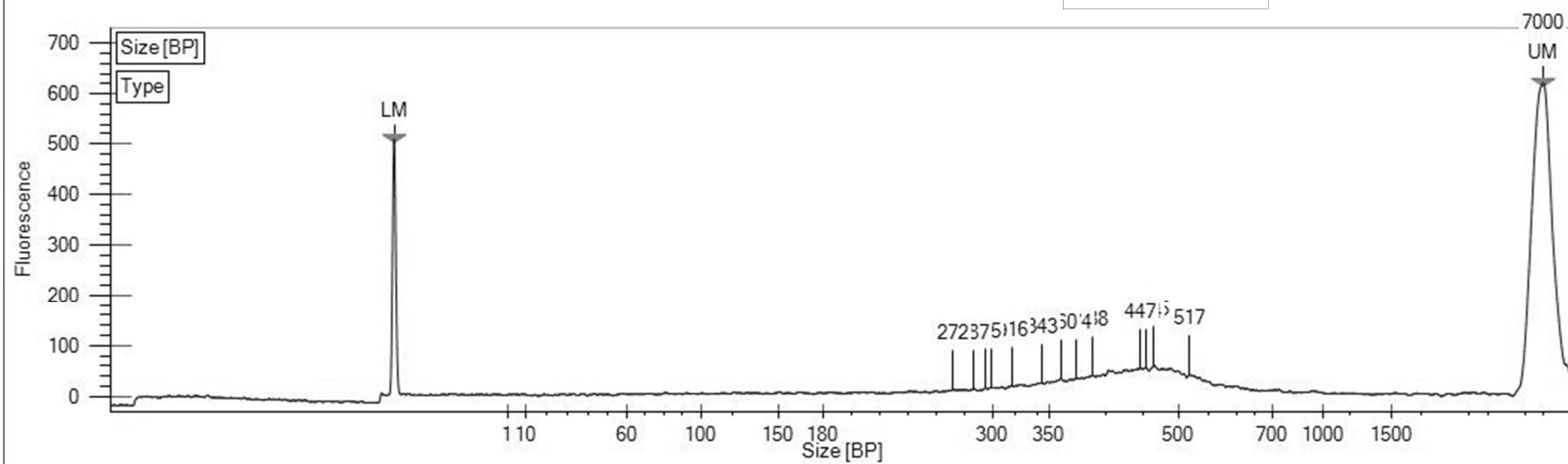


Sample ID	Index Sequencing	Library volume (μL)	Fragment size (bp)	Con. (ng/μL)	Molarity (nmol/L)	Conclusion	Remarks
15	ATGTCA	26.3	436.252	0.001	0.6415	Fail	Large Insert Size, Tailing
16	CCGTCC	43.2	349.48	0.518	1.8408	Fail	Small Fragment, Large Insert Size, Tailing
18	GTCCGC	52.8	324.9999	0.552	2.1655	Fail	Small Fragment, Tailing
19	GTGAAA	22.2	356.1812	0.512	1.2769	Fail	Small Fragment, Tailing
20	GTGGCC	33	373.8985	0.682	1.7912	Fail	Small Fragment, Tailing
21	GTTTCG	13	340.522	0.506	3.0746	Fail	Small Fragment, Tailing
22	CGTACG	41.8	343.2168	0.518	1.6349	Fail	Small Fragment, Tailing
23	GAGTGG	23.9	316.2991	0.226	1.5293	Fail	Small Fragment, Tailing
25	ACTGAT	51	323.4607	0.676	2.6643	Fail	Small Fragment, Tailing
27	ATTCCT	21.2	347.1122	0.558	1.9015	Fail	Small Fragment, Tailing

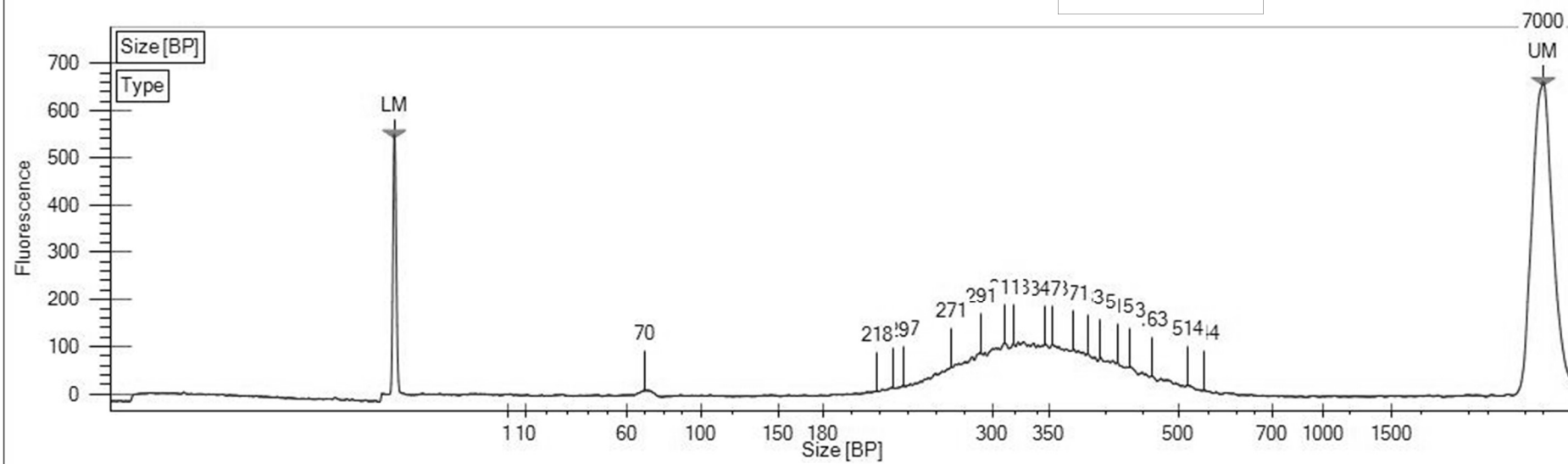
[Labchip_2019-03-28_11-12-21_20190328-NGS3K-1/K18]

#15



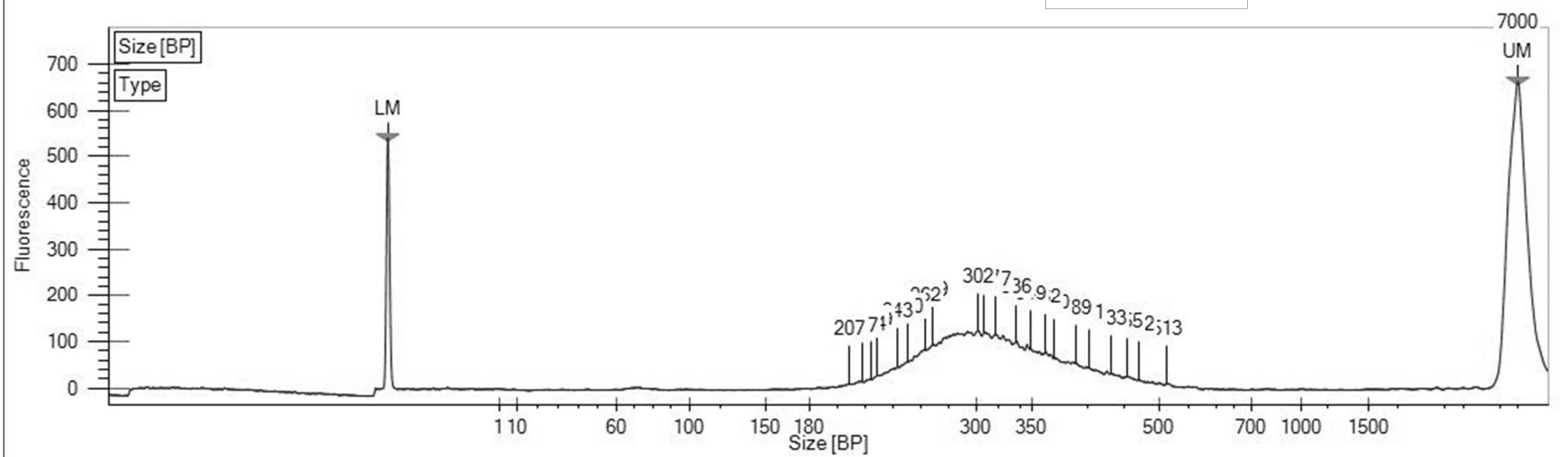
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#16



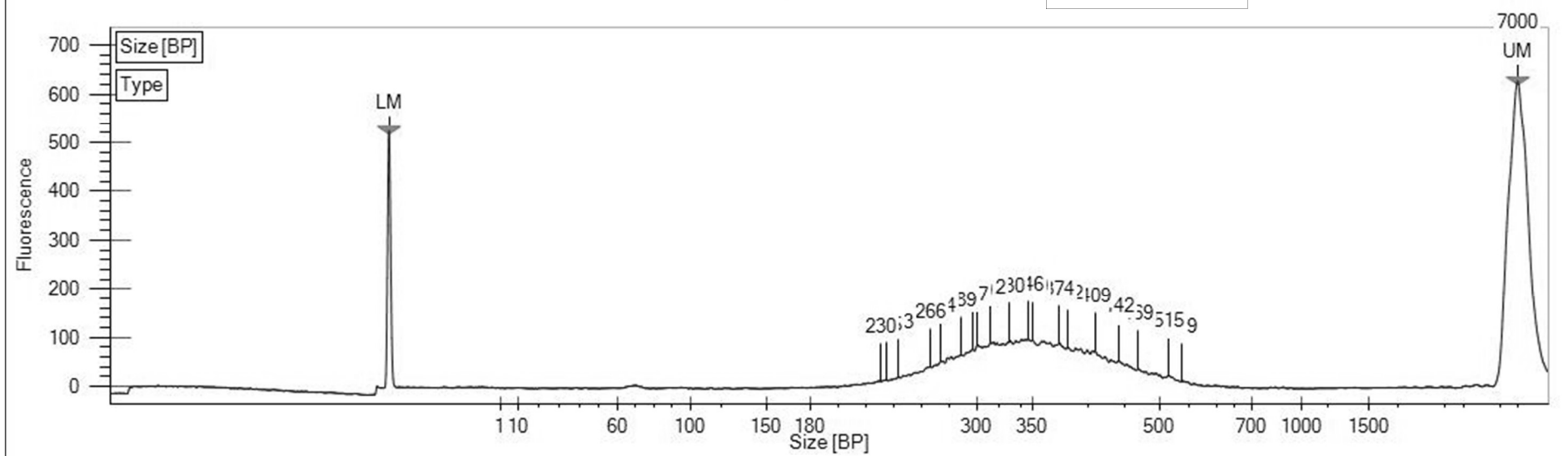
[Labchip_2019-03-28_11-12-21_20190328-NGS3K-1/K20]

#18



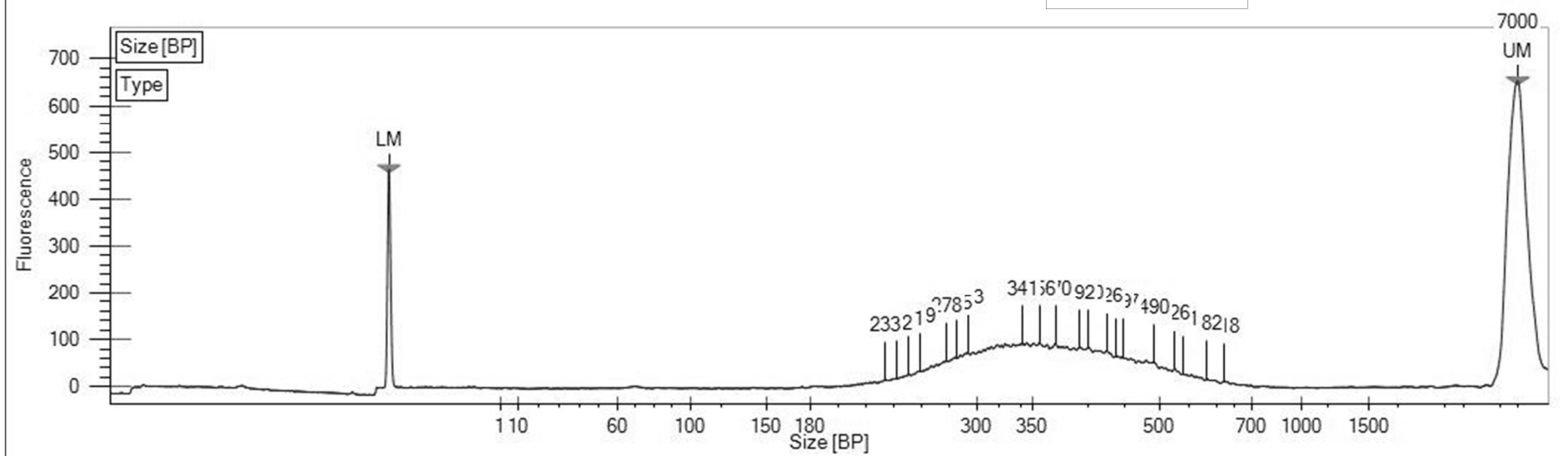
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#19



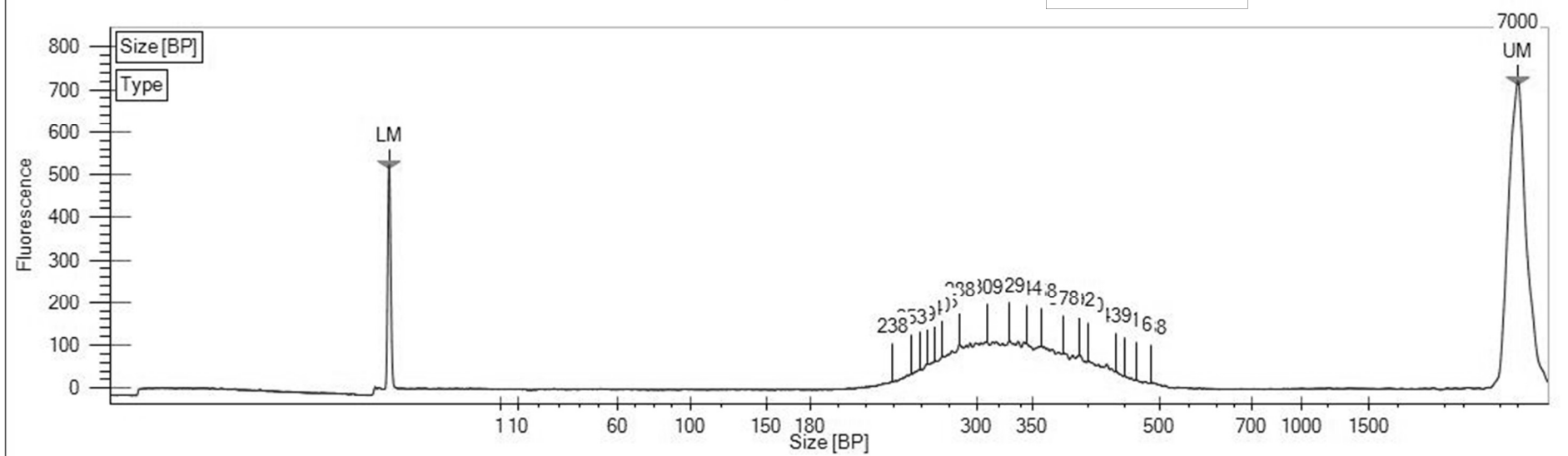
[Labchip_2019-03-28_11-12-21_20190328-NGS3K-1/K22]

#20



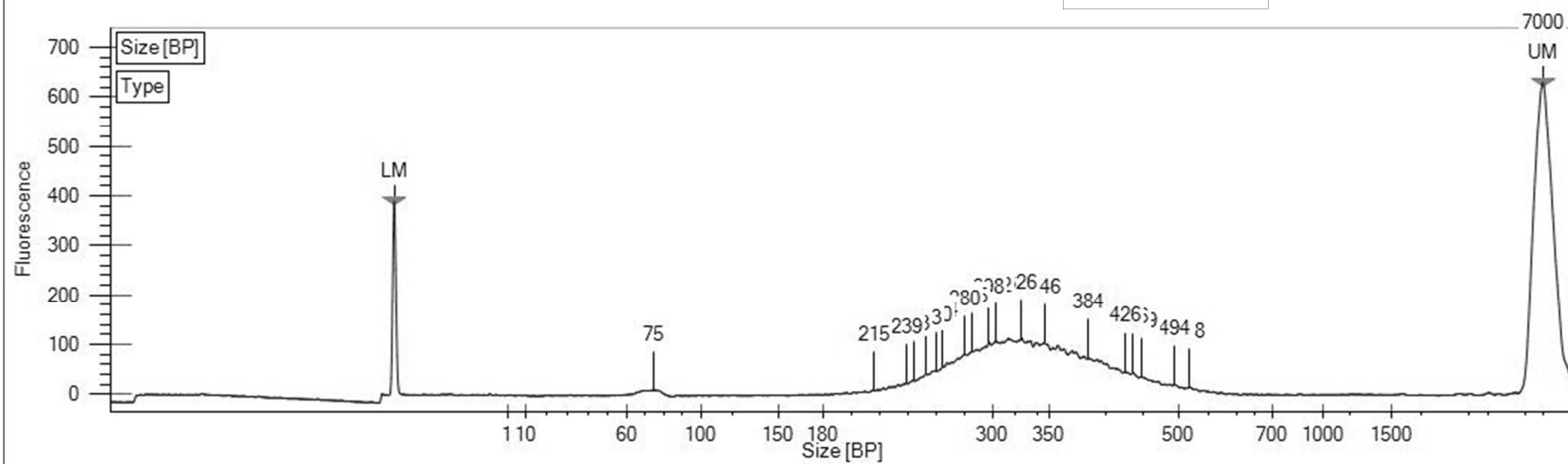
[Labchip_2019-03-28_11-12-21_20190328-NGS3K-1/K23]

#21



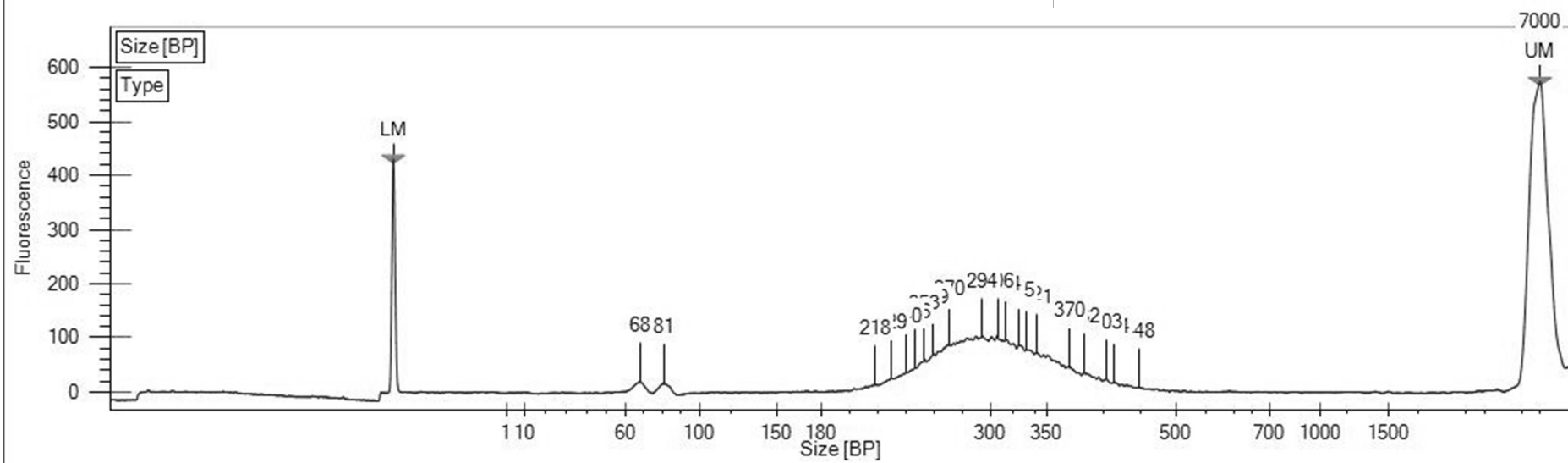
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#22



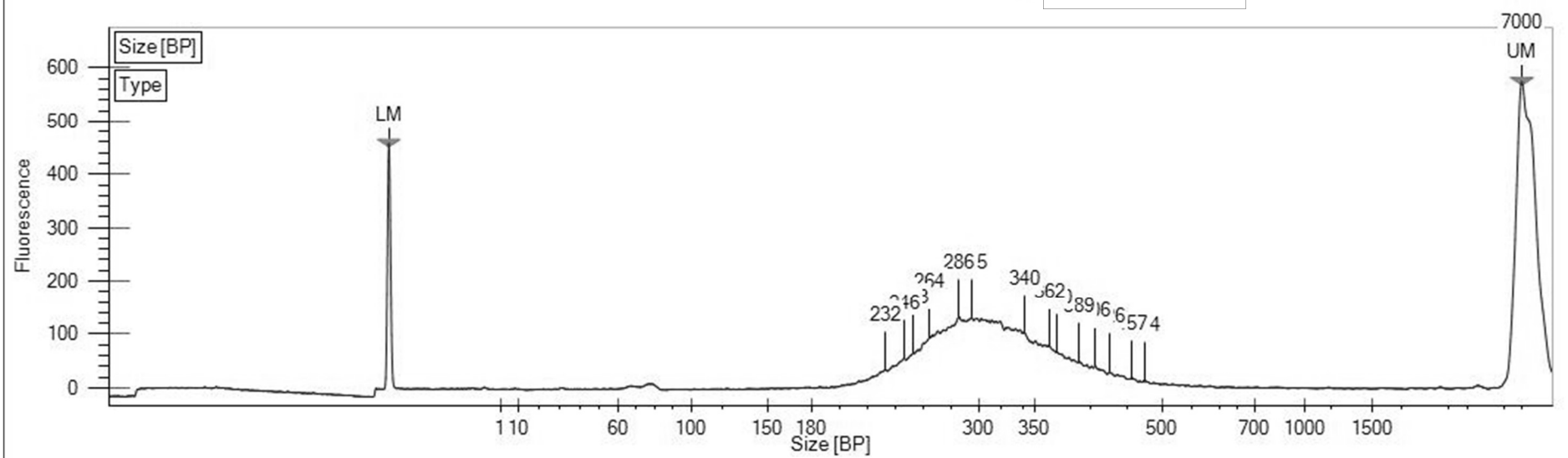
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#23



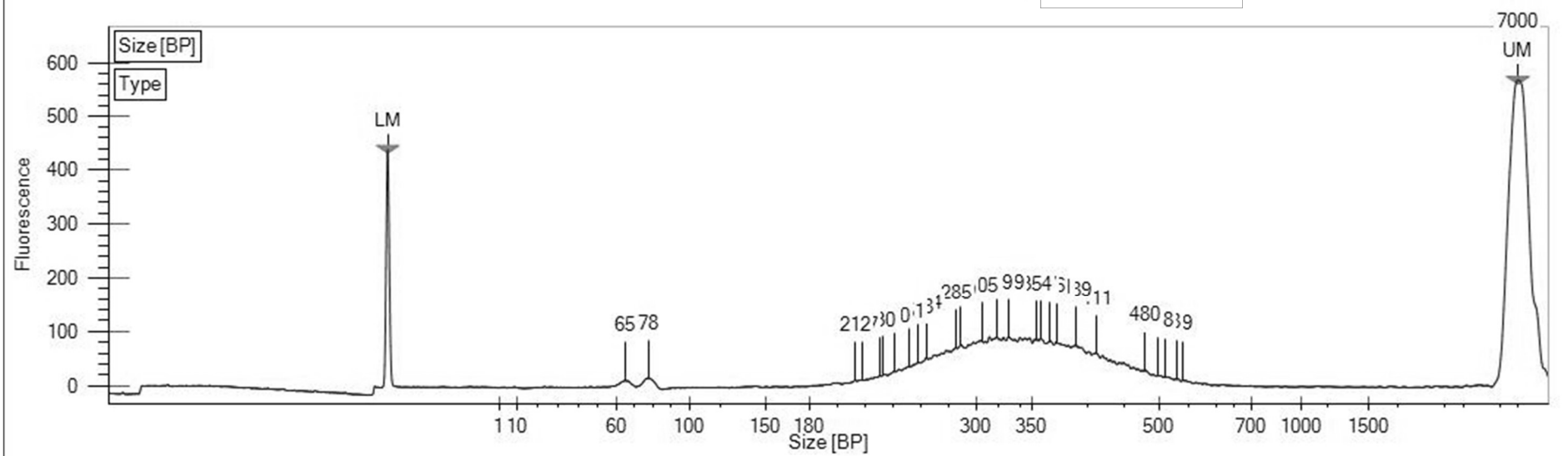
[Labchip_2019-03-28_11-12-21_20190328-NGS3K-1/L2]

#25



[Labchip_2019-03-28_11-12-21_20190328-NGS3K-1/L3]

#27



EXAMPLE:

Figure from the kit manual I used showing a successful library prep.

Here I see:

- (1) very small “small fragments” (<200 bp);
- (2) slight tiling (not symmetrical);
- (3) a small bump for HMW DNA

Apparently a library like this shall be OK..
(looks like the chip was overloaded though)

