	
H2	3-4	TTACCTAGAAATTTTTTTTTTTTTTTTTTACCCGATGATTTTTTTTTTTTTTTTTGCAGATGTTGTTTTTTTTTTTTTTTTTACAATGCGTC	
A3	3-5	GAAGCTGGCAAGTTTTTTTTTTTTTTTTTGTTGCTATATTTTTTTTTTTTTTTTTCCGCGGCAGATTTTTTTTTTTTTTTTTCTACAGCTGC	
B3	3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAGCAACTA	
C3	4-1	TTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTTCGAGATTTTTTTTTTTTTTTTTTGCCGTTCCGTGTTTTTTTTTTTTTTTTTTTTTTTT	
D3	4-2	GATTAGAGCATTTTTTTTTTTTTTTTTTAATCTCTTTCTTTTTTTTTTTTTTTTTGGCCTAGGACGATTTTTTTTTTTTTTTTTCACGTTCGA	
E3	4-3	GCTGAGGTGTGTTTTTTTTTTTTTTTTTCCGAGAAACATTTTTTTTTTTTTTTTTGTCGATCCGGAATTTTTTTTTTTTTTTTTGAAGTCCAG	
F3	4-4	TCTAGGAAACCTTTTTTTTTTTTTTTTTCGGATATGTGTTTTTTTTTTTTTTTTTATTTCTAGGTAATTTTTTTTTTTTTTTTTATGGCGAGG	
G3	4-5	CGGCAGTTTAATTTTTTTTTTTTTTTTTGACCTGCTCTTTTTTTTTTTTTTTTTTCTTGCCAGCTTCTTTTTTTTTTTTTTTTTTCATCGGGT	
H3	4-6	GAACAAATATCTTTTTTTTTTTTTTTTTTTACACCCTATTTTTTTTTTTTTTTTTTCCATCTTCCCGTTTTTTTTTTTTTTTTTTATAGCAAC	
A4	5-1	GGTCGGATCACTTTTTTTTTTTTTTTTTTCCCGCCAACTTTTTTTTTTTTTTTTTTATGCTCTAATCTTTTTTTTTTTTTTTTTTCTCGAAACC	
B4	5-2	GAACTCGTCTCCTTTTTTTTTTTTTTTTTTGCTCAGGGTTTTTTTTTTTTTTTTTTCACACCTCAGCTTTTTTTTTTTTTTTTTGAAAGAGATT	
C4	5-3	CTAATAATAAGCTTTTTTTTTTTTTTTTTTGTGCCTAGCTTTTTTTTTTTTTTTTTGGTTTCCTAGATTTTTTTTTTTTTTTTTGTTTCTCGG	
D4	5-4	TGAGCAAAGCAGTTTTTTTTTTTTTTTTTACACAAAGGTTTTTTTTTTTTTTTTTTAAACTGCCGTTTTTTTTTTTTTTTTCACATATCCG	
E4	5-5	ACCATCACCCTATTTTTTTTTTTTTTTTTCGATTCTCATTTTTTTTTTTTTTTTTGATATTTGTTCTTTTTTTTTTTTTTTTTAGAGCAGGTC	
F4	5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGGGTGTA	
G4	6-1	TTTTTTTTTTTTTTTTTTTTTTTTTTTCTAGCTCACCTTTTTTTTTTTTTTTTTTAGTGATCCGACCTTTTTTTTTTTTTTTTTTTTTTT	
H4	6-2	ACTTCACTATTTTTTTTTTTTTTTTTTTAAGGTGTTGTTTTTTTTTTTTTTTTTTGGAGACGAGTTCTTTTTTTTTTTTTTTTTGTTGGCGGG	
A5	6-3	ATTTAGACTAGTTTTTTTTTTTTTTTTTTCGCCTGGATTTTTTTTTTTTTTTTTTGCTTATTATTAGTTTTTTTTTTTTTTTTACCCTGAGC	
B5	6-4	CAGAAAGTGAGTTTTTTTTTTTTTTTTTGGCCTCAGGTTTTTTTTTTTTTTTTTCTGCTTTGCTCATTTTTTTTTTTTTTTTGCTAGGCAC	
C5	6-5	GGTCAGGTCAATTTTTTTTTTTTTTTTTCGGTCATCTCTTTTTTTTTTTTTTTTTTAGGGTGATGGTTTTTTTTTTTTTTTTCCTTTGTGT	
D5	6-6	AAAGCTCGGATTTTTTTTTTTTTTTTTTTAGCGCCCGGTTTTTTTTTTTTTTTTTCTGAGTTTGCTATTTTTTTTTTTTTTTTTGAGAATCG	
E5	7-1	TTGCACGACCGTTTTTTTTTTTTTTTTTTATCGTCTCTTTTTTTTTTTTTTTTTTAATAGTGAAGTTTTTTTTTTTTTTTTTGGTGAGCTAG	
F5	7-2	ACTTACAACGCCTTTTTTTTTTTTTTTTTTGAAATAAGTTTTTTTTTTTTTTTTTCTAGTCTAAATTTTTTTTTTTTTTTTCAACACCTTA	
G5	7-3	AATAATTACCTCTTTTTTTTTTTTTTTTTACATACGCTTTTTTTTTTTTTTTTTCTCACTTTCTGTTTTTTTTTTTTTTTTATCCAGGCGA	
H5	7-4	CTGGTCATCTCATTTTTTTTTTTTTTTTTGAATGAGAATTTTTTTTTTTTTTTTTGACCTGACCTTTTTTTTTTTTTTTTACCTGAGGCC	
A6	7-5	TAGCGTGAATGGTTTTTTTTTTTTTTTTTATGAGACGCTTTTTTTTTTTTTTTTTATCCGAGCTTTTTTTTTTTTTTTTTGAGATGACCG	
B6	7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCGGGCGCTA	
C6	8-1	TTTTTTTTTTTTTTTTTTTTTTTTTTTGGACATTCCTTTTTTTTTTTTTTTTTTACGGTCGTGCAATTTTTTTTTTTTTTTTTTTTTTT	
D6	8-2	TGCGAAGGCCGTTTTTTTTTTTTTTTTTAAGCTGGCAGTTTTTTTTTTTTTTTTTGGCGTTGTAAGTTTTTTTTTTTTTTTTTAGAGACGAT	
E6	8-3	TGCAGGCGGGCTTTTTTTTTTTTTTTTTCAAAGGATAATTTTTTTTTTTTTTTTTGAGGTAATTATTTTTTTTTTTTTTTTCTTATTTCA	
F6	8-4	GCTTCCGTTGCTTTTTTTTTTTTTTTTTTGATGCCATTTTTTTTTTTTTTTTTTGAGATGACCAGTTTTTTTTTTTTTTTTTAGCGTATGT	
G6	8-5	CAGGCGAAATCTTTTTTTTTTTTTTTTTTAGCGTTGGCTTTTTTTTTTTTTTTTTCCATTCACGCTATTTTTTTTTTTTTTTTTCTCATTC	
H6	8-6	AGCGCTGGAGGTTTTTTTTTTTTTTTTTGCTCAATGTTTTTTTTTTTTTTTTTTGACTTGAGTGACTTTTTTTTTTTTTTTTGCGTCTCAT	
A7	9-1	AATCTCCCACGCTTTTTTTTTTTTTTTTTATTGGACCTTTTTTTTTTTTTTTTTCGGCCTTCGCATTTTTTTTTTTTTTTTAGGAATGTCC	
B7	9-2	TCAGTGTATACCTTTTTTTTTTTTTTTTTGACTGTAAATTTTTTTTTTTTTTTTTGCCCGCCTGCATTTTTTTTTTTTTTTTCTGCCAGCTT	
C7	9-3	GCCTTCGCACAGTTTTTTTTTTTTTTTTTGGTCTGACTTTTTTTTTTTTTTTTTGCAACGGAAGCTTTTTTTTTTTTTTTTTATCCTTTG	
D7	9-4	GTCTAGGTATCCTTTTTTTTTTTTTTTTCTGCTGGGATTTTTTTTTTTTTTTTGATTTCGCCTGTTTTTTTTTTTTTTTTAATGGCATCA	
E7	9-5	GCCGGAATTTGCTTTTTTTTTTTTTTTTTTAGCATTTATTTTTTTTTTTTTTTTCCTCCAGCGCTTTTTTTTTTTTTTTTAGCCAACGCT	

F7	9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAACATTGAGC
G7	10-1	TTTTTTTTTTTTTTTTTTTTTTTTTTTCTGTCTCGTATTTTTTTTTTTTTTTTGCGTGGGAGATTTTTTTTTTTTTTTTTTTTTTTTTTT
H7	10-2	TAGTAAACTCCTTTTTTTTTTTTTTTTAAGGCTACCCTTTTTTTTTTTTTTTTGGTATACACTGATTTTTTTTTTTTTTTTAGGTCCAAT
A8	10-3	TGTAAGTCGATTTTTTTTTTTTTTTTTTAAACCACTGTTTTTTTTTTTTTTTTCTGTGCGAAGGCTTTTTTTTTTTTTTTTTTTACAGTC
B8	10-4	CAGAAATATTGTTTTTTTTTTTTTTTTAACTGTGATTTTTTTTTTTTTTTTTTGGATACCTAGACTTTTTTTTTTTTTTTTGTCAGACCA
C8	10-5	TGAGAGCTCTGTTTTTTTTTTTTTTTTATGAATTCGCTTTTTTTTTTTTTTTTGCAAATTCCGGCTTTTTTTTTTTTTTTTTCCCAGCAG
D8	10-6	TTTCCTAGTTGTTTTTTTTTTTTTTTTAATATCCACGTTTTTTTTTTTTTTTTAATAAAGGTAATTTTTTTTTTTTTTTTTTAAATGCTA
E8	11-1	GGAGTTTACTATTTTTTTTTTTTTTTTTACGAGACAG
F8	11-2	ATCGACTTACATTTTTTTTTTTTTTTTGGGTAGCCTT
G8	11-3	CAATATTTCTGTTTTTTTTTTTTTTTTCAGTGGTTTA
H8	11-4	CAGAGCTCTCATTTTTTTTTTTTTTTTAATCACAGTT
A9	11-5	CAACTAGGAAATTTTTTTTTTTTTTTTGCGAATTCAT
B9	11-6	TTTTTTTTTTTTTTTTTTTTTTTTTTTCGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m14	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	TCCGCCGTCGGCGTCTCGGGA	
B1	1-2	ACTTGTACCAAGAGGCCAGTG	
C1	1-3	GTCTGTGCCCTAGCTGCATCG	
D1	1-4	CGTAGACGTTAAGACCTCGGA	
E1	1-5	AGGTGGTTTATACGGACTGTA	
F1	1-6	TTTTTTTTTTTTTAATACCCA	
G1	2-1	TTTTTTTTTTGCCCAATGCGTTTCCGACGGCGGATTTTTTTTTT	
H1	2-2	GTGCAGCAAGTCCGTTAACCATTTTGGTACAAGTTCCCGAGACG	
A2	2-3	GAATGAACTAGGGATAATAAGTTAGGGCACAGACCACTGGCCTC	
B2	2-4	ACCGACTAAATGATTGAGTCCTTTAACGTCTACGCGATGCAGCT	
C2	2-5	TACAAAGTTCAACCATAGACGTTATAAACCACCTTCCGAGGTCT	
D2	2-6	TGGGATAGTAGACACCTGCCCTTACGCATAGTCCTACAGTCCGT	
E2	3-1	AGTTATCCCTCATCGGTTACTTTCTTGCTGCACACGCATTGGGC	
F2	3-2	TAGAAGGGCCCTCAAGATGCATTTAGTTCATTCTGGTTAACGGA	
G2	3-3	ATGCGGGCCTAGCATGTAAGCTTTTTAGTCGGTCTTATTATCCC	
H2	3-4	TCCGTAAATTTAGTTTAGGACTTGAACTTTGTAGGACTCAATCA	
A3	3-5	GTTTACTGCACCAACTTGAAGTTTACTATCCCACGTCTATGGTT	
B3	3-6	ACTCGCAGCACTTTTTTTTTTTTTTTTTTTTTTGGGCAGGTGTC	
C3	4-1	TTTTTTTTTTCACGTGGGCATTTGAGGGATAACTTTTTTTTTTT	
D3	4-2	CGAGTCCGCGAGGTCCGAATCTTGGGCCCTTCTAAGTAACCGAT	
E3	4-3	CGCGCCAACGGGTGGAGCTGTTTTAGGCCCGCATTGCATCTTGA	
F3	4-4	CCATCGCGCCCTAAGTGTATGTTAAATTTACGGAGCTTACATGC	
G3	4-5	GGTACCGGACCGTGGTCACCGTTGTGCAGTAAACGTCCTAAACT	
H3	4-6	AGGTAATCTAATAGCAGCAGTTTGTGCTGCGAGTCTTCAAGTTG	
A4	5-1	ACATAGCGAGTCAAACGGTGATTCGCGGACTCGATGCCCACGTG	
B4	5-2	ATGGGCGGGCCGGTCACAAGTTTCGTTGGCGCGGATTCGGACCT	
C4	5-3	CCGGAGCCCTAAGTCCGAGGTTTGGCGCGATGGACAGCTCCACC	
D4	5-4	AAGGATCTGGAGGAAGTTCCATTGTCCGGTACCCATACACTTAG	
E4	5-5	TTAGGGAAATAAAGGATTGACTTTAGATTACCTCGGTGACCACG	
F4	5-6	TCAGCGCTTCATTTTTTTTTTTTTTTTTTTTTACTGCTGCTAT	
G4	6-1	TTTTTTTTTTGTATCTGCACATTACTCGCTATGTTTTTTTTTTT	
H4	6-2	CCGCATGATCCGCAAGAGCTTTTGGCCCGCCCATTCACCGTTTG	
A5	6-3	AGTGCTTATGACCCTAAATTGTTTAGGGCTCCGGACTTGTGACC	
B5	6-4	CGTCAGAAAGATAAAGAGGGCTTTCCAGATCCTTACCTCGGACT	
C5	6-5	CATACGCTGTCCCTAACGTTATTTATTTCCCTAATGGAACTTCC	
D5	6-6	GCCAATCCAGGTTTAAAGAGATTTGAAGCGCTGAGTCAATCCTT	
E5	7-1	TATTTGGCATCTGACTATAGGTTGATCATGCGGTGTGCAGATAC	
F5	7-2	GTACGCCCTGACCCACCGATGTTCATAAGCACTAAGCTCTTGCG	
G5	7-3	GTTAAAGGCGTTCGCGAAATTTTCTTTCTGACGCAATTTAGGGT	
H5	7-4	CCTTTGACTTTCACTGAACAGTTACAGCGTATGGCCCTCTTTAT	
A6	7-5	GCCCTGACGGGAGCTGCGGGCTTCTGGATTGGCTAACGTTAGGG	
B6	7-6	GACGTTGAATTTTTTTTTTTTTTTTTTTTTTTTCTCTTTAAAC	
C6	8-1	TTTTTTTTTTACAGAAAGGTCTTGATGCCAAATATTTTTTTTTT	
D6	8-2	TGGCGGTTGGATTAATTAGGCTTTCAGGGCGTACCCTATAGTCA	
E6	8-3	AATCCCTGTGGCTACCGAGGCTTACGCCTTTAACCATCGGTGGG	
F6	8-4	AACTGAAGCGGCTTGGCCACTTTAAAGTCAAAGGAATTTCGCGA	
G6	8-5	ACCGTGACGCAACTAAACAATTTCCCGTCAGGGCCTGTTCAGTG	
H6	8-6	GGACTCTATCCCTACGGAACCTTAATTCAACGTCGCCCGCAGCT	
A7	9-1	GGGACCCTTCACTAACGACCATTCCAACCGCCAGACCTTTCTGT	
B7	9-2	GCCTGATATTGCAATCACTCCTTCACAGGGATTGCCTAATTAAT	
C7	9-3	GGGTACCGACTCCCTTTACGGTTCGCTTCAGTTGCCTCGGTAGC	
D7	9-4	CTTCCGAGAAGTCATTTGGAATTGCGTCACGGTAGTGGCCAAGC	
E7	9-5	GTCTCAGGCGCTTGAGAATGATTGATAGAGTCCATTGTTTAGTT	

F7	9-6	TCGAACACTTCTTTTTTTTTTTTTTTTTTTTTGGTTCCGTAGG
G7	10-1	TTTTTTTTTTCACATAGGCCGTTTGAAGGGTCCCTTTTTTTTTT
H7	10-2	CCCACCTAGAAGAAGAAAGGGTTCAATATCAGGCTGGTCGTTAG
A8	10-3	TAGAACTGAGAGACAGGGCTATTAGTCGGTACCCGGAGTGATTG
B8	10-4	TATAGCGCGTCTGTGGCGCGATTCTTCTCGGAAGCCGTAAAGGG
C8	10-5	CTGGCGGTACCATAAACTCGCTTGCGCCTGAGACTTCCAAATGA
D8	10-6	ATTTCCCTGACCTTGAGGGAGTTGAAGTGTTCGATCATTCTCAA
E8	11-1	TCTAGGTGGGCGGCCTATGTG
F8	11-2	CTCAGTTCTACCCTTTCTTCT
G8	11-3	ACGCGCTATATAGCCCTGTCT
H8	11-4	GTACCGCCAGTCGCGCCACAG
A9	11-5	TCAGGGAAATGCGAGTTTATG
B9	11-6	TTTTTTTTTTCTCCCTCAAGG
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m14_10T	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	TCCGCCGTCGGTTTTTTTTTTCGTCTCGGGA	
B1	1-2	ACTTGTACCAATTTTTTTTTTGAGGCCAGTG	
C1	1-3	GTCTGTGCCCTTTTTTTTTTTAGCTGCATCG	
D1	1-4	CGTAGACGTTATTTTTTTTTTAGACCTCGGA	
E1	1-5	AGGTGGTTTATTTTTTTTTTTACGGACTGTA	
F1	1-6	TTTTTTTTTTTTTTTTTTTTTTTAATACCCA	
G1	2-1	TTTTTTTTTTTTTTTTTTTTGCCCAATGCGTTTTTTTTTTTCCGACGGCGGATTTTTTTTTTTTTTTTTT	
H1	2-2	GTGCAGCAAGTTTTTTTTTTCCGTTAACCATTTTTTTTTTTTGGTACAAGTTTTTTTTTTTCCCGAGACG	
A2	2-3	GAATGAACTATTTTTTTTTTGGGATAATAAGTTTTTTTTTTAGGGCACAGACTTTTTTTTTCACTGGCCTC	
B2	2-4	ACCGACTAAATTTTTTTTTTTGATTGAGTCCTTTTTTTTTTTAACGTCTACGTTTTTTTTTCGATGCAGCT	
C2	2-5	TACAAAGTTCTTTTTTTTTAACCATAGACGTTTTTTTTTATAAACCACCTTTTTTTTTTTCCGAGGTCT	
D2	2-6	TGGGATAGTATTTTTTTTTGACACCTGCCCTTTTTTTTTACGCATAGTCCTTTTTTTTTTACAGTCCGT	
E2	3-1	AGTTATCCCTCTTTTTTTTTCATCGGTTACTTTTTTTTTCTTGCTGCACTTTTTTTTTACGCATTGGGC	
F2	3-2	TAGAAGGGCCCTTTTTTTTTCTCAAGATGCTTTTTTTTTTAGTTCATTCTTTTTTTTTGGTTAACGGA	
G2	3-3	ATGCGGGCCTATTTTTTTTTAGCATGTAAGTTTTTTTTTTAGTCGGTTTTTTTTTCTTATTATCCC	
H2	3-4	TCCGTAAATTTTTTTTTTTAGTTTAGGATTTTTTTTTGAACTTTGTATTTTTTTTGGACTCAATCA	
A3	3-5	GTTTACTGCACTTTTTTTTTCCAACTTGAATTTTTTTTTACTATCCCATTTTTTTTTCGTCTATGGTT	
B3	3-6	ACTCGCAGCACTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGCAGGTGTC	
C3	4-1	TTTTTTTTTTTTTTTTTTTCACGTGGGCATTTTTTTTTTGAGGGATAACTTTTTTTTTTTTTTTTTT	
D3	4-2	CGAGTCCGCGTTTTTTTTTAGGTCCGAATCTTTTTTTTTGGGCCCTTCTATTTTTTTTTAGTAACCGAT	
E3	4-3	CGCGCCAACGTTTTTTTTTGGTGGAGCTGTTTTTTTTTTAGGCCCGCATTTTTTTTTTGCATCTTGA	
F3	4-4	CCATCGCGCCTTTTTTTTTCTAAGTGTATGTTTTTTTTTAAATTTACGGATTTTTTTTTGCTTACATGC	
G3	4-5	GGTACCGGACTTTTTTTTTCGTGGTCACCGTTTTTTTTTGTGCAGTAAACTTTTTTTTTGTCCTAAACT	
H3	4-6	AGGTAATCTATTTTTTTTTATAGCAGCAGTTTTTTTTTGTGCTGCGAGTTTTTTTTTCTTCAAGTTG	
A4	5-1	ACATAGCGAGTTTTTTTTTTCAAACGGTGTTTTTTTTTCGCGGACTCGTTTTTTTTTATGCCCACGTG	
B4	5-2	ATGGGCGGGCCTTTTTTTTTCGGTCACAAGTTTTTTTTTCGTTGGCGCGTTTTTTTTTGATTCGGACCT	
C4	5-3	CCGGAGCCCTATTTTTTTTTAAGTCCGAGGTTTTTTTTTGGCGCGATGGTTTTTTTTTACAGCTCCACC	
D4	5-4	AAGGATCTGGATTTTTTTTTAGGAAGTTCCTTTTTTTTTGTCCGGTACCTTTTTTTTTCATACACTTAG	
E4	5-5	TTAGGGAAATATTTTTTTTTAAAGGATTGATTTTTTTTTAGATTACCTTTTTTTTTCGGTGACCACG	
F4	5-6	TCAGCGCTTCATTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACTGCTGCTAT	
G4	6-1	TTTTTTTTTTTTTTTTTTTGTATCTGCACATTTTTTTTTACTCGCTATGTTTTTTTTTTTTTTTTTT	
H4	6-2	CCGCATGATCTTTTTTTTTCGCAAGAGCTTTTTTTTTTGGCCCGCCCATTTTTTTTTTCACCGTTTG	
A5	6-3	AGTGCTTATGTTTTTTTTTACCCTAAATTGTTTTTTTTTAGGGCTCCGGTTTTTTTTTACTTGTGACC	
B5	6-4	CGTCAGAAAGTTTTTTTTTATAAAGAGGGCTTTTTTTTTCCAGATCCTTTTTTTTTACCTCGGACT	
C5	6-5	CATACGCTGTTTTTTTTTCCCTAACGTTATTTTTTTTTATTTCCCTAATTTTTTTTTGGAACTTCC	
D5	6-6	GCCAATCCAGTTTTTTTTTGTTTAAAGAGATTTTTTTTTGAAGCGCTGATTTTTTTTTGTCAATCCTT	
E5	7-1	TATTTGGCATCTTTTTTTTTCTGACTATAGTTTTTTTTTGATCATGCGGTTTTTTTTTGTGCAGATAC	
F5	7-2	GTACGCCCTGATTTTTTTTTACCCACCGATTTTTTTTTCATAAGCACTTTTTTTTTAAGCTCTTGCG	
G5	7-3	GTTAAAGGCGTTTTTTTTTCGCGAAATTTTTTTTTCTTTCTGACGTTTTTTTTTCAATTTAGGGT	
H5	7-4	CCTTTGACTTTTTTTTTTCACTGAACATTTTTTTTTACAGCGTATGTTTTTTTTGCCCTCTTTAT	
A6	7-5	GCCCTGACGGGTTTTTTTTTGAGCTGCGGGTTTTTTTTTCTGGATTGGCTTTTTTTTTAACGTTAGGG	
B6	7-6	GACGTTGAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTTTAAAC	
C6	8-1	TTTTTTTTTTTTTTTTTTTACAGAAAGGTCTTTTTTTTTGATGCCAAATATTTTTTTTTTTTTTTTT	
D6	8-2	TGGCGGTTGGTTTTTTTTTATTAATTAGGCTTTTTTTTTTCAGGGCGTACTTTTTTTTTCCTATAGTCA	
E6	8-3	AATCCCTGTGTTTTTTTTTGCTACCGAGGCTTTTTTTTTACGCCTTTAACTTTTTTTTTCATCGGTGGG	
F6	8-4	AACTGAAGCGTTTTTTTTTGCTTGGCCACTTTTTTTTTTAAAGTCAAAGGTTTTTTTTTAATTTCGCGA	
G6	8-5	ACCGTGACGCTTTTTTTTTAACTAAACAATTTTTTTTTCCCGTCAGGGCTTTTTTTTTCTGTTCAGTG	
H6	8-6	GGACTCTATCTTTTTTTTTCCTACGGAACCTTTTTTTTTAATTCAACGTCTTTTTTTTTGCCCGCAGCT	
A7	9-1	GGGACCCTTCATTTTTTTTTACTAACGACCTTTTTTTTTCCAACCGCCATTTTTTTTTGACCTTTCTGT	
B7	9-2	GCCTGATATTGTTTTTTTTTGCAATCACTCTTTTTTTTTCACAGGGATTTTTTTTTTGCCTAATTAAT	
C7	9-3	GGGTACCGACTTTTTTTTTTCCCTTTACGTTTTTTTTTCGCTTCAGTTTTTTTTTGCCTCGGTAGC	
D7	9-4	CTTCCGAGAAGTTTTTTTTTGTCATTTGGATTTTTTTTTGCGTCACGGTTTTTTTTTAGTGGCCAAGC	
E7	9-5	GTCTCAGGCGCTTTTTTTTTCTTGAGAATGTTTTTTTTTGATAGAGTCCTTTTTTTTTATTGTTTAGTT	

F7	9-6	TCGAACACTTCTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTCCGTAGG
G7	10-1	TTTTTTTTTTTTTTTTTTTTCACATAGGCCGTTTTTTTTTTTGAAGGGTCCCTTTTTTTTTTTTTTTTTT
H7	10-2	CCCACCTAGATTTTTTTTTTAGAAGAAAGGGTTTTTTTTTTCAATATCAGGCTTTTTTTTTTTGGTCGTTAG
A8	10-3	TAGAACTGAGTTTTTTTTTTAGACAGGGCTATTTTTTTTTTAGTCGGTACCCTTTTTTTTTTGGAGTGATTG
B8	10-4	TATAGCGCGTTTTTTTTTTTCTGTGGCGCGATTTTTTTTTTCTTCTCGGAAGTTTTTTTTTCCGTAAAGGG
C8	10-5	CTGGCGGTACTTTTTTTTTTCATAAACTCGCTTTTTTTTTTGCGCCTGAGACTTTTTTTTTTTCCAAATGA
D8	10-6	ATTTCCCTGATTTTTTTTTTCCTTGAGGGAGTTTTTTTTTTGAAGTGTTCGATTTTTTTTTTCATTCTCAA
E8	11-1	TCTAGGTGGGTTTTTTTTTCGGCCTATGTG
F8	11-2	CTCAGTTCTATTTTTTTTTCCCTTTCTTCT
G8	11-3	ACGCGCTATATTTTTTTTTTAGCCCTGTCT
H8	11-4	GTACCGCCAGTTTTTTTTTTCGCGCCACAG
A9	11-5	TCAGGGAAATTTTTTTTTTGCGAGTTTATG
B9	11-6	TTTTTTTTTTTTTTTTTTTCTCCCTCAAGG
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m3.1

Well	Name	Sequence
A1	1-1	ATACAACACCGCCAAACACGC
B1	1-2	GGGCGACCGCATACTGTGTAT
C1	1-3	CCAGGTACGATGAGTAGTTGT
D1	1-4	TAATTTGGTACGCGCATTCAA
E1	1-5	GTCCACGGCGGCTAATAAGTT
F1	1-6	TTTTTTTTTTGTTCTCGTCAT
G1	2-1	TTTTTTTTTTGCGTGTTTGGCGATTTGACTAACCTGTGTGAG
H1	2-2	GGTGTTGTATATACACAGTATTCATGATATCTCATAGGGCCT
A2	2-3	GCGGTCGCCCACAACTACTCAGCATTGGGCGGTTGGGCTACC
B2	2-4	TCGTACCTGGTTGAATGCGCGAGGCCTCCGCCTAAGTAGATT
C2	2-5	TACCAAATTAAACTTATTAGCGTGGTTGACGCAATTTCGAGA
D2	2-6	CGCCGTGGACATGACGAGAACATGGGAATGGCTTTTTTTTTT
E2	3-1	GCTGCTATATCCCTGCTTCTCTTAGTCAAATCTTTTTTTTTT
F2	3-2	ACCTTTCTGCAGAAAGTGATCAGATATCATGACTCACACAGG
G2	3-3	CAGGTGGAAGGGCCAAAGAATCCGCCCAATGCAGGCCCTATG
H2	3-4	AGCCAAACTGCTTGCATGATGGGCGGAGGCCTGGTAGCCCAA
A3	3-5	ATACTGGTTTGTTCAGCCGTGGCGTCAACCACAATCTACTTA
B3	3-6	TTTTTTTTTTCGAGTAGTCTGGCCATTCCCATTCTCGAAATT
C3	4-1	TTTTTTTTTTGAGAAGCAGGGACTCACGGATGCTTAGGACCC
D3	4-2	ATATAGCAGCGATCACTTTCTAAGCTCATCCTCATTATCAAT
E3	4-3	GCAGAAAGGTATTCTTTGGCCTTACATGAGCGTGGACCAACT
F3	4-4	CTTCCACCTGCATCATGCAAGGCAAACGCTCGCGTACGACAC
G3	4-5	CAGTTTGGCTCACGGCTGAACAGTTATTTGTACTCGGTATAG
H3	4-6	AAACCAGTATCAGACTACTCGAGCTCCAACCCTTTTTTTTTT
A4	5-1	ACGGCAGGATGATCTGTGATTCATCCGTGAGTTTTTTTTTTT
B4	5-2	TGGCGCCAGCACGCGGTACTTAGGATGAGCTTGGGTCCTAAG
C4	5-3	ACCGACGTTCTTCGACTGCTACGCTCATGTAAATTGATAATG
D4	5-4	AGACAGTGTGCTGACATAATTCGAGCGTTTGCAGTTGGTCCA
E4	5-5	TATCACGTGATGATGTAAACGTACAAATAACTGTGTCGTACG
F4	5-6	TTTTTTTTTTAGCTAGATCACGGGTTGGAGCTCTATACCGAG
G4	6-1	TTTTTTTTTTAATCACAGATCAGTTCCTACTAGGGCACCAGT
H4	6-2	ATCCTGCCGTAAGTACCGCGTGAGCGTGCCAGTCGGACTGGG
A5	6-3	GCTGGCGCCATAGCAGTCGAAAGACAGTATCTCTACCCGTAG
B5	6-4	GAACGTCGGTAATTATGTCAGCGCCCGTGGAGGATGATTCAT
C5	6-5	CACACTGTCTCGTTTACATCAGAATTCCCGGCAAGCGGGCCG
D5	6-6	TCACGTGATAGTGATCTAGCTACAAGCGCTGATTTTTTTTTT
E5	7-1	TTGAACGATAATCAATGGAAGTAGTAGGAACTTTTTTTTTTT
F5	7-2	CCGTTCTGCTGCAACCGCCGGCTGGCACGCTCACTGGTGCCC
G5	7-3	ACTCCGCGTAGATCCAAAGATAGATACTGTCTCCCAGTCCGA
H5	7-4	AATGACCGCTCCACACGCTCACTCCACGGGCGCTACGGGTAG
A6	7-5	CTTCAAGGATCCTATTTCTCCGCCGGGAATTCATGAATCATC
B6	7-6	TTTTTTTTTTCGACTCTCGGATCAGCGCTTGTCGGCCCGCTT
C6	8-1	TTTTTTTTTTCTTCCATTGATATATGCCTAATACTGAACGTT
D6	8-2	TATCGTTCAACCGGCGGTTGCGTGGTACTCTTATACCCTCGC
E6	8-3	AGCAGAACGGATCTTTGGATCAAACGACTCGAATCAAAGGCT
F6	8-4	TACGCGGAGTTGAGCGTGTGGGTCTTGTGTCCTGCTAATATG
G6	8-5	AGCGGTCATTGGAGAAATAGGGTCTATTCTGAACTCTAGTAG
H6	8-6	ATCCTTGAAGTCCGAGAGTCGCGCCGAGCGATTTTTTTTTTT
A7	9-1	CTCATTTACCTACCATAATATATTAGGCATATTTTTTTTTTT
B7	9-2	AATAGTGAGGCACGCTTCATTAAGAGTACCACAACGTTCAGT
C7	9-3	GATATTTAAACGTCCGCTCCCTCGAGTCGTTTGCGAGGGTAT
D7	9-4	CATCCCGGCAGCATAAGAGGAGGACACAAGACAGCCTTTGAT
E7	9-5	ACGCCTACAGGCGCCTTACTGTCAGAATAGACCATATTAGCA

Back to overview

F7	9-6	TTTTTTTTTTAATGCACAACGATCGCTCGGCGCTACTAGAGT
G7	10-1	TTTTTTTTTTATATTATGGTAGGACCGCTGTAACTTTACTAA
H7	10-2	GGTAAATGAGAATGAAGCGTGAGCAGGATGAATTCAAAGTCG
A8	10-3	CCTCACTATTGGGAGCGGACGTCTTCTCATGTTGCTTGTGGG
B8	10-4	TTTAAATATCTCCTCTTATGCCGGCAAACTGAACTGGGCTGC
C8	10-5	TGCCGGGATGCAGTAAGGCGCCGTCCTCCGGTTCACTTACGT
D8	10-6	CTGTAGGCGTCGTTGTGCATTCCTCTAGCATATTTTTTTTTT
E8	11-1	TACAGCGGTCCTTTTTTTTT
F8	11-2	TTCATCCTGCTTTAGTAAAGT
G8	11-3	ACATGAGAAGACGACTTTGAA
H8	11-4	TCAGTTTGCCGCCCACAAGCA
A9	11-5	ACCGGAGGACGGCAGCCCAGT
B9	11-6	TATGCTAGAGGACGTAAGTGA
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m3.1_10T

[Back to overview]

Well	Name	Sequence
A1	1-1	ATACAACACCTTTTTTTTTTGCCAAACACGC
B1	1-2	GGGCGACCGCTTTTTTTTTTATACTGTGTAT
C1	1-3	CCAGGTACGATTTTTTTTTTTGAGTAGTTGT
D1	1-4	TAATTTGGTATTTTTTTTTTCGCGCATTCAA
E1	1-5	GTCCACGGCGTTTTTTTTTTGCTAATAAGTT
F1	1-6	TTTTTTTTTTTTTTTTTTTTGTTCTCGTCAT
G1	2-1	TTTTTTTTTTTTTTTTTTTTGCGTGTTTGGCTTTTTTTTTTGATTTGACTAATTTTTTTTTTCCTGTGTGAG
H1	2-2	GGTGTTGTATTTTTTTTTTTATACACAGTATTTTTTTTTTTTCATGATATCTTTTTTTTTTTCATAGGGCCT
A2	2-3	GCGGTCGCCCTTTTTTTTTTACAACTACTCATTTTTTTTTTGCATTGGGCGGTTTTTTTTTTTGGGCTACC
B2	2-4	TCGTACCTGGTTTTTTTTTTTTGAATGCGCGTTTTTTTTTTAGGCCTCCGCCTTTTTTTTTTTAAGTAGATT
C2	2-5	TACCAAATTATTTTTTTTTTAACTTATTAGCTTTTTTTTTTGTGGTTGACGCTTTTTTTTTTAATTTCGAGA
D2	2-6	CGCCGTGGACTTTTTTTTTTATGACGAGAACTTTTTTTTTTATGGGAATGGCTTTTTTTTTTTTTTTTTTT
E2	3-1	GCTGCTATATTTTTTTTTTCCCTGCTTCTCTTTTTTTTTTTTAGTCAAATCTTTTTTTTTTTTTTTTTTT
F2	3-2	ACCTTTCTGCTTTTTTTTTTAGAAAGTGATCTTTTTTTTTTAGATATCATGATTTTTTTTTTCTCACACAGG
G2	3-3	CAGGTGGAAGTTTTTTTTTTGGCCAAAGAATTTTTTTTTTCCGCCCAATGCTTTTTTTTTTAGGCCCTATG
H2	3-4	AGCCAAACTGTTTTTTTTTTCTTGCATGATGTTTTTTTTTTGGCGGAGGCCTTTTTTTTTTGGTAGCCCAA
A3	3-5	ATACTGGTTTTTTTTTTTTTGTTCAGCCGTGTTTTTTTTTTGCGTCAACCACTTTTTTTTTTAATCTACTTA
B3	3-6	TTTTTTTTTTTTTTTTTTTTCGAGTAGTCTGTTTTTTTTTTGCCATTCCCATTTTTTTTTTTCTCGAAATT
C3	4-1	TTTTTTTTTTTTTTTTTTTTGAGAAGCAGGGTTTTTTTTTTACTCACGGATGTTTTTTTTTTCTTAGGACCC
D3	4-2	ATATAGCAGCTTTTTTTTTTGATCACTTTCTTTTTTTTTTTAAGCTCATCCTTTTTTTTTTTCATTATCAAT
E3	4-3	GCAGAAAGGTTTTTTTTTTTATTCTTTGGCCTTTTTTTTTTTTACATGAGCGTTTTTTTTTTGGACCAACT
F3	4-4	CTTCCACCTGTTTTTTTTTTCATCATGCAAGTTTTTTTTTTGCAAACGCTCGTTTTTTTTTTCGTACGACAC
G3	4-5	CAGTTTGGCTTTTTTTTTTTCACGGCTGAACTTTTTTTTTTAGTTATTTGTATTTTTTTTTTCTCGGTATAG
H3	4-6	AAACCAGTATTTTTTTTTTTCAGACTACTCGTTTTTTTTTTAGCTCCAACCCTTTTTTTTTTTTTTTTTTT
A4	5-1	ACGGCAGGATTTTTTTTTTGATCTGTGATTTTTTTTTTTTCATCCGTGAGTTTTTTTTTTTTTTTTTTTT
B4	5-2	TGGCGCCAGCTTTTTTTTTTACGCGGTACTTTTTTTTTTTTAGGATGAGCTTTTTTTTTTTGGGTCCTAAG
C4	5-3	ACCGACGTTCTTTTTTTTTTTCGACTGCTATTTTTTTTTCGCTCATGTAATTTTTTTTTTATTGATAATG
D4	5-4	AGACAGTGTGTTTTTTTTTTCTGACATAATTTTTTTTTTTCGAGCGTTTGCTTTTTTTTTTAGTTGGTCCA
E4	5-5	TATCACGTGATTTTTTTTTTTGATGTAAACGTTTTTTTTTTTACAAATAACTTTTTTTTTTGTGTCGTACG
F4	5-6	TTTTTTTTTTTTTTTTTTTTAGCTAGATCACTTTTTTTTTTGGGTTGGAGCTTTTTTTTTTCTATACCGAG
G4	6-1	TTTTTTTTTTTTTTTTTTTTAATCACAGATCTTTTTTTTTTAGTTCCTACTATTTTTTTTTGGGCACCAGT
H4	6-2	ATCCTGCCGTTTTTTTTTTTAAGTACCGCGTTTTTTTTTTGAGCGTGCCAGTTTTTTTTTTCGGACTGGG
A5	6-3	GCTGGCGCCATTTTTTTTTTAGCAGTCGAATTTTTTTTTTAGACAGTATCTTTTTTTTTTCTACCCGTAG
B5	6-4	GAACGTCGGTTTTTTTTTTAATTATGTCAGTTTTTTTTTCGCCCGTGGAGTTTTTTTTTGATGATTCAT
C5	6-5	CACACTGTCTTTTTTTTTTCGTTTACATCATTTTTTTTTGAATTCCCGGCTTTTTTTTTAAGCGGGCCG
D5	6-6	TCACGTGATATTTTTTTTTGTGATCTAGCTTTTTTTTTTACAAGCGCTGATTTTTTTTTTTTTTTTTT
E5	7-1	TTGAACGATATTTTTTTTTATCAATGGAAGTTTTTTTTTTAGTAGGAACTTTTTTTTTTTTTTTTTT
F5	7-2	CCGTTCTGCTTTTTTTTTTGCAACCGCCGGTTTTTTTTTCTGGCACGCTCTTTTTTTTTTACTGGTGCCC
G5	7-3	ACTCCGCGTATTTTTTTTTTGATCCAAAGATTTTTTTTTTAGATACTGTCTTTTTTTTTTCCCAGTCCGA
H5	7-4	AATGACCGCTTTTTTTTTTCCACACGCTCATTTTTTTTTCTCCACGGGCGTTTTTTTTTCTACGGGTAG
A6	7-5	CTTCAAGGATTTTTTTTTTCCTATTTCTCCTTTTTTTTTGCCGGGAATTCTTTTTTTTTATGAATCATC
B6	7-6	TTTTTTTTTTTTTTTTTTTCGACTCTCGGATTTTTTTTTTCAGCGCTTGTTTTTTTTTCGGCCCGCTT
C6	8-1	TTTTTTTTTTTTTTTTTTTCTTCCATTGATTTTTTTTTTATATGCCTAATTTTTTTTTTACTGAACGTT
D6	8-2	TATCGTTCAATTTTTTTTTCCGGCGGTTGCTTTTTTTTTGTGGTACTCTTTTTTTTTTATACCCTCGC
E6	8-3	AGCAGAACGGTTTTTTTTTATCTTTGGATCTTTTTTTTTAAACGACTCGATTTTTTTTTATCAAAGGCT
F6	8-4	TACGCGGAGTTTTTTTTTTGAGCGTGTGGTTTTTTTTTGTCTTGTGTCCTTTTTTTTTGCTAATATG
G6	8-5	AGCGGTCATTTTTTTTTTTGGAGAAATAGGTTTTTTTTTGTCTATTCTGATTTTTTTTTACTCTAGTAG
H6	8-6	ATCCTTGAAGTTTTTTTTTTCCGAGAGTCGTTTTTTTTTCGCCGAGCGATTTTTTTTTTTTTTTTTT
A7	9-1	CTCATTTACCTTTTTTTTTTACCATAATATTTTTTTTTTATTAGGCATATTTTTTTTTTTTTTTTTT
B7	9-2	AATAGTGAGGTTTTTTTTTCACGCTTCATTTTTTTTTTAAGAGTACCACTTTTTTTTTAACGTTCAGT
C7	9-3	GATATTTAAATTTTTTTTTCGTCCGCTCCCTTTTTTTTTCGAGTCGTTTTTTTTTTTGCGAGGGTAT
D7	9-4	CATCCCGGCATTTTTTTTTGCATAAGAGGATTTTTTTTTGGACACAAGACTTTTTTTTTAGCCTTTGAT
E7	9-5	ACGCCTACAGTTTTTTTTTGCGCCTTACTGTTTTTTTTTTCAGAATAGACTTTTTTTTTCATATTAGCA

F7	9-6	TTTTTTTTTTTTTTTTTTTTAATGCACAACGTTTTTTTTTTATCGCTCGGCGTTTTTTTTTTCTACTAGAGT
G7	10-1	TTTTTTTTTTTTTTTTTTTTATATTATGGTATTTTTTTTTTGGACCGCTGTATTTTTTTTTTACTTTACTAA
H7	10-2	GGTAAATGAGTTTTTTTTTTAATGAAGCGTGTTTTTTTTTTAGCAGGATGAATTTTTTTTTTTTCAAAGTCG
A8	10-3	CCTCACTATTTTTTTTTTTTGGGAGCGGACGTTTTTTTTTTTCTTCTCATGTTTTTTTTTTTTGCTTGTGGG
B8	10-4	TTTAAATATCTTTTTTTTTTCCTCTTATGCTTTTTTTTTTCGGCAAACTGATTTTTTTTTTACTGGGCTGC
C8	10-5	TGCCGGGATGTTTTTTTTTTCAGTAAGGCGCTTTTTTTTTTCGTCCTCCGGTTTTTTTTTTTCACTTACGT
D8	10-6	CTGTAGGCGTTTTTTTTTTTCGTTGTGCATTTTTTTTTTTTCCTCTAGCATATTTTTTTTTTTTTTTTTT
E8	11-1	TACAGCGGTCCTTTTTTTTTTTTTTTTTT
F8	11-2	TTCATCCTGCTTTTTTTTTTTTTAGTAAAGT
G8	11-3	ACATGAGAAGATTTTTTTTTTCGACTTTGAA
H8	11-4	TCAGTTTGCCGTTTTTTTTTTCCCACAAGCA
A9	11-5	ACCGGAGGACGTTTTTTTTTTGCAGCCCAGT
B9	11-6	TATGCTAGAGGTTTTTTTTTTACGTAAGTGA
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m4.1

Well	Name	Sequence
A1	1-1	ACTAAGCACTTTTTTTTTTT
B1	1-2	TGTATAGTATCCAGCAGCTTA
C1	1-3	CATCGTTACCGAGATTGATGG
D1	1-4	GGACTAGACCGTTAACCAGTT
E1	1-5	AATTCAAGCGTAGCCATCCTC
F1	1-6	TGGAGTTTCACCTGATGTTCG
G1	2-1	AGTGCTTAGTTAAGCTGCTGGGCCTGCTGGATCGGCATGTAG
H1	2-2	ATACTATACACCATCAATCTCAGAAAGACTTTGACGATACTC
A2	2-3	GGTAACGATGAACTGGTTAACTCGCGCGAGCGACCCTCAGTG
B2	2-4	GGTCTAGTCCGAGGATGGCTAACTATTATTTATGGACCGAAA
C2	2-5	CGCTTGAATTCGAACATCAGGGTATGCTCCCTACTGAAATAG
D2	2-6	TGAAACTCCATTTTTTTTTTTCCTCAGCTTTTTTTTTTTTT
E2	3-1	TCCAGCAGGCTTTTTTTTTTTTACCGTTTGTTTTTTTTTTT
F2	3-2	AAGTCTTTCTCTACATGCCGACTTTAACCTAGATGCTCATTC
G2	3-3	GCTCGCGCGAGAGTATCGTCATGCTTAATACGAATCCTGACT
H2	3-4	AAATAATAGTCACTGAGGGTCTTCCCATCAAGTGGTTTGCCA
A3	3-5	GGGAGCATACTTTCGGTCCATTCCCGTACAGAGGTACGAGGT
B3	3-6	AAAGCTGAGGCTATTTCAGTATAGCCATACTCGAAGGTCTTA
C3	4-1	ACAAACGGTAGAATGAGCATCCAGGGCGTGAGCCCTTGAGTT
D3	4-2	TAGGTTAAAGAGTCAGGATTCAGACATAGCGTCCGCGATCAG
E3	4-3	GTATTAAGCATGGCAAACCACGCCAGTATGTAAATCCCGGGC
F3	4-4	TTGATGGGAAACCTCGTACCTCGGCTCGGCCCAGTGGTCAAG
G3	4-5	CTGTACGGGATAAGACCTTCGGTGGTAGCCCACCACTCGCCT
H3	4-6	AGTATGGCTATTTTTTTTTTTCCCGACCACTTTTTTTTTTTT
A4	5-1	TCACGCCCTGTTTTTTTTTTTCCTACACTCATTTTTTTTTTT
B4	5-2	CGCTATGTCTAACTCAAGGGCCAGTTACGTAAATCCGCGCAA
C4	5-3	ACATACTGGCCTGATCGCGGACCATAGACCATCGGACCCGCA
D4	5-4	GGCCGAGCCGGCCCGGGATTTATTCCTGCTGCTCAGATCAGA
E4	5-5	GGGCTACCACCTTGACCACTGCTTAGATTTATGTGTTCGTAC
F4	5-6	AGTGGTCGGGAGGCGAGTGGTATGAGTGGCACATCGCATTTA
G4	6-1	TGAGTGTAGGTTGCGCGGATTGACCCATGTGCGCACGACTCC
H4	6-2	TACGTAACTGTGCGGGTCCGATCCCGTCTGAGTCTATTCATC
A5	6-3	TGGTCTATGGTCTGATCTGAGAGTGCACTTCAAGCAAAGTTG
B5	6-4	CAGCAGGAATGTACGAACACATAGTGACACGGTGCGGAGCGT
C5	6-5	TAAATCTAAGTAAATGCGATGGGCACAACCCTCCACAATGAA
D5	6-6	TGCCACTCATTTTTTTTTTTTATTGCACTTTTTTTTTTTTTT
E5	7-1	CACATGGGTCTTTTTTTTTTTCCTCCGATAGTTTTTTTTTTT
F5	7-2	TCAGACGGGAGGAGTCGTGCGGTTCGCATTACGAGGTAAGTA
G5	7-3	GAAGTGCACTGATGAATAGACAAACTGTTTAGGCTAGGATAT
H5	7-4	CGTGTCACTACAACTTTGCTTATAGGTCCTGGGCCGCCTCCT
A6	7-5	GGGTTGTGCCACGCTCCGCACGATACTTATTCTAGAACTAGC
B6	7-6	AAAGTGCAATTTCATTGTGGAATCCGGTTTCCATTTGTTCTA
C6	8-1	CTATCGGAGGTACTTACCTCGAGAAAGGGCGATTCCGATCGC
D6	8-2	TAATGCGAACATATCCTAGCCACCTTTCAGCATGCAAAGTTC
E6	8-3	TAAACAGTTTAGGAGGCGGCCAGAACTCCACCTGCCACGTGA
F6	8-4	CAGGACCTATGCTAGTTCTAGTAGCTAGTCGTAGAATCTACT
G6	8-5	AATAAGTATCTAGAACAAATGGTGGCTTGTACCCGGAATGTG
H6	8-6	GAAACCGGATTTTTTTTTTTTTCGACCGTGTTTTTTTTTTTT
A7	9-1	CGCCCTTTCTTTTTTTTTTTTATAGAATTCATTTTTTTTTTT
B7	9-2	GCTGAAAGGTGCGATCGGAATGACGTAAACGACAAAGTAAGG
C7	9-3	GTGGAGTTCTGAACTTTGCATAGTGAAATGTTGGAACATTGG
D7	9-4	CGACTAGCTATCACGTGGCAGGTGCACAGAATGAGCGGAAAT
E7	9-5	TACAAGCCACAGTAGATTCTATTTGATCATCGATGCCCGCAG

Back to overview

F7	9-6	ACACGGTCGACACATTCCGGGAACCAAGTCTGTTTAAAGTAC
G7	10-1	TGAATTCTATCCTTACTTTGTTTCGAAAGTAATCCCATTGTC
H7	10-2	CGTTTACGTCCCAATGTTCCACGACTGTGACGACAATTGTCG
A8	10-3	ACATTTCACTATTTCCGCTCAGGCTATGGCATGCAACGATAC
B8	10-4	TTCTGTGCACCTGCGGGCATCCATCCAGTGCCGTATGATACT
C8	10-5	GATGATCAAAGTACTTTAAACTCATCCCTGTTCAACTCTGCA
D8	10-6	AGACTTGGTTTTTTTTTTTTTGCAAGACATCTTTTTTTTTTT
E8	11-1	TACTTTCGAATTTTTTTTTT
F8	11-2	GTCACAGTCGGACAATGGGAT
G8	11-3	TGCCATAGCCCGACAATTGTC
H8	11-4	GCACTGGATGGTATCGTTGCA
A9	11-5	ACAGGGATGAAGTATCATACG
B9	11-6	GATGTCTTGCTGCAGAGTTGA
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m4.1_10T	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	ACTAAGCACTTTTTTTTTTTTTTTTTTTT	
B1	1-2	TGTATAGTATTTTTTTTTTTCCAGCAGCTTA	
C1	1-3	CATCGTTACCTTTTTTTTTTGAGATTGATGG	
D1	1-4	GGACTAGACCTTTTTTTTTTGTTAACCAGTT	
E1	1-5	AATTCAAGCGTTTTTTTTTTTAGCCATCCTC	
F1	1-6	TGGAGTTTCATTTTTTTTTTCCTGATGTTCG	
G1	2-1	AGTGCTTAGTTTTTTTTTTTTAAGCTGCTGGTTTTTTTTTTGCCTGCTGGATTTTTTTTTTTCGGCATGTAG	
H1	2-2	ATACTATACATTTTTTTTTTCCATCAATCTCTTTTTTTTTTAGAAAGACTTTTTTTTTTTTTGACGATACTC	
A2	2-3	GGTAACGATGTTTTTTTTTTAACTGGTTAACTTTTTTTTTTCGCGCGAGCTTTTTTTTTTGACCCTCAGTG	
B2	2-4	GGTCTAGTCCTTTTTTTTTTGAGGATGGCTATTTTTTTTTTACTATTATTTTTTTTTTTTATGGACCGAAA	
C2	2-5	CGCTTGAATTTTTTTTTTTCGAACATCAGGTTTTTTTTTGTATGCTCCCTTTTTTTTTTACTGAAATAG	
D2	2-6	TGAAACTCCATTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTCAGCTTTTTTTTTTTTTTTTTTTTT	
E2	3-1	TCCAGCAGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACCGTTTGTTTTTTTTTTTTTTTTTTT	
F2	3-2	AAGTCTTTCTTTTTTTTTTCTACATGCCGATTTTTTTTTCTTTAACCTATTTTTTTTTTGATGCTCATTC	
G2	3-3	GCTCGCGCGATTTTTTTTTGAGTATCGTCATTTTTTTTTTGCTTAATACTTTTTTTTTGAATCCTGACT	
H2	3-4	AAATAATAGTTTTTTTTTTCACTGAGGGTCTTTTTTTTTTTCCCATCAATTTTTTTTTGTGGTTTGCCA	
A3	3-5	GGGAGCATACTTTTTTTTTTTTCGGTCCATTTTTTTTTTTCCCGTACAGTTTTTTTTTAGGTACGAGGT	
B3	3-6	AAAGCTGAGGTTTTTTTTTCTATTTCAGTATTTTTTTTTTAGCCATACTTTTTTTTTTCGAAGGTCTTA	
C3	4-1	ACAAACGGTATTTTTTTTTGAATGAGCATCTTTTTTTTTCAGGGCGTGATTTTTTTTTGCCCTTGAGTT	
D3	4-2	TAGGTTAAAGTTTTTTTTTAGTCAGGATTCTTTTTTTTTAGACATAGCGTTTTTTTTTCCGCGATCAG	
E3	4-3	GTATTAAGCATTTTTTTTTTGGCAAACCACTTTTTTTTTGCCAGTATGTTTTTTTTTAAATCCCGGGC	
F3	4-4	TTGATGGGAATTTTTTTTTACCTCGTACCTTTTTTTTTCGGCTCGGCCTTTTTTTTCAGTGGTCAAG	
G3	4-5	CTGTACGGGATTTTTTTTTAAGACCTTCGTTTTTTTTGTGGTAGCCCTTTTTTTTTACCACTCGCCT	
H3	4-6	AGTATGGCTATTTTTTTTTTTTTTTTTTTTTTTTTTCCCGACCACTTTTTTTTTTTTTTTTTTT	
A4	5-1	TCACGCCCTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTACACTCATTTTTTTTTTTTTTTTTT	
B4	5-2	CGCTATGTCTTTTTTTTTTAACTCAAGGGCTTTTTTTTTCAGTTACGTATTTTTTTTTAATCCGCGCAA	
C4	5-3	ACATACTGGCTTTTTTTTTCTGATCGCGGATTTTTTTTTCCATAGACCATTTTTTTTTTCGGACCCGCA	
D4	5-4	GGCCGAGCCGTTTTTTTTTGCCCGGGATTTTTTTTTTTTATTCCTGCTGTTTTTTTTTCTCAGATCAGA	
E4	5-5	GGGCTACCACTTTTTTTTTCTTGACCACTGTTTTTTTTTCTTAGATTTATTTTTTTTTTGTGTTCGTAC	
F4	5-6	AGTGGTCGGGTTTTTTTTTAGGCGAGTGGTTTTTTTTTTATGAGTGGCATTTTTTTTTCATCGCATTTA	
G4	6-1	TGAGTGTAGGTTTTTTTTTTGCGCGGATTTTTTTTTTTGACCCATGTGTTTTTTTTTCGCACGACTCC	
H4	6-2	TACGTAACTGTTTTTTTTTTGCGGGTCCGATTTTTTTTTTCCCGTCTGATTTTTTTTTGTCTATTCATC	
A5	6-3	TGGTCTATGGTTTTTTTTTCTGATCTGAGTTTTTTTTTAGTGCACTTCTTTTTTTTTAAGCAAAGTTG	
B5	6-4	CAGCAGGAATTTTTTTTTTGTACGAACACATTTTTTTTTTAGTGACACGTTTTTTTTTGTGCGGAGCGT	
C5	6-5	TAAATCTAAGTTTTTTTTTTAAATGCGATGTTTTTTTTTGGCACAACCCTTTTTTTTTCCACAATGAA	
D5	6-6	TGCCACTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTGCACTTTTTTTTTTTTTTTTTTT	
E5	7-1	CACATGGGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTCCGATAGTTTTTTTTTTTTTTTTTT	
F5	7-2	TCAGACGGGATTTTTTTTTGGAGTCGTGCGTTTTTTTTTGTTCGCATTATTTTTTTTTCGAGGTAAGTA	
G5	7-3	GAAGTGCACTTTTTTTTTTGATGAATAGACTTTTTTTTTAAACTGTTTATTTTTTTTTGGCTAGGATAT	
H5	7-4	CGTGTCACTATTTTTTTTTCAACTTTGCTTTTTTTTTTTTATAGGTCCTGTTTTTTTTTGGCCGCCTCCT	
A6	7-5	GGGTTGTGCCTTTTTTTTTTACGCTCCGCACTTTTTTTTTGATACTTATTTTTTTTTTTCTAGAACTAGC	
B6	7-6	AAAGTGCAATTTTTTTTTTTTCATTGTGGATTTTTTTTTTATCCGGTTTCTTTTTTTTTCATTTGTTCTA	
C6	8-1	CTATCGGAGGTTTTTTTTTTACTTACCTCGTTTTTTTTTAGAAAGGGCGTTTTTTTTTATTCCGATCGC	
D6	8-2	TAATGCGAACTTTTTTTTTATATCCTAGCCTTTTTTTTTACCTTTCAGCTTTTTTTTTATGCAAAGTTC	
E6	8-3	TAAACAGTTTTTTTTTTTTAGGAGGCGGCCTTTTTTTTTAGAACTCCACTTTTTTTTTCTGCCACGTGA	
F6	8-4	CAGGACCTATTTTTTTTTTGCTAGTTCTAGTTTTTTTTTAGCTAGTCGTTTTTTTTTAGAATCTACT	
G6	8-5	AATAAGTATCTTTTTTTTTTAGAACAAATGTTTTTTTTTGTGGCTTGTATTTTTTTTTCCCGGAATGTG	
H6	8-6	GAAACCGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTCGACCGTGTTTTTTTTTTTTTTTTTTT	
A7	9-1	CGCCCTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGAATTCATTTTTTTTTTTTTTTTTT	
B7	9-2	GCTGAAAGGTTTTTTTTTTGCGATCGGAATTTTTTTTTTGACGTAAACGTTTTTTTTTTACAAAGTAAGG	
C7	9-3	GTGGAGTTCTTTTTTTTTTGAACTTTGCATTTTTTTTTTAGTGAAATGTTTTTTTTTTTGGAACATTGG	
D7	9-4	CGACTAGCTATTTTTTTTTTCACGTGGCAGTTTTTTTTTGTGCACAGAATTTTTTTTTGAGCGGAAAT	
E7	9-5	TACAAGCCACTTTTTTTTTAGTAGATTCTATTTTTTTTTTTGATCATCTTTTTTTTTGATGCCCGCAG	

F7	9-6	ACACGGTCGATTTTTTTTTTCACATTCCGGGTTTTTTTTTTAACCAAGTCTTTTTTTTTTTTGTTTAAAGTAC
G7	10-1	TGAATTCTATTTTTTTTTTTCCTTACTTTGTTTTTTTTTTTTTCGAAAGTATTTTTTTTTTATCCCATTGTC
H7	10-2	CGTTTACGTCTTTTTTTTTTCCAATGTTCCATTTTTTTTTTCGACTGTGACTTTTTTTTTTGACAATTGTCG
A8	10-3	ACATTTCACTTTTTTTTTTTATTTCCGCTCATTTTTTTTTTGGCTATGGCATTTTTTTTTTTGCAACGATAC
B8	10-4	TTCTGTGCACTTTTTTTTTTCTGCGGGCATCTTTTTTTTTTCATCCAGTGCTTTTTTTTTTCGTATGATACT
C8	10-5	GATGATCAAATTTTTTTTTGTACTTTAAACTTTTTTTTTTCATCCCTGTTTTTTTTTTTCAACTCTGCA
D8	10-6	AGACTTGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAAGACATCTTTTTTTTTTTTTTTTTTT
E8	11-1	TACTTTCGAATTTTTTTTTTTTTTTTTTT
F8	11-2	GTCACAGTCGTTTTTTTTTGACAATGGGAT
G8	11-3	TGCCATAGCCTTTTTTTTTTCGACAATTGTC
H8	11-4	GCACTGGATGTTTTTTTTTTGTATCGTTGCA
A9	11-5	ACAGGGATGATTTTTTTTTTAGTATCATACG
B9	11-6	GATGTCTTGCTTTTTTTTTTTGCAGAGTTGA
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m14_lowGC

Back to overview

Well	Name	Sequence
A1	1-1	GAAGTACAATTTTTTTTTTTTCTACAGATTC
B1	1-2	ATGATTGTTGATTTTTTTTTTTAACTCTAAA
C1	1-3	CGAAGTAACTATTTTTTTTTTCATAATCGAA
D1	1-4	GATAGAAAGACTTTTTTTTTTTAGTAAATGC
E1	1-5	ATCATTTGTGATTTTTTTTTTACTTATGTGA
F1	1-6	AACTTCTTAGATTTTTTTTTTTTTTTTTTT
G1	2-1	TTTTTTTTTTTTTTTTTTTTAATGGTTCTAGTTTTTTTTTTAATTGTACTTCTTTTTTTTTTTTTTTTTT
H1	2-2	ATACATCTATTTTTTTTTTTTGATACGTTACTTTTTTTTTTTCAACAATCATTTTTTTTTTTGAATCTGTAG
A2	2-3	TACAATCTCATTTTTTTTTTAATAGGTTACATTTTTTTTTTTAGTTACTTCGTTTTTTTTTTTTTAGAGTTA
B2	2-4	ATGTCATAAATTTTTTTTTTGACAGTTCTATTTTTTTTTTTGTCTTTCTATCTTTTTTTTTTTTCGATTATG
C2	2-5	TCAATGAATGTTTTTTTTTTTTTACCGTTATTTTTTTTTTTTCACAAATGATTTTTTTTTTTGCATTTACTA
D2	2-6	CTTACTCTTCTTTTTTTTTTTAGTTTCTTTGTTTTTTTTTTTCTAAGAAGTTTTTTTTTTTTCACATAAGT
E2	3-1	ATTAGATATAGTTTTTTTTTTCATCTAAAGATTTTTTTTTTATAGATGTATTTTTTTTTTTCTAGAACCATT
F2	3-2	TTGCTTATGATTTTTTTTTTAAACCAACAGTTTTTTTTTTGAGATTGTATTTTTTTTTTGTAACGTATCA
G2	3-3	TTTAGTGATATTTTTTTTTTACCATGTTTCTTTTTTTTTTTTATGACATTTTTTTTTTTGTAACCTATT
H2	3-4	AGTAAAGAATCTTTTTTTTTTTATAGTGAATTTTTTTTTCATTCATTGATTTTTTTTTATAGAACTGTC
A3	3-5	CATTTAGGTAGTTTTTTTTTTATTACAGAAGTTTTTTTTTGAAGAGTAAGTTTTTTTTTATAACGGTAAA
B3	3-6	AATTACGTAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAAAGAAACTA
C3	4-1	TTTTTTTTTTTTTTTTTTTTTAACCATAGTTTTTTTTTTCTATATCTAATTTTTTTTTTTTTTTTTT
D3	4-2	AATTGCAGTTTTTTTTTTTAGAATGAACAATTTTTTTTTATCATAAGCAATTTTTTTTTTCTTTAGATG
E3	4-3	ACTAAAGCATTTTTTTTTTATACATATTGGTTTTTTTTTATATCACTAAATTTTTTTTTCTGTTGGTTT
F3	4-4	AAAGTCTTACTTTTTTTTTATTTGCTATGATTTTTTTTTGATTCTTTACTTTTTTTTTTGAAACATGGT
G3	4-5	TTTGCATTAATTTTTTTTTGATCTATACAATTTTTTTTTCTACCTAAATGTTTTTTTTTTTCACTATAA
H3	4-6	CTTGTATTAGTTTTTTTTTGTTGTTATTGGTTTTTTTTTACTACGTAATTTTTTTTTTTCTTCTGTAAT
A4	5-1	TTAGTAAGTGATTTTTTTTTAATCTCTAGTTTTTTTTTTAACTGCAATTTTTTTTTTACTATGGTTAA
B4	5-2	AGTATGATGAATTTTTTTTTTTAGTATAGTTTTTTTTTTATGCTTTAGTTTTTTTTTTTTGTTCATTCT
C4	5-3	TGTTCTAAATCTTTTTTTTTAGTGTACATGTTTTTTTTTGTAAGACTTTTTTTTTTTCCAATATGTAT
D4	5-4	TTAACTGTAACTTTTTTTTTATCATGTAGATTTTTTTTTTTAATGCAAATTTTTTTTTTCATAGCAAAT
E4	5-5	TAAAGTAGCATTTTTTTTTTTATGGTACTTTTTTTTTTTCTAATACAAGTTTTTTTTTTTGTATAGATC
F4	5-6	TGTTAAGAACATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCAATAACAAC
G4	6-1	TTTTTTTTTTTTTTTTTTTTCTACTTCATTTTTTTTTTTTTTCACTTACTAATTTTTTTTTTTTTTTTT
H4	6-2	CAGATTATCTTTTTTTTTTTGTGATCAATTTTTTTTTTTTTTCATCATACTTTTTTTTTTACTAGAGATT
A5	6-3	GACTTTAAGTTTTTTTTTTAATCGTAATGTTTTTTTTTTGATTTAGAACATTTTTTTTTTACTATACTAA
B5	6-4	CTACAAATCTTTTTTTTTTTATGCTAACAAGTTTTTTTTTTGTTACAGTTAATTTTTTTTTCATGTACACT
C5	6-5	AATGTATTTGTTTTTTTTTTGAATTTCTTATTTTTTTTTTTATGCTACTTTATTTTTTTTTTCTACATGAT
D5	6-6	CTCTTGTAATTTTTTTTTTAGGATCATCTTTTTTTTTTTTTGTTCTTAACATTTTTTTTTAAGTACCATA
E5	7-1	AGTACATCAACTTTTTTTTTTAACTTTGAGTTTTTTTTTAGATAATCTGTTTTTTTTTAAATGAAGTAG
F5	7-2	TATGTAATGACTTTTTTTTTTTCTAATTGGTTTTTTTTTACTTAAAGTCTTTTTTTTTAAATTGATCAC
G5	7-3	TATTGAACGATTTTTTTTTTAGATAGTGTATTTTTTTTTAGATTTGTAGTTTTTTTTACATTACGATT
H5	7-4	AAGTTGAGTTTTTTTTTTTGATGATTAACTTTTTTTTTCAAATACATTTTTTTTTTCTTGTTAGCAT
A6	7-5	GAAATGCTTAGTTTTTTTTTATTGAGAAATTTTTTTTTTATTACAAGAGTTTTTTTTTATAAGAAATTC
B6	7-6	ACGTACTATCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGATGATCCT
C6	8-1	TTTTTTTTTTTTTTTTTTTTAGTATAACATTTTTTTTTTTTGTTGATGTACTTTTTTTTTTTTTTTTTT
D6	8-2	GCTGTTTGTATTTTTTTTTTTGTCAATCAATTTTTTTTTTTGTCATTACATATTTTTTTTTCTCAAAGTTA
E6	8-3	GTGATACTATTTTTTTTTTTTGTGATTTCTGTTTTTTTTTTATCGTTCAATATTTTTTTTTCCAATTAGAA
F6	8-4	ACTATGTTAGTTTTTTTTTTTCTATATGTCTTTTTTTTTTTAAACTCAACTTTTTTTTTTTTACACTATCT
G6	8-5	CTATCATTGTTTTTTTTTTTCATTCAACATATTTTTTTTTTCTAAGCATTTCTTTTTTTTTTGTTAATCATC
H6	8-6	ACAGAAACAGTTTTTTTTTTTATCTTTGTGTTTTTTTTTTTTGATAGTACGTTTTTTTTTTTATTTCTCAAT
A7	9-1	AAGTATTACCATTTTTTTTTTTCAAGATCATTTTTTTTTTTTACAAACAGCTTTTTTTTTAATGTTATACT
B7	9-2	ATGTTTGAAGTTTTTTTTTTTTCTTCAAGTTTTTTTTTTTTATAGTATCACTTTTTTTTTTATTGATTGACA
C7	9-3	TACTCAGAATTTTTTTTTTTTTGGTTGTAAATTTTTTTTTTCTAACATAGTTTTTTTTTTCAGAAATCACA
D7	9-4	TCGATGATATTTTTTTTTTTTCGTTGTTTAATTTTTTTTTTACAATGATAGTTTTTTTTTAGACATATAGA
E7	9-5	GCTTGAATTGATTTTTTTTTTAAGTTTGGATTTTTTTTTTCTGTTTCTGTTTTTTTTTTTTATGTTGAATG

F7	9-6	GTAACTTAAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACACAAAGATA
G7	10-1	TTTTTTTTTTTTTTTTTTTTTTGAAATTGGATTTTTTTTTTTGGTAATACTTTTTTTTTTTTTTTTTTTTTT
H7	10-2	TCTTTCATTATTTTTTTTTTTCCTACTATAGTTTTTTTTTTACTTCAAACATTTTTTTTTTTATGATCTTGA
A8	10-3	AATCGTTTGTTTTTTTTTTTCTATGAAATAGTTTTTTTTTTAATTCTGAGTATTTTTTTTTTAACTTGAAGA
B8	10-4	CTTATCGATCTTTTTTTTTTATTAGTTCATCTTTTTTTTTTAATATCATCGATTTTTTTTTTTTTACAACCA
C8	10-5	TACTTATCCATTTTTTTTTTTTGTTACTGTATTTTTTTTTTTCAATTCAAGCTTTTTTTTTTTTAAACAACG
D8	10-6	TAAGTCAGTTTTTTTTTTTATAGGAAGATTTTTTTTTTTTTCCTTAAGTTACTTTTTTTTTTATCCAAACTT
E8	11-1	TAATGAAAGATTTTTTTTTTTCCAATTTCAA
F8	11-2	ACAAACGATTTTTTTTTTTTCTATAGTAGGA
G8	11-3	GATCGATAAGTTTTTTTTTTCTATTTCATAG
H8	11-4	TGGATAAGTATTTTTTTTTTGATGAACTAAT
A9	11-5	AACTGACTTATTTTTTTTTTTACAGTAACAA
B9	11-6	TTTTTTTTTTTTTTTTTTTTAATCTTCCTAT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

		m10	
Well	**Name**	**Sequence**	Back to overview
A1	1-1	AGCCCACTCGGGCGCGGACGG	
B1	1-2	TCAGCGATATTAGGCTGTTAA	
C1	1-3	ATCTCGACGATCGCATGCAGC	
D1	1-4	CAACGCTCCTAGTCATCTTTC	
E1	1-5	GATATAGCACCCGATTCACCT	
F1			
G1	2-1	TTTTTTTTTTTTTTTTTTTTTACTTTCTCTCGCAACTTAGTA	
H1	2-2	TTTTTTTTTTTTTTTTTTTTTCCGTCCGCGCCCGAGTGGGCT	
A2	2-3	TTAACAGAAGACAGGTGATAACCCTGGCACACCTCGATTAAC	
B2	2-4	GAGTTTACCTAATATCGCTGAGCTGCATGCGATCGTCGAGAT	
C2	2-5	GAAAGATGAAGGCGGGCGAGCCGGCTCACTAACGTCGGTTCG	
D2	2-6	TTTAGCAGACTAGGAGCGTTGAGGTGAATCGGGTGCTATATC	
E2	3-1	TTATCACCTGTCTTTAAACTCTACTAAGTTGCGAGGTGCCGA	
F2	3-2	TAGCAATGGATGACCCGGGATCATTCGGATTAGACAGAAAGT	
G2	3-3	GCTCGCCCGCCTTCTGCTAAAGTTAATCGAGGTGTAAATTGT	
H2	3-4	ACGTGTTTGTACGACCGTTGATGTGTCTGTGAGTTGCCAGGG	
A3	3-5	TTTTTTTTTTTTTTTTTTTTTCGAACCGACGTTAGCATAGTC	
B3	3-6	TTTTTTTTTTTTTTTTTTTTTCATTCCCTGTGGTCTGAGCCG	
C3	4-1	TTTTTTTTTTTTTTTTTTTTTGCCCACCCTCCCTTCAAGATC	
D3	4-2	TTTTTTTTTTTTTTTTTTTTTCGGCACGTCTAATCCGAATG	
E3	4-3	ATCCCGGCCATTGAGGTACCGTCGAAGCAGCGACCCAAGCTT	
F3	4-4	TCAATCTGTCATCCATTGCTAACAATTTAACTCACAGACACA	
G3	4-5	TCAACGGCAATGGTCACTACAGTACATGGTTGACAGGTTGGT	
H3	4-6	GGAGCACTCGTACAAACACGTGACTATGGACCACAGGGAATG	
A4	5-1	CGGTACCTCAATGGAGATTGAGATCTTGAAGGGAGTCTGAAG	
B4	5-2	CAGGATCCACGGTAAAGCTATTCCCTCTTCGAACAGGTGGGC	
C4	5-3	TGTAGTGACCATTGGTGCTCCAAGCTTGGGTCGCTAGCTGGT	
D4	5-4	CGAGTGTTTAACGAGCCCTAATCTCGAGTATCCCTGCTTCGA	
E4	5-5	TTTTTTTTTTTTTTTTTTTTTACCAACCTGTCAACTTTAGCG	
F4	5-6	TTTTTTTTTTTTTTTTTTTTTCTCTACGGTGGGTACATGTAC	
G4	6-1	TTTTTTTTTTTTTTTTTTTTTACGGCGAAAGATGCATATACG	
H4	6-2	TTTTTTTTTTTTTTTTTTTTTCTTCAGATGTTCGAAGAGGGA	
A5	6-3	ATAGCTTGAATAGGGCGTTAATCTGGAAGGGATACCCTGACA	
B5	6-4	CGTTAAATACCGTGGATCCTGACCAGCTAGGGATACTCGAGA	
C5	6-5	TTAGGGCAAATTCCTCGAGCAGCCAGAGATCATGTCTCTAGA	
D5	6-6	TCCAGTTTCGTTAAACACTCGCGCTAAATACCCACCGTAGAG	
E5	7-1	TTAACGCCCTATTCTTTAACGCGTATATGCATCTTTAATTGT	
F5	7-2	TGTTACCCGTTATCATCGTATGGTCTACTCGGATTTCGCCGT	
G5	7-3	TGCTCGAGGAATTTAACTGGATGTCAGGGTATCCCAGGTTAA	
H5	7-4	GCGCTTTCGCTTGTGAATTAGACGAGACATCGAGCTTCCAGA	
A6	7-5	TTTTTTTTTTTTTTTTTTTTTTCTAGAGACATGATAAGGCAG	
B6	7-6	TTTTTTTTTTTTTTTTTTTTTATACTGCCGGTGAGCTCTGGC	
C6	8-1	TTTTTTTTTTTTTTTTTTTTTTACTGCCGGAACGCTGCCCT	
D6	8-2	TTTTTTTTTTTTTTTTTTTTTACAATTAAATCCGAGTAGACC	
E6	8-3	ATACGATCGATTTCTTAGCAGGCCAAAGGAGCGTTGGTCACA	
F6	8-4	GCTATTGGATAACGGGTAACATTAACCTGCTCGATGTCTCGT	
G6	8-5	CTAATTCGATATACGGGTTGCTGGCATTATACGAACTTGATT	
H6	8-6	TGGGCCCACAAGCGAAAGCGCCTGCCTTCTCACCGGCAGTAT	
A7	9-1	CTGCTAAGAAATCGCAATAGCAGGGCAGCGTTCCGGCTAAAT	
B7	9-2	TGTCGTGTATGGTGCAAAGACACTGAAGCTGGGCCGCAGTAA	
C7	9-3	GCAACCCGTATATCGGGCCCATGTGACCAACGCTCTTGGGTT	
D7	9-4	GACAAGGTCTAGCGTTACTTGGTACTGTGTGTGTACTTTGGC	
E7	9-5	TTTTTTTTTTTTTTTTTTTTTAATCAAGTTCGTATAGCTCAG	

F7	9-6	TTTTTTTTTTTTTTTTTTTTTTCTACGGACGCTCCAATGCCA
G7	10-1	TTTTTTTTTTTTTTTTTTTTTGGGCTACCGAGGGTCTGGGCC
H7	10-2	TTTTTTTTTTTTTTTTTTTTTATTTAGCGGCCCAGCTTCAGT
A8	10-3	GTCTTTGGGTCCGCAGGGCTCGGAACGCTATGCCGCCCTCTA
B8	10-4	GGTTCATCACCATACACGACAAACCCAATACACACACAGTAC
C8	10-5	CAAGTAATCCGGCGCTCCCGCGCGCACATGGGCATACGCCTG
D8	10-6	TATCGCGCGCTAGACCTTGTCCTGAGCTGGAGCGTCCGTAGA
E8	11-1	GGCCCAGACCCTCGGTAGCCC
F8	11-2	GAGCCCTGCGGACCATGAACC
G8	11-3	TAGAGGGCGGCATAGCGTTCC
H8	11-4	GCGGGAGCGCCGGACGCGATA
A9	11-5	CAGGCGTATGCCCATGTGCGC
B9		
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m10_highGC

[Back to overview]

Well	Name	Sequence
A1	1-1	GCAGACTGGACTCGGCATCCT
B1	1-3	CGGACCCGTAGCGTCCGTGCA
C1	1-5	GGAGGTCCCGCAACGCGCGTT
D1	1-2	CGCCATGGGCTGAGCTCGGGC
E1	1-4	AGGGAGCTGGGACCAGCGTGA
F1	1-6	
G1	2-2	TTTTTTTTTTTTTTTTTTTTTAGGATGCCGAGTCCAGTCTGC
H1	2-4	CGCACAGCTCAGCCCATGGCGTGCACGGACGCTACGGGTCCG
A2	2-6	GGCATGGGGTCCCAGCTCCCTAACGCGCGTTGCGGGACCTCC
B2	2-1	TTTTTTTTTTTTTTTTTTTTTGTGGGAGACCGCGTGGCCGTC
C2	2-3	GCCCGAGCAGGCTACCCACGGGACACGTCGGTGTGGCAGCGA
D2	2-5	TCACGCTCTCCCAGGTCCGCACGACGTCTGGCCACTGCACCC
E2	3-1	CCGTGGGTAGCCTGCTGTGCGGACGGCCACGCGGTTGGGTGA
F2	3-3	TGCGGACCTGGGAGCCATGCCTCGCTGCCACACCGCGCAGGT
G2	3-5	TTTTTTTTTTTTTTTTTTTTTGGGTGCAGTGGCCAGGTGGGT
H2	3-2	GCTGGACCCAGCGCACTGCCCTAGGCAGCTGGCACCTCCCAC
A3	3-4	TCGCTCCGTCTCCGACGCACTCCCGCGGTTTCCCTACGTGTC
B3	3-6	TTTTTTTTTTTTTTTTTTTTTGCCAGAGCCGACCAGACGTCG
C3	4-2	TTTTTTTTTTTTTTTTTTTTTCACCCAGTGCCAGCTGCCTA
D3	4-4	CTGGCGCGCGCTGGGTCCAGCACCTGCGAGGGAAACCGCGGG
E3	4-6	ATCCGGCCGGAGACGGAGCGAACCCACCTGGTCGGCTCTGGC
F3	4-1	TTTTTTTTTTTTTTTTTTTTTAGACGCGTGAGAGCAGCCTCG
G3	4-3	GGGCAGTTCCACGGTGGCACGGTTCCCTCCGGACACCCGCAT
H3	4-5	AGTGCGTCGAGGTCGTGGGCCGCTGTGGAGCCTGCGCGCCTG
A4	5-1	CGTGCCACCGTGGAGCGCCAGCGAGGCTGCTCTCAACGGTGA
B4	5-3	GGCCCACGACCTCGGCCGGATATGCGGGTGTCCGGGGGCACC
C4	5-5	TTTTTTTTTTTTTTTTTTTTTCAGGCGCGCAGGCTTGGTCGC
D4	5-2	TCACCTCGGAGCCACTCGGTCCTGGGCGAAGGACCCGCGTCT
E4	5-4	CTCGTGCTCCTGCGGTCACGGGCCTGGTGCCTGCAAGGGAAC
F4	5-6	TTTTTTTTTTTTTTTTTTTTTGCCCGTCGCGTGCCCCACAGC
G4	6-2	TTTTTTTTTTTTTTTTTTTTTCACCGTGGTCCTTCGCCCAG
H4	6-4	TTCGGGATGGCTCCGAGGTGAGGTGCCCTGCAGGCACCAGGC
A5	6-6	CTCCTGGCGCAGGAGCACGAGGCGACCAGGCACGCGACGGGC
B5	6-1	TTTTTTTTTTTTTTTTTTTTTCCTCCGCGTAGCAGCTCTGCG
C5	6-3	GACCGAGTGCACCGAGCGGTAGGGCTGTGCAGGGCGCTCGAC
D5	6-5	CCGTGACGACGCCCACACTGCGGGCCATTGCCAGGCGTAGGG
E5	7-1	TACCGCTCGGTGCATCCCGAACGCAGAGCTGCTACTGGTCCA
F5	7-3	GCAGTGTGGGCGTCCCAGGAGGTCGAGCGCCCTGCCCCGTCC
G5	7-5	TTTTTTTTTTTTTTTTTTTTTCCCTACGCCTGGCACTCTCGC
H5	7-2	ACCGTAGGCGTGTGGTGCGCCGCATTGCGGCAAGCGCGGAGG
A6	7-4	GAGGAGGTGGGCTCTCCTCCCTGGCTGCGGAAGGCACAGCCC
B6	7-6	TTTTTTTTTTTTTTTTTTTTTCATCGACCCTGCTGATGGCCC
C6	8-2	TTTTTTTTTTTTTTTTTTTTTGGACCAGCTTGCCGCAATGC
D6	8-4	CTGGCTCCACACGCCTACGGTGGACGGGGCCTTCCGCAGCCA
E6	8-6	GTCGCACGAGCCCACCTCCTCGCGAGAGCAGCAGGGTCGATG
F6	8-1	TTTTTTTTTTTTTTTTTTTTTGGGTTCGTGGCGCGAGTCTCC
G6	8-3	GGCGCACACCAGCCGCCTCCCGGGCGTTGCGAGCCCGCTGCG
H6	8-5	GGGAGGAAGGCCGGGCTAGAGCTCCAGGGCCCGACTGGCCCA
A7	9-1	GGGAGGCGGCTGGTGAGCCAGGGAGACTCGCGCCAAGCGTGC
B7	9-3	CTCTAGCCCGGCCTGTGCGACCGCAGCGGGCTCGCGCGACCG
C7	9-5	TTTTTTTTTTTTTTTTTTTTTTGGGCCAGTCGGGCTGAGCCC
D7	9-2	TGACCGTCGACCGGATCCCGCTCTGACCCGGACGACGAACCC
E7	9-4	ACGGACGTGGGACGACCGCTGGCCGAGACGCCAGCAACGCCC

F7	9-6	TTTTTTTTTTTTTTTTTTTTTCAAGGAGGGCCAAGCCTGGAG
G7	10-2	TTTTTTTTTTTTTTTTTTTTTGCACGCTTCGTCCGGGTCAGA
H7	10-4	CCTCCAGCCGGTCGACGGTCACGGTCGCGCTGGCGTCTCGGC
A8	10-6	CCTGTGGCGTCCCACGTCCGTGGGCTCACTTGGCCCTCCTTG
B8	10-1	TTTTTTTTTTTTTTTTTTTTTCCTGTCGGGTCGCCCTTTGGC
C8	10-3	GCGGGATACCGGCACCCGGTCCGAAGCAGGTCGAGGCAGGCC
D8	10-5	CAGCGGTGTGTCTCGAGCACCGCGATCGGTCGGACAGGGACC
E8	11-2	GACCGGGTGCCGGTCTGGAGG
F8	11-4	GGTGCTCGAGACACCCACAGG
G8	11-6	
H8	11-1	GCCAAAGGGCGACCCGACAGG
A9	11-3	GGCCTGCCTCGACCTGCTTCG
B9	11-5	GGTCCCTGTCCGACCGATCGC
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m4.1_10T_split

Back to overview

Well	Name	Sequence
A1	1-1	ACTAATGCACTTTTTTTTTTTTTTTTTTTTT
B1	1-2	TGTATTAGTATTTTTTTTTTTCCAGCTAGCTTA
C1	1-3	CATCGTTTACCTTTTTTTTTTGAGATTTGATGG
D1	1-4	GGACTTAGACCTTTTTTTTTTGTTAATCCAGTT
E1	1-5	AATTCTAAGCGTTTTTTTTTTAGCCTATCCTC
F1	1-6	TGGAGTTTTCATTTTTTTTTTCCTGATTGTTCG
G1	2-1	AGTGCTTTAGTTTTTTTTTTTTAAGCTTGCTGGTTTTTTTTTTGCCTGTCTGGATTTTTTTTTTTCGGCTATGTAG
H1	2-2	ATACTTATACATTTTTTTTTTCCATCATATCTCTTTTTTTTTTAGAAATGACTTTTTTTTTTTTTGACGTATACTC
A2	2-3	GGTAATCGATGTTTTTTTTTTAACTGGTTTAACTTTTTTTTTTCGCGTCGAGCTTTTTTTTTTGACCCTTCAGTG
B2	2-4	GGTCTTAGTCCTTTTTTTTTTGAGGATTGGCTATTTTTTTTTTACTATTTATTTTTTTTTTTTATGGATCCGAAA
C2	2-5	CGCTTTGAATTTTTTTTTTTCGAACATTCAGGTTTTTTTTTTGTATGTCTCCCTTTTTTTTTTACTGTAAATAG
D2	2-6	TGAAATCTCCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTCATGCTTTTTTTTTTTTTTTTTTTTTTT
E2	3-1	TCCAGTCAGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACCGTTTTGTTTTTTTTTTTTTTTTTTTTT
F2	3-2	AAGTCTTTTCTTTTTTTTTTTCTACATTGCCGATTTTTTTTTTCTTTATACCTATTTTTTTTTTGATGCTTCATTC
G2	3-3	GCTCGTCGCGATTTTTTTTTTGAGTATTCGTCATTTTTTTTTTTGCTTTAATACTTTTTTTTTTGAATCTCTGACT
H2	3-4	AAATATATAGTTTTTTTTTTTCACTGATGGGTCTTTTTTTTTTTTCCCTATCAATTTTTTTTTTGTGGTTTTGCCA
A3	3-5	GGGAGTCATACTTTTTTTTTTTTTTCGGTTCCATTTTTTTTTTTTCCCGTTACAGTTTTTTTTTTAGGTATCGAGGT
B3	3-6	AAAGCTTGAGGTTTTTTTTTTCTATTTTCAGTATTTTTTTTTTTAGCCTATACTTTTTTTTTTTCGAAGTGTCTTA
C3	4-1	ACAAATCGGTATTTTTTTTTTGAATGATGCATCTTTTTTTTTTCAGGGTCGTGATTTTTTTTTTGCCCTTTGAGTT
D3	4-2	TAGGTTTAAAGTTTTTTTTTTAGTCAGTGATTCTTTTTTTTTTAGACATTAGCGTTTTTTTTTTTCCGCTGATCAG
E3	4-3	GTATTTAAGCATTTTTTTTTTTGGCAATACCACTTTTTTTTTTGCCAGTTATGTTTTTTTTTTTAAATCTCCGGGC
F3	4-4	TTGATTGGGAATTTTTTTTTACCTCGTTACCTTTTTTTTTTTCGGCTTCGGCCTTTTTTTTTTCAGTGTGTCAAG
G3	4-5	CTGTATCGGGATTTTTTTTTTAAGACTCTTCGTTTTTTTTTTGTGGTTAGCCCTTTTTTTTTTACCACTTCGCCT
H3	4-6	AGTATTGGCTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCGATCCACTTTTTTTTTTTTTTTTTTTTTT
A4	5-1	TCACGTCCCTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTACTACTCATTTTTTTTTTTTTTTTTTTT
B4	5-2	CGCTATTGTCTTTTTTTTTTTAACTCATAGGGCTTTTTTTTTTCAGTTTACGTATTTTTTTTTTAATCCTGCGCAA
C4	5-3	ACATATCTGGCTTTTTTTTTTCTGATCTGCGGATTTTTTTTTTCCATATGACCATTTTTTTTTTTCGGATCCCGCA
D4	5-4	GGCCGTAGCCGTTTTTTTTTTGCCCGGTGATTTTTTTTTTTTTTATTCCTTGCTGTTTTTTTTTTCTCAGTATCAGA
E4	5-5	GGGCTTACCACTTTTTTTTTTCTTGACTCACTGTTTTTTTTTTCTTAGTATTTATTTTTTTTTTTGTGTTTCGTAC
F4	5-6	AGTGGTTCGGGTTTTTTTTTTAGGCGATGTGGTTTTTTTTTTTATGAGTTGGCATTTTTTTTTTCATCGTCATTTA
G4	6-1	TGAGTTGTAGGTTTTTTTTTTTGCGCTGGATTTTTTTTTTTGACCCTATGTGTTTTTTTTTTCGCACTGACTCC
H4	6-2	TACGTTAACTGTTTTTTTTTTGCGGGTTCCGATTTTTTTTTTCCCGTTCTGATTTTTTTTTGTCTATTTCATC
A5	6-3	TGGTCTTATGGTTTTTTTTTTCTGATTCTGAGTTTTTTTTTAGTGCTACTTCTTTTTTTTTAAGCATAAGTTG
B5	6-4	CAGCATGGAATTTTTTTTTTGTACGATACACATTTTTTTTTTAGTGTACACGTTTTTTTTTGTGCGTGAGCGT
C5	6-5	TAAATTCTAAGTTTTTTTTTTAAATGTCGATGTTTTTTTTTGGCACTAACCCTTTTTTTTTTCCACTAATGAA
D5	6-6	TGCCATCTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTGCTACTTTTTTTTTTTTTTTTTTTTTT
E5	7-1	CACATTGGGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTCCTGATAGTTTTTTTTTTTTTTTTTTTT
F5	7-2	TCAGATCGGGATTTTTTTTTGGAGTCTGTGCGTTTTTTTTTGTTCGTCATTATTTTTTTTTCGAGGTTAAGTA
G5	7-3	GAAGTTGCACTTTTTTTTTTGATGAATTAGACTTTTTTTTTAAACTTGTTTATTTTTTTTTGGCTATGGATAT
H5	7-4	CGTGTTCACTATTTTTTTTTCAACTTTGCTTTTTTTTTTTTATAGGTTCCTGTTTTTTTTTGGCCGTCCTCCT
A6	7-5	GGGTTTGTGCCTTTTTTTTTACGCTCTCGCACTTTTTTTTTGATACTTTATTTTTTTTTTCTAGATACTAGC
B6	7-6	AAAGTTGCAATTTTTTTTTTTCATTTGTGGATTTTTTTTTATCCGTGTTTCTTTTTTTTTCATTTTGTTCTA
C6	8-1	CTATCTGGAGGTTTTTTTTTTACTTATCCTCGTTTTTTTTTAGAAATGGGCGTTTTTTTTTATTCCTGATCGC
D6	8-2	TAATGTCGAACTTTTTTTTTATATCCTTAGCCTTTTTTTTTACCTTTTCAGCTTTTTTTTTATGCATAAGTTC
E6	8-3	TAAACTAGTTTTTTTTTTTTAGGAGGTCGGCCTTTTTTTTTAGAACTTCCACTTTTTTTTTCTGCCTACGTGA
F6	8-4	CAGGATCCTATTTTTTTTTTGCTAGTTTCTAGTTTTTTTTTTAGCTTAGTCGTTTTTTTTTAGAATTCTACT
G6	8-5	AATAATGTATCTTTTTTTTTTAGAACTAAATGTTTTTTTTTGTGGCTTTGTATTTTTTTTTCCCGGTAATGTG
H6	8-6	GAAACTCGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGACTCGTGTTTTTTTTTTTTTTTTTTTTT
A7	9-1	CGCCCTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAGATATTCATTTTTTTTTTTTTTTTTTTT
B7	9-2	GCTGATAAGGTTTTTTTTTTGCGATCTGGAATTTTTTTTTTGACGTTAAACGTTTTTTTTTTACAAATGTAAGG
C7	9-3	GTGGATGTTCTTTTTTTTTTGAACTTTTGCATTTTTTTTTTTAGTGATAATGTTTTTTTTTTTGGAATCATTGG
D7	9-4	CGACTTAGCTATTTTTTTTTTCACGTTGGCAGTTTTTTTTTGTGCATCAGAATTTTTTTTTTGAGCTGGAAAT
E7	9-5	TACAATGCCACTTTTTTTTTTAGTAGATTTCTATTTTTTTTTTTTTGATTCATCTTTTTTTTTTGATGCTCCGCAG

F7	9-6	ACACGTGTCGATTTTTTTTTTCACATTTCCGGGTTTTTTTTTTAACCATAGTCTTTTTTTTTTTTGTTTATAAGTAC
G7	10-1	TGAATTTCTATTTTTTTTTTTCCTTACTTTTGTTTTTTTTTTTTTCGATAAGTATTTTTTTTTTATCCCTATTGTC
H7	10-2	CGTTTTACGTCTTTTTTTTTTCCAATGTTTCCATTTTTTTTTTCGACTTGTGACTTTTTTTTTTGACAATTTGTCG
A8	10-3	ACATTTTCACTTTTTTTTTTTATTTCCTGCTCATTTTTTTTTTGGCTATTGGCATTTTTTTTTTTGCAATCGATAC
B8	10-4	TTCTGTTGCACTTTTTTTTTTCTGCGGTGCATCTTTTTTTTTTCATCCTAGTGCTTTTTTTTTTCGTATTGATACT
C8	10-5	GATGATTCAAATTTTTTTTTGTACTTTTAAACTTTTTTTTTTCATCTCCTGTTTTTTTTTTTCAACTTCTGCA
D8	10-6	AGACTTTGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCAAGTACATCTTTTTTTTTTTTTTTTTTTT
E8	11-1	TACTTTTCGAATTTTTTTTTTTTTTTTTTT
F8	11-2	GTCACTAGTCGTTTTTTTTTGACAATTGGGAT
G8	11-3	TGCCATTAGCCTTTTTTTTTTCGACAATTTGTC
H8	11-4	GCACTTGGATGTTTTTTTTTTGTATCGTTTGCA
A9	11-5	ACAGGTGATGATTTTTTTTTTAGTATCTATACG
B9	11-6	GATGTTCTTGCTTTTTTTTTTTGCAGATGTTGA
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		

m1_10A

Well	Name	Sequence
A1	1-1	GCCGGTGTCATAAAAAAAAAAAGGACCAGAG
B1	1-2	GCCTCAACGGCTAAAAAAAAAATTAGCACGT
C1	1-3	AACAGAGAGGTAAAAAAAAAAACTCCAAAGA
D1	1-4	ACTTAGTTACCGAAAAAAAAAAGCTCGTTGA
E1	1-5	GTGTAAAGCTGGAAAAAAAAAACGGTGACGC
F1	1-6	GGTTACAGATACAAAAAAAAAAAAAAAAAA
G1	2-1	AAAAAAAAAAAAAAAAAAAAAAGCCATTGAGCAAAAAAAAAATATGACACCGGCAAAAAAAAAAAAAAAAAA
H1	2-2	GAGACGGCGTCAAAAAAAAAAGTCGGCGAACAAAAAAAAAAAGCCGTTGAGGCAAAAAAAAAACTCTGGTCC
A2	2-3	CTGGGCGGATGAAAAAAAAAATTACAGTGCGAAAAAAAAAATACCTCTCTGTTAAAAAAAAAAACGTGCTAA
B2	2-4	TCCGATTGCTAAAAAAAAAAAGACGCATTGTAAAAAAAAAAACGGTAACTAAGTAAAAAAAAAATCTTTGGAG
C2	2-5	CAACATCTGCAAAAAAAAAAAGCAGCTGTAGAAAAAAAAAACCAGCTTTACACAAAAAAAAAATCAACGAGC
D2	2-6	ATCTGCCGCGGAAAAAAAAAATAGTTGCTGCAAAAAAAAAAGTATCTGTAACCAAAAAAAAAAGCGTCACCG
E2	3-1	CACGGAACGGCAAAAAAAAAAATCGAACGTGAAAAAAAAAAGACGCCGTCTCAAAAAAAAAAGCTCAATGGC
F2	3-2	TCGTCCTAGGCCAAAAAAAAAACTGGACTTCAAAAAAAAAACATCCGCCCAGAAAAAAAAAAGTTCGCCGAC
G2	3-3	TTCCGGATCGACAAAAAAAAAACCTCGCCATAAAAAAAAAAATAGCAATCGGAAAAAAAAAAACGCACTGTAA
H2	3-4	TTACCTAGAAATAAAAAAAAAAACCCGATGAAAAAAAAAAATGCAGATGTTGAAAAAAAAAAACAATGCGTC
A3	3-5	GAAGCTGGCAAGAAAAAAAAAAGTTGCTATAAAAAAAAAAACCGCGGCAGATAAAAAAAAAACTACAGCTGC
B3	3-6	CGGGAAGATGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAGCAACTA
C3	4-1	AAAAAAAAAAAAAAAAAAAAAGGTTTCGAGAAAAAAAAAAAATGCCGTTCCGTGAAAAAAAAAAAAAAAAAA
D3	4-2	GATTAGAGCATAAAAAAAAAAAATCTCTTTCAAAAAAAAAAGGCCTAGGACGAAAAAAAAAAACACGTTCGA
E3	4-3	GCTGAGGTGTGAAAAAAAAAACCGAGAAACAAAAAAAAAAAGTCGATCCGGAAAAAAAAAAAAGAAGTCCAG
F3	4-4	TCTAGGAAACCAAAAAAAAAACGGATATGTGAAAAAAAAAAATTTCTAGGTAAAAAAAAAAAAATGGCGAGG
G3	4-5	CGGCAGTTTAAAAAAAAAAAAGACCTGCTCTAAAAAAAAAACTTGCCAGCTTCAAAAAAAAAATCATCGGGT
H3	4-6	GAACAAATATCAAAAAAAAAATACACCCTATAAAAAAAAAAATCCATCTTCCCGAAAAAAAAAATATAGCAAC
A4	5-1	GGTCGGATCACTAAAAAAAAAACCCGCCAACAAAAAAAAAAAATGCTCTAATCAAAAAAAAAATCTCGAAACC
B4	5-2	GAACTCGTCTCCAAAAAAAAAAGCTCAGGGTAAAAAAAAAACACACCTCAGCAAAAAAAAAAGAAAGAGATT
C4	5-3	CTAATAATAAGCAAAAAAAAAAGTGCCTAGCAAAAAAAAAAGGTTTCCTAGAAAAAAAAAAATGTTTCTCGG
D4	5-4	TGAGCAAAGCAGAAAAAAAAAAACACAAAGGAAAAAAAAAATTAAACTGCCGAAAAAAAAAACACATATCCG
E4	5-5	ACCATCACCCTAAAAAAAAAAACGATTCTCAAAAAAAAAAAGATATTTGTTCAAAAAAAAAAAGAGCAGGTC
F4	5-6	TAGCAAACTCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATAGGGTGTA
G4	6-1	AAAAAAAAAAAAAAAAAAAAAACTAGCTCACCAAAAAAAAAAAAGTGATCCGACCAAAAAAAAAAAAAAAAAA
H4	6-2	ACTTCACTATTAAAAAAAAAATAAGGTGTTGAAAAAAAAAAGGAGACGAGTTCAAAAAAAAAAGTTGGCGGG
A5	6-3	ATTTAGACTAGAAAAAAAAAATCGCCTGGATAAAAAAAAAAGCTTATTATTAGAAAAAAAAAAACCCTGAGC
B5	6-4	CAGAAAGTGAGAAAAAAAAAAGGCCTCAGGTAAAAAAAAAACTGCTTTGCTCAAAAAAAAAAAGCTAGGCAC
C5	6-5	GGTCAGGTCAAAAAAAAAAAACGGTCATCTCAAAAAAAAAATAGGGTGATGGTAAAAAAAAAACCTTTGTGT
D5	6-6	AAAGCTCGGATAAAAAAAAAATAGCGCCCGGAAAAAAAAAACTGAGTTTGCTAAAAAAAAAAATGAGAATCG
E5	7-1	TTGCACGACCGTAAAAAAAAAAATCGTCTCTAAAAAAAAAAAATAGTGAAGTAAAAAAAAAAGGTGAGCTAG
F5	7-2	ACTTACAACGCCAAAAAAAAAATGAAATAAGAAAAAAAAAACTAGTCTAAATAAAAAAAAAACAACACCTTA
G5	7-3	AATAATTACCTCAAAAAAAAAAACATACGCTAAAAAAAAAACTCACTTTCTGAAAAAAAAAAATCCAGGCGA
H5	7-4	CTGGTCATCTCAAAAAAAAAAAGAATGAGAAAAAAAAAAAATTGACCTGACCAAAAAAAAAAACCTGAGGCC
A6	7-5	TAGCGTGAATGGAAAAAAAAAAATGAGACGCAAAAAAAAAAATCCGAGCTTTAAAAAAAAAAGAGATGACCG
B6	7-6	GTCACTCAAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCGGGCGCTA
C6	8-1	AAAAAAAAAAAAAAAAAAAAAGGACATTCCTAAAAAAAAAAAACGGTCGTGCAAAAAAAAAAAAAAAAAAAA
D6	8-2	TGCGAAGGCCGAAAAAAAAAAAAGCTGGCAGAAAAAAAAAAGGCGTTGTAAGTAAAAAAAAAAAGAGACGAT
E6	8-3	TGCAGGCGGGCAAAAAAAAAACAAAGGATAAAAAAAAAAAAGAGGTAATTATTAAAAAAAAAACTTATTTCA
F6	8-4	GCTTCCGTTGCAAAAAAAAAATGATGCCATTAAAAAAAAAAATGAGATGACCAGAAAAAAAAAAAGCGTATGT
G6	8-5	CAGGCGAAATCAAAAAAAAAAAGCGTTGGCTAAAAAAAAAACCATTCACGCTAAAAAAAAAAATTCTCATTC
H6	8-6	AGCGCTGGAGGAAAAAAAAAAGCTCAATGTTAAAAAAAAAAGACTTGAGTGACAAAAAAAAAAGCGTCTCAT
A7	9-1	AATCTCCCACGCAAAAAAAAAAATTGGACCTAAAAAAAAAACGGCCTTCGCAAAAAAAAAAAAGGAATGTCC
B7	9-2	TCAGTGTATACCAAAAAAAAAAGACTGTAAAAAAAAAAAAAGCCCGCCTGCAAAAAAAAAAACTGCCAGCTT
C7	9-3	GCCTTCGCACAGAAAAAAAAAATGGTCTGACAAAAAAAAAAGCAACGGAAGCAAAAAAAAAATTATCCTTTG
D7	9-4	GTCTAGGTATCCAAAAAAAAAACTGCTGGGAAAAAAAAAAAGATTTCGCCTGAAAAAAAAAAAATGGCATCA
E7	9-5	GCCGGAATTTGCAAAAAAAAAATAGCATTTAAAAAAAAAAACCTCCAGCGCTAAAAAAAAAAAGCCAACGCT

Back to overview

F7	9-6	ATTACCTTTATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACATTGAGC
G7	10-1	AAAAAAAAAAAAAAAAAAAAAACTGTCTCGTAAAAAAAAAAAAGCGTGGAGATTAAAAAAAAAAAAAAAAAAAA
H7	10-2	TAGTAAACTCCAAAAAAAAAAAAAGGCTACCCAAAAAAAAAAAGGTATACACTGAAAAAAAAAAAAGGTCCAAT
A8	10-3	TGTAAGTCGATAAAAAAAAAAATAAACCACTGAAAAAAAAAAACTGTGCGAAGGCAAAAAAAAAATTTACAGTC
B8	10-4	CAGAAATATTGAAAAAAAAAAAAACTGTGATTAAAAAAAAAAAGGATACCTAGACAAAAAAAAAAGTCAGACCA
C8	10-5	TGAGAGCTCTGAAAAAAAAAAAATGAATTCGCAAAAAAAAAAAGCAAATTCCGGCAAAAAAAAAATCCCAGCAG
D8	10-6	TTTCCTAGTTGAAAAAAAAAAAAATATCCACGAAAAAAAAAAAAATAAAGGTAATAAAAAAAAAATAAATGCTA
E8	11-1	GGAGTTTACTAAAAAAAAAAAATACGAGACAG
F8	11-2	ATCGACTTACAAAAAAAAAAAAGGGTAGCCTT
G8	11-3	CAATATTTCTGAAAAAAAAAAACAGTGGTTTA
H8	11-4	CAGAGCTCTCAAAAAAAAAAAAAATCACAGTT
A9	11-5	CAACTAGGAAAAAAAAAAAAAAGCGAATTCAT
B9	11-6	AAAAAAAAAAAAAAAAAAAAAACGTGGATATT
C9		
D9		
E9		
F9		
G9		
H9		
A10		
B10		
C10		
D10		
E10		
F10		
G10		
H10		
A11		
B11		
C11		
D11		
E11		
F11		
G11		
H11		
A12		
B12		
C12		
D12		
E12		
F12		
G12		
H12		