> meth.data :List of 8 (one for each locus)

$ [locus1 name] :List of 2

..$ CpG.sum :List of 3

.. ..$ coverage :'data.frame': 96 obs. of X variables (number of reads, one row per sample, one column per CpG site; X=number of CpG sites at the locus)

.. ..$ freq.meth :'data.frame': 96 obs. of X variables (number of methylated reads, one row per sample, one column per CpG site)

.. ..$ freq.meth :'data.frame': 96 obs. of X variables (number of reads with something other than a C or T, one row per sample, one column per CpG site)

..$ non.CpG.sum :List of 3 (same as CpG.sum, except for non-CpG C’s in the sequence)