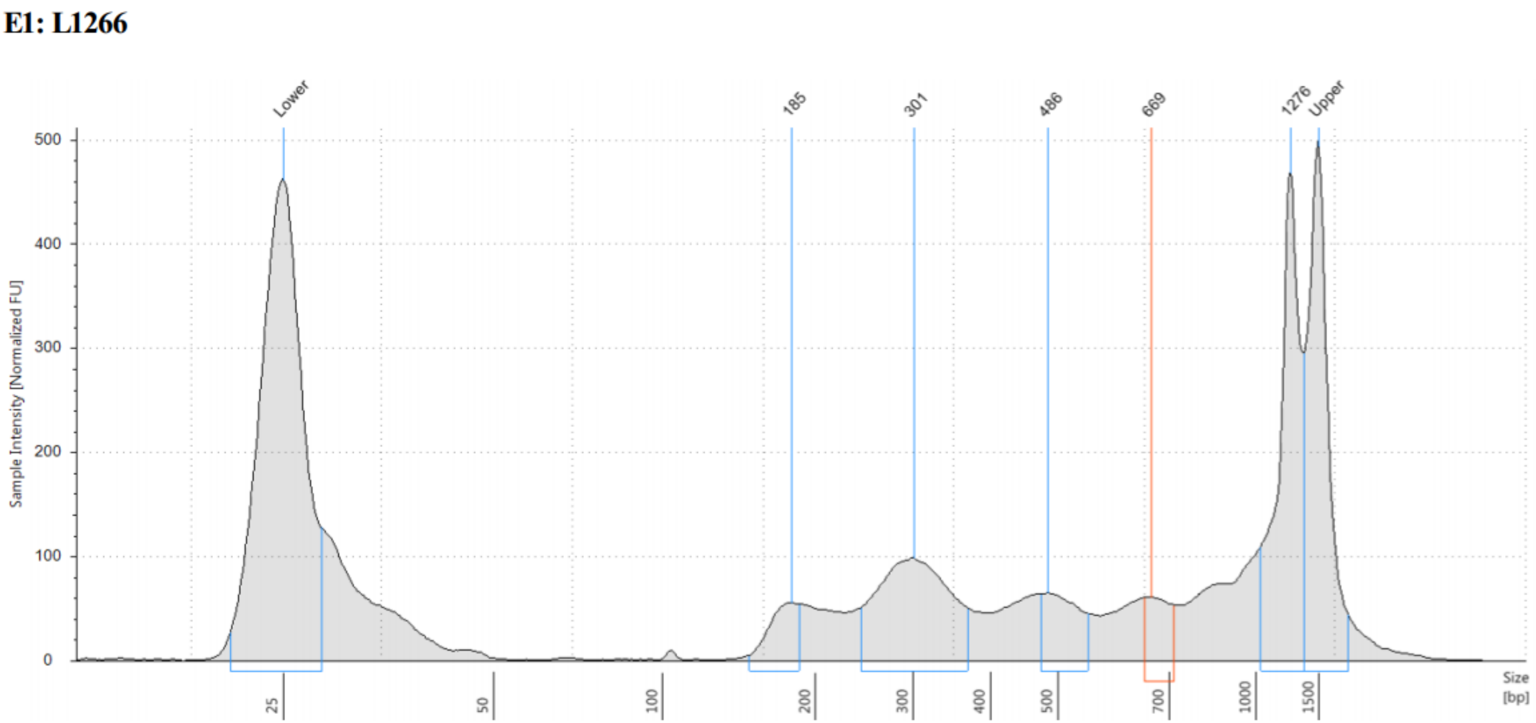
TEST #1

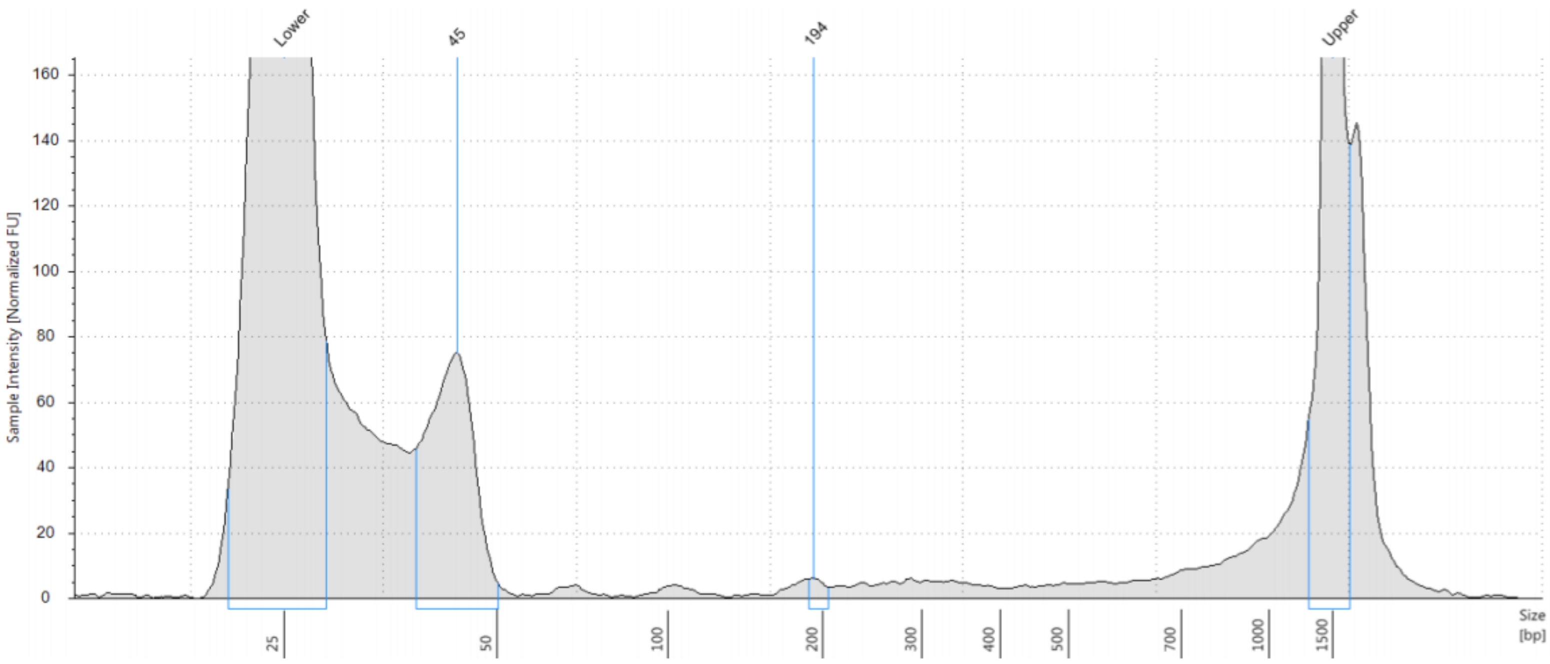
Tapestation


E1: L1266

This is conventional ATAC-seq done side by side

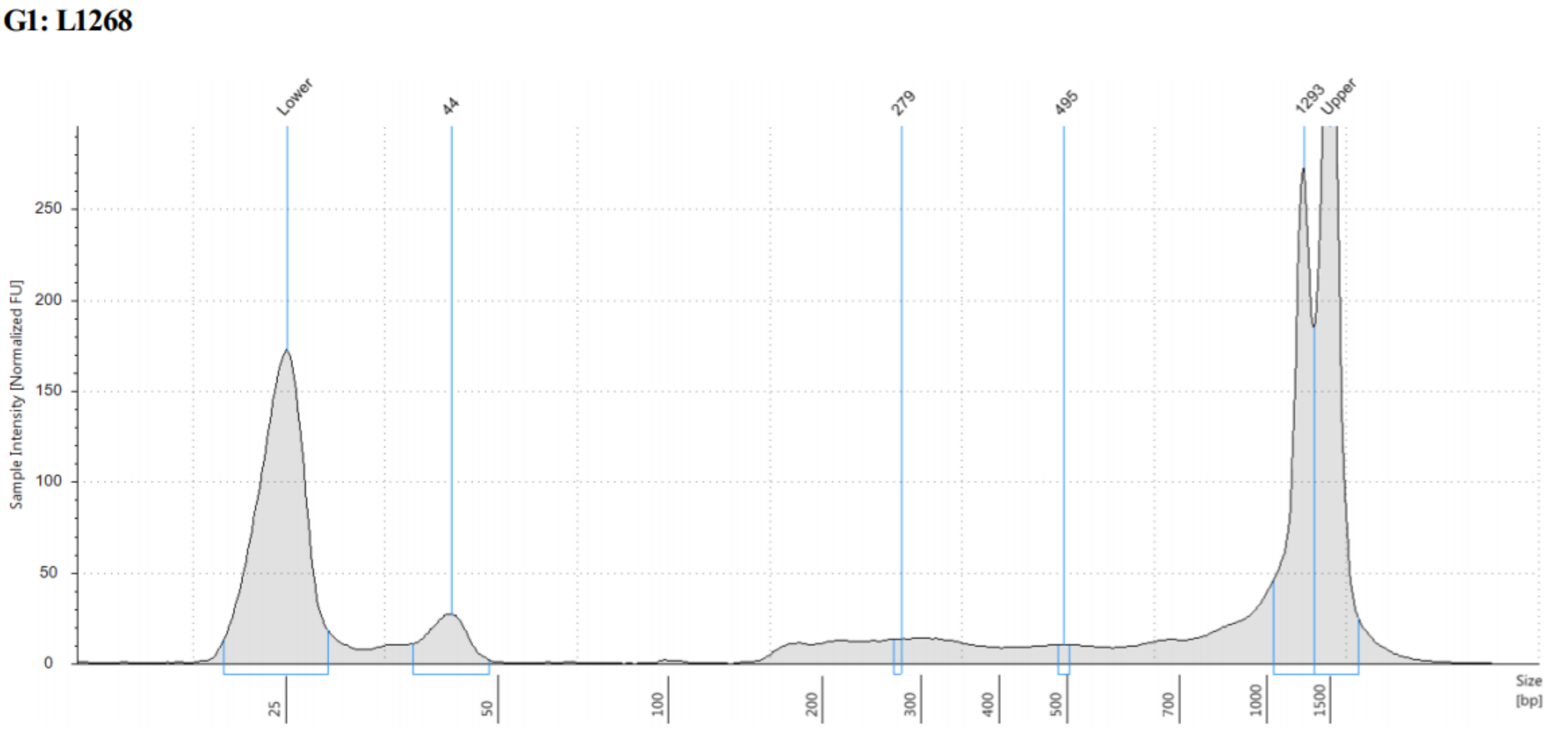
Tapestation

F1: L1267



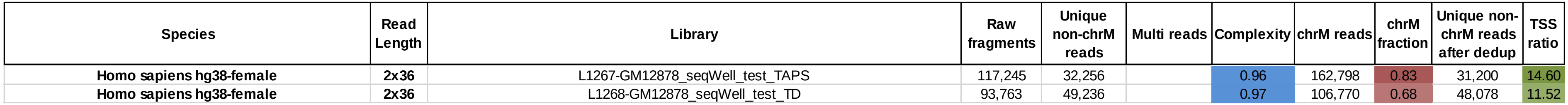
seqWell ATAC-seq in TAPS buffer

Tapestation



seqWell ATAC-seq in TD buffer

Dataset stats; test #1

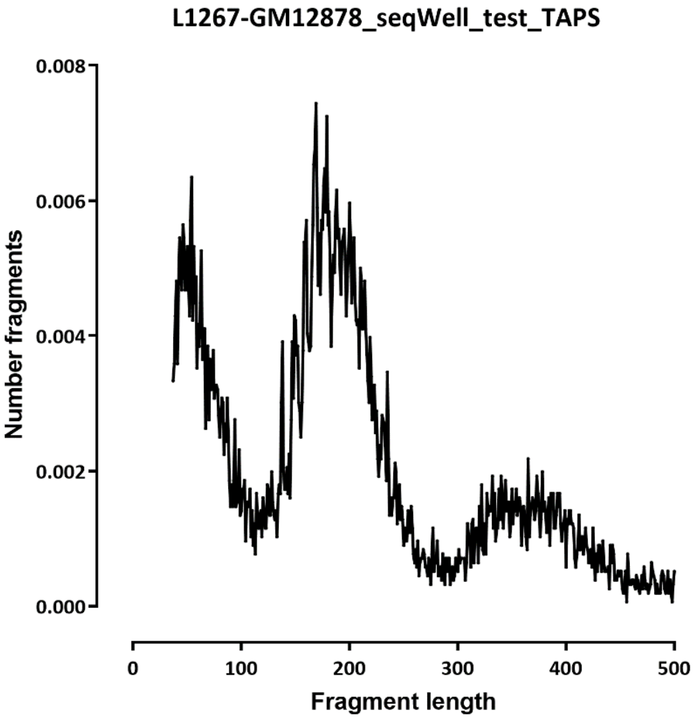


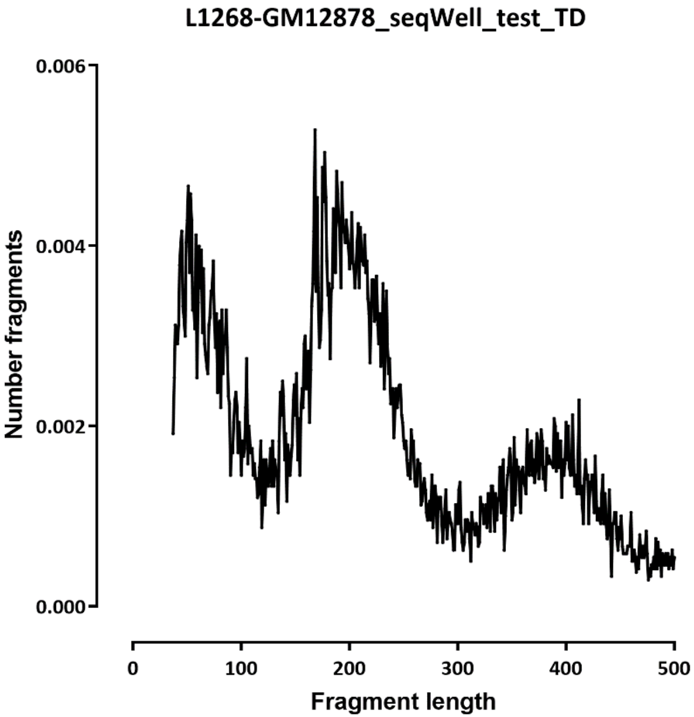
Species	Read Length	Library	Raw fragments	Unique non-chrM reads	Multi reads	Complexity	chrM reads	chrM fraction	Unique non-chrM reads after dedup	TSS ratio
Homo sapiens hg38-female	**2x36**	L1267-GM12878_seqWell_test_TAPS	117,245	32,256		0.96	162,798	0.83	31,200	14.60
Homo sapiens hg38-female	**2x36**	L1268-GM12878_seqWell_test_TD	93,763	49,236		0.97	106,770	0.68	48,078	11.52

Notes:

1. This is a very high mitochondrial fraction
2. The TSS ratio is, on the other hand, good
3. They did not sequence well (aimed for 5M reads, got 100K)

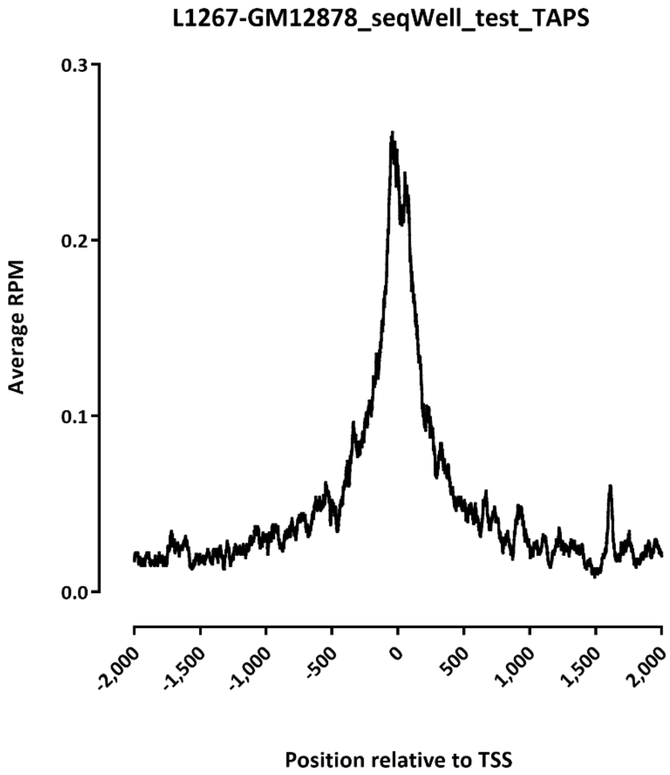
Fragment length

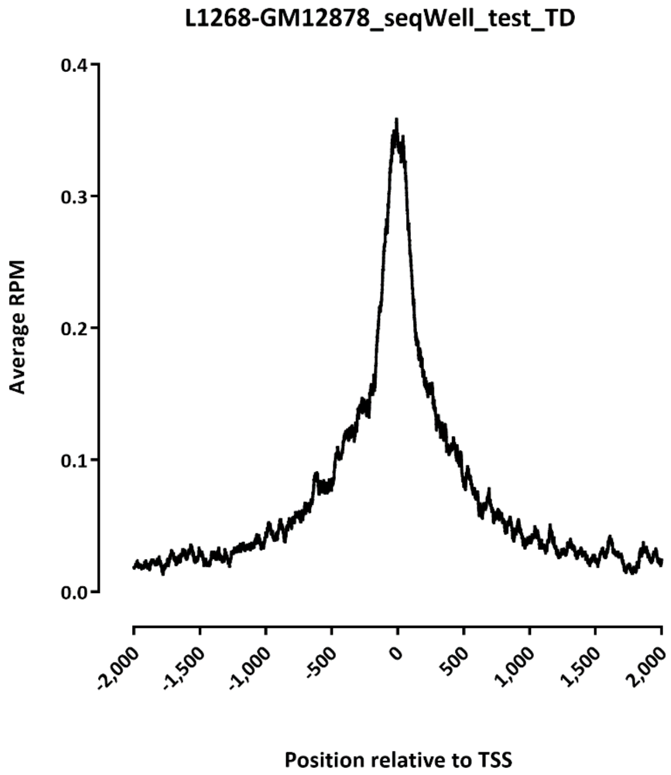

L1267-GM12878_seqWell_test_TAPS


L1268-GM12878_seqWell_test_TD

Note: this is what it should look like in a good mammalian dataset

TSS profiles


L1267-GM12878_seqWell_test_TAPS


L1268-GM12878_seqWell_test_TD

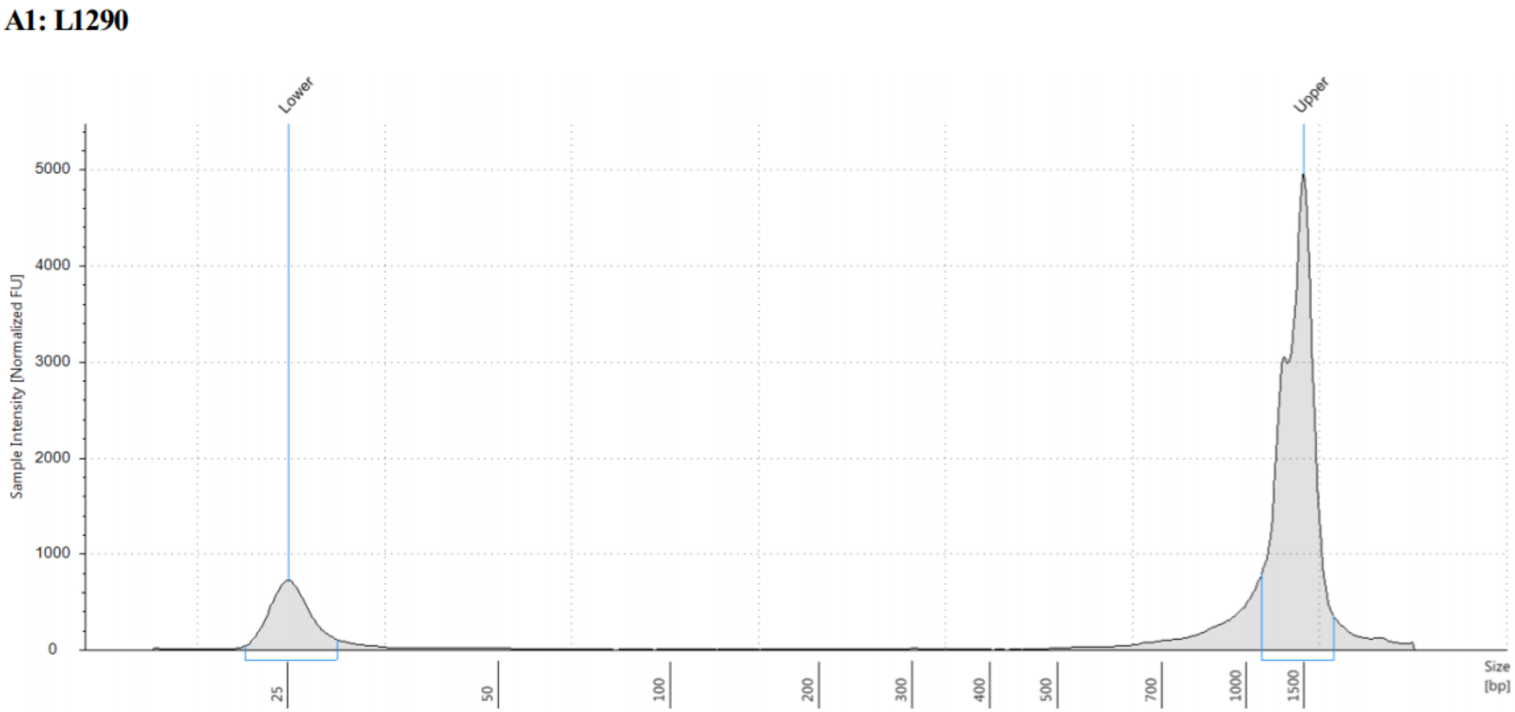
TEST #2

Libraries:

#Library	cell line	buffer	Tn5 volume	primers used	PCR protocol	Library concentration (ng/uL)
L1286	GM12878	TAPS	5uL	P7+P5	seqWell	1.30
L1287	GM12878	TD	5uL	P7+P5	seqWell	2.62
L1288	GM12878	TAPS	1.5uL	P7+P5	seqWell	1.85
L1289	GM12878	TD	1.5uL	P7+P5	seqWell	0.76
L1290	GM12878	TAPS	5uL	i7+i5	Greenleaf	42.40
L1291	GM12878	TD	5uL	i7+i5	Greenleaf	2.82
L1292	GM12878	TAPS	1.5uL	i7+i5	Greenleaf	8.80
L1293	GM12878	TD	1.5uL	i7+i5	Greenleaf	2.38
L1294	GM12878	TAPS	5uL	P7+i5	seqWell	58.60
L1295	GM12878	TD	5uL	P7+i5	seqWell	2.63
L1296	GM12878	TAPS	1.5uL	P7+i5	seqWell	16.60
L1297	GM12878	TD	1.5uL	P7+i5	seqWell	2.86

- i5/i7 – our own indexed primers
- P7/P5 – seqWell primers (not indexed)

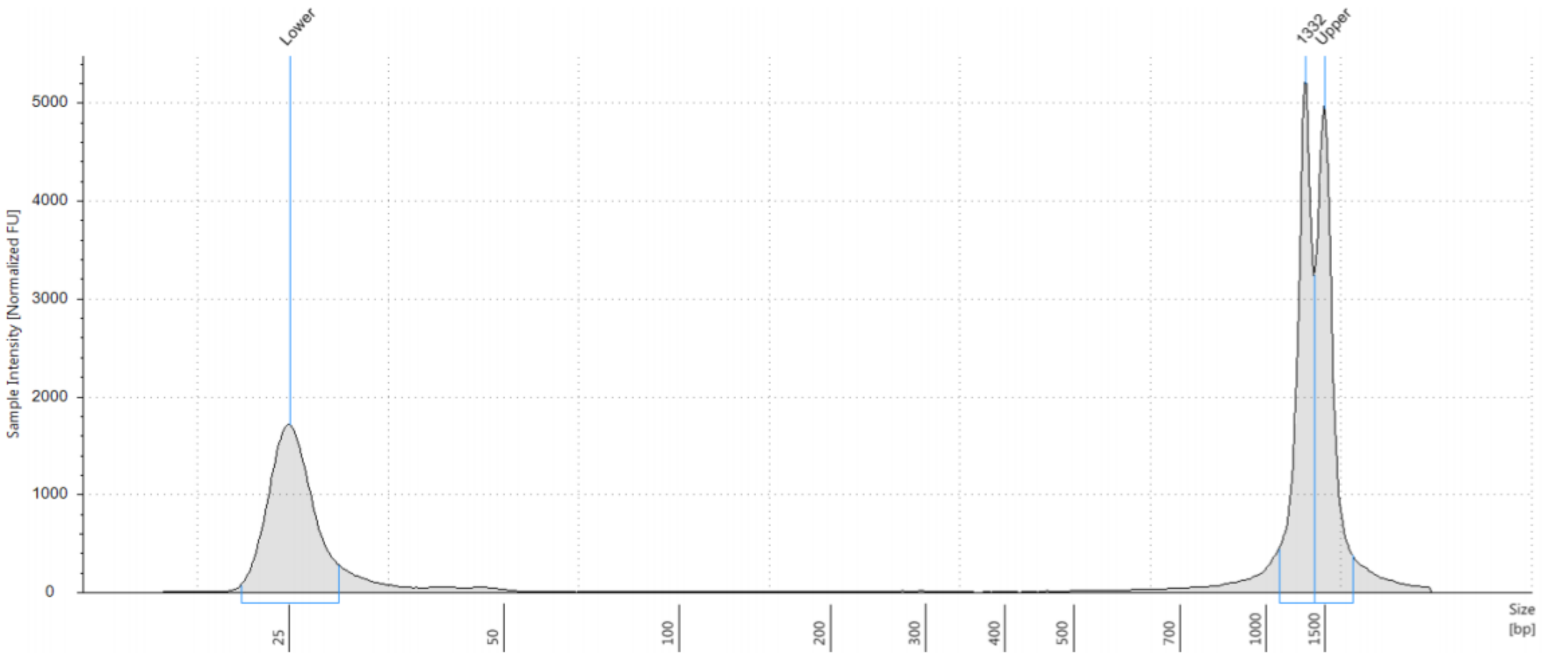
Tapestation



Concentration was high, but the library contains only HMW fragments;
A possibility is that transposition failed due to the volume of the enzyme being too high

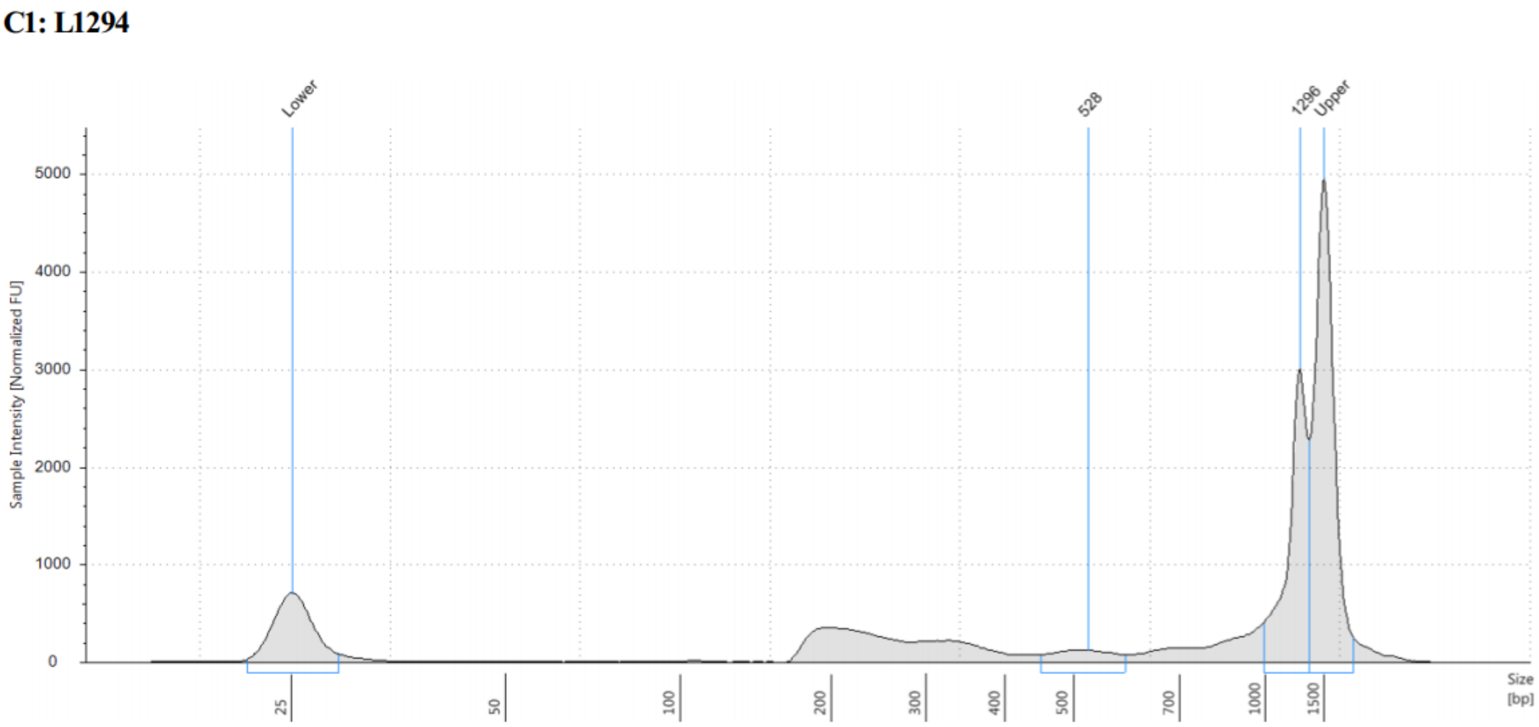
Tapestation

B1: L1292



However, we see a similar picture with the 1.5 uL Tn5 reaction

Tapestation

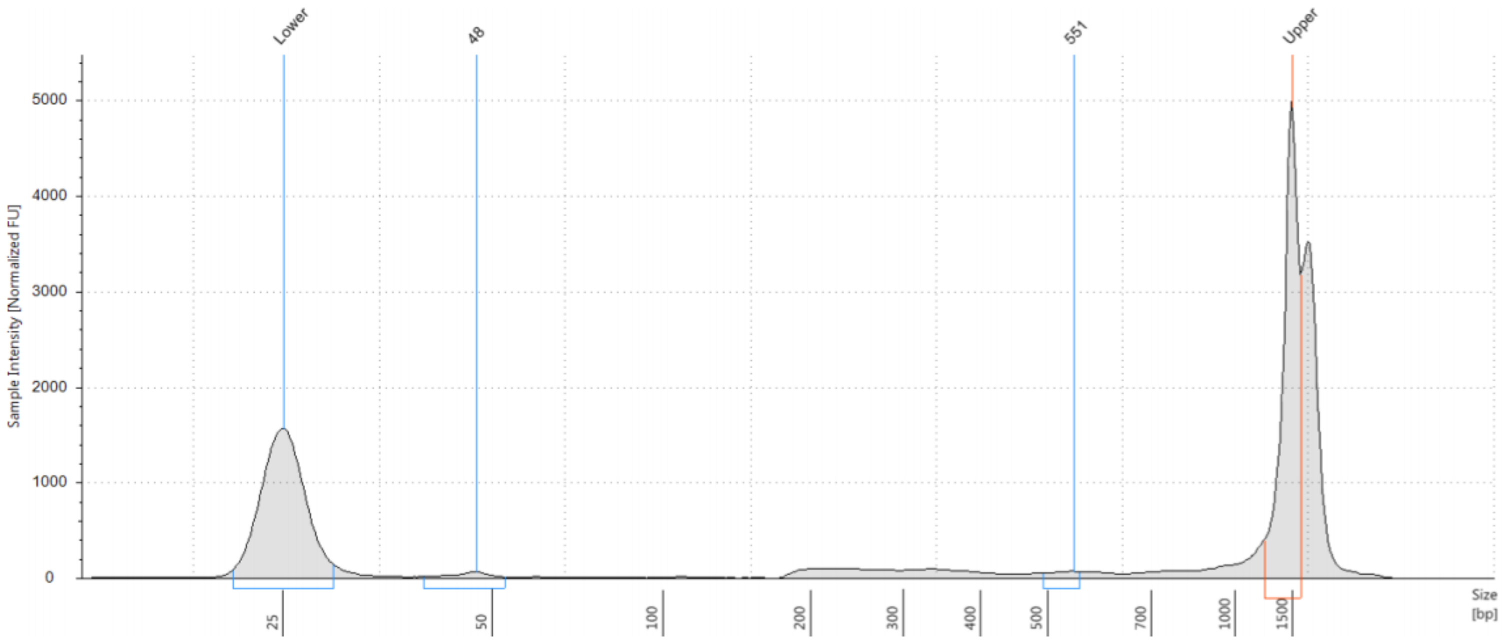


C1: L1294

And this (also 5 uL) is the best library, as it shows a nucleosomal signature, though it still has HMW DNA and is not as strong as our usual libraries in the meaningful range

Tapestation

D1: L1296



This is probably also a good library, as it shows a nucleosomal signature, but it too has HMW DNA, and is weaker than the 5 uL reaction