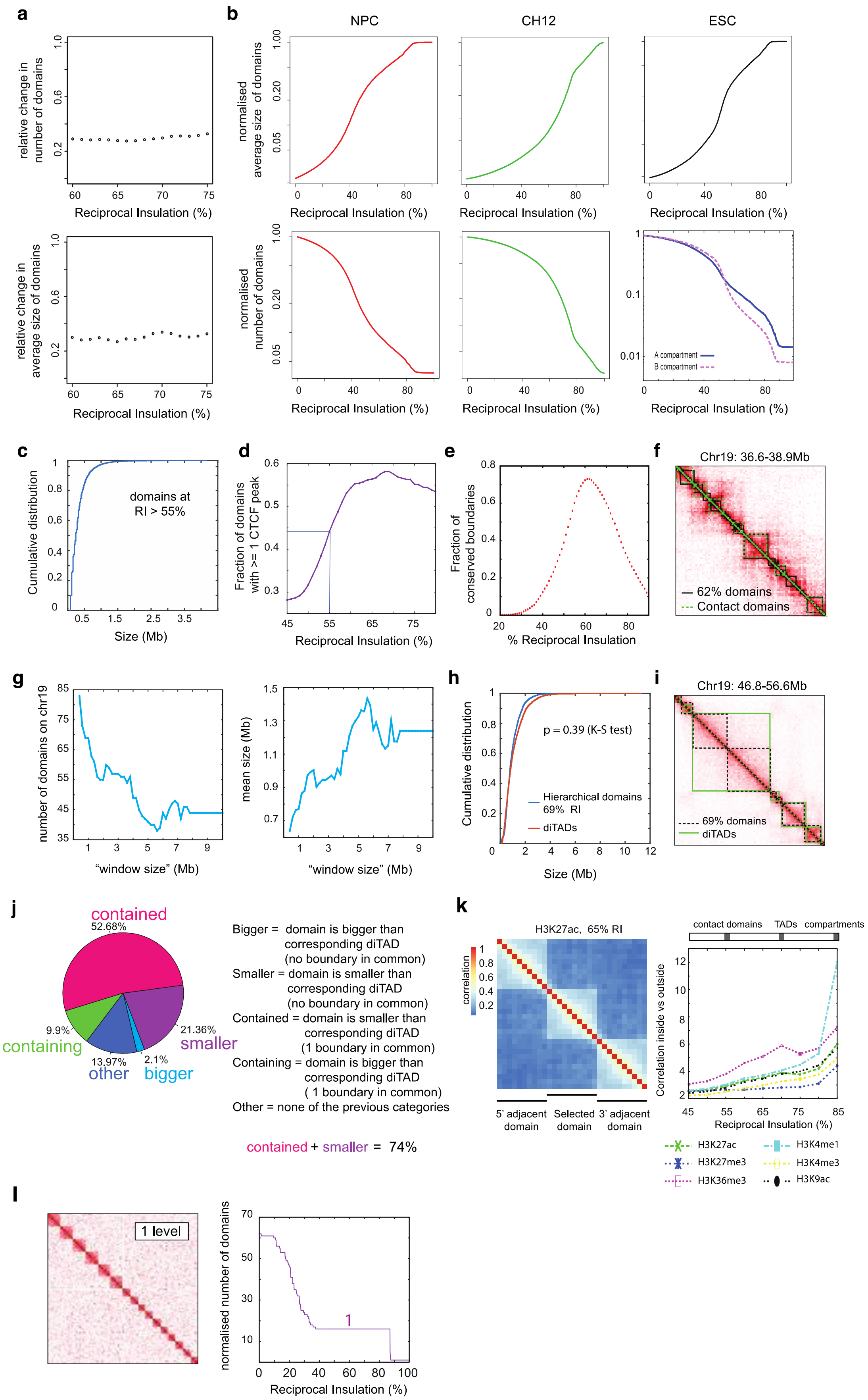

Bigger = domain is bigger than corresponding diTAD (no boundary in common)
Smaller = domain is smaller than corresponding diTAD (no boundary in common)
Contained = domain is smaller than corresponding diTAD (1 boundary in common)
Containing = domain is bigger than corresponding diTAD (1 boundary in common)
Other = none of the previous categories

contained + smaller = 74%

Supplemental Figure S1.

a. Changes in the number (top) and the mean size (bottom) of domains between when the threshold RI value is increased by 5% with respect to the x coordinate of the data point (i.e. the point at 60% represent changes when increasing from 60% to 65% etc).

b. Normalized mean size (upper panels) and number (lower panels) of domains as a function of the minimal RI threshold used to define them (semi-log scale), in NPC, CH12 and ESC. The normalized number of domains detected in regions belonging exclusively to either the A and B compartment is shown for ESCs. Normalized number of domains genome-wide for ESC is plotted in main Figure 1c.

c. Cumulative distribution of the size of domains at 55% (median 180 kb).

d. Fraction of domains with at least one CTCF bound site at both boundaries, as a function of the RI used to define domains. Straight lines indicate domains whose size is most similar to contact domains (7).

e. Fraction of boundaries of contact domains in CH12 cells (7), which are detected by the CaTCH algorithm applied to same Hi-C dataset, as a function of the RI used to define hierarchical domains. Maximal overlap is found at 62% RI.

f. Example of domains at 62% of RI in CH12 (black lines) and contact domains (7) (green lines) for a small region of chromosome 19 in CH12 cells.

g. Number (left panel) and mean size (right panel) of domains detected by the directionality index method (diTADs) (7) as a function of the “window size” parameter required by the method. No intrinsic rule allows to choose any window size below 8 Mbps from these plots.

h. Cumulative distribution of domains size for diTADs (red curve) and domains at 69% RI (blue curve). KS-test shows that these two sets of domains are not significantly different.

i. Example of domains at 69% of RI (black squares) and diTADs (green squares) for a small region of chromosome 19 in ESCs. The CaTCH algorithm is more sensitive to small variations in contact probabilities within large, uniform domains.

j. Pie chart representing the properties of non-conserved domains between diTADs and the set of domains at 69%. Most domains at 69% divide a diTAD into smaller domains.

k. Enrichment in correlation of histone marks within vs. across domains (7). Correlation is maximal at the scale of compartments, consistent with the notion that compartments A and B represent stretches of active and inactive chromatin respectively.

l. Right: Number of domains detected by CaTCH as a function of RI in computationally generated contact maps with one preferential folding level and different domain sizes. Left: The corresponding heat map.