

# Our “must have” list with essential for replication checkpoints

By Alexandra Belyaeva, Alexandr Zhuravlev



**Give link to the common popset**



Say we have 95 sequences in our research



Skip this step, cause it is obvious



**Mark the settings, which were used in programmes**



**Accept trimming as a pre-analyse method**



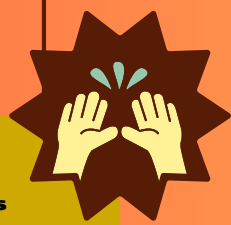
Say not a single word about it



Immediately specify all the data we are working with



**Say after the alignment description that the sequences from the previous study were added**



**Describe which subsets the data is divided into**



Dedicate one sentence to this and not to tell what tools were used

