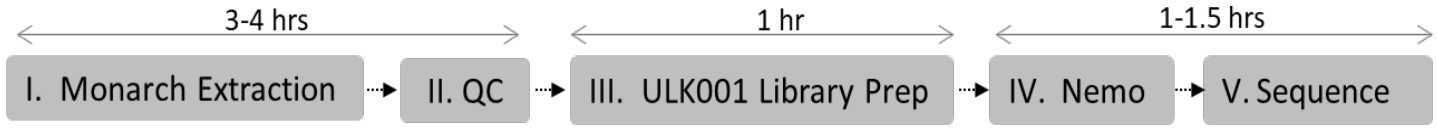
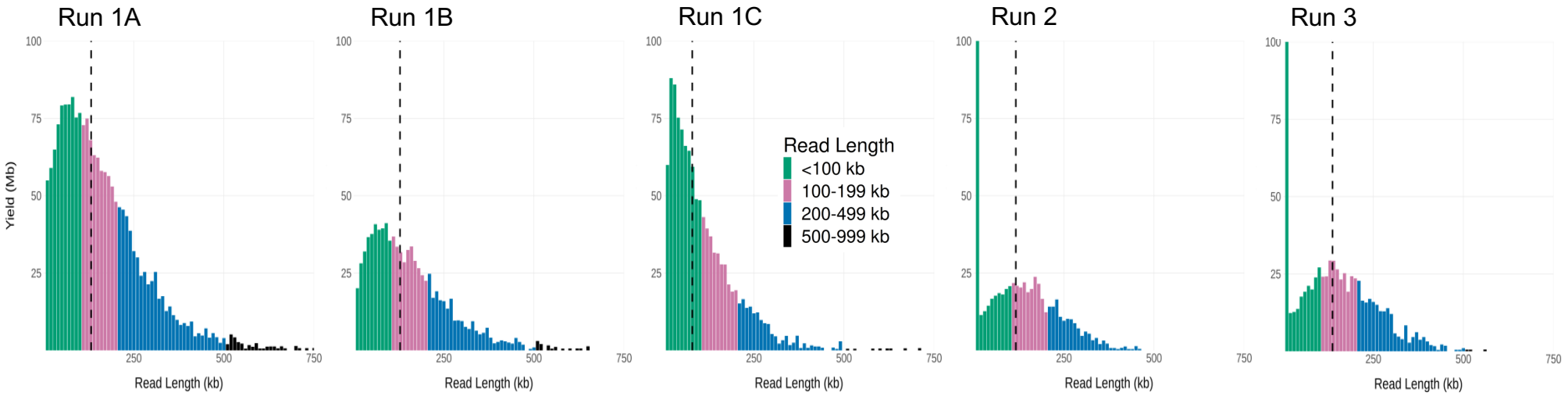
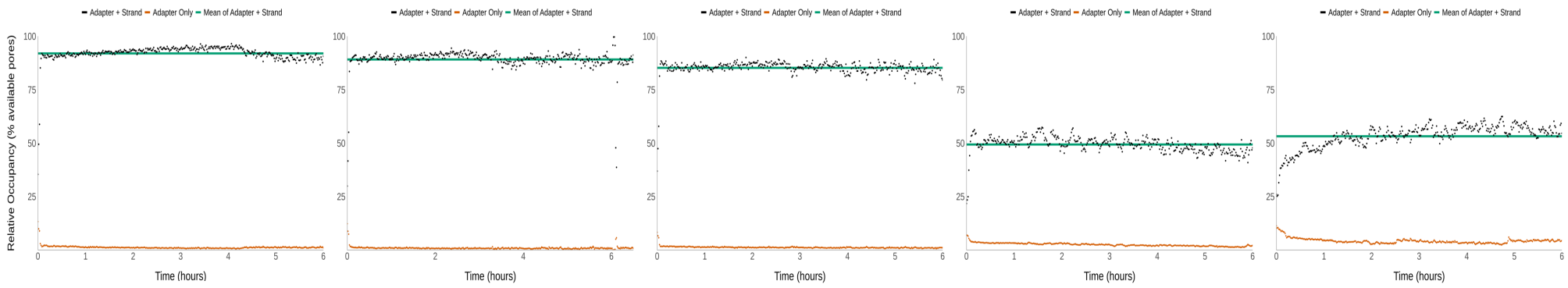
A


3-4 hrs
1 hr
1-1.5 hrs
I. Monarch Extraction
II. QC
III. ULK001 Library Prep
IV. Nemo
V. Sequence

B


Run 1A
Run 1B
Run 1C
Run 2
Run 3
Yield (Mb)
Read Length (kb)
Read Length
<100 kb
100-199 kb
200-499 kb
500-999 kb

C


Adapter + Strand
Adapter Only
Mean of Adapter + Strand
Relative Occupancy (% available pores)
Time (hours)

D

Run	Monarch Extraction Type	%CV of Input Concentration (by Nanodrop)	Input DNA (est. μg)	Reaction Volume (ml)	Reaction Time (min)	%CV of Library Concentration (by Nanodrop)	Loaded Library Amount (μg)	N50 (bp)	Yield (% Bases ≥ 100 kb)	Average Occupancy (%)	Yield per Pore (Mb)
1A	Nuclei Prep	130	10	0.5	5	55.9	3.4	133,867	1.84 Gb (62.59%)	92.4	1.81
1B	Nuclei Prep			0.5	10	72.9	4.4	131,329	0.86 Gb (61.86%)	89.8	2.13
1C	Nuclei Prep			1	5	91.6	11.4	80,395	1.09 Gb (41.59%)	85.52	2.40
2	Nuclei Prep	1.8	42	1	10	Not measured*	11	118,360	0.59 Gb (56.65%)	53.81	1.00
3	Direct Lysis	7.8	36	1	10	Not measured*	12	138,751	0.72 Gb (64.03%)	49.56	1.03

(*) %CV was not measured by Nanodrop as input DNA samples were relatively homogeneous

Figure S9. *FindingNemo in one day*: an UL sequencing protocol that extracts UHMW DNA from human cells and sequencing it in a working day (a) The protocol workflow along with the estimated step durations (b) Read length distributions of the libraries extracted using the Monarch kit; dashed black vertical lines denote N50s (c) Occupancy time lapses, (d) DNA and sequencing metrics of the libraries. Samples were extracted from GM12878 cells, each library was loaded on a MinION flow cell and run on the GridION platform. Data are after 6 hours of sequencing (excluding the first 10 minutes).