

miRBase Best Hit/Cluster ID	Sort by Read Counts	Sort by Length	Sort by Sequence
pre-gga-miR-10a		74	-cuauaugUACCCUGUAGAUCCGAAUUUGuaaagga
gga-miR-10a		22	-----UACCCUGUAGAUCCGAAUUUGU-----
173510	26443	22	-TACCCTGTAGATCCGAATTTGTG-----
173519	10431	23	-----TACCCTGTAGATCCGAATTTGTg-----
173520	523	24	-----TACCCTGTAGATCCGAATTTGTga-----
173529	360	24	-----TACCCTGTAGATCCGAATTTGTgt-----
173511	135	23	-----TACCCTGTAGATCCGAATTTGTa-----
173532	84	23	-----TACCCTGTAGATCCGAATTTGTt-----
173512	56	24	-----TACCCTGTAGATCCGAATTTGTaa-----
173521	18	25	-----TACCCTGTAGATCCGAATTTGTgaa-----
173516	5	23	-----TACCCTGTAGATCCGAATTTGTc-----
173527	5	27	-----TACCCTGTAGATCCGAATTTGTggaac-----

**(f)**

JOB_ID	1268806910
No. of total reads	3257227
No. of sequence tags	329334
No. of tags after 3'adaptor clean up	269002
No. of tags after 5'adaptor Clean up	261902
No. of tags after poly N cleanup	261592
No. of tags after poly-ATCG Clean up	261289
No. of cleaned sequence tags	261289
No. of reads in cleaned sequence tags	3076497
Percentage of reliable reads #	94.45
#Percentage of reliable reads=(No. of reads in cleaned sequence tags/No. of total reads)*100	
No. of Unique Sequence Clusters (USC)	225501
No. of matched ncRNA in Rfam	188
No. of USC matched to Rfam	18406
No. of total reads matched to Rfam	95979
Percentage of reads matched to Rfam	3.12
No. of matched miRNA in miRBase	415
No. of USC matched to miRBase	2555
No. of total reads matched to miRBase	1687442
Percentage of reads matched to miRNA	54.85
USC Unmatched	204540

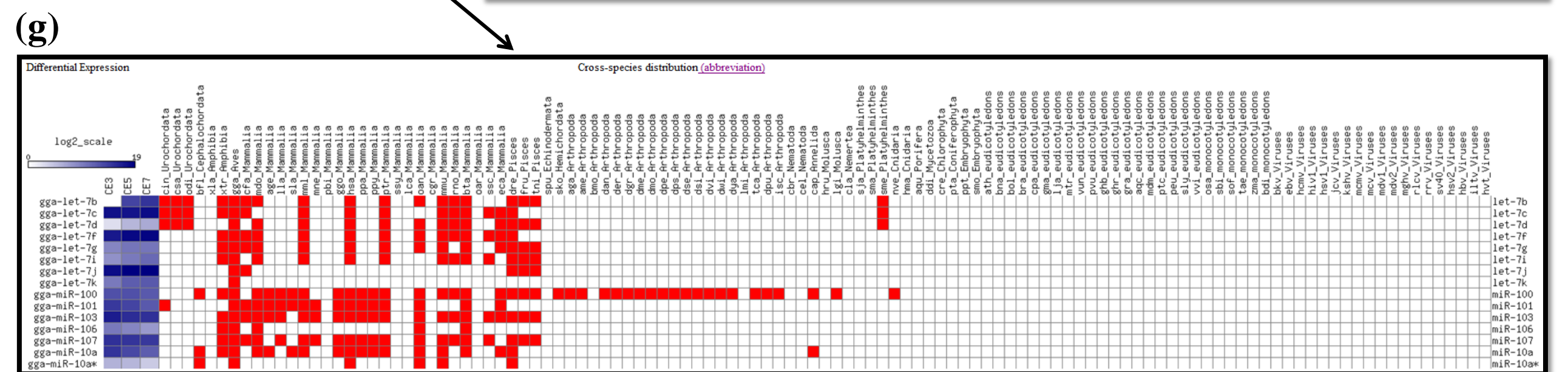


Figure S1 - Output pages of DSAP.

All the results of DSAP are summarized in figures and clickable charts for better visualization. Figure S1a shows the current status of the process and exact run time of each step in a dynamic meter graph. Figure S1b shows a bar chart dynamically recording the number of sequence tags during the cleanup process. Figure S1c shows the clustering state of the cleaned sequence tags and provides each unique sequence cluster and its member information in a tab-delimited file. Figure S1d and S1e summarize the results of the unique sequence clusters matched to Rfam and miRBase respectively. Figure S1f shows a summary of the job. Figure S1g shows cross-experiment and cross-species miRNA distribution comparison results through a color scaling matrix.

miRNA	CE5	CE7	CE9
gga-let-7b	1	12352	29903
gga-let-7c	163164	156621	198263
gga-let-7d	6	44	81
gga-let-7f	128541	255562	346444
gga-let-7g	532	1156	1075
gga-let-7i	250	936	1877
gga-let-7j	232980	37351	446116
gga-let-7k	837	3414	4844
gga-miR-100	7358	6871	4168
gga-miR-101	23497	12104	4654
gga-miR-103	89271	41329	34030

Figure S2 - Input format for comparative miRNA analysis.

The first column is a miRNA descriptor using the standard format as in miRBase. The remaining columns are numeric data such as read counts or fold difference with headings to indicate each individual experiment.