**Detailed description of our analysis pipeline**

To reproduce all results in this paper, run all scripts in the order in which they are listed in this file.

**Part A**

run: generating\_RNA\_RawCount.R

generates

- a\_results / rnaRawData.Rda

- a\_results / rnaMatrix\_meta.csv

- a\_results / rnaMatrix\_mRNA.csv

- a\_results / rnaMatrix\_RNA.csv

- a\_results / rnaMatrix\_rRNA.csv

- a\_results / rnaMatrix\_tRNA.csv

- a\_results / rnaMatrix.csv

- a\_figures / log2AmountDensity.pdf

run: generating\_Protein\_RawCount.R

generates

- a\_results / proteinMatrix\_w\_NA.csv

- a\_results / proteinMatrix\_wo\_NA.csv

- a\_results / proteinMatrix.csv

run: generating\_Meta\_data.R

generates

- a\_results / sampleSizeDf.csv

- a\_results / metaData.csv

- a\_results / metaProtein.csv

- a\_results / metaRNA.csv

- a\_results / metaRawData.Rda

run: data.normalization.R with parameters.R (RUNS 1 to 15) with given parameters

|  |  |  |  |
| --- | --- | --- | --- |
|  | All Data | Exp | Sta |
| mRNA | 1 DONE | 2 DONE | 3 DONE |
| Protein | 4 DONE | 5 DONE | 6 DONE |
| Int\_mRNA | 7 DONE | 8 DONE | 9 DONE |
| Int\_protein | 10 DONE | 11 DONE | 12 DONE |
| Int\_mrna\_protein | 13 DONE | 14 DONE | 15 DONE |

With parameters

* Data type: TABLE
* Bad data set: set00 (No bad sample is excluded)
* Reference parameter order: growthPhase, Mg\_mM\_Levels, Na\_mM\_Levels, carbonSource, experiment
* Referece levels: exponential(stationary), baseMg, baseNa, glucose, glucose\_time\_course
* experimentVector: allEx
* carbonSourceVector: SYAN
* MgLevelVector: allMg
* NaLevelVector: allNa
* growthPhaseVector: TABLE
* filterGenes: noMatchFilter
* threshold: NA
* roundData: TRUE
* sumTechnicalReplicates: TRUE
* deSeqSfChoice: P1Sf
* normalizationMethodChoice: vst

those runs generate

output of run No 1:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 2:

- a\_results / metaData\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 3:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 4:

- a\_results / metaData\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 5:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 6:

- a\_results / metaData\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 7:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 8:

- a\_results / metaData\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 9:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 10:

- a\_results / metaData\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 11:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 12:

- a\_results / metaData\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 13:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 14:

- a\_results / metaData\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_protein\_trT\_set00\_StcYtcNasAgrNgrMgh\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

output of run No 15:

- a\_results / metaData\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

- a\_results / resDf\_mrna\_trT\_set00\_StcAllEx\_SYAN\_baseMgAllMg\_baseNaAllNa\_ExpAllPhase\_noMatchFilter\_p1Sf\_noNorm.csv

**PART B**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | **All Data** | **Exp** | **Sta** |
| **mRNA** | **All** | 1 |  |  |
| **Growth** | 4 |  |  |
| **Carbon** | 7 |  |  |
| **Mg** | 10 |  |  |
| **Na** | 13 |  |  |
| **Protein** | **All** | 2 |  |  |
| **Growth** | 5 |  |  |
| **Carbon** | 8 |  |  |
| **Mg** | 11 |  |  |
| **Na** | 14 |  |  |
| **int\_mrna\_protein** | **All** | 3 |  |  |
| **Growth** | 6 |  |  |
| **Carbon** | 9 |  |  |
| **Mg** | 12 |  |  |
| **Na** | 15 |  |  |
| **int\_mRNA** | **All** | 16 |  |  |
| **Growth** | 17 |  |  |
| **Carbon** | 18 |  |  |
| **Mg** | 19 |  |  |
| **Na** | 20 |  |  |
| **int\_protein** | **All** | 21 |  |  |
| **Growth** | 22 |  |  |
| **Carbon** | 23 |  |  |
| **Mg** | 24 |  |  |
| **Na** | 25 |  |  |