3. Bioinformatics Analysis

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| **Standard Analysis** |
| Data quality control (get rid of reads containing adapter or with low quality; Q20, Q30, error rate distribution, GC distribution, total bases) |
| Mapping onto reference genome (mapping rate, reads distribution, rRNA content) |
| Peak calling |
| Motif prediction |
| Peak annotation (downstream or overlapping gene, peak distribution in functional region of gene and transcript) |
| Functional analysis of peak-associated genes (Gene Ontology, pathway) |
| Visualization of RIP-seq data |