

Table 1: Overview of the Pool-Seq data used in this work. For all replicates (rep) and generations (gen) we show the lane ID, the sequencing technology (platform), the read length (rl.), the inner distance (id.) and the number of sequenced paired-end reads in millions. Samples from naive flies not having the *P-element* are also included.

rep	gen	lane ID	platform	rl.	id.	reads [M]
naive	-	CEBYBANXX	Illumina HiSeq 2500	125	xx	13.2
naive	-	CD67CANXX	Illumina HiSeq 2500	125	xx	19.0
R1	G1	CDMKUANXX	Illumina HiSeq 2500	125	55	27.6
R1	G10	CDMKUANXX	Illumina HiSeq 2500	125	52	25.9
R1	G20	CDMKUANXX	Illumina HiSeq 2500	125	52	28.8
R1	G34	CE7UPANXX	Illumina HiSeq 2500	125	45	22.2
R1	G40	CEBYBANXX	Illumina HiSeq 2500	125	60	30.1
R1	G48	CD67CANXX	Illumina HiSeq 2500	125	43	23.7
R2	G1	CDMKUANXX	Illumina HiSeq 2500	125	44	31.7
R2	G10	CDMKUANXX	Illumina HiSeq 2500	125	50	25.9
R2	G20	CDMKUANXX	Illumina HiSeq 2500	125	56	26.4
R2	G34	CE7UPANXX	Illumina HiSeq 2500	125	39	30.8
R2	G40	CEBYBANXX	Illumina HiSeq 2500	125	72	25.6
R2	G48	CD67CANXX	Illumina HiSeq 2500	125	34	26.9
R4	G1	CDMKUANXX	Illumina HiSeq 2500	125	44	27.1
R4	G10	CDMKUANXX	Illumina HiSeq 2500	125	55	24.5
R4	G20	CDMKUANXX	Illumina HiSeq 2500	125	57	25.8
R4	G34	CE7UPANXX	Illumina HiSeq 2500	125	51	23.0
R4	G40	CEBYBANXX	Illumina HiSeq 2500	125	79	22.9
R4	G48	CD67CANXX	Illumina HiSeq 2500	125	50	18.8