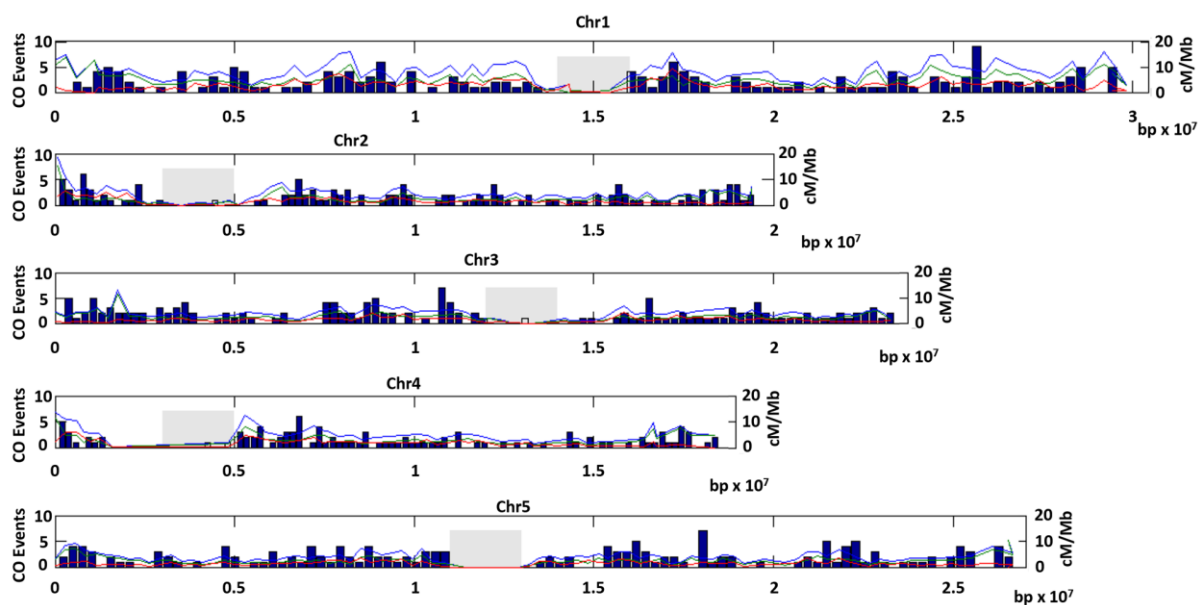
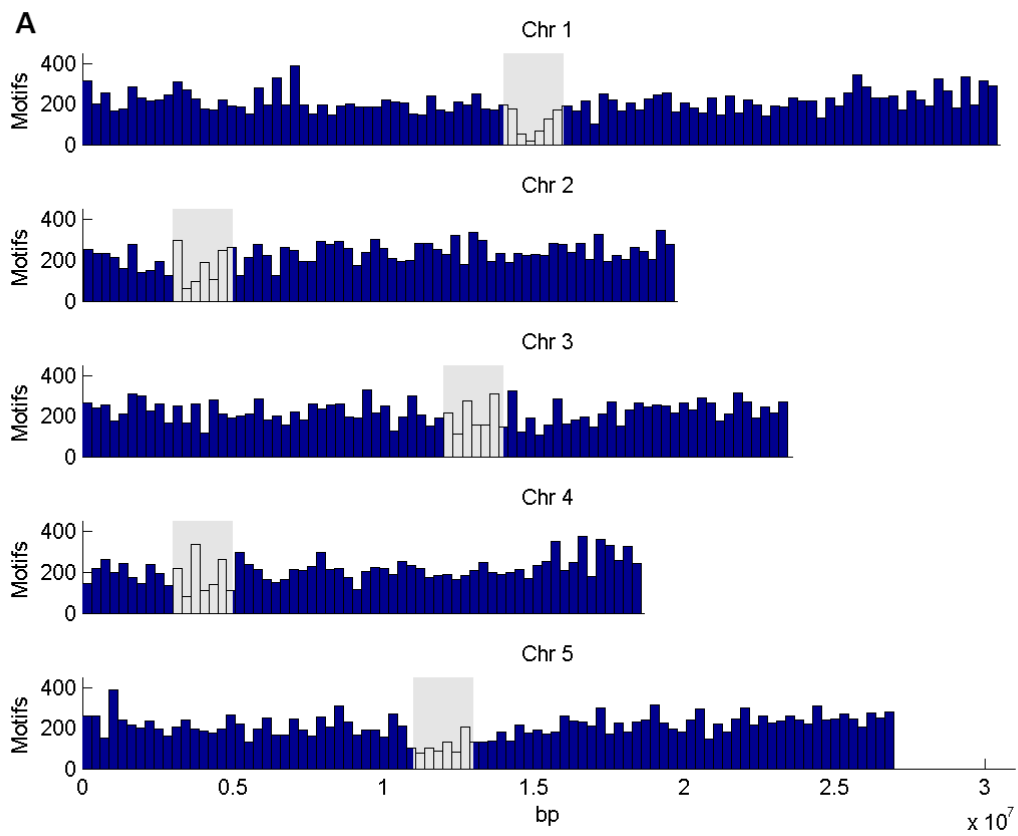


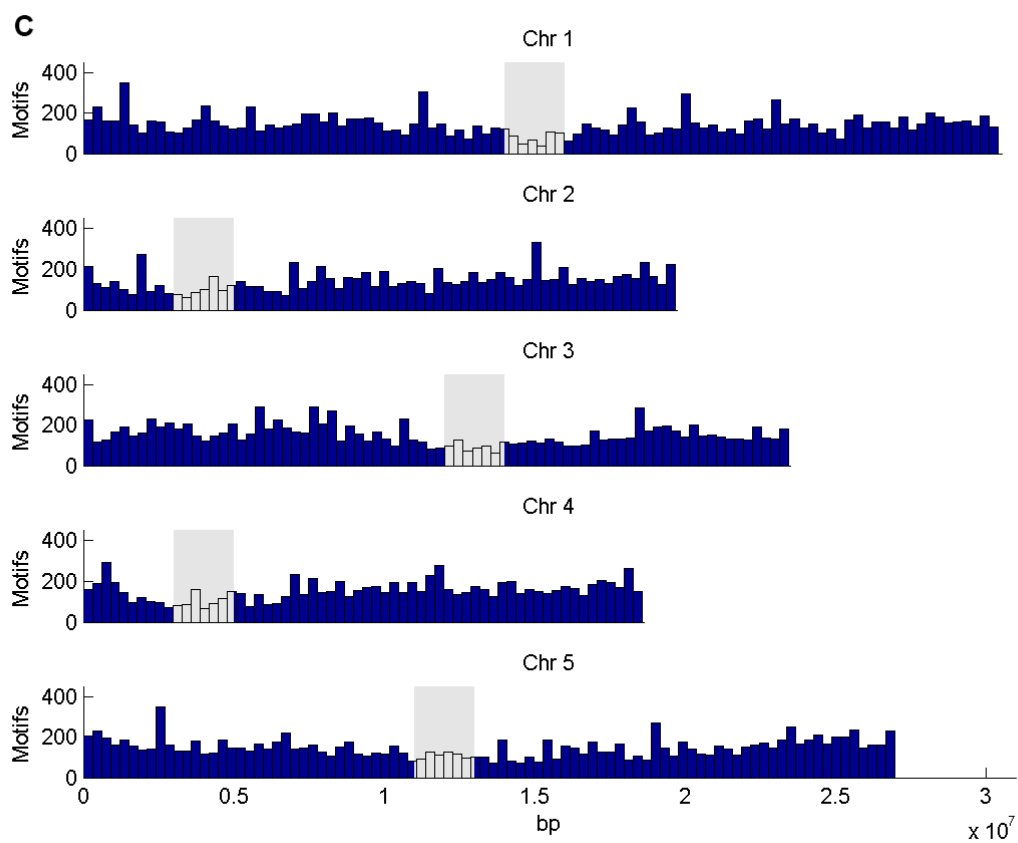
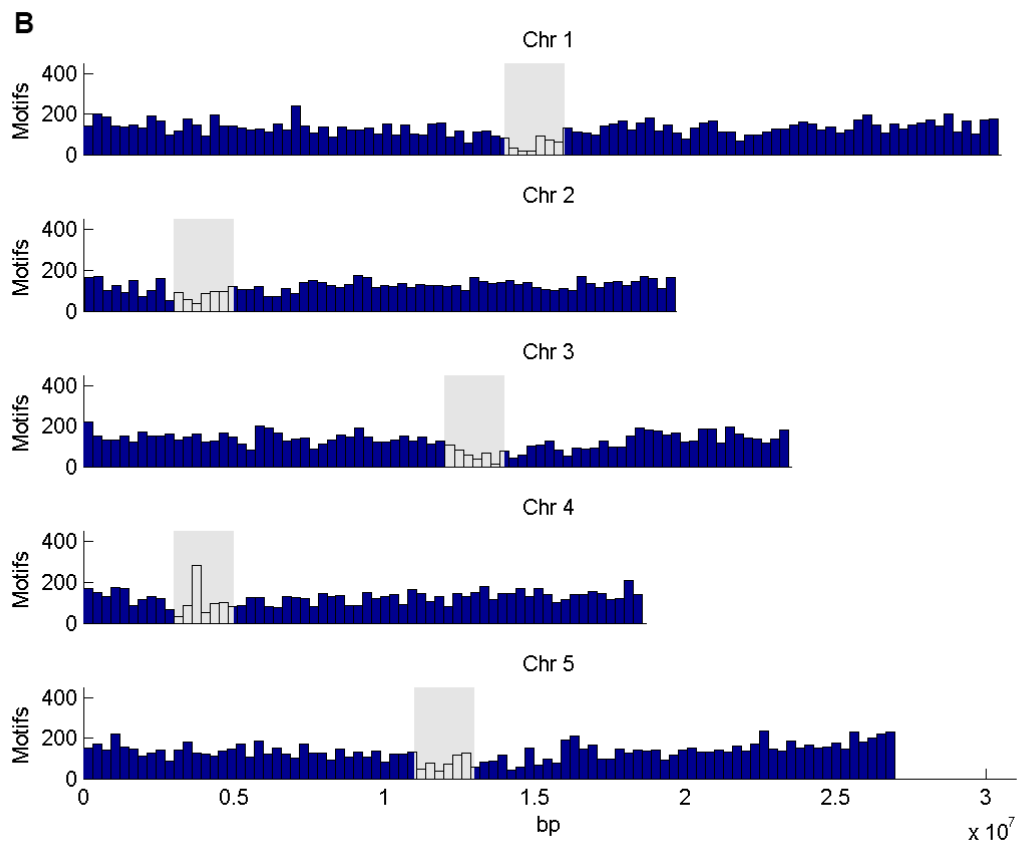
## Supplemental data



### Supplemental Figure 1. Distribution of CO events.

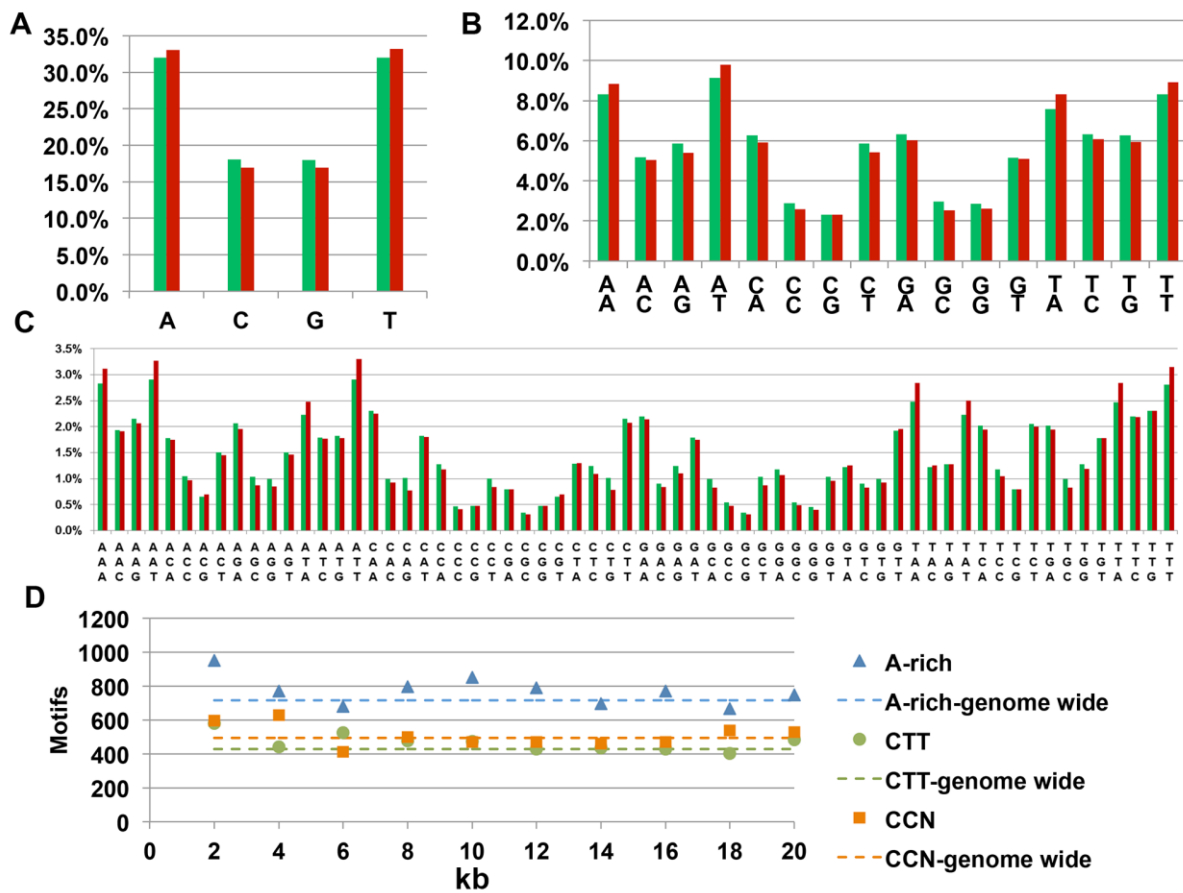
Distribution of the 737 CO events dataset along 5 chromosomes of *A. thaliana* (blue bars). The lines show the CO rate of male (green), female (red) and the sum of both (blue) (Giraut et al., 2011). Pericentric region (~ 2 Mb around the centromere) is shown as a grey box.





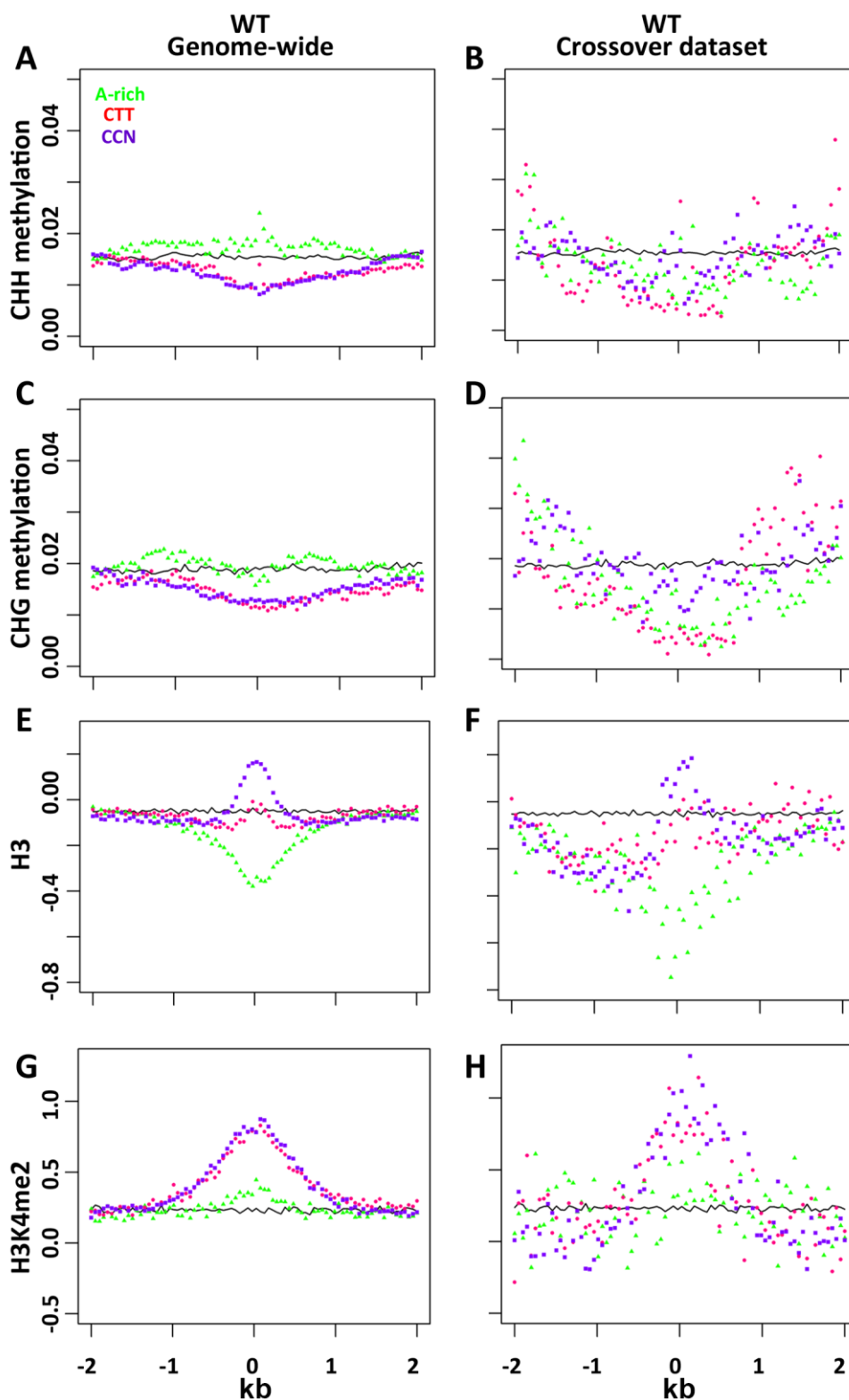
**Supplemental Figure 2. Distribution of the three crossover motifs.**

The distribution of the (A) A-rich, (B) CTT and (C) CCN motifs (blue bars) is shown for all 5 chromosomes. The pericentric region (~ 2 Mb around the centromere) is shown as a grey box.



**Supplemental Figure 3. AT/GC content and motif signal.**

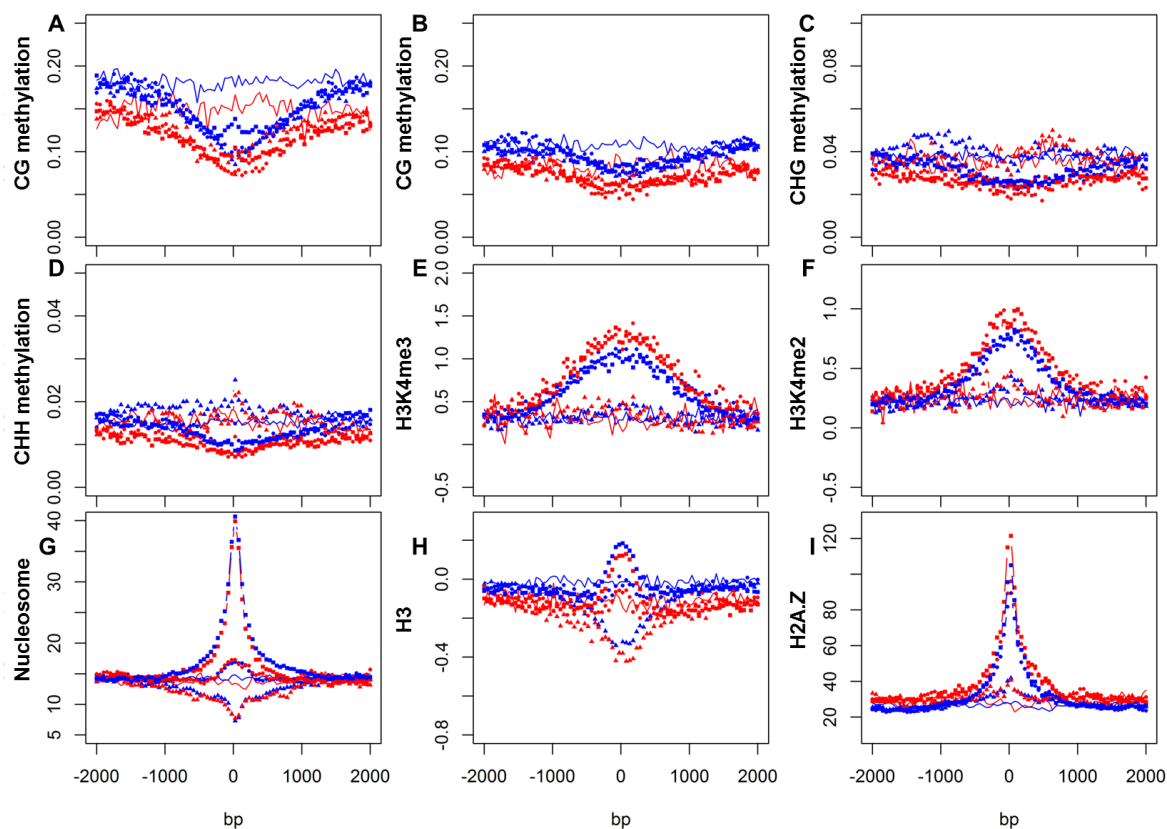
The AT content in CO sites (red) in comparison to the genome wide rate (green) for (A) mono (B) di and (C) tri nucleotides. (D) Motif abundance in windows of 2 kb distance from the CO site. A-rich (triangles), CTT-repeat (circles), CCN motifs (squares).



**Supplemental Figure 4. Epigenetic modifications around all the motifs.**

Epigenetic markers around the CCN-repeat (purple square), CTT-repeat (red circle), the A-rich CO motifs (green triangle) and the randomly picked control sequences (continuous black lines) are shown. The data are the average from hot and cold

recombination regions around the three motifs and are shown on the Y-axis for 50 bp bins from the centre of the X axis and up to 2000 bp upstream and downstream of the motifs. The analysis was performed on genome wide dataset (A,C,E,G) and the crossover dataset (B,D,F,H). The epigenetic markers analysed are CHH methylation (A,B); CHG methylation (C,D); H3 occupancy (E,F) and H3K4me2 (G,H).



**Supplemental Figure 5. Average epigenetic modifications 2000 bp around all the motifs in hot and cold intervals.**

Averaged data are shown for the A-rich (triangles), CTT (circles), CCN motifs (squares) and a clear line for random control, in hot (red) or cold (blue) intervals. (A) CG methylation in wild-type plants. (B) CG methylation in *ddm1* mutant. (C) CHG methylation. (D) CHH methylation. (E) H3K4me3. (F) H3K4me2. (G) Nucleosome occupancy (H) H3 occupancy. (I) H2A.Z.

**Supplemental Table 1. Number of reads yield from a lane of hi-seq Illumina machine of two different library preparation protocols.**

Library preparation	Sample	Paired reads	% of lane	Fold
Illumina	GFP5	22859951	15.08	19.04
Illumina	GFP6	19981382	13.18	16.65
Illumina	GFP7	10766399	7.11	8.97
Illumina	GFP8	6802176	4.49	5.67
Illumina	RFP5	13562178	8.954	11.32
Illumina	RFP6	12864547	8.49	10.72
Illumina	RFP7	14521412	9.58	12.1
Illumina	RFP8	50167156	33.11	41.81
	sum	151525201	100	126.271
ChIP seq (Blecher-Gonen et al., 2013)	GFP10	8471940	5.78	7.06
ChIP seq (Blecher-Gonen et al., 2013)	GFP11	10490252	7.16	8.74
ChIP seq (Blecher-Gonen et al., 2013)	GFP12	9118655	6.23	7.6
ChIP seq (Blecher-Gonen et al., 2013)	GFP14	8049317	5.5	6.71
ChIP seq (Blecher-Gonen et al., 2013)	GFP15	8126462	5.55	6.77
ChIP seq (Blecher-Gonen et al., 2013)	GFP16	8680000	5.93	7.23
ChIP seq (Blecher-Gonen et al., 2013)	GFP17	11054374	7.55	9.21
ChIP seq (Blecher-Gonen et al., 2013)	RFP10	6774641	4.63	5.65
ChIP seq (Blecher-Gonen et al., 2013)	RFP11	8401876	5.74	7
ChIP seq (Blecher-Gonen et al., 2013)	RFP12	8412500	5.74	7.01
ChIP seq (Blecher-Gonen et al., 2013)	RFP13	10875360	7.43	9.06
ChIP seq (Blecher-Gonen et al., 2013)	RFP14	9682359	6.61	8.07
ChIP seq (Blecher-Gonen et al., 2013)	RFP15	14545559	9.93	12.12
ChIP seq (Blecher-Gonen et al., 2013)	RFP16	7399680	5.05	6.17
ChIP seq (Blecher-Gonen et al., 2013)	RFP17	8010410	5.45	6.68
ChIP seq (Blecher-Gonen et al., 2013)	RFP19	8360097	5.71	6.97
	sum	146453482	100	122.05
Difference between the methods		5071719	3.4	4.23