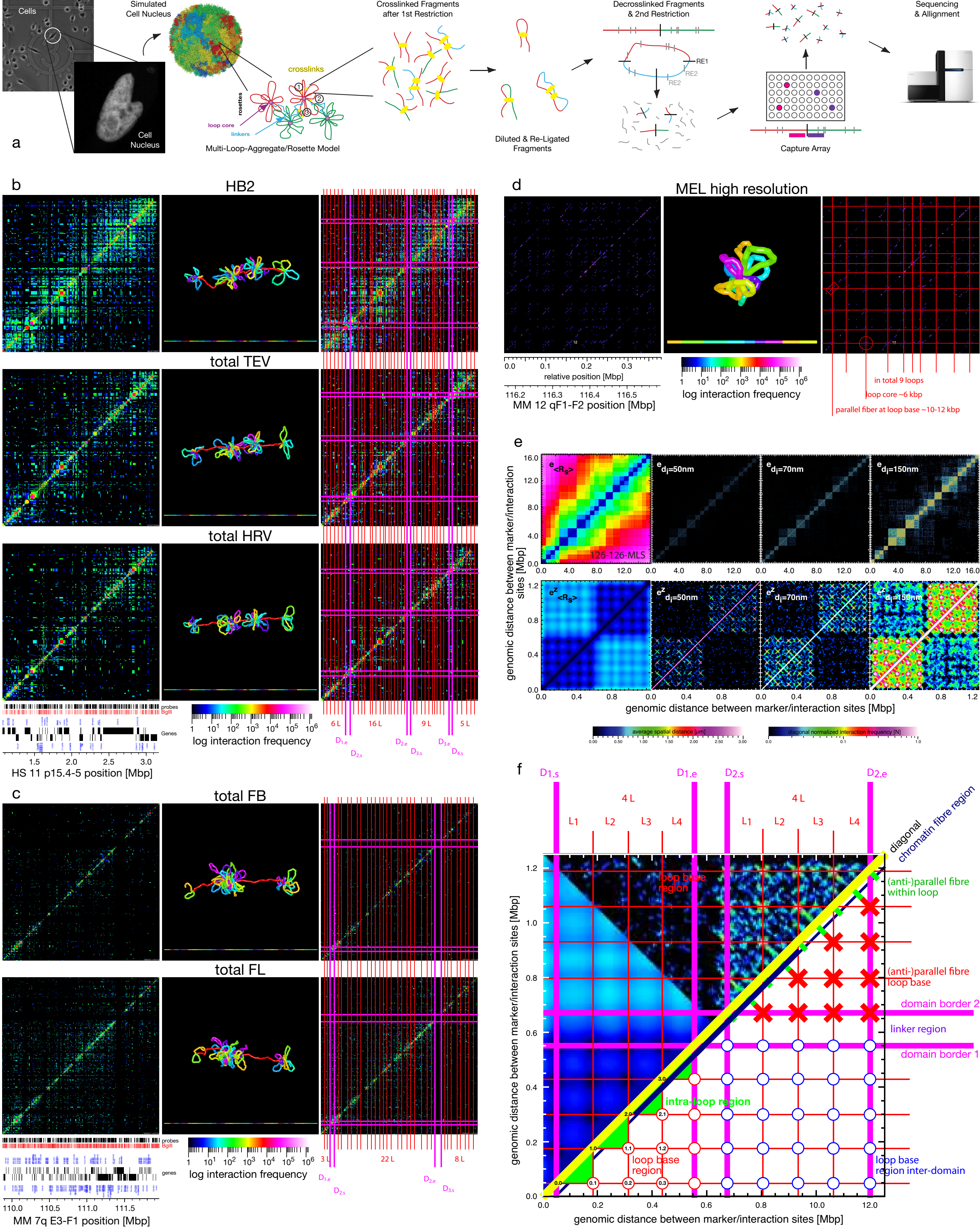
a
Cells
Cell Nucleus
Simulated Cell Nucleus
crosslinks
rosettes
loop core
linkers
Multi-Loop-Aggregate/Rosette Model
Crosslinked Fragments after 1st Restriction
Diluted & Re-Ligated Fragments
Decrosslinked Fragments & 2nd Restriction
RE1
RE2
Capture Array
Sequencing & Allignment
b
HB2
total TEV
total HRV
probes
BglII
Genes
1.5
2.0
2.5
3.0
HS 11 p15.4-5 position [Mbp]
1
10^1
10^2
10^3
10^4
10^5
10^6
log interaction frequency
6 L
16 L
9 L
5 L
$D_{1,e}$
$D_{2,s}$
$D_{2,e}$
$D_{3,s}$
$D_{3,e}$
$D_{4,s}$
c
total FB
total FL
probes
BglII
genes
110.0
110.5
111.0
111.5
MM 7q E3-F1 position [Mbp]
log interaction frequency
3 L
22 L
8 L
$D_{1,e}$
$D_{2,s}$
$D_{2,e}$
$D_{3,s}$
d
MEL high resolution
0.0
0.1
0.2
0.3
relative position [Mbp]
116.2
116.3
116.4
116.5
MM 12 qF1-F2 position [Mbp]
log interaction frequency
in total 9 loops
loop core ~6 kbp
parallel fiber at loop base ~10-12 kbp
e
$e_{\langle R_S \rangle}$
126-126-MLS
$e_{d_i=50nm}$
$e_{d_i=70nm}$
$e_{d_i=150nm}$
$e^z_{\langle R_S \rangle}$
$e^z_{d_i=50nm}$
$e^z_{d_i=70nm}$
$e^z_{d_i=150nm}$
16.0
12.0
8.0
4.0
0.0
1.2
0.8
0.4
genomic distance between marker/interaction sites [Mbp]
average spatial distance [µm]
0.00
0.50
1.00
1.50
2.00
2.50
3.00
diagonal normalized interaction frequency [N]
0.0
0.1
1.0
f
$D_{1,s}$
$D_{1,e}$
$D_{2,s}$
$D_{2,e}$
4 L
L1
L2
L3
L4
diagonal chromatin fibre region
loop base region
(anti-)parallel fibre within loop
(anti-)parallel fibre loop base
domain border 2
linker region
domain border 1
intra-loop region
loop base region
loop base region inter-domain
0.0
1.0
2.0
3.0
0.1
0.2
0.3
1.1
1.2
2.1
0.2
0.4
0.6
0.8
1.0
1.2
genomic distance between marker/interaction sites [Mbp]