Supplementary table 1. Comparison of CPSS 2.0 and current sRNA analysis web-servers.

Terms	CPSS 2.0	sRNAtoolbox	Oasis	Chimira	MAGI
Input format	FASTA or FASTA files compressed in *.tar.gz format	FASTQ, FASTA or read counts file compressed in *.gz format	FASTQ file compressed in *.gz format	FASTA or FASTQ files compressed in *.gz format	FASTQ (This server is currently closed. This assessment is based on the available demo data.)
Finish the whole analysis process by single submission	Yes	No (specific submission required for miRNA target prediction, miRNA expression difference, et al.)	No (specific submission required for sRNA detection, differently expression and classification)	Yes	Yes
Species	48 species in total, including 31 animals (*Homo sapiens* , *Mus musculus* , et al.).	60 species in total, including 20 animals (*Homo sapiens* , *Mus musculus* , et al.).	14 animal species (*Homo sapiens* , *Mus musculus* , et al.).	180 species including (*Homo sapiens, Mus musculus* , et al.).	*Homo sapiens*
miRNA reference	miRBase (V.21)	miRBase (V.21)	miRBase (V.21)	miRBase (Not mentioned)	miRBase (Not mentioned)
General results	Genome mapping result, Length distribution, Chromosome distribution, miRNA family matching results, statistics results of matched ncRNA and ncRNA matching distribution including miRNA, piRNA, rRNA, snRNA, snoRNA, circRNA and lncRNA.	Genome mapping result, Length distribution, miRNA matching distribution, isomiR fraction, sRNA matching statistics including piRNA, Repeat, mRNA and tRNA.	FastQC report, Genome mapping result, Length distribution, ncRNA matching result including miRNA, piRNA, snoRNA, snRNA and rRNA	QC plot, miRNA count table and miRNA modification	Base quality, read length, base distribution, GC ratio, statistics of genome mapping and sRNA (miRNA, lincRNA, rRNA, snRNA, snoRNA, tRNA) matching results.
Differentially expressed ncRNA	miRNA, piRNA, rRNA, snRNA, snoRNA, circRNA and lncRNA differentially expressed detection are conducted on paired and multiple samples.	miRNA differentially expressed detection is conducted on multiple samples.	miRNA, piRNA, rRNA, snRNA, snoRNA differently expressed detection are conducted on multiple samples	miRNA differentially expressed detection is conducted on paired multiple samples.	miRNA differentially expressed detection is conducted on multiple samples.
Novel miRNA prediction	Predicted with miReep, strcuture illustration using RNAfold and detailed information including Precusor (ID, Location, Length, MFE and sequence), Mature-5p/3P (sequence and expression count)	This module is not provided in all my tests.	This module is not provided in all my tests.	Not provided	Predicted with miRdeep2, detailed information including expression statistics and P value.
Functional analysis	GO (DAVID 6.7), Pathway (KEGG DAVID 6.7), Protein domain (DAVID 6.7) and Protein-protein interaction (STRING V.10).	GO (Annotation-Modules)	Submit selected miRNA targets to third-party web based tools to perform functional annotation and enrichment analysis.	Not provided	KEGG pathway
Visualization	Graphical interface are provided for: 1) status of the job (queue, running or finished); 2) general results; 3) statistic result for each type of sRNA (miRNA, Rfam, Repeat, mRNA, circRNA, lncRNA and piRNA); 4) clustered bar graph illustration of each differently expressed sRNA among paired or multiple samples; 5) novel miRNA prediction results; 6) functional analysis, including GO, Pathway, Protein domain annotation and enrichment analysis; 7) Protein-protein interaction.	Graphical interface are provided for: 1) status of the job (queue, running or finished); 2) general results; 3) heat-map and statistics of miRNA expression; 4) miRNA targets and GO term analysis.	Graphical interface are provided for: 1) general results; 2) multiple sample comparison and detailed information for each sample; 3) miRNA detailed table and specific enrichment analysis; 4) biomarker detection.	Graphical interface are provided for: 1) status of the job (queue, running or finished); 2) general results and miRNA modification.	Graphical interface are provieded for: 1) general results; 2) known and novel miRNA statistics; 3) Pathway analysis.
Demo case	Four single sample and three multiple samples demo data and results	One multiple samples demo data and results	Three multiple samples demo data and results	One multiple samples demo results	One multiple samples demo data and results