Table S4 Number of times the defined TAD boundaries appeared in the iteration.

PAX3 Human: TAD size from 15 to 40

Boundary	Times appeared	Comment
Chr2: 222,451,756	25 (100%)	TAD boundary
Chr2: 222,871,756	25 (100%)	TAD boundary
Chr2: 223,171,756	25 (100%)	Sub-TAD boundary
Chr2: 223,511,756	25 (100%)	TAD boundary
Chr2: 223,871,756	25 (100%)	TAD boundary

FOXO1 human: TAD size from 20 to 50

Boundary	Times appeared	Comment
Chr13: 39,502,000	30 (100%)	TAD boundary
Chr13: 40,262,000	30 (100%)	TAD boundary
Chr13: 41,362,000	30 (100%)	TAD boundary
Chr13: 41,902,000	30 (100%)	TAD boundary

Pax3 Mouse: TAD size from 15 to 30

Boundary	Times appeared	Comment
Chr1: 77,530,000	15 (100%)	TAD boundary
Chr1: 77,950,000	15 (100%)	TAD boundary
Chr1: 78,200,000	13 (86.7%)	Sub-TAD boundary
Chr1: 78,490,000	15 (100%)	TAD boundary
Chr1: 78,740,000	13 (86.7%)	TAD boundary

Foxo1 mouse: TAD size from 20 to 40

Boundary	Times appeared	Comment
Chr3: 51,220,000	20 (100%)	TAD boundary
Chr3: 51,500,000	20 (100%)	TAD boundary
Chr3: 52,060,000	20 (100%)	TAD boundary
Chr3: 52,780,000	20 (100%)	TAD boundary

RMS Translocation: TAD size from 30 to 90

Boundary	Times appeared	Comment
Chr2: 223,815,327	60 (100%)	TAD boundary
Chr13: 40,249,897	58 (96%)	TAD boundary
Chr2: 223,512,553	45 (75%)	TAD boundary
Chr13: 39,799,255	31 (52%)	TAD boundary

Column 1 shows the predicted chromosomal location of the boundaries identified by D.I. analysis (±20 kb); Column 2 shows the number of times it was selected as a boundary in the iterative process and the percentage it represents; Column 3 shows the interpretation of the defined boundary.