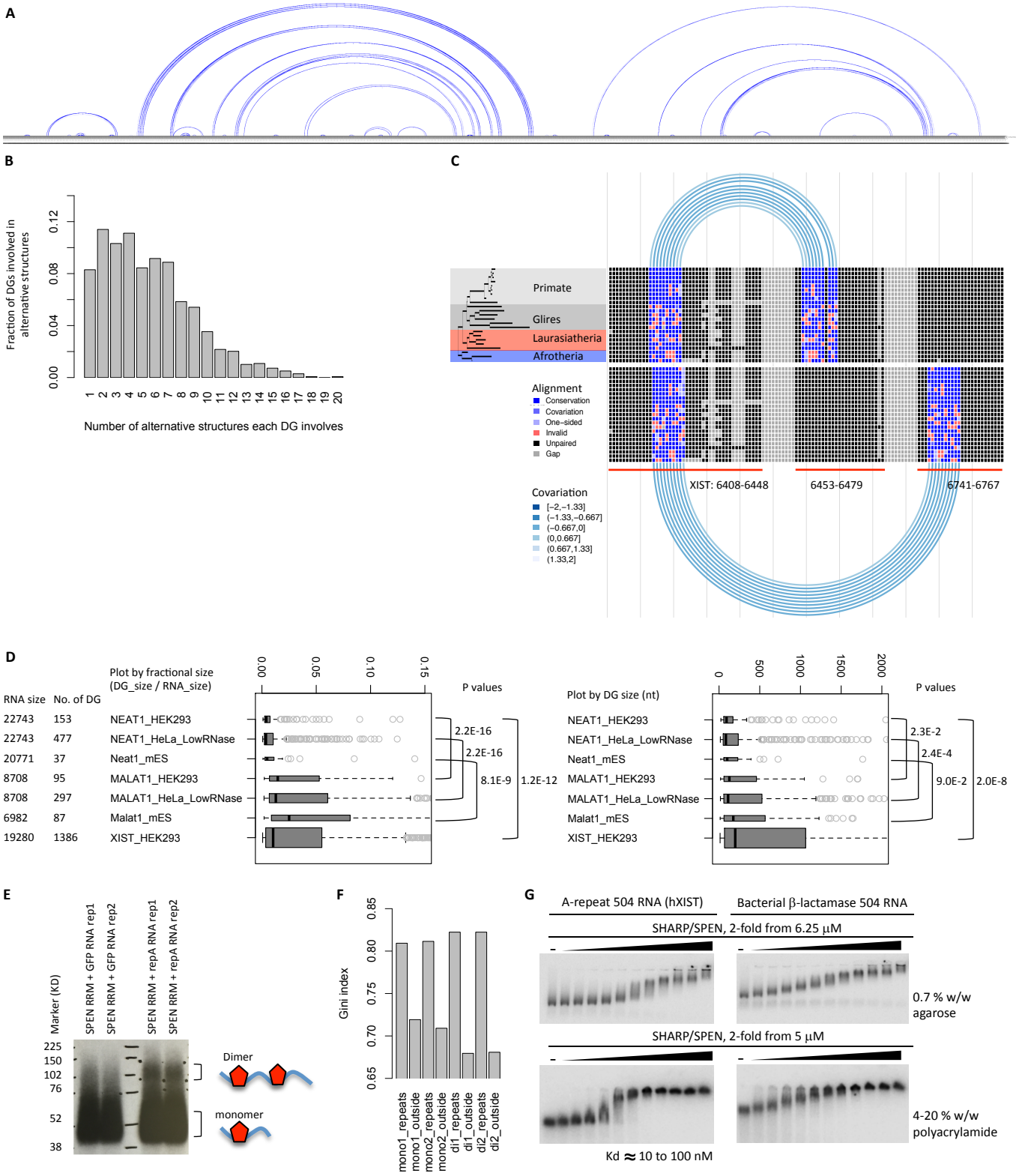
A
B
Fraction of DGs involved in alternative structures
0.00
0.04
0.08
0.12
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Number of alternative structures each DG involves
C
Primate
Glires
Laurasiatheria
Afrotheria
Alignment
Conservation
Covariation
One−sided
Invalid
Unpaired
Gap
Covariation
[−2,−1.33]
(−1.33,−0.667]
(−0.667,0]
(0,0.667]
(0.667,1.33]
(1.33,2]
XIST: 6408-6448
6453-6479
6741-6767
D
Plot by fractional size (DG_size / RNA_size)
0.00
0.05
0.10
0.15
P values
RNA size
No. of DG
22743 153 NEAT1_HEK293
22743 477 NEAT1_HeLa_LowRNase
20771 37 Neat1_mES
8708 95 MALAT1_HEK293
8708 297 MALAT1_HeLa_LowRNase
6982 87 Malat1_mES
19280 1386 XIST_HEK293
2.2E-16
2.2E-16
8.1E-9
1.2E-12
Plot by DG size (nt)
0
500
1000
1500
2000
P values
NEAT1_HEK293
NEAT1_HeLa_LowRNase
Neat1_mES
MALAT1_HEK293
MALAT1_HeLa_LowRNase
Malat1_mES
XIST_HEK293
2.3E-2
2.4E-4
9.0E-2
2.0E-8
E
Marker (KD)
SPEN RRM + GFP RNA rep1
SPEN RRM + GFP RNA rep2
SPEN RRM + repA RNA rep1
SPEN RRM + repA RNA rep2
225
150
102
76
52
38
Dimer
monomer
F
Gini index
0.65
0.70
0.75
0.80
0.85
mono1_repeats
mono1_outside
mono2_repeats
mono2_outside
di1_repeats
di1_outside
di2_repeats
di2_outside
G
A-repeat 504 RNA (hXIST)
Bacterial β-lactamase 504 RNA
SHARP/SPEN, 2-fold from 6.25 μM
0.7 % w/w agarose
SHARP/SPEN, 2-fold from 5 μM
4-20 % w/w polyacrylamide
Kd ≈ 10 to 100 nM