A Reanalysis of an Existing *Drosophila melanogaster* Dataset Reveals a New Set of Genes Involved in Post-Mating Response

Analysis Commands

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1 Constructing the 000_t2g (Transcript to Gene File) Commands

- Starting files:
  - Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fasta.ids
  - Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fasta.ids

```
paste \
    <(awk '{print $1}' \
  Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fasta.ids) \
    <(awk '{print $4}' \
  Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fasta.ids | \
  sed 's/gene://') \
    <(awk '{print $7}' \
  Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fasta.ids | \
  sed 's/gene_symbol://') \
    > 000_t2g
```

2 Master Tables Generation Commands

```
grep ">" zzDrosophila_melanogaster.BDGP6.28.cdna.all.ncrna.fa | \
    sed 's/^>//' | \
    awk '{print $3 "\t" $4 "\t" $1 "\t" $6 "\t" $7}' \
> zzMasterTableChrGeneTransName_01

awk -F":" '{print $3 ":" $4 "\t" $7 "\t" $9 "\t" $10 }' zzMasterTableChrGeneTransName_01 | \
    awk '{print $1 "\t" $2 "\t" $3 "\t" $5 "\t" $6}' \
> zzMasterTableChrGeneTransName_02
```

3 Converting Fowler Data Gene IDs to Transcript IDs

```
grep -f 00_Fowler_SigHits_mRNA_Ab_Genes.org zzMasterTableChrGeneTransName_02 | \
    awk '{print $3}' | \
    sort -u \
 > 00_Fowler_SigHits_mRNA_Ab_Transcripts.org

grep -f 00_Fowler_SigHits_mRNA_HT_Genes.org zzMasterTableChrGeneTransName_02 | \
    awk '{print $3}' | \
    sort -u \
 > 00_Fowler_SigHits_mRNA_HT_Transcripts.org
```

4 mRNA

4.1 Abdomen

4.1.1 Testing Command

```
for i in 00_E*_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;do echo $i;done;
```

4.1.2 Affected Files:

```
00_E01_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
00_E02_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
00_E03_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
00_E04_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
```

```
for i in 00_E*_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;do
 tail -n+2 $i | \
     awk -F, '{print $2}' | \
     sed 's/"//g';
      done | \
      sort | \
      uniq | \
      wc -l;
```

```
for i in 00_E*_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;do \
     tail -n+2 $i | \
      awk -F, '{print $2}' | \sed 's/"//g';
      done | \
      sort | \
      uniq \
  > 01_TotalNumberUniqueHits_E1234_mRNA_F_VxM_Ab_Transcripts.csv;
```

```
tail -n+2 00_E01_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E01_mRNA_F_VxM_Ab_Transcripts.csv
```

```
tail -n+2 00_E02_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E02_mRNA_F_VxM_Ab_Transcripts.csv
```

```
tail -n+2 00_E03_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E03_mRNA_F_VxM_Ab_Transcripts.csv
```

```
tail -n+2 00_E04_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | \
    sed ’s/"//g’ | \
    sort -u \
 > 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts.csv
```

```
grep -f 01_TotalNumberUniqueHits_E1234_mRNA_F_VxM_Ab_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $2}’ | \
    sort -u | \
    wc -l;
```

```
grep -f 01_TotalNumberUniqueHits_E1234_mRNA_F_VxM_Ab_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $2}’ | \
    sort -u \
 > 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv;
```

```
for i in 00_E*_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, ’{print $2}’ | \
sed ’s/"//g’;
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk ’{print $2}’ | wc -l;
```

```
for i in 00_E*_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, ’{print $2}’ | \
sed ’s/"//g’;
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk ’{print $2}’ \
> 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_Ab_Transcripts_PresentAll4Experiments.csv;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_Ab_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $2}’ | \
    sort -u | \
    wc -l;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_Ab_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u \
 > 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv;
```

```
tail -n+2 00_E01_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E02_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E03_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E04_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

4.2 Head-Thorax

4.2.1 Testing Command

```
for i in 00_E*_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;do echo $i;done;
```

4.2.2 Affected Files:

```
00_E01_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
00_E02_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
00_E03_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
00_E04_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
```

```
for i in 00_E*_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq | \
    wc -l;
```

```
for i in 00_E*_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq \
> 01_TotalNumberUniqueHits_E1234_mRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E01_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E01_mRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E02_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E02_mRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E03_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E03_mRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E04_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts.csv;
```

```
grep -f 01_TotalNumberUniqueHits_E1234_mRNA_F_VxM_HT_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u | \
    wc -l;
```

```
grep -f 01_TotalNumberUniqueHits_E1234_mRNA_F_VxM_HT_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u \
 > 02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv;
```

```
for i in 00_E*_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk '{print $2}' | \
    wc -l;
```

```
for i in 00_E*_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk '{print $2}' \
> 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_HT_Transcripts_PresentAll4Experiments.csv;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_HT_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u | \
    wc -l;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_HT_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u \
 > 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv;
```

```
tail -n+2 00_E01_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E02_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E03_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E04_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort | \
    uniq | \
    wc -l;
```

4.3 Canonical Analysis

```
tail -n+2 \
     00_E04_mRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05_canonical_r28.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv;
```

```
grep -f 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u \
 > 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv;
```

```
comm -23 \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) | \
    wc -l;
comm -23 \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) \
     > 19_Significant_Ab_mRNA_Genes_E1234_x_canonical_r28_E1234.org;
```

```
comm -13 \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) | \
    wc -l;
comm -13 \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) \
     > 19_Significant_Ab_mRNA_Genes_E1234_x_canonical_r28_canonical_r28.org;
```

```
comm -12 \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) | \
    wc -l;
comm -12 \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) \
     > 19_Significant_Ab_mRNA_Genes_E1234_x_canonical_r28_Overlap.org;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) | \
    wc -l;
comm -23 \
```

```
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) \
     > 20_Significant_Ab_mRNA_Genes_Fowlers_x_canonical_r28_Fowlers.org;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) | \
    wc -l;
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) \
     > 20_Significant_Ab_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) | \
    wc -l;
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv) \
     > 20_Significant_Ab_mRNA_Genes_Fowlers_x_canonical_r28_Overlap.org;
```

```
tail -n+2 \
     00_E04_mRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05_canonical_r28.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv;
```

```
grep -f 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u \
 > 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv;
```

```
comm -23 \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) | \
    wc -l;
comm -23 \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) \
     > 21_Significant_HT_mRNA_Genes_E1234_x_canonical_r28_E1234.org;
```

```
comm -13 \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) | \
    wc -l;
comm -13 \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) \
     > 21_Significant_HT_mRNA_Genes_E1234_x_canonical_r28_canonical_r28.org;
```

```
comm -12 \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) | \
    wc -l;
comm -12 \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) \
     > 21_Significant_HT_mRNA_Genes_E1234_x_canonical_r28_Overlap.org;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) | \
    wc -l;
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) \
     > 22_Significant_HT_mRNA_Genes_Fowlers_x_canonical_r28_Fowlers.org;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) |
    wc -l;
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) \
     > 22_Significant_HT_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) | \
    wc -l;
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv) \
     > 22_Significant_HT_mRNA_Genes_Fowlers_x_canonical_r28_Overlap.org;
```

```
cat 20_Significant_Ab_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
    22_Significant_HT_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org | \
```

```
    sort | \
    uniq \
> 23_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org;
```

```
#eliminate genes removed from r28
diff -y --suppress-common-lines \
     <(sort \
   23_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org) \
     <(grep -f \
    23_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
    Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids | \
   awk '{print $1}' | \
   sort);
```

```
grep -f \
     23_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
     Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids \
     > 24_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org;
```

```
grep -f \
     20_Significant_Ab_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
     24_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org | \
    awk '{print $0}' \
> 25_Ab_GenesIDs_TranscriptsIDs_Ours;
```

```
grep -f \
     20_Significant_Ab_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
     24_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org | \
    awk '{print $1}' \
> 25_Ab_GenesIDs_Ours;
```

```
grep -f \
     20_Significant_Ab_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
     24_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org | \
    awk '{print $2}' \
> 25_Ab_TranscriptsIDs_Ours;
```

```
grep -f \
     22_Significant_HT_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
     24_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org | \
    awk '{print $0}' \
> 26_HT_GenesIDs_TranscriptsIDs_Ours;
```

```
grep -f \
     22_Significant_HT_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
     24_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org | \
    awk '{print $1}' \
> 26_HT_GenesIDs_Ours;
```

```
grep -f \
     22_Significant_HT_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org \
     24_Significant_All_mRNA_Genes_Fowlers_x_canonical_r28_canonical_r28.org | \
    awk '{print $2}' > 26_HT_TranscriptsIDs_Ours;
```

5 sRNA

5.1 Abdomen

5.1.1 Testing Command

```
for i in 00_E*_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;do echo $i;done;
```

5.1.2 Affected Files:

```
00_E01_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
00_E02_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
00_E03_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
00_E04_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv
```

```
for i in 00_E*_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;do
 tail -n+2 $i | \
     awk -F, '{print $2}' | \
     sed 's/"//g';
      done | \
      sort | \
      uniq | \
      wc -l;
```

```
for i in 00_E*_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;do
 tail -n+2 $i | \
     awk -F, '{print $2}' | \
     sed 's/"//g';
      done | \
      sort | \
      uniq \
  > 01_TotalNumberUniqueHits_E1234_sRNA_F_VxM_Ab_Transcripts.csv;
```

```
tail -n+2 00_E01_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E01_sRNA_F_VxM_Ab_Transcripts.csv
```

```
tail -n+2 00_E02_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
      awk -F, '{print $2}' | \
      sed 's/"//g' | \
      sort -u \
   > 01_TotalNumberUniqueHits_E02_sRNA_F_VxM_Ab_Transcripts.csv
```

```
tail -n+2 00_E03_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E03_sRNA_F_VxM_Ab_Transcripts.csv
```

```
tail -n+2 00_E04_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E04_sRNA_F_VxM_Ab_Transcripts.csv
```

```
grep -f 01_TotalNumberUniqueHits_E1234_sRNA_F_VxM_Ab_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u | \
    wc -l;
```

```
grep -f 01_TotalNumberUniqueHits_E1234_sRNA_F_VxM_Ab_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u \
 > 02_TotalHits_E1234_sRNA_F_VxM_Ab_Genes.csv;
```

```
for i in 00_E*_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk '{print $2}' | \
    wc -l;
```

```
for i in 00_E*_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk '{print $2}' \
> 03_TotalNumberUniqueHits_E1234_sRNA_F_VxM_Ab_Transcripts_PresentAll4Experiments.csv
```

```
grep -f 03_TotalNumberUniqueHits_E1234_sRNA_F_VxM_Ab_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $2}’ | \
    sort -u | \
    wc -l;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_sRNA_F_VxM_Ab_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $2}’ | \
    sort -u \
 > 04_All_Experiments_sRNA_F_VxM_Ab_Genes.csv;
```

```
tail -n+2 00_E01_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E02_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E03_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E04_sRNA_F_VxM_Ab_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

5.2 Head-Thorax

5.2.1 Testing Command

```
for i in 00_E*_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;do echo $i;done
```

5.2.2 Affected Files:

```
00_E01_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
00_E02_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
00_E03_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
00_E04_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv
```

```
for i in 00_E*_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq | \
    wc -l;
```

```
for i in 00_E*_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq \
> 01_TotalNumberUniqueHits_E1234_sRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E01_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E01_sRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E02_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E02_sRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E03_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E03_sRNA_F_VxM_HT_Transcripts.csv;
```

```
tail -n+2 00_E04_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, '{print $2}' | \
    sed 's/"//g' | \
    sort -u \
 > 01_TotalNumberUniqueHits_E04_sRNA_F_VxM_HT_Transcripts.csv;
```

```
grep -f 01_TotalNumberUniqueHits_E1234_sRNA_F_VxM_HT_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u | \
    wc -l;
```

```
grep -f 01_TotalNumberUniqueHits_E1234_sRNA_F_VxM_HT_Transcripts.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $2}' | \
    sort -u \
 > 02_TotalHits_E1234_sRNA_F_VxM_HT_Genes.csv;
```

```
for i in 00_E*_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk '{print $2}' | \
    wc -l;
```

```
for i in 00_E*_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv;
do
    tail -n+2 $i | \
awk -F, '{print $2}' | \
sed 's/"//g';
done | \
    sort | \
    uniq -c | \
    sort -nr | \
    grep -Pw "4" | \
    awk '{print $2}' \
> 03_TotalNumberUniqueHits_E1234_sRNA_F_VxM_HT_Transcripts_PresentAll4Experiments.csv;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_sRNA_F_VxM_HT_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $2}’ | \
    sort -u | \
    wc -l;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_sRNA_F_VxM_HT_Transcripts_PresentAll4Experiments.csv \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $2}’ | \
    sort -u \
 > 04_All_Experiments_sRNA_F_VxM_HT_Genes.csv;
```

```
tail -n+2 00_E01_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E02_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E03_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

```
tail -n+2 00_E04_sRNA_F_VxM_HT_Table04_Sleuth_wald_test_sig_0.05.csv | \
    awk -F, ’{print $2}’ | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    wc -l;
```

6 Calculating Overlaps

6.1 Abdomen

```
cat 00_Fowler_SigHits_mRNA_Ab_Genes.org 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv  | \
    sort | \
    uniq | \
    wc -l;
```

```
cat 00_Fowler_SigHits_mRNA_Ab_Genes.org 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv  | \
    sort | \
    uniq \
> 05_Combined_Unique_Significant_Ab_mRNA_Genes.org;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv) | \
    wc -l;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv) \
     > 06_Significant_Ab_mRNA_Genes_Overlap.org;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv) | \
    wc -l;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv) \
     > 06_Significant_Ab_mRNA_Genes_Fowlers.org;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv) | \
    wc -l;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_Ab_Genes.csv) \
     > 06_Significant_Ab_mRNA_Genes_This_Study.org;
```

```
cat 00_Fowler_SigHits_mRNA_Ab_Genes.org 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv | \
    sort | \
    uniq | \
    wc -l;
```

```
cat 00_Fowler_SigHits_mRNA_Ab_Genes.org 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv | \
    sort | \
    uniq \
> 07_Combined_Unique_Significant_Ab_mRNA_Genes_Stringent.org;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) | \
    wc -l;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     > 08_Significant_Ab_mRNA_Genes_Overlap_Stringent.org;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) | \
    wc -l;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     > 08_Significant_Ab_mRNA_Genes_Fowlers_Stringent.org;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) | \
    wc -l;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_Ab_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv) \
     > 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org;
```

```
grep -f 06_Significant_Ab_mRNA_Genes_This_Study.org \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $3}' | \
    sort -u | \
    wc -l;
```

```
grep -f 06_Significant_Ab_mRNA_Genes_This_Study.org \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $3}' | \
    sort -u \
 > 09_Significant_Ab_mRNA_Transcripts_This_Study.org;
```

```
grep -f 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $3}' | \
    sort -u | \
    wc -l;
```

```
grep -f 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $3}' | \
    sort -u \
 > 10_Significant_Ab_mRNA_Transcripts_This_Study_Stringent.org;
```

```
grep -f 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org \
     zzMasterTableChrGeneTransName_02 | \
    awk '{print $0}' | \
    sort -k4r;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_Ab_Transcripts_PresentAll4Experiments.csv \
     <(grep -f 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org \
    zzMasterTableChrGeneTransName_02 | \
   awk '{print $0}' | \
   sort -k4r);
```

6.2 Head-Thorax

```
cat 00_Fowler_SigHits_mRNA_HT_Genes.org \
    02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv  | \
    sort | \
    uniq | \
    wc -l;
```

```
cat 00_Fowler_SigHits_mRNA_HT_Genes.org \
    02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv  | \
    sort | \
    uniq \
> 05_Combined_Unique_Significant_HT_mRNA_Genes.org
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv) | \
    wc -l;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv) \
     > 06_Significant_HT_mRNA_Genes_Overlap.org;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv) | \
    wc -l;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv) \
     > 06_Significant_HT_mRNA_Genes_Fowlers.org;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv) | \
    wc -l;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 02_TotalHits_E1234_mRNA_F_VxM_HT_Genes.csv) \
     > 06_Significant_HT_mRNA_Genes_This_Study.org;
```

```
cat 00_Fowler_SigHits_mRNA_HT_Genes.org \
    04_All_Experiments_mRNA_F_VxM_HT_Genes.csv | \
    sort | \
    uniq | \
    wc -l;
```

```
cat 00_Fowler_SigHits_mRNA_HT_Genes.org \
    04_All_Experiments_mRNA_F_VxM_HT_Genes.csv | \
    sort | \
    uniq \
> 07_Combined_Unique_Significant_HT_mRNA_Genes_Stringent.org;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) | \
    wc -l;
```

```
comm -12 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     > 08_Significant_HT_mRNA_Genes_Overlap_Stringent.org;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) | \
    wc -l;
```

```
comm -23 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     > 08_Significant_HT_mRNA_Genes_Fowlers_Stringent.org;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) | \
    wc -l;
```

```
comm -13 \
     <(sort 00_Fowler_SigHits_mRNA_HT_Genes.org) \
     <(sort 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv) \
     > 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org;
```

```
grep -f 06_Significant_HT_mRNA_Genes_This_Study.org \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $3}’ | \
    sort -u | \
    wc -l;
```

```
grep -f 06_Significant_HT_mRNA_Genes_This_Study.org \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $3}’ | \
    sort -u \
 > 09_Significant_HT_mRNA_Transcripts_This_Study.org;
```

```
grep -f 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $3}’ | \
    sort -u | \
    wc -l;
```

```
grep -f 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $3}’ | \
    sort -u \
 > 10_Significant_HT_mRNA_Transcripts_This_Study_Stringent.org;
```

```
grep -f 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org \
     zzMasterTableChrGeneTransName_02 | \
    awk ’{print $0}’ | \
    sort -k4r;
```

```
grep -f 03_TotalNumberUniqueHits_E1234_mRNA_F_VxM_HT_Transcripts_PresentAll4Experiments.csv \
     <(grep -f 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org \
    zzMasterTableChrGeneTransName_02 | \
   awk ’{print $0}’ | \
   sort -k4r);
```

6.3 sRNA Classes

```
# zTotalHits_sRNA_Abdomen_Genes_Filtered.org
awk -F: '{print $3}' zTotalHits_sRNA_Abdomen_Genes_Filtered.org | \
    sort | \
    uniq -c | \
    sort -nr | \
    awk '{print $2 "\t" $1}';

awk -F: '{print $2}' zTotalHits_sRNA_Abdomen_Genes_Filtered.org | \
    awk '{print $1}' | \
    sort -u \
 > zTotalHits_sRNA_Abdomen_Genes_Filtered_GeneIDs.org;
```

```
# zTotalHits_sRNA_Head_Thorax_Genes_Filtered.org
awk -F: '{print $3}' zTotalHits_sRNA_Head_Thorax_Genes_Filtered.org | \
    sort | \
    uniq -c | \
    sort -nr | \
    awk '{print $2 "\t" $1}';

awk -F: '{print $2}' zTotalHits_sRNA_Head_Thorax_Genes_Filtered.org | \
    awk '{print $1}' | \
    sort -u \
 > zTotalHits_sRNA_Head_Thorax_Genes_Filtered_GeneIDs.org;
```

6.4 Extracting Chromosomal Coordinates

```
cat 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org | \
    grep -f - zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\tgene\t" | \
    awk '{print $1 ":" $4 "-" $5}' | \
    sort | \
    uniq \
> 09_Significant_Ab_mRNA_Genes_This_Study_Stringent_Chr_Coordinates.org;
```

```
cat 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org | \
    grep -f - zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\tgene\t" | \
    awk '{print $1 ":" $4 "-" $5}' | \
    sort | \
    uniq \
> 09_Significant_HT_mRNA_Genes_This_Study_Stringent_Chr_Coordinates.org;
```

```
cat \
    09_Significant_Ab_mRNA_Genes_This_Study_Stringent_Chr_Coordinates.org \
    09_Significant_HT_mRNA_Genes_This_Study_Stringent_Chr_Coordinates.org \
    > 10_Significant_Ab_HT_mRNA_Genes_This_Study_Stringent_Chr_Coordinates_IGV_pics;

cat 12_Control_Genes_List.org \
    grep -f - zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\tgene\t" | \
    awk '{print $1 ":" $4 "-" $5}' | \
    sort | \
    uniq \
> 13_Control_Genes_List_Chr_Coordinates_pics;
```

6.5 Extracting Isoforms from Gene Lists and Calculating Gene To Isoforms Ratios

```
cat 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org | \
    grep -f - zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F'"' '{print $4}' | \
    sort -u;

cat 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org | \
    grep -f - zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F'"' '{print $4}' | \
    sort -u | \
    wc -l;

cat 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org | \
    grep -f - zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F'"' '{print $4}' | \
    sort -u;

cat 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org | \
    grep -f - zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F'"' '{print $4}' | \
    sort -u | \
    wc -l;

while read r;
do
    echo -e "====\n$r\n" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F'"' '{print $4}' | \
    sort -u;
done < <(sort -n 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org)

while read r;
do
    echo -e "====\n$r\n" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F'"' '{print $4}' | \
    sort -u;
done < <(sort -n 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org) \
     > 17_Ab_GenesIDs_TranscriptsIDs

while read r;
do
    echo -e "====\n$r\n" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F'"' '{print $4}' | \
    sort -u;
done < <(sort -n 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org)

while read r;
```

```
do
    echo -e "====\n$r\n" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F’"’ ’{print $4}’ | \
    sort -u;
done < <(sort -n 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org) \
     > 17_HT_GenesIDs_TranscriptsIDs

while read r;
do
    echo -ne "$r\t" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F’"’ ’{print $4}’ | \
    sort -u | \
    wc -l;
done < <(sort -n 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org) | \
    awk '{print $2 "\t" $1}’ | \
    sort -nr;

while read r;
do
    echo -ne "$r\t" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F’"’ ’{print $4}’ | \
    sort -u | \
    wc -l;
done < <(sort -n 08_Significant_Ab_mRNA_Genes_This_Study_Stringent.org) | \
    awk '{print $2 "\t" $1}’ | \
    sort -nr > 18_Ab_GenesIDs_TranscriptsIDs;

while read r;
do
    echo -ne "$r\t" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F’"’ ’{print $4}’ | \
    sort -u | \
    wc -l;
done < <(sort -n 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org) | \
    awk '{print $2 "\t" $1}’ | \
    sort -nr;

while read r;
do
    echo -ne "$r\t" && grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F’"’ ’{print $4}’ | \
    sort -u | \
    wc -l;
done < <(sort -n 08_Significant_HT_mRNA_Genes_This_Study_Stringent.org) | \
    awk '{print $2 "\t" $1}’ | \
    sort -nr > 18_HT_GenesIDs_TranscriptsIDs;

while read r;
do
```

```
    open *$r*;
done < <(cat ../18_All_GenesIDs_TranscriptsIDs | \
     sort -nr | \
     grep -w "1" | \
     sort -k2 | \
     awk ’{print $2}’ | \
     sort)

  while read r;
  do echo -ne "$r\t" && \
  grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
      grep -P "\ttranscript\t" | \
      awk -F’"’ ’{print $4}’ | \
      sort -u | \
      wc -l;
  done < \
       <(sort -n 25_Ab_GenesIDs_Ours) | \
      awk ’{print $2 "\t" $1}’ | \
      sort -nr;

   while read r;
   do echo -ne "$r\t" && \
   grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
       grep -P "\ttranscript\t" | \
       awk -F’"’ ’{print $4}’ | \
       sort -u | \
       wc -l;
   done < \
<(sort -n 25_Ab_GenesIDs_Ours) | \
       awk ’{print $2 "\t" $1}’ | \
       sort -nr \
    > 25_Ab_GenesIDs_TranscriptsIDs_Ours_Ratios;

   while read r;
   do echo -ne "$r\t" && \
   grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
       grep -P "\ttranscript\t" | \
       awk -F’"’ ’{print $4}’ | \
       sort -u | \
       wc -l;
   done < \
<(sort -n 26_HT_GenesIDs_Ours) | \
       awk ’{print $2 "\t" $1}’ | \
       sort -nr;

while read r;
do echo -ne "$r\t" && \
grep $r zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    awk -F’"’ ’{print $4}’ | \
    sort -u | \
    wc -l;
done < \
```

```
    <(sort -n 26_HT_GenesIDs_Ours) | \
   awk '{print $2 "\t" $1}' | \
   sort -nr \
> 26_HT_GenesIDs_TranscriptsIDs_Ours_Ratios;
```

6.6 Calculating Gene/Transcripts Ratios

```
tail -n+4 Drosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\tgene\t" | \
    grep -P "\; gene_biotype \"protein_coding\"\;" | \
    wc -l;
# 13947
```

```
tail -n+4 Drosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\tgene\t" | \
    grep -Pv "\; gene_biotype \"protein_coding\"\;" | \
    wc -l;
# 3860
```

```
tail -n+4 Drosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    grep -P "\; gene_biotype \"protein_coding\"\;" | \
    wc -l;
# 30588
```

```
tail -n+4 Drosophila_melanogaster.BDGP6.28.47.gtf | \
    grep -P "\ttranscript\t" | \
    grep -Pv "\; gene_biotype \"protein_coding\"\;" | \
    wc -l;
# 4332
```

6.7 Generating BED Files form GTF

```
tail -n+4 zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    cut -d";" -f8 | \
    cut --delimiter=" " -f3 | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    sed ’/^$/d’;
```

```
tail -n+4 zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    cut -d";" -f8 | cut --delimiter=" " -f3 | \
    sed ’s/"//g’ | \
    sort | \
    uniq | \
    sed ’/^$/d’ \
> zzDrosophila_melanogaster.BDGP6.28.47.gtf.features;
```

```
tail -n+4 zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    sed -e ’s/"//g’ -e ’/^$/d’ -e ’s/;//g’ | \
    grep -Pi "transcript" | \
    grep -Pi "protein_coding" |  \
    grep -P "\texon\t" | \
    awk ’{print $1 "\t" $4 "\t" $5 "\t" $12}’ \
> zzDrosophila_melanogaster.protein_coding_exons.bed
```

```
tail -n+4 zzDrosophila_melanogaster.BDGP6.28.47.gtf | \
    sed -e ’s/"//g’ -e ’/^$/d’ -e ’s/;//g’ | \
    grep -Pi "transcript" | \
    grep -Piv "protein_coding" | \
    grep -Pv "pseudogene" | \
    grep -P "\texon\t" | \
    awk ’{print $1 "\t" $4 "\t" $5 "\t" $12}’ \
> zzDrosophila_melanogaster.non_protein_coding_exons.bed
```

6.8 Canonical Work

```
#Calculating Number Combined Unique
cat 04_All_Experiments_mRNA_F_VxM_Ab_Genes.csv 02_TotalHits_E04_mRNA_F_VxM_Ab_Genes_canonical_r28.csv
cat 04_All_Experiments_mRNA_F_VxM_HT_Genes.csv 02_TotalHits_E04_mRNA_F_VxM_HT_Genes_canonical_r28.csv

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 03_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 03_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_Ab_Transcripts_canonical_r28.csv) <(sort 03_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 01_Tot

comm -23 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 03_Tot
comm -13 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 03_Tot
comm -12 <(sort 01_TotalNumberUniqueHits_E04_mRNA_F_VxM_HT_Transcripts_canonical_r28.csv) <(sort 03_Tot
```

```
while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
 1 5
 1 4
 2 3
19 2
48 1

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
2 2
6 1

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
2 2
18 1

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
      1 12
      2 11
      3 10
      4 9
      6 8
      4 7
      8 6
     23 5
     49 4
     97 3
    335 2
   1183 1

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
      1 22
      1 19
      1 18
      1 13
      1 11
      4 9
      1 8
      3 7
      6 6
      6 5
     17 4
     30 3
     77 2
    210 1

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
      1 5
      1 4
     11 3
     42 2
    389 1

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
      1 5
```

```
      1 4
      2 3
     21 2
     66 1
     # 92%

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
      4 2
     24 1
   # 85%

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
      1 12
      2 11
      3 10
      4 9
      6 8
      4 7
      8 6
     24 5
     50 4
    108 3
    377 2
   1572 1
   # 72%

while read r;do grep -Pw $r *gtf | grep -Pw "transcript_id" | awk -F’"’ ’{print $4}’ | sort -u | wc -l
      1 22
      1 19
      1 18
      1 13
      1 11
      4 9
      1 8
      3 7
      6 6
      7 5
     18 4
     41 3
    119 2
    599 1
    # 74.5%
```

7 Other_Commands

7.1 CD-HIT-EST_Commands

```
cd-hit-est \
    -c 1.0 \
    -n 8 \
    -r 1 \
    -p 1 \
    -g 1 \
    -T 40 \
    -d 40 \
    -M 0 \
    -s 1.0 \
    -aL 1.0 \
    -i Drosophila_melanogaster.BDGP6.28.ncrna.fa \
    -o Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.fa;
```

```
cd-hit-est \
    -c 1.0 \
    -n 8 \
    -r 1 \
    -p 1 \
    -g 1 \
    -T 40 \
    -d 40 \
    -M 0 \
    -s 1.0 \
    -aL 1.0 \
    -i Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    -o Drosophila_melanogaster.BDGP6.28.cdna.all.cd-hit-est.fa;
```

```
cd-hit-est \
    -c 1.0 \
    -n 8 \
    -r 1 \
    -p 1 \
    -g 1 \
    -T 40 \
    -d 40 \
    -M 0 \
    -s 1.0 \
    -aL 1.0 \
    -i Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa \
    -o Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.cd-hit-est.fa;
```

```
cd-hit-est \
    -c 1.0 \
    -n 8 \
```

```
-r 1 \
-p 1 \
-g 1 \
-T 40 \
-d 40 \
-M 0 \
-s 1.0 \
-aL 1.0 \
-i Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fa \
-o Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.cd-hit-est.fa;
```

7.2 rRNA_Biotype_Filtration_Commands

```
grep -i "rRNA" \
     Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.fa | \
    sed 's/^>//' \
> Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.fa.biotype-rRNA_GeneIDs;
```

7.3 Fasta_Files_Construction_Commands

```
faSomeRecords \
    -exclude \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.fa \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.fa.biotype-rRNA_GeneIDs \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.filtered-biotype-rRNA.fa;
```

```
faSomeRecords \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.fa \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.fa.biotype-rRNA_GeneIDs \
    Drosophila_melanogaster.BDGP6.28.ncrna.cd-hit-est.biotype-rRNA.fa;
```

```
> head Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids
FBgn0000008 FBtr0071764
FBgn0000014 FBtr0083388
FBgn0000015 FBtr0415463
FBgn0000017 FBtr0330133
FBgn0000018 FBtr0080168
FBgn0000022 FBtr0070072
FBgn0000024 FBtr0082780
FBgn0000028 FBtr0074015
FBgn0000032 FBtr0085610
FBgn0000036 FBtr0330310
```

```
awk '{print $2}' \
    Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids | \
    grep -f - Drosophila_melanogaster.BDGP6.28.cdna.all.fa | \
    wc -l;

awk '{print $2}' \
    Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids | \
    grep -f - Drosophila_melanogaster.BDGP6.32.cdna.all.fa | \
    wc -l;
```

```
diff --suppress-common-lines -y \
     <(awk '{print $2}' \
   Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids | \
   grep -f - Drosophila_melanogaster.BDGP6.28.cdna.all.fa | \
   sort) \
     <(awk '{print $2}' \
   Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids | \
   grep -f - Drosophila_melanogaster.BDGP6.32.cdna.all.fa | \
   sort);
```

```
awk '{print $2}' \
    Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids | \
```

```
    grep -f - Drosophila_melanogaster.BDGP6.28.cdna.all.fa | \
    sed ’s/>//’ \
> Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fasta.ids;
```

```
awk ’{print $2}’ \
    Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.ids | \
    grep -f - Drosophila_melanogaster.BDGP6.32.cdna.all.fa | \
    sed ’s/>//’ \
> Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fasta.ids;
```

```
faSomeRecords \
    Drosophila_melanogaster.BDGP6.28.cdna.all.fa \
    Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fasta.ids \
    Drosophila_melanogaster.BDGP6.28.cdna.canonical_only.fa
```

```
faSomeRecords \
    Drosophila_melanogaster.BDGP6.32.cdna.all.fa \
    Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fasta.ids \
    Drosophila_melanogaster.BDGP6.32.cdna.canonical_only.fa
```
