Do I have all correct output files??

**Kimo Script Readme**

Identification of Top 30 truncating mutations (Readme file)

1: Identification of TCGA truncating mutations >> NOT Correct as uses **Genbankkinases**

2: Identification of CCLE truncating mutations >> As above

3: Scoring of Top 30 truncating mutations

4: Alignment of this data (Or is that what 1.3 is doing)

Application of hotspot motifs (Readme file)

5: Identification of Motifs from Genbank

6: Applying Genbank data to put out TCGA data

7: Applying Genbank data to put out CCLE data

8: Merge TCGA and CCLE outputs