Notes on 450k data

1. It may have duplicate genomic position with different ref id
2. It may have overlapping genomic position in the same file

Bedtools unionbedg Wont work properly if above are true. So run <https://github.com/Irfanwustl/Research_code/tree/master/450k_data_analysis/450k_supporting_tools/merge_onlyoverlapping>

After TCGA preprocess step

Or: Pending task:should I change the TCGA process file to include: <https://github.com/Irfanwustl/Research_code/tree/master/450k_data_analysis/450k_supporting_tools/merge_onlyoverlapping>

?

uniq\_pos.sh: I have code this and working (but if not necessary for 450k data preprocess. merge\_onlyoverlapping.sh is enough): <https://github.com/Irfanwustl/Research_code/tree/master/450k_data_analysis/450k_supporting_tools/uniq_pos>