

Table S4. Permutation results after controlling for chromatin compartment (HindIII).

Dataset	Total # Unique Translo- cations	Mean Hi-Score		Permutation Method				T-test	Rank Sum	# of individually significant translocations	% Genome Covered	% Interactions Covered*
		Translo- cations	Permut- ations	1	2	3	4					
Mitelman Database (total)	577	0.167	0.124	<0.001	0.002	<0.001	<0.001	7.8 E-04	1.2 E-03	6	79.7%	1.12%
Multiple myeloma (cytogenetic band mapping)	89	0.166	0.091	<0.001	0.003	0.007	0.001	9.7 E-02	1.7 E-01	5	44.8%	0.21%
Prostate cancer (cytogenetic band mapping)	89	0.071	0.014	<0.001	0.018	0.026	0.002	7.1 E-03	4.5 E-03	0	43.1%	0.19%
Mendelian	779	-0.047	-0.071	<0.001	0.004	<0.001	<0.001	1.6 E-02	2.1 E-01	6	91.5%	0.79%

*Percentage of inter-chromosomal 1-Mb bins that are covered by translocations.