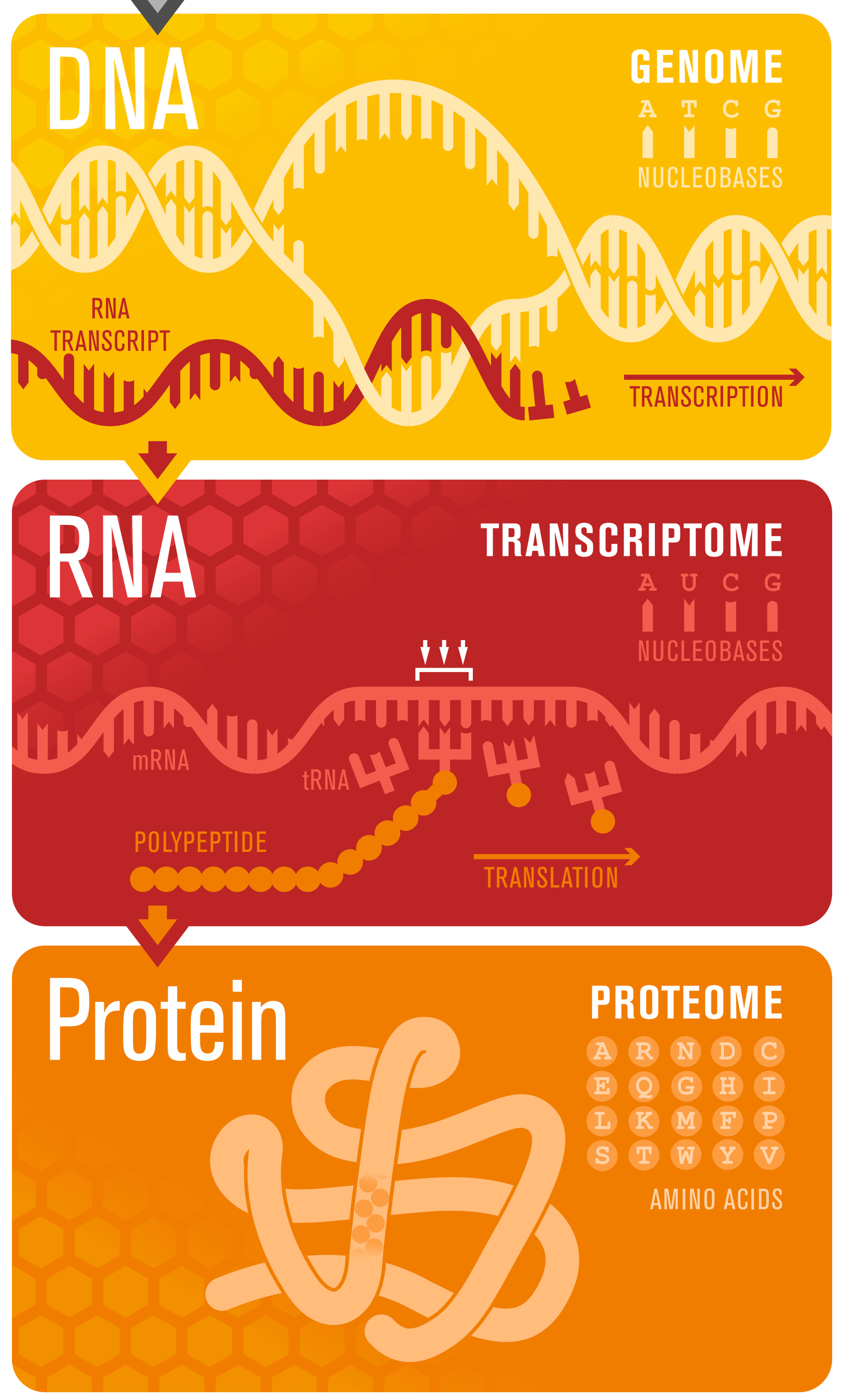
THE HUMAN TRANSCRIPTOME

The human genome consists of DNA, a molecule that contains the instructions needed to build and maintain cells. These instructions are spelled out in the form of four "base pairs", organized into approximately 20,000 protein-coding genes. For the instructions to be carried out, DNA must be "read" and transcribed into RNA transcripts. The transcriptome is a collection of all the transcripts present in a cell. Here, we focus on the protein-coding transcriptome to explore when and where each transcript and the corresponding protein is present in the various cells.

molecular systems biology

The central dogma in molecular biology

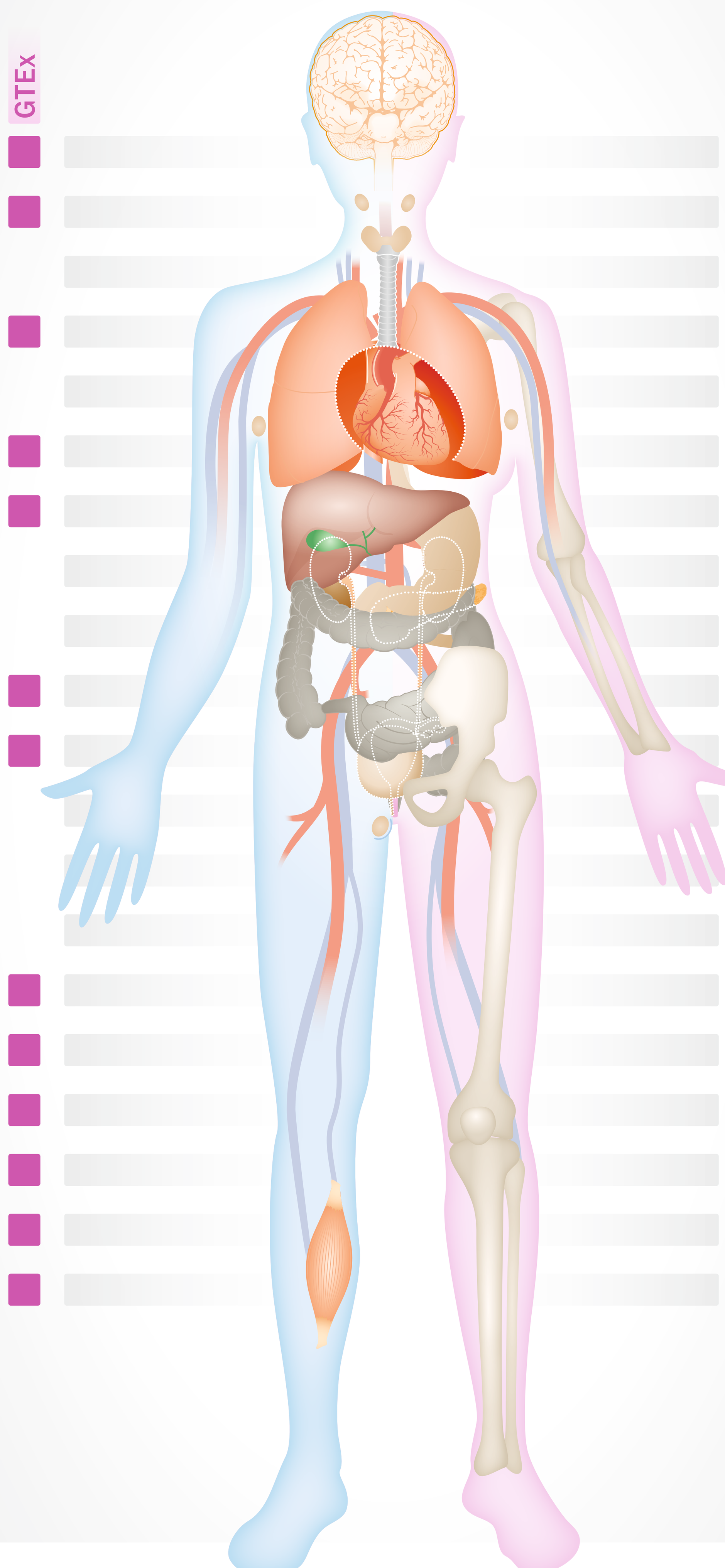
The central dogma of molecular biology explains that DNA codes for RNA, which codes for proteins. DNA is the molecule of heredity that passes from parents to offspring. It contains the instructions for building RNA and proteins, which make up the structure of the body and carry out most of its functions.



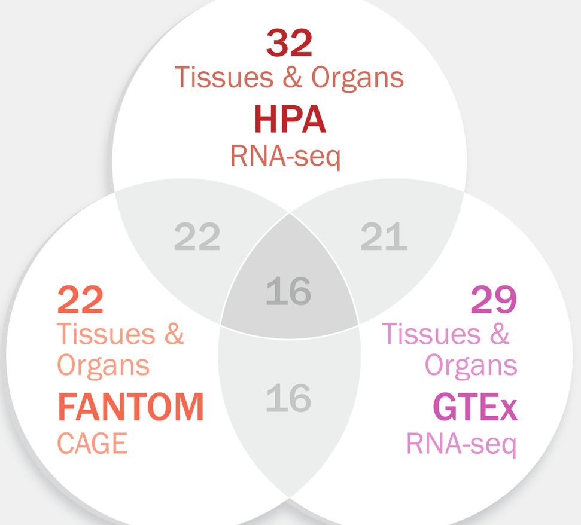
Global transcriptomics analysis of human tissues and organs

Overview of the tissues and organs analyzed using RNA-seq by the Human Protein Atlas consortium (HPA, dark red), using cap analysis gene expression (CAGE) by the FANTOM consortium (light red), and using RNA-seq by the genome-based tissue expression consortium (GTEx, pink). Altogether, 22 tissues and organs were studied by both the HPA and FANTOM, while 21 tissues overlapped between the HPA and GTEx datasets.

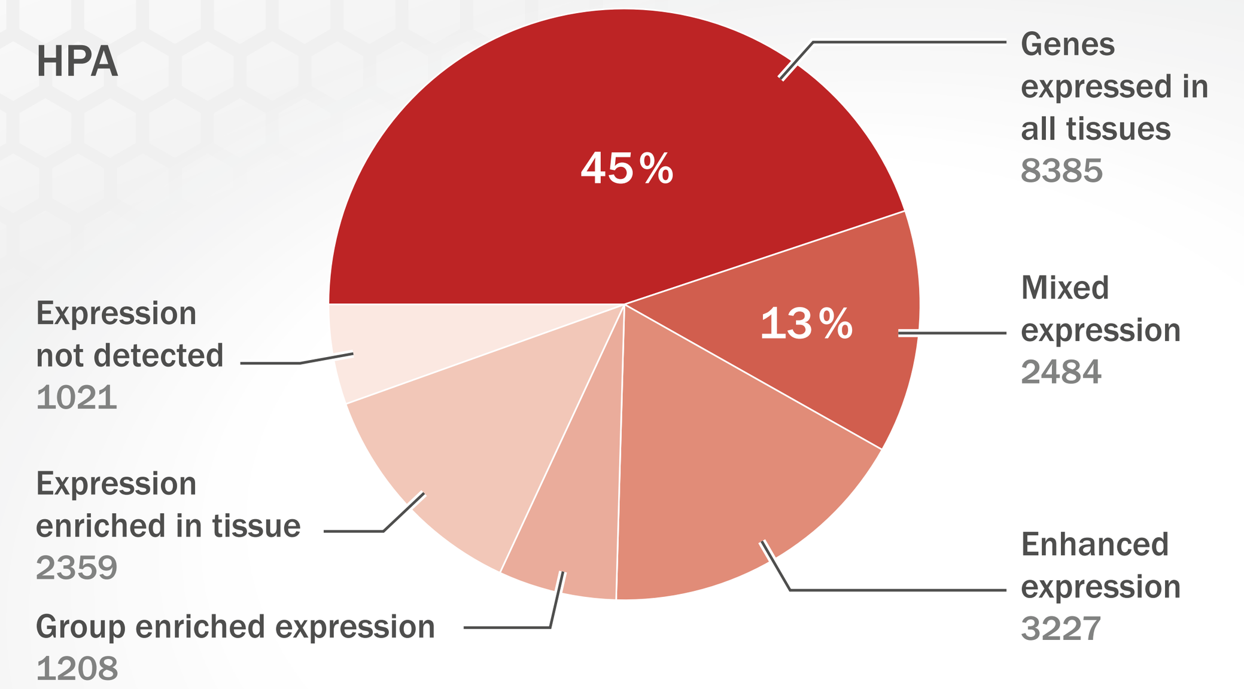
Tissue	HPA	FANTOM	GTEx
Cerebrum	■	■	■
Pituitary			■
Salivary gland	■	■	
Lung	■	■	■
Lymph node	■	■	
Liver	■	■	■
Adrenal gland	■		■
Gallbladder	■	■	
Duodenum	■		
Small intestine	■	■	■
Colon	■	■	■
Appendix	■	■	
Rectum	■		
Smooth muscle	■		
Prostate	■	■	■
Urinary bladder	■	■	■
Testis	■	■	■
Skeletal muscle	■		■
Adipose tissue	■	■	■
Skin	■		■

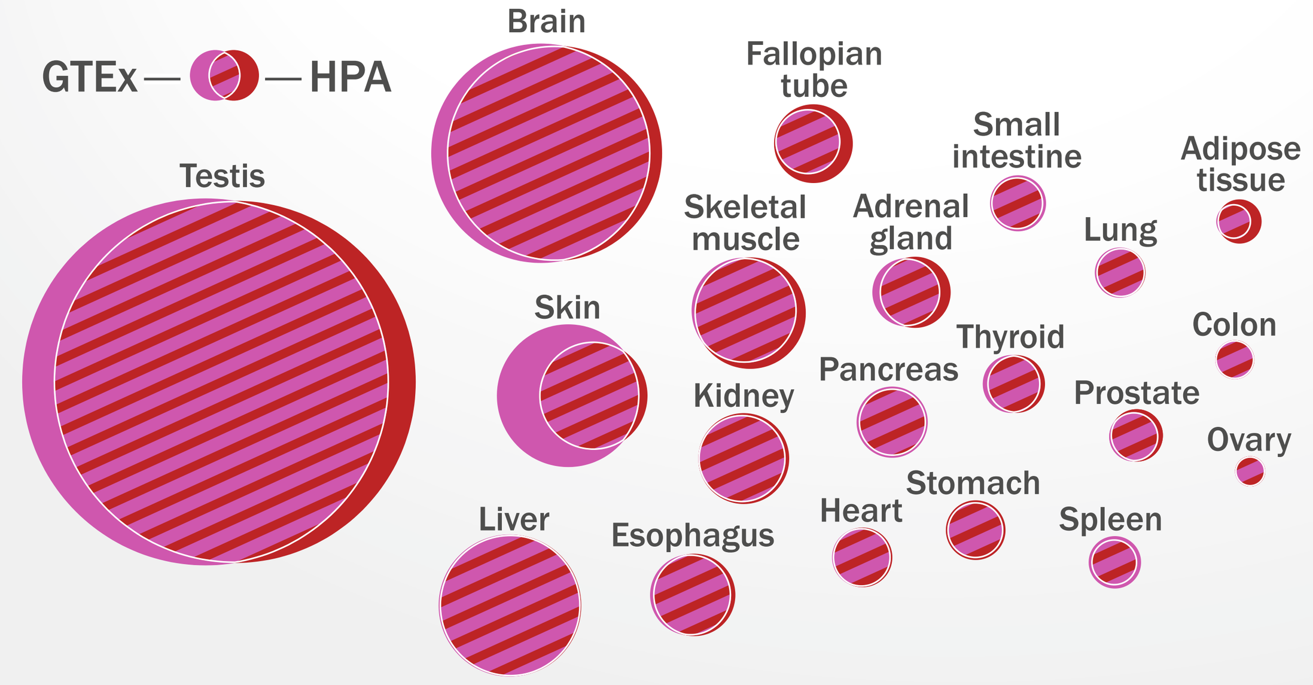


Tissue	HPA	FANTOM	GTEx
Cerebellum			■
Tonsil	■		
Thyroid gland	■	■	■
Esophagus	■	■	■
Heart muscle	■	■	■
Breast			■
Stomach	■		■
Spleen	■	■	■
Kidney	■	■	■
Pancreas	■	■	■
Fallopian tube	■		■
Ovary	■	■	■
Placenta	■	■	
Endometrium	■	■	
Cervix			■
Vagina			■
Bone marrow	■		
Blood			■
Artery			■
Nerve			■



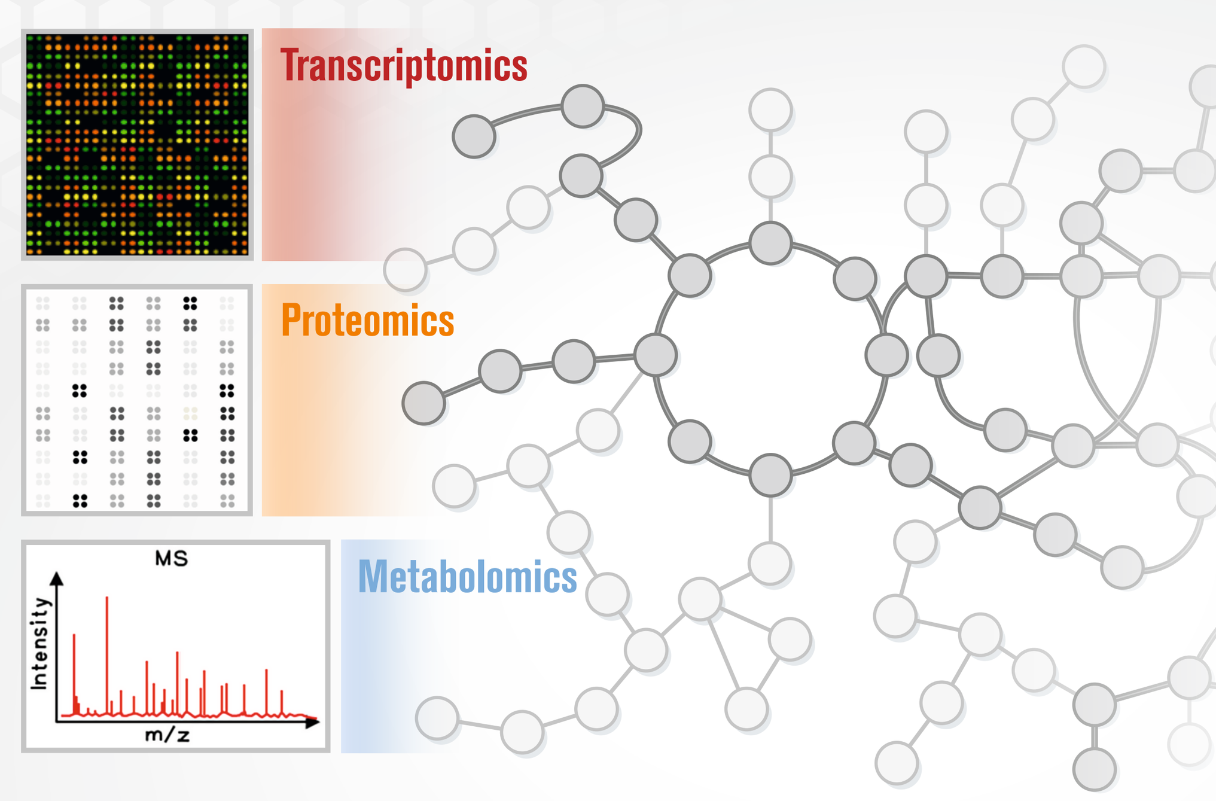
Classification of all human genes based on tissue expression





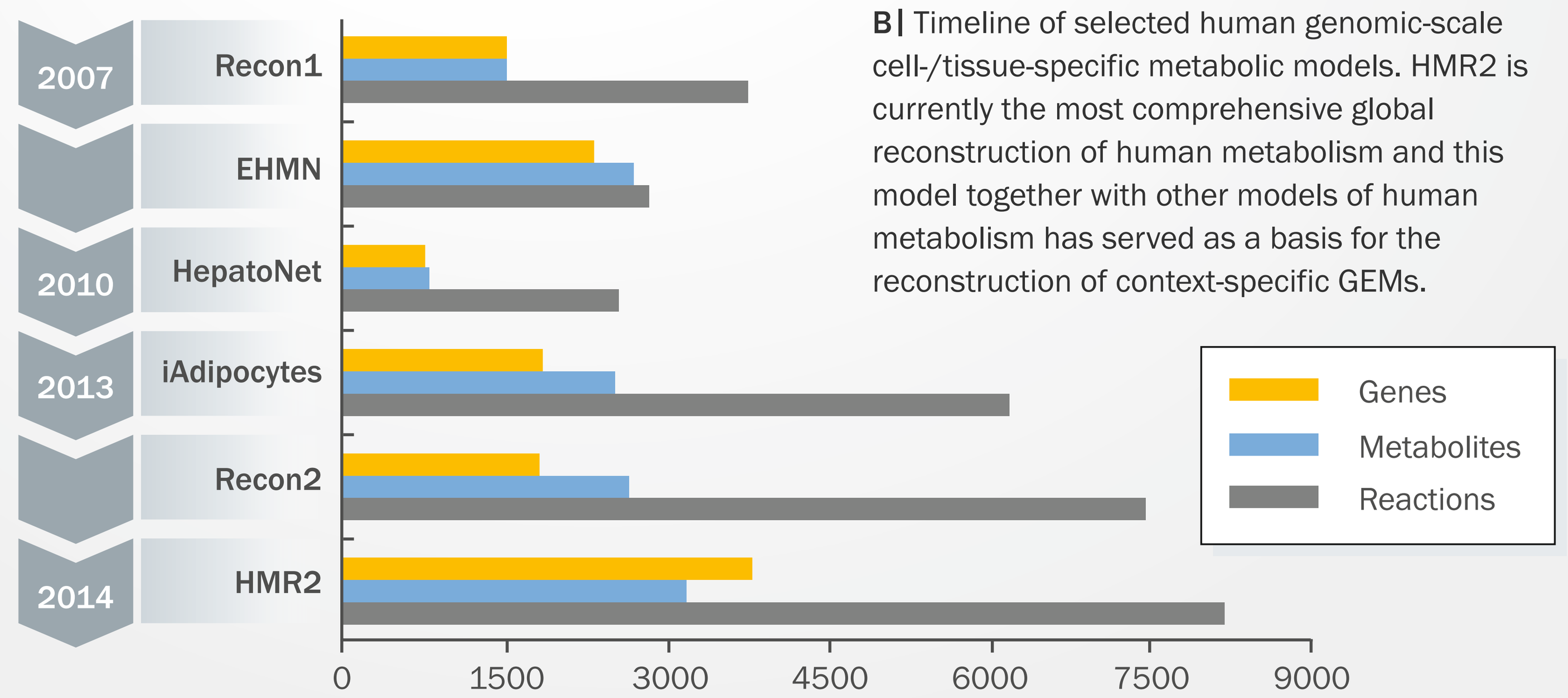
A| The classification of the human protein-coding transcriptome shows that almost half of the genes are detected in all tissues, while 13% show a mixed expression. The number of tissue-enriched genes in the different tissues and the overlap between the Human Protein Atlas consortium (HPA) and the genome-based tissue expression consortium (GTEx) are shown in **B.** Overall, it is reassuring that there is a significant overlap in the tissue classification of the genes based on the two independent datasets. The fact that similar results are obtained when using fresh frozen tissue (HPA) and postmortem tissue (GTEx) suggests negligible effects of the sampling procedures used by the GTEx consortium on RNA degradation.

Genome-scale metabolic models for human cells and tissues



A| Proteomics and transcriptomics data can be used for generating and improving context-specific biological networks including protein–protein interaction, regulatory, signaling, and metabolic networks in order to gain further insights into the differences in cellular functions across tissues. Genome-scale metabolic models (GEMs) that can be reconstructed directly from proteomics or transcriptomics data are particularly well suited for analyzing biological functions, since they can be applied to examine the metabolic functions associated with a given cell type.

B| Timeline of selected human genome-scale cell-/tissue-specific metabolic models. HMR2 is currently the most comprehensive global reconstruction of human metabolism and this model together with other models of human metabolism has served as a basis for the reconstruction of context-specific GEMs.



Human transcriptome resources

Several genome-wide transcriptome profiling methods have been used for quantifying global gene expression patterns. Some of these publicly available repositories for transcriptomics data are summarized in the table of QR codes with a focus on datasets from RNA-seq experiments. The resources include repositories for external data, such as Expression Atlas from the European Bioinformatics Institute (EBI) and Gene Expression Omnibus from the National Center for Biotechnology Information (NCBI), as well as repositories with internally generated transcriptome data, such as the GTEx, the Human Protein Atlas, and the Allen Brain Atlas.

Human Protein Atlas
KTH Royal Institute of Technology (Sweden)
Tissue-based RNA data based on surgically removed tissues (RNA-seq)
UHLÉN *et al*, 2015
www.proteinatlas.org

FANTOM
Riken Institute (Japan)
Tissue-based RNA data based on CAGE
YU *et al*, 2015
fantom.gsc.riken.jp

GTEx
Broad Institute (USA)
Tissue-based RNA data based on post mortem samples (RNA-seq)
KEEN & MOORE, 2015
www.gtexportal.org

RNA-Seq Atlas
J. Gutenberg University (Germany)
A reference database for gene expression profiling in normal tissue by next-generation sequencing
KRUPP *et al*, 2012
medicalgenomics.org/rna_seq_atlas

Gene Expression Omnibus
National Center for Biotechnology Information NCBI (USA)
Repository for RNA expression data (both microarray and RNA-seq)
BARRETT *et al*, 2013
www.ncbi.nlm.nih.gov/geo

Evolution of gene expression
University of Lausanne (Switzerland)
The evolution of gene expression levels in mammalian organs
BRAWAND *et al*, 2011
www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE30352

AltIso
Massachusetts Institute of Technology MIT (USA)
Alternative isoform regulation in human tissue transcriptomes
WANG *et al*, 2008
www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE12946

Expression Atlas
The European Bioinformatics Institute EMBL-EBI (UK)
Repository for RNA expression data (both microarray and RNA-seq)
PETRYSZAK *et al*, 2015
www.ebi.ac.uk/gxa

ArrayExpress
The European Bioinformatics Institute EMBL-EBI (UK)
International functional genomics public data repositories
RUSTICI *et al*, 2013
www.ebi.ac.uk/arrayexpress

Illumina Body Map
Illumina (USA)
RNA-seq of 16 human individual tissues
RUSTICI *et al*, 2013
www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-513

Allen Brain Atlas
Allen Institute (USA)
An anatomically comprehensive atlas of the adult human brain transcriptome
HAWRYLYCZ *et al*, 2012
human.brain-map.org

Scan the QR code with a mobile device to visit the web sites.

To explore the human proteome in depth, visit
www.proteinatlas.org

THE HUMAN PROTEIN ATLAS

Knut och Alice Wallenbergs Stiftelse

SciLifeLab

KTH VETENSKAP OCH KONST
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Mol Syst Biol. 12(4):862
msb.embopress.org/content/12/4/862