

### 5 accessions analysis pipeline

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graph TD
    prepare_tfdb_R[prepare_tfdb_R] --> hirano_hormone_genes_R[hirano_hormone_genes_R]
    hirano_hormone_genes_R --> genewise_homology_ensembl_R[genewise_homology_ensembl_R]
    genewise_homology_ensembl_R --> download_pettko_cycle_genes_R[download_pettko_cycle_genes_R]
    download_pettko_cycle_genes_R --> osiReads[osiReads]
    osiReads --> osjReads[osjReads]
    osjReads --> ogReads[ogReads]
    ogReads --> obReads[obReads]
    obReads --> orReads[orReads]
    orReads --> downloadGenome_sh[downloadGenome_sh]
    
    osiReads --> cutadapt_sh[cutadapt_sh]
    osjReads --> cutadapt_sh
    ogReads --> cutadapt_sh
    obReads --> cutadapt_sh
    orReads --> cutadapt_sh
    
    cutadapt_sh --> starGenomeGenerate_sh[starGenomeGenerate_sh]
    cutadapt_sh --> loadGenome_sh[loadGenome_sh]
    
    starGenomeGenerate_sh --> loadGenome_sh
    loadGenome_sh --> firstMapping_sh[firstMapping_sh]
    firstMapping_sh --> unloadGenome_sh[unloadGenome_sh]
    unloadGenome_sh --> secondMapping_sh[secondMapping_sh]
    
    firstMapping_sh --> secondMapping_sh
    
    secondMapping_sh --> compressUnmappedReads_sh[compressUnmappedReads_sh]
    secondMapping_sh --> deseq2_R{{deseq2_R}}
    secondMapping_sh --> parseStarStats_R{{parseStarStats_R}}
    secondMapping_sh --> htseq_shuffle[htseq_shuffle]
    
    compressUnmappedReads_sh --> remap_sh[remap_sh]
    remap_sh --> download_gwas_crowell_R[download_gwas_crowell_R]
    download_gwas_crowell_R --> retrieve_gwas_genes_biomart_R[retrieve_gwas_genes_biomart_R]
    retrieve_gwas_genes_biomart_R --> gwas_domestication_genes_R{{gwas_domestication_genes_R}}
    
    deseq2_R --> wald_tests[wald_tests]
    parseStarStats_R --> tpm_R[tpm_R]
    htseq_shuffle --> tpm_R
    htseq_shuffle --> calculate_cutoffs_R[calculate_cutoffs_R]
    calculate_cutoffs_R --> wald_tests
    
    tpm_R --> extract_dom_lists_R[extract_dom_lists_R]
    extract_dom_lists_R --> gwas_lmi_R{{gwas_lmi_R}}
    
    calculate_feature_lengths_R[calculate_feature_lengths_R] --> shuffle[shuffle]
    shuffle --> htseq_shuffle
    calculate_feature_lengths_R --> tpm_R
  
```

Key:

The diagram shows a yellow box labeled 'Up-to-date Final target' with a green border. A grey arrow points down from this box to a yellow box labeled 'Final target' with an orange border.

```
graph TD; A[Up-to-date Final target] --> B[Final target]
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Key:

The diagram consists of two orange rectangular boxes with green outlines. The top box contains the text 'Up-to-date Final target'. A grey arrow points downwards from the bottom center of the top box to the top center of the bottom box. The bottom box contains the text 'Final target'.

Key:

The diagram consists of two orange rectangular boxes with green outlines. The top box contains the text 'Up-to-date Final target'. A grey arrow points downwards from the bottom center of the top box to the top center of the bottom box. The bottom box contains the text 'Final target'.