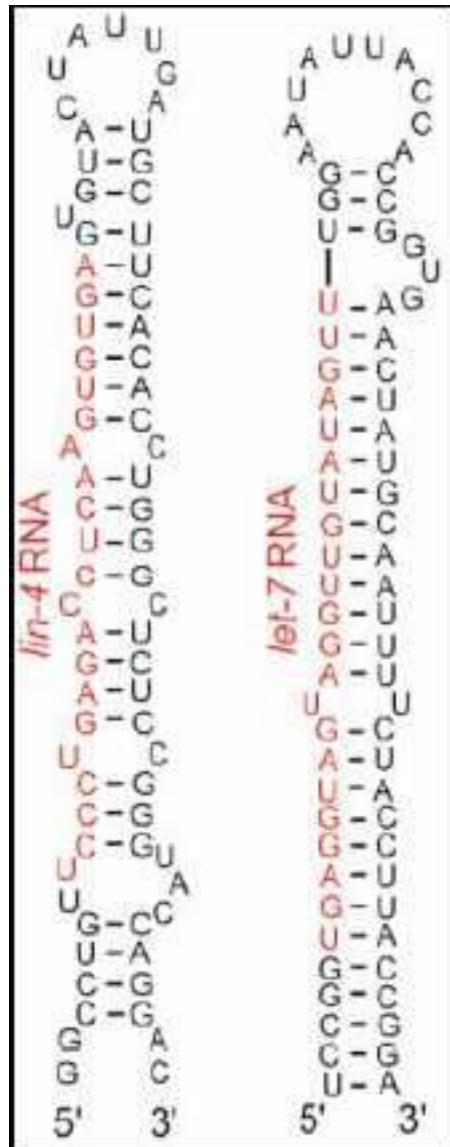


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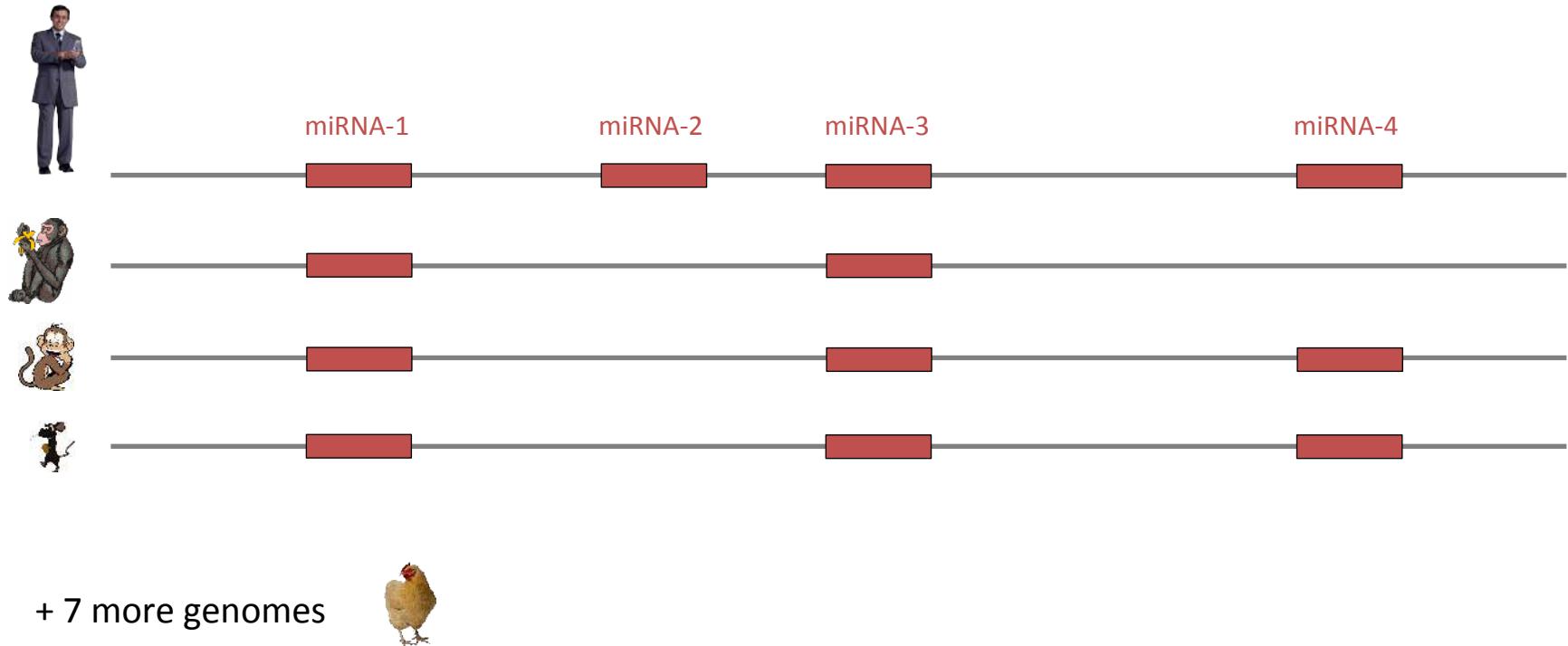
Human-specific transcripts

Human-specific transcripts | microRNA (miRNA)

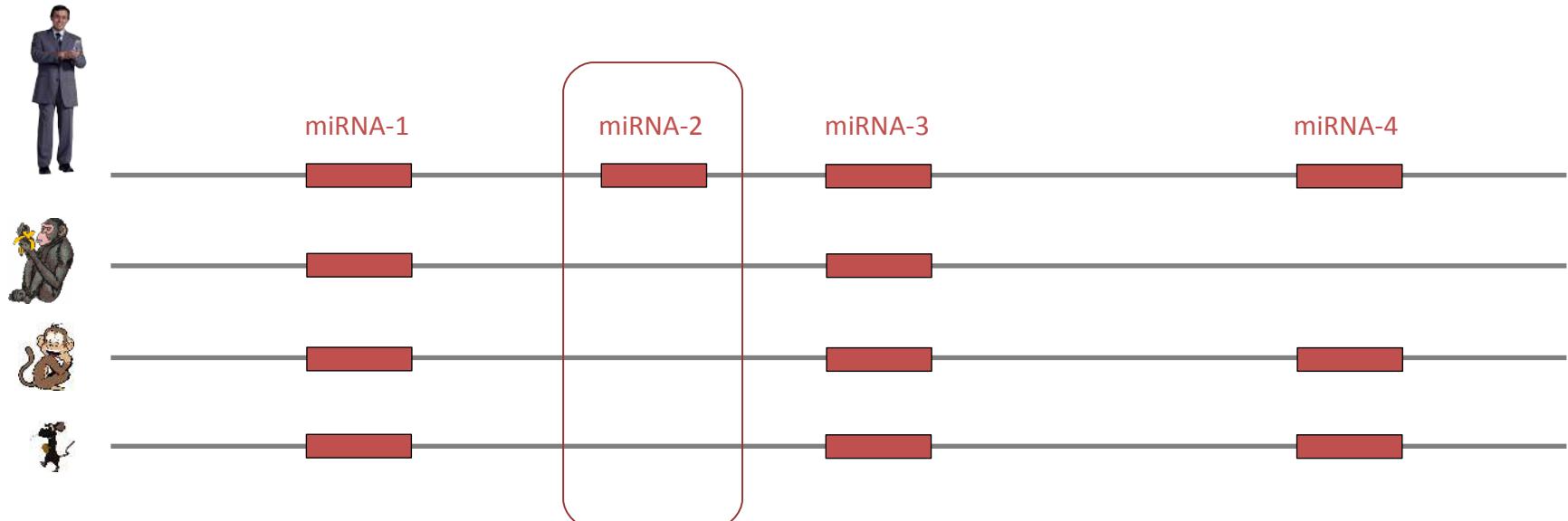


miRNA

Novel miRNA | genome analysis



Novel miRNA | genome analysis

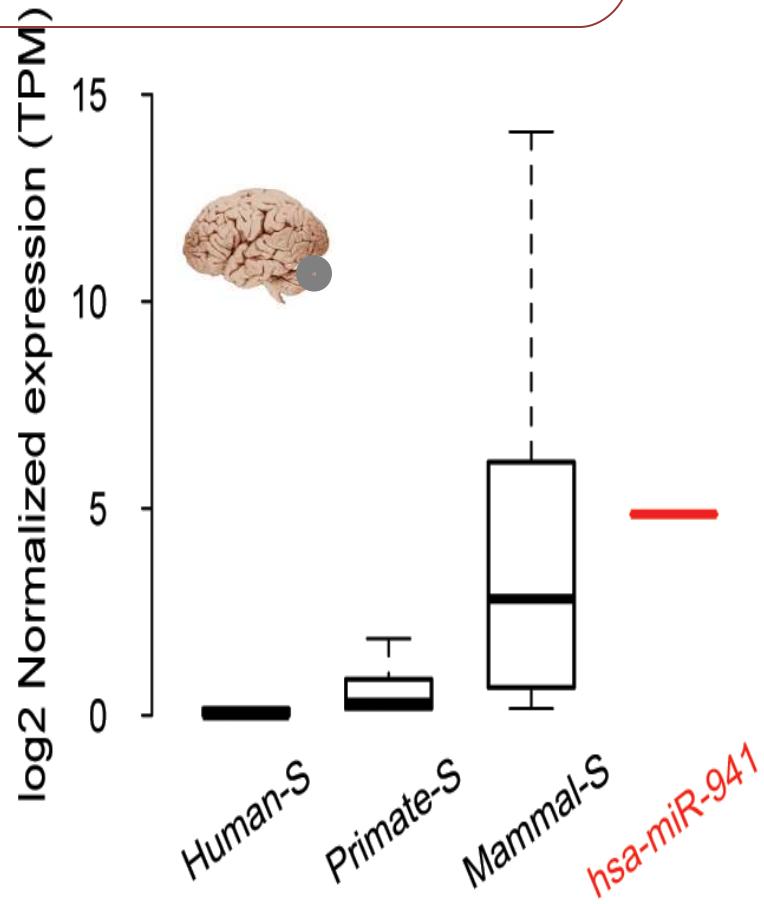
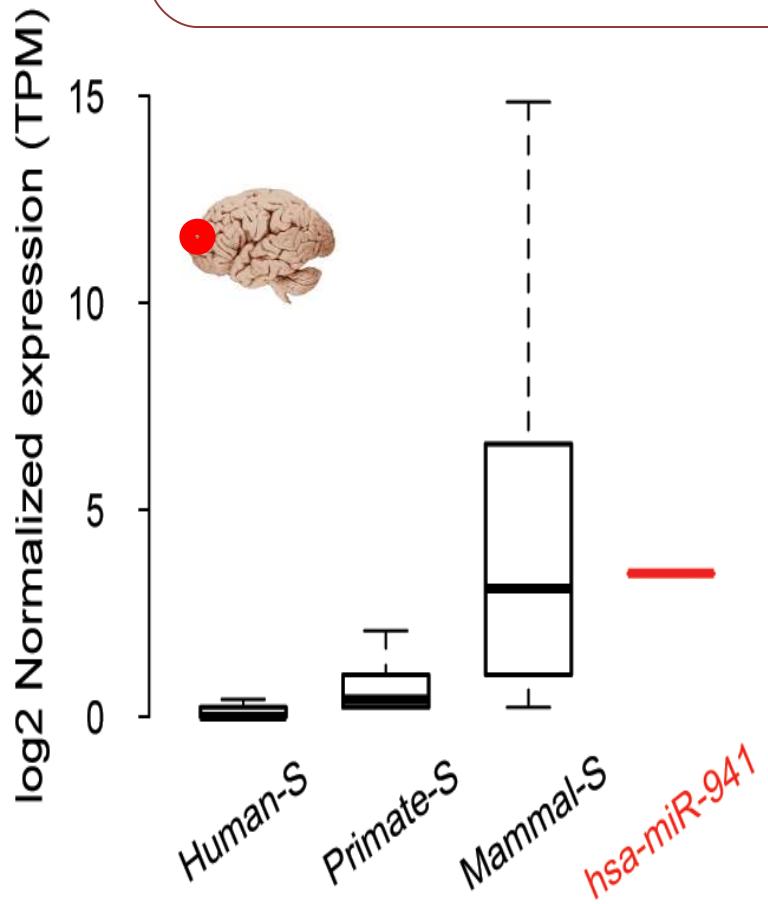


+ 7 more genomes

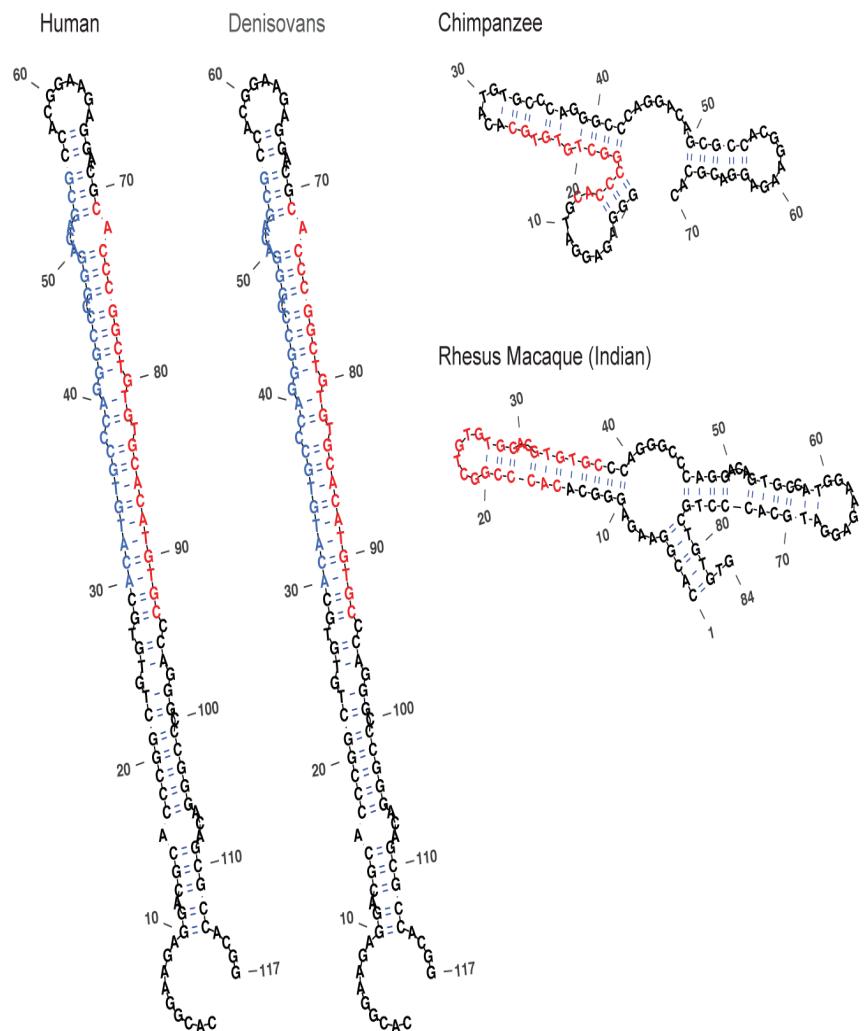
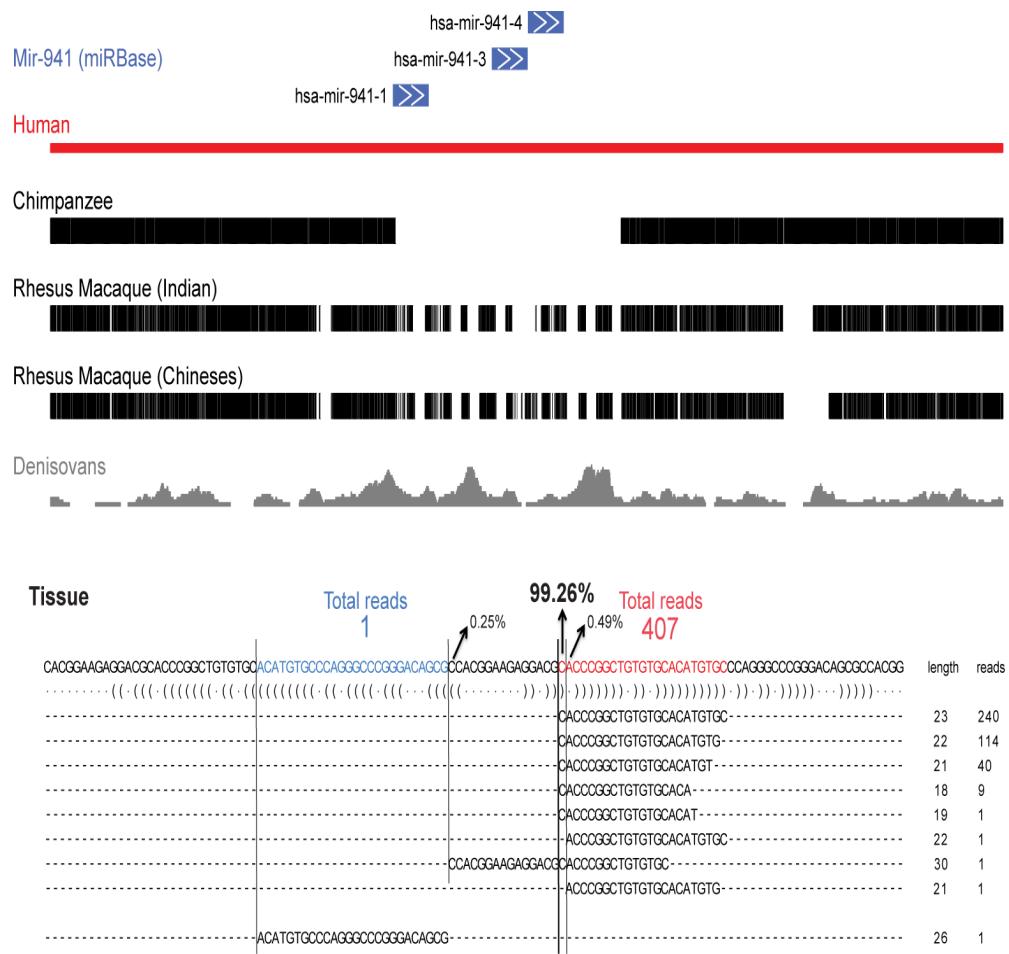


21 human-specific microRNA
1017 primate-specific microRNA
677 conserved among mammals

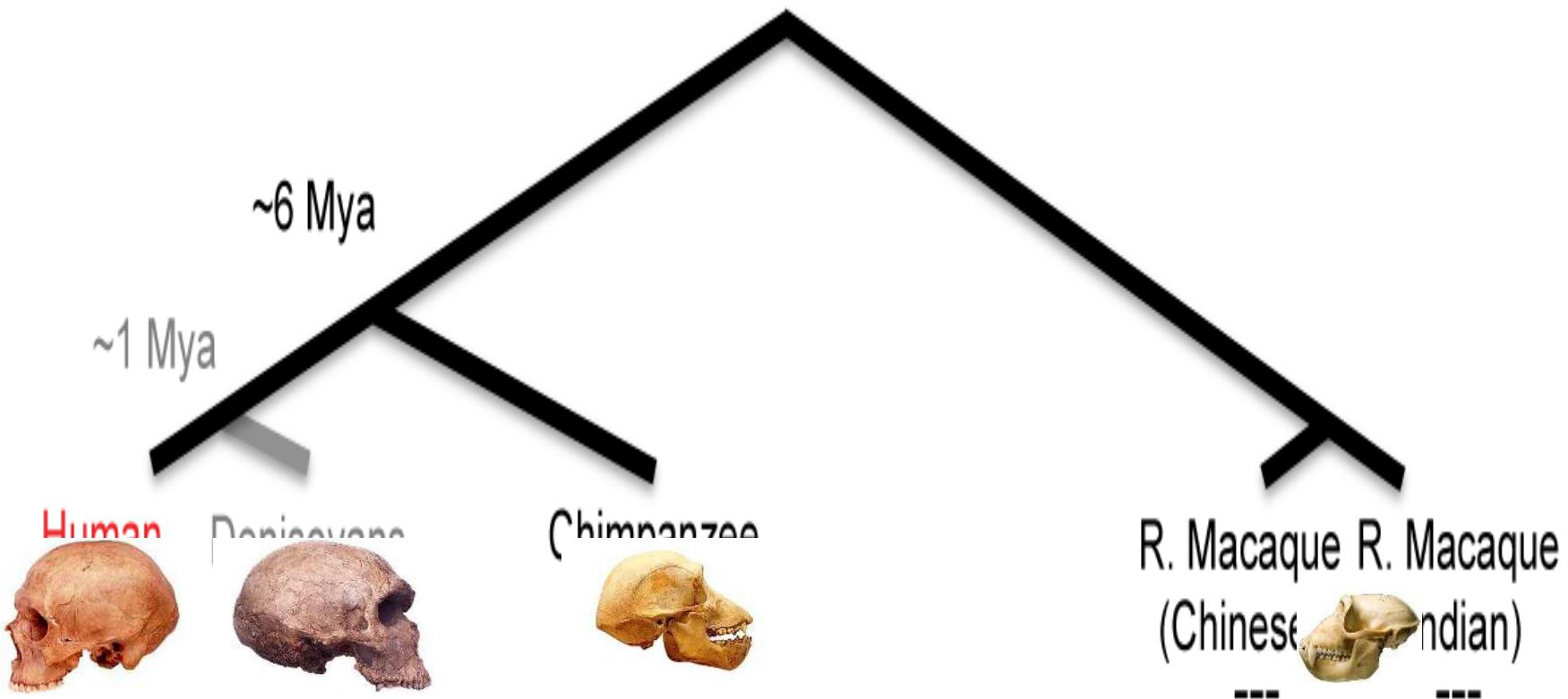
Novel miRNA | expression in brain



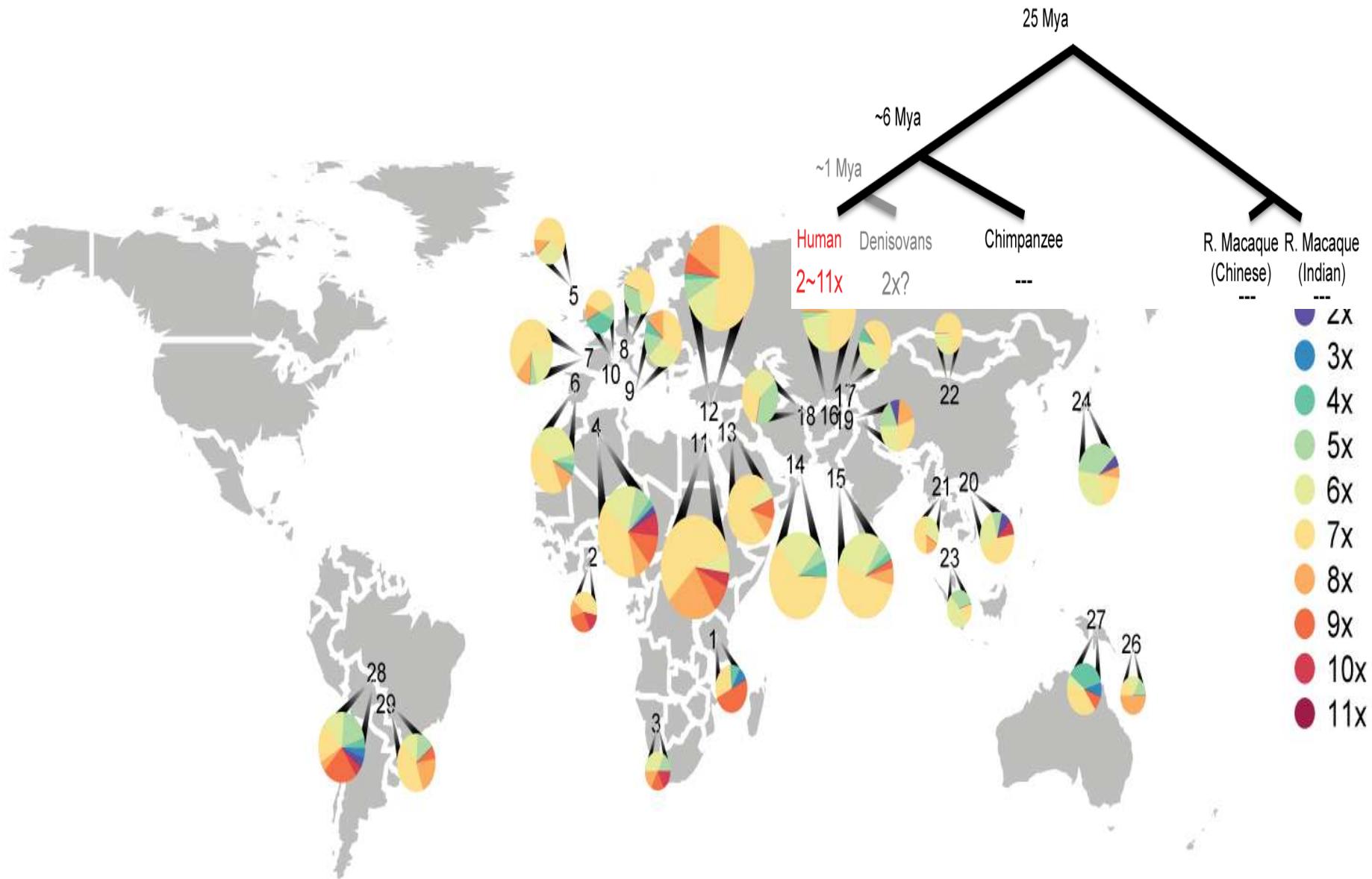
miRNA 941 | sequence evolution



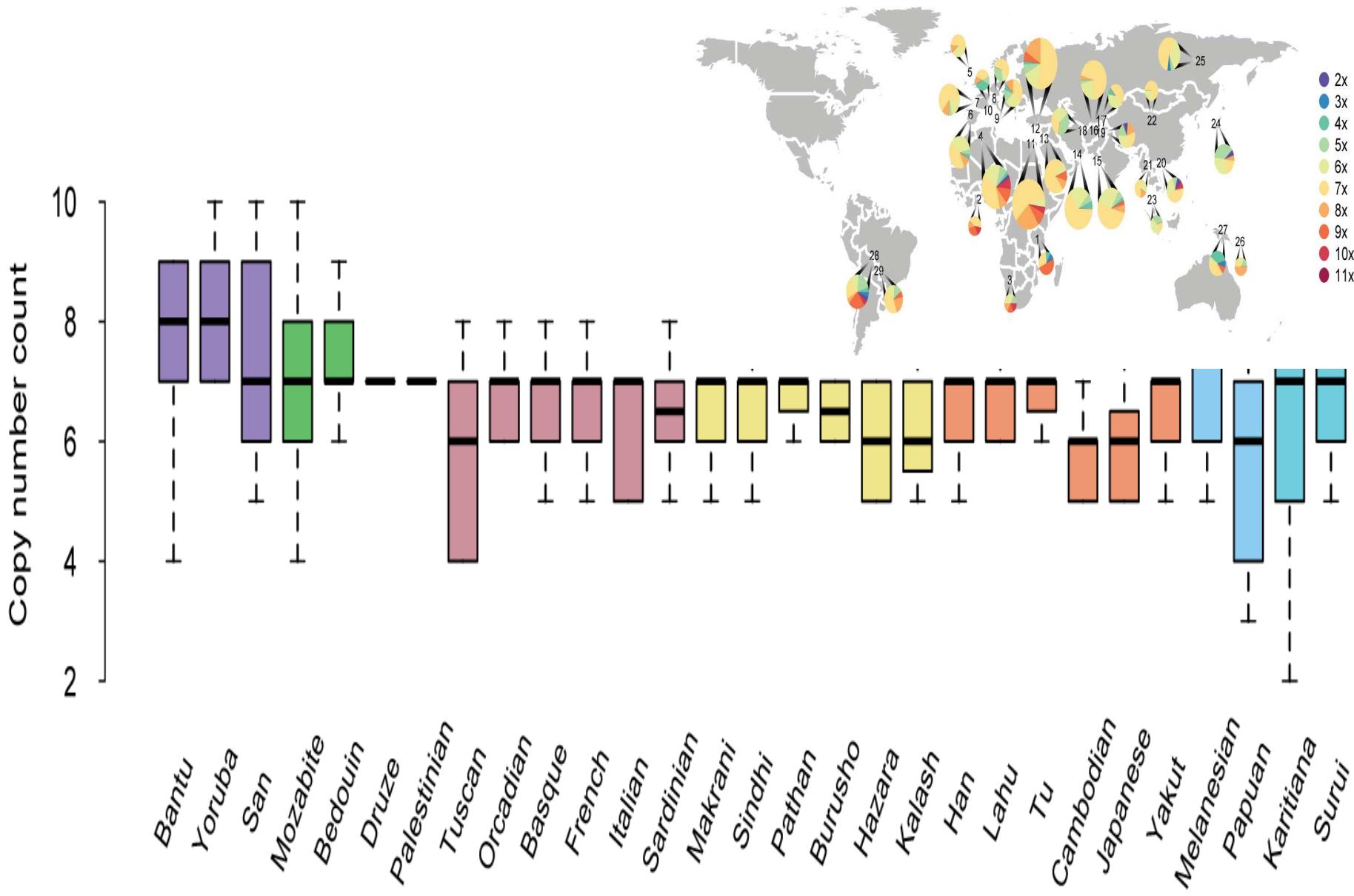
miRNA 941 | precursor copy number



miRNA 941 | copy number variation in modern humans



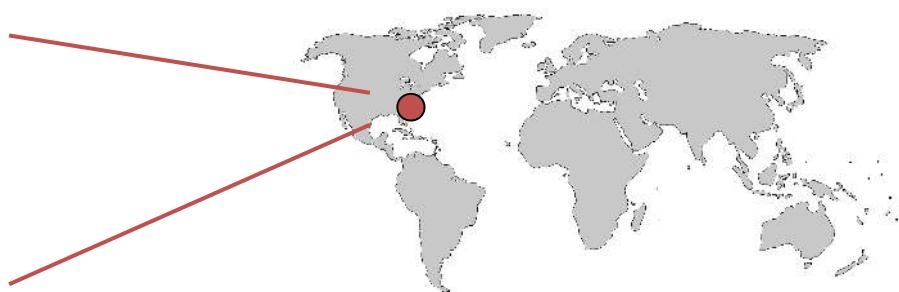
miRNA 941 | copy number variation in modern humans



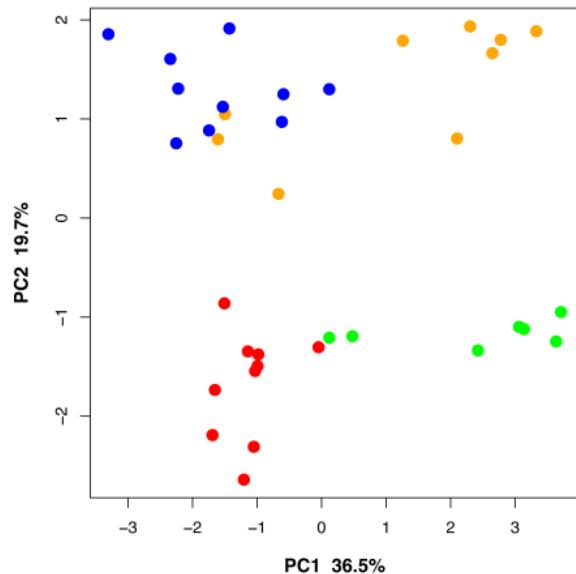
miRNA 941 expression variation among populations | placenta

Placenta samples:

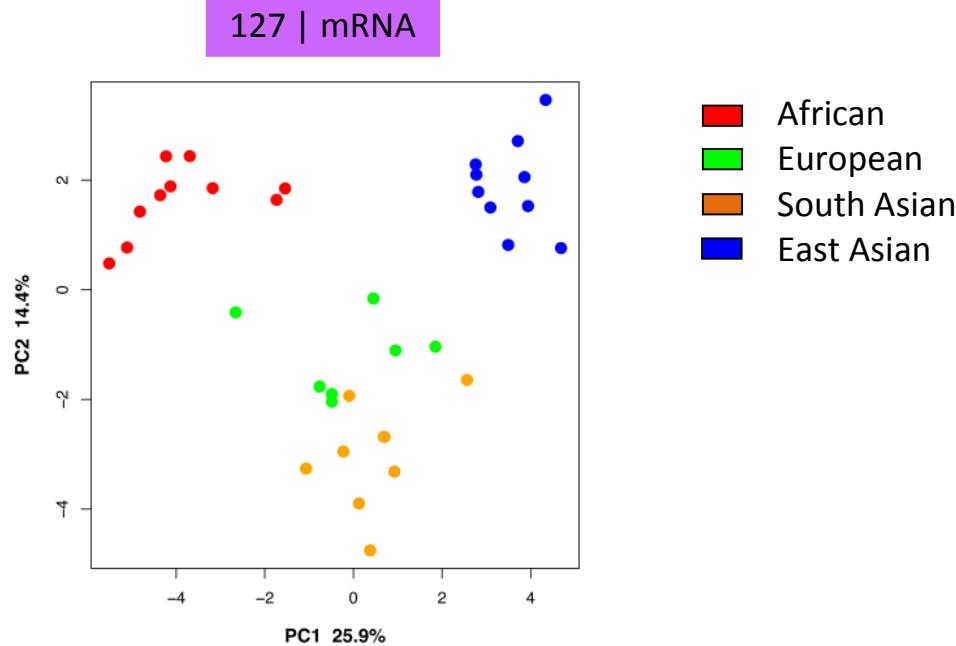
- 10 African (AF)
- 10 European (EU)
- 10 South Asian (SA)
- 10 East Asian (EA)



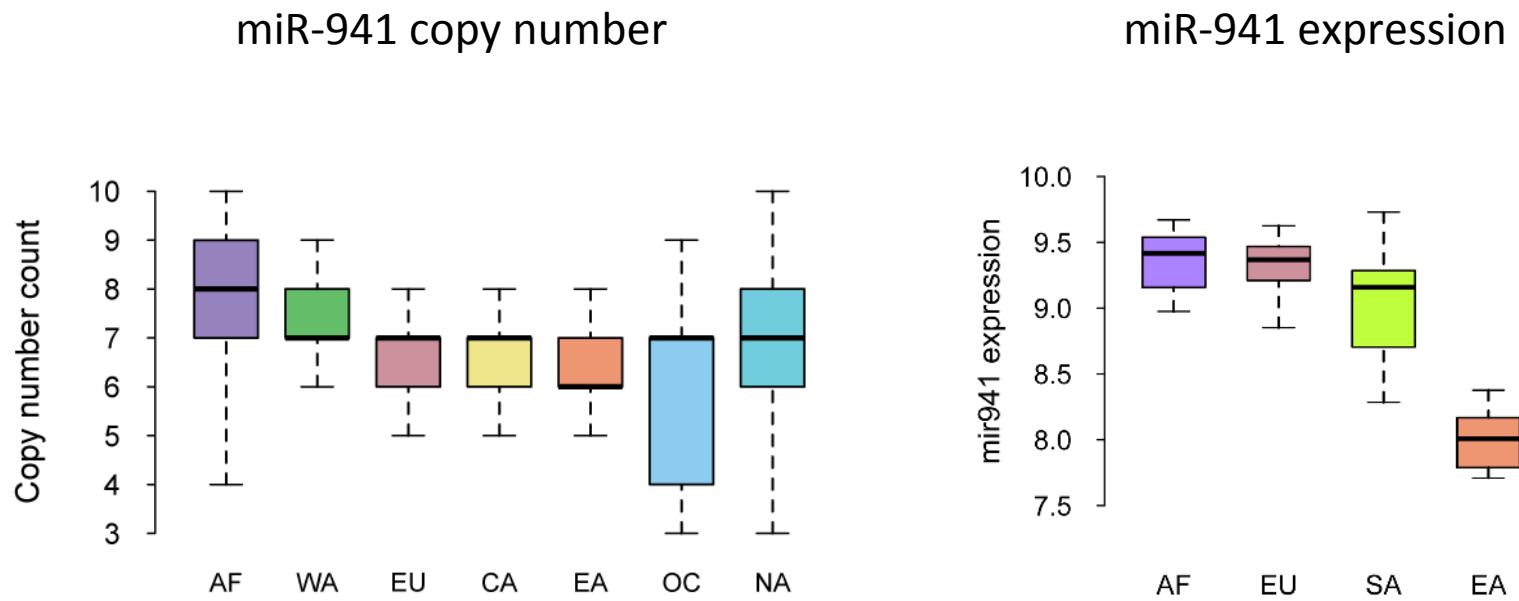
40 | miRNA



127 | mRNA

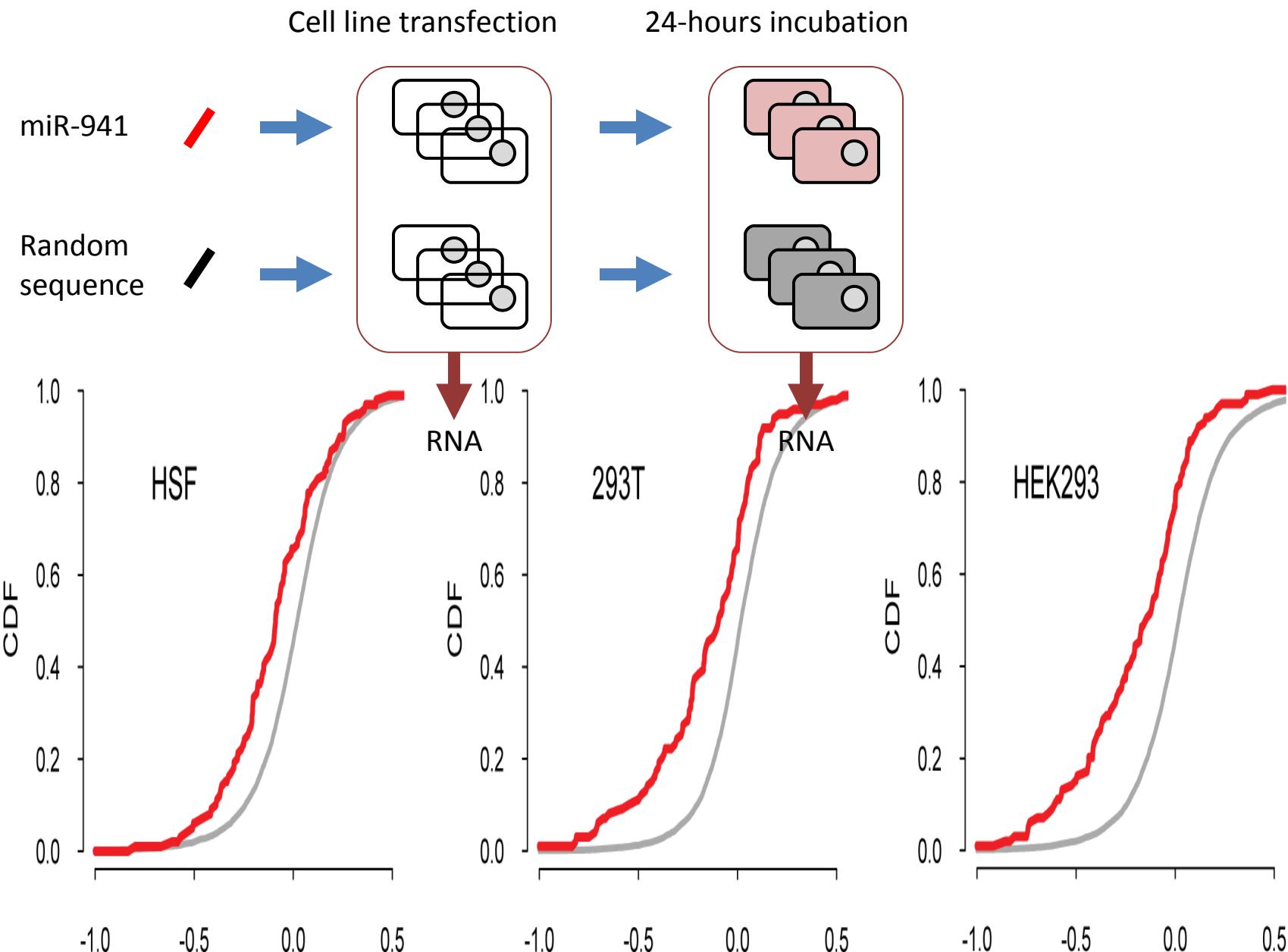


miRNA 941 expression variation among populations | placenta



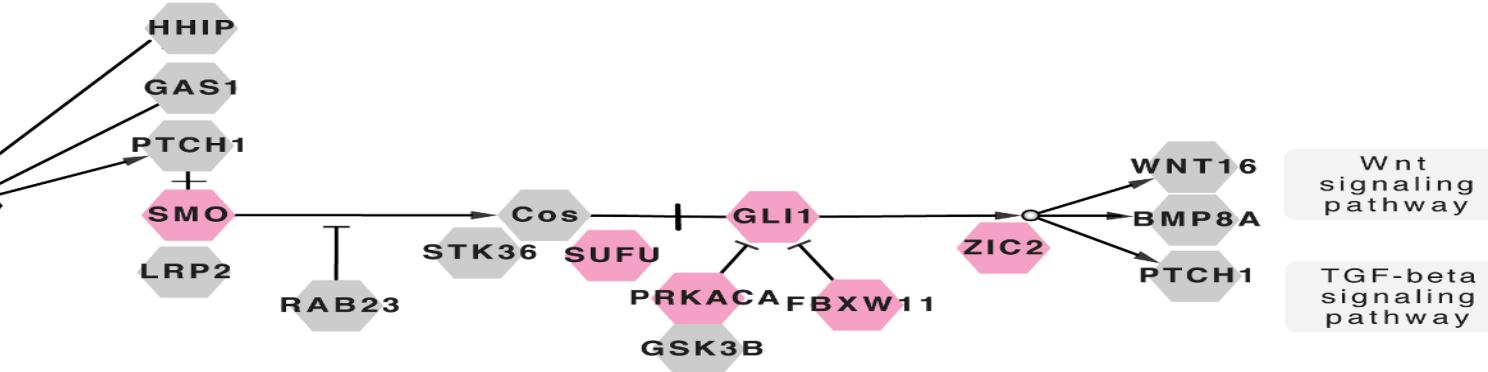
There is substantial expression variation among human populations

miRNA 941 | functional analysis – target genes

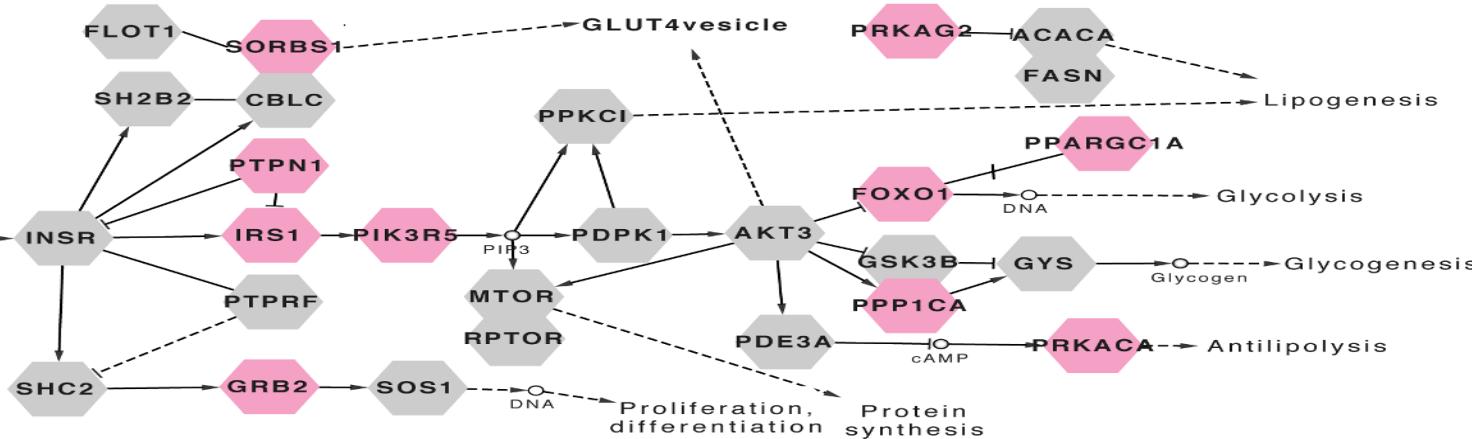


miRNA 941 | functional analysis – target pathways

Hedgehog signaling pathway

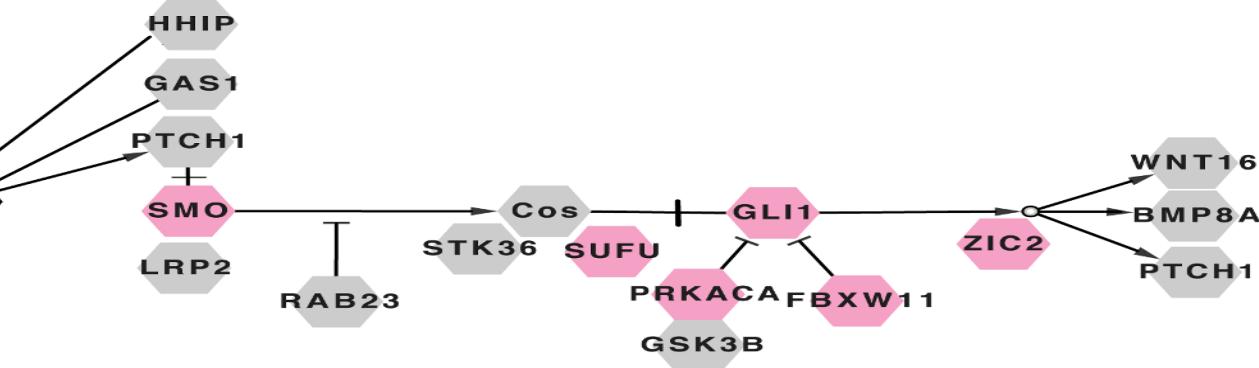


Insulin signaling pathway

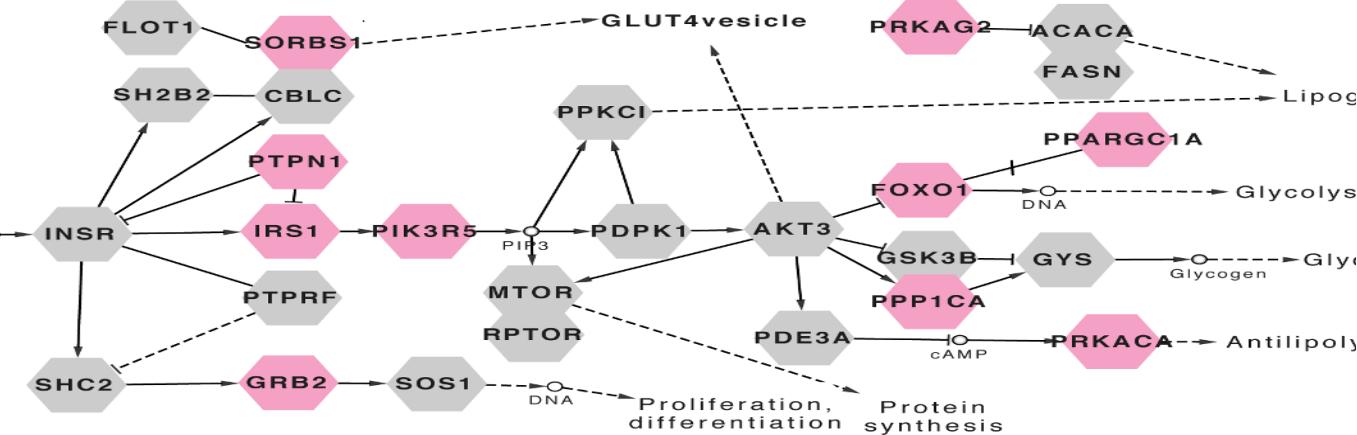


miRNA 941 | functional analysis – role in proliferation?

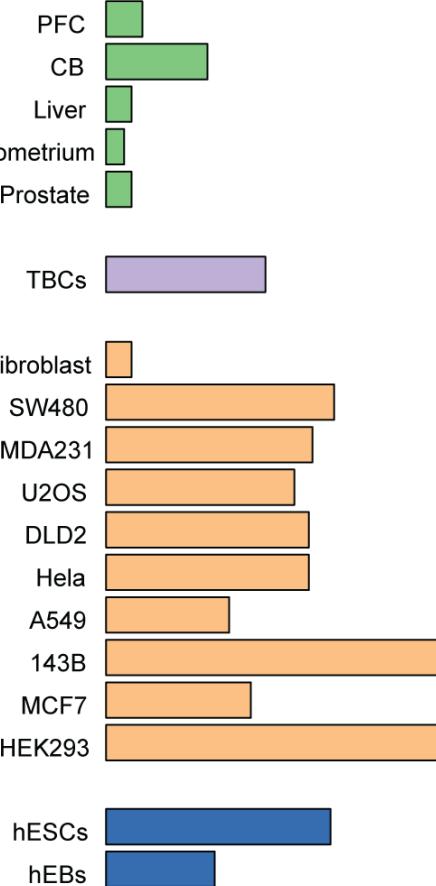
Hedgehog signaling pathway



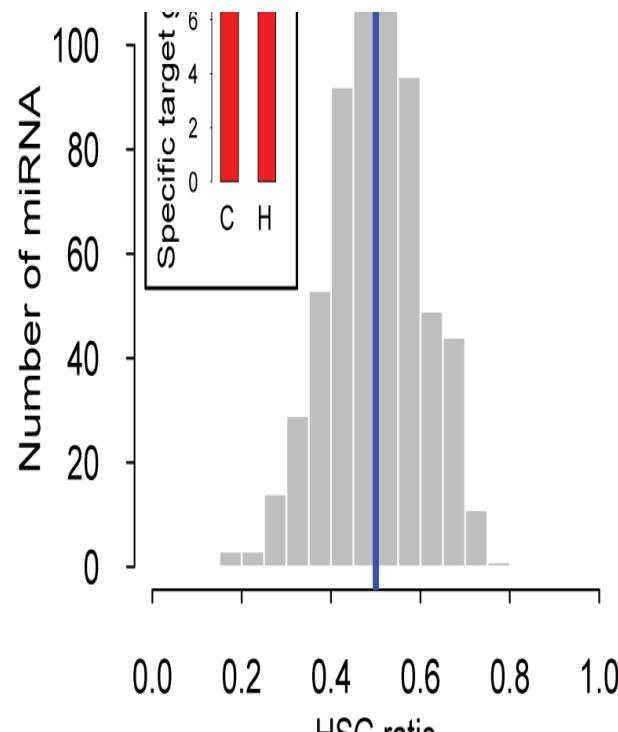
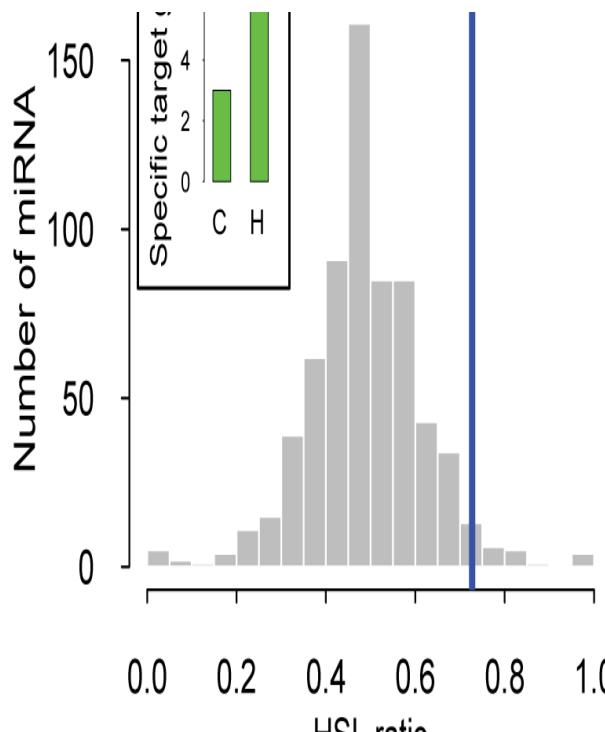
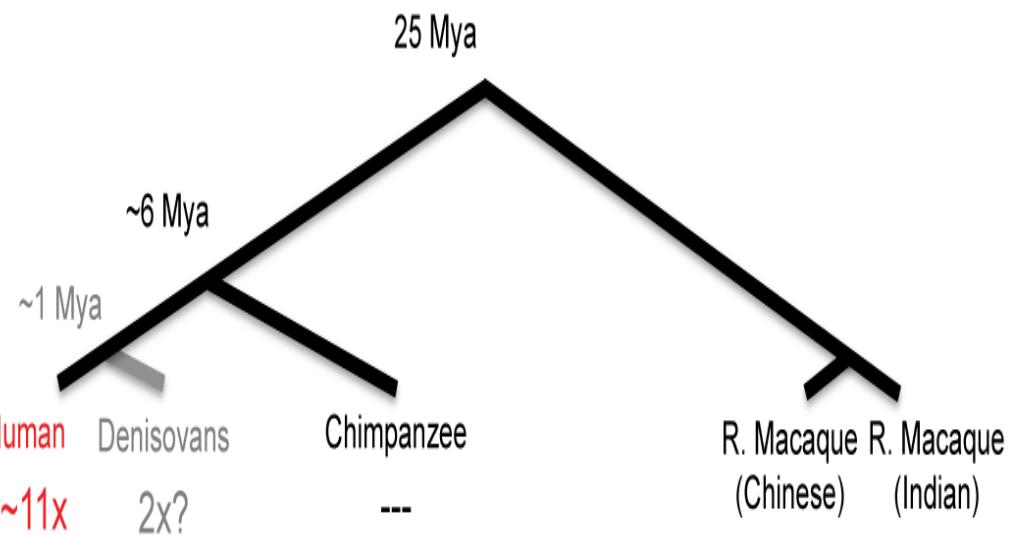
Insulin signaling pathway



Normalized expression (TPM)

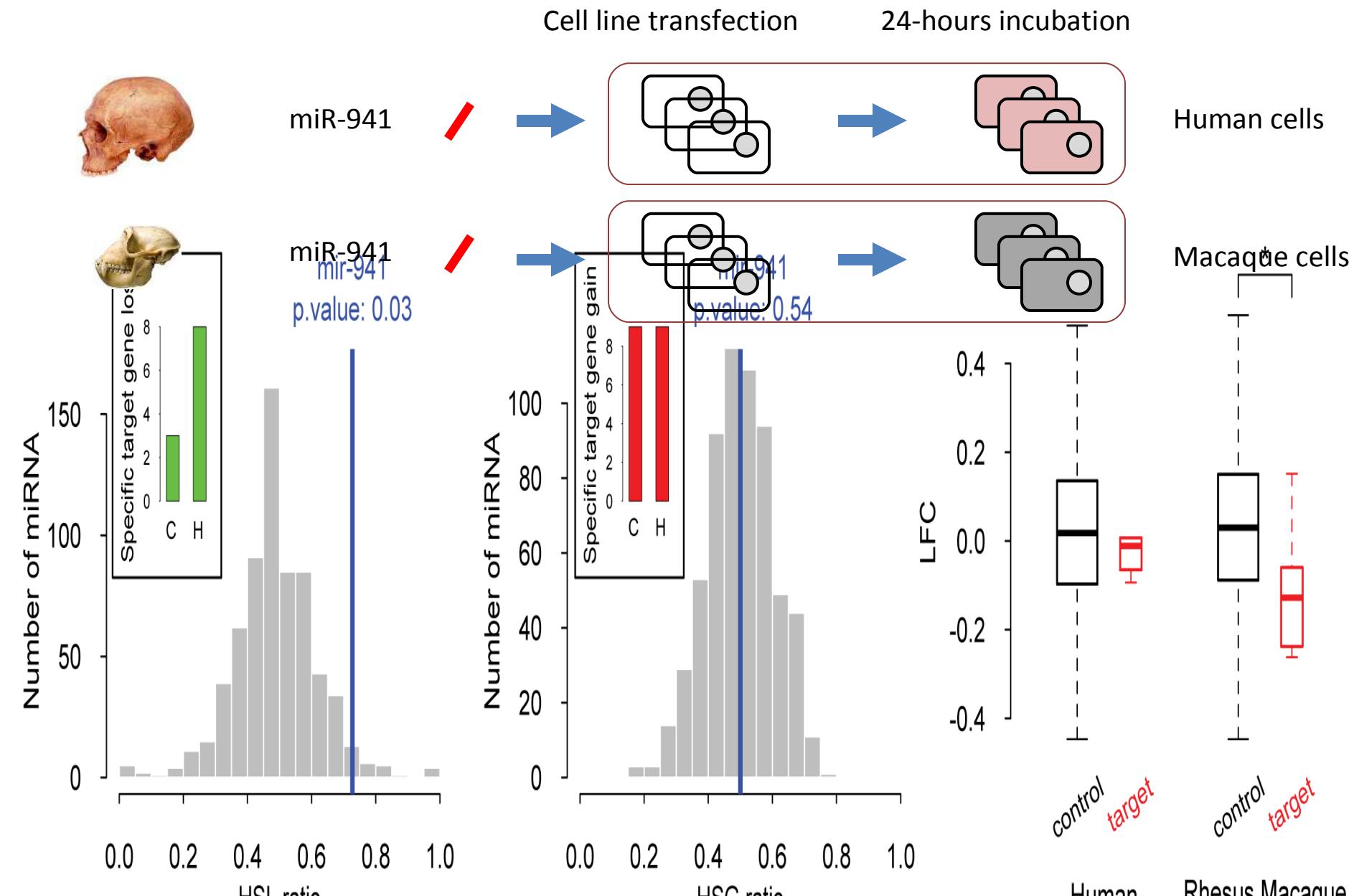


miRNA 941 | regulatory evolution – binding sites



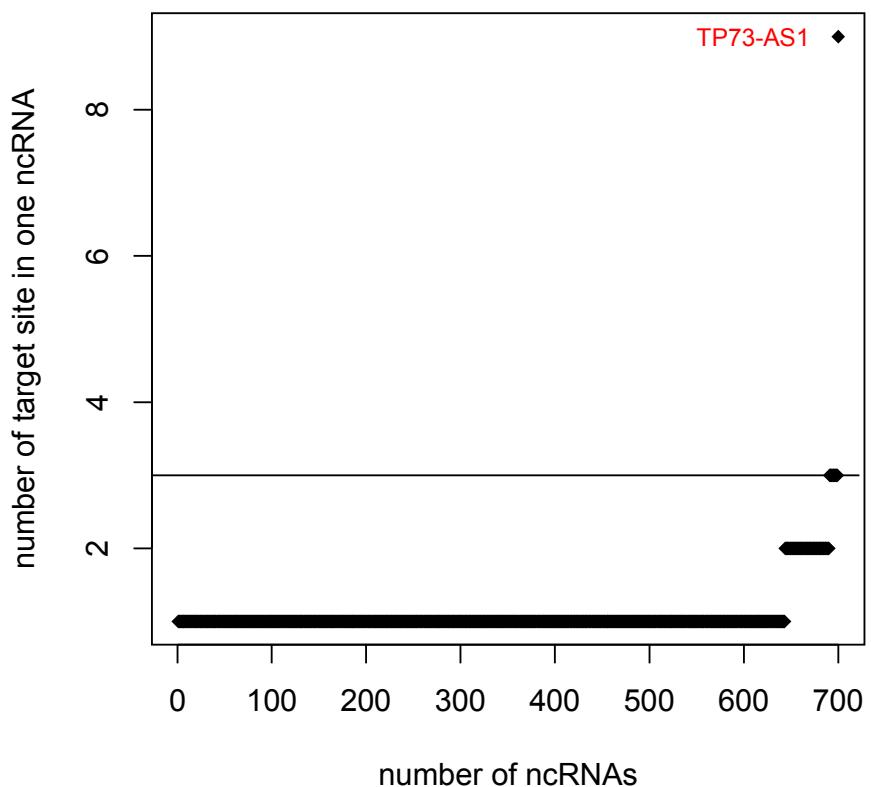
C⁰⁺ R⁰⁺ C⁰⁺ R⁰⁺ Human Rhesus Macaque

miRNA 941 | regulatory evolution – binding sites

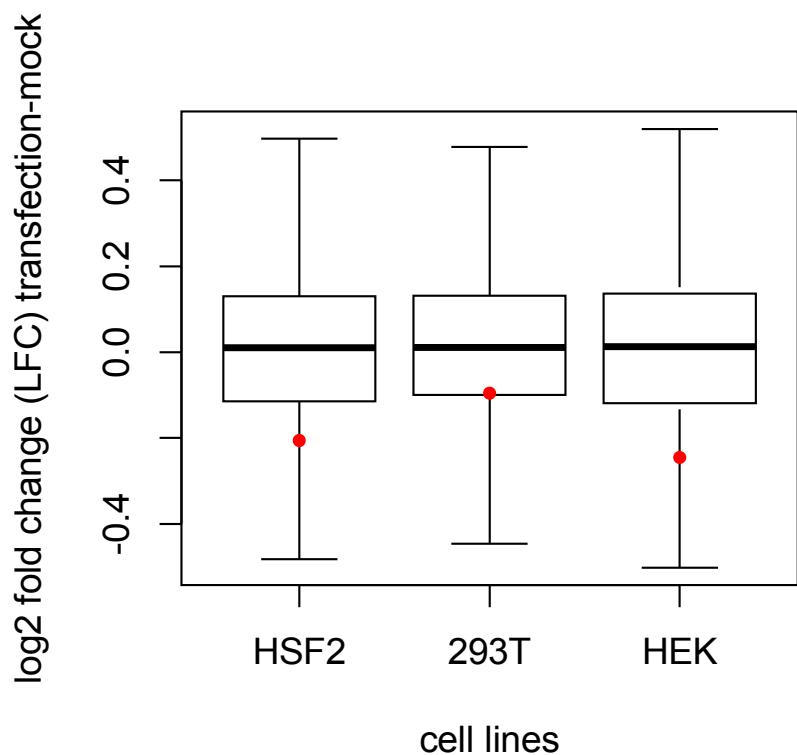


miRNA 941 | regulatory evolution – sponge

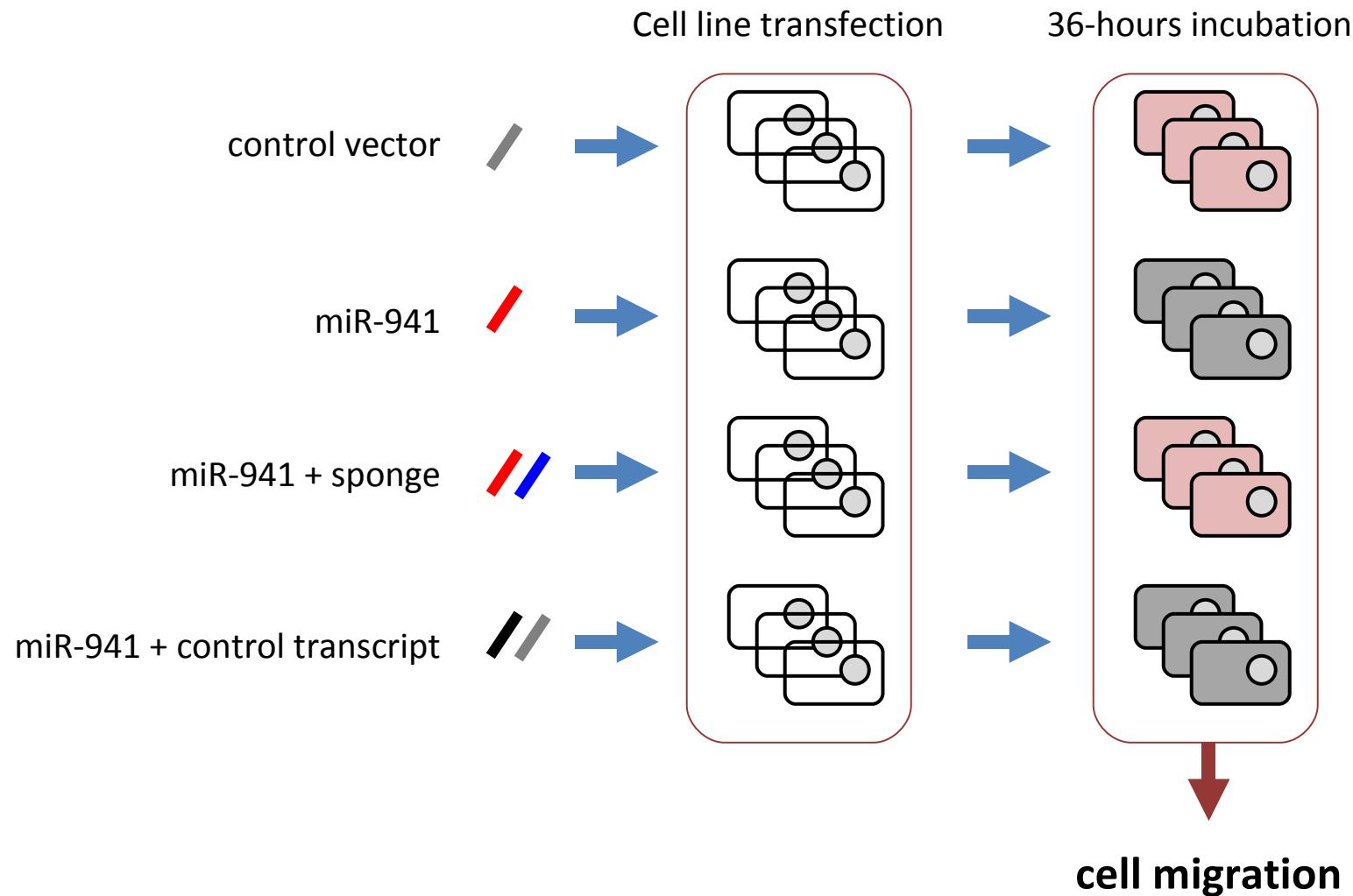
miR-941 binding sites



miR-941 inhibits sponge



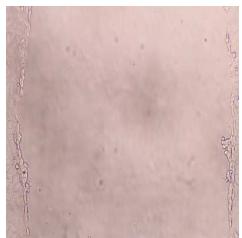
miRNA 941 | regulatory evolution – sponge



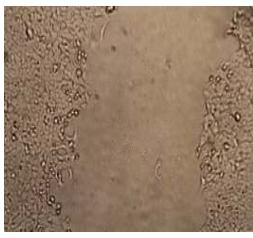
miRNA 941 | regulatory evolution – sponge

Phenotype

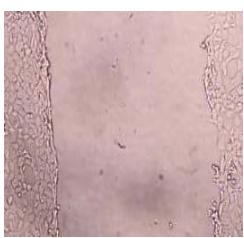
0 hours



36 hours



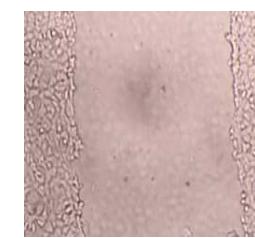
0 hours



36 hours



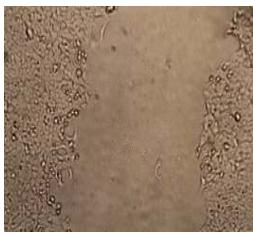
0 hours



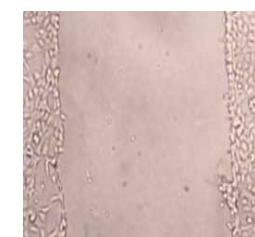
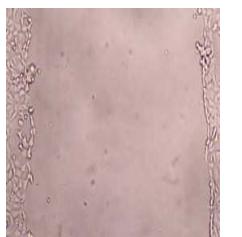
36 hours



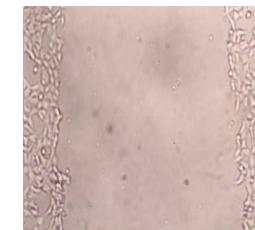
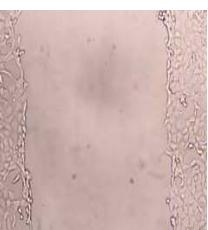
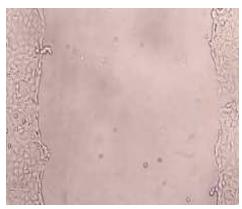
1



2



3



miR-941



miR-941 + sponge

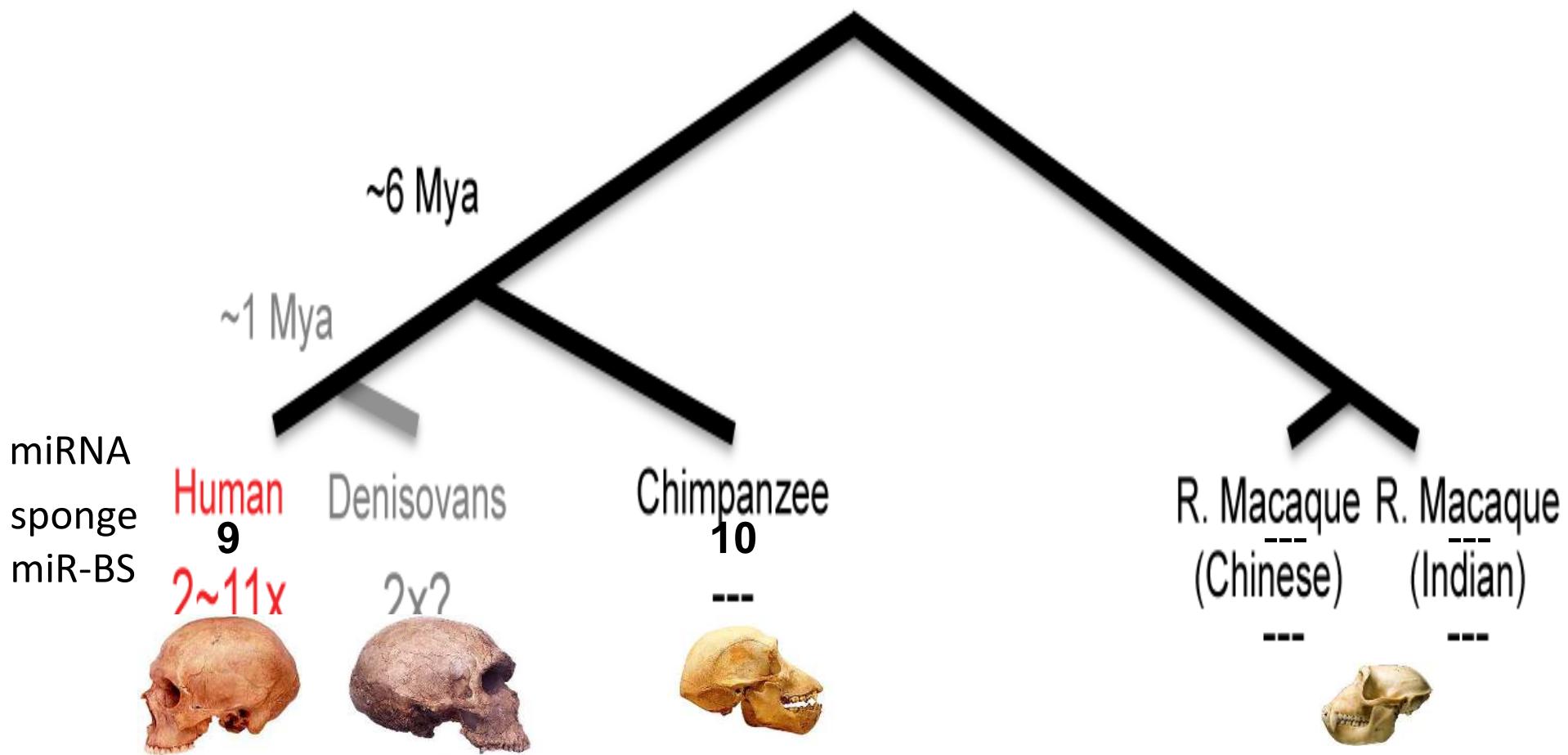


miR-941 + control transcript



14.8.13

miRNA 941 | regulatory evolution 25 Mya sponge



Conclusions

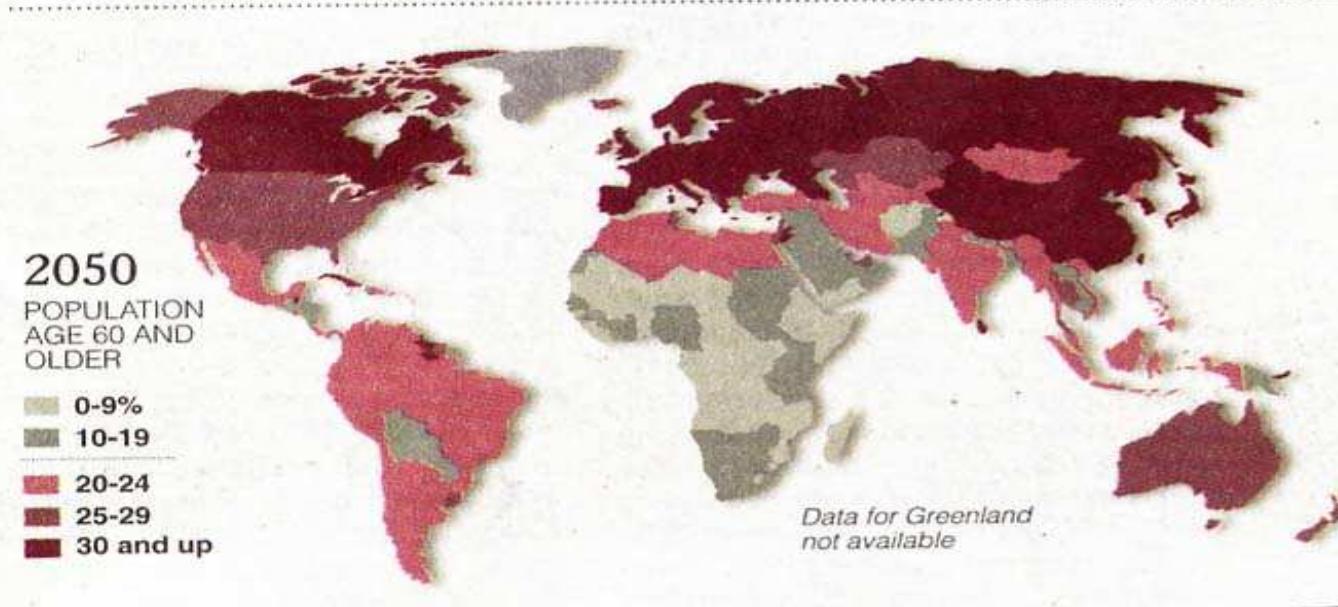
Transcriptome regulation driven by non-coding RNA evolves rapidly and complexly



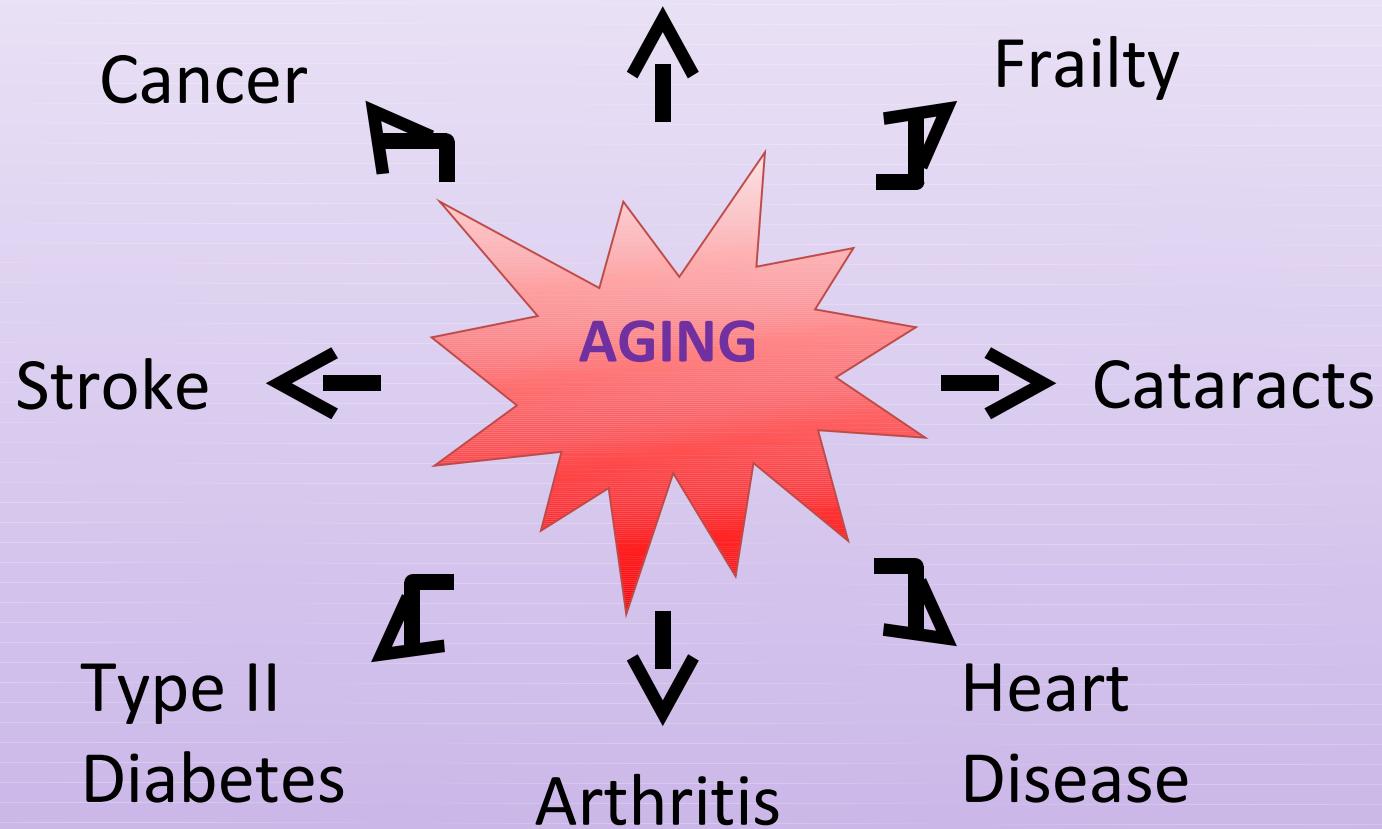
Brain aging

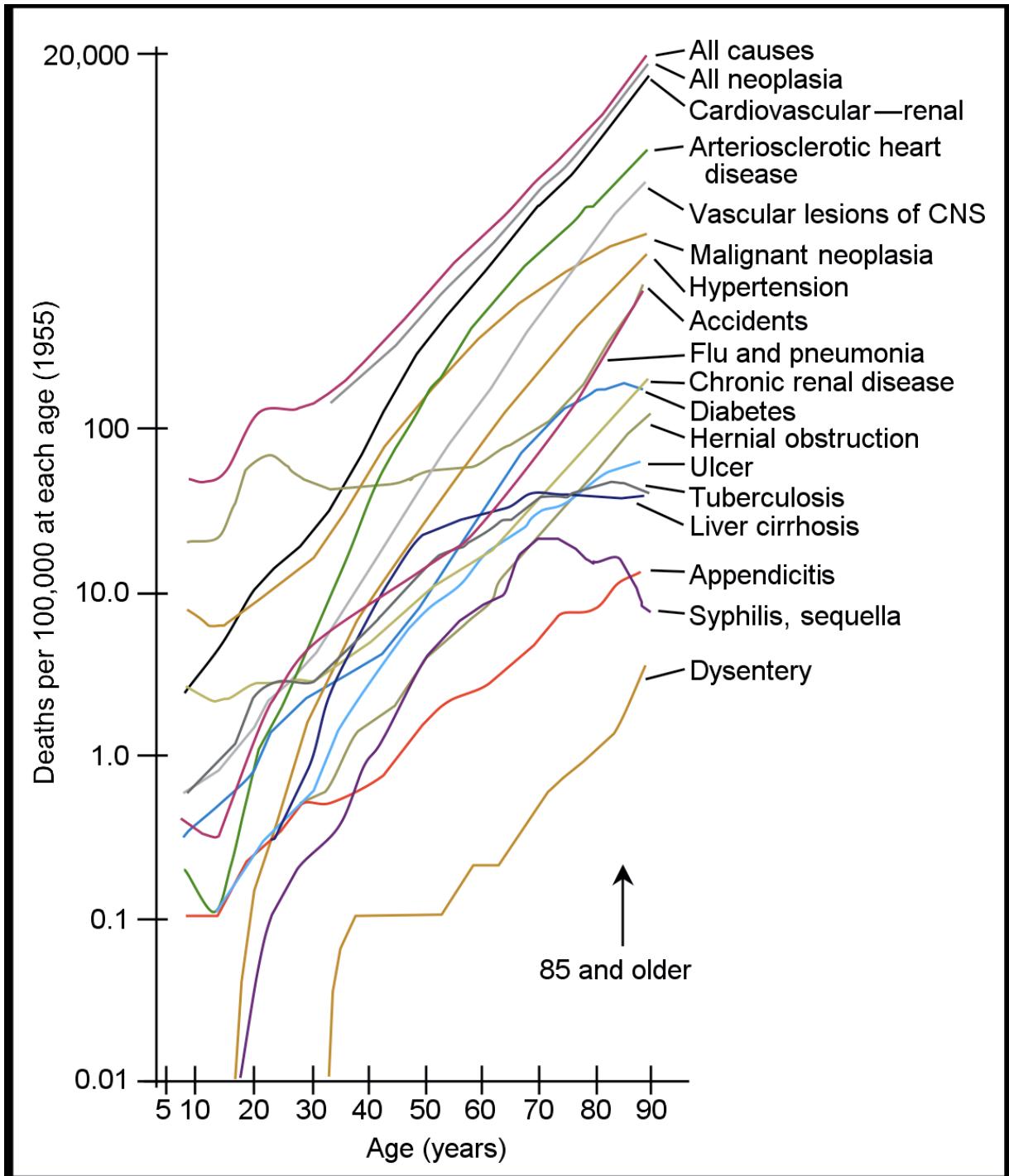
A Growing Tide of Elderly Citizens . . .

The percentage of the world's population that is age 60 and older is expected to grow steadily over the next 50 years, so that by 2050 the elderly will make up a full 25 percent of many countries' populations.



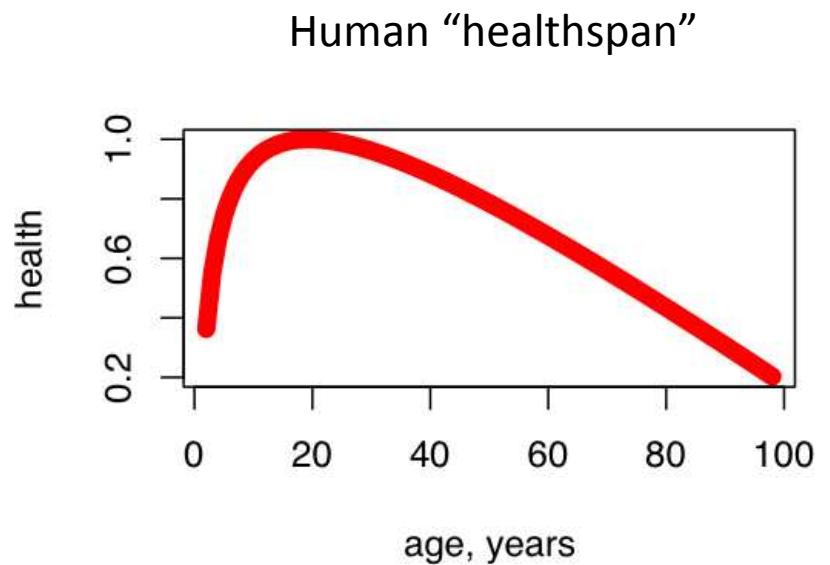
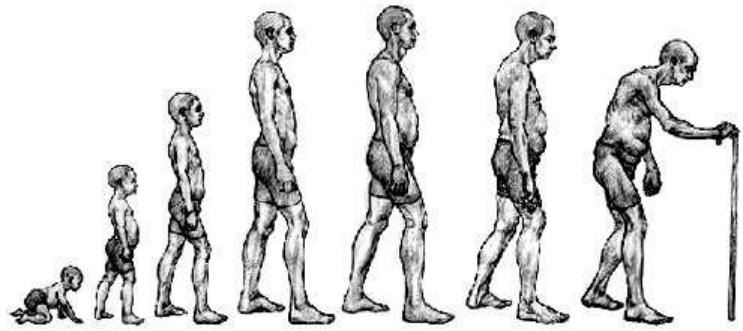
Neurodegeneration



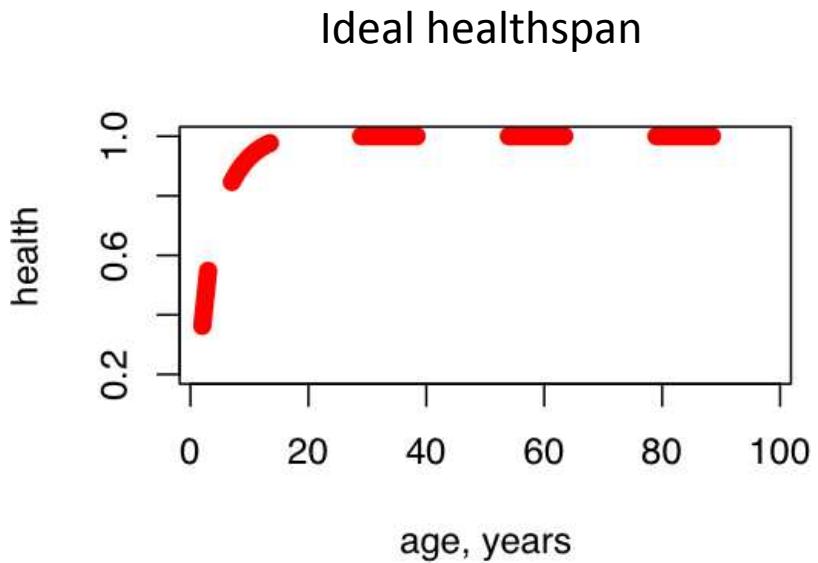
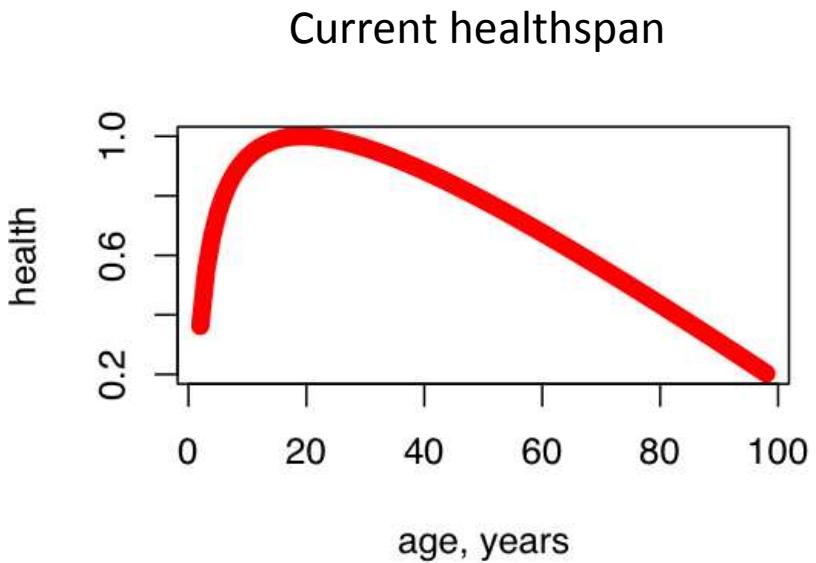


Kohn
1978

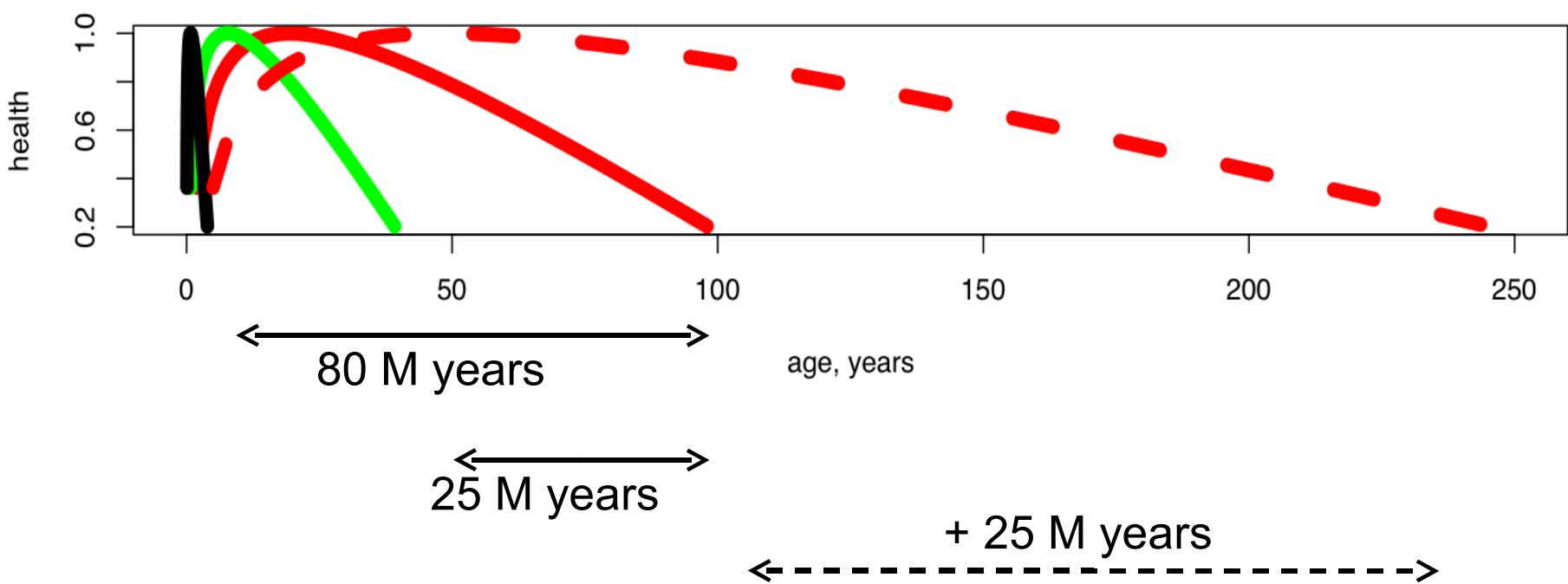
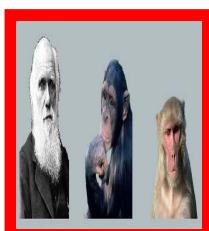
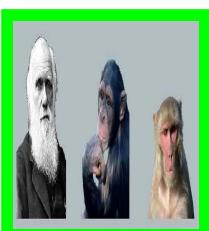
Human aging | health decrease with age



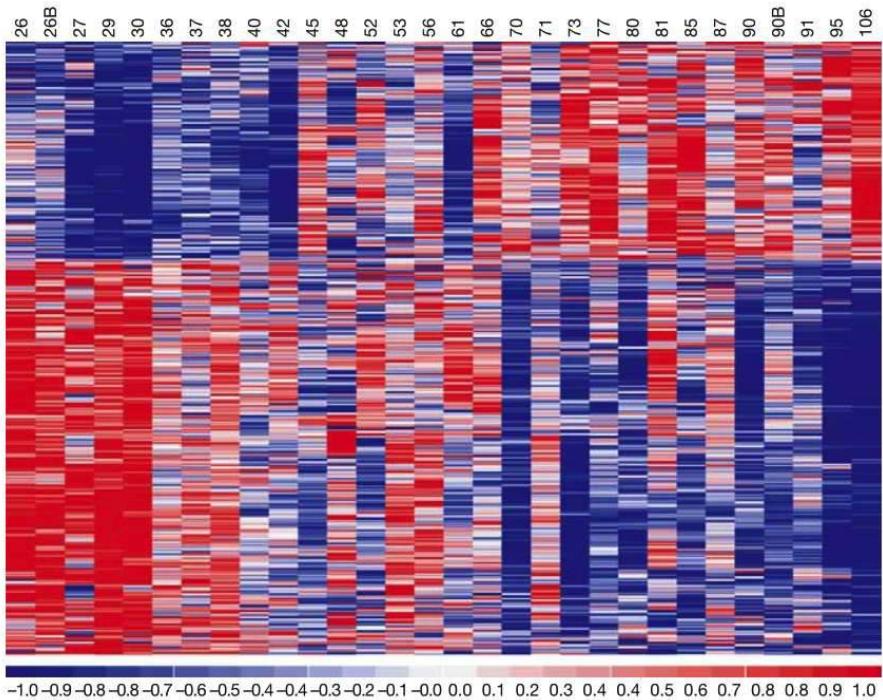
Human aging | health decrease with age



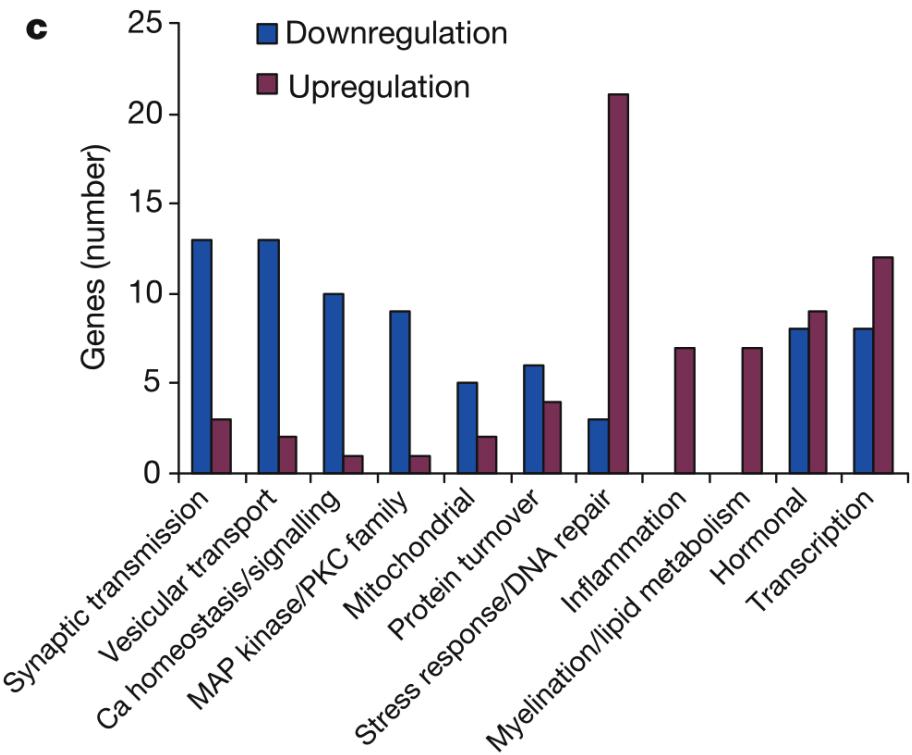
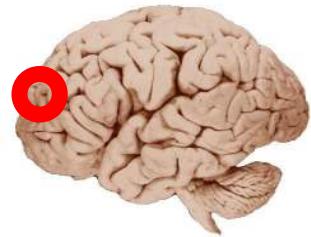
Human aging | variation among species



Human aging | background



mRNA



Lu et al. Nature (2004)

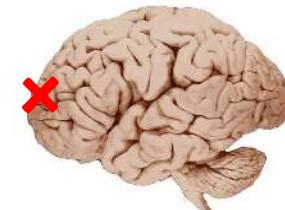
Human aging | human-macaque comparison



24 humans 0 - 98 years



24 rhesus macaques 0 - 28 years



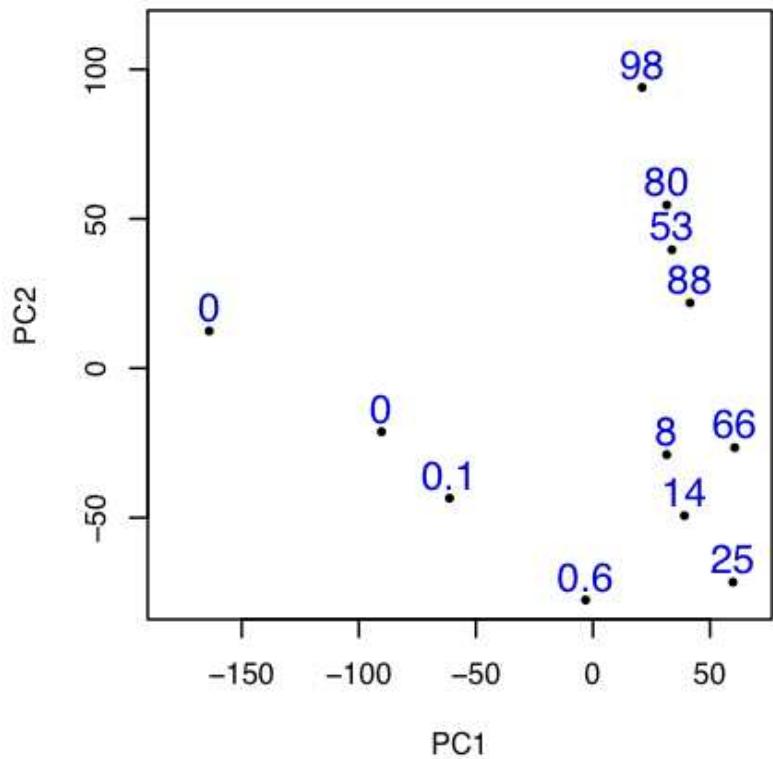
mRNA Affymetrix microarrays ~12,000 genes



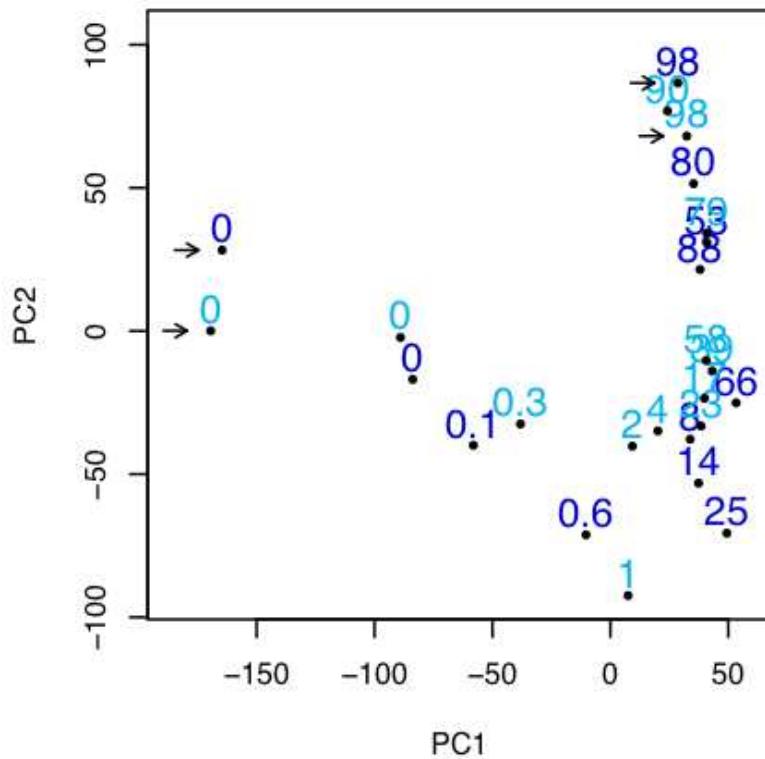
miRNA Illumina sequencing ~400 miRNAs

Human aging | expression changes with age

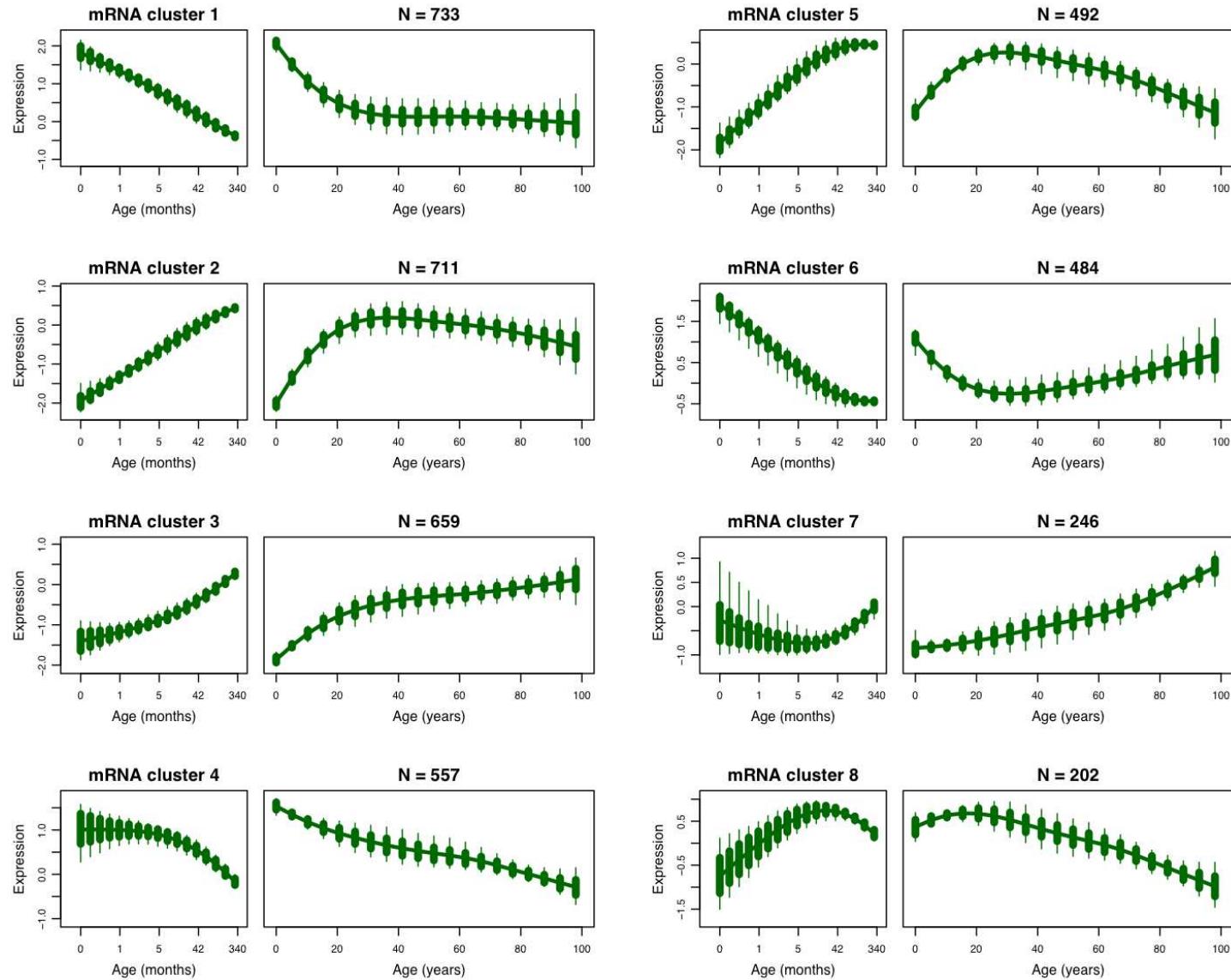
Human mRNA | set 1



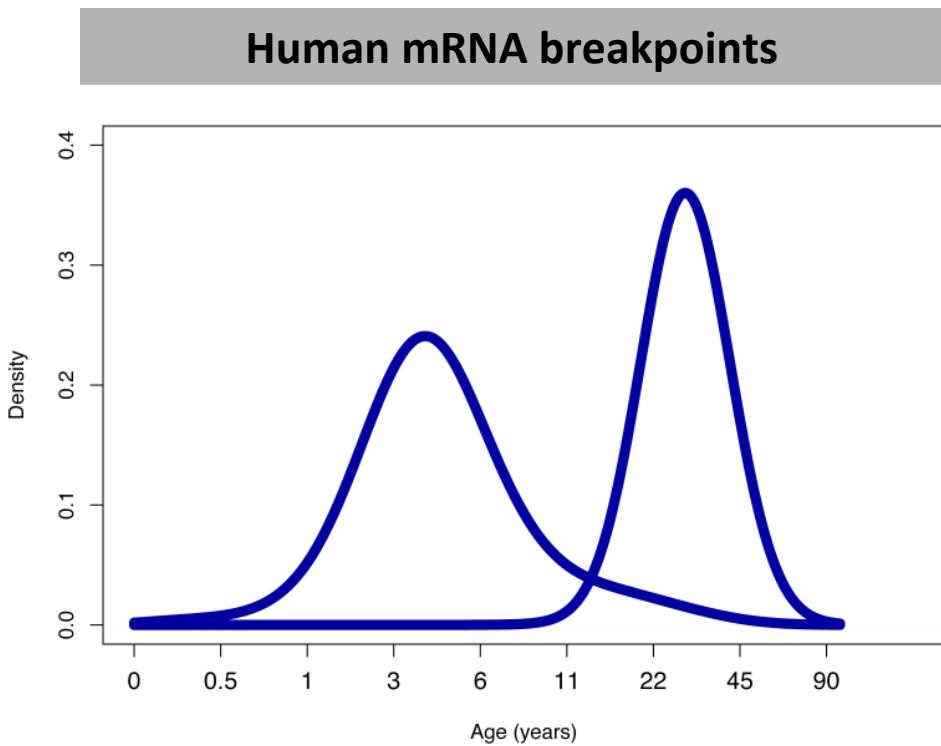
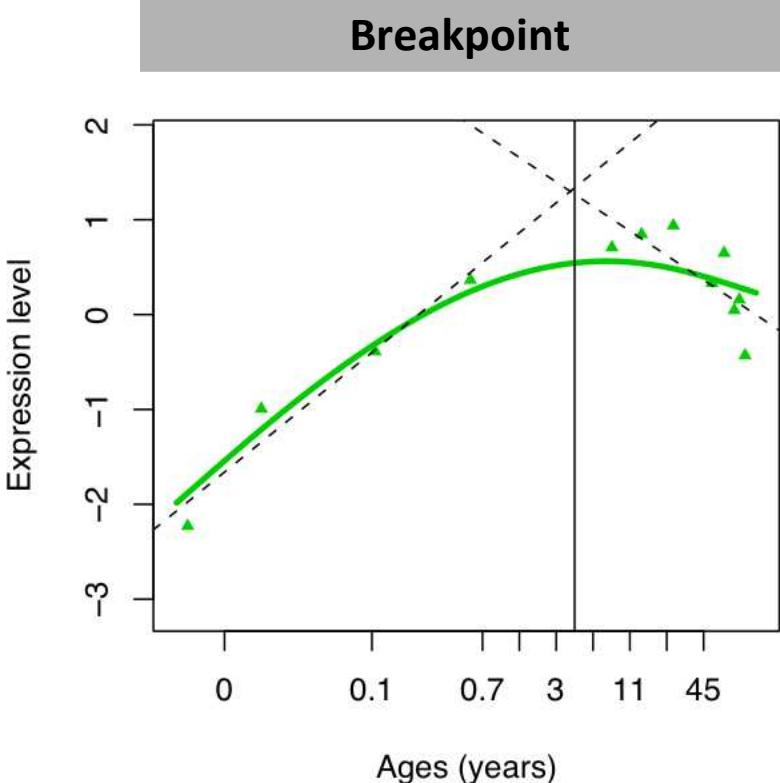
Human mRNA | sets 1&2



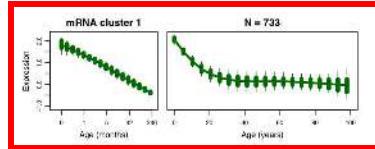
Human aging | expression patterns



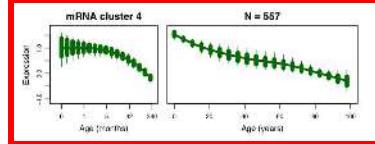
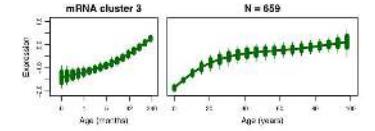
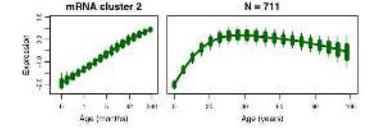
Human aging | expression “breakpoints”



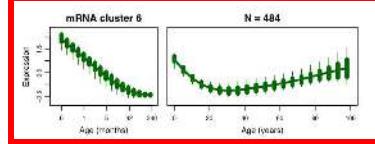
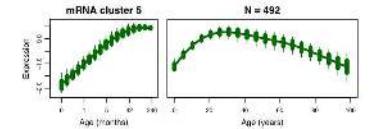
Human aging | expression “breakpoints” and gene functions



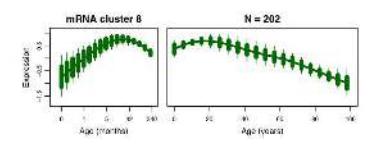
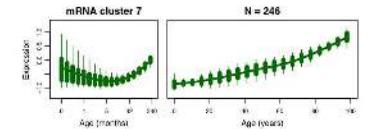
■ Nervous system development ↗ ~25 years



■ Neuron development ↗ ~5 years

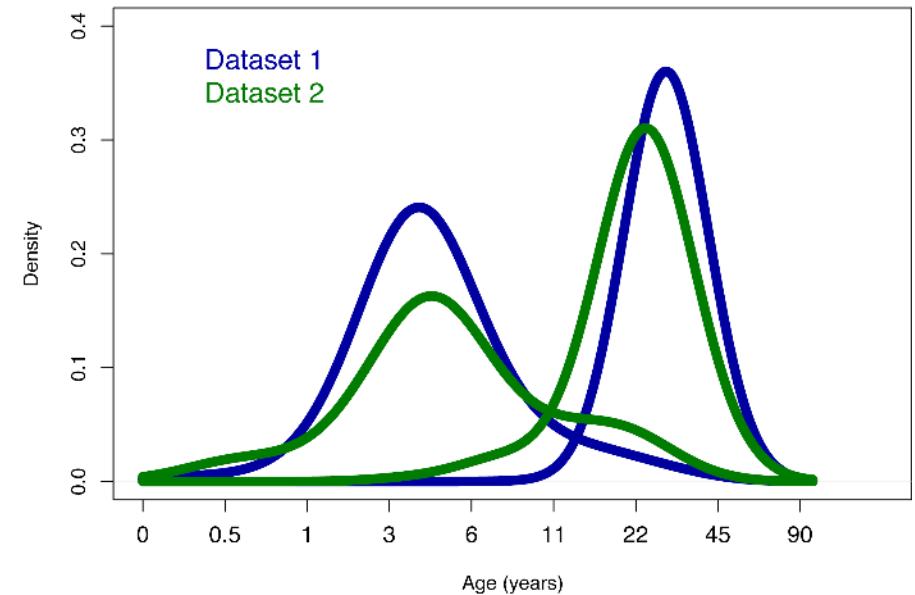


■ Chromatin modification ↗ ~25 years

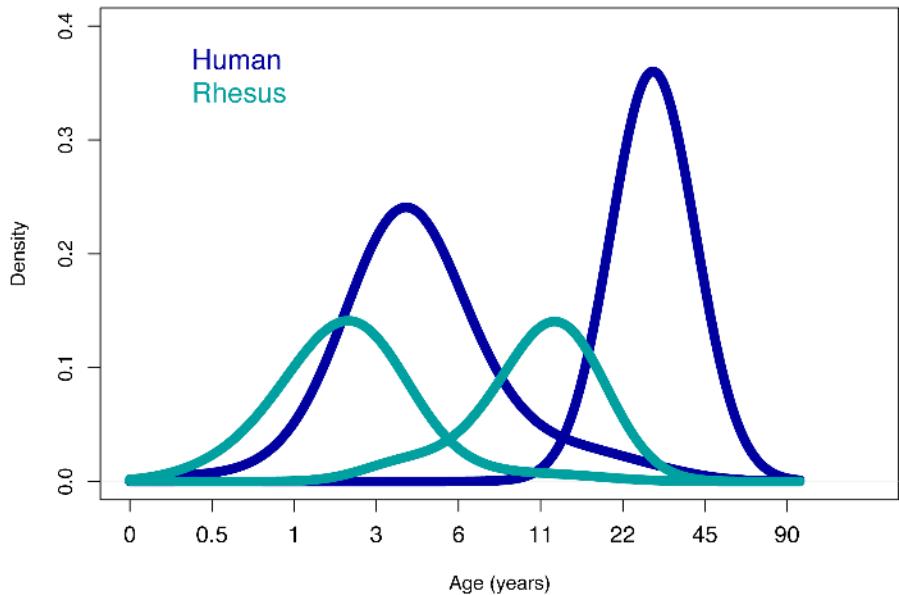


Human aging | expression “breakpoints”

Human mRNA | two datasets



Human & Macaque mRNA

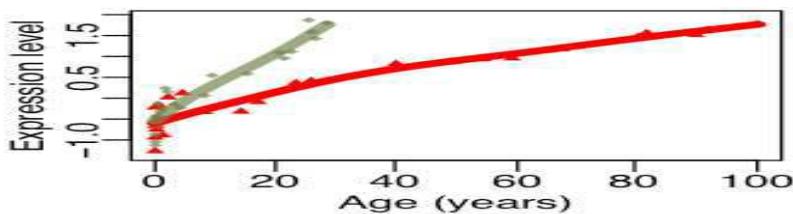


Human aging | rate of gene expression changes reflects species' lifespan

mRNA

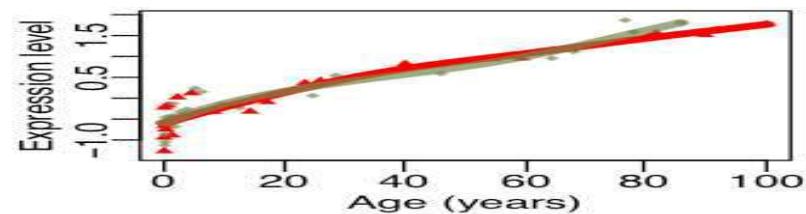
Maximum lifespan:

humans 120 years
macaques 40 years

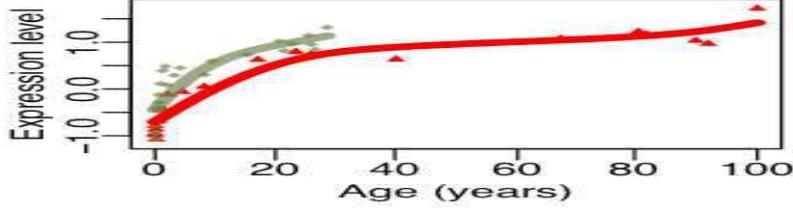


Maximum lifespan:

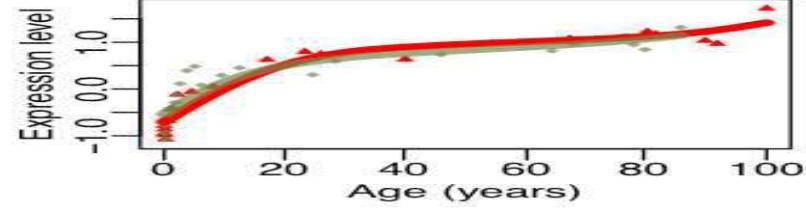
humans 120 years
macaques 120 years



N=5

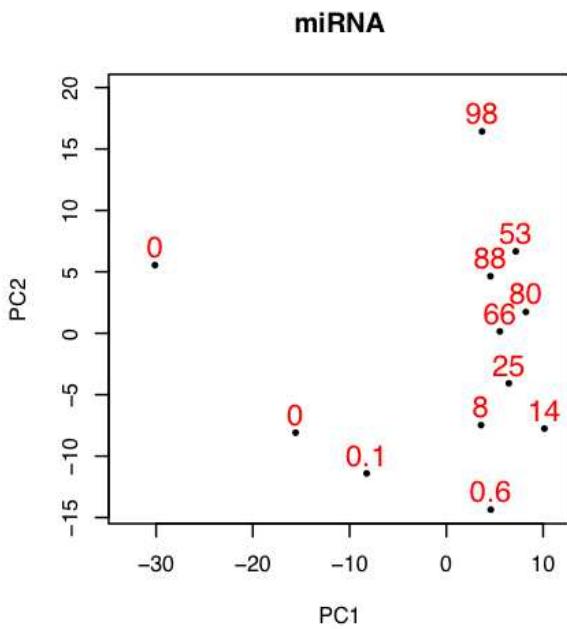


N=5

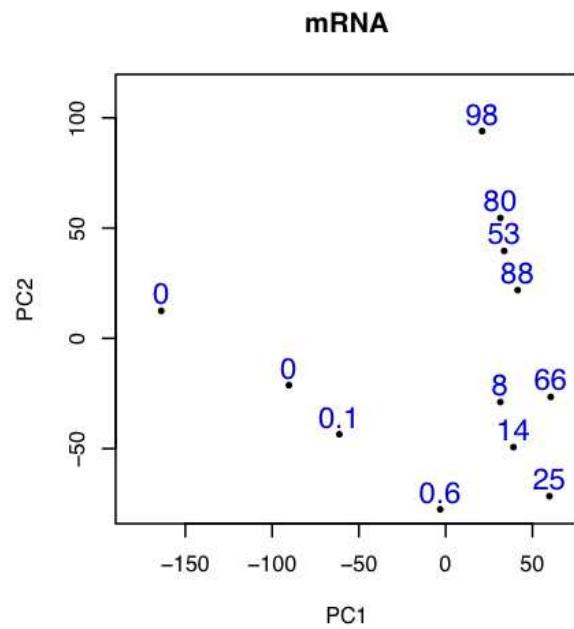


Human aging | miRNA expression

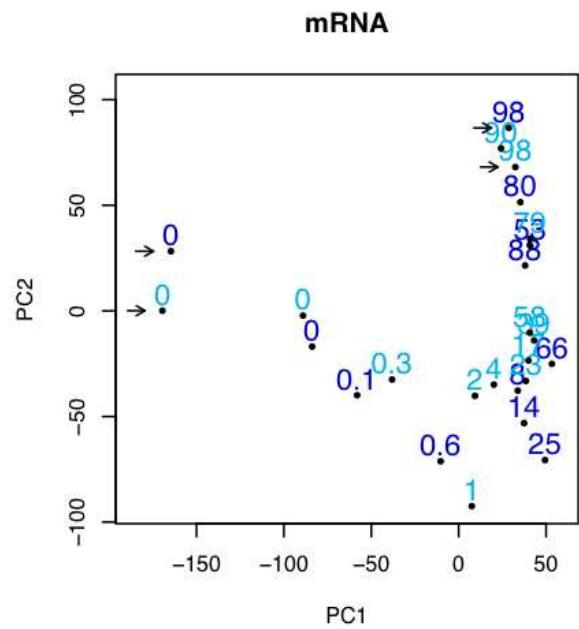
Human miRNA | 1



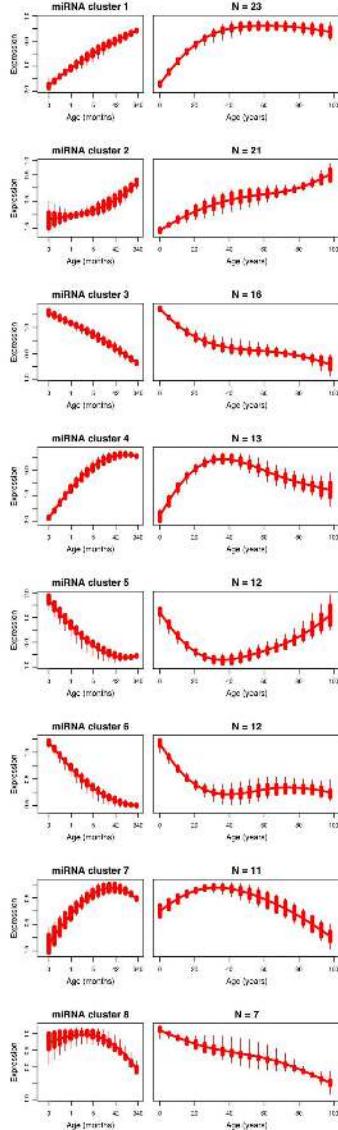
Human mRNA | 1



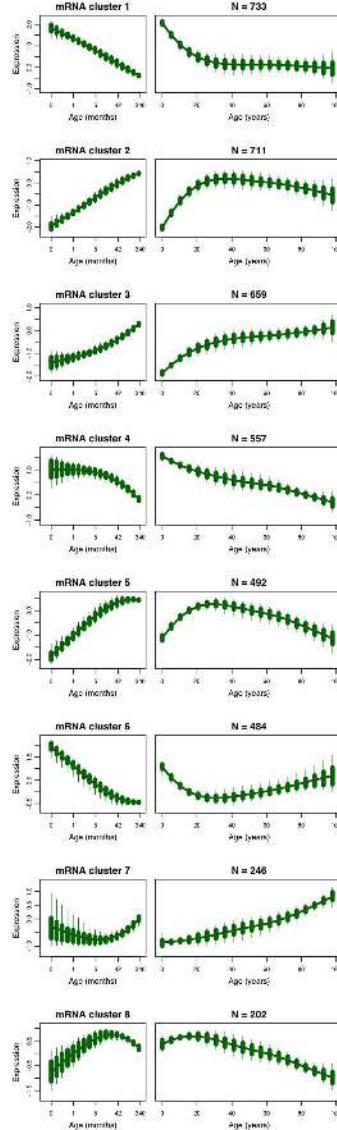
Human mRNA | 1&2



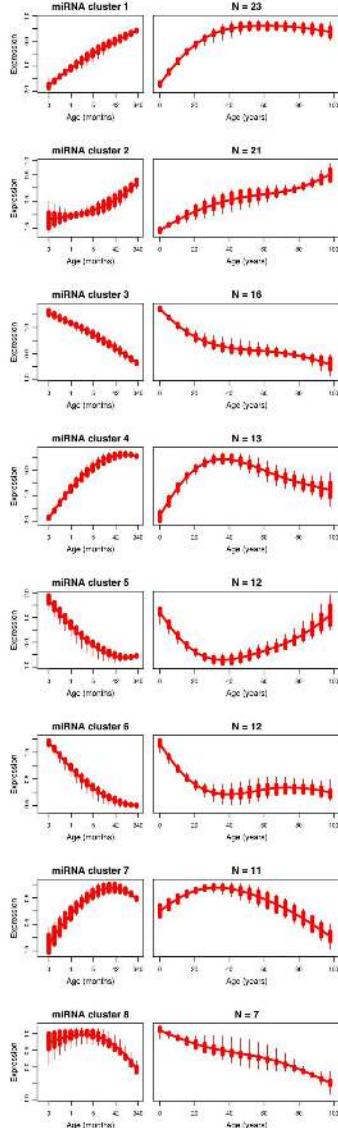
miRNA



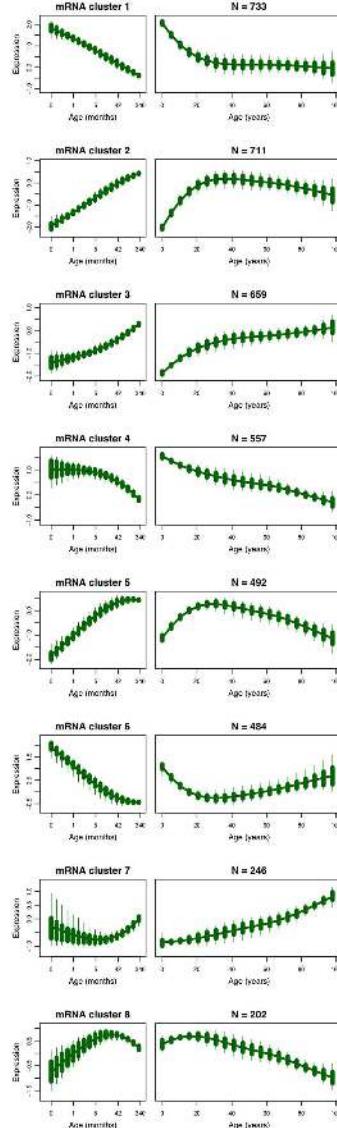
mRNA



miRNA



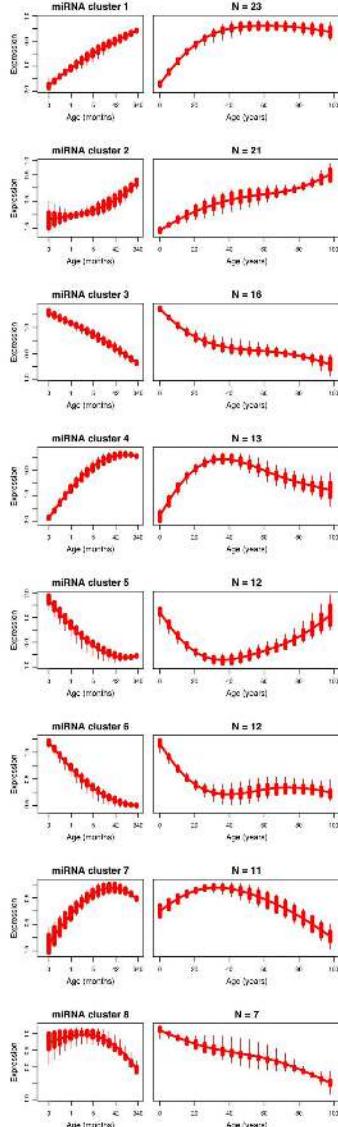
mRNA



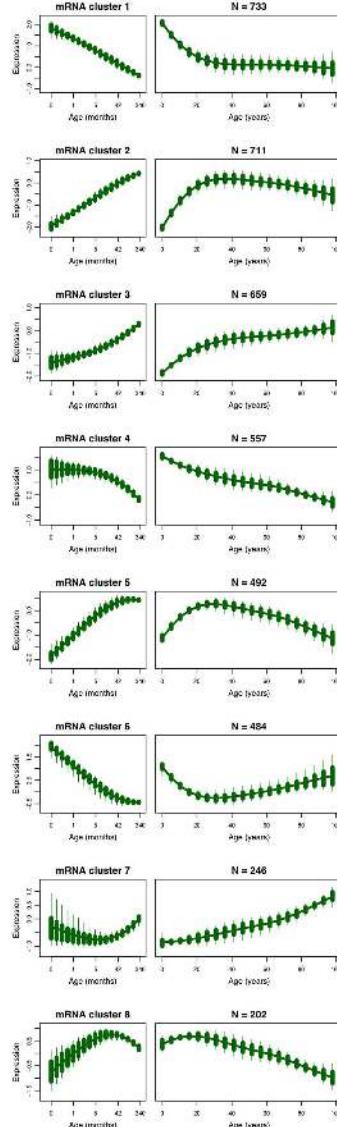
Regulation of mRNA

- microRNA
- Transcription Factors

miRNA



mRNA



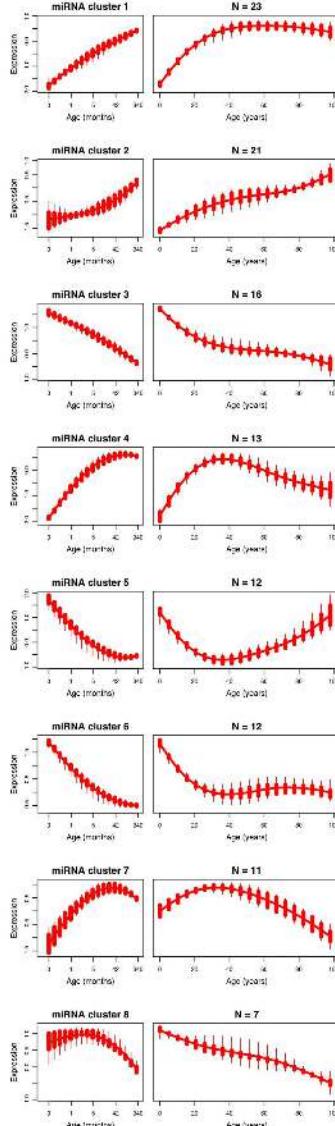
Regulation of mRNA

- microRNA
- Transcription Factors (TFs)

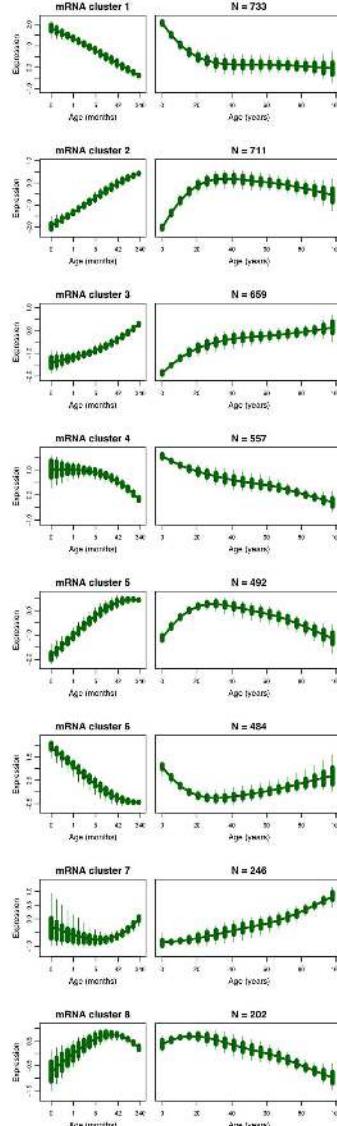


Excess of miRNA/TF target genes

miRNA

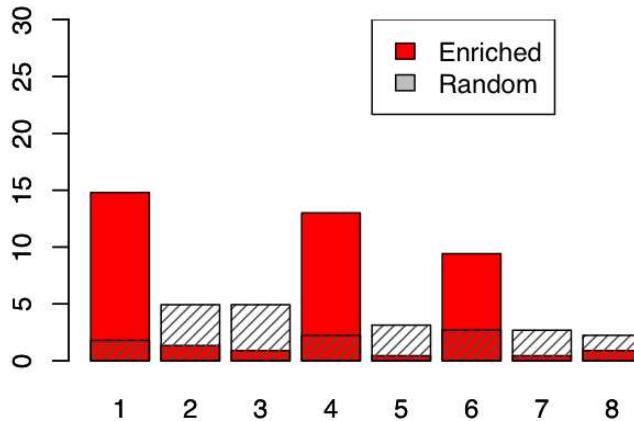


mRNA



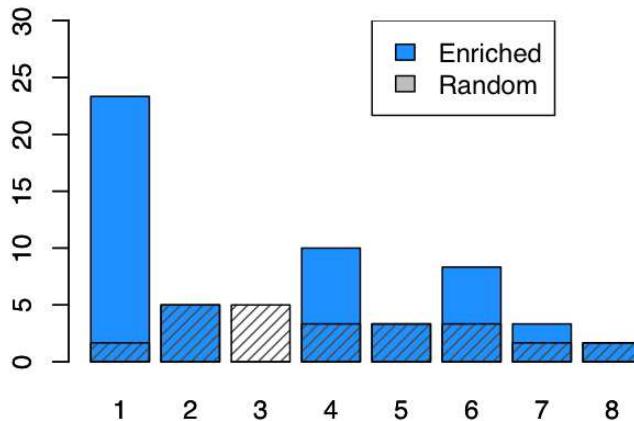
miRNA/TF target genes

Enrichment in miRNA targets



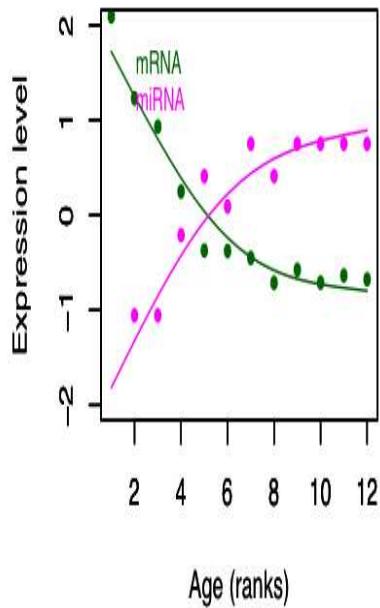
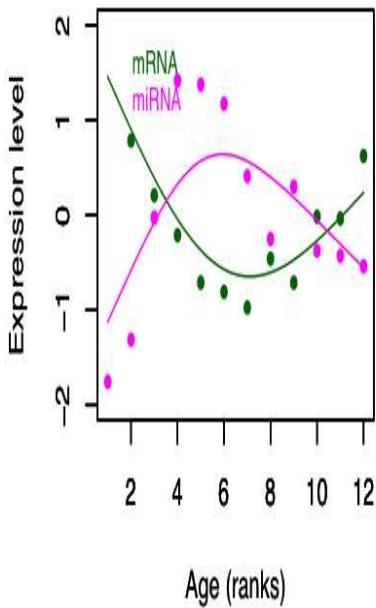
total 223 miRNAs

Enrichment in TF targets



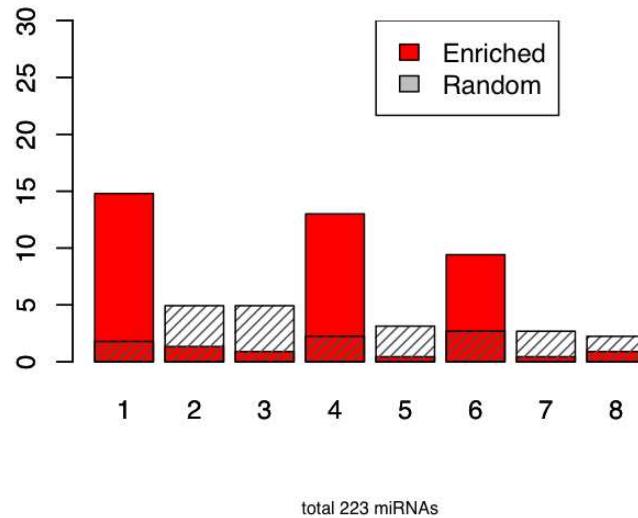
total 60 TFs

miRNA-target gene expression

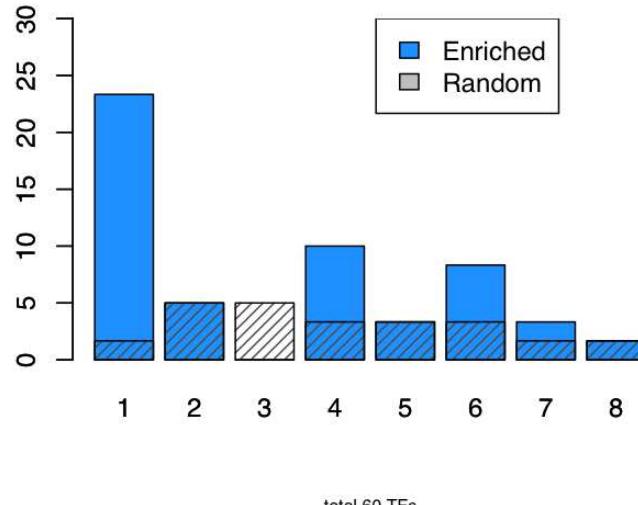


miRNA/TF target genes

Enrichment in miRNA targets



Enrichment in TF targets



Human

Rhesus macaque

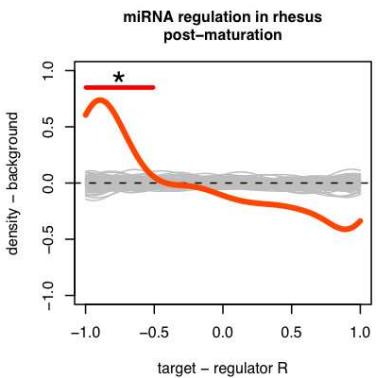
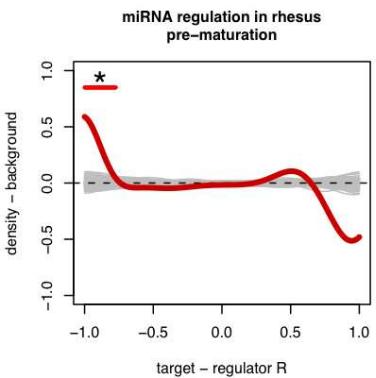
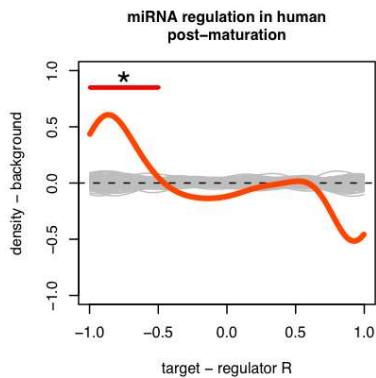
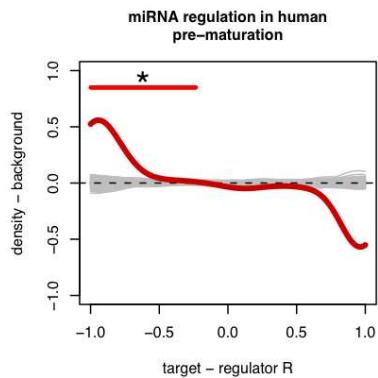
0-30 years

30-98 years

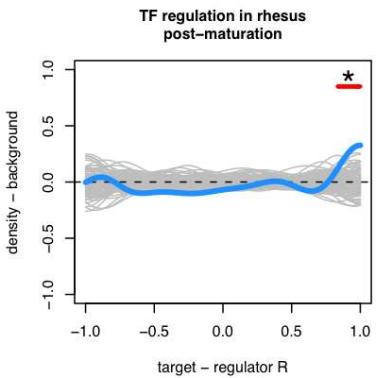
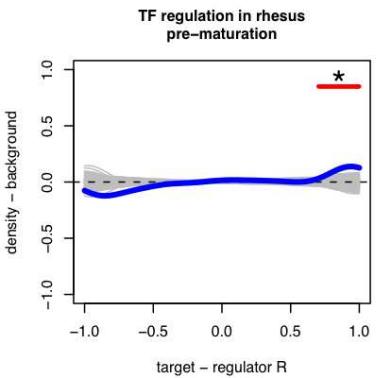
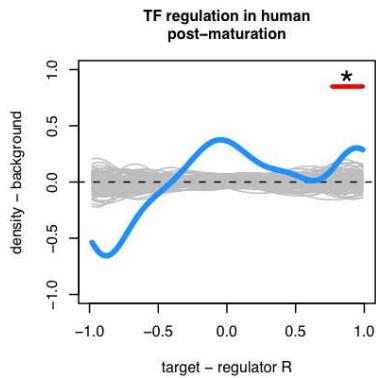
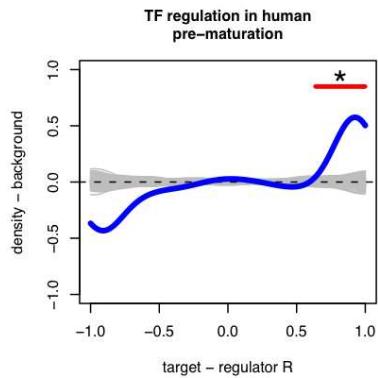
0-10 years

10-28 years

miRNA

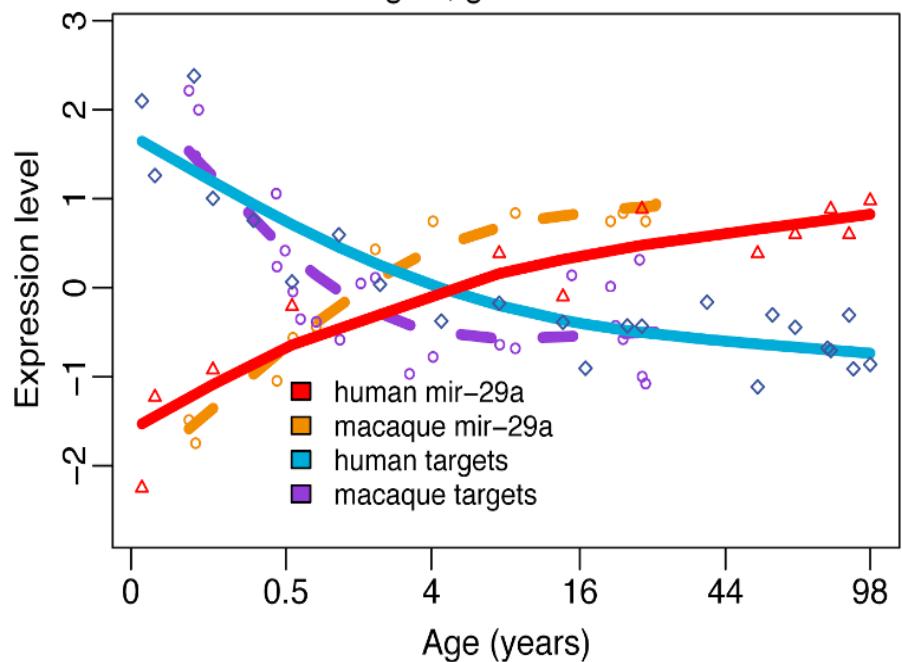


TF

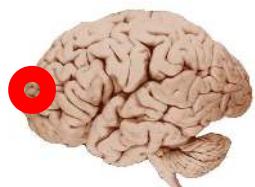
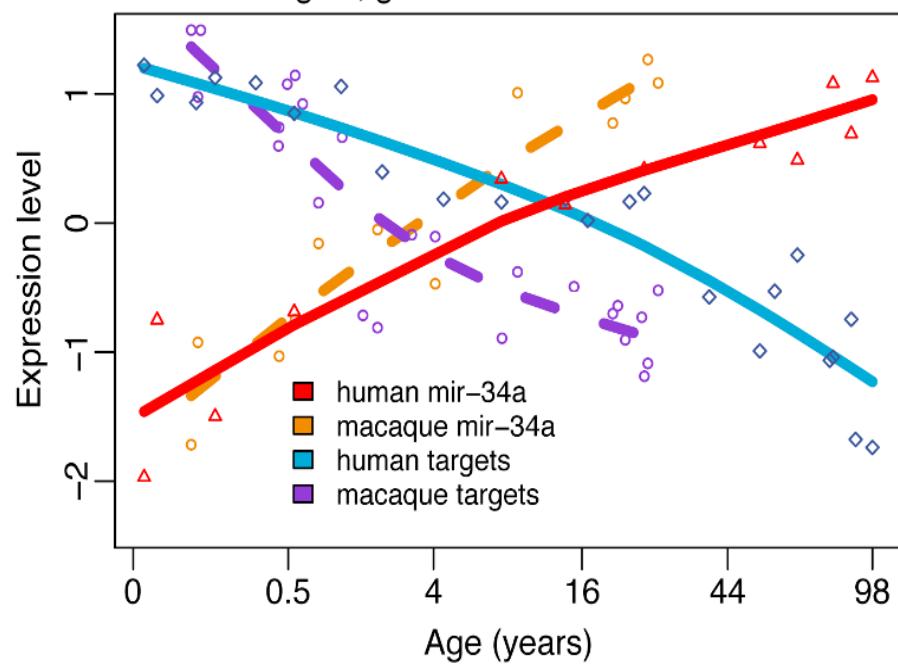


Human aging | developmental regulators might drive aging

Cancer-related targets, gr. 1



Neuronal targets, gr. 4



microRNA

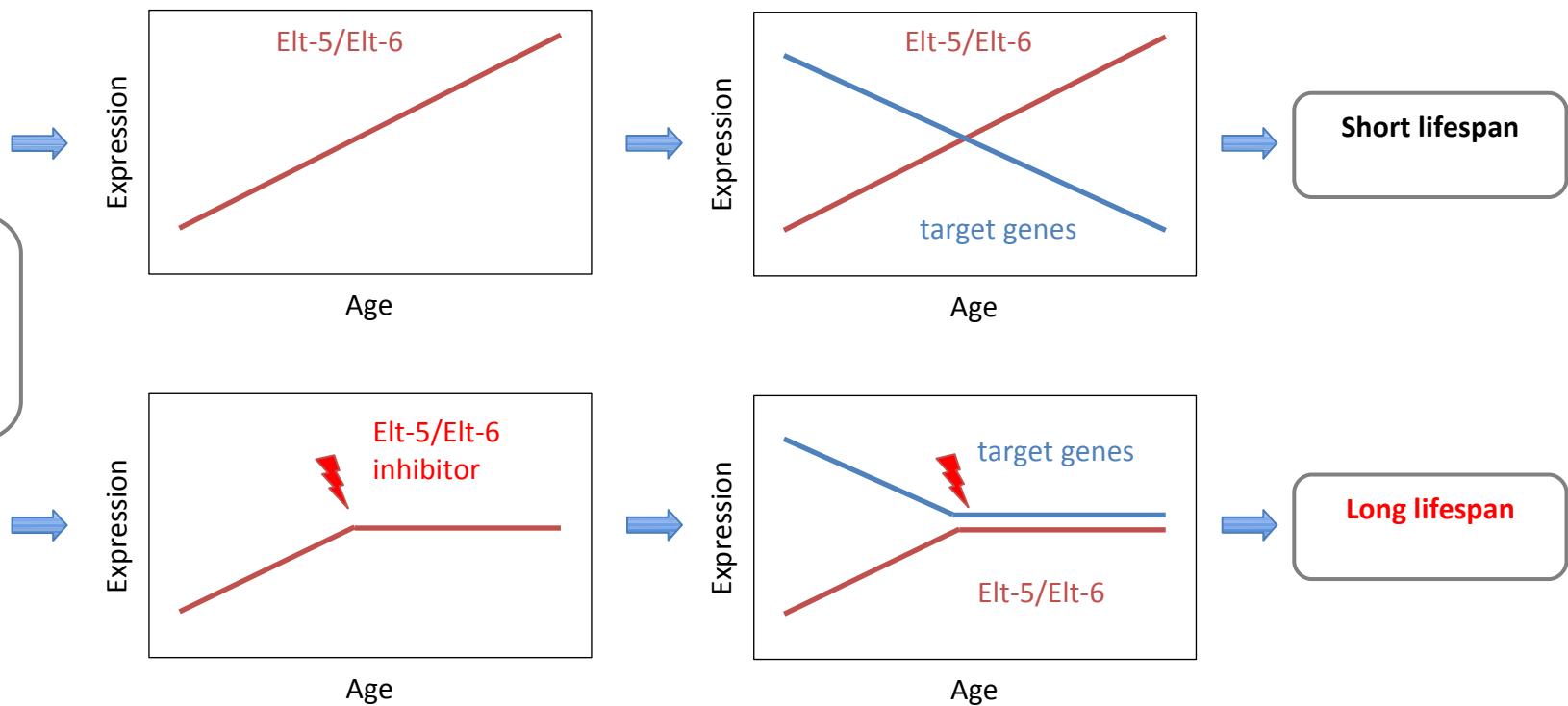
mRNA

Binding site
enrichment

Expression level
correlation

Aging regulation | model organisms

Experiments in *C. elegans* demonstrate that regulatory intervention during aging can extend lifespan



Budovskaya et al *Cell* 2008

Conclusions

Runaway developmental regulation may drive aging process

Main collaborations | research

short RNA



long RNA



Proteins



Metabolites



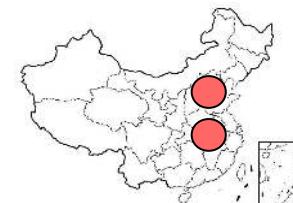
Phenotype



MPI Golm



MDC Berlin
MPI Leipzig



BIG
SIBS



Beijing Chip
Center



SIBS Proteomics
Center



SIBS Institute of
Neuroscience

Main collaborations | sample collection



> 600 individuals

Holland
USA
China
Germany



> 80 individuals

Germany
Japan
USA



> 100 individuals

China
USA
Japan



Lab members

postdocs



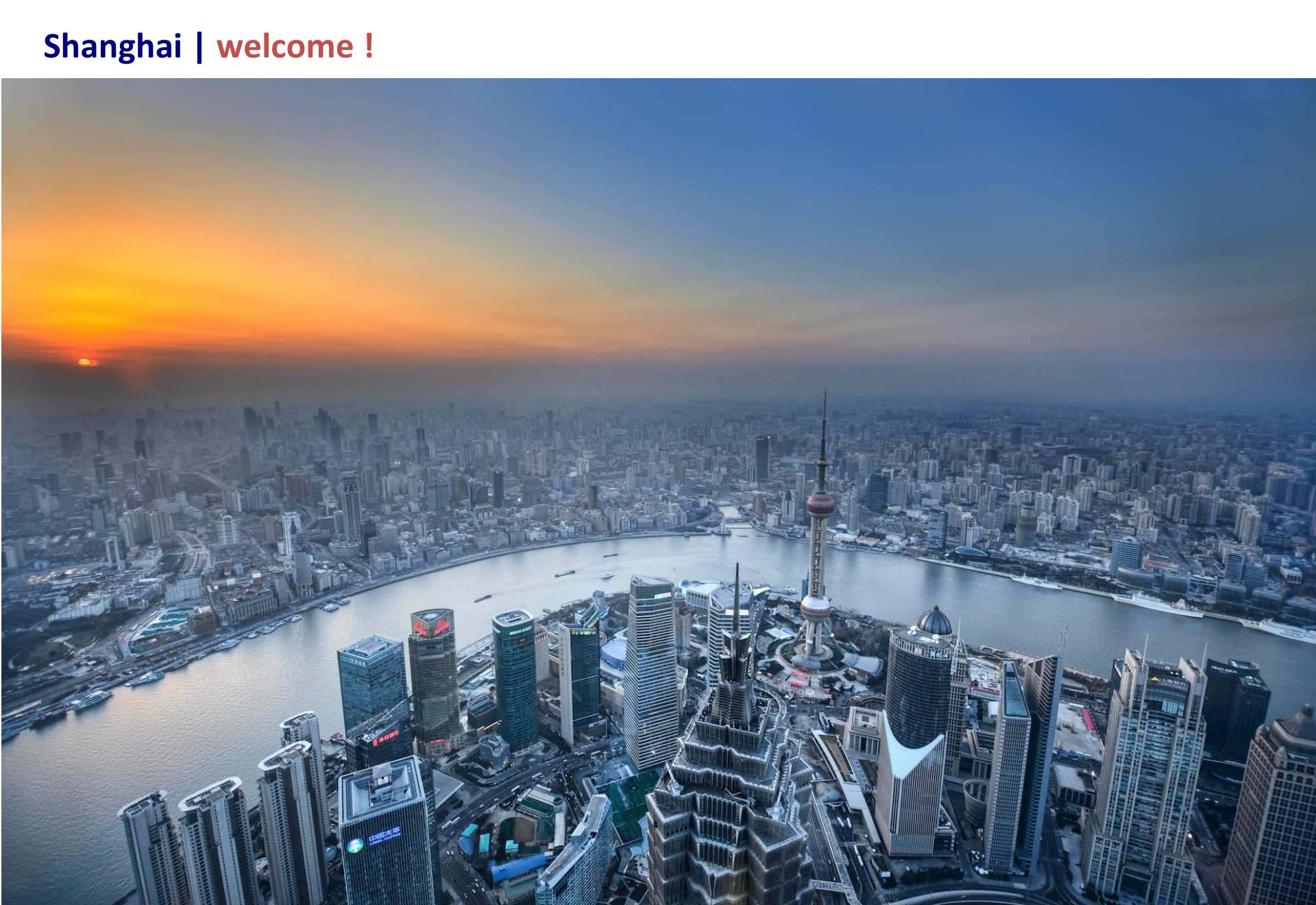
research assistants



students



Shanghai | welcome !



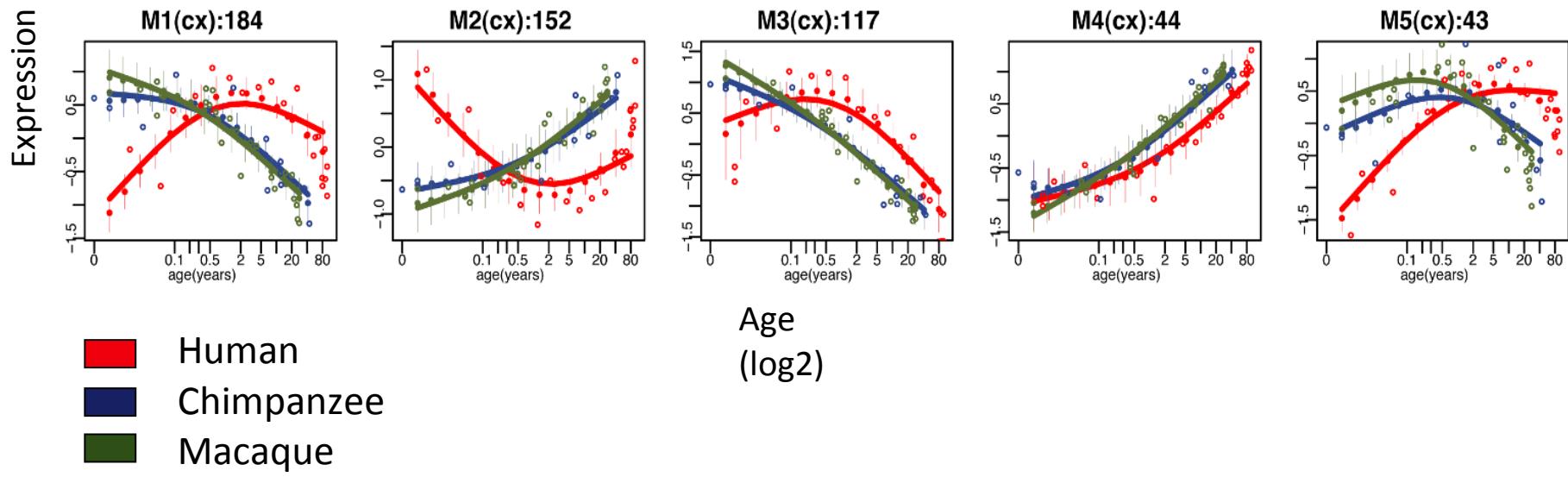
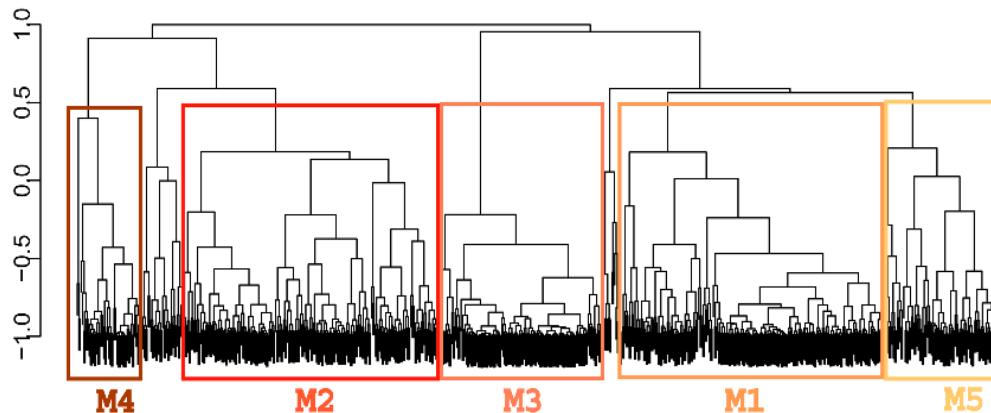
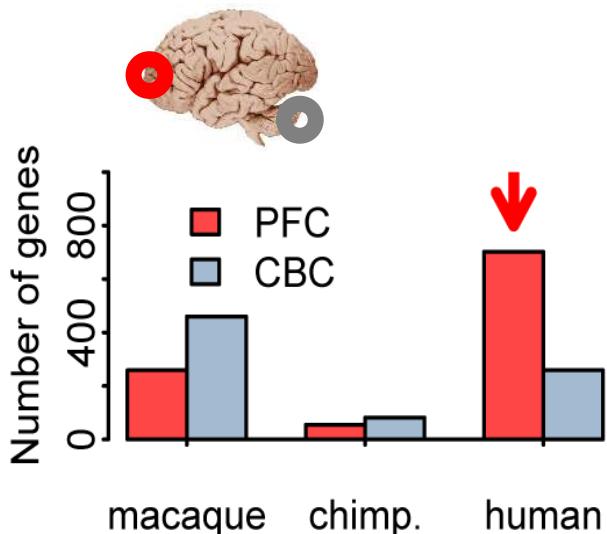
14.8.13



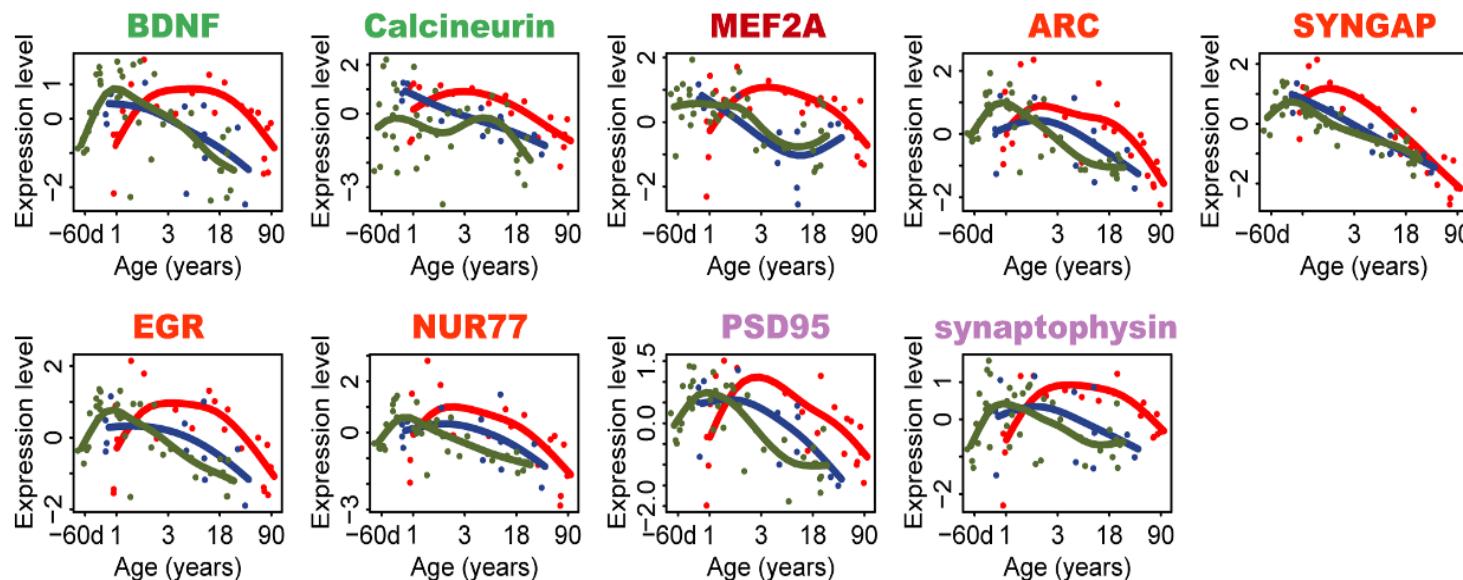
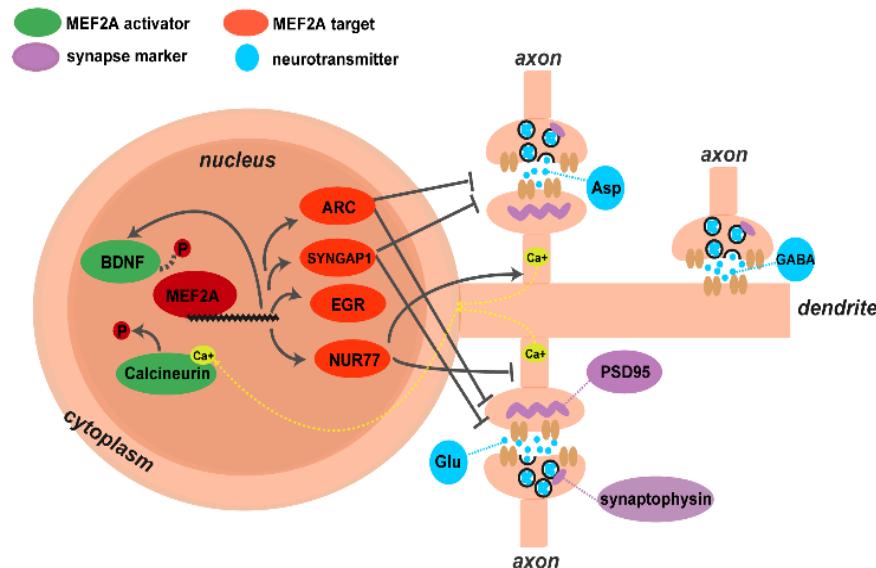
Thank you!

Human-specific expression

mRNA



Human-specific changes | model



Conclusions

Genetic flow from Neanderthals may have shaped contemporary human phenotypes

macaque



chimpanzee



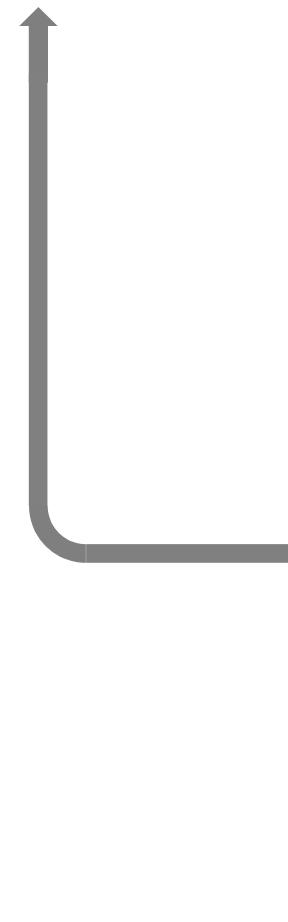
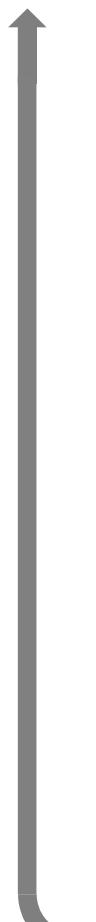
modern humans



neanderthal



14.8.13



↑

0.03 M

0.5 M

6-7 M

25 M





Long non-coding RNA in human brain

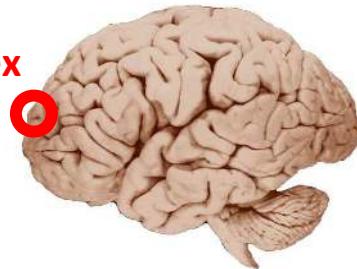
Experiment

birth
↓

postnatal development



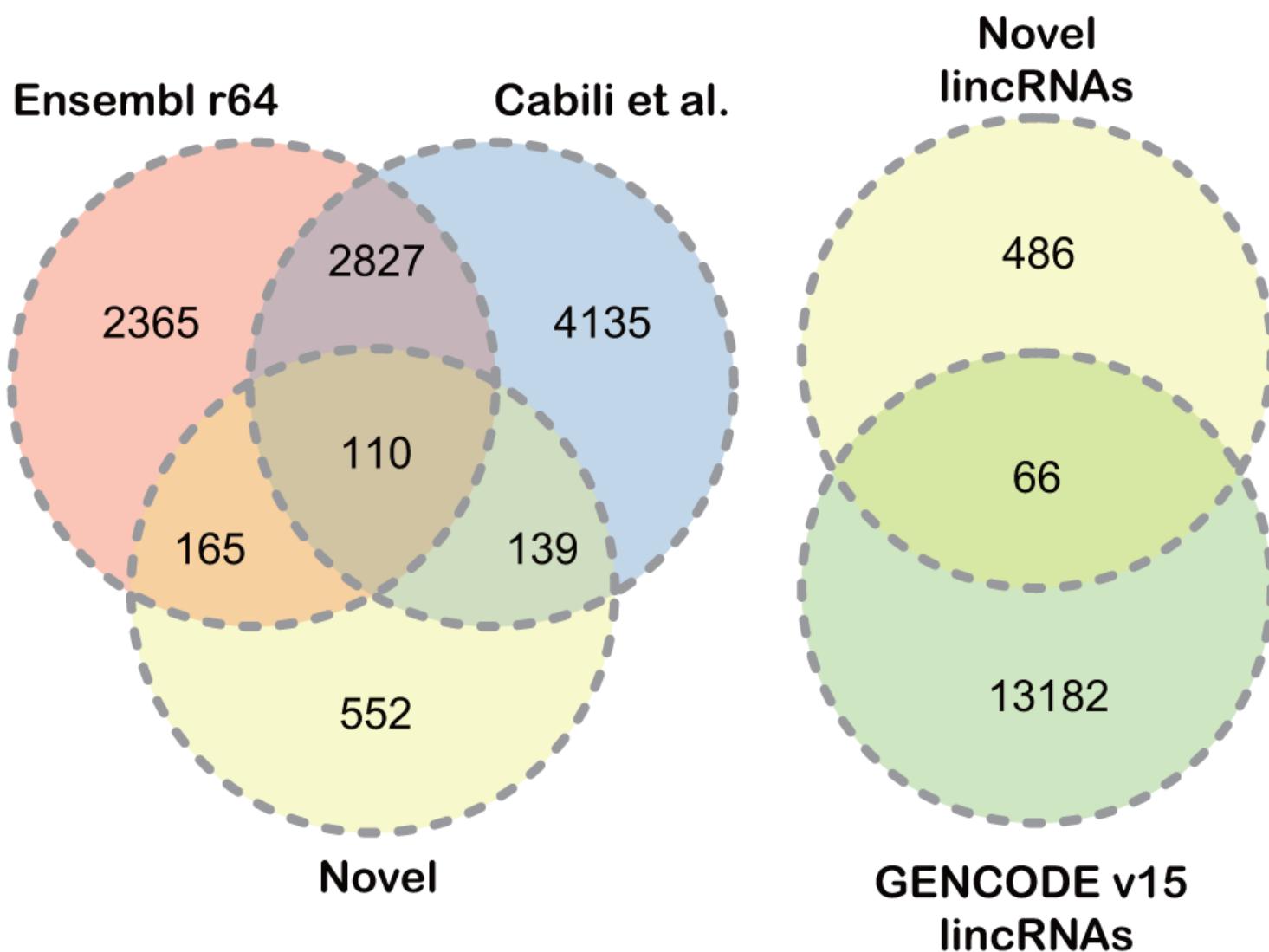
prefrontal cortex



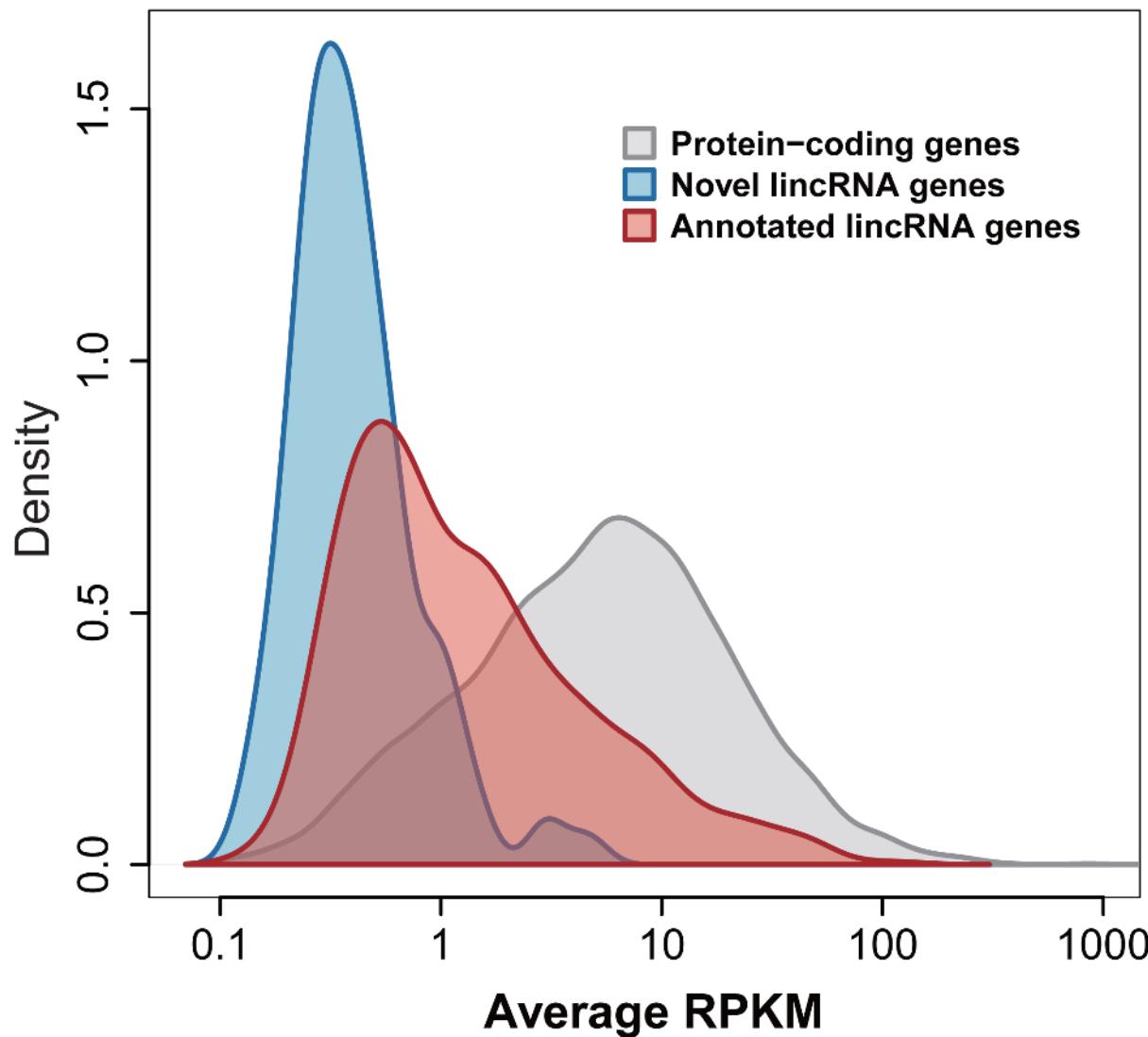
RNA-seq



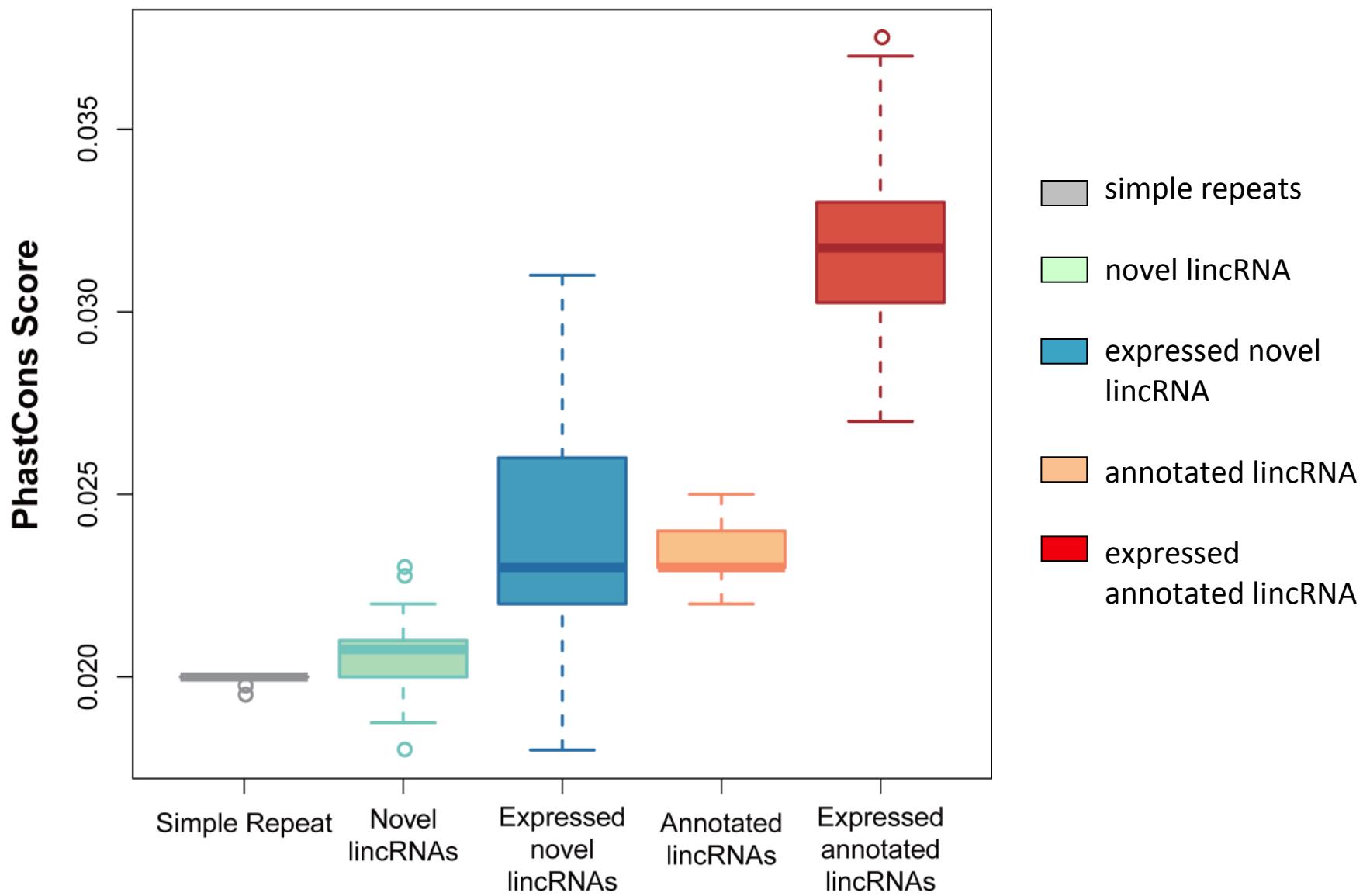
lincRNA numbers



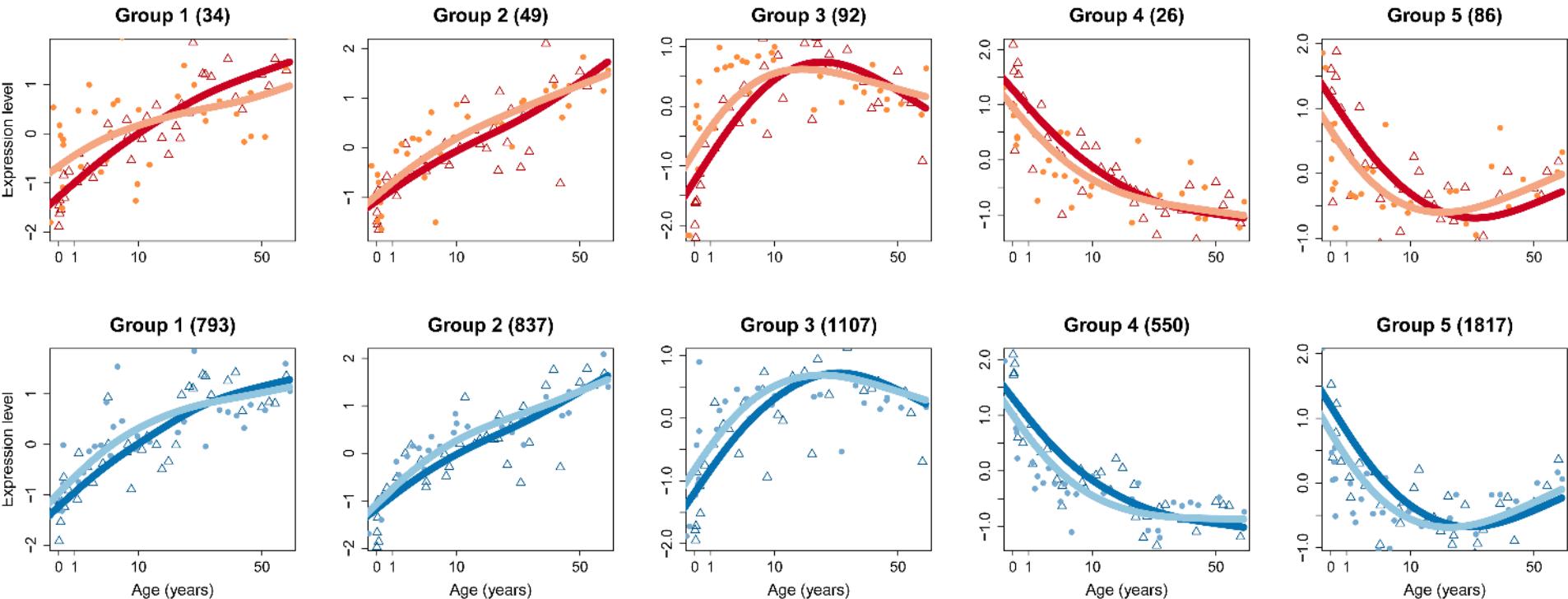
lincRNA expression levels



lincRNA sequence conservation



lincRNA expression conservation

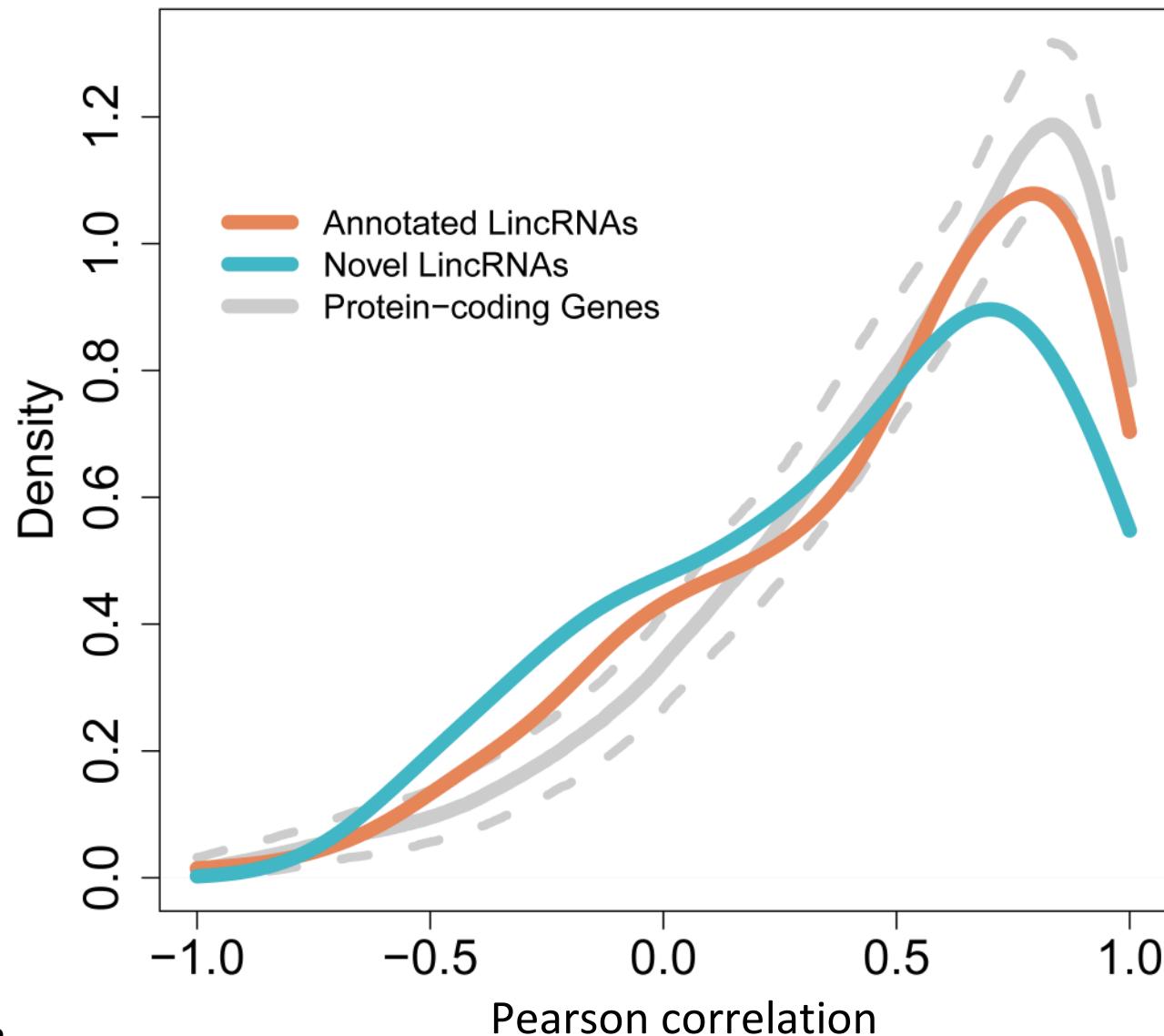


protein-coding
non-coding

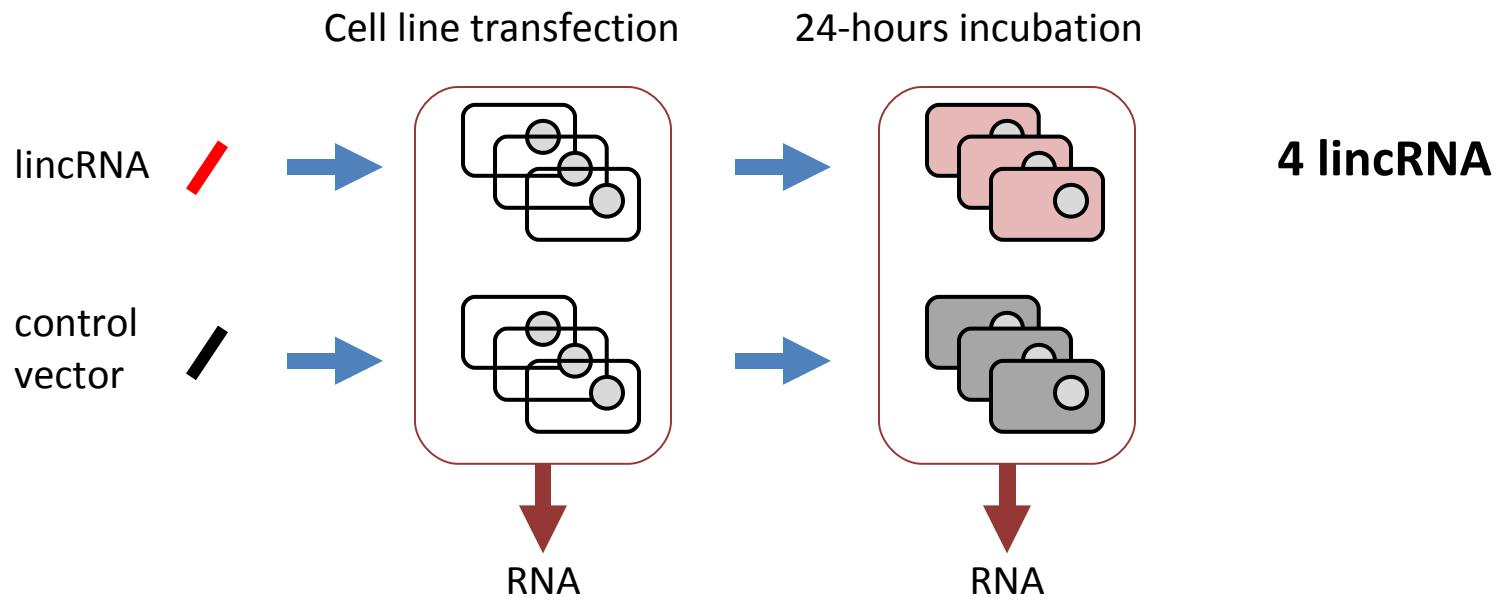
protein-coding
non-coding

14.8.13

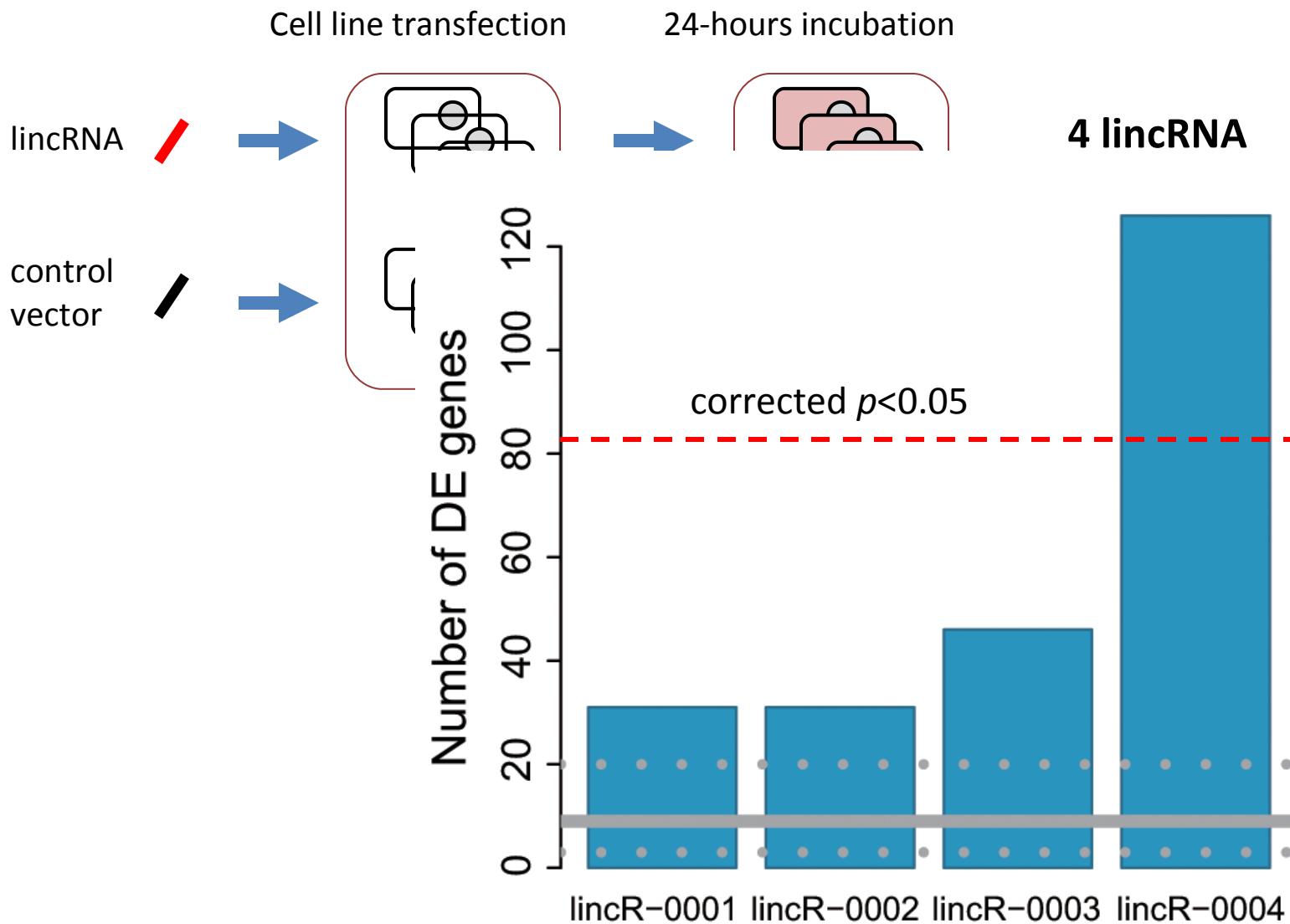
lincRNA expression conservation



lincRNA overexpression in a cell line



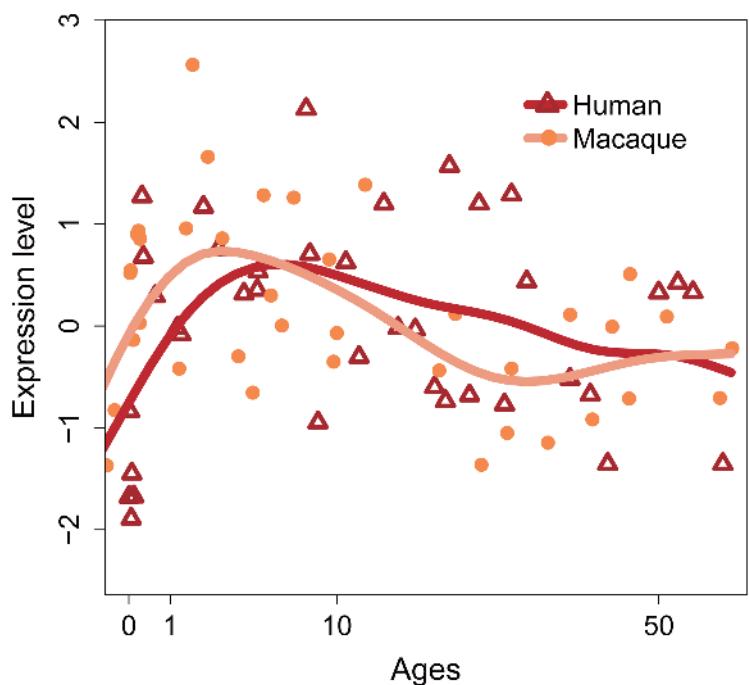
lincRNA overexpression in a cell line



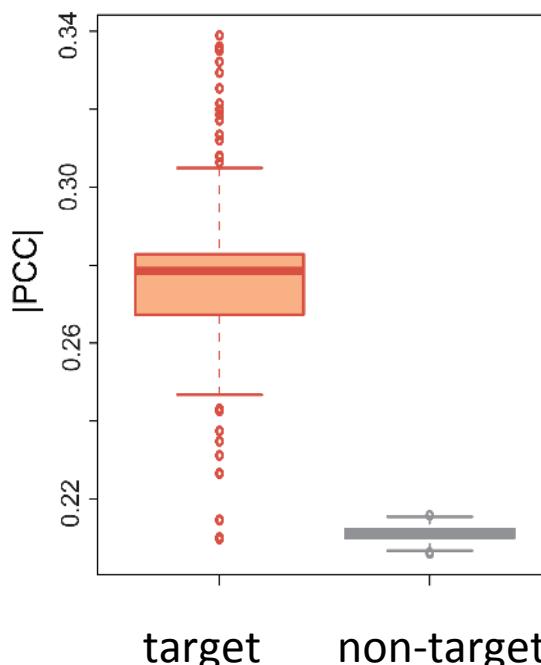
lincR-0004 targets in brain development



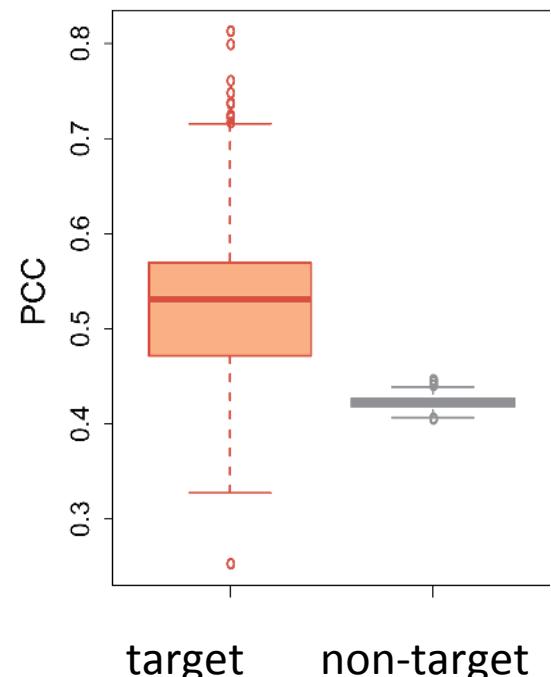
lincRNA expression



correlation with targets



expression conservation



Conclusions

lncRNA are not conserved on the sequence level, but expression patterns in brain development are conserved

Overexpression of lncRNA not always results in [molecular]phenotype