

Supplementary Table 1. Read counts during meta3C/Hi-C analysis

Dataset	G_3C	M_3C	Y_3C		D_HiC	P_HiC	K_HiC*
			Y_3C_A	Y_3C_B			
Processed reads	198,493,086	366,961,002	2,921,579,828	1,239,950,680	133,509,800	157,755,162	37,984,239
Reads mapped (MAPQ>20)	181,467,148	278,726,053	2,868,601,794	1,155,939,113	108,556,752	124,877,330	32,412,518
Percentage mapped	91.42%	75.96%	98.19%	93.22%	81.31%	79.16%	85.66%
Intercontig reads	3,271,007	35,717,451	188,322,547	94,104,831	9,488,683	21,679,019	192,510
Percentage intercontig	1.65%	9.73%	6.45%	7.59%	7.11%	13.74%	0.64%
Filtered intercontig reads	1,574,468	28,773,234	90,197,910	63,855,164	6,880,255	18,917,493	53,157
Percentage intercontig after filtering	0.79%	7.84%	3.09%	5.15%	5.15%	11.99%	0.18%

*for K_HiC, an average of 43 samples is presented in this table; For datasets that used multiple restriction enzymes, numbers presented are a combined total; MAPQ = mapping quality