

IRF1_Decoy_ChIPseq

Prepared by Zhe Zhang

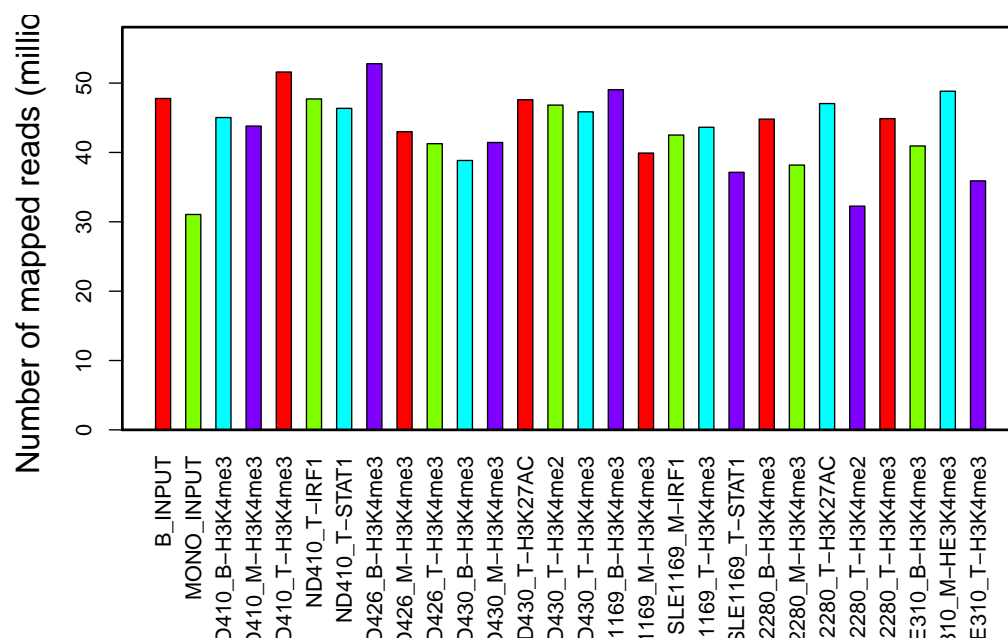
August 20, 2014

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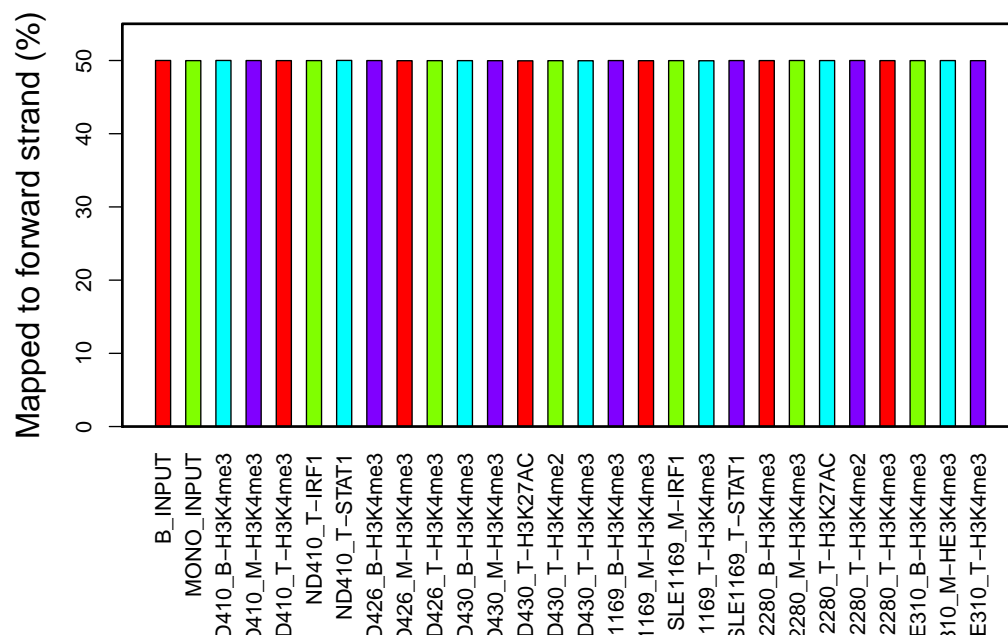
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1 Summary statistics

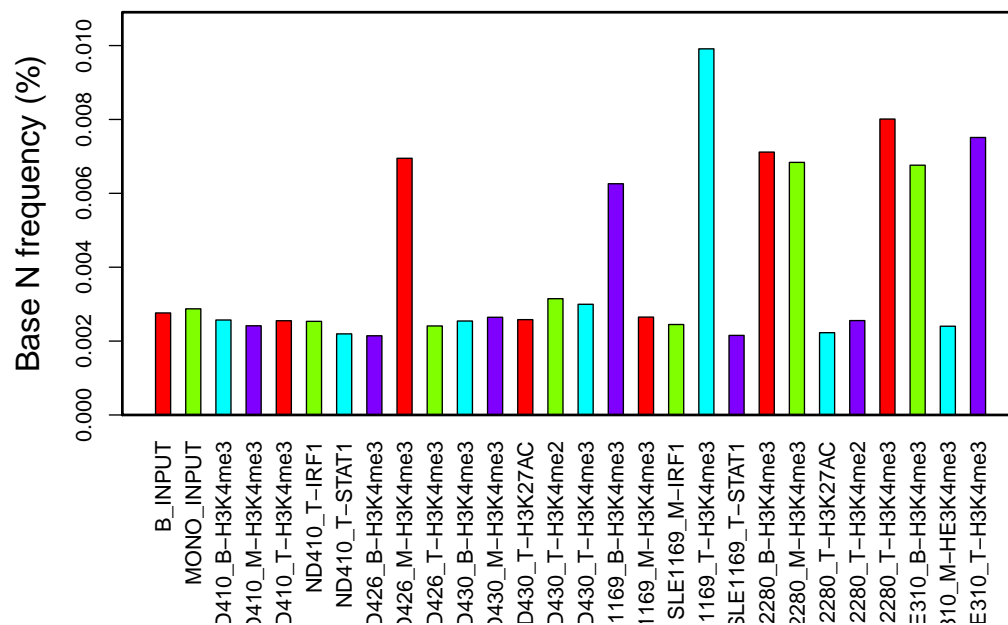
1.1 Total number of mapped reads



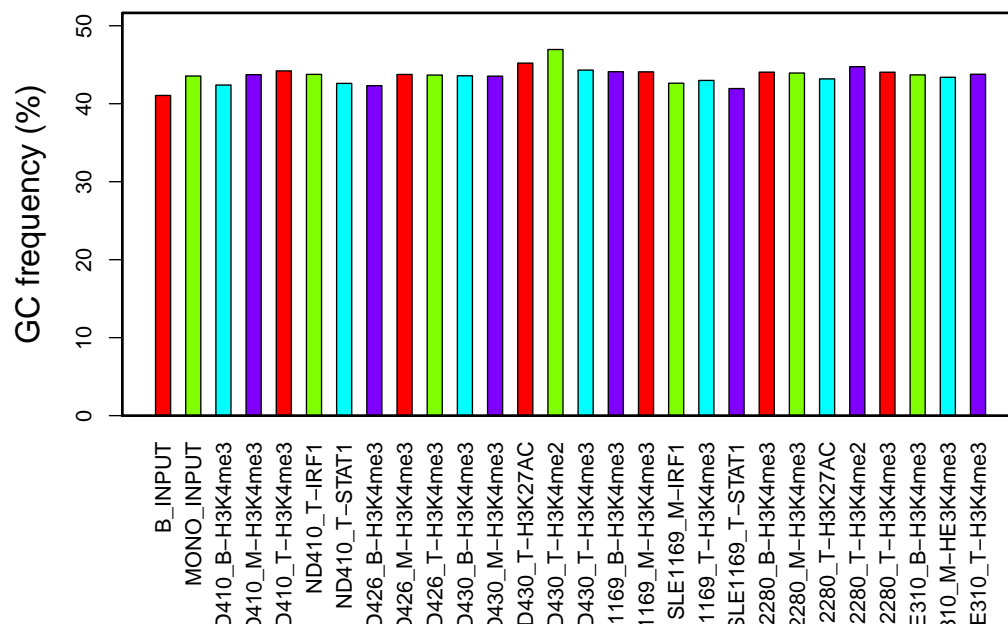
1.2 Strand frequency



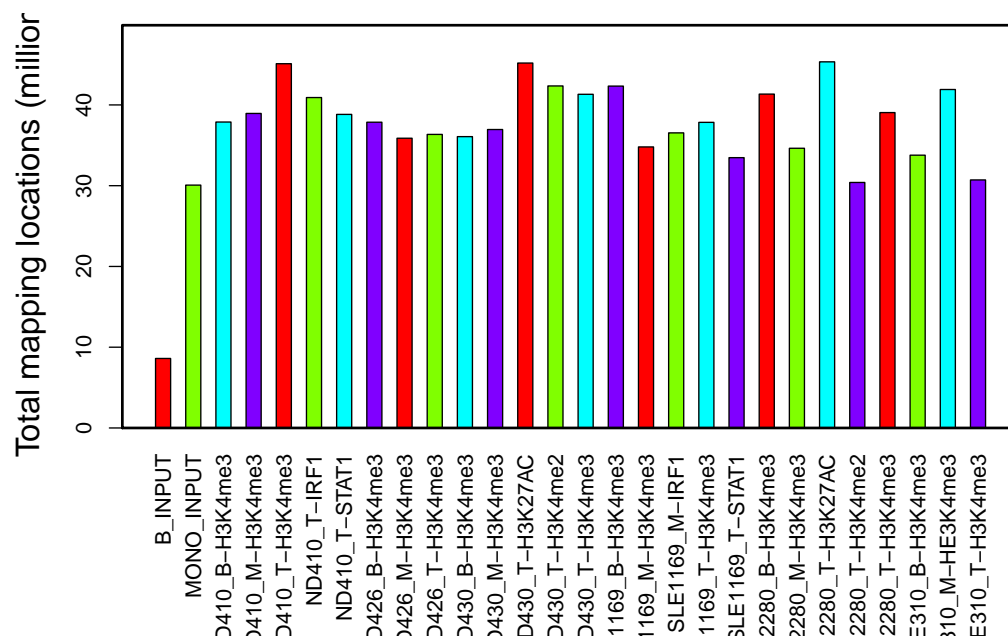
1.3 Base N frequency



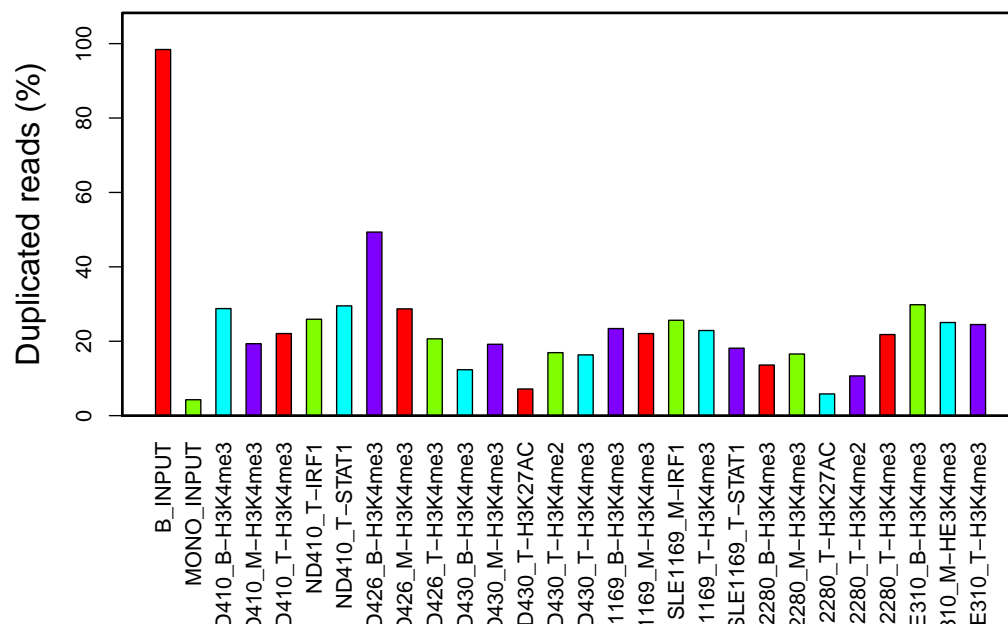
1.4 GC frequency



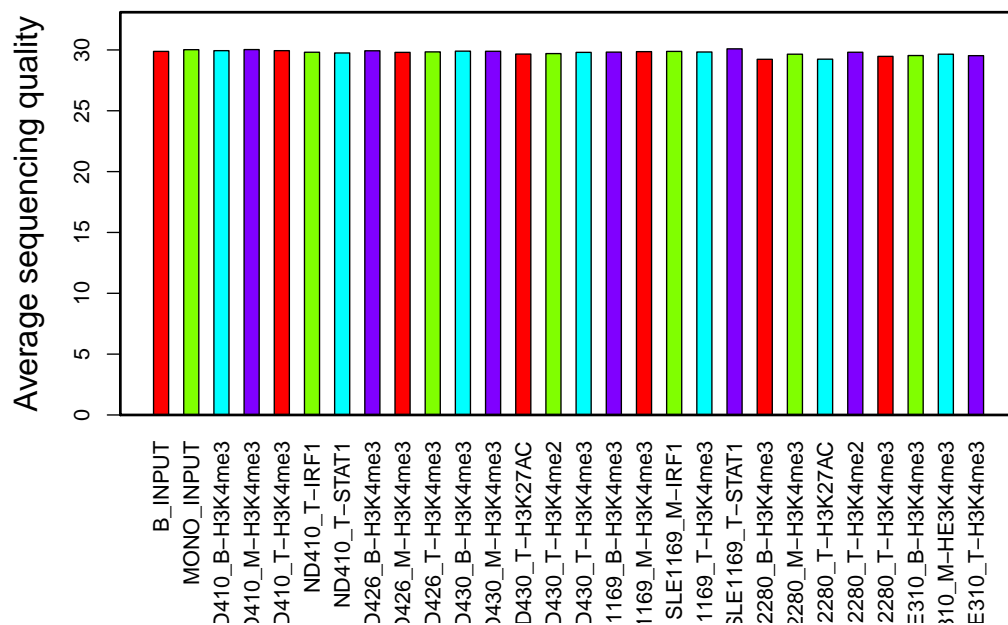
1.5 Total mapping locations



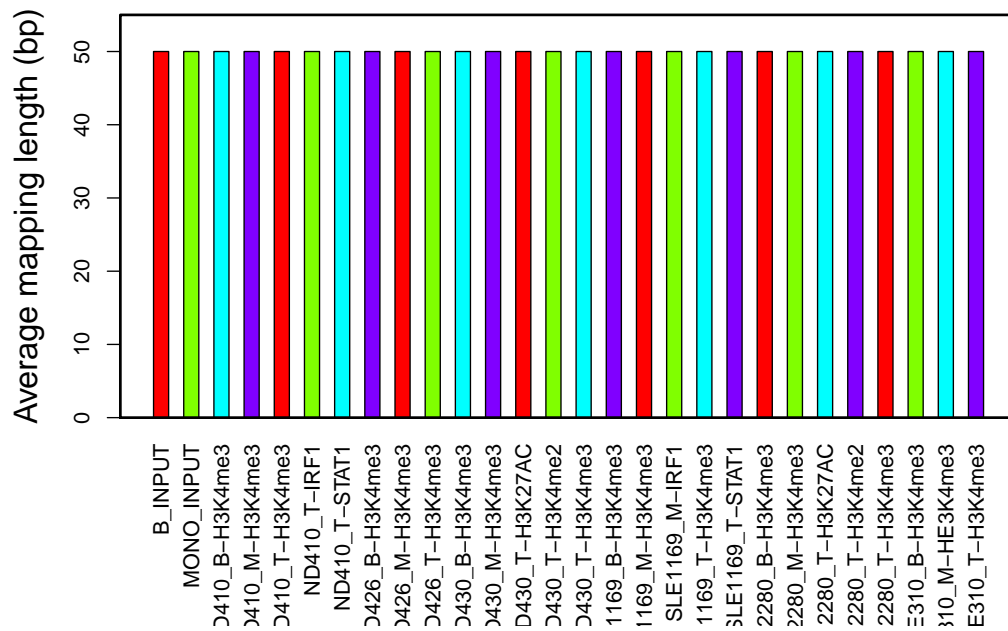
1.6 Duplicated mapping frequency



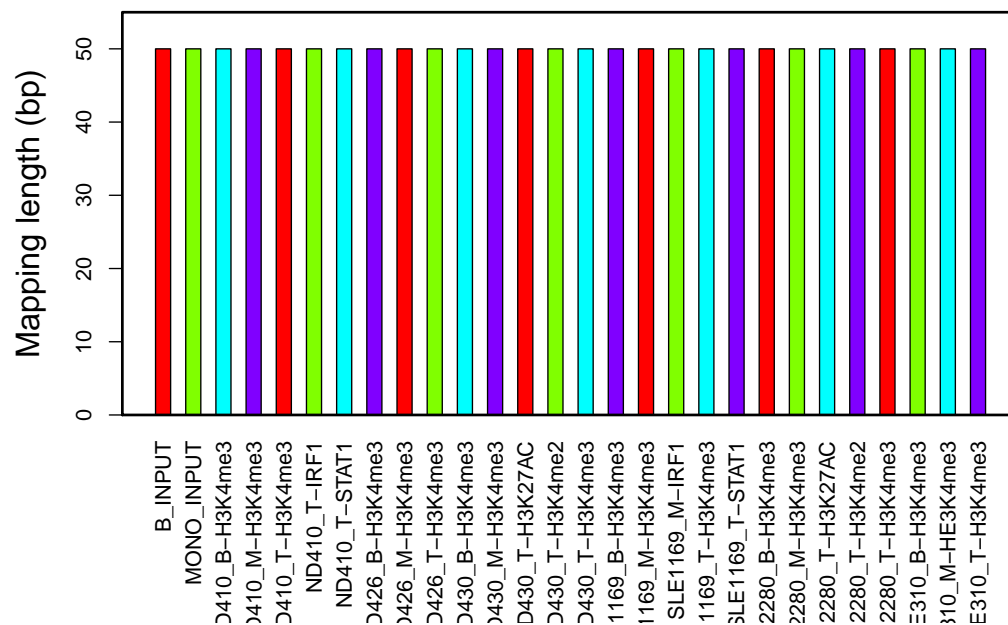
1.7 Sequencing quality



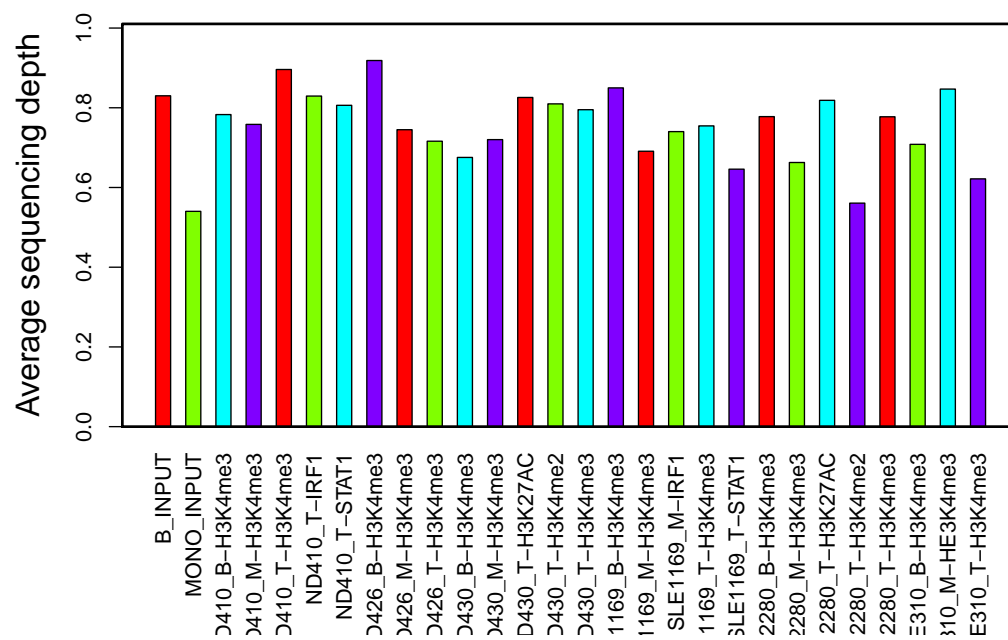
1.8 Mapping quality



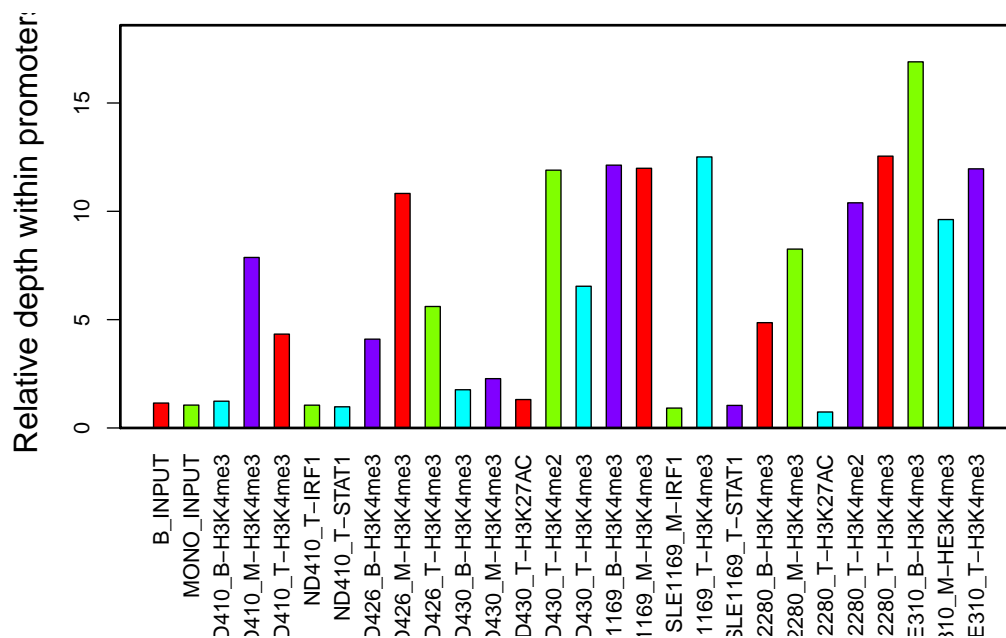
1.9 Mapping length



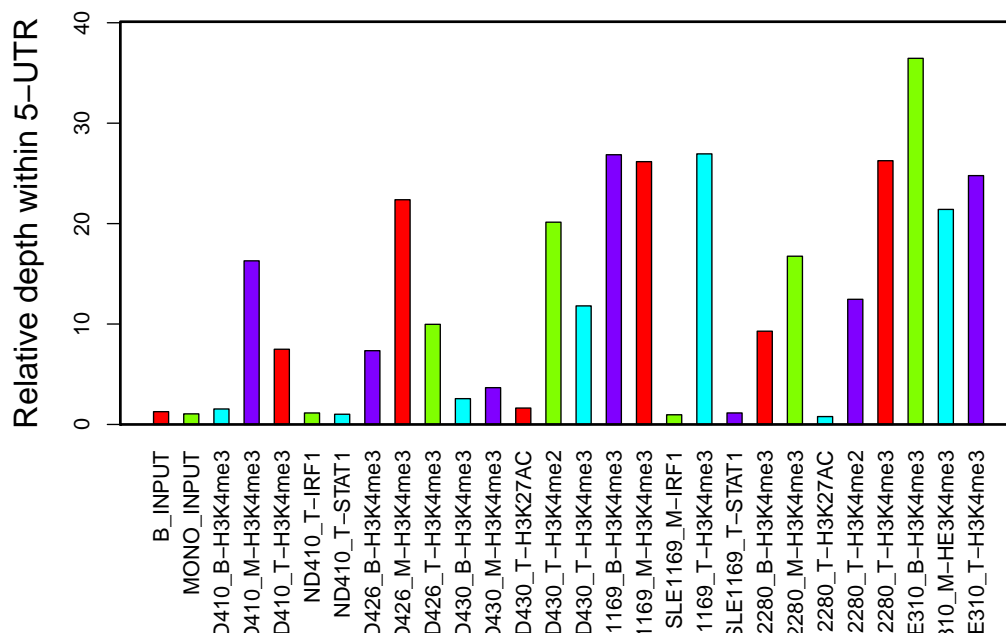
1.10 Sequencing depth



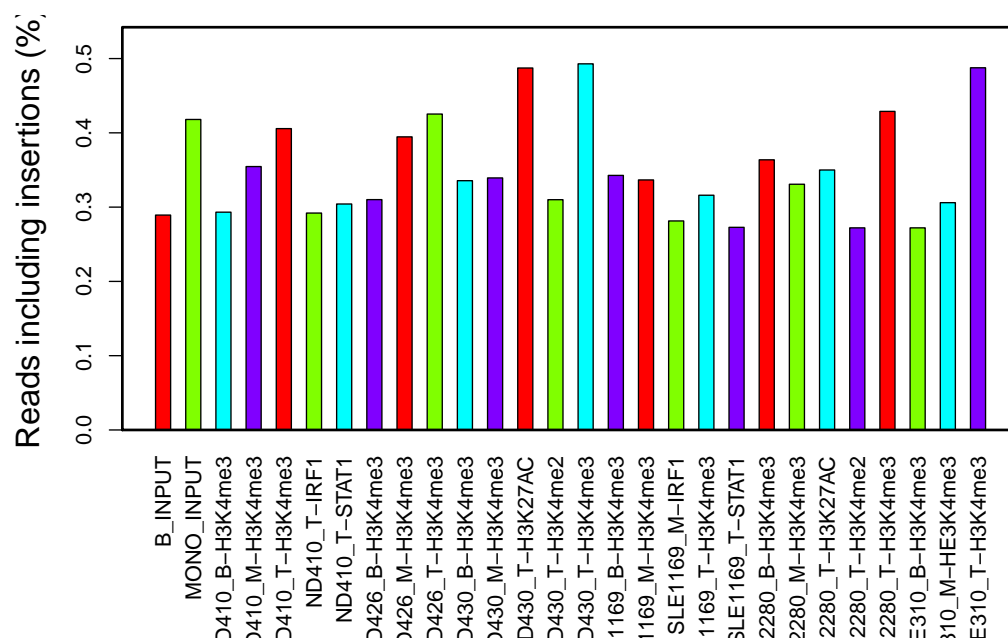
1.11 Read enrichment within promoters



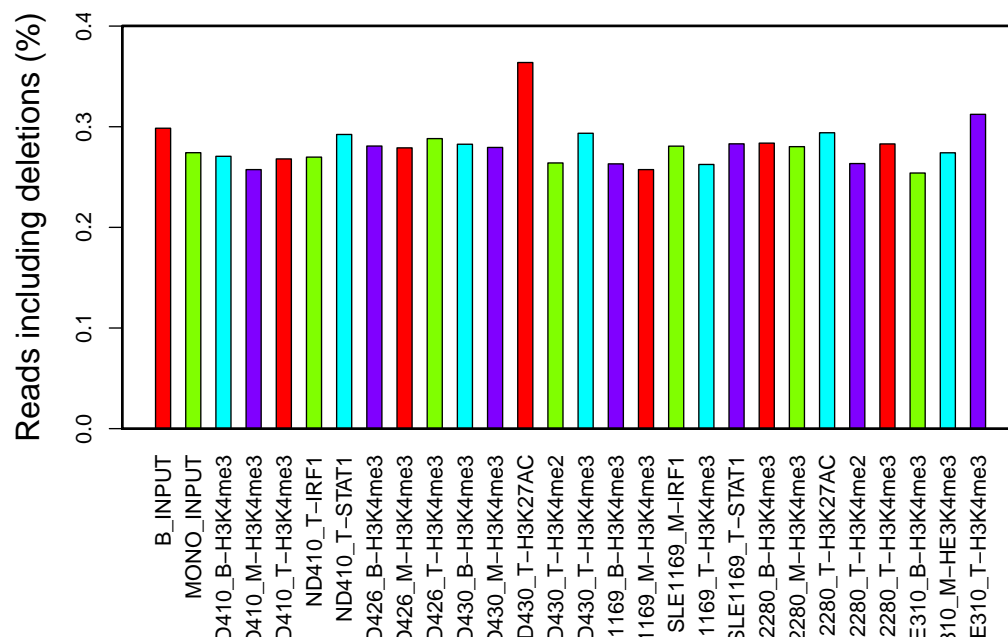
1.12 Read enrichment within 5-UTR



1.13 Mapping with insertions



1.14 Mapping with deletions

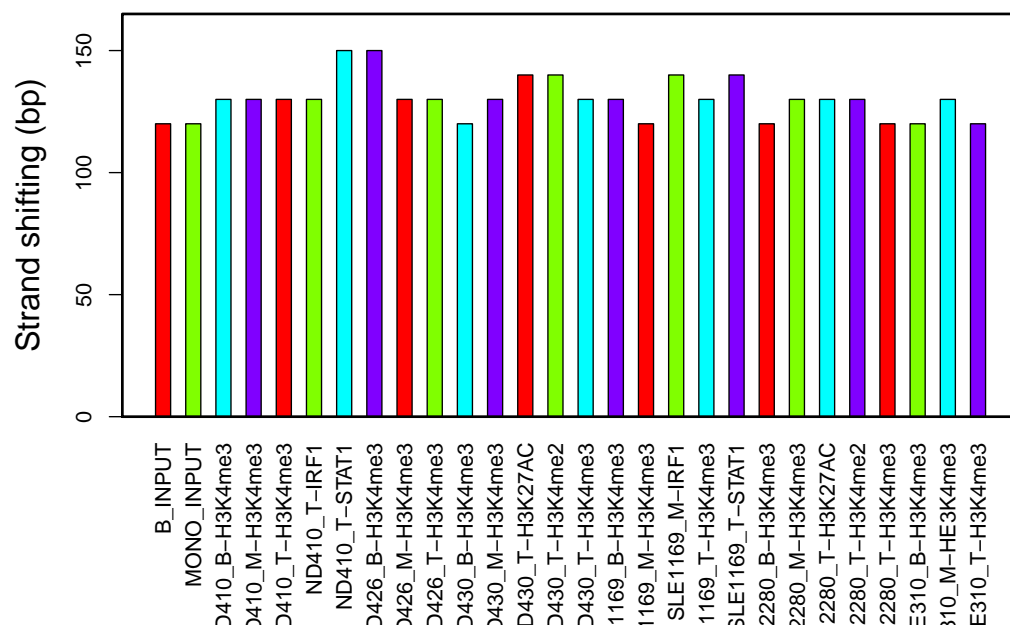


1.15 K-mer frequency

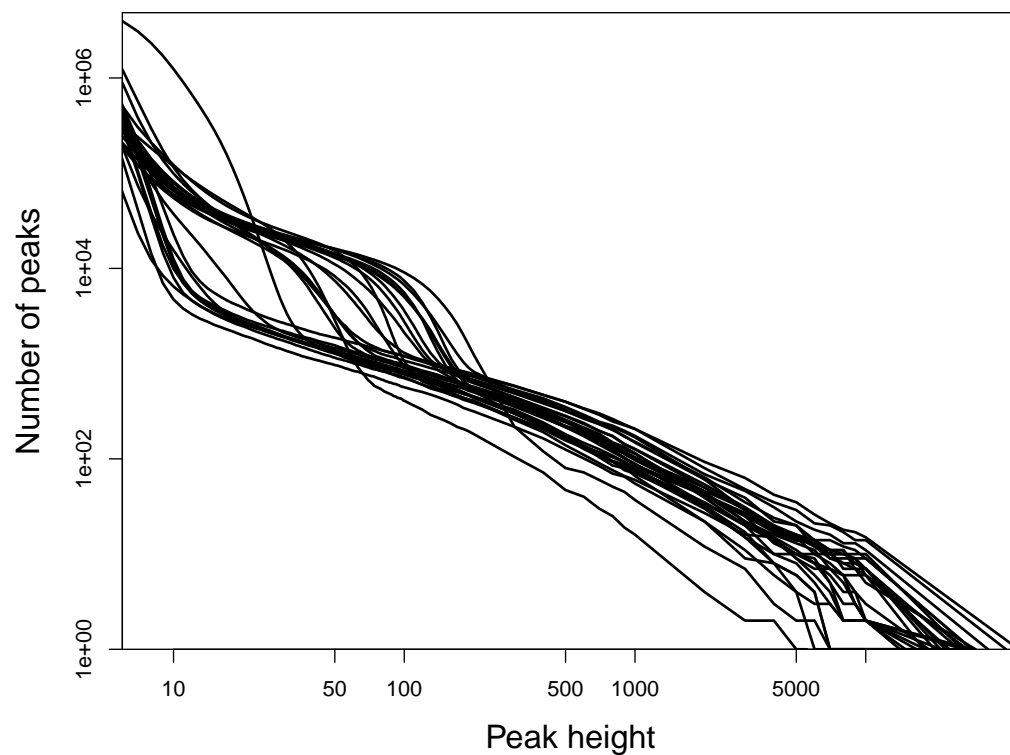
	MEAN	BINPUT	MONOINPUT	ND410B.H3K4me3	ND410M.H3K4me3	ND410T.H3K4me3	ND410T.IRF1	ND410T.STAT1	ND426B.H3K4me3	ND426M.H3K4me3	ND426T.H3K4me3
CCCAG	3.55	5.05	3.54	3.31	3.67	3.45	3.46	3.63	3.25	3.10	
CTGGG	3.52	4.43	3.21	3.60	3.66	3.34	3.83	4.08	3.68	3.34	
CCCAG	3.51	2.97	3.17	3.47	3.59	3.23	3.53	3.55	3.65	3.30	
CCAGG	3.37	3.51	3.24	3.04	2.94	3.58	3.47	3.06	3.49	3.24	
CTGGG	3.24	2.51	3.21	3.51	3.26	2.99	3.42	3.56	3.22	3.47	
GGAGG	3.23	3.12	3.29	2.82	3.19	3.18	2.76	3.17	3.05	3.07	
CCAGG	3.12	3.61	3.01	2.96	3.49	2.74	2.98	3.06	3.05	3.27	
CCTGG	3.11	3.60	2.91	3.32	2.82	2.95	3.33	3.38	3.14	3.69	
CCTGG	3.03	3.61	2.92	2.83	3.03	3.04	2.78	2.97	3.21	2.88	
GCTGG	3.03	1.61	2.67	2.83	2.90	3.21	3.35	2.60	2.89	3.20	
GGCTG	3.00	3.32	2.66	2.89	3.06	2.96	3.03	3.10	3.25	2.94	

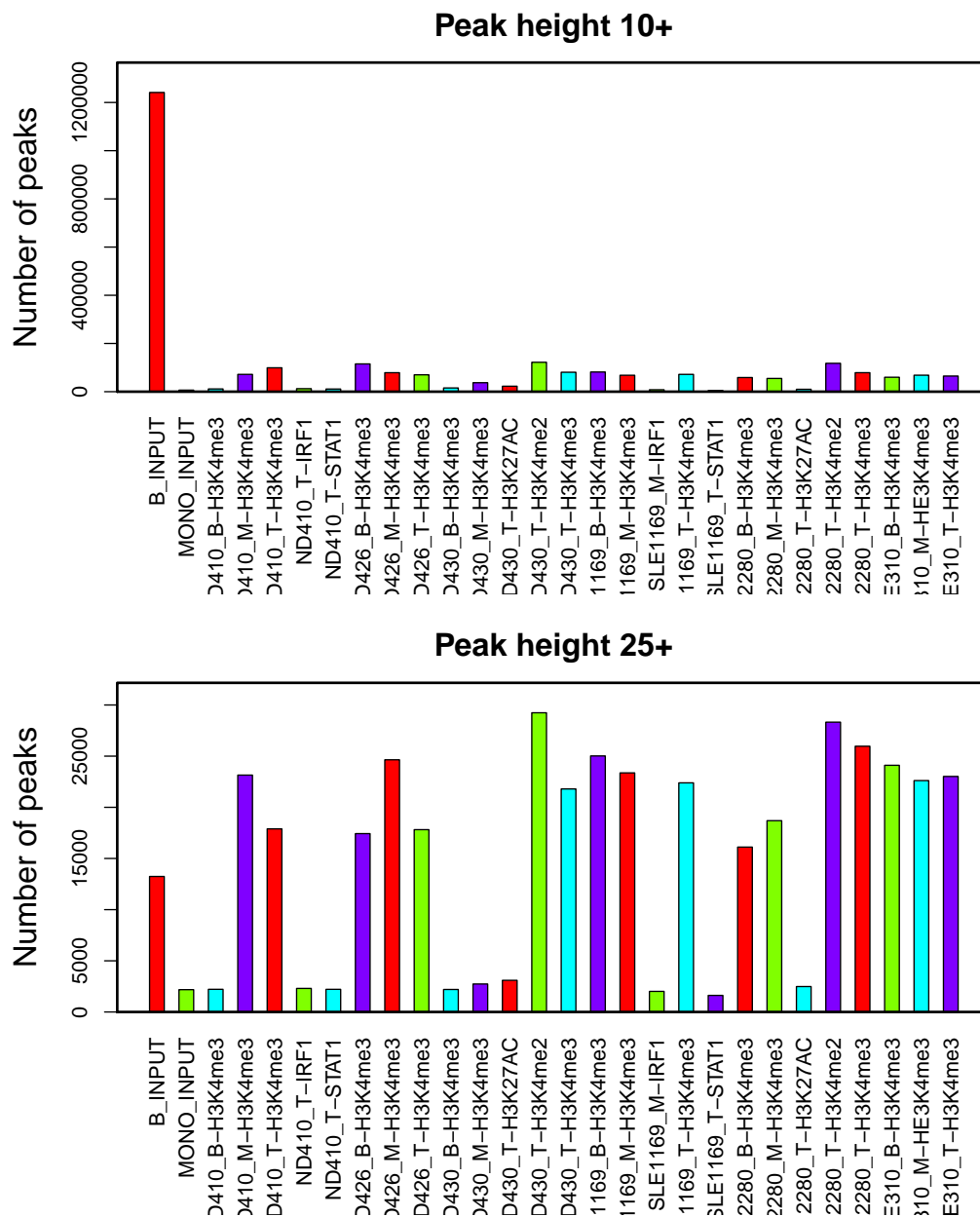
2 ChIP-seq

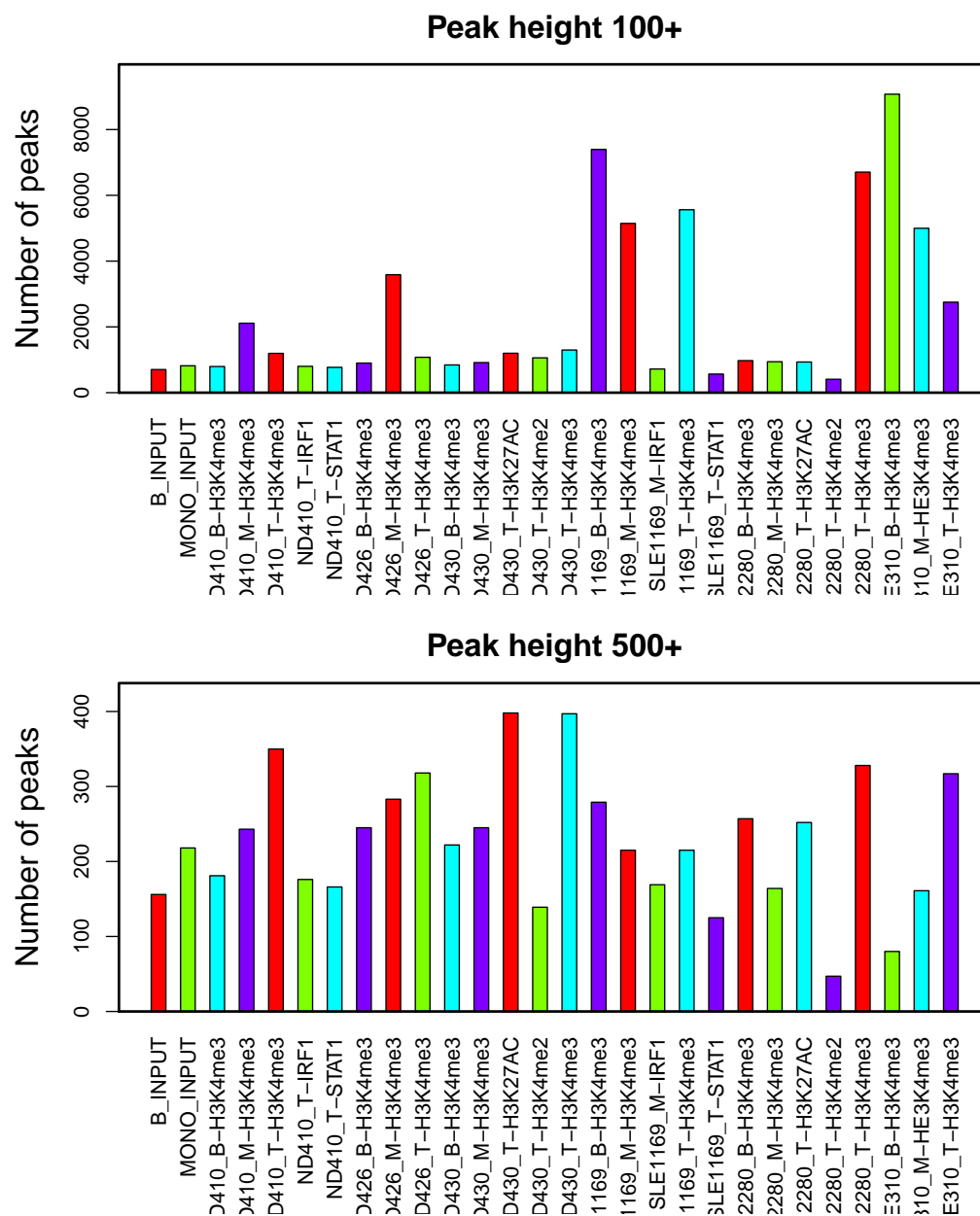
2.1 Strand-strand correlation

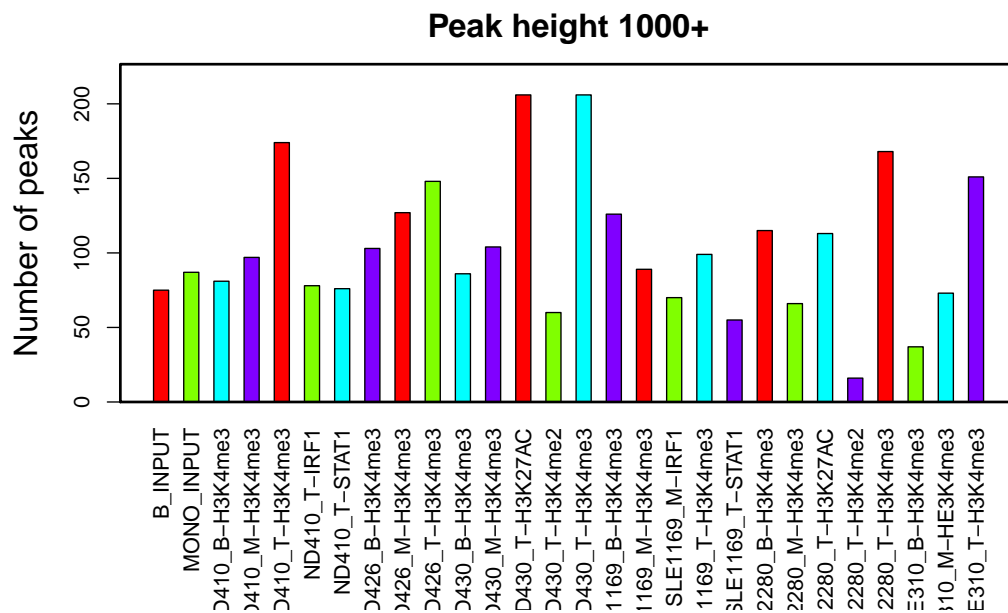


2.2 Total peaks

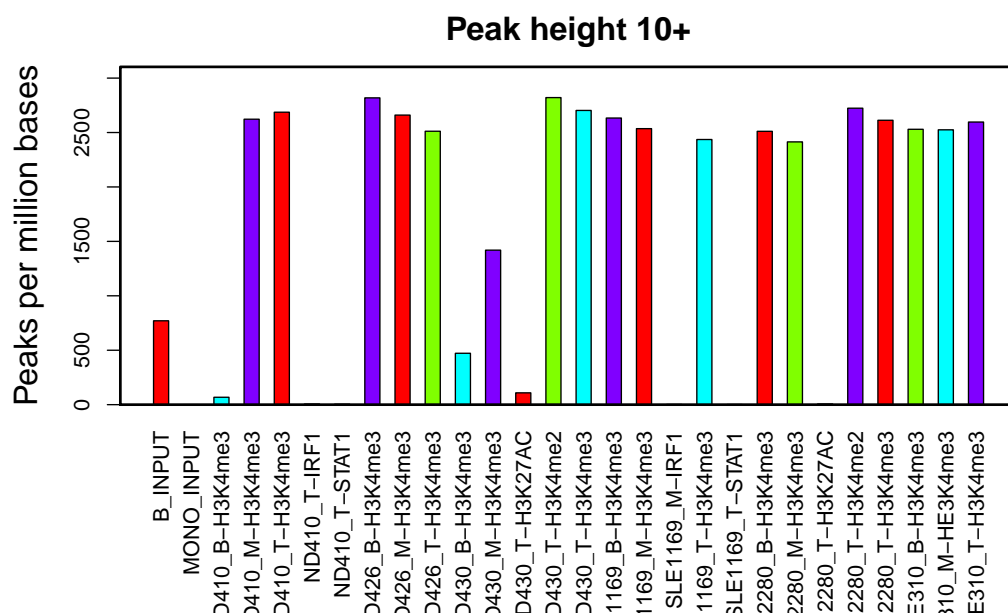


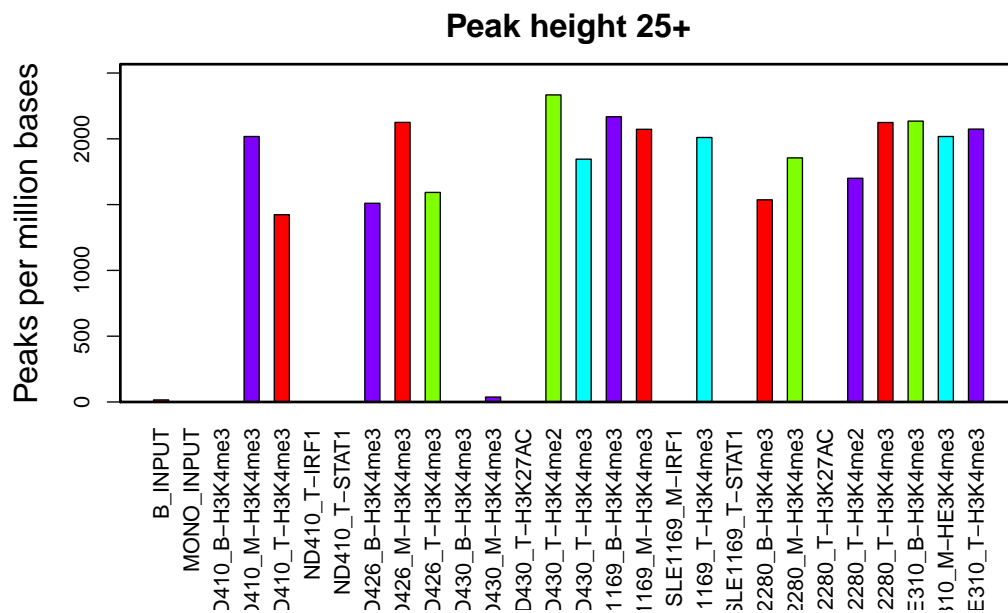






2.3 5-UTR peaks





2.4 TSS reads

