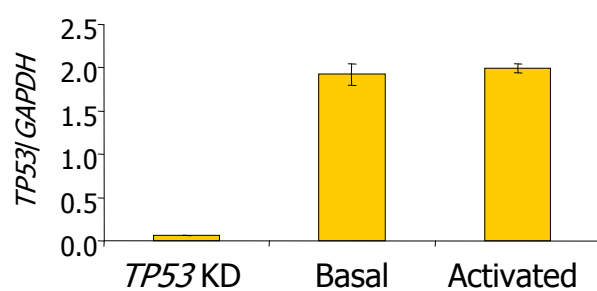


Supp. Table 1

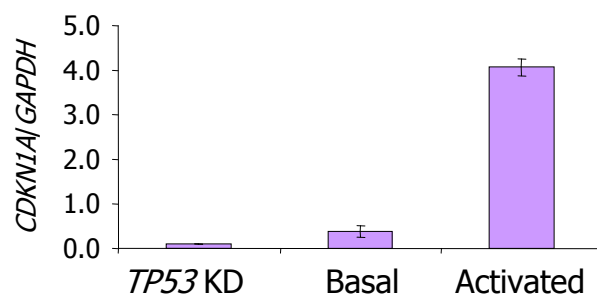
Site Id	Sequence (hg18 coordinates)	PSSM score (Wei '06)
Bound 1	AGACCTGCCCCGACATGTCC chr19:18345757-18345776	19.2973
Bound 2 (<i>CDKN1A</i>)	GAACATGTCCCAACATGTTG chr6:36752204-36752223	12.8359
Bound 3	GAACATGTCAGAGCATGTGG chr10:45254000-45254019	7.771
Bound 4 (<i>GADD45A</i>)	GAACATGTCTAAGCATGCTG chr1:67925046-67925065	11.7558
Bound 5 (<i>MDM2-p53RE1</i>)	GGTCAAGTTCAGACACGTTC chr12:67488970-67488989	4.64871
Unbound 1	AGACTTGTTCTTACATGTTT chr10:58715379-58715398	10.3955
Unbound 2	TTACAAGTTCAGACATGTCA chr9:26079023-26079042	10.5914
Unbound 3	CTACAAGTTCTTAACATGCCC chr12:24354054-24354074	11.4014
Unbound 4	ATGCATGGTCAAGCATGCCC chr6:55606032-55606051	9.9681
Unbound 5	TTACATGTTGTGACATGCCT chr1:71589086-71589105	9.5916

Site Id	Forward primer	Reverse primer
Bound1	CAGGAGTGCCTCAGACCTGC	AGCACCATACAGGGAAGGGA
Bound2	AGCAGGCTGTGGCTCTGATT	CAAAATAGCCACCAGCCTCTTCT
Bound3	CAGGCAGCCCAGCATTCTAG	CAGCTCTCAGGGTCCCCAC
Bound4	TGGACTTTAGCCGAGATGTG	GATCTCTTCCGCTGCTGGC
Bound5	GGTTGACTCAGCTTTTCTCTTG	GGAAAATGCATGTTTAAATAGCC
Unbound1	TCTGTTCTTGTCAAATTCTATAGACTTGTT	TTACCCATATTTTCTCTGAGCTTTCA
Unbound2	GTTACTTTATTATATTGTCTTTCATTGAATGACTT	CACATACACATTTATTATTCATCTTCAAGAA
Unbound3	ACATTACATAAAGATTTCTTTTACACTAGGTTT	TGGAAGTAGTACTGATAGGGCATGTT
Unbound4	AATACCTATGGTTAATGCATGGTCAAG	ACTAATAACTAGCCCAACCATATTTGACTA
Unbound5	AATGTTGAAAGTGTGGAACATAATCTG	GCAAAAGCTAAGGCACCTAATGAG

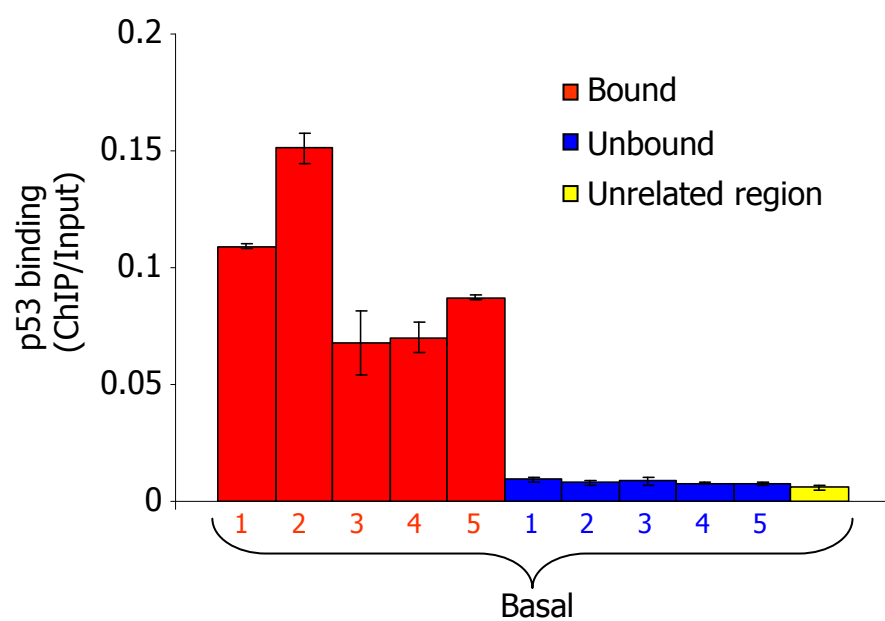
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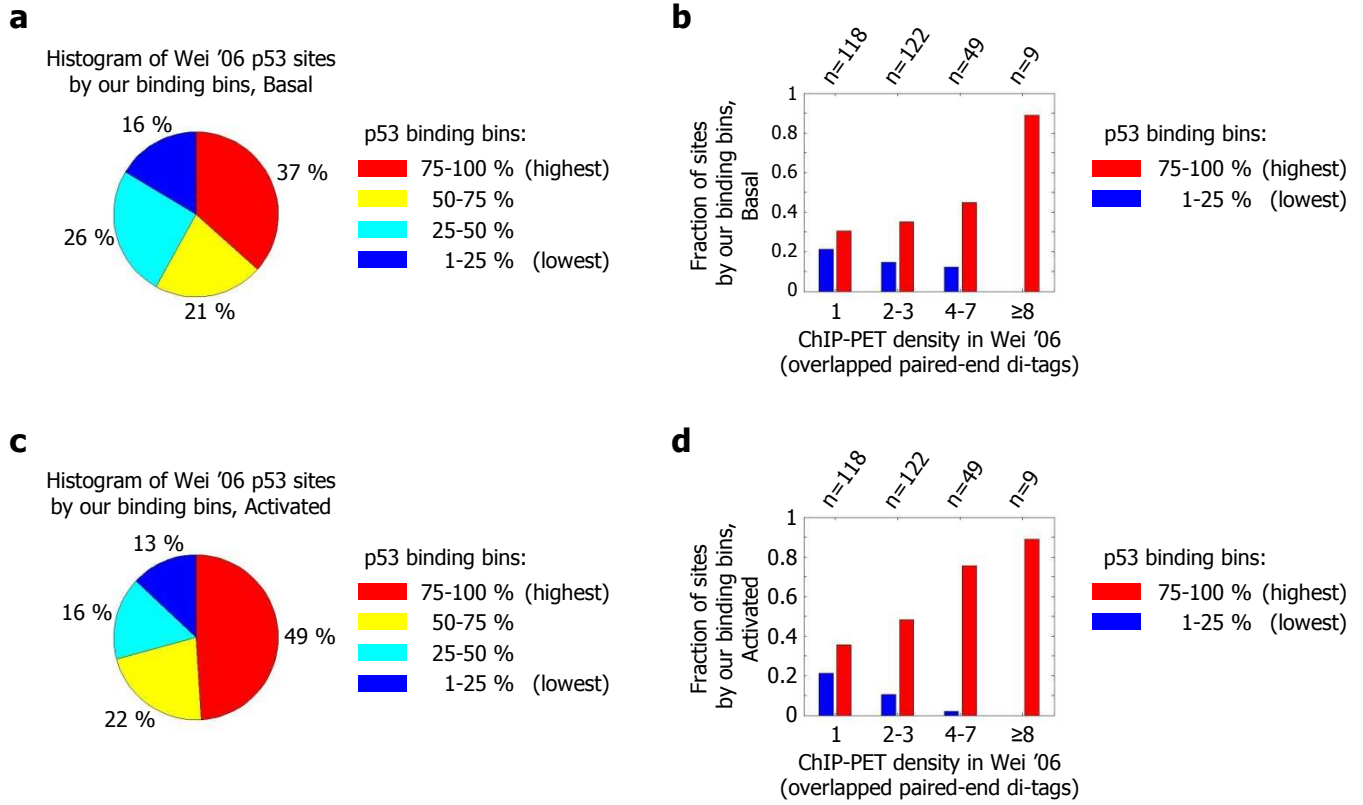


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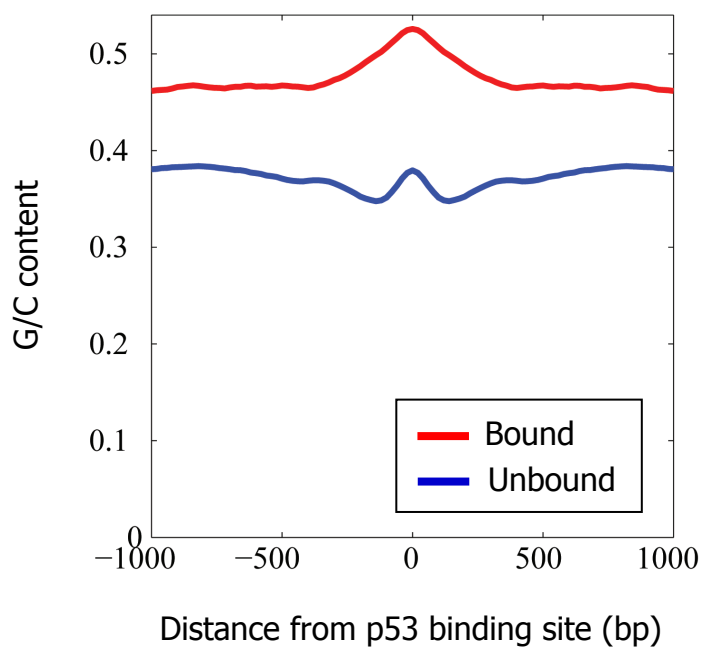


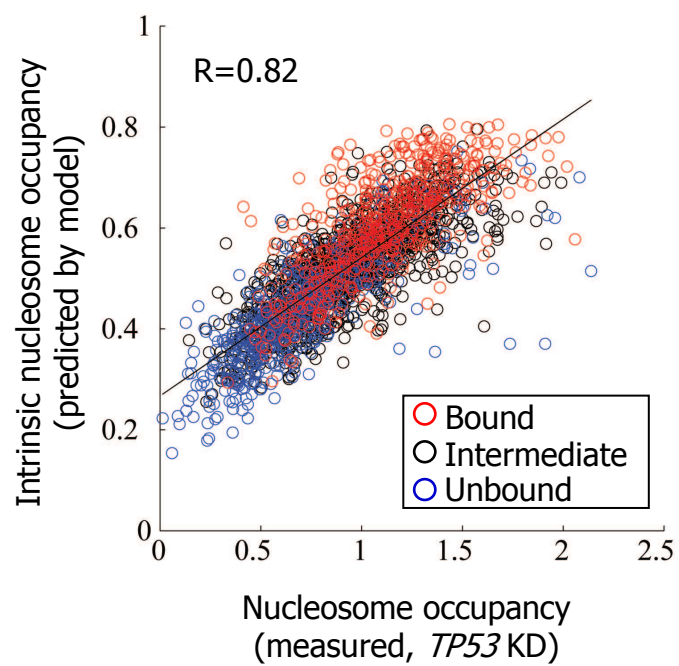
Supp. Figure 2

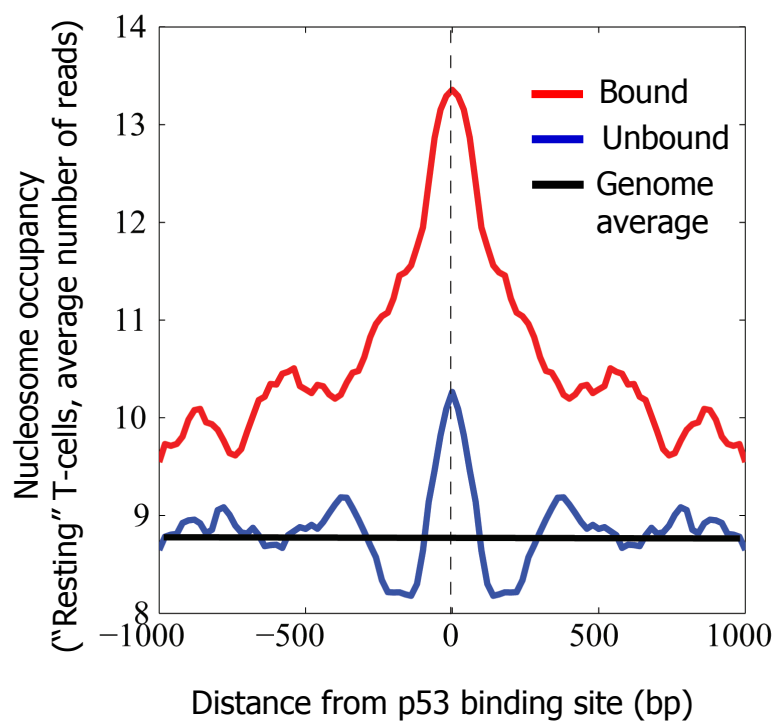


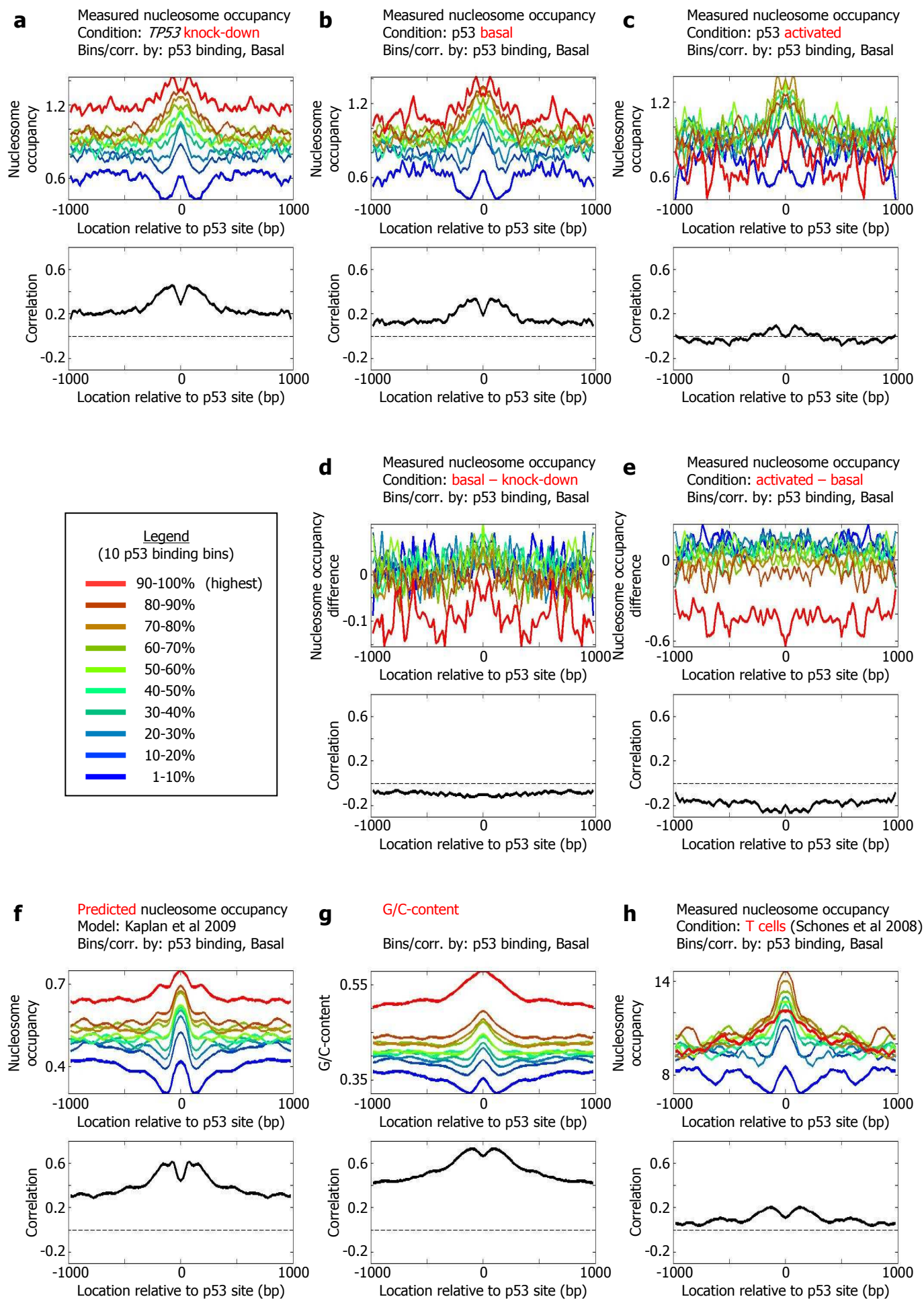


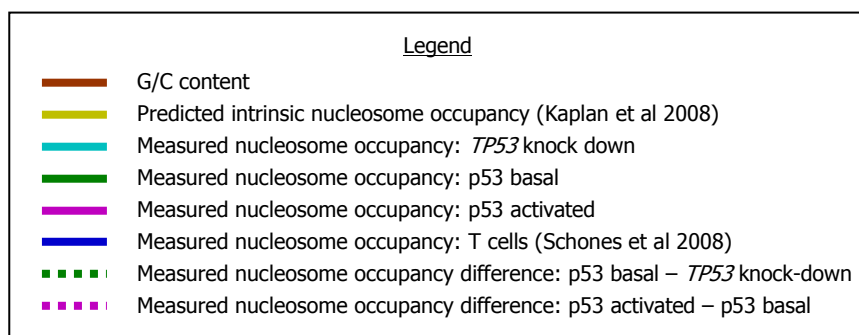
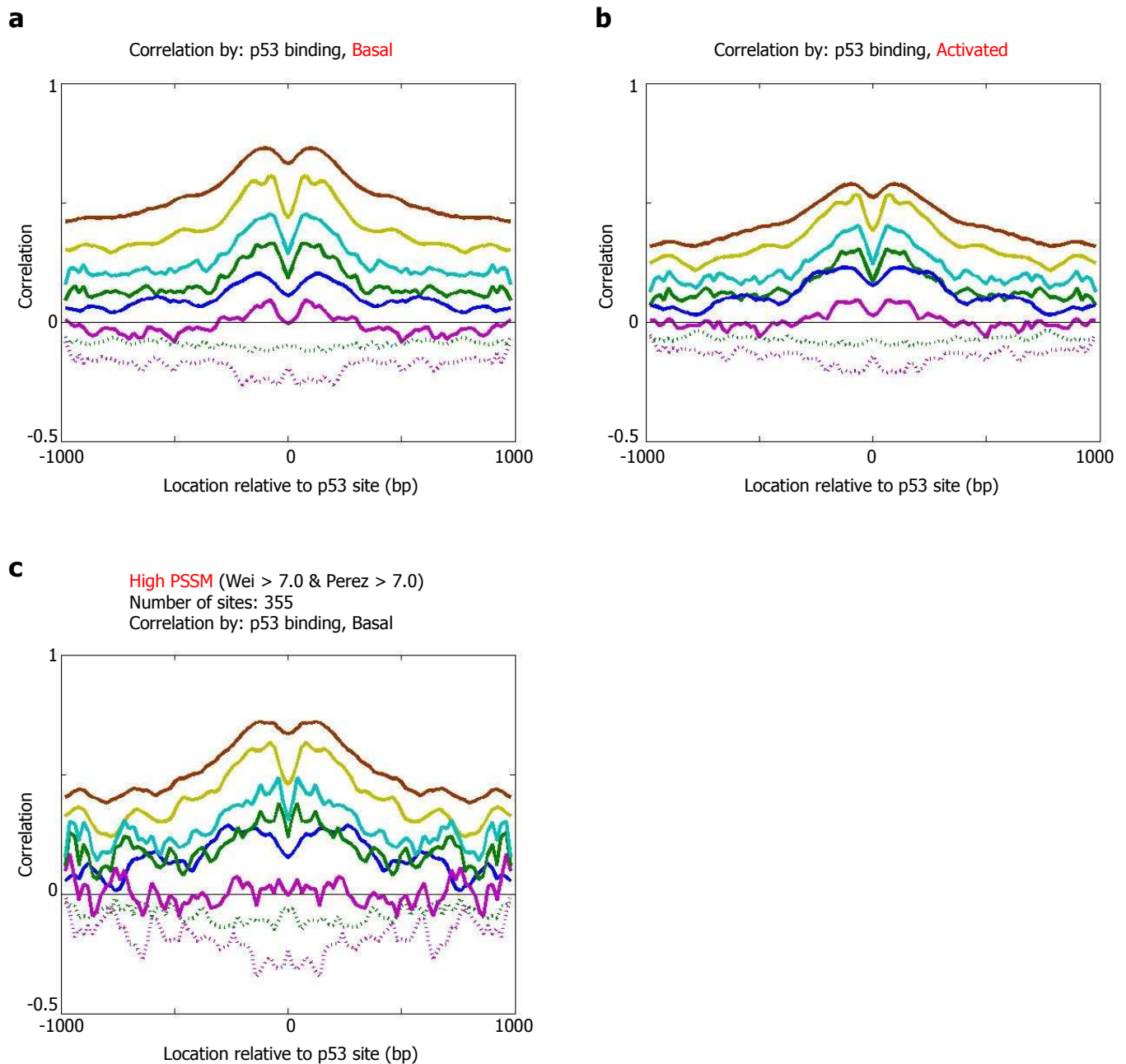
Supp. Figure 4

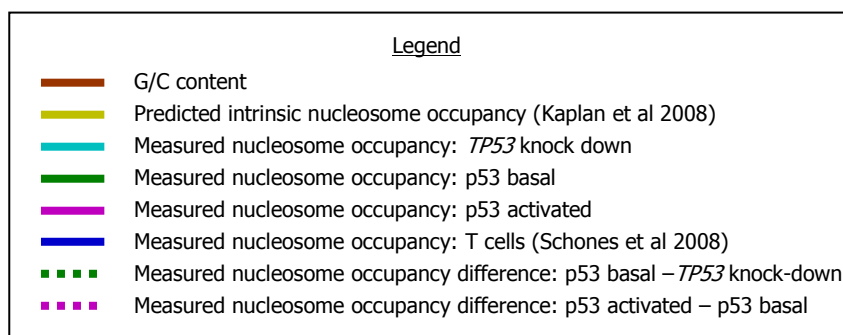
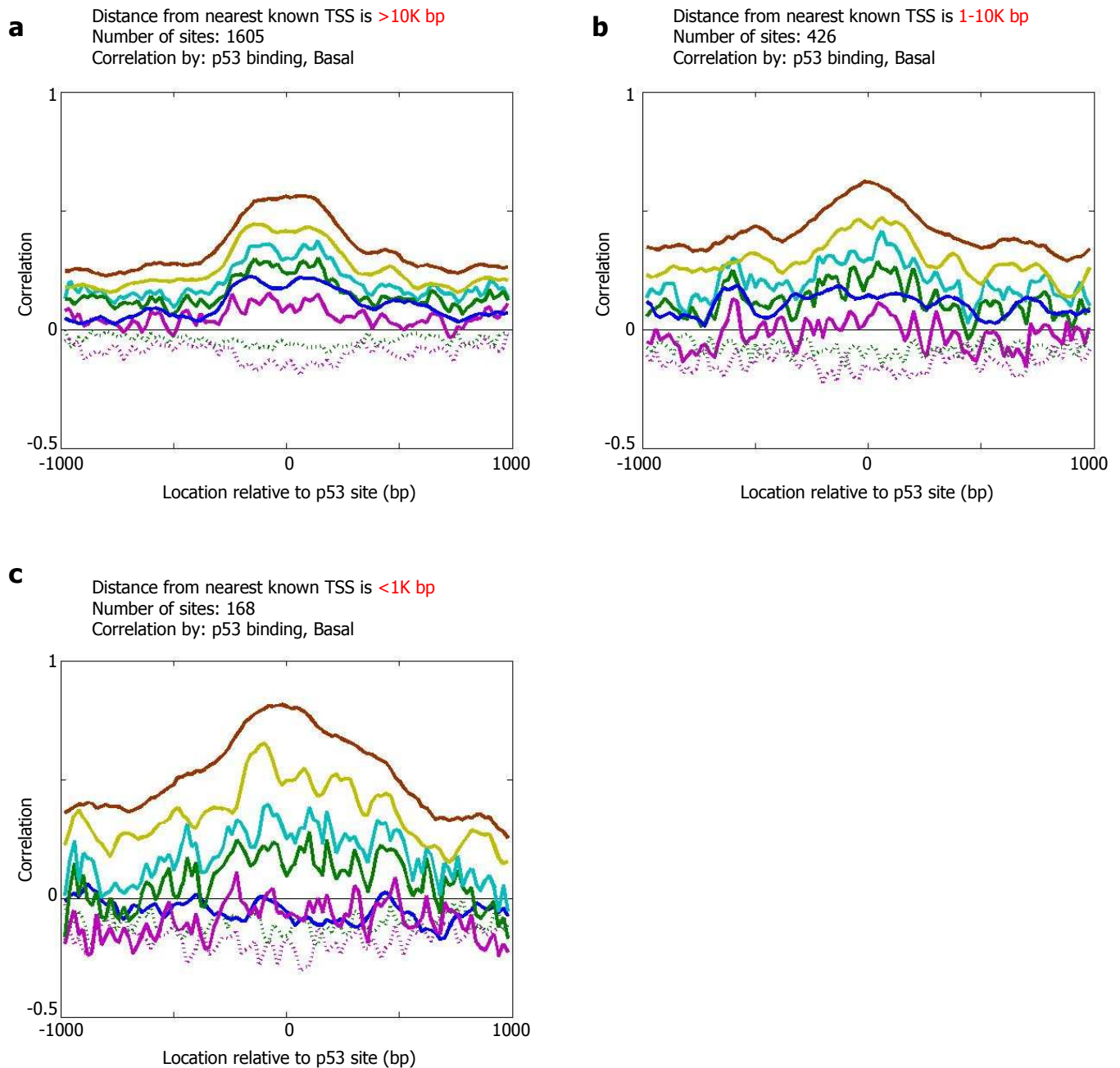


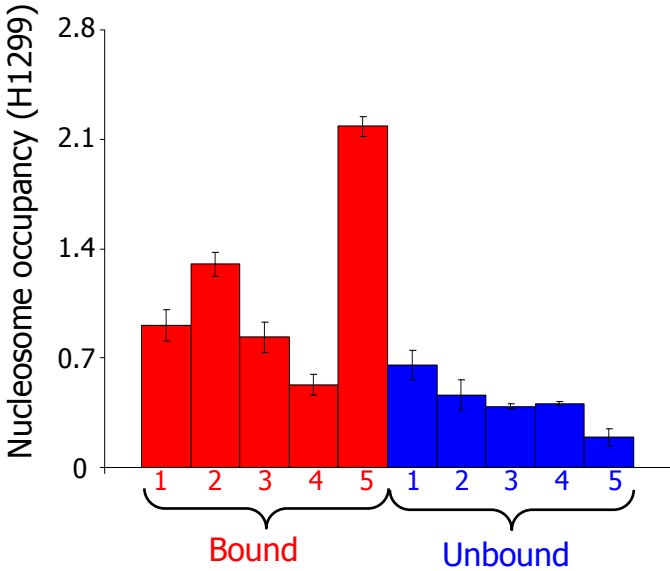




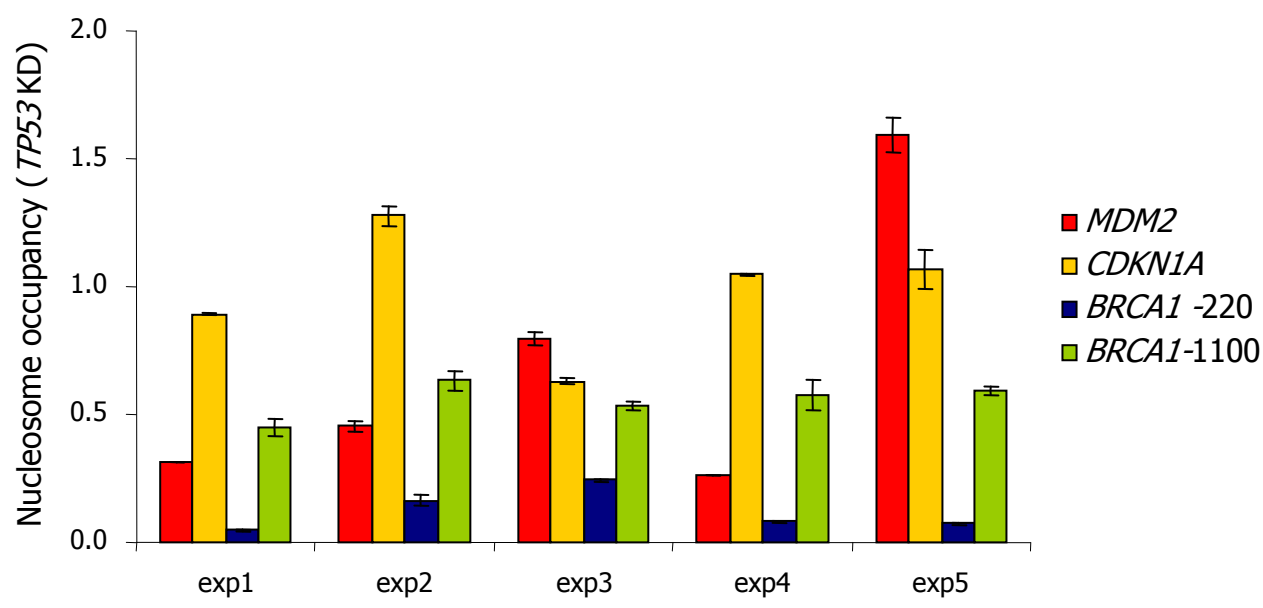


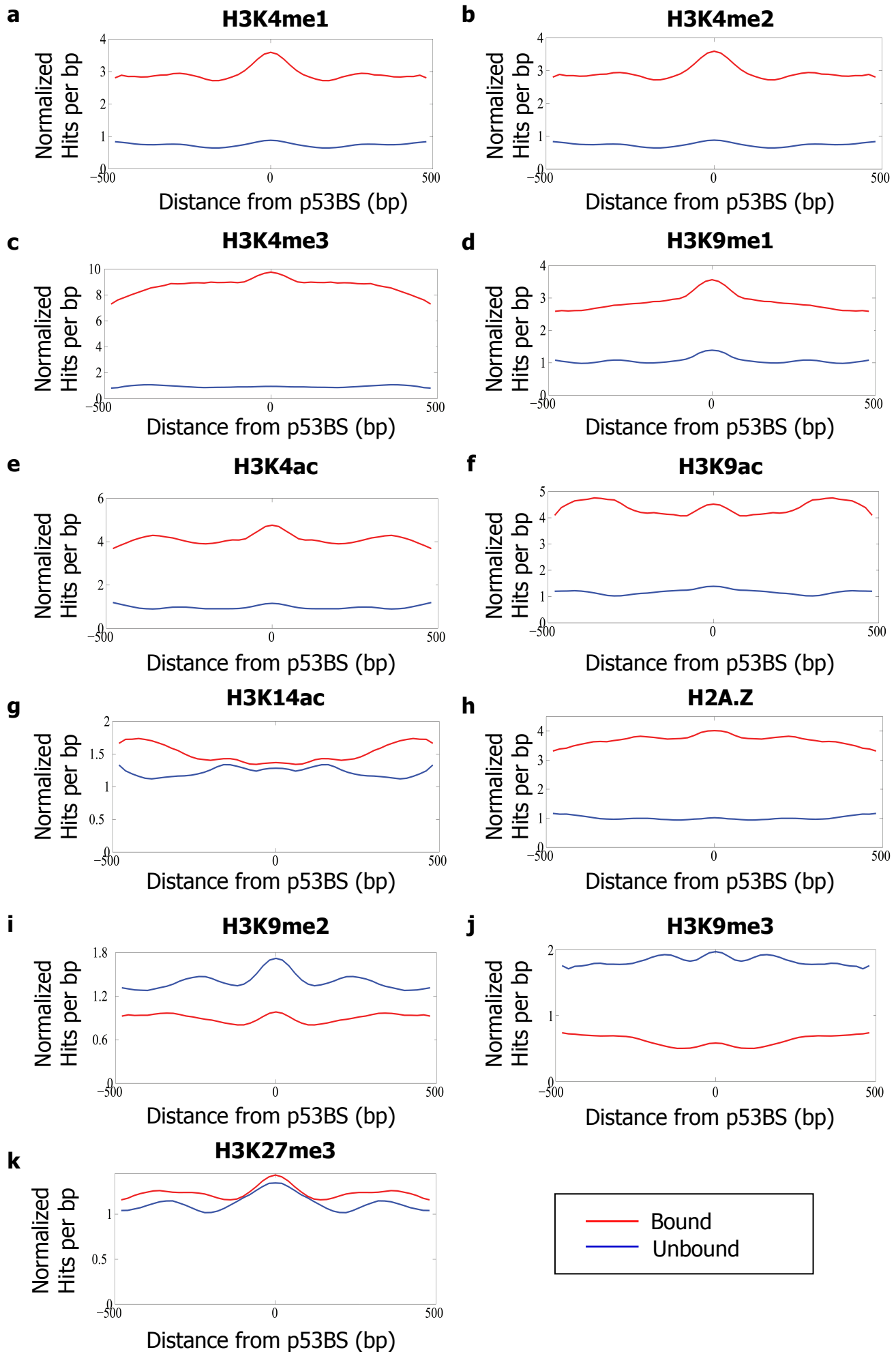


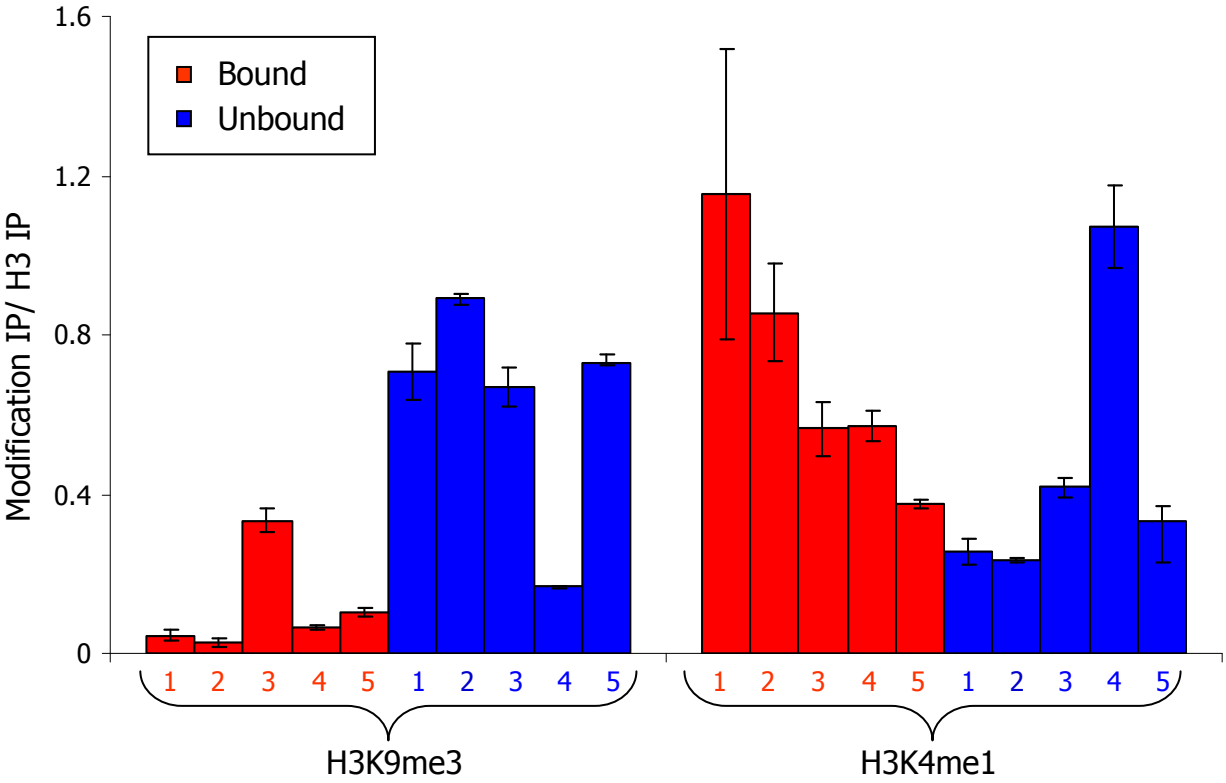


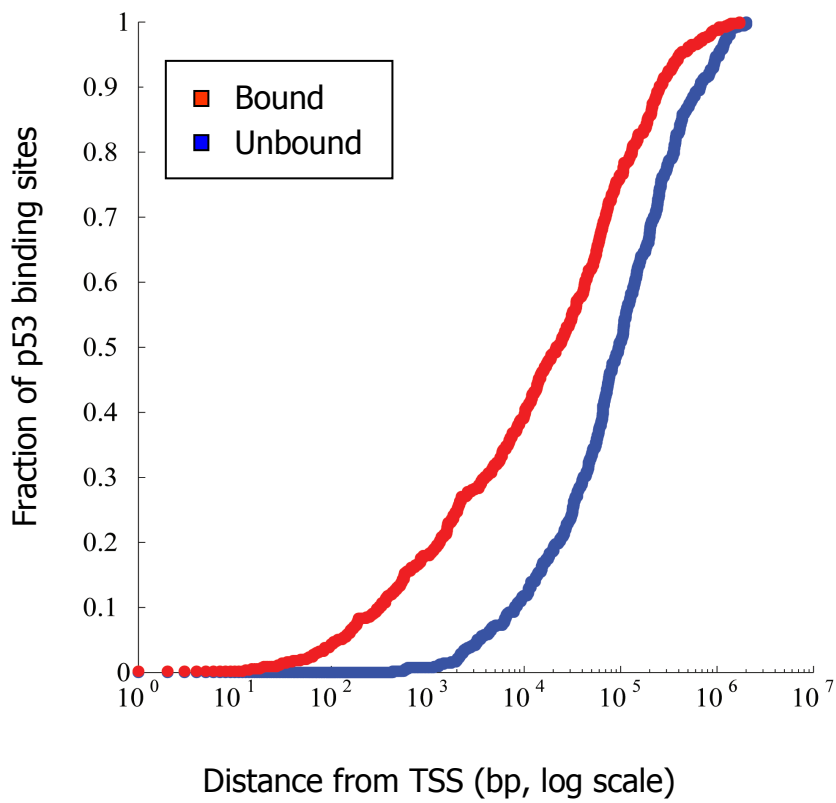


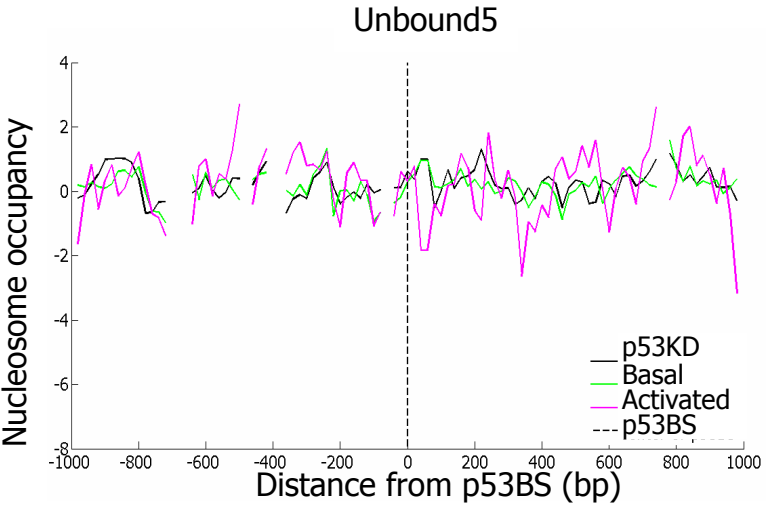
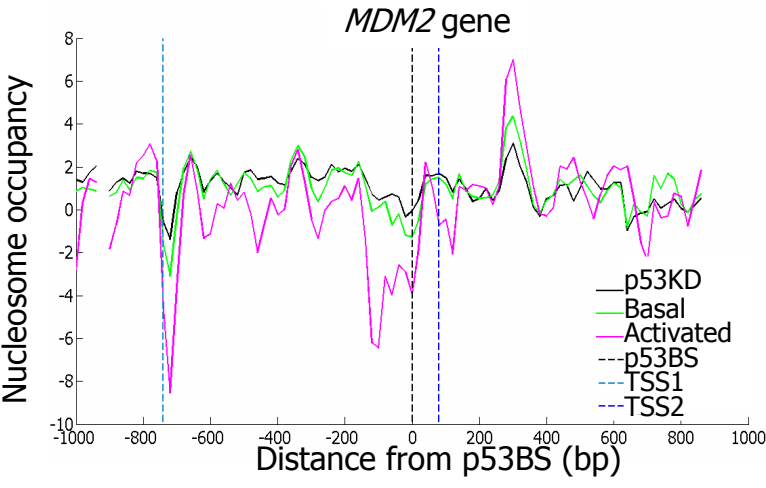
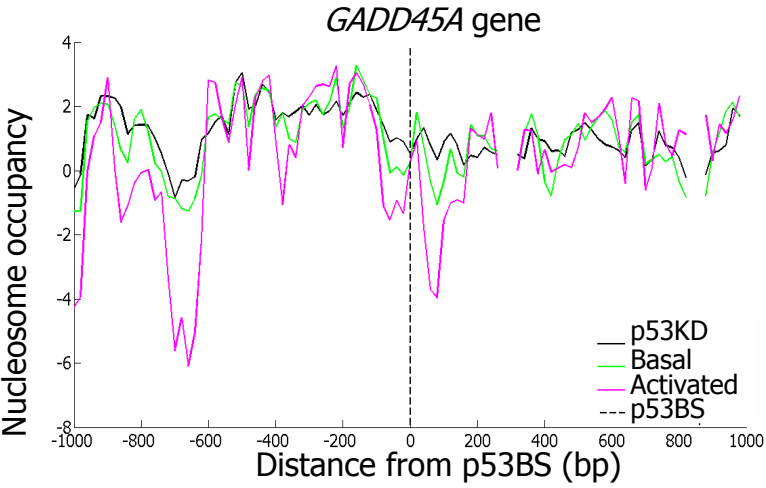
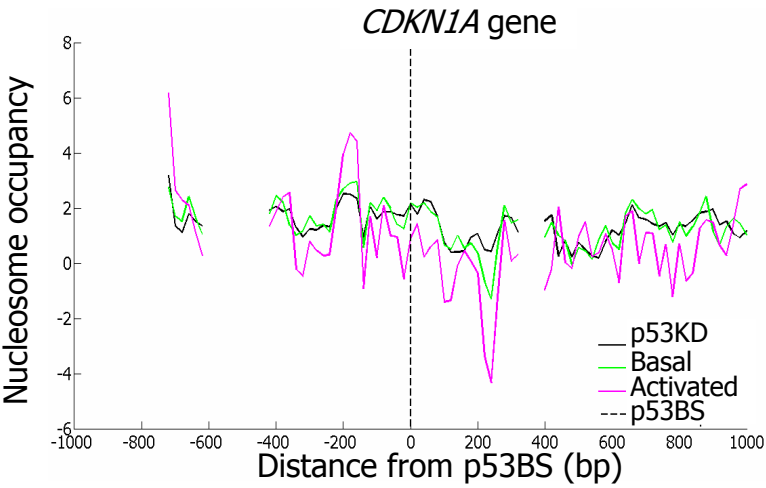
Supp. Figure 11











Supp. Figure 16

