

SEQUENCES (.zip)    TPA (.txt)    METADATA (.txt)



**Manage files**



*stats\_log (.txt)*



*all\_dataset*



**Filtering and trimming**

- T ( Tags ~)
- P ( Primers ~)
- C ( Tag Combination ~)
- N ( Ns ~)
- L ( Length ~)
- H ( Homopolymers ~)
- A ( Trim Adaptors ~)
- G ( Trim Tags/Primers ~)
- D ( Duplicates ~)



*summary (.txt)*



*\*stats\_log (.txt)*



*homopolymers (.html)*



*rejected (.fas)*



*accepted (.fas)*



**Cluster (BLASTCLUST & CD-HIT)**

- C ( Coverage % ~)
- I ( Identity % ~)
- S ( Remove Singletons~)



*cluster\_info (.txt)*



*\*stats\_log (.txt)*



*matrix\_table\_1 (.xls)*



*singleton (.fas)*



*cluster\_out (.fas)*



**Blast , Blast Parsing  
&  
Presenting Outfiles**



*output\_bp (.txt, .xls, .html)*



*\*stats\_log (.txt)*



*\*matrix\_table\_2 (.xls)*



*blastout.txt*

