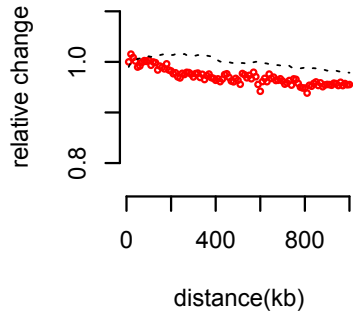
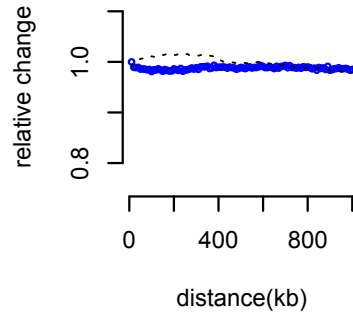
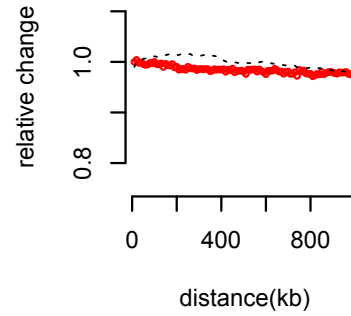
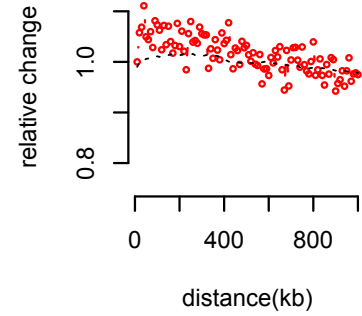
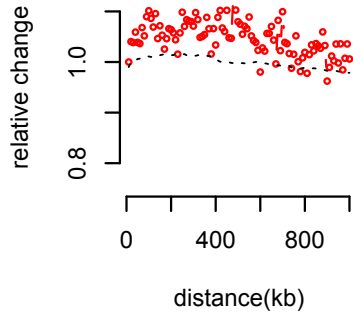
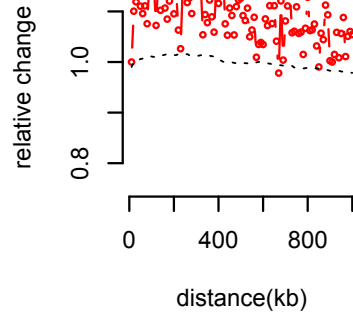
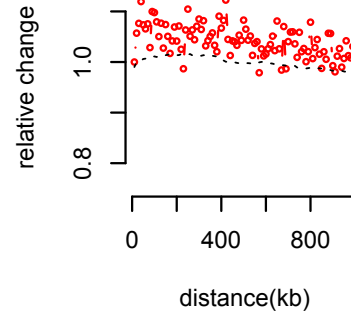
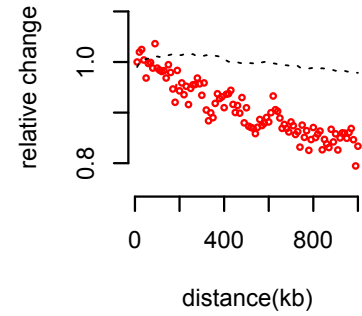
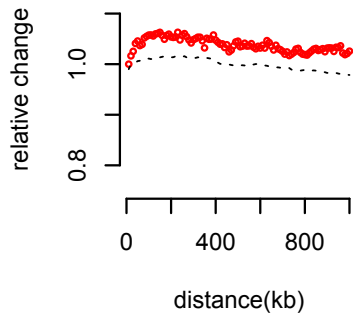
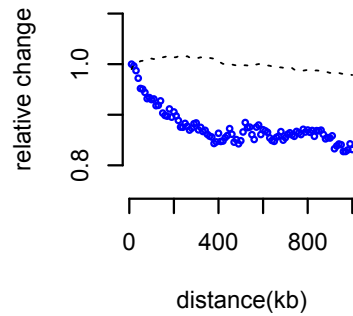
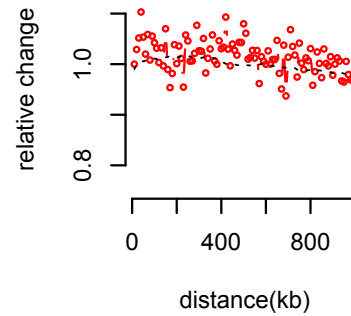
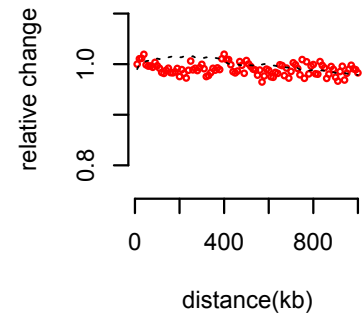


# Workflow

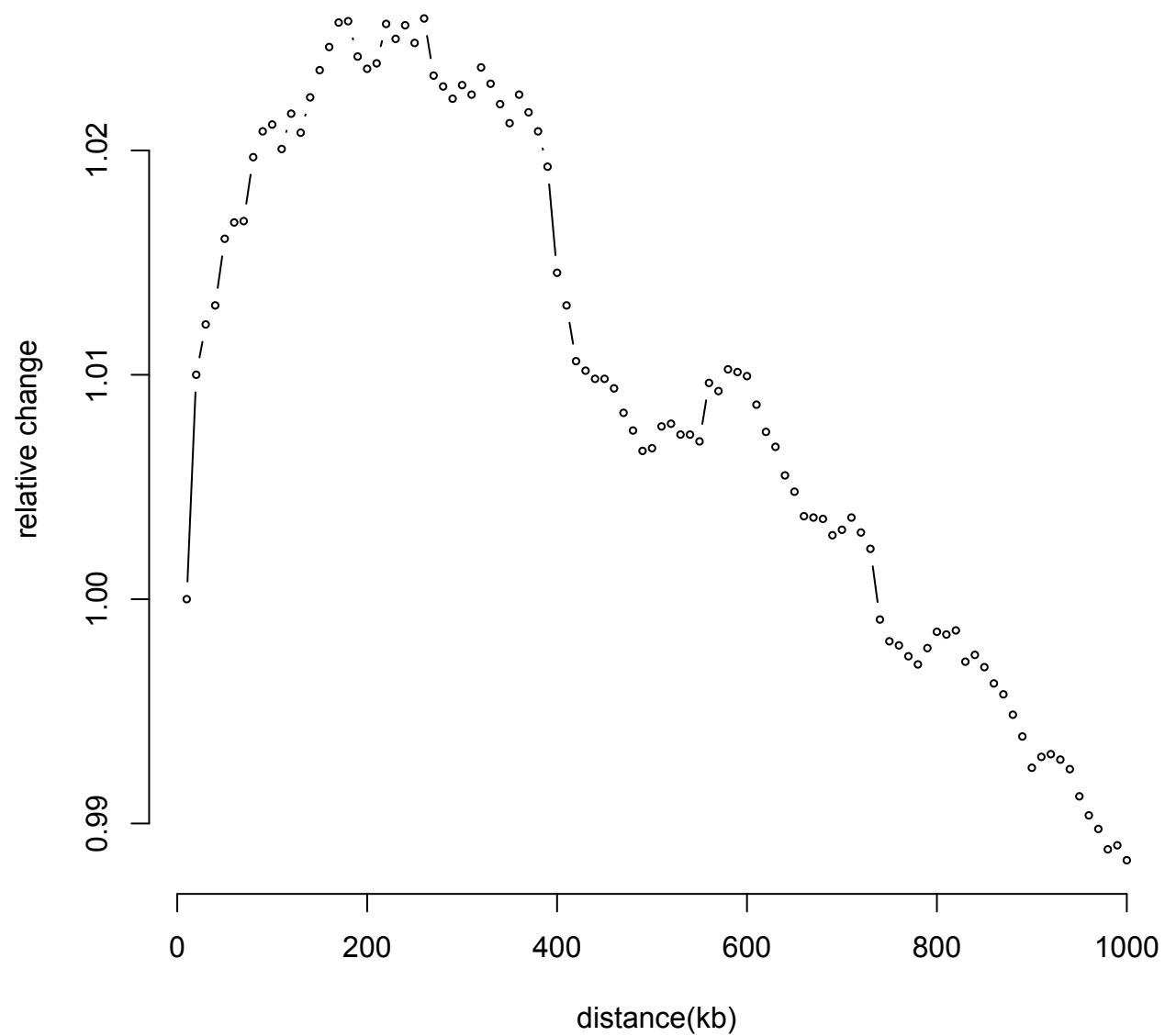
- Took care of the up-/downstream (directional)
- Removed blacklist
- 10kb bin size, starting right at the bkpts(union), thus random phasing
- 12 Histone modifications in K562
  - K562\_H2AFZ
  - K562\_H3K27ac
  - K562\_H3K27me3 (2)
  - K562\_H3K36me3 (2)
  - K562\_H3K4me1 (2)
  - K562\_H3K4me2
  - K562\_H3K4me3 (4)
  - K562\_H3K79me2
  - K562\_H3K9ac (2)
  - K562\_H3K9me1
  - K562\_H3K9me3
  - K562\_H4K20me1

Type of modification	Histone							
	H3K4	H3K9	H3K14	H3K27	H3K79	H3K122	H4K20	H2BK5
mono-methylation	activation <sup>[6]</sup>	activation <sup>[7]</sup>		activation <sup>[7]</sup>	activation <sup>[7][8]</sup>		activation <sup>[7]</sup>	activation <sup>[7]</sup>
di-methylation	activation	repression <sup>[3]</sup>		repression <sup>[3]</sup>	activation <sup>[8]</sup>			
tri-methylation	activation <sup>[9]</sup>	repression <sup>[7]</sup>		repression <sup>[7]</sup>	activation, <sup>[8]</sup> repression <sup>[7]</sup>			repression <sup>[3]</sup>
acetylation		activation <sup>[9]</sup>	activation <sup>[9]</sup>	activation <sup>[10]</sup>		activation <sup>[11]</sup>		

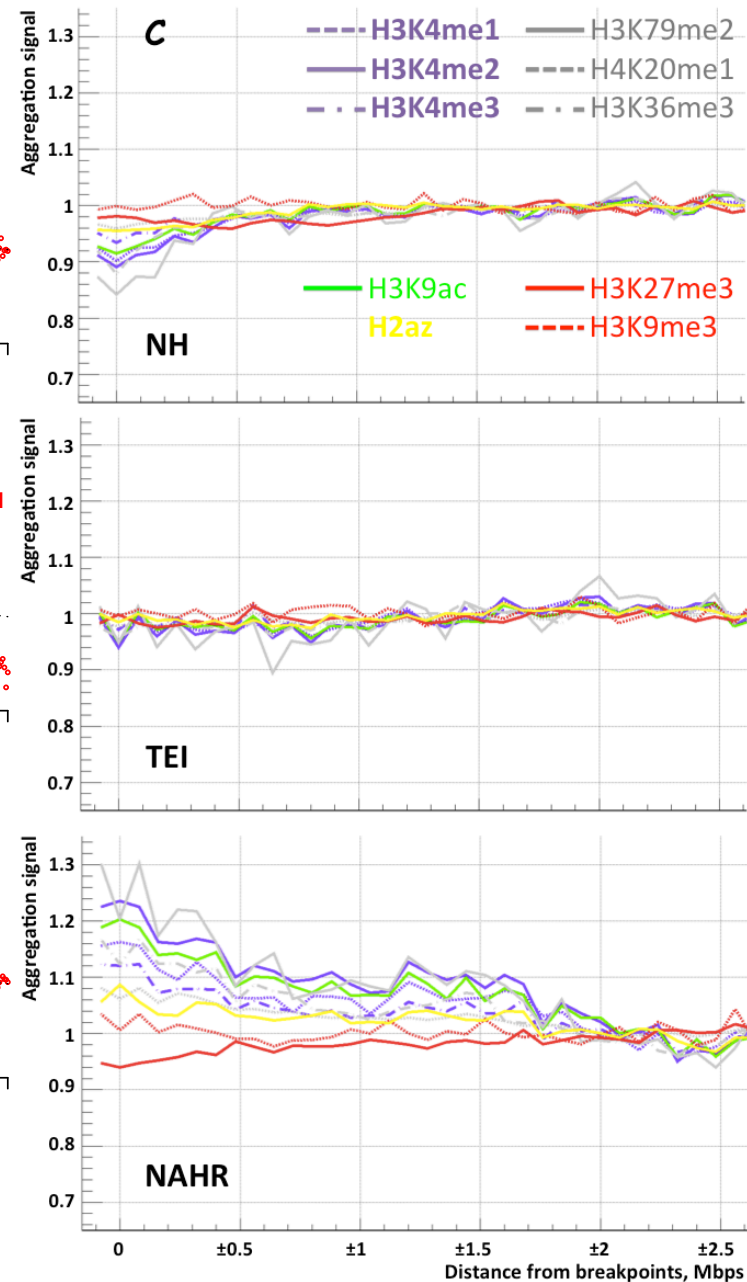
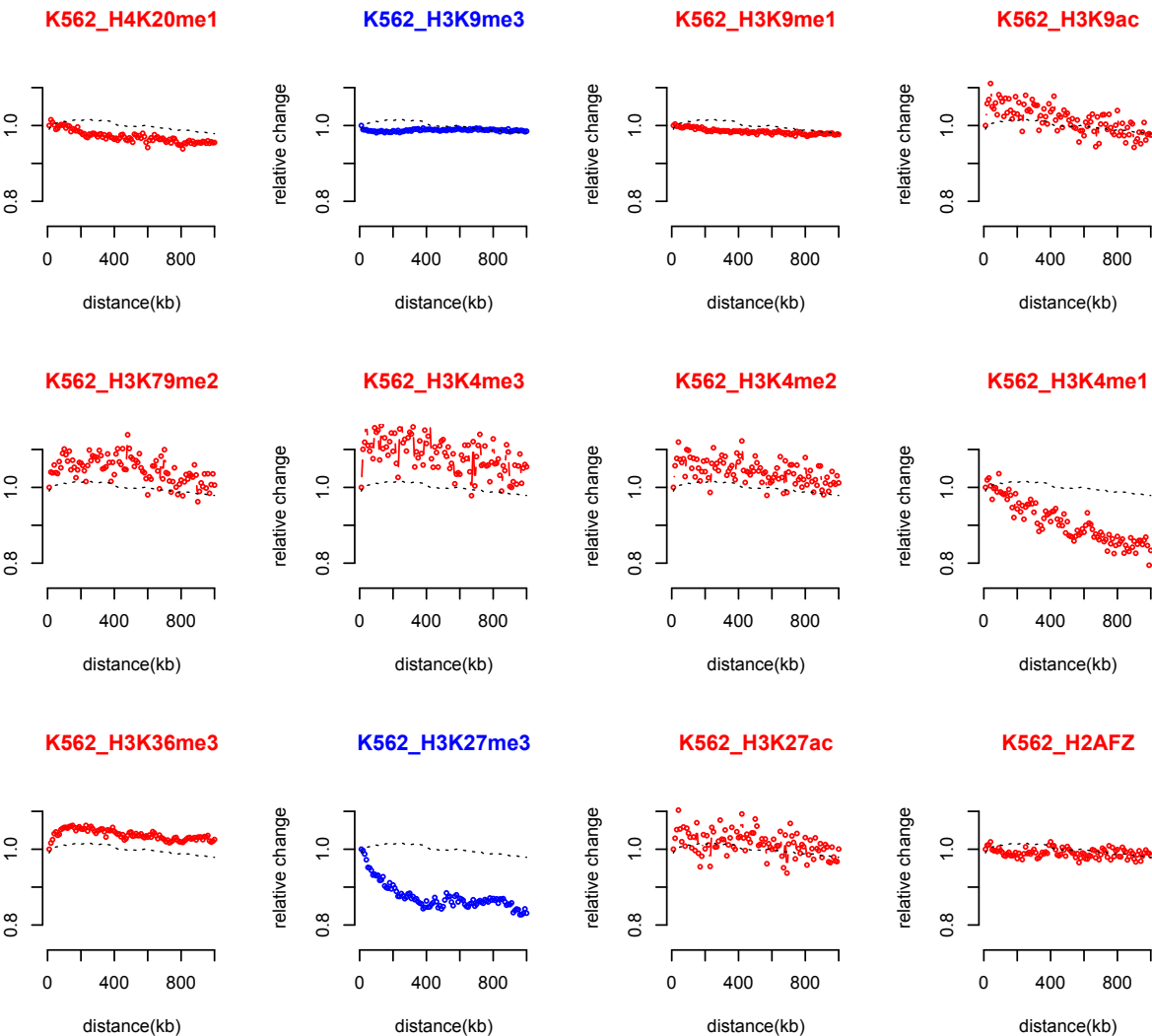
- **H3K4me3** is enriched in transcriptionally active promoters.<sup>[12]</sup>
- **H3K9me3** is found in constitutively repressed genes.
- **H3K27me3** is found in facultatively repressed genes.<sup>[7]</sup>
- **H3K36me3** is found in actively transcribed gene bodies.
- **H3K9ac** is found in actively transcribed promoters.
- **H3K14ac** is found in actively transcribed promoters.
- **H3K27ac** distinguishes active enhancers from poised enhancers.
- **H3K122ac** is enriched in poised promoters and also found in a different type of putative enhancer that lacks H3K27ac.

**K562\_H4K20me1****K562\_H3K9me3****K562\_H3K9me1****K562\_H3K9ac****K562\_H3K79me2****K562\_H3K4me3****K562\_H3K4me2****K562\_H3K4me1****K562\_H3K36me3****K562\_H3K27me3****K562\_H3K27ac****K562\_H2AFZ**

# total data points







- Filtered using dbSNP138
  - 69,546/3,088,918 → SNPs (2.25%)
  - 149,457/712,041 → InDels(21%)

# SNPs/InDels density

