

**Supplement:** exceRpt: A Comprehensive Analytic Platform for Extracellular RNA Profiling

**Figure S1:** miRNA quantification comparison with miRDeep2  
miRDeep2 (Friedländer et al. 2012) is a commonly used software package for the identification of miRNAs in deep sequenced RNA data. Read count quantifications for miRNAs based on results from processing exRNA samples from representative biofluids are displayed. Plasma, saliva and urine (3 samples from each) from miRDeep2 and exceRpt are highly correlated, with Pearson correlations ranging from 0.93 to 0.99. This suggests that miRNA quantification results from exceRpt are highly consistent with existing tools.

**Figure S2:** miRNA abundance for exRNA samples  
exceRpt produces miRNA quantifications for exRNA samples, which can be used to see which miRNAs are enriched within which samples. Here, enriched miRNAs in samples from four different biofluids are shown.

**Figure S3:** Exogenous sequence characterization algorithm  
For exogenous sequence alignment, reads are assigned to most specific node possible.

**Figure S4:**

**(A):** Genboree interface for exceRpt

Signing up for an account on genboree.org is the quickest and easiest way to start processing exRNA samples using exceRpt. The Genboree Workbench offers a graphical, browser-based interface for processing exRNA samples and storing exceRpt results. Shown is the working interface for Genboree, including navigation functionalities and locations for inputs and outputs.

**(B):** Docker implementation for exceRpt

exceRpt is also available as a Docker image at [github.gersteinlab.org/exceRpt](https://github.com/gersteinlab.org/exceRpt). Shown are example commands for processing a sample with the exceRpt pipeline using Docker. Detailed instructions are on the GitHub webpage.

# Figure S1

## miRNA quantification comparison of exceRpt and miRDeep2

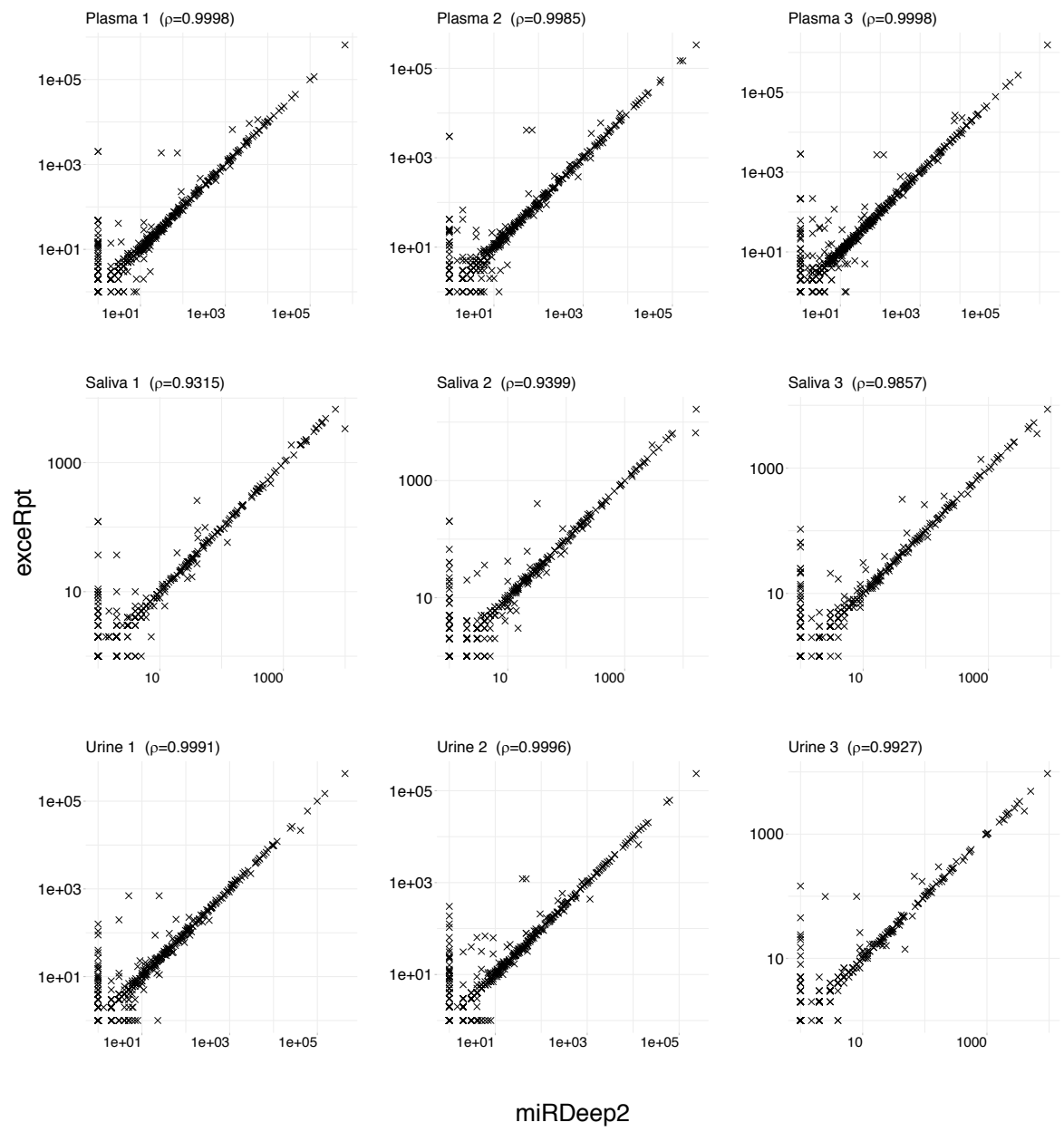
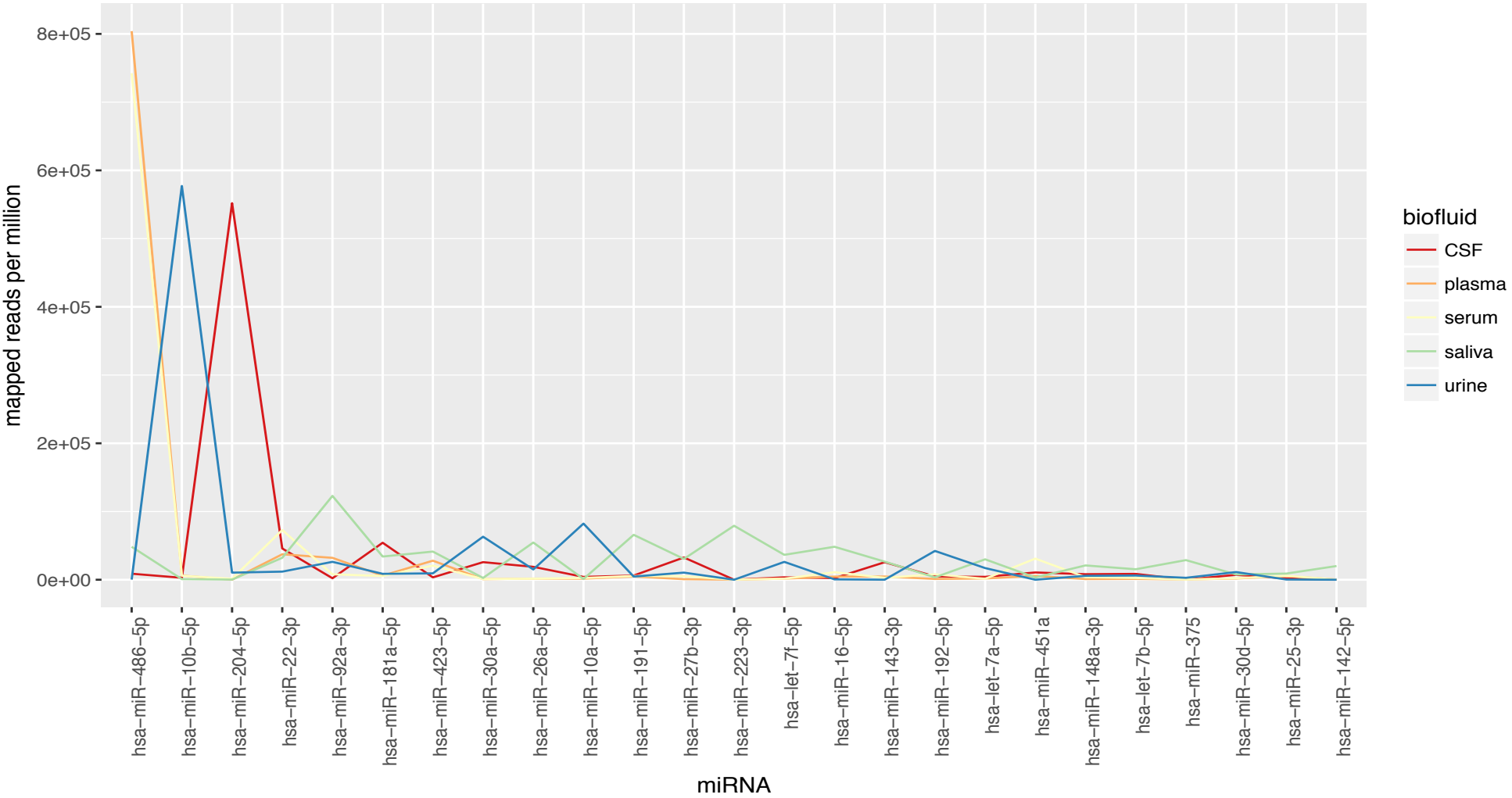


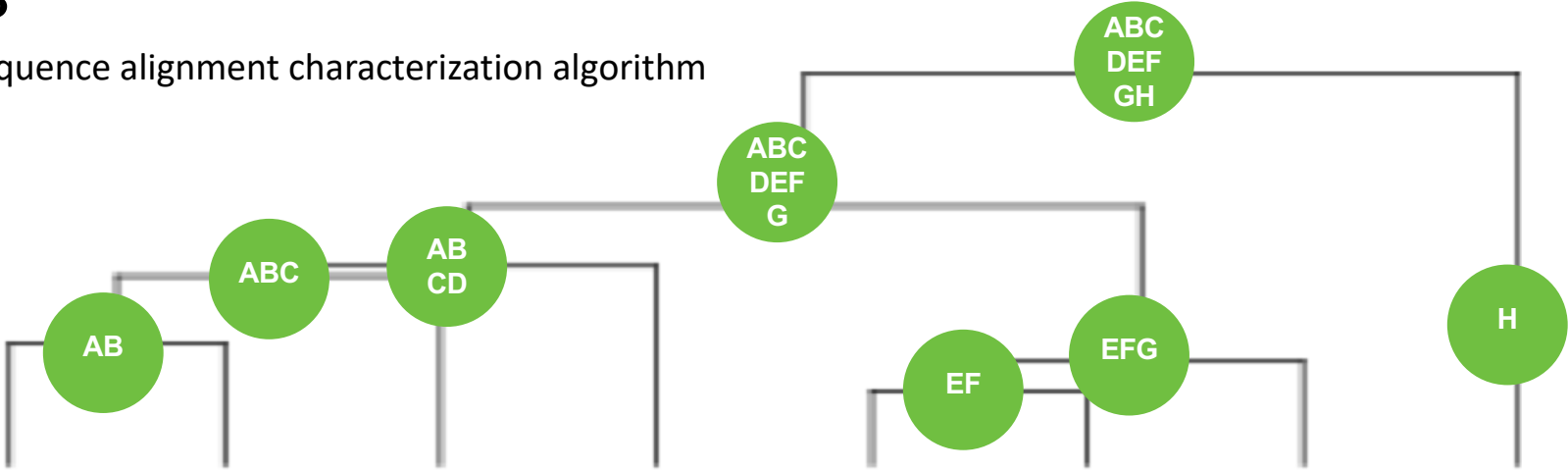
Figure S2

miRNA abundance for exRNA samples



# Figure S3

Exogenous sequence alignment characterization algorithm



reads

	A	B	C	D	E	F	G	H	
1	x	x	x	x					AB CD
2	x	x							AB
3					x	x	x		EFG
4	x	x	x	x	x	x	x		ABC DEF G
5	x	x	x		x	x		x	ABC DEF GH

# Figure S4

## (A) Genboree interface for exceRpt

**Data Selector**

Refresh Data Filter: Select a filter...

- exceRpt small RNA-seq Pipeline Post-processing - Example Data
  - Tracks
  - Lists & Selections
  - SampleSets
  - Samples
  - Files
    - postProcessedResults\_v4.6.3
      - sample\_C1\_non\_pregnant1\_SRR822433\_fastq\_Circulating%20microRNAs%20from%
      - sample\_C3\_non\_pregnant3\_SRR822434\_fastq\_Circulating%20microRNAs%20from%
      - sample\_C4\_non\_pregnant4\_SRR822435\_sra\_Circulating%20microRNAs%20from%2
      - sample\_C5\_non\_pregnant5\_SRR822436\_fastq\_Circulating%20microRNAs%20from%
    - FastQC - Example Data
    - Import Samples - Example Data
    - KNIFE - Example Data
    - Pathway Finder - Example Data
    - RSEQtools hg18 - Example Data
    - RSEQtools hg19 - Example Data
    - Target Interaction Finder - Example Data
  - exRNAAtlas
  - Extracellular RNA Atlas
  - Genboree Videos

**Details**

Attribute	Value
Group	parkji_group
Role	administrator
Name	Exrna-atlasOutput
Description	Database from Exrna-atlas
Species	Homo sapiens

**Input Data**

- sample\_C5\_non\_pregnant5\_SRR822436\_fastq\_Circulating%20microRNAs%20from%20serum%20plas

**Output Targets**

- Exrna-atlasOutput

## (B) Docker implementation for exceRpt

```
docker run -v ~/DirectoryContainingMyInputSample:/exceRptInput \  
-v ~/DirectoryInWhichToPutMyResults:/exceRptOutput \  
-v ~/DirectoryContainingMyexceRptDatabase/hg38:/exceRpt_DB/hg38 \  
-t rkitchen/excerpt \  
INPUT_FILE_PATH=/exceRptInput/SRR026761.sra
```