

# From transcription to translation: RNA dynamics in a transdifferentiation model

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Computational Biology of RNA Processing - CRG

Post-doc Symposium - 06/07/2016



# Outline

## Introduction

- Our model

- Experimental outline

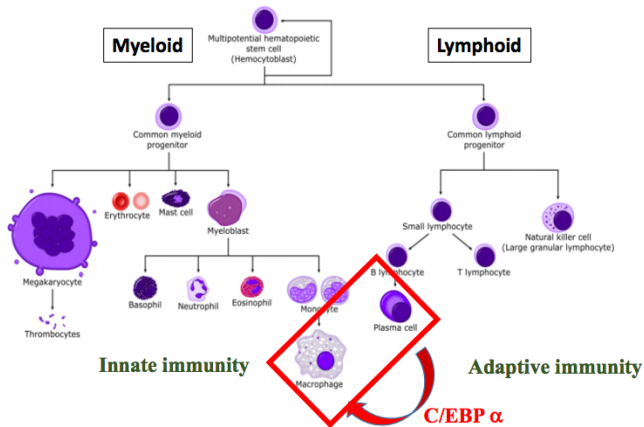
## Results

- Correlation between RNA-Seq fractions and among data types

- correlation between gene expression and H3K4me3 signal

# Transdifferentiation model

C/EBP  $\alpha$  induces transdifferentiation of B cells into macrophages



# Outline

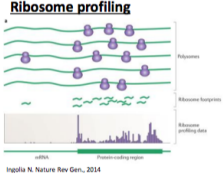
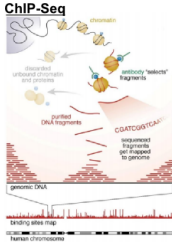
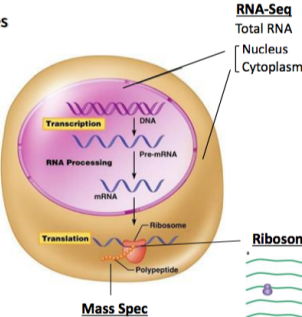
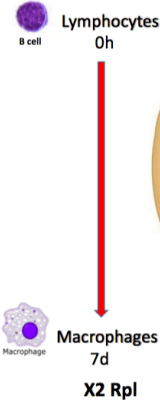
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Our model

Experimental outline

## Results

# Experimental outline



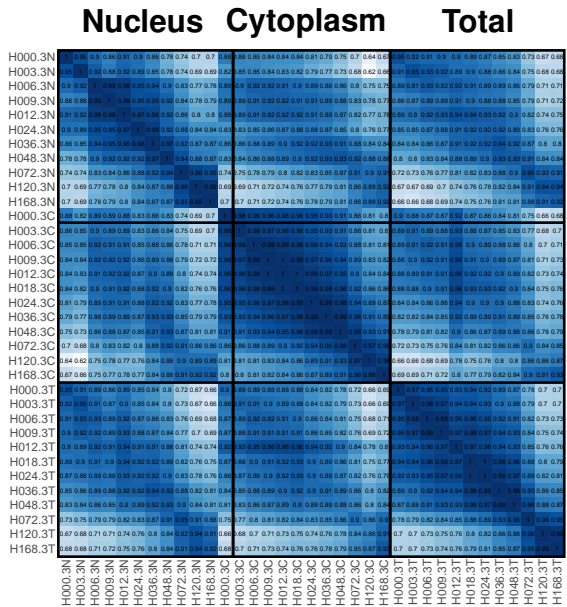
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# RNA-Seq fractions

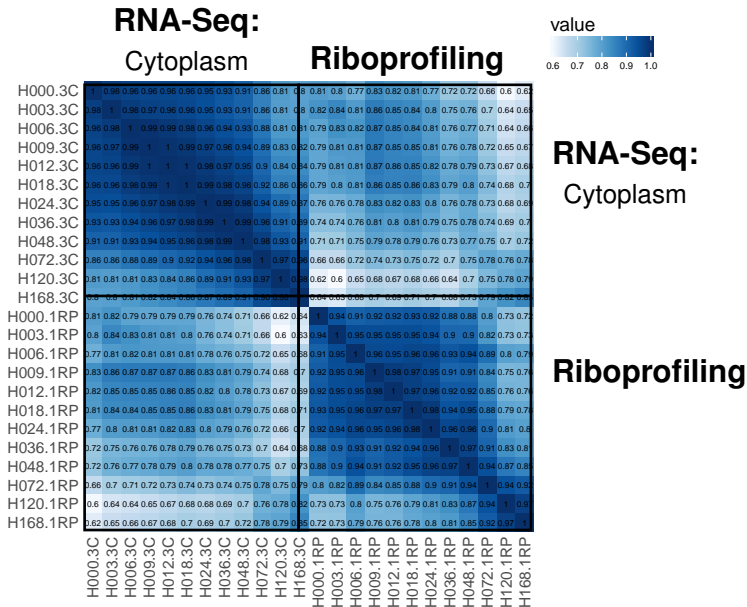


Nucleus

Cytoplasm

Total

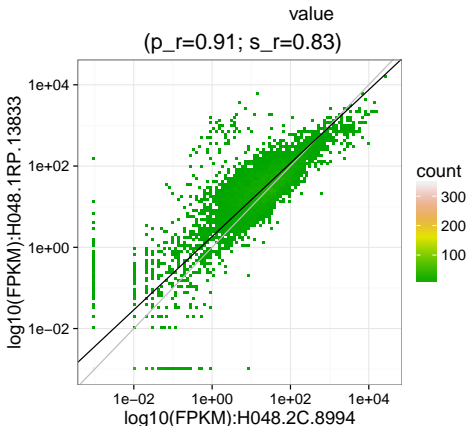
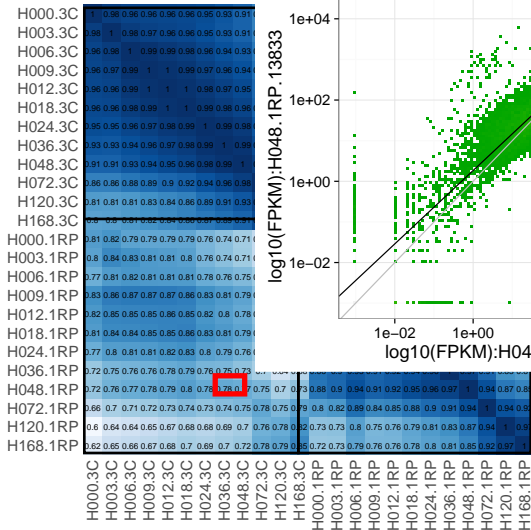
# RNA-Seq and Riboprofiling



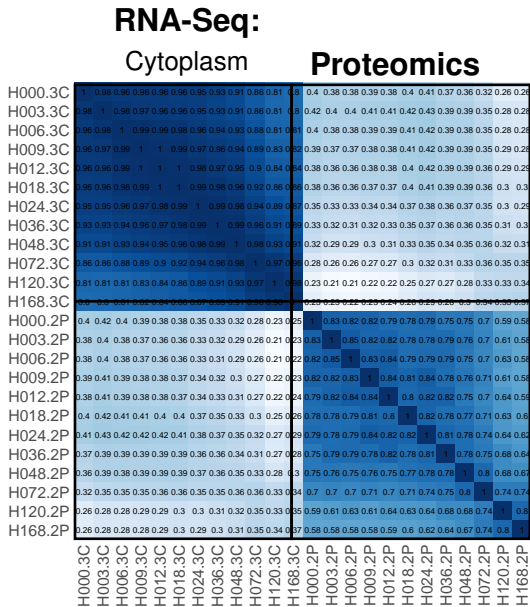


# RNA-Seq and Riboprofiling

## RNA-Seq: Cytoplasm



# RNA-Seq and proteomics



value



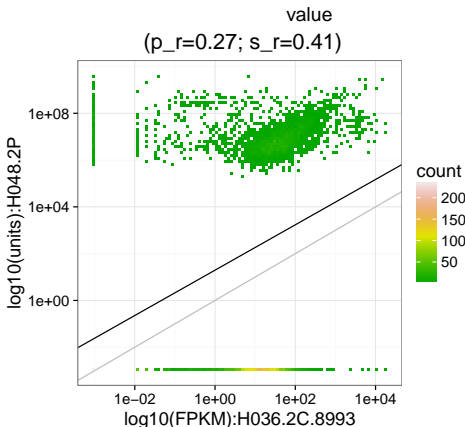
**RNA-Seq:**  
Cytoplasm

**Proteomics**

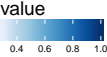
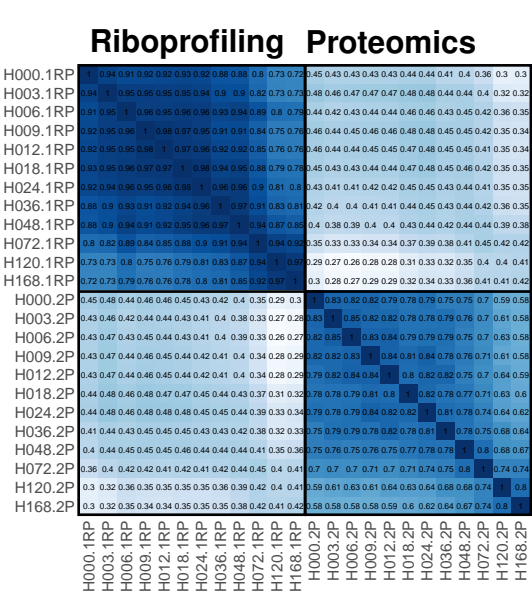
# RNA-Seq and proteomics

**RNA-Seq:**  
Cytoplasm

|         |      |      |      |      |      |      |      |      |      |      |
|---------|------|------|------|------|------|------|------|------|------|------|
| H000.3C | 1    | 0.98 | 0.96 | 0.96 | 0.96 | 0.96 | 0.95 | 0.93 | 0.91 | 0    |
| H003.3C | 0.98 | 1    | 0.98 | 0.97 | 0.96 | 0.96 | 0.95 | 0.93 | 0.91 | 0    |
| H006.3C | 0.96 | 0.96 | 1    | 0.99 | 0.99 | 0.98 | 0.96 | 0.94 | 0.93 | 0    |
| H009.3C | 0.96 | 0.97 | 0.99 | 1    | 1    | 0.99 | 0.97 | 0.96 | 0.94 | 0    |
| H012.3C | 0.96 | 0.96 | 0.96 | 1    | 1    | 1    | 0.98 | 0.97 | 0.95 | 0    |
| H018.3C | 0.96 | 0.96 | 0.98 | 0.99 | 1    | 1    | 0.99 | 0.98 | 0.96 | 0    |
| H024.3C | 0.95 | 0.95 | 0.96 | 0.97 | 0.98 | 0.99 | 1    | 0.99 | 0.98 | 0    |
| H036.3C | 0.93 | 0.93 | 0.94 | 0.96 | 0.97 | 0.96 | 0.99 | 1    | 0.99 | 0    |
| H048.3C | 0.91 | 0.91 | 0.93 | 0.94 | 0.95 | 0.96 | 0.98 | 0.99 | 1    | 0    |
| H072.3C | 0.86 | 0.86 | 0.88 | 0.89 | 0.9  | 0.92 | 0.94 | 0.96 | 0.98 | 0    |
| H120.3C | 0.81 | 0.81 | 0.81 | 0.83 | 0.84 | 0.86 | 0.89 | 0.91 | 0.93 | 0    |
| H168.3C | 0.79 | 0.79 | 0.81 | 0.82 | 0.84 | 0.86 | 0.87 | 0.89 | 0.91 | 0    |
| H000.2P | 0.4  | 0.42 | 0.4  | 0.39 | 0.38 | 0.38 | 0.35 | 0.33 | 0.32 | 0    |
| H003.2P | 0.38 | 0.4  | 0.38 | 0.37 | 0.36 | 0.36 | 0.33 | 0.32 | 0.29 | 0    |
| H006.2P | 0.38 | 0.4  | 0.38 | 0.37 | 0.36 | 0.36 | 0.33 | 0.31 | 0.29 | 0    |
| H009.2P | 0.39 | 0.41 | 0.39 | 0.38 | 0.38 | 0.37 | 0.34 | 0.32 | 0.3  | 0    |
| H012.2P | 0.38 | 0.41 | 0.39 | 0.38 | 0.38 | 0.37 | 0.34 | 0.33 | 0.31 | 0    |
| H018.2P | 0.4  | 0.42 | 0.41 | 0.41 | 0.4  | 0.4  | 0.37 | 0.35 | 0.33 | 0    |
| H024.2P | 0.41 | 0.43 | 0.42 | 0.42 | 0.42 | 0.41 | 0.38 | 0.37 | 0.35 | 0    |
| H036.2P | 0.37 | 0.39 | 0.39 | 0.39 | 0.39 | 0.39 | 0.36 | 0.34 | 0.31 | 0.27 |
| H048.2P | 0.36 | 0.39 | 0.38 | 0.39 | 0.39 | 0.39 | 0.36 | 0.35 | 0.33 | 0.28 |
| H072.2P | 0.32 | 0.35 | 0.35 | 0.35 | 0.36 | 0.36 | 0.35 | 0.35 | 0.36 | 0.33 |
| H120.2P | 0.26 | 0.28 | 0.28 | 0.29 | 0.29 | 0.3  | 0.3  | 0.31 | 0.32 | 0.35 |
| H168.2P | 0.26 | 0.28 | 0.28 | 0.28 | 0.29 | 0.3  | 0.29 | 0.3  | 0.31 | 0.35 |



# Riboprofiling and proteomics



**Riboprofiling**

**Proteomics**



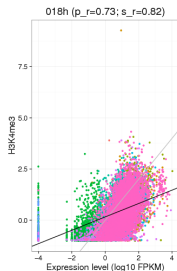
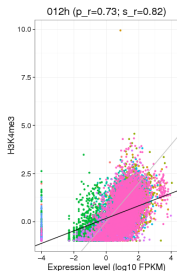
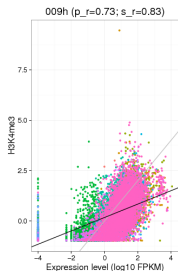
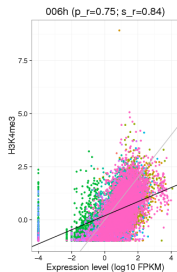
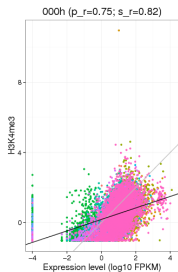
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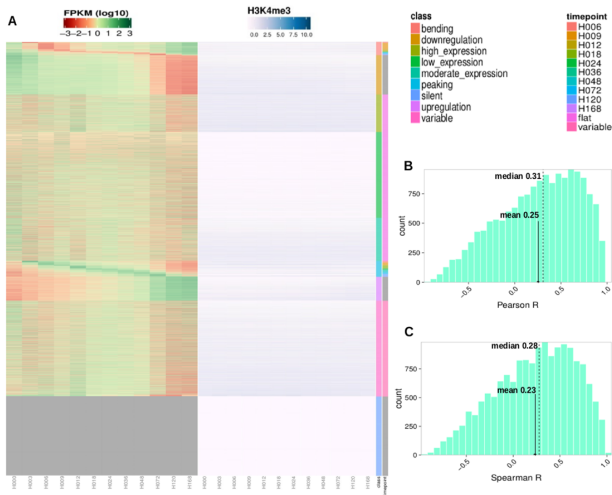
Results

Correlation between RNA-Seq fractions and among data types  
correlation between gene expression and H3K4me3 signal

# Correlation between gene expression and H3K4me3 signal



# Correlation between gene expression and H3K4me3 signal





# Acknowledgements



- ▶ Alex Esteban
- ▶ Amaya Abad
- ▶ Beatrice Borsari
- ▶ Emilio Palumbo
- ▶ Sebastian Ullrich
- ▶ Rory Johnson
- ▶ Ramil Nurtdinov
- ▶ Alessandra Breschi
- ▶ Silvia Perez Lluch
- ▶ Marina Ruiz Romero
- ▶ Roderic Guigo





obrigado

Dank U

Merci

mahalo

Köszi

chnacuóo

Grazie

Thank  
you

mauruuru

Takk

Gracias

Dziękuję

Děkuju

danke

Kiitos

