

Table S1. Sequences of Y-motifs. Each strand was named Y-*N-i_D*, where ‘*N*’ represents the sequence for which motif, ‘*i*’ is a strand identification number, and ‘*D*’ is a fluorescent molecular dye. Complementary sequences for the same motif are shown in the same color.

Name	Sequence (5'→3')
YA ₁	GCTCGAGCCAGTGAGGACGGAAGTTTGTCTAGCATCGCACC
YA ₂	GCTCGAGCCAAACCACGCCTGTCCATTACTTCCGTCCTCACTG
YA ₃	GCTCGAGCGGTGCGATGCTACGACTTTGGACAGGCGTGGTTG
YA ₂ _FAM	[FAM]-AAACCACGCCTGTCCATTACTTCCGTCCTCACTG
YB ₁	CTCGCGAGAAAGGAACTCTCCGCGTTGACAAAGCCGACACGT
YB ₂	CTCGCGAGGCCTCTGTGTGCGATCTTCGCGGAGAGTTCCTTT
YB ₃	CTCGCGAGACGTGTCGGCTTTGTCTTGATGCGACACAGAGGC
YB ₂ _Alexa405	[Alexa405]-GCCTCTGTGTGCGATCTTCGCGGAGAGTTCCTTT
YC ₁	CGCTAGCGTGGTTACACTGAGCTTTATGAACCTAGTGTGGC
YC ₂	CGCTAGCGGCCACACTAGGTTCAATTCGCTTGATACGATGTC
YC ₃	CGCTAGCGGACATCGTATCAAGCGTTAGCTCAGTGTAACCAG
YC ₂ _Cy3	[Cy3]-GCCACACTAGGTTCAATTCGCTTGATACGATGTC

Table S2. T_m of the Y-motif stem part with neighbouring sequences. The T_m of each stem part was estimated using the DINAMelt server (<http://www.unafold.org/hybrid2.php>) with 0.35 M Na^+ and 5 μM DNA. The T_m of each stem was higher than the reaction temperature (50°C) and the observation temperature (60°C). Since Y-motif structures are stabilized by the hybridization of three stems cooperatively, the Y-motif structures are sufficiently stable at the experimental temperatures.

Y-motif	Stem sequences	T_m [°C]
YA	5'- CAGTGAGGACGGAAGT-3' 3'- GTCACTCCTGCCTTCA-5'	67
	5'- GTCGTAGCATCGCACCC-3' 3'-CAGCATCGTAGCGTGG-5'	67.8
	5'-CAACCACGCCTGTCCA-3' 3'-GTTGGTGCGGACAGGT-5'	72.7
YB	5'- AAAGGAACTCTCCGCG-3' 3'- TTTCTTGAGAGGCGC-5'	69.6
	5'- GACAAAGCCGACACGT-3' 3'-CTGTTTCGGCTGTGCA-5'	69.5
	5'-GCCTCTGTGTCGCATC-3' 3'-CGGAGACACAGCGTAG-5'	68.9
YC	5'- CTGGTTACACTGAGCT-3' 3'- GACCAATGTGACTCGA-5'	63
	5'- ATGAACCTAGTGTGGC-3' 3'-TACTTGGATCACACCG-5'	64.2
	5'-CGCTTGATACGATGTC-3' 3'-GCGAACTATGCTACAG-5'	62.5

Table S3. Sequences of 6-branched, 4-branched, and linear AB-linkers. Strands for linkers were named *sLMN-i_e*, where ‘*s*’ represents the structure type (*s* = 6, 4, or 2; 2 is for linear), ‘*L*’ is short for ‘Linker’, ‘*M*’ and ‘*N*’ represent for which two motifs (*M* and *N* = A, B, or C), ‘*i*’ is a strand identification number (*i* = 1, 2, ..., 6), and ‘*e*’ is the number of nucleotides for toehold. Complementary sequences for the same linker are shown in the same color.

Name	Sequence (5'→3')
6LAB-1	GCTCGAGC CGGCGCTGTAAATTTGCGTT CCCCGGG CCGGT
6LAB-2	GCTCGAGC CAGACGTC ACTCTCCA ACTTCGCAAATTTACAGCGCCG
6LAB-3	GCTCGAGC TCTCCTGTCCTGGGTCCCTCATTGTTGGAGAGTGACGTCTG
6LAB-4	CTCGCGAG GCTGGACTAACGGAACGGTTTGAGGGACCCAGG
6LAB-5	CTCGCGAG CTCAGAGAGGTGACAGCATTCCGTTCCGTTAGTCCAGC
6LAB-6	CTCGCGAG CGGCGCGACCGGCCCGGGGTTTGCTGTACCTCTCTGAG
6LAC-1	GCTCGAGC CACGACCGACGCCACGCCGAGTTTGGTGGCTTATACAGACGT
6LAC-2	GCTCGAGC ACGTCTGTATAAGCCACCTTTCGGTTCTCTCCAAAGCA
6LAC-3_11	GCTCGAGC TGCTTTGGAGAGAACCGATTAAATGGATT
6LAC-3_8	GCTCGAGC TGCTTTGGAGAGAACCGATTAAATGGATTTTTT
6LAC-3_5	GCTCGAGC TGCTTTGGAGAGAACCGATTAAATGGATTTTTTGGA
6LAC-4	CGCTAGCG CCTGCTCCAAAAATCCATTTTTCGCAAATTGATGGCTGC
6LAC-5	CGCTAGCG GCAGCCATCAATTTTCGCATTTCGGTCACATAACTGGAGA
6LAC-6	CGCTAGCG TCTCCAGTTATGTGACCGTTACTCGGCGTGG
6LAB-1_DNA	GCTCGAGC CGGCGCTGTAAATTTGCGTT CATCACTTGGGACCATGG
6LAB-2_DNA	GCTCGAGC CAGACGTC ACTCTCCA ACTTCGCAAATTTACAGCGCCG
6LAB-3_DNA	GCTCGAGC TAGGACCATCAGTGCTGGCATACTGACTTTGTTGGAGAGTGAC GTCTG
6LAB-4_DNA	CTCGCGAG GCTGGACTAACGGAACGGTTAGTCAGGTATGCCAGCAC

6LAB- CTCGCGAGCTCAGAGAGGTGACAGCA~~TTCCGTTCCGTTAGTCCAGC~~
5_DNA

6LAB- CTCGCGAGTGACTGCATAACCCATGGTCCCAAGTGATGTTTGCTGTCACCTCTC
6_DNA TGAG

4LAB-1 GCTCGAGCCGGCGCTGTAAATTTGCGTTCATCACTTGGGACCATGG

4LAB-2 GCTCGAGCTCAGGACCATCACAGACGTCACCTCTCCAAC~~TTCGCAAATTTACAGCGCCG~~

4LAB-3 CTCGCGAGGCTGGACTAACGGAACGGTTGTTGGAGAGTGACGTCTG

4LAB-4 CTCGCGAGTGACTGCATAACCCATGGTCCCAAGTGATGTTCCGTTCCGTTAGT
CCAGC

2LAB-1 GCTCGAGCGTGCTGGCATACTGACT

2LAB-2 CTCGCGAGAGTCAGGTATGCCAGCAC

Table S4. Sequences of microRNAs.

Name	Sequence (5'→3')
hsa-miR-1307-3p	ACUCGGCGUGGCGUCGGUCGUG
hsa-miR-1204	AAUGGAUUUUUGGAGCAGG
hsa-miR-6875-5p	UGAGGGACCCAGGACAGGAGA
hsa-miR-4634	CGGCGCGACCGGCCCGGGG

Table S5. T_m of the stem part with neighbouring sequences as the toehold of 14, 11, 8 nucleotides. These parameters were obtained using the DINAMelt server with 0.35 M Na⁺ and 5 μ M DNA.

Sequence pair	T_m [°C]
5'-AATGGATT-3' 3'-TTACCTAA-5'	28.9
5'-AATGGATTTTT-3' 3'-TTACCTAAAAA-5'	42.5
5'-AATGGATTTTTGGA-3' 3'-TTACCTAAAAACCT-5'	55.7

Table S6. Strand concentration for the characterization of AB-linker for AB-mixed-droplet to achieve the logical operations.

	DNA strand name	Final concentration
AB-mixed-droplet with linear linker	Y-motif-A	5 μ M
	YA ₂ _FAM	0.5 μ M
	Y-motif-B	5 μ M
	YB ₂ _Alexa405	0.5 μ M
	Linear AB-linker	5 μ M
AB-mixed-droplet with 4-branched linker	Y-motif-A	5 μ M
	YA ₂ _FAM	0.5 μ M
	Y-motif-B	5 μ M
	YB ₂ _Alexa405	0.5 μ M
	4-branched AB-linker	2.5 μ M
AB-mixed-droplet with 6-branched linker	Y-motif-A	5 μ M
	YA ₂ _FAM	0.5 μ M
	Y-motif-B	5 μ M
	YB ₂ _Alexa405	0.5 μ M
	6-branched AB-linker	1.67 μ M

Table S7. Strand concentration for the characterization of the logical operation by AB-mixed-droplets.

	DNA strand name	Final concentration
AB-mixed-droplet fabrication	Y-motif-A	5 μ M
	YA ₂ _FAM	0.5 μ M
	Y-motif-B	5 μ M
	YB ₂ _Alexa405	0.5 μ M
	6-branched AB-linker	3.3 μ M
Reaction with Input DNAs	Input-DNA-1	4 μ M
	Input-DNA-2	4 μ M

Table S8. Strand concentration for the AND operation based on AC-mixed-droplets accepting two miRNA inputs miRNA-1 and miRNA-2.

	DNA/RNA strand name	Final concentration
AC-mixed-droplet fabrication	Y-motif-A	5 μ M
	YA ₂ _FAM	0.5 μ M
	Y-motif-C	5 μ M
	YC ₂ _Cy3	0.5 μ M
	6-branched AC-linker-miR_ <i>n</i>	3.3 μ M
Reaction with Input miRNAs	miRNA-1	4 μ M
	miRNA-2	4 μ M

Table S9. Strand concentration for the logic operation ($\text{miRNA-3} \wedge \neg \text{miRNA-4}$) based on AB-mixed-droplets accepting two miRNA inputs miRNA-3 and miRNA-4.

	DNA/RNA strand name	Final concentration
AB-mixed-droplet fabrication	Y-motif-A	5 μM
	YA ₂ _FAM	0.5 μM
	Y-motif-B	5 μM
	YB ₂ _Alexa405	0.5 μM
	6-branched AB-linker-miR	3.3 μM
Characterization of NOT gate miRNA-4* DNA for input (1,1)	miRNA-3	4 μM
	miRNA-4	4 μM
	miRNA-4* DNA	0 μM / 2 μM / 4 μM / 6 μM / 8 μM
Reactions with 4 types of input patterns	miRNA-3	4 μM
	miRNA-4	4 μM
	miRNA-4* DNA	3.6 μM

Table S10. Strand concentration for the logic operation ($\text{miRNA-3} \wedge \neg \text{miRNA-4}$) based on AB-mixed-droplets accepting two miRNA inputs miRNA-3 and miRNA-4.

	DNA/RNA strand name	Final concentration
ABC-mixed-droplet fabrication	Y-motif-A	5 μM
	YA ₂ _FAM	0.5 μM
	Y-motif-B	5 μM
	YB ₂ _Alexa405	0.5 μM
	Y-motif-C	5 μM
	YC ₂ _Cy3	0.5 μM
	6-branched AB-linker-miR	3.3 μM
	6-branched AC-linker-miR ₁₄	3.3 μM
Reactions with 16 types of input patterns	miRNA-1	3 μM
	miRNA-2	3 μM
	miRNA-3	3 μM
	miRNA-4	3 μM
	miRNA-4* DNA	2.7 μM