			unbiased			**biased**			**Pattern matched**		
			D_{max}	p-value	confidence interval	D_{max}	p-value	confidence interval	D_{max}	p-value	confidence interval
L1	truncated	all	0.1952	<0.0001	0.0000-0.0004	0.1482	<0.0001	0.0000-0.0004	0.1768	<0.0001	0.0000-0.0004
		TA	0.2188	0.0010	0.0005-0.0018	0.1738	0.0114	0.0094-0.0137	0.2024	0.0020	0.0017-0.0023
		TSD≥14	0.1385	<0.0001	0.0000-0.0004	0.0915	<0.0001	0.0000-0.0004	not determined		
	full-length	all	0.0726	<0.0001	0.0000-0.0004	0.0622	0.0002	0.0000-0.0007	0.0413	0.0268	0.0237-0.0302
		TA	0.0481	0.5763	0.5665-0.5860	0.0770	0.1502	0.1433-0.1574	0.0673	0.4025	0.3994-0.4055
		TSD≥14	0.0618	0.0053	0.0040-0.0069	0.0889	<0.0001	0.0000-0.0004	not determined		
Alu	truncated	all	0.0343	0.0281	0.0249-0.0315	0.0546	0.0003	0.0001-0.0009	0.0426	0.0043	0.0031-0.0058
		TSD≥14	0.0373	0.0532	0.0489-0.0578	0.0483	0.0089	0.0072-0.0109	not determined		
	full-length	all	0.0296	<0.0001	0.0000-0.0004	0.0566	<0.0001	0.0000-0.0004	0.0069	0.1243	0.1179-0.1309
		TSD≥14	0.0229	0.0002	0.0000-0.0007	0.0814	<0.0001	0.0000-0.0004	not determined		

Supplementary Table 1: Statistical data characterizing biased, unbiased and pattern-matched expected distributions of microhomologies associated with preexisting human L1 and *Alu* insertions