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## Ramp Sequences Change Across Tissues: How Ramps Correlate with Differing Tissue-Specific Expression Levels

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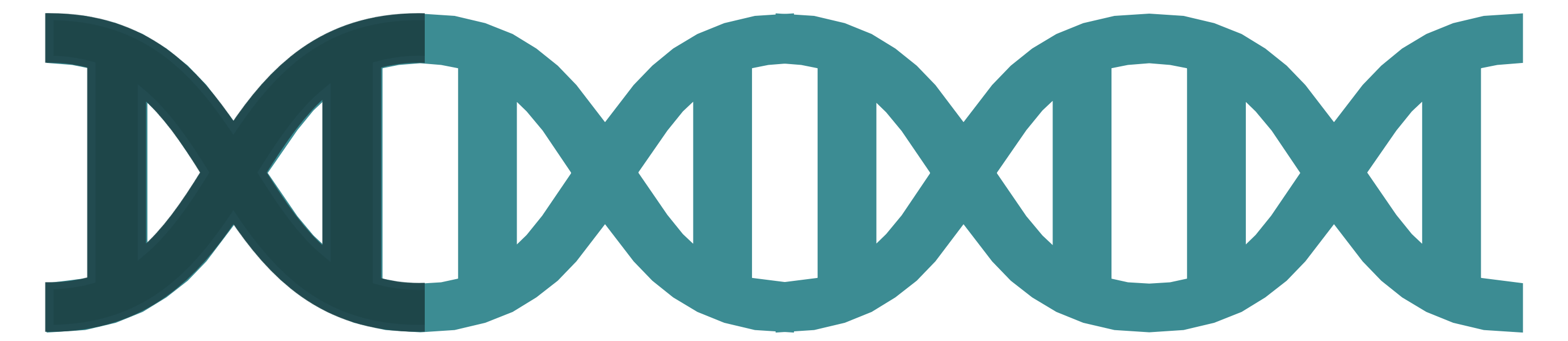
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# RAMP SEQUENCES CHANGE ACROSS TISSUES

— How ramps correlate with differing tissue-specific expression levels —

Authors: Taylor Meurs, Justin Miller, and Ben Song at Brigham Young University March 6, 2020



19% of genes in each tissue use a ramp sequence

## Introduction

Our bodies are made of proteins. They help our cells function, give them structure, and cause some diseases. Different amounts of proteins are required for different functions, which makes regulation of protein production a scientific concern. Genes produce quantities of proteins dependent on many factors. Rare regions at the beginning of genes have recently been attributed to variation in protein expression. These regions, called ramp sequences, correlate with higher production. Protein expression differs across tissue types, but it has yet to be explored if ramp sequences correlate with these differences.

## Questions

- Do different tissues use different percentages of ramp sequences?
- Can we confirm that highly expressed genes use more ramps than lowly expressed genes?

## Materials

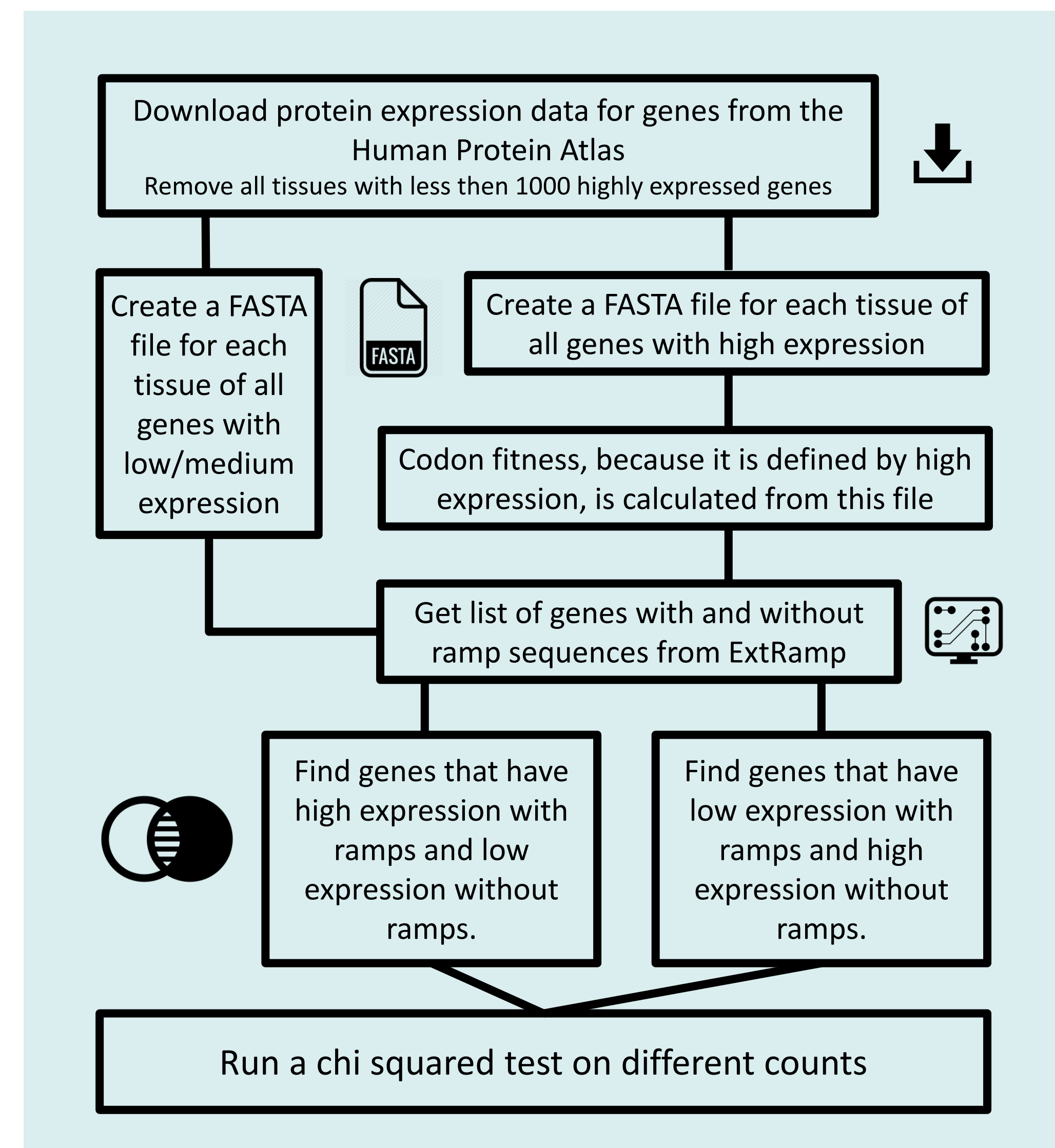
### Tissue Data from the Human Protein Atlas

- Genes in each tissue
- Protein expression in each tissue

### Ramp Sequence Data extracted from reference genome with ExtRamp

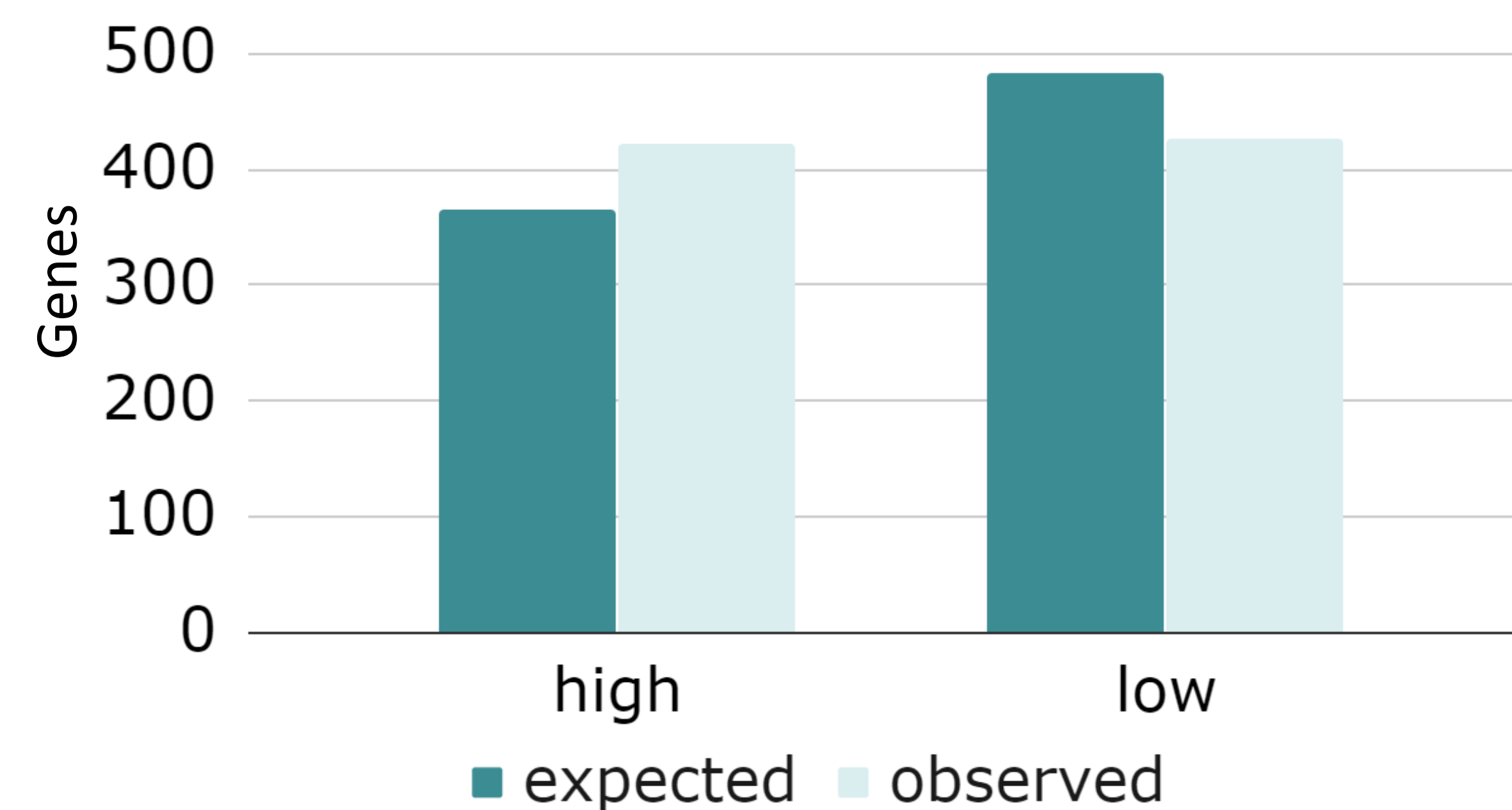
- List of genes with and without ramp sequences activated in each tissue type

## Methods

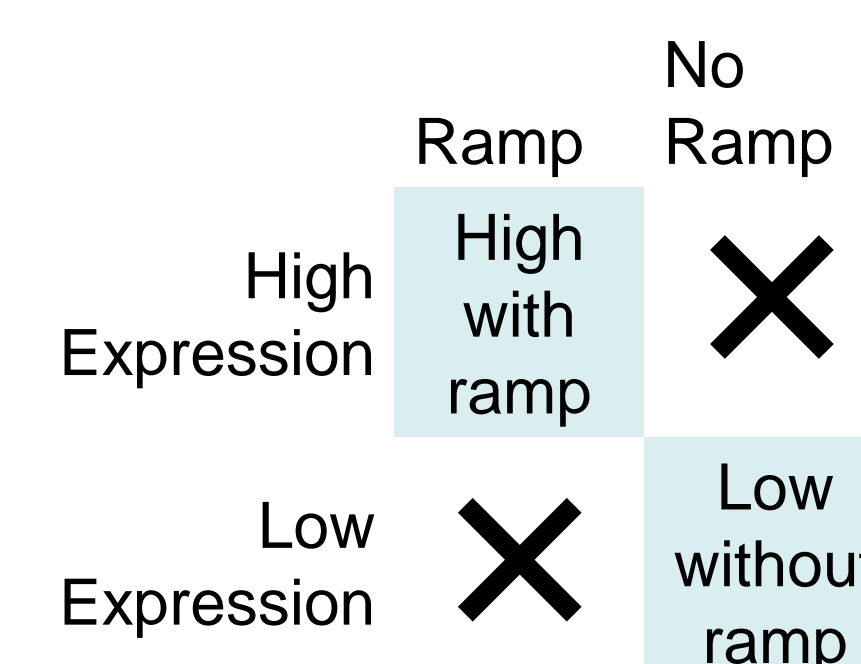


## Results

### High vs Low Expression Overlap Chi Squared Analysis



The category "high" represents genes that fall into the two light blue boxes in the chart to the right. The category "low" represents genes in the boxes marked X. The observed values show that it is more likely than expected that genes fall in the "high" category ( $p\text{-value} = 7.97 \times 10^{-5}$ )



## Ramp Presence in Selected Genes

Expression in different tissues correlates with ramps

Gene	Expression	heart	placenta	skin	colon	bone marrow	brain
WDR36	High	Light Blue	Light Blue	White	White	Light Blue	White
	Low	Light Blue	White	Grey	Light Blue	White	Grey
TSC1	High	Light Blue	Light Blue	White	White	Light Blue	Light Blue
	Low	White	White	Grey	Light Blue	White	White
PCDH10	High	White	White	White	Light Blue	White	Light Blue
	Low	Light Blue	Grey	Light Blue	White	Grey	White

Ramp activated (light blue)  
No ramp (grey)  
Gene not expressed at this level (white)

Here are several examples of genes that fall in the "high" category of the chi squared analysis. These genes have active ramp sequences in tissues where they are highly expressed. Often, the very same gene will not use a ramp sequence when its expression level is lower.

## Conclusions

- On average, 19% of genes in each tissue contain ramp sequences
- Although the same percentage of tissues use ramps, those ramps correspond to different genes in each tissue that correlate with higher protein expression ( $p = 7.97 \times 10^{-5}$ )
- Genes such as WDR11, TSC1, PCDH10, GNAI1, and WDR36 express ramp sequences correlating with expression

## Future Research

- Which specific tissues have more ramps in their highly expressed genes?
- Do different cell types affect codon fitness in different tissues? Does this change the presence of ramp sequences?