Deconvolution of Nucleic-acid Length Distributions: A gel electrophoresis analysis tool and applications

SUPPLEMENTARY FIGURES AND TABLES

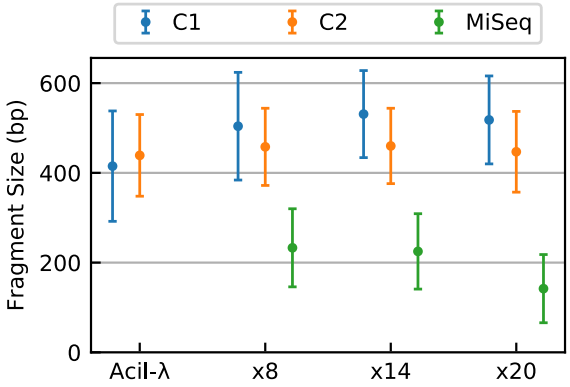


Figure S1. Comparison of average DNA-fragment size obtained from plug-in and MiSeq analysis of NGS libraries. NGS data are for phage-λ DNA libraries subjected to increasing numbers of PCR-amplification cycles as shown in Figure 2a. The same data are also reported in Table S1.

Table S1. Comparison of plug-in output for four camera systems (Table 1) used in acquiring images of the high-resolution gel, shown in Figure 2a. Uncertainty values in Tables are conservatively reported in terms of the standard deviation of the fragment-size distribution, $\pm 1\sigma_d$, as quantified by the plug-in. For this gel-purified sample, *MiSeq*® bioinformatic data are also available.

	C1	**C2**	**MiSeq®**
λ-*Aci*I Digest	415±123	439±91	-
8 PCR Cycles	504±120	458±86	233±87
14 PCR Cycles	531±97	460±84	225±84
20 PCR Cycles	518±98	447±90	142±76

Table S2. Comparison of plug-in output for four camera systems (Table 1.) used in acquiring images of the mini-gel, shown in Figure 2c. Uncertainty values in Tables are conservatively reported in terms of the standard deviation of the fragment-size distribution, $\pm 1\sigma_d$, as quantified by the plug-in.

	C1	**C2**	**C3**	**C4**
λ-*Aci*I Digest	588±140	568±126	672±131	638±150
8 PCR Cycles	714±124	659±138	688±128	678±137
14 PCR Cycles	726±112	672±138	695±122	695±131
20 PCR Cycles	680±124	667±135	679±125	670±134

Table S3. Tabular data for the plot in Figure 6b, 6c. Size distribution average $\pm 1\sigma_d$, standard deviation. The estimated average fragment size for the λ-*Aci*I sample is 329 and 734 bp for the *low*-MW and *high*-MW fractions, respectively.

ROI	**Low Cut**		**High Cut**	
	Low Ex.	**High Ex.**	**Low Ex.**	**High Ex.**
2	378±66	400±54	736±125	723±111
3	385±62	405±51	755±136	742±125
4	386±81	354±87	763±138	761±131
5	397±61	416±55	718±135	724±122
6	366±83	325±72	830±135	850±128
7	385±64	403±52	712±131	737±130

Table S4. Comparison of the distributions' average fragment size calculations when using different subsets of the reference fragment distribution, the λ-*Aci*I digest. Size distribution average $\pm 1\sigma_d$, standard deviation.

ROI	Full λ-*Aci*I	3:4 λ-*Aci*I	2:3 λ-*Aci*I	1:2 λ-*Aci*I	Ladder	MiSeq®
2	841±174	857±180	869±188	845±183	829±145	-
3	728±191	706±172	749±222	694±181	719±151	-
4	753±177	740±171	752±197	773±200	747±148	617±199
5	830±178	838±180	859±194	837±194	837±145	609±101
6	724±172	735±171	728±186	750±191	733±147	610±193
7	761±203	737±184	727±176	725±179	735±159	-
8	788±194	784±193	786±192	822±223	774±172	-

Table S5. Profile fit accuracy as absolute RMS for the fits for the gel in Figure 5a

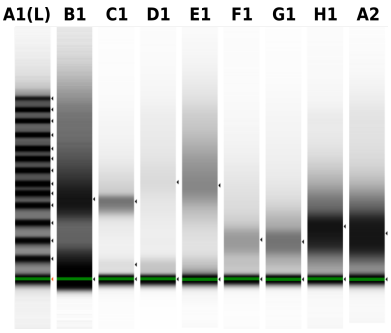
ROI	Full λ-*Aci*I	3:4 λ-*Aci*I	2:3 λ-*Aci*I	1:2 λ-*Aci*I	Ladder
1	467.6	467.6	467.6	467.6	461.5
2	179.7	119.7	109.9	212.1	641.2
3	74.1	94.3	85.6	132.5	662.9
4	160.4	27.2	65.6	201.6	111.9
5	140.5	57.2	101.2	169.4	673.6
6	188.7	27.9	142.8	159.7	108.4
7	121.1	190.9	48.2	98.4	482.8
8	17.8	17.9	72.9	46.0	124.0

Table S6. Plug-in output compared with TapeStation results. Size-distribution average $\pm 1\sigma_d$, standard deviation, for the plugin output. The calculated average for the λ-*Aci*I sample is 398 and 871 bp for the *low* and *high* gel portions respectively. The labels in the 2nd and 5th columns, as well as the TS sizes, refer to the plots in section TapeStation Output.

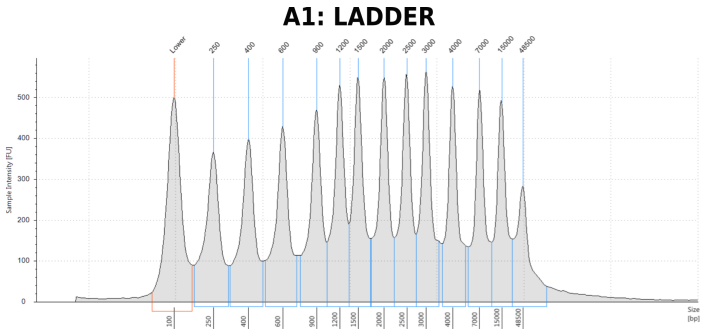
ROI		Low Cut			High Cut	
		Plugin	TS		Plugin	TS
2	λ-*Aci*I	378±66	-	λ-*Aci*I	736±125	-
3	λ-*Aci*I	385±62	-	λ-*Aci*I	755±136	-
4	F1:5	386±81	410	B1:1	763±138	1046
5	G1:6	397±61	391	C1:2	718±135	985
6	H1:7	366±83	555	D1:3	830±135	1554
7	A2:8	385±64	475	E1:4	712±131	1448

TAPESTATION OUTPUT

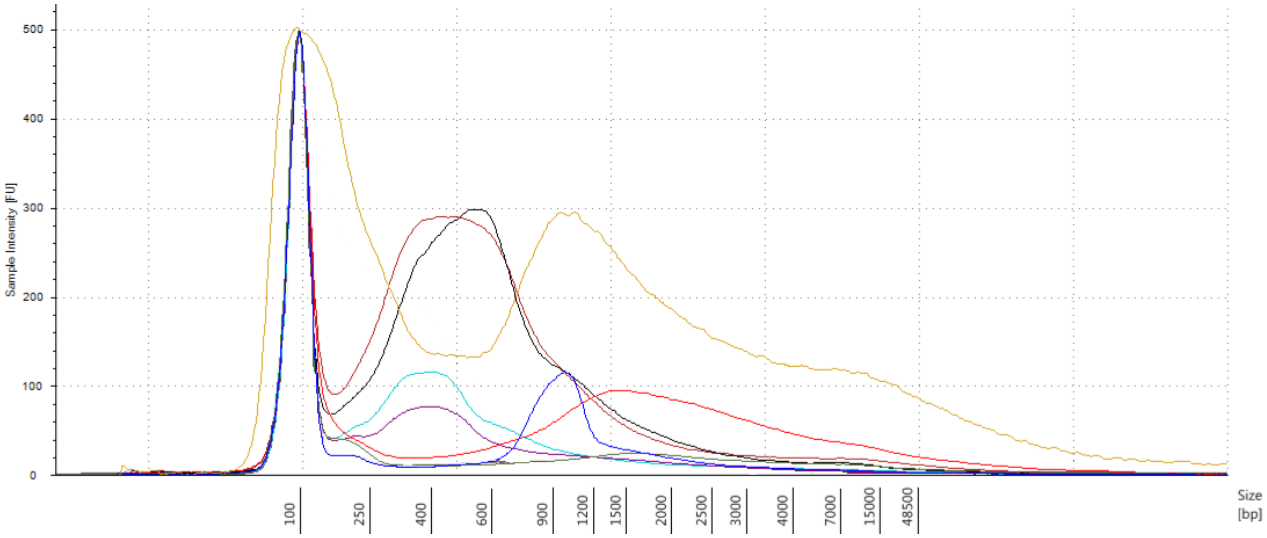
(a)



(b)



(c)



Well ID	Size (bp)	Well ID	Size (bp)	Well ID	Size (bp)	Well ID	Size (bp)
B1	1046	D1	1554	F1	410	H1	555
C1	985	E1	1448	G1	391	A2	475

Figure S2. TapeStation® capillary-electrophoretic analysis of tagmented libraries prepared from *C. elegans* genomic DNA. Standard agarose-gel characterization of these libraries is shown in Figure 6. **(a)** original sample profile from the TS, **(b)** the line profile for the ladder of standards ((a), A1(L)) with the location of the peaks; **(c)** line profiles of the analyzed samples and respective main peak location (bp).