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# Supplementary figures

## Figure S1

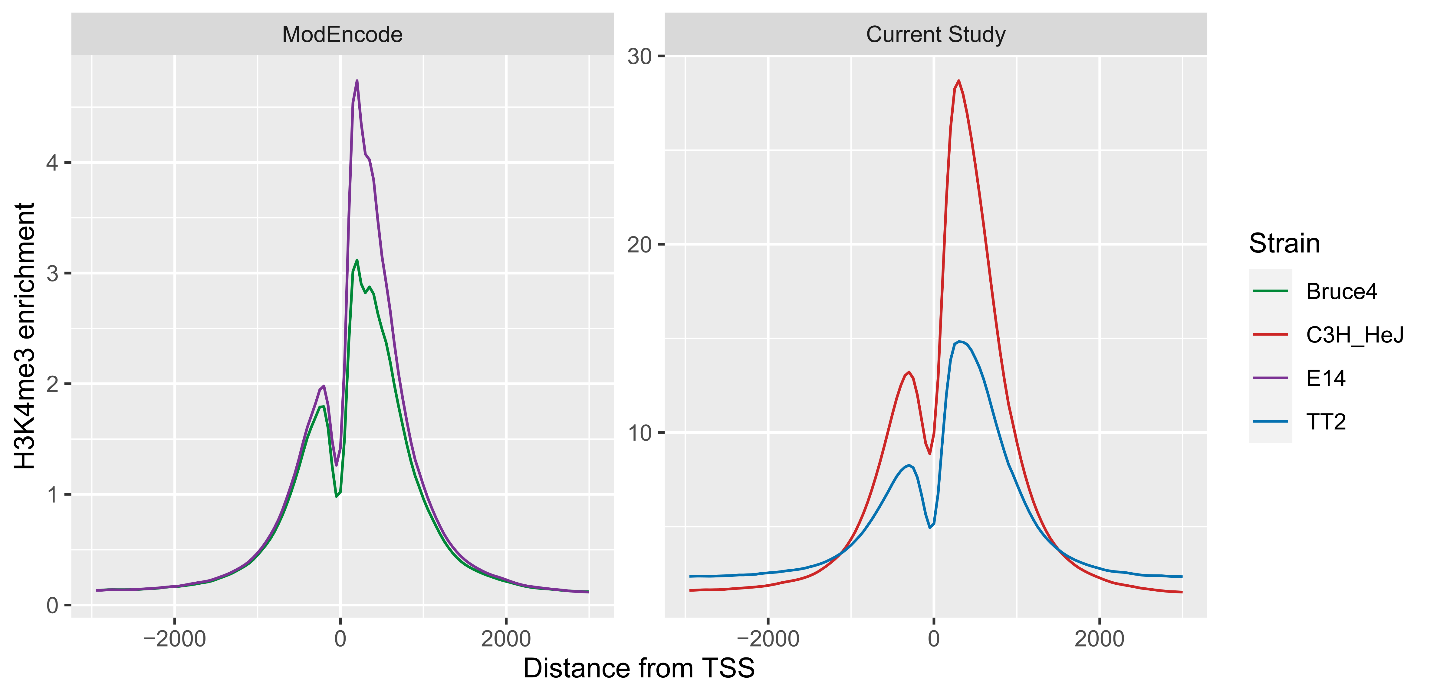


Figure S1. H3K4me3 enrichment around TSS for the datasets produced in this manuscript ( C3H/HeJ and TT2) and for the ModEncode datasets (Bruce4 and E14).

## Figure S2

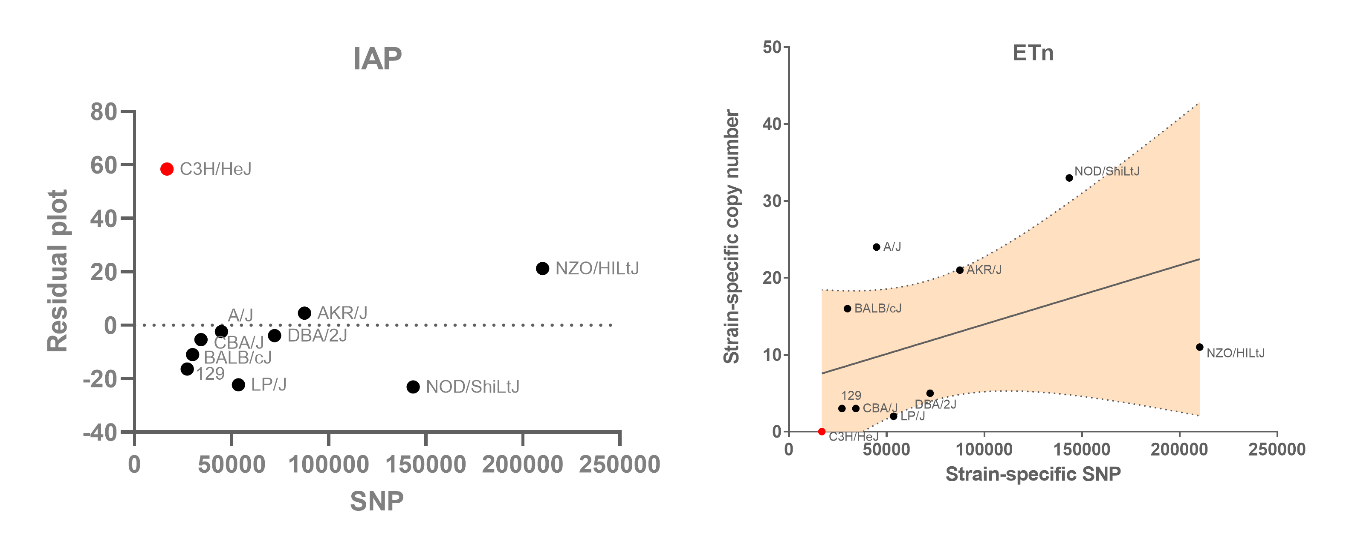


Figure S2. Supporting data for Figure 1. Left panel shows residuals standard deviation for private IAP copies versus private SNPs (see linear regression, Figure 1C). Right panel depicts private ETn copy number versus private SNPs across mouse strains.

## Figure S3

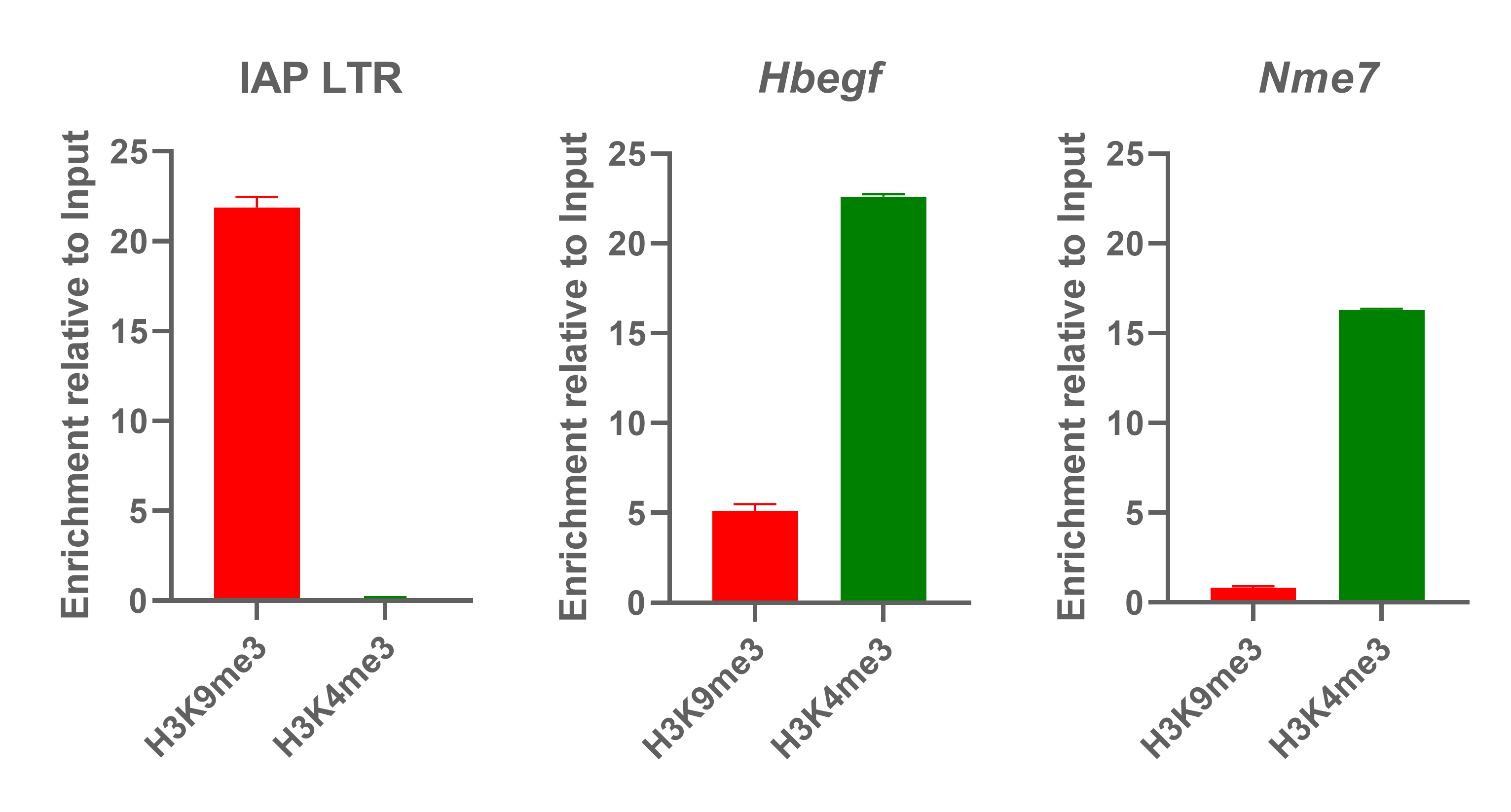


Figure S3: ChIP-qPCR of H3K9me3 and H3K4me3 for all IAP copies (non-specific copy primers targeting LTR-int), and for two H3K4me3 copies found only in C3H/HeJ, located inside the *Hbegf* (IAP # 30) and *Nme7* (IAP #3) genes (see Table S2).

## Figure S4

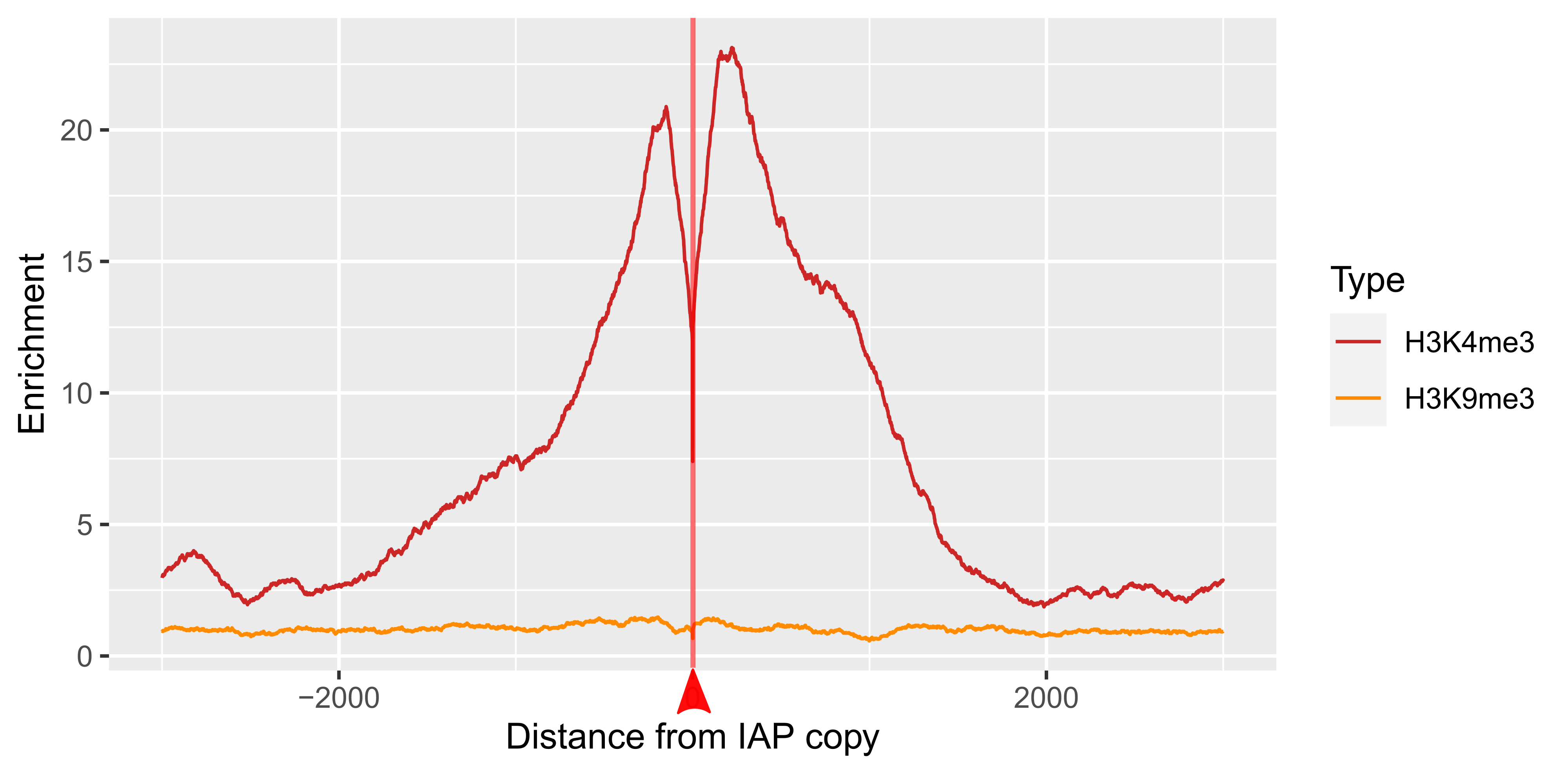


Figure S4. H3K4me3 and H3K9me3 enrichment in flanking sites of all H3K4me3-marked C3H/HeJ copies present in Table S2. Figure shows lack of H3K9me3 in in K4me3 flanking sites.

## Figure S5

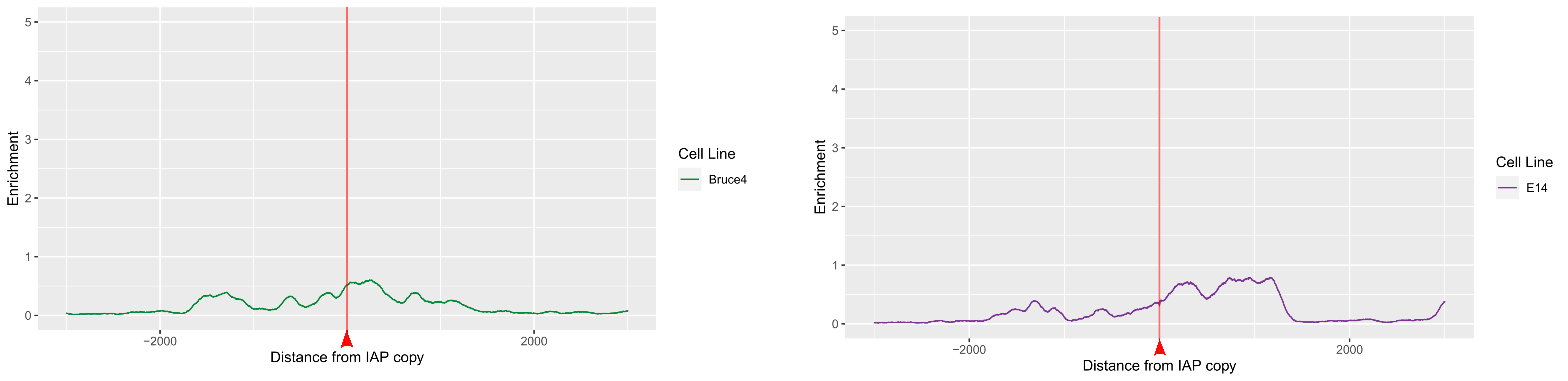


Figure S5. H3K4me3 enrichment in empty sites of Bruce4 and E14. Figure show lack of H3K4me3 in empty sites.

## Figure S6

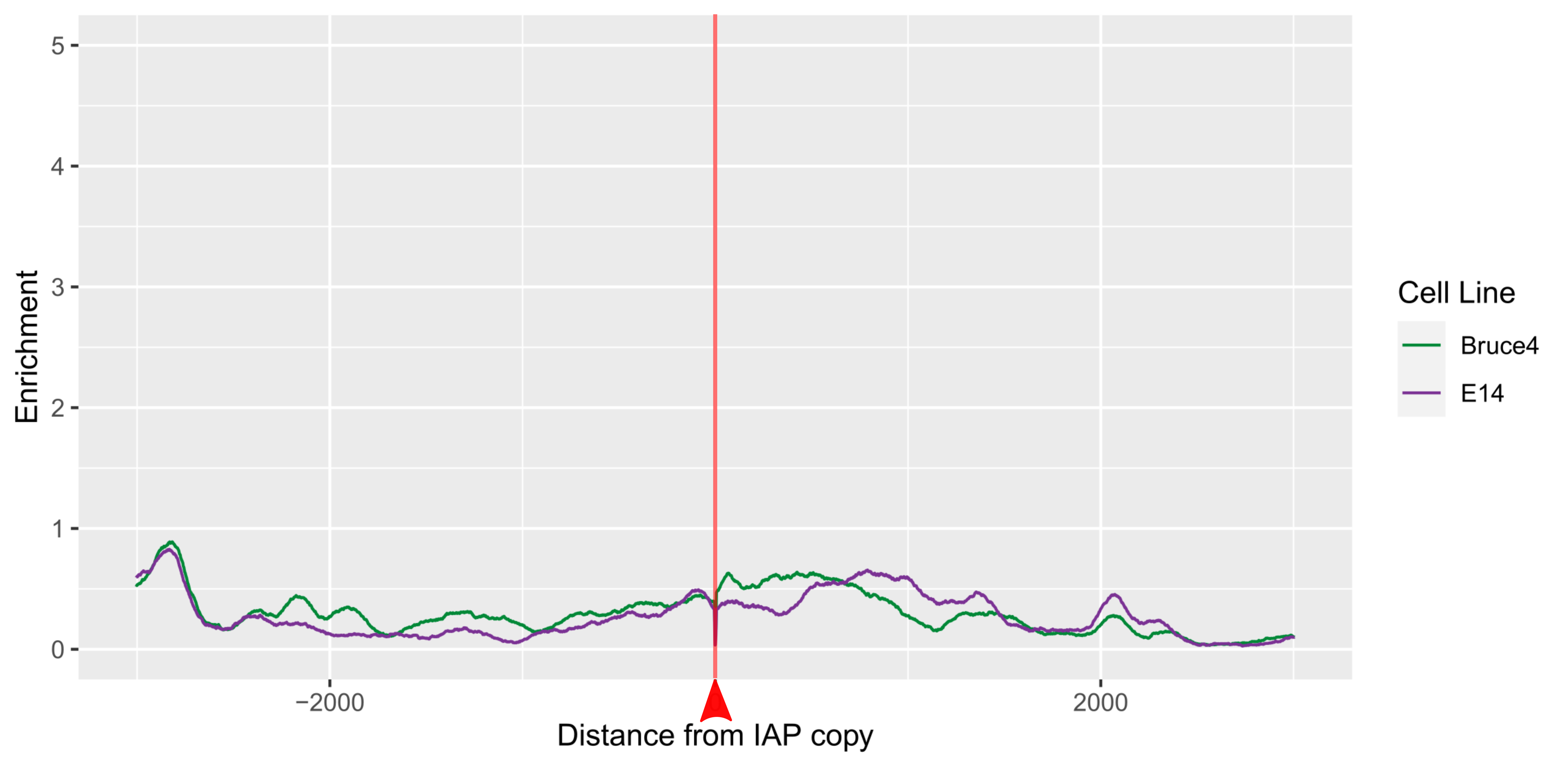


Figure S6. H3K4me3 enrichment in flanking sites of IAP copies present in C3H/HeJ, C57BL/6 and 129 of Bruce4 and E14. Figure show lack of H3K4me3 in flanking sites of common copies.

# Supplementary data

## C3H\_HeJ IAP #60 full length copy - DNA

Legend

LTR PBS GAG SHIN PRO POL

>C3H-FL

TGTGGGAAGCCGCCCCCACATTCGCCGTCACAAGATGGCGCTGACATCCTGTGTTCTAAGTTGGTAAACAAATAATCTGCGCATGAGCCAAGGGTATTTACGACTACTTGTACTCTGTTTTTCCCGTGAACGTCAGCTCGGCCATGGGCTGCAGCCAATCAGGGAGTGATGCGCCCTAGGCAATGGTTGTTCTCTTTAAAATAGAAGGGGTTTCGTTTTTCTCGCTCTCTTGCTTCCCTCTCTTGCTTCTTACACTCTGGCCCGATAAAGATATAAGCAATAAAGCTTTGCCGTAGAAGATTCTGGTTGTTGTGTTCTTCCTGGCCGGTCGTGAGAACGCGTCGAATAACAATTGGTGCCGAATTCCGGGACGAGAAAATCCGGGACGAGAAAAAACTCCGGACTGGCGCAGGAGGGATACTTCATTTCAGAACCAGAACTACGGATCACGTTTATAAAGGTTCCCGTAACACAGACTGTTGAGAAGGATCAACTGCCGAATTCAGACTCATCAGCTGGGGAACGACGGTGATAAAGGTCCCGTAAGCAGACTGTTAAGAAGGATTCAACTGTATGAATTCAGAACTTTTCAGCTGGGGAACGAGAGTACCAGTGAGTATGTTTGGCCTTGAATTTTTTCTGGTGTTAGGAGCCCTTTTGTTCCTTTTCACATGTTATATAGTGGTTAAGGCAGGGCTGAAAATTCTGGATGAAATTCAGGGCAGTCTATCAGAAGTAAAGCGGGGAGAGAGAGTAGGAGCAAGGAGAAACGGTAAGTATACAGGCCTTTCCAAGGGTCTTGAACCCGAGGAAAAGTTAAGGTTAGGTAGGAATACCTGGAGAGAGATTAGAAGAAAAAGAGGAAAAAGGGAAAAGAAAAAAGATCGATTAGCGGAGGTCTCTAGGAGATACTCGTCACTAGATGAGCTCAGGAAGCCAGCTCTTAGTAGCTCTGAAGCAAGTGAAGAATCCTCCTCTGAGGAAACAGACTGGGAGGAAGAAGCAGCCCATTACCAGCCAGCTAATTGGTCAAGAAAAAAGCCAAAAGCGGCTGGCGAAAGTCAGCGTACTGTTCAACCTCCCGGCAGTCGGTTTCAAGGTCCGCCCTATGCGGAGCCCCCGCCCTGCGTAGTGCGTCAGCAATGCGCAGAGAGGCAATGCGCAGAGAGGTGCGCAGAGAGGCAGTGCGCAGACAGGTGCGCAGAGAGGCAGTGCGCAGAGAGGCAGTGCGCAGACTCATTCATTCCCCGAGAGGAACAAAAGAAAATAGAACAGGCATTTCCAGTCTTTGAAGGAGCCGAGGGTGGGCGTGTCCACGCTCCGGTAGAATACGTACAGATTAAGGAAATTGCCGAGTCGGTTCGTAAATACGGAACCAATGCTAATTTCACCTTGGTGCAGTTAGACAGGCTCGCTGGTATGGCACTAACGCCTGCTGATTGGCAGACGGTTGTAAAAGCCGCTCTTCCTAGTATGGGCAAATATATGGAATGGAAAGCGCTTTGGCACGAAGCTGCACAGGCGCAGGCCCGAGCAAACGCAGCTGCTTTGACTCCAGAGCAGATAGATTGGACTTTTGACTTGTTAACGGGTCAGGGGGCTTATTCTGCTGATCAGACAAGCTACCATTGGGGAGCTTATGCCCAGATTTCTTCCACGGCTATTAGGGCCTGGAAGGCGCTCTCTCGAGCAGGTGAAACCACTGGTCAGTTAACAAAAATAATCCAGGGACCTCAGGAATCTTTCTCAGATTTTGTGGCCAGAATGACAGAGGCAGCAGAGCGTATTTTTGGAGAGTCAGAGCAAGCTGCGCCTCTCATAGAACAGCTAATCTACGAGCAAGCCACAAAGGAGTGCCGAGCGGCCATAGCCCCAAGAAAGAACAAAGGCTTACAAGACTGGCTCAGGGTCTGTCGAGAGCTTGGGGGACCCCTTAGCAATGCAGGTTTAGCGGCTGCCATCCTTCAATCCCAAAACCGCTCCATGGGCAGAAATGATCAGAGGACATGTTTTAACTGCGGAAAGCCTGGGCATTTTAAGAAAGATTGCAGAGCTCCAGATAAACAGGGAGGGGCTCTCACTCTTTGCTCTAAGTGTGGCAAGGGTTATCATAGAGCTGACCAGTGTCGCTCTGTGAGGGATATAAAGGGCAGAATTCTTCCCCCACCTGATAGTCAATCAGCTGATGTGCCAAAAAACGGGTCACCGGGCCCTCGGTCCCAGGGCCCTCAAAGATATGGGAACCGGTTTGTCAGGACCCAGGAAGCAGTCAGAGAGACGACCCAGGAAGACCCACAAGGGTGGACCTGCGTGCCGCCTCCGACTTCCTATTAATGCCTCAAATGAGTATTCAGCCGGTGCCGGTGGAGCCTATACCATCCTTGCCCCCGGGAACCATGGGCCTTATTCTCGGCCGAGGTTCACTCACCTTGCAGGGCTTAGTAGTCCACCCTGGAATTATGGATTGTCAACATTCCCCTGAAATACAGGTCCTGTGCTCAAGCCCTAAAGGCGTTTTTTCTATTAGTAAAGGAGATAGGATAGCTCAGCTGCTGCTCCTCCCTGATAATACCAGGGAGAAATCTGCAGGACCTGAGATAAAGAAAATGGGCTCCTCAGGAAATGATTCTGCCTATTTGGTTGTATCTTTAAATGATAGACCTAAGCTCCGCCTTAAGATTAATGGAAAAGAGTTTGAAGGCATCCTTGATACCGGAGCAGATAAAAGTATAATTTCTACACATTGGTGGCCCAAAGCATGGCCCACCACAGAGTCATCTCATTCATTACAGGGCCTAGGATATCAATCATGTCCCACTATAAGCTCCGTTGCCTTGACGTGGGAATCCTCTGAAGGGCAGCAAGGGAAATTCATACCTTATGTGCTCCCACTCCCGGTTAACCTCTGGGGAAGGGATATTATGCAGCATTTGGGCCTTATTTTGTCCAATGAAAACGCCCCATCAGGAGGGTATTCAGCTAAAGCAAAAAATATCATGGCAAAGATGGGTTATAAAGAAGGAAAAGGGTTAGGACATCAAGAACAGGGAAGGATAGAGCCCATCTCACCTAATGGAAACCAAGACAGACAGGGTCTGGGTTTTCCATAGCGGCCATTGGGGCAGCACGACCCATACCATGGAAAACAGGGGACCCAGTGTGGGTTCCTCAATGGCACCCATCCTCTGAAAAACTAGAAGCTGTGATTCAACTGGTAGAGGAACAATTAAAATTAGGCCATATTGAACCCTCTACCTCACCTTGGAATACTCCAATTTTTGTAATTAAGAAAAAGTCAGGAAAGTGGAGACTGCTCCATGACCTCAGAGCCATTAATGAGCAAATGAACTTATTTGGCCCAGTACAGAGGGGTCTCCCTGTACTTTCCGCCTTACCACGTGGCTGGAATTTAATCATTATAGATATTAAAGATTGTTTCTTTTCTATACCTTTGTGTCCAAGGGATAGGCCCAGATTTGCCTTTACCATCCCCTCTATTAATCACATGGAACCTGATAAGAGGTATCAATGGAAGGTCTTACCACAGGGAATGTCCAATAGTCCTACTATGTGTCAACTTTATGTACAAGAAGCTCTTTTGCCAGTGAGGGAACAATTCCCCTCTTTAATTTTGCTCCTTTACATGGATGACATCCTCCTGTGCCATAAAGACCTTACCATGCTACAAAAGGCATATCCTTTTCTACTTAAAACTTTAAGTCAGTGGGGTCTACAGATAGCCACAGAAAAGGTCCAAATTTCTGATACAGGACAATTCTTGGGCTCTGTGGTGTCCCCAGATAAGATTGTGCCCCAAAAGGTAGAGATAAGAAGAGATCACCTCCATACCTTAAATGATTTTCAAAAGCTGTTGGGAGATATTAATTGGCTCAGACCCTTTTTAAAGATTCCTTCTGCTGAATTAAGGCCTTTGTTTAGTATTTTAGAAGGAGATCCTCATATCTCCTCCCCTAGGACTCTTACTCTAGCTGCTAACCAGGCCTTACAAAAAGTGGAAAAAGCCTTACAGAATGCACAATTACAACGTATTGAGGATTCGCAGCCTTTCAGTTTGTGTGTCTTTAAGACAGCACAATTGCCAACTGCAGTTTTGTGGCAAAATGGGCCATTGTTGTGGATCCATCCAAACGTATCCCCAGCTAAAATAATAGATTGGTATCCTGATGCAATTGCACAGCTTGCCCTTAAAGGCCTAAAAGCAGCAATCACCCACTTTGGGCAAAGTCCATATCTTTTAATTGTACCTTATACCGCTGCACAGGTTCAAACCTTGGCAGCCGCATCTAATGATTGGGCAGTTTTAGTTACCTCCTTTTCAGGAAAAGTAGATAACCATTATCCAAAGCATCCAATCTTACAGTTTGCCCAAAATCAATCTGTTGTGTTTCCACAAATAACAGTAAGAAACCCACTTAAAAATGGGATTGTGGTATATACTGATGGATCAAAAACTGGCATAGGTGCCTATGTGGCTAATGGTAAAGTGGTATCCAAACAATATAATGAAAATTCACCTCAAGTGGTAGAATGTTTAGTGGTCTTAGAAGTTTTAAAAACCTTTTTAGAACCCCTTAATATTGTGTCAGATTCCTGTTATGTGGTAAATGCAGTAAATCTTTTAGAAGTGGCCGGAGTGATTAAGCCTTCCAGTAGAGTTGCCAATATTTTTCAGCAGATACAATTAGTTTTGTTATCTAGAAGATCTCCTGTTTATATTACTCATGTTAGAGCCCATTCAGGCCTACCTGGCCCCATGGCTCTGGGAAATGATTTGGCAGATAAGGCCACTAAAGTGGTGGCTGCTGCCCTATCATCCCCGGTAGAGGCTGCAAGAAATTTTCATAATAATTTTCATGTGACGGCTGAAACATTACGCAGTCGTTTCTCCTTGACAAGAAAAGAAGCCCGTGACATTGTTACTCAATGTCAAAGCTGCTGTGAGTTCTTGCCAGTTCCTCATGTGGGAATTAACCCACGCG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## C3H\_HeJ full length IAP #60 copy - proteins

>GAG

MNSELFSWGTRVPVSMFGLEFFLVLGALLFLFTCYIVVKAGLKILDEIQGSLSEVKRGERVGARRNGKYTGLSKGLEPEEKLRLGRNTWREIRRKRGKREKKKDRLAEVSRRYSSLDELRKPALSSSEASEESSSEETDWEEEAAHYQPANWSRKKPKAAGESQRTVQPPGSRFQGPPYAEPPPCVVRQQCAERQCAERCAERQCADRCAERQCAERQCADSFIPREEQKKIEQAFPVFEGAEGGRVHAPVEYVQIKEIAESVRKYGTNANFTLVQLDRLAGMALTPADWQTVVKAALPSMGKYMEWKALWHEAAQAQARANAAALTPEQIDWTFDLLTGQGAYSADQTSYHWGAYAQISSTAIRAWKALSRAGETTGQLTKIIQGPQESFSDFVARMTEAAERIFGESEQAAPLIEQLIYEQATKECRAAIAPRKNKGLQDWLRVCRELGGPLSNAGLAAAILQSQNRSMGRNDQRTCFNCGKPGHFKKDCRAPDKQGGALTLCSKCGKGYHRADQCRSVRDIKGRILPPPDSQSADVPKNGSPGPRSQGPQRYGNRFVRTQEAVRETTQEDPQGWTCVPPPTSY

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>POL

MNLFGPVQRGLPVLSALPRGWNLIIIDIKDCFFSIPLCPRDRPRFAFTIPSINHMEPDKRYQWKVLPQGMSNSPTMCQLYVQEALLPVREQFPSLILLLYMDDILLCHKDLTMLQKAYPFLLKTLSQWGLQIATEKVQISDTGQFLGSVVSPDKIVPQKVEIRRDHLHTLNDFQKLLGDINWLRPFLKIPSAELRPLFSILEGDPHISSPRTLTLAANQALQKVEKALQNAQLQRIEDSQPFSLCVFKTAQLPTAVLWQNGPLLWIHPNVSPAKIIDWYPDAIAQLALKGLKAAITHFGQSPYLLIVPYTAAQVQTLAAASNDWAVLVTSFSGKVDNHYPKHPILQFAQNQSVVFPQITVRNPLKNGIVVYTDGSKTGIGAYVANGKVVSKQYNENSPQVVECLVVLEVLKTFLEPLNIVSDSCYVVNAVNLLEVAGVIKPSSRVANIFQQIQLVLLSRRSPVYITHVRAHSGLPGPMALGNDLADKATKVVAAALSSPVEAARNFHNNFHVTAETLRSRFSLTRKEARDIVTQCQSCCEFLPVPHVGINPRGIRPLQVWQMDVTHVSSFGKLQYLHVSIDTCSGIMFASPLTGEKASHVIQHCLEAWSAWGKPRLLKTDNGPAYTSQKFQQFCRQMDVTHLTGLPYNPQGQGIVERAHRTLKAYLIKQKRGTFEETVPRAPRVSVSLALFTLNFLNIDAHGHTAAERHCSEPDRPNEMVKWKNVLDNKWYGPDPILIRSRGAICVFPQNEDNPFWVPERLTRKIQTDQGNTNVPRLGDVQGVNNKERAALGDNVDISTPNDGDV

## DNA alignment of the full-length copy between C3H/HeJ (IAP #60) and the 129 genome

In bold underlined, the SHIN region

**C3H** 1 TGTGGGAAGCCGCCCCCACATTCGCCGTCACAAGATGGCGCTGACATCCTGTGTTCTAAGTTGGTAAACAAATAATCTGCGCATGAGCCAAGGGTATTTA

**129** 1 TGTGGGAAGCCGCCCCCACATTCGCCGTCACAAGATGGCGCTGACATCCTGTGTTCTAAGTTGGTAAACAAATAATCTGCGCATGAGCCAAGGGTATTTA

**C3H** 101 CGACTACTTGTACTCTGTTTTTCCCGTGAACGTCAGCTCGGCCATGGGCTGCAGCCAATCAGGGAGTGATGCGCCCTAGGCAATGGTTGTTCTCTTTAAA

**129** 101 CGACTACTTGTACTCTGTTTTTCCCGTGAACGTCAGCTCGGCCATGGGCTGCAGCCAATCAGGGAGTGATGCGCCCTAGGCAATGGTTGTTCTCTTTAAA

**C3H** 201 ATAGAAGGGGTTTCGTTTTTCTCGCTCTCTTGCTTCCCTCTCTTGCTTCTTACACTCTGGCCCGATAAAGATATAAGCAATAAAGCTTTGCCGTAGAAGA

**129** 201 ATAGAAGGGGTTTCGTTTTTCTCGCTCTCTTGCTTCCCTCTCTTGCTTCTTACACTCTGGCCCGATAAAGATATAAGCAATAAAGCTTTGCCGTAGAAGA

**C3H** 301 TTCTGGTTGTTGTGTTCTTCCTGGCCGGTCGTGAGAACGCGTCGAATAACAATTGGTGCCGAATTCCGGGACGAGAAAATCCGGGACGAGAAAAAACTCC

**129** 301 TTCTGGTTGTTGTGTTCTTCCTGGCCGGTCGTGAGAACGCGTCGAATAACAATTGGTGCCGAATTCCGGGACGAGAAAATCCGGGACGAGAAAAAACTCC

**C3H** 401 GGACTGGCGCAGGAGGGATACTTCATTTCAGAACCAGAACTACGGATCACGTTTATAAAGGTTCCCGTAACACAGACTGTTGAGAAGGAT-CAACTGCCG

**129** 401 GGACTGGCGCAGGAGGGATACTTCATTTCAGAACCAGAACTACGGATCACGTTTATAAAGGTTCCCGTAACACAGACTGTTGAGAAGGATTCAACTGCCG

**C3H** 500 AATTCAGA-CTCATCAGCTGGGGAACGACGGTGATAAAGGT-CCCGTAA-GCAGACTGTTAAGAAGGATTCAACTGTATGAATTCAGAACTTTTCAGCTG

**129** 501 AATTCAGAACTCATCAGCTGGGGAACGACGGTGATAAAGGTTCCCGTAAAGCAGACTGTTAAGAAGGATTCAACTGTATGAATTCAGAACTTTTCAGCTG

**C3H** 597 GGGAACGAGAGTACCAGTGAGTATGTTTGGCCTTGAATTTTTTCTGGTGTTAGGAGCCCTTTTGTTCCTTTTCACATGTTATATAGTGGTTAAGGCAGGG

**129** 601 GGGAACGAGAGTACCAGTGAGTATGTTTGGCCTTGAATTTTTTCTGGTGTTAGGAGCCCTTTTGTTCCTTTTCACATGTTATATAGTGGTTAAGGCAGGG

**C3H** 697 CTGAAAATTCTGGATGAAATTCAGGGCAGTCTATCAGAAGTAAAGCGGGGAGAGAGAGTAGGAGCAAGGAGAAACGGTAAGTATACAGGCCTTTCCAAGG

**129** 701 CTGAAAATTCTGGATGAAATTCAGGGCAGTCTATCAGAAGTAAAGCGGGGAGAGAGAGTAGGAGCAAGGAGAAACGGTAAGTATACAGGCCTTTCCAAGG

**C3H** 797 GTCTTGAACCCGAGGAAAAGTTAAGGTTAGGTAGGAATACCTGGAGAGAGATTAGAAGAAAAAGAGGAAAAAGGGAAAAGAAAAAAGATCGATTAGCGGA

**129** 801 GTCTTGAACCCGAGGAAAAGTTAAGGTTAGGTAGGAATACCTGGAGAGAGATTAGAAGAAAAAGAGGAAAAAGGGAAAAGAAAAAAGATCGATTAGCGGA

**C3H** 897 GGTCTCTAGGAGATACTCGTCACTAGATGAGCTCAGGAAGCCAGCTCTTAGTAGCTCTGAAGCAAGTGAAGAATCCTCCTCTGAGGAAACAGACTGGGAG

**129** 901 GGTCTCTAGGAGATACTCGTCACTAGATGAGCTCAGGAAGCCAGCTCTTAGTAGCTCTGAAGCAAGTGAAGAATCCTCCTCTGAGGAAACAGACTGGGAG

**C3H** 997 GAAGAAGCAGCCCATTACCAGCCAGCTAATTGGTCAAGAAAAAAGCCAAAAGCGGCTGGCGAAAGTCAGCGTACTGTTCAACCTCCCGGCAGTCGGTTTC

**129** 1001 GAAGAAGCAGCCCATTACCAGCCAGCTAATTGGTCAAGAAAAAAGCCAAAAGCGGCTGGCGAAAGTCAGCGTACTGTTCAACCTCCCGGCAGTCGGTTTC

**C3H** 1097 AAGGTCCGCCCTATGCGGAGCCCCCGCCCTGCGTAGTGCGTCAGCAATGCGCAGAGAGGCAATGCGCAGAGAGGTGCGCAGAGAGGCAGTGCGCAGACAG

**129** 1101 AAGGTCCGCCCTATGCGGAGCCCCCGCCCTGCGTAGTGCGTCAGCAATGCGCAGAGAGGCAATGCGCAGAGAGGTGCGCAGAGAGGCAGTGCGCAGACAG

**C3H** 1197 GTGCGCAGAGAGGCAGTGCGCAGAGAGGCAGTGCGCAGACTCATTCATTCCCCGAGAGGAACAAAAGAAAATAGAACAGGCATTTCCAGTCTTTGAAGGA

**129** 1201 GTGCGCAGAGAGGCAGTGCGCAGAGAGGCAGTGCGCAGACTCATTCATTCCCCGAGAGGAACAAAAGAAAATAGAACAGGCATTTCCAGTCTTTGAAGGA

**C3H** 1297 GCCGAGGGTGGGCGTGTCCACGCTCCGGTAGAATACGTACAGATTAAGGAAATTGCCGAGTCGGTTC**GTAAATACGGAACCAATGCTAATTTCACCTTGG**

**129** 1301 GCCGAGGGTGGGCGTGTCCACGCTCCGGTAGAATACGTACAGATTAAGGAAATTGCCGAGTCGGTTCGTAAATACGGAACCAATGCTAATTTCACCTTGG

**C3H** 1397 **TGCAGTTAGACAGGCTCGCTGGTATGGCACTAACGCCTGCTGATTGGCAGACGGTTGTAAAAGCCGCTCTTCCTAGTATGGGCAAATATATGGAATGGAA**

**129** 1401 TGCAGTTAGACAGGCTCGCTGGTATGGCACTAACGCCTGCTGATTGGCAGACGGTTGTAAAAGCCGCTCTTCCTAGTATGGGCAAATATATGGAATGGAA

**C3H** 1497 **AGC**GCTTTGGCACGAAGCTGCACAGGCGCAGGCCCGAGCAAACGCAGCTGCTTTGACTCCAGAGCAGATAGATTGGACTTTTGACTTGTTAACGGGTCAG

**129** 1501 AGCGCTTTGGCACGAAGCTGCACAGGCGCAGGCCCGAGCAAACGCAGCTGCTTTGACTCCAGAGCAGAGAGATTGGACTTTTGACTTGTTAACGGGTCAG

**C3H** 1597 GGGGCTTATTCTGCTGATCAGACAAGCTACCATTGGGGAGCTTATGCCCAGATTTCTTCCACGGCTATTAGGGCCTGGAAGGCGCTCTCTCGAGCAGGTG

**129** 1601 GGAGCTTATTCTGCTGATCAGACAAACTACCATTGGGGAGCTTATGCCCAGATTTCTTCCACGGCTATTAGGGCCTGGAAGGCGCTCTCTCGAGCAGGTG

**C3H** 1697 AAACCACTGGTCAGTTAACAAAAATAATCCAGGGACCTCAGGAATCTTTCTCAGATTTTGTGGCCAGAATGACAGAGGCAGCAGAGCGTATTTTTGGAGA

**129** 1701 AAACCACTGGTCAGTTAACAAAAATAATCCAGGGACCTCAGGAATCTTTCTCAGATTTTGTGGCCAGAATGACAGAGGCAGCAGAGCGTATTTTTGGAGA

**C3H** 1797 GTCAGAGCAAGCTGCGCCTCTCATAGAACAGCTAATCTACGAGCAAGCCACAAAGGAGTGCCGAGCGGCCATAGCCCCAAGAAAGAACAAAGGCTTACAA

**129** 1801 GTCAGAGCAAGCTGCGCCTCTCATAGAACAGCTAATCTACGAGCAAGCCACAAAGGAGTGCCGAGCGGCCATAGCCCCAAGAAAGAACAAAGGCTTACAA

**C3H** 1897 GACTGGCTCAGGGTCTGTCGAGAGCTTGGGGGACCCCTTAGCAATGCAGGTTTAGCGGCTGCCATCCTTCAATCCCAAAACCGCTCCATGGGCAGAAATG

**129** 1901 GACTGGCTCAGGGTCTGTCGAGAGCTTGGGGGACCCCTTAGCAATGCAGGTTTAGCGGCTGCCATCCTTCAATCCCAAAACCGCTCCATGGGCAGAAATG

**C3H** 1997 ATCAGAGGACATGTTTTAACTGCGGAAAGCCTGGGCATTTTAAGAAAGATTGCAGAGCTCCAGATAAACAGGGAGGGGCTCTCACTCTTTGCTCTAAGTG

**129** 2001 ATCAGAGGACATGTTTTAACTGCGGAAAGCCTGGGCATTTTAAGAAAGATTGCAGAGCTCCAGATAAACAGGGAGGGACTCTCACTCTTTGCTCTAAGTG

**C3H** 2097 TGGCAAGGGTTATCATAGAGCTGACCAGTGTCGCTCTGTGAGGGATATAAAGGGCAGAATTCTTCCCCCACCTGATAGTCAATCAGCTGATGTGCCAAAA

**129** 2101 TGGCAAGGGTTATCATAGAGCTGACCAGTGTCGCTCTGTGAGGGATATAAAGGGCAGAATTCTTCCCCCACCTGATAGTCAATCAGCTGATGTGCCAAAA

**C3H** 2197 AACGGGTCACCGGGCCCTCGGTCCCAGGGCCCTCAAAGATATGGGAACCGGTTTGTCAGGACCCAGGAAGCAGTCAGAGAGACGACCCAGGAAGACCCAC

**129** 2201 AACGGGTCACCGGGCCCTCGGTCCCAGGGCCCTCAAAGATATGGGAACCGGTTTGTCAGGACCCAGGAAGCAGTCAGAGAGACGACCCAGGAAGACCCAC

**C3H** 2297 AAGGGTGGACCTGCGTGCCGCCTCCGACTTCCTATTAATGCCTCAAATGAGTATTCAGCCGGTGCCGGTGGAGCCTATACCATCCTTGCCCCCGGGAACC

**129** 2301 AAGGGTGGACCTGCGTGCCGCCTCCGACTTCCTATTAATGCCTCAAATGAGTATTCAGCCGGTGCCGGTGGAGCCTATACCATCCTTGCCCCCGGGAACC

**C3H** 2397 ATGGGCCTTATTCTCGGCCGAGGTTCACTCACCTTGCAGGGCTTAGTAGTCCACCCTGGAATTATGGATTGTCAACATTCCCCTGAAATACAGGTCCTGT

**129** 2401 ATGGGCCTTATTCTCGGCCGAGGTTCACTCACCTTGCAGGGCTTAGTAGTCCACCCTGGAATTATGGATTGTCAACATTCCCCTGAAATACAGGTCCTGT

**C3H** 2497 GCTCAAGCCCTAAAGGCGTTTTTTCTATTAGTAAAGGAGATAGGATAGCTCAGCTGCTGCTCCTCCCTGATAATACCAGGGAGAAATCTGCAGGACCTGA

**129** 2501 GCTCAAGCCCTAAAGGCGTTTTTTCTATTAGTAAAGGAGATAGGATAGCTCAGCTGCTGCTCCTCCCTGATAATACCAGGGAGAAATCTGCAGGACCTGA

**C3H** 2597 GATAAAGAAAATGGGCTCCTCAGGAAATGATTCTGCCTATTTGGTTGTATCTTTAAATGATAGACCTAAGCTCCGCCTTAAGATTAATGGAAAAGAGTTT

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**C3H** 2697 GAAGGCATCCTTGATACCGGAGCAGATAAAAGTATAATTTCTACACATTGGTGGCCCAAAGCATGGCCCACCACAGAGTCATCTCATTCATTACAGGGCC

**129** 2701 GAAGGCATCCTTGATACCGGAGCAGATAAAAGTATAATTTCTACACATTGGTGGCCCAAAGCATGGCCCACCACAGAGTCATCTCATTCATTACAGGGCC

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**129** 3001 ATGGCAAAGATGGGTTATAAAGAAGGAAAAGGGTTAGGACATCAAGAACAGGGAAGGATAGAGCCCATCTCACCTAATGGAAACCAAGACAGACAGGGTC

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**129** 3201 GAAGCTGTGATTCAACTGGTAGAGGAACAATTAAAATTAGGCCATATTGAACCCTCTACCTCACCTTGGAATACTCCAATTTTTGTAATTAAGAAAAAGT

**C3H** 3297 CAGGAAAGTGGAGACTGCTCCATGACCTCAGAGCCATTAATGAGCAAATGAACTTATTTGGCCCAGTACAGAGGGGTCTCCCTGTACTTTCCGCCTTACC

**129** 3301 CAGGAAAGTGGAGACTGCTCCATGACCTCAGAGCCATTAATGAGCAAATGAACTTATTTGGCCCAGTACAGAGGGGTCTCCCTGTACTTTCCGCCTTACC

**C3H** 3397 ACGTGGCTGGAATTTAATCATTATAGATATTAAAGATTGTTTCTTTTCTATACCTTTGTGTCCAAGGGATAGGCCCAGATTTGCCTTTACCATCCCCTCT

**129** 3401 ACGTGGCTGGAATTTAATCATTATAGATATTAAAGATTGTTTCTTTTCTATACCTTTGTGTCCAAGGGATAGGCCCAGATTTGCCTTTACCATCCCCTCT

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**129** 3701 TCCTTTTCTACTTAAAACTTTAAGTCAGTGGGGTCTACAGATAGCCACAGAAAAGGTCCAAATTTCTGATACAGGACAATTCTTGGGCTCTGTGGTGTCC

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**129** 3901 CCTTTTTAAAGATTCCTTCTGCTGAATTAAGGCCTTTGTTTAGTATTTTAGAAGGAGATCCTCATATCTCCTCCCCTAGGACTCTTACTCTAGCTGCTAA

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**129** 4001 CCAGGCCTTACAAAAAGTGGAAAAAGCCTTACAGAATGCACAATTACAACGTATTGAGGATTCGCAGCCTTTCAGTTTGTGTGTCTTTAAGACAGCACAA

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**129** 4101 TTGCCAACTGCAGTTTTGTGGCAAAATGGGCCATTGTTGTGGATCCATCCAAACGTATCCCCAGCTAAAATAATAGATTGGTATCCTGATGCAATTGCAC

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**129** 4201 AGCTTGCCCTTAAAGGCCTAAAAGCAGCAATCACCCACTTTGGGCAAAGTCCATATCTTTTAATTGTACCTTATACCGCTGCACAGGTTCAAACCTTGGC

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**129** 4801 CAGATAAGGCCACTAAAGTGGTGGCTGCTGCCCTATCATCCCCGGTAGAGGCTGCAAGAAATTTTCATAATAATTTTCATGTGACGGCTGAAACATTACG

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**129** 4901 CAGTCGTTTCTCCTTGACAAGAAAAGAAGCCCGTGACATTGTTACTCAATGTCAAAGCTGCTGTGAGTTCTTGCCAGTTCCTCATGTGGGAATTAACCCA

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**129** 5201 GACTGATAATGGACCAGCTTATACGTCCCAAAAATTTCAGCAGTTCTGCCGTCAGATGGACGTAACCCACCTGACTGGACTTCCATACAACCCTCAAGGA

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**129** 5301 CAGGGTATTGTTGAGCGTGCGCATCGCACCCTCAAAGCCTATCTTATAAAACAGAAGAGGGGAACTTTTGAGGAGACTGTACCCCGAGCACCAAGAGTGT

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**129** 5401 CGGTGTCTTTGGCACTCTTTACACTCAATTTTTTAAATATTGATGCTCATGGCCATACTGCGGCTGAACGTCATTGTTCAGAGCCAGATAGGCCCAATGA

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**129** 5501 GATGGTTAAATGGAAAAATGTCCTTGATAATAAATGGTATGGCCCGGATCCTATCTTGATAAGATCCAGGGGAGCTATCTGTGTTTTCCCACAGAATGAA

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**C3H** 7097 TCGAATAACA

**129** 7041 TCGAATAACA