Supporting Information:

Rapid and accurate quantification of paramylon produced from *Euglena gracilis* using an ssDNA aptamer

Jee Young Kim[a,1], Jeong-Joo Oh[a,1], Da Hee Kim[a], Jaewon Park[b], Hyun Soo Kim[c], and Yoon-E Choi[a,*]

[a]Division of Environmental Science & Ecological Engineering, Korea University, Seoul
02841, Korea

[b]Department of Electrical and Electronic Engineering, Southern University of Science and Technology, Shenzhen 518055, China

[c]Korea Institute of Machinery and Materials, Daegu Research Center for Medical Devices and Rehabilitation, Daegu 42994, Korea

*Corresponding author

Tel: +82 2 3290 3042, Fax: +82 2 3290 3040,

E-mail address: yechoi@korea.ac.kr

Table S1

Name	Sequences
ssDNA random library	5’- CGA CTG ACG CCT CCA AGC - N_{60} - GCA TGC ATC GCT ACG TG - 3’
Forward primer	5’ – CGA CTG ACG CCT CCA AGC – 3’
Reverse primer	5’ – CAC GTA GCG ATG CAT GC – 3’
Modified forward primer	5’ – (FAM) CGA CTG ACG CCT CCA AGC – 3’
Modified reverse primer	5’ – (Biotin) CAC GTA GCG ATG CAT GC – 3’

Table S2

Group	Sequence name	Central region 5′-3′	Gibbs free energy (kcal/mol)	Number of clones
1	Par-1	GACAGCGCAGGAGCGTATGGAGACCGGCTCTTGTCTGAATATGTATTCCGAGAATTATTT	-16.39	1
	Par-7	**GACAGCGCAGGAGCGTATGGAGACCGGCTCTTGTCTGAATATGTATTCCAAGAATTATTT**	-16.57	4
	Par-9	GACAGCGCAGGAGCGTATGGAGACCGACTCTTGTCTGAATATGTATTCCAAGAATTATTT	-16.68	1
	Par-13	GACAGCGCAGGAGCGTATGGAAACCGGCTCTTGTCTGAATATGTATTCCAAGAATTATTT	-18.03	1
	Par-15	**GACAGCGCAGGAGCGTATGGAGACCGGCTCTCGTCTGAATATGTATTCCAAGAATTATTT**	-16.7	2
	Par-21	GACAGCGCAGGAGCGTATGGAGACCGGCTCTTGTCTGAATACGTATTCCAAGAATTATTT	-16.78	1
2	Par-6	TTCACATCTGGTGTGCTGTCTACTTTGGACGATTTTTTCCGCTGTCTTGACTTGCCACCA	-13.23	1
	Par-11	TAACCCTGCTATCAAATTGCGCTGGAGGCATTTTCAAAAGATAGTCAAGAGTTGTACTAT	-14.63	1
	Par-12	TCCAAGGTGAATCGGGACTGAATTTTCACTTTTTGCGAATCTCTTTGACTGTTCAATATC	-11.17	1
	Par-22	**CACCCTGCATTAGGGTGGCGCTGTTGCGAGTTTATGCTCATAATTGTACTTACTGGACAG**	-20.26	1
	Par-23	AGTACTTTTTCCATTACTTTACTTGCCAGGTTAACGTCTTATTCAGTGTTATTTGTTTGG	-8.55	1
3	Par-3	CTTGCTTGGAGGGTAAAGGTACGTGGAATTTCTACCGCGGGGGTCTAATTGGGACTGGTG	-21.41	1
	Par-8	CTTACGGGGTCTATACTCAGAGTAGGAACAGCGATGAACCGGTCGCGAGCTGGGAGCAAG	-16.87	1
	Par-14	TTCACGGGTGATCGGAAAAAGCTAGAGCTGGCGTCGCCAGCGTGGGGGGCGGGGCGGCGC	-23.79	1
	Par-20	**GCCCGGGTACTGGGCGCTAAAGAGGGCAAACAGGGCGGGAGGAGCGGCGCAGCGGGGGGG**	-25.32	1
4	Par-2	GGGTCGTAAGAAATTAACGCTTTTGATAACTTAAGAGAGCTATGTCTACTTGAGCACTTA	-13.34	1
	Par-5	GACATGAGATGATAATCATATAAGAGACCTAGTTCGGTTAGAGATATGTCAATCTACTTA	-13.93	1
	Par-10	CCATCTTGGCTAAGACAACCTTACACTGAAAAACCATAAGGTGACCTGATTCCAATCTAT	-13.09	1
	Par-18	**GGCAGGCGTGAATTCTATCCATCTAGGAGTATATCAGGACCCATGTATTGCAGTAGCAAT**	-23.08	1
	Par-24	GTAGCTTGGAGATTACAGCGTTACCGGATGTATAATCGTTCTTCGGTAATTTCACAATTT	-20.99	1
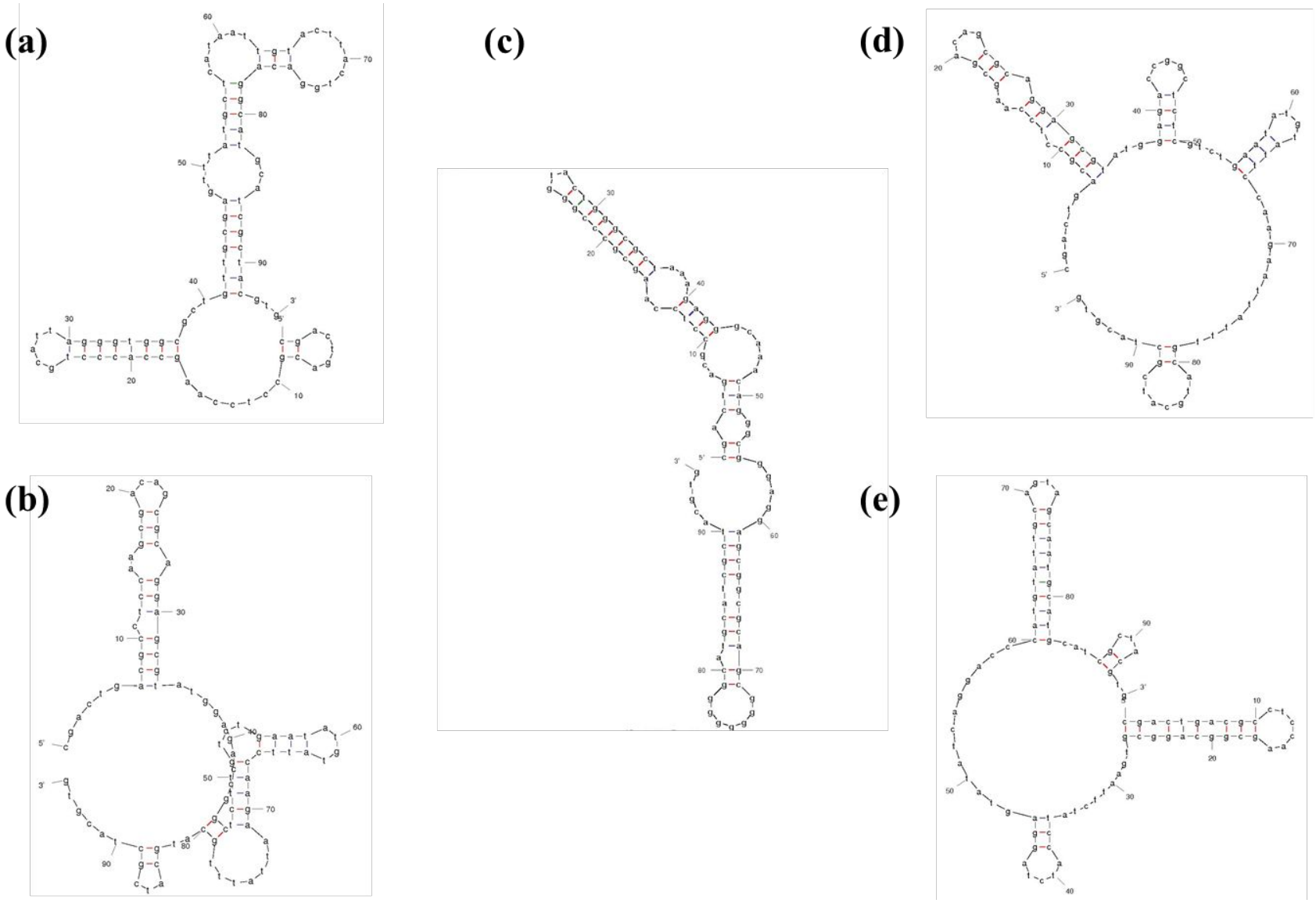
Figure S1