



Supplementary Material

10.1302/2046-3758.109.BJR-2020-0421.R2

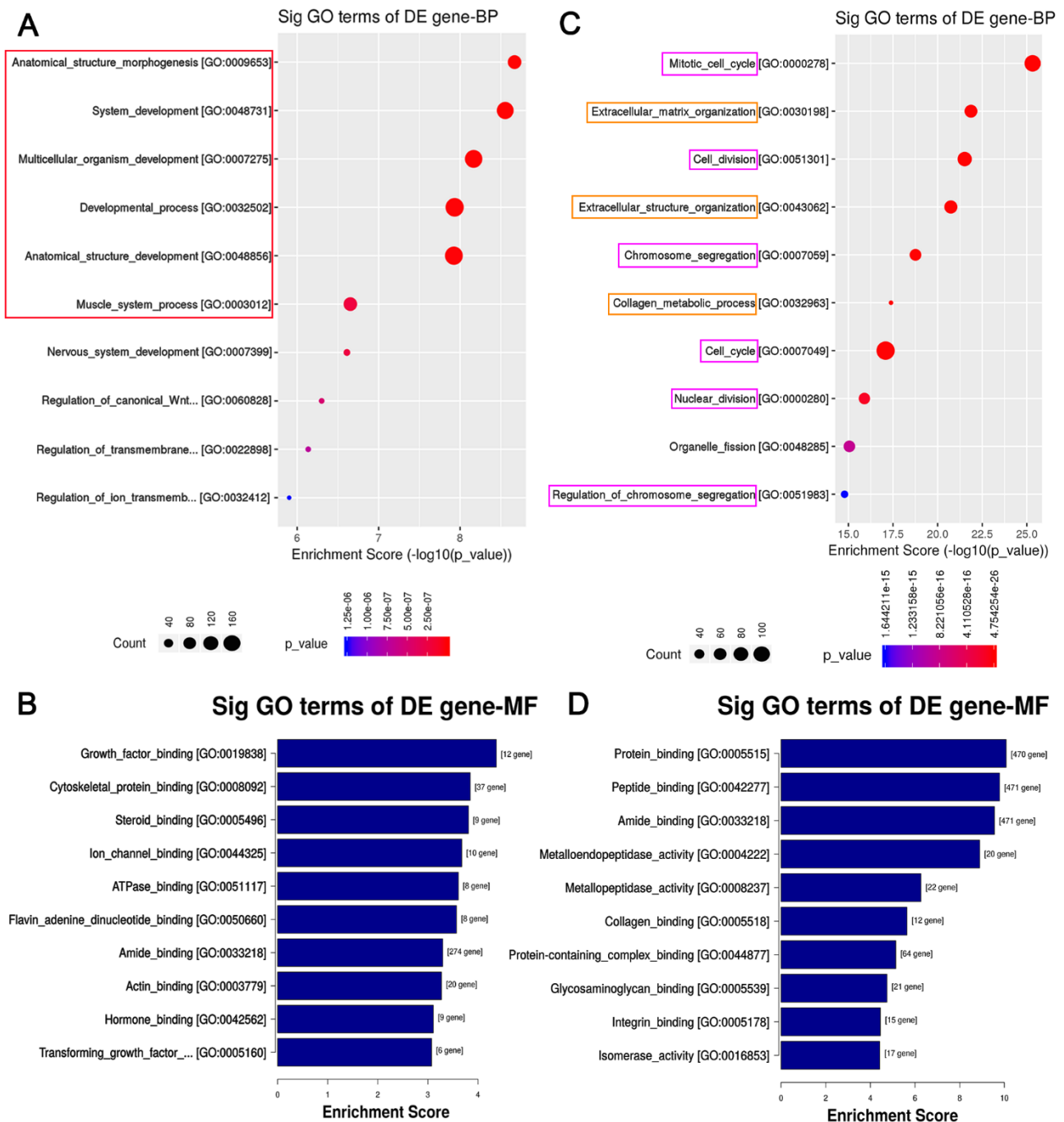


Fig a. Gene ontology (GO) analysis of the differentially expressed genes. The upregulated genes (developmental dysplasia of the hip (DDH) vs control group) were subjected to GO analysis with two

categories: a) biological processes (BP), and b) molecular functions (MF). The results are shown as bubble and column diagrams. The biological processes and molecular functions were ranked according to the enrichment score. Similar methods were also adopted for the downregulated genes with two categories: c) BPs, and d) MFs. DE, dysregulated genes.

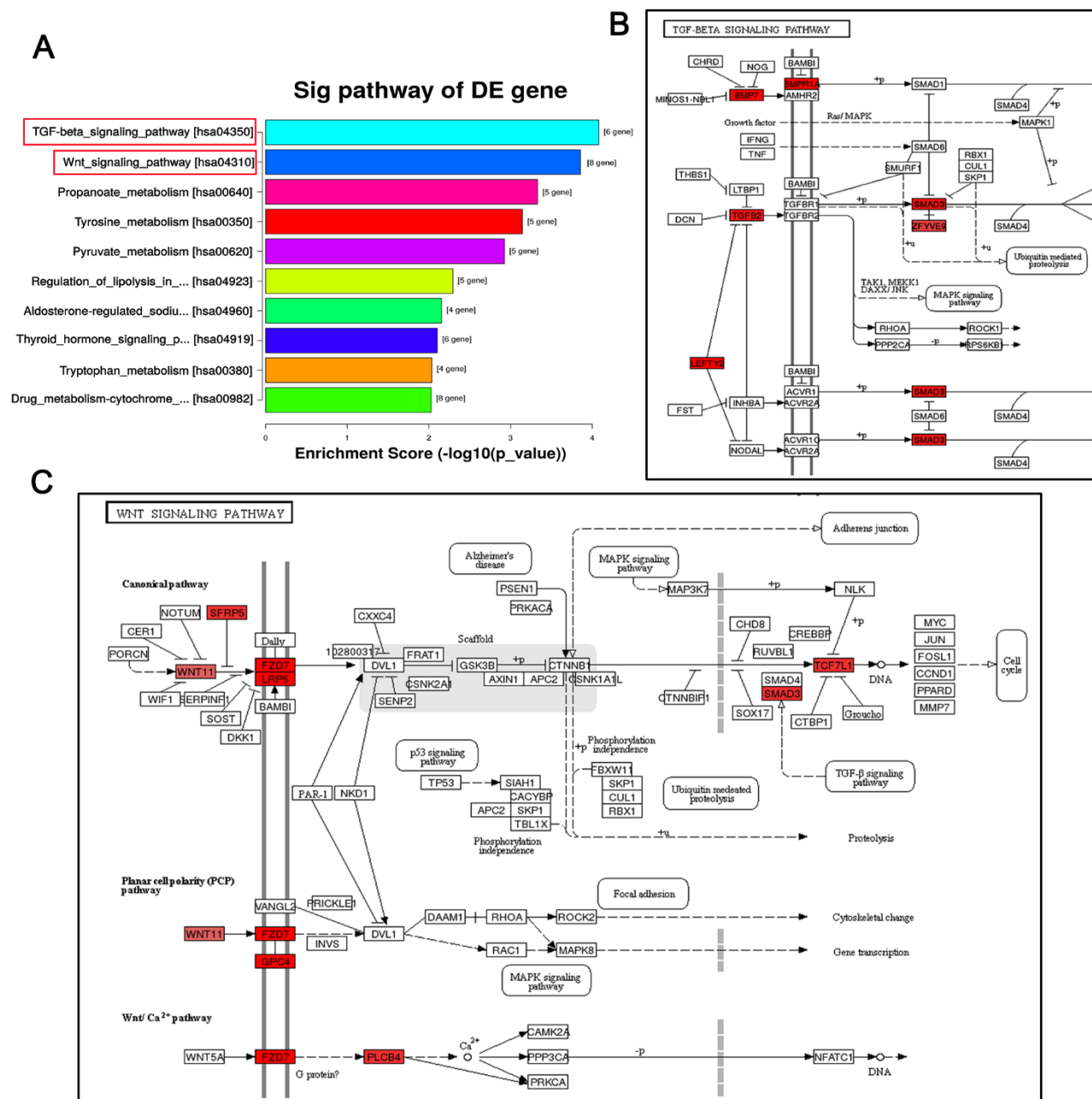


Fig b. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of the upregulated genes (developmental dysplasia of the hip (DDH) vs control group), which were subjected to KEGG analysis. a) The results are shown as a column diagram and ranked by the enrichment score. b) Graphical KEGG pathway maps showed the dendrogram of the genes in tumour growth factor beta (TGF- β), and c) Wnt signalling pathways. Genes upregulated in the pathway are highlighted in red. DE, dysregulated gene.

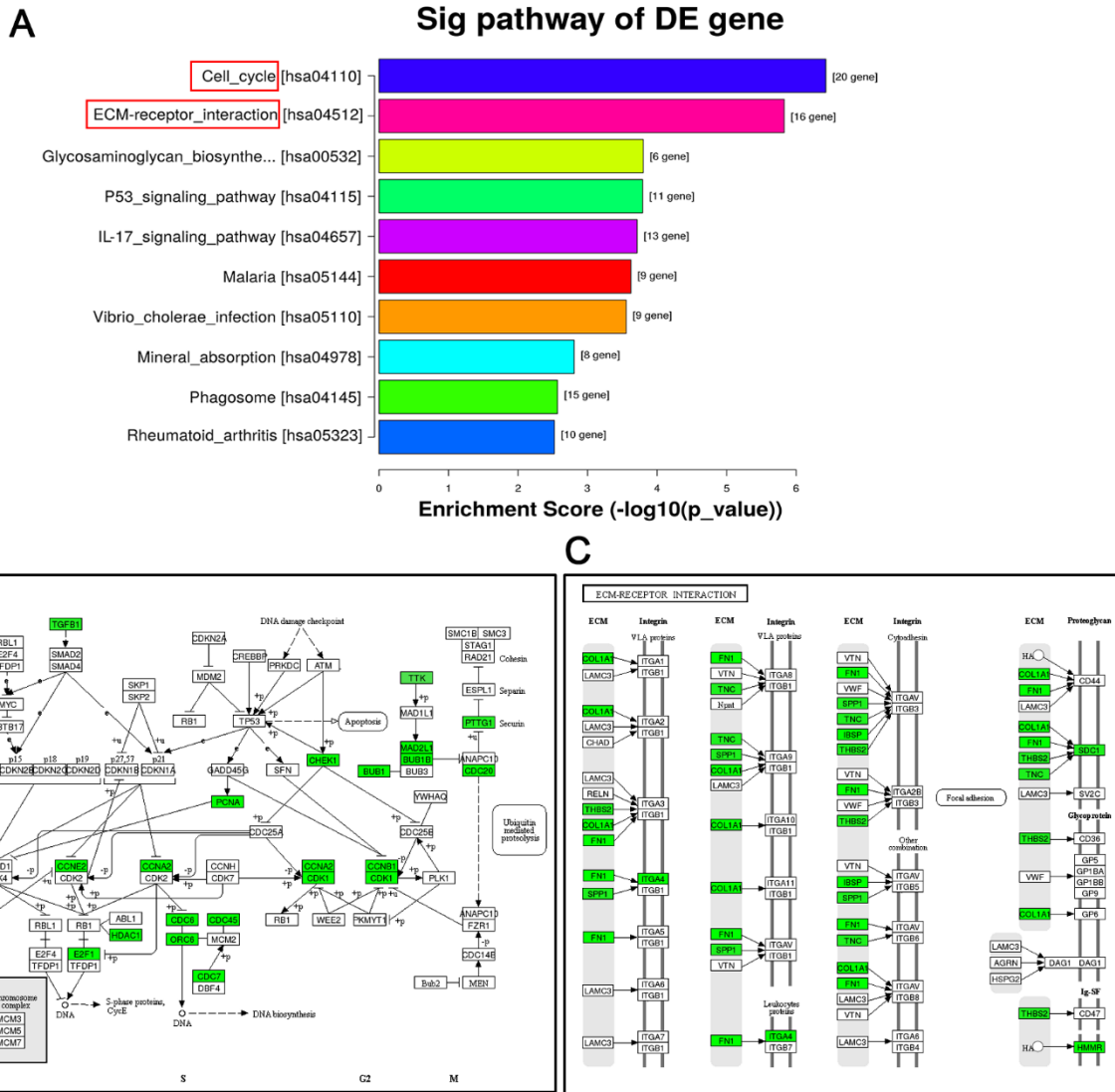


Fig c. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of the downregulated genes. The downregulated genes (developmental dysplasia of the hip (DDH) vs control group) were subjected to KEGG analysis. The results are shown as: a) a column diagram and ranked by the enrichment score; b) graphical KEGG pathway maps which show the dendrogram of the genes in the cell cycle; and c) extracellular matrix (ECM)-receptor interaction signalling pathways. Genes downregulated in the pathway are highlighted in green.

RNA QC EUK

1. RNA Quantification and Quality Assurance by NanoDrop ND-1000

Sample ID	OD260/280 Ratio	OD260/230 Ratio	Conc. (ng/μl)	Volume (μl)	Quantity (ng)	QC Purity Pass or Fail
Case1	1.90	1.85	263.54	15	3953.10	Pass
Case2	1.92	1.98	315.46	30	9463.80	Pass
Case3	1.85	2.18	266.36	15	3995.40	Pass
Case4	2.05	2.08	410.59	15	6158.85	Pass
Case5	1.81	2.03	314.95	20	6299.00	Pass
Case6	1.88	1.81	445.39	20	8907.80	Pass
Ctl1	1.91	2.05	518.83	15	7782.45	Pass
Ctl2	1.94	1.81	429.41	30	12882.30	Pass
Ctl3	1.86	1.80	277.02	15	4155.30	Pass
Ctl4	1.91	2.24	708.60	15	10629.00	Pass
Ctl5	1.96	2.13	515.90	15	7738.50	Pass
Ctl6	1.93	2.27	729.10	15	10936.50	Pass

*For spectrophotometer, the O.D. A260 /A280 ratio should be close to 2.0 for pure RNA (ratios between 1.8 and 2.1 are acceptable). The O.D. A260/A230 ratio should be more than 1.8.

Quality Assessment of Sequencing Library

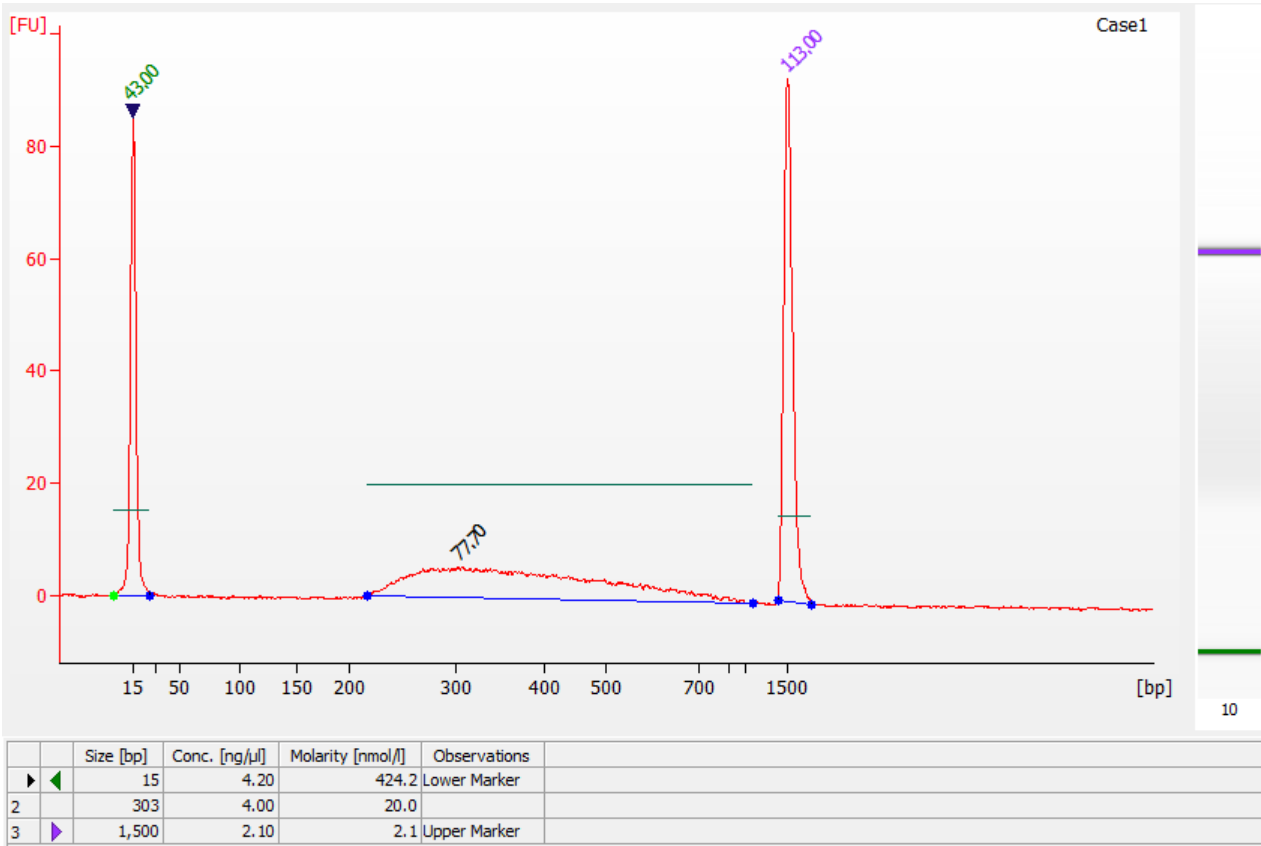
Sequencing library was determined by Agilent 2100 Bioanalyzer using the Agilent DNA 1000 chip kit (Agilent, part # 5067-1504)

Sample Name	Size (bp)	Conc. (ng/μl)	Conc. (nmol/L)	Volume (μl)	Total Amount (ng)
Case1	303	4	20	20	80
Case2	307	5.49	27.1	20	109.8
Case3	299	5.75	29.2	20	115
Case4	456	5.48	18.2	20	109.6
Case5	304	8.49	42.4	20	169.8
Case6	310	7.26	35.4	20	145.2
Ctl1	297	6.21	31.7	20	124.2
Ctl2	355	3.97	16.9	20	79.4
Ctl3	280	4.16	22.5	20	83.2
Ctl4	297	5.98	30.5	20	119.6
Ctl5	280	3.55	19.2	20	71
Ctl6	313	4.23	20.5	20	84.6

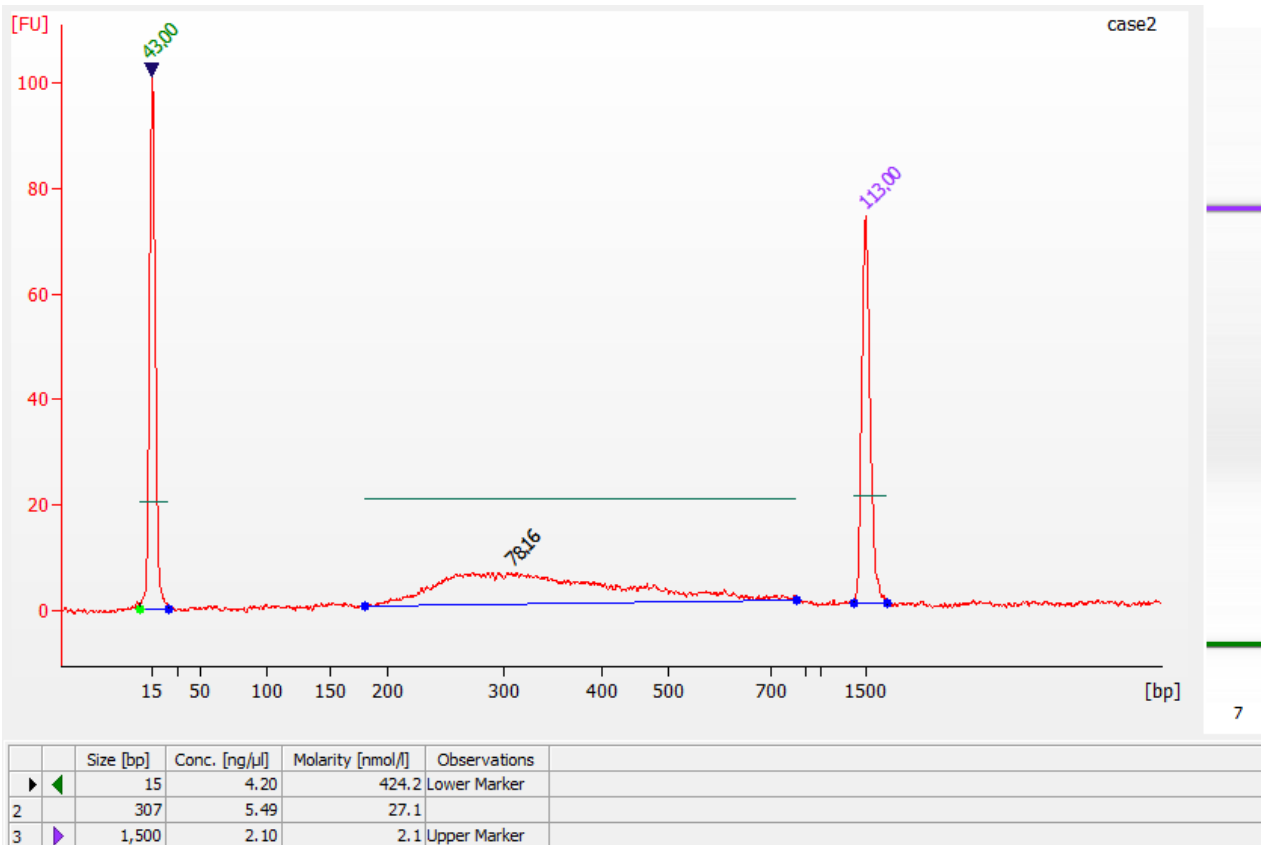
**The libraries were adjusted to 10nM before cluster generation.

Quality control analysis on an Agilent 2100 Bioanalyzer

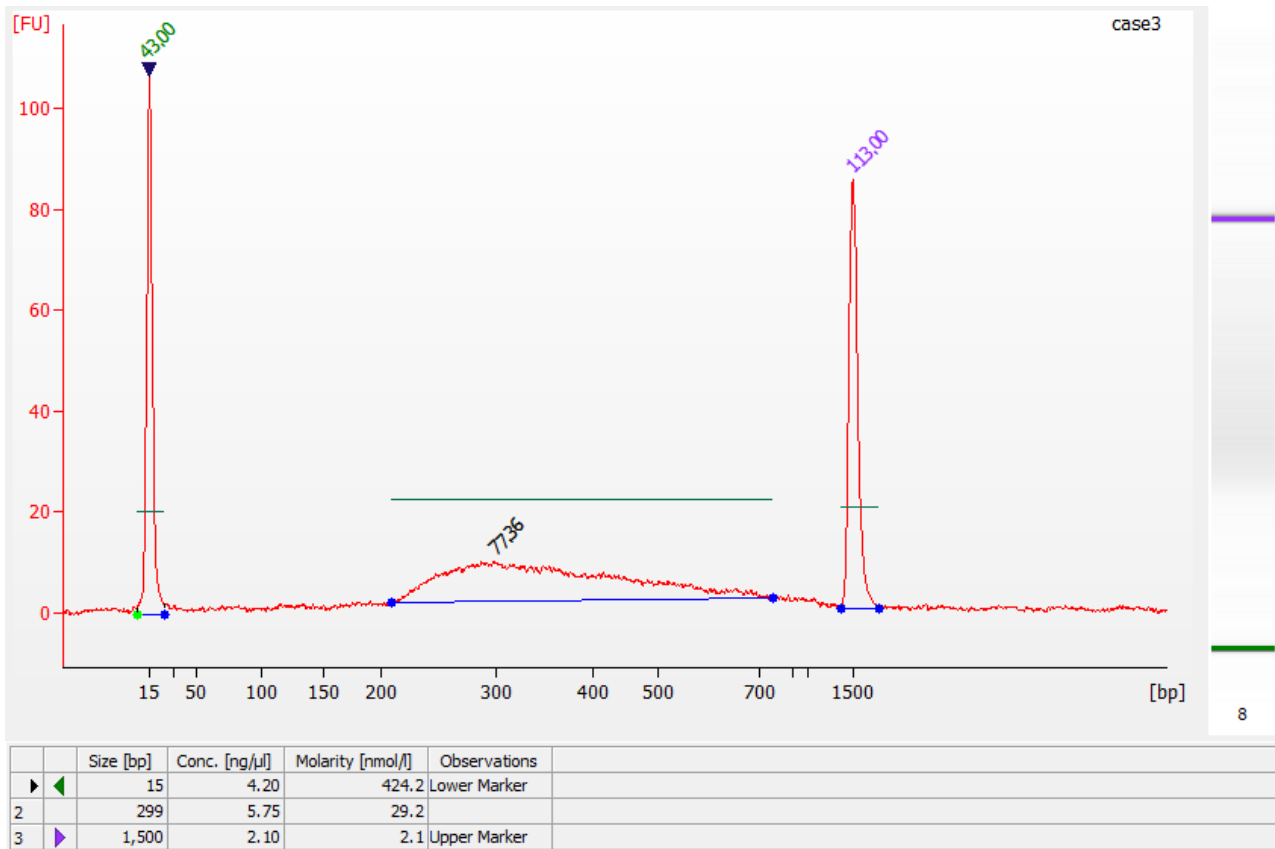
Sample Case1:



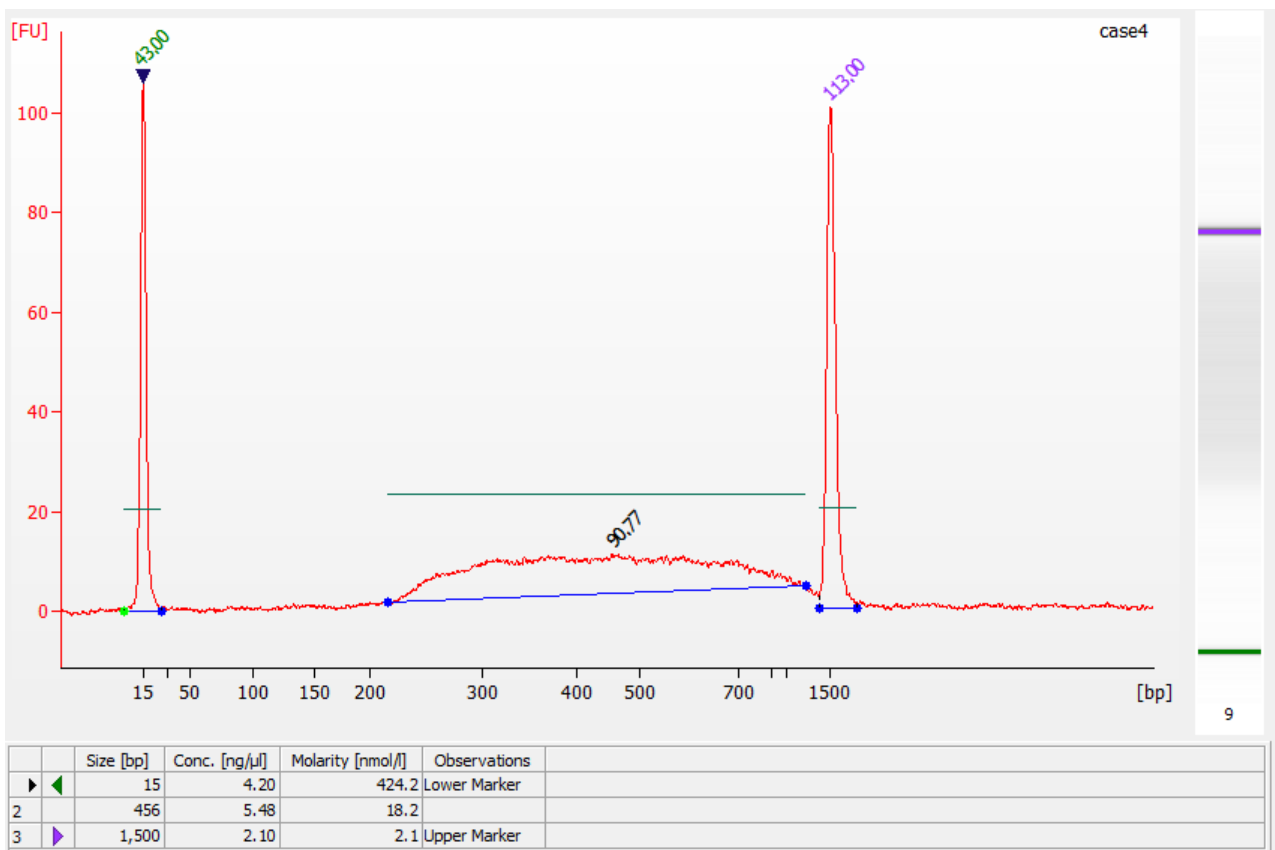
Sample Case2:



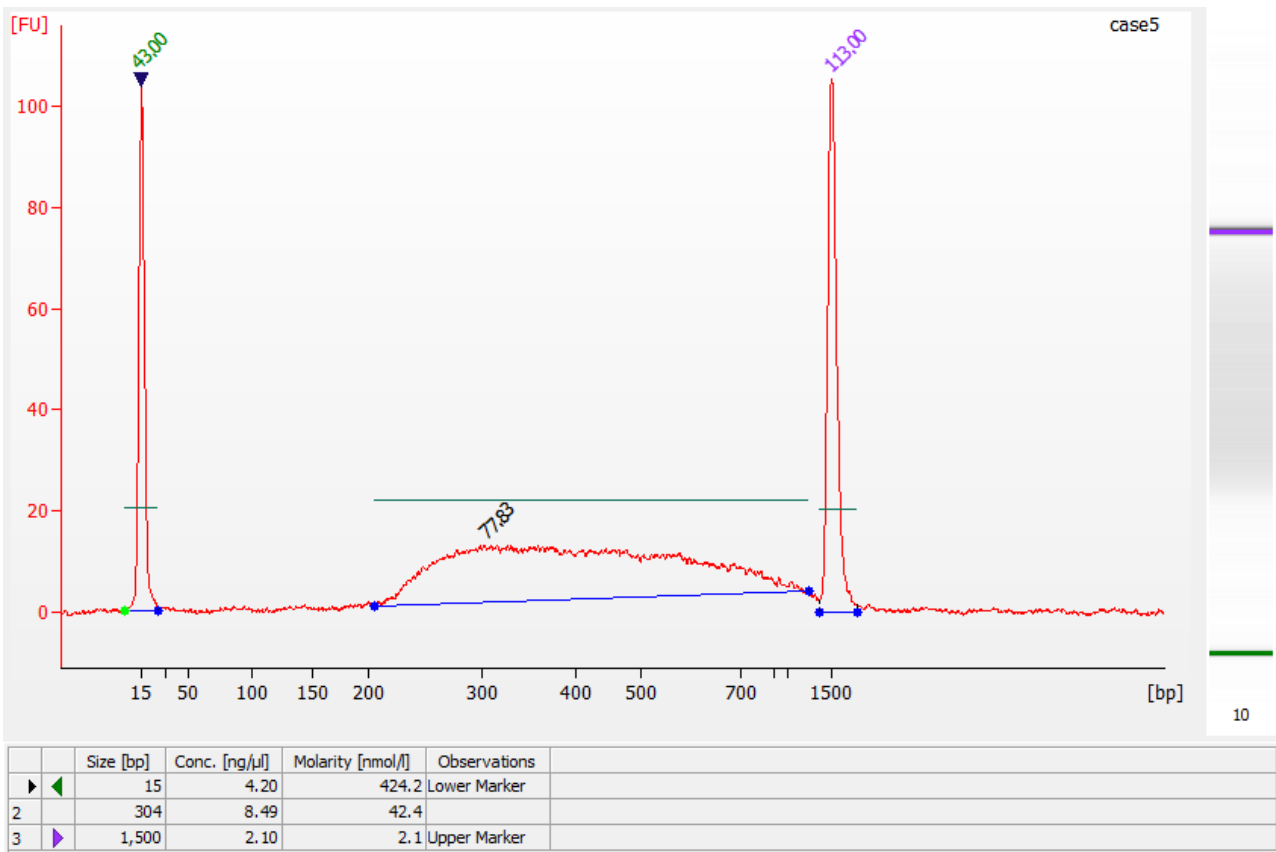
Sample Case3:



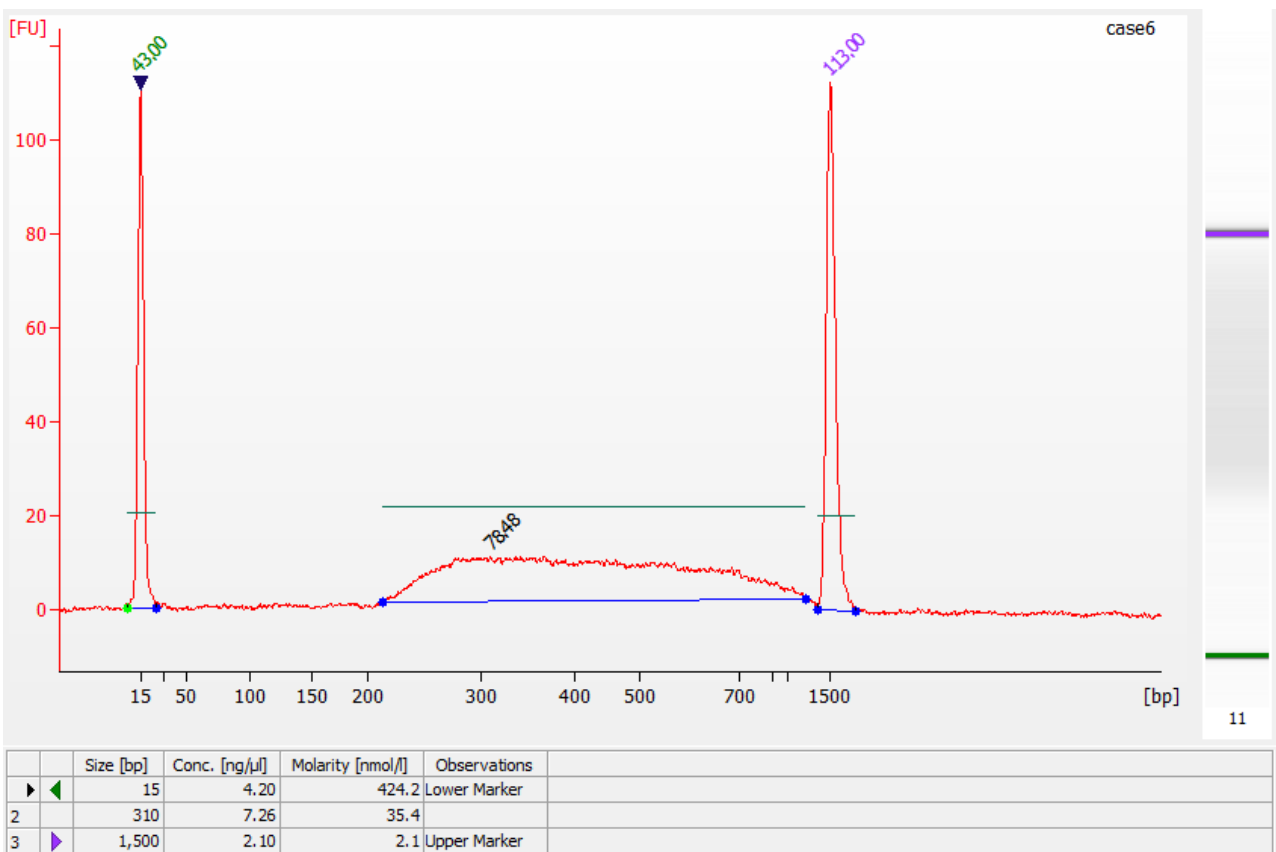
Sample Case4:



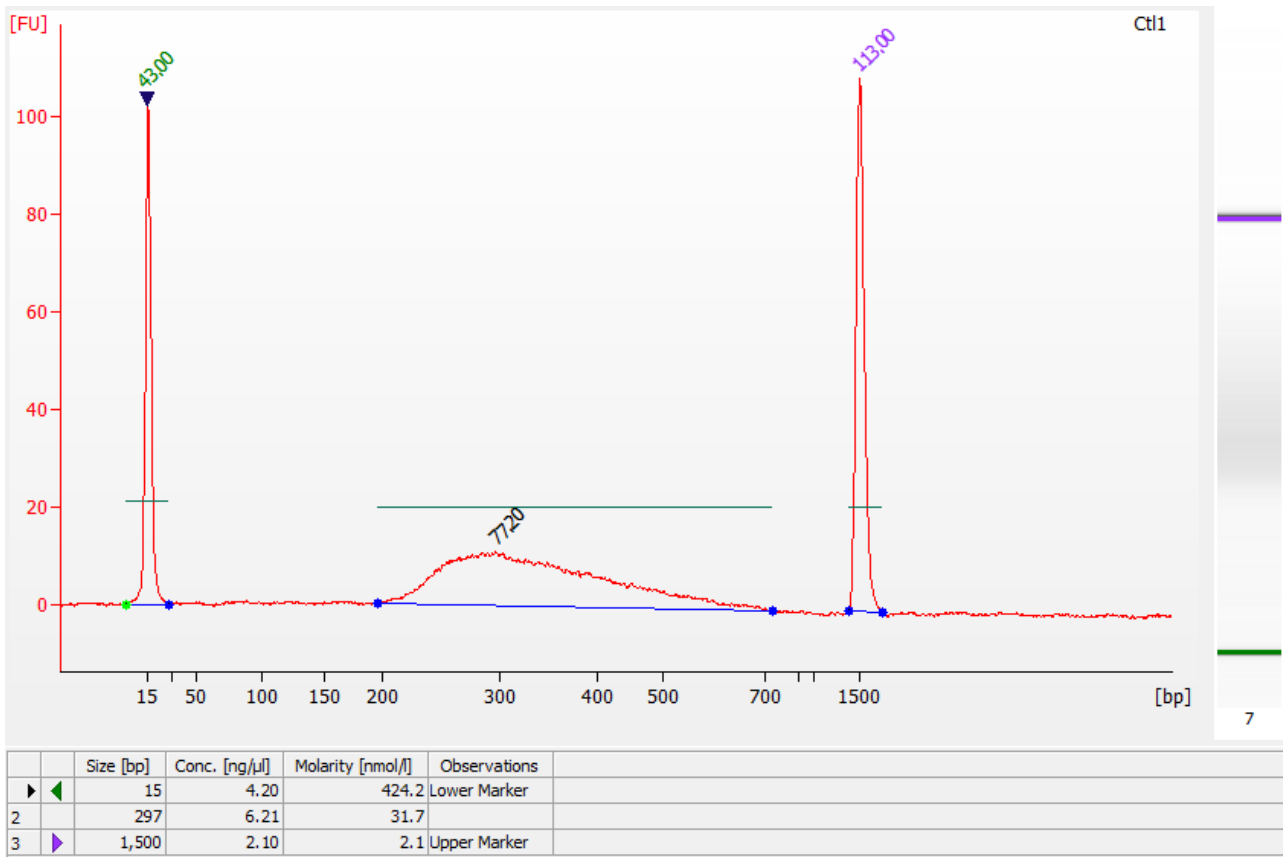
Sample Case5:



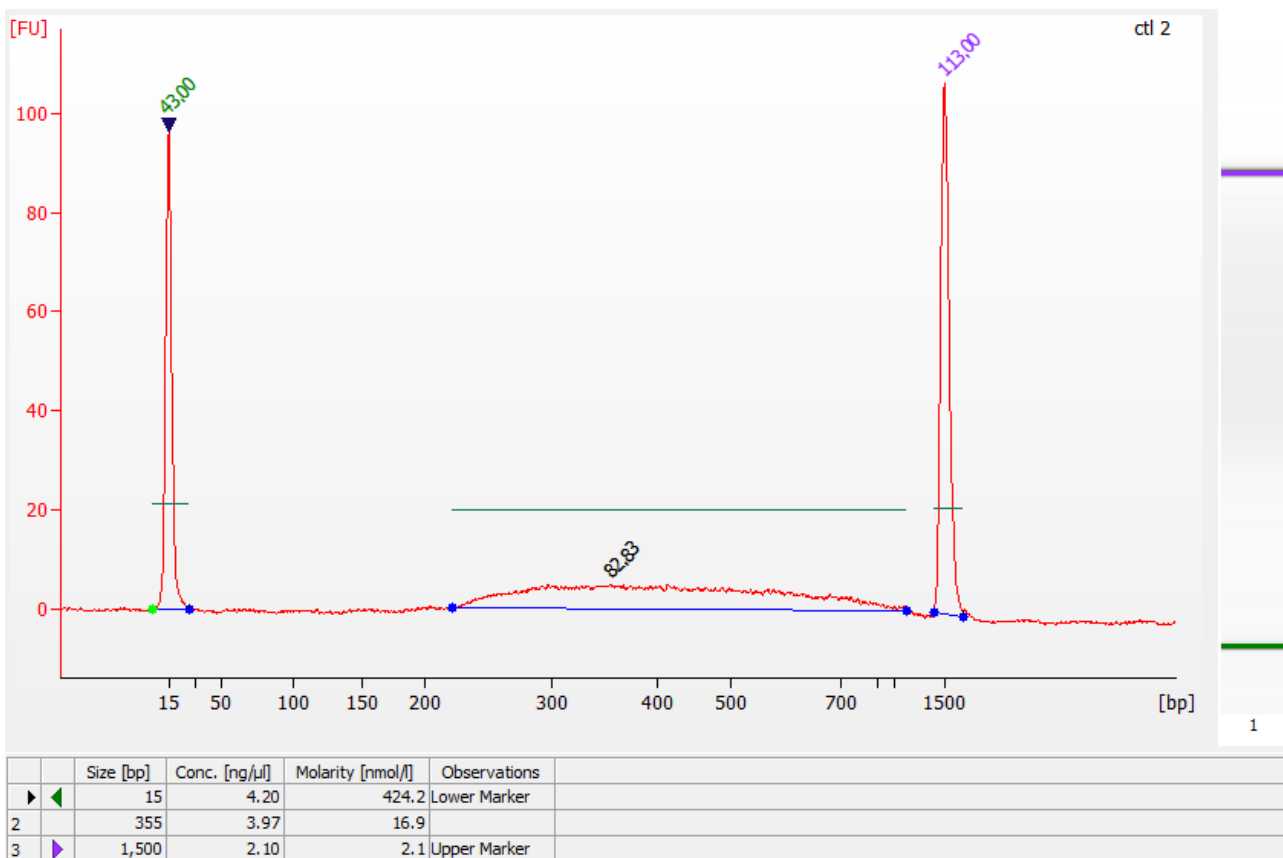
Sample Case6:



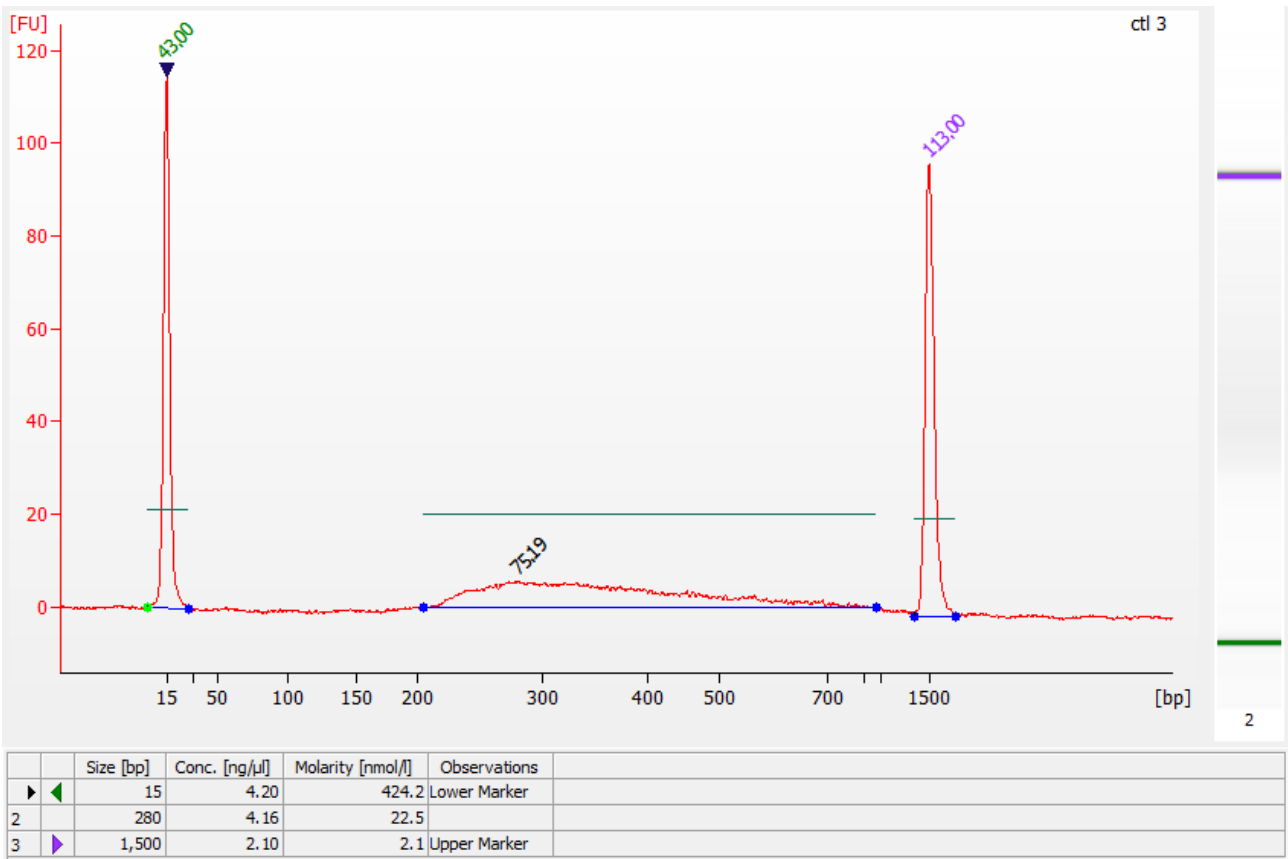
Sample Ctl1:



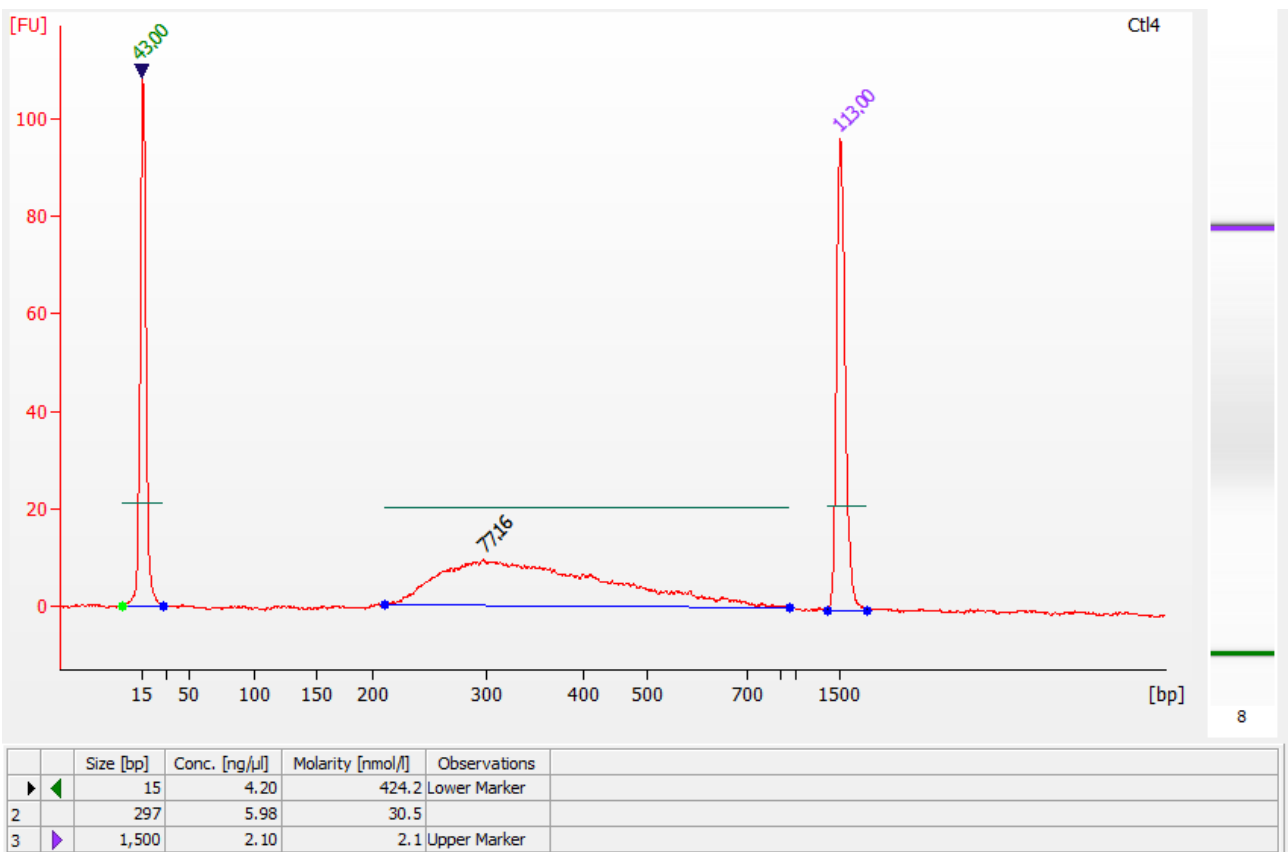
Sample Ctl2:



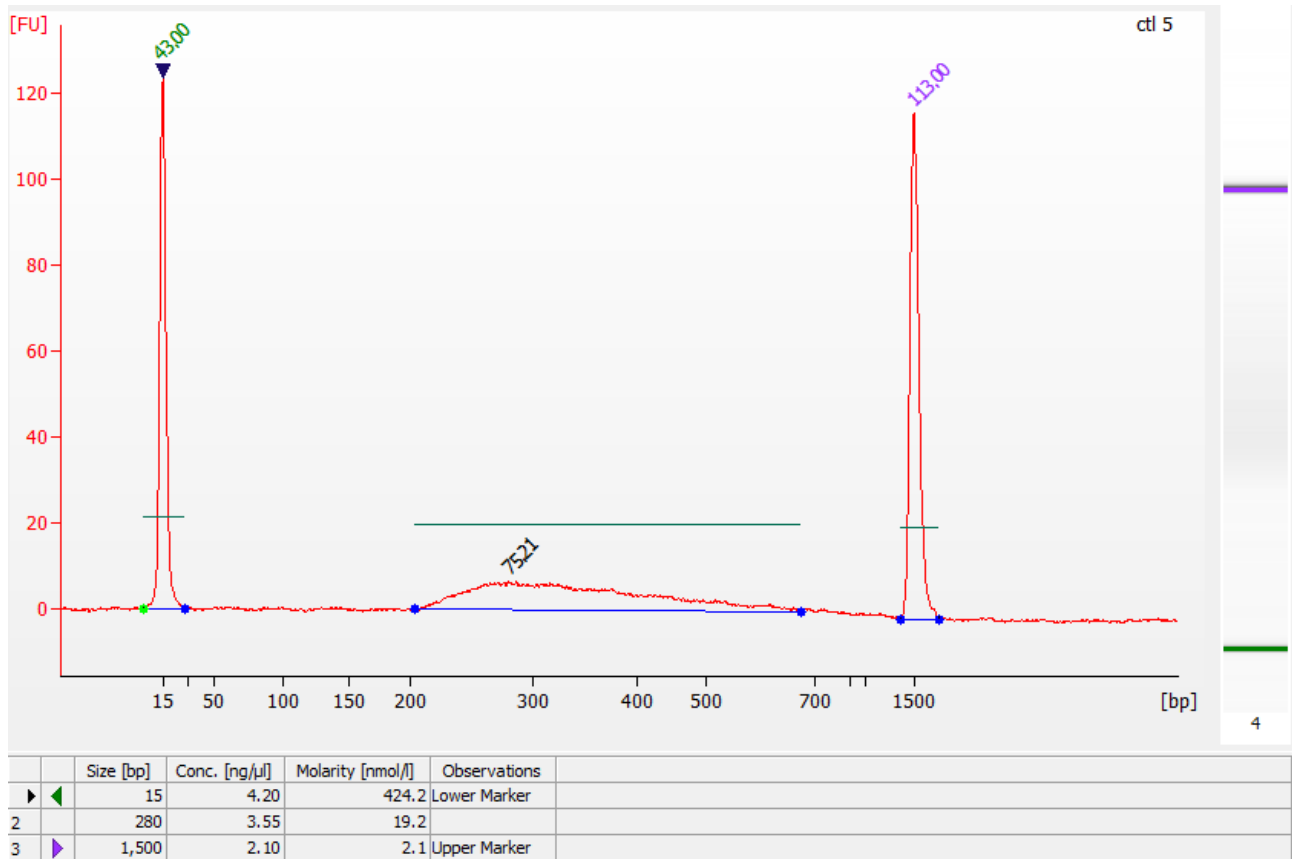
Sample Ctl3:



Sample Ctl4:



Sample Ctl5:



Sample Ctl6:

