



## **iSEQ lunch seminar series**

**Talk:**

The evolution of mammalian tissue transcriptomes.

**Speaker:**

Henrik Kaessmann, PhD, Associate Professor, University of Lausanne, Switzerland.

**Venue:** Merete Barker Auditory, The Lakeside Theatres

**Time:** 2 April 2014 at 12.00 – 13.00

**Abstract:**

Shared mammalian traits include lactation, hair and relatively large brains with unique structures. Individual lineages have, in turn, evolved distinct anatomical, physiological and behavioral characteristics relating to differences in reproduction, life span, cognitive abilities and disease susceptibility.

Regulatory mutations affecting gene expression (rather than mutations altering the sequence of the gene product) probably explain many or even most phenotypic differences among species.

The advent of high-throughput RNA sequencing (RNA-seq) approaches now allows for accurate and sensitive assessments of transcript sequences and expression levels at a genome-wide scale.

We have generated comprehensive sets of RNA-seq data for a large collection of germline and somatic tissues from representatives of all major mammalian lineages (placental mammals, marsupials, and the egg-laying monotremes) and evolutionary outgroups (e.g., birds).

In conjunction with various high-throughput genomic and epigenomic data, we are using these transcriptome datasets to study the functional (expression) evolution of mammalian genomes across gene types, lineages, tissues, chromosomes and sexes. I will present recent selected highlights of this endeavor.

**Refreshments:**

Sandwiches will be provided.

Therefore, please email Anne Hedemand ([anneh@hum-gen.au.dk](mailto:anneh@hum-gen.au.dk)) no later than 31 March 2014, if you would like to participate.