**Questions**

Could you ask to the Canada people some question? Considering the table "CpG-islands-DMR-calls", and the values in the columns "IwtAP2R4a", "IwtAP6c", "IwtAPB" etc I have these questions:

1. Does these columns contain the methylation values for a sample and all the regions?
2. Which kind of pre-processing has been performed?
3. Why the ranges of these data are between 0 and >100?
4. There is a cut-off that we can consider to identify if a region is hypo or hyper-methylated without looking at the fold changes and p-values?  
   For example considering the sample IwtAP2R4a the minum value reported in this column is 0, whereas the maximum of 161. Is there any cut-off that I can employ to stratify the regions of these samples in 1) hypo 2) partial methylated 3) hyper-methylated?