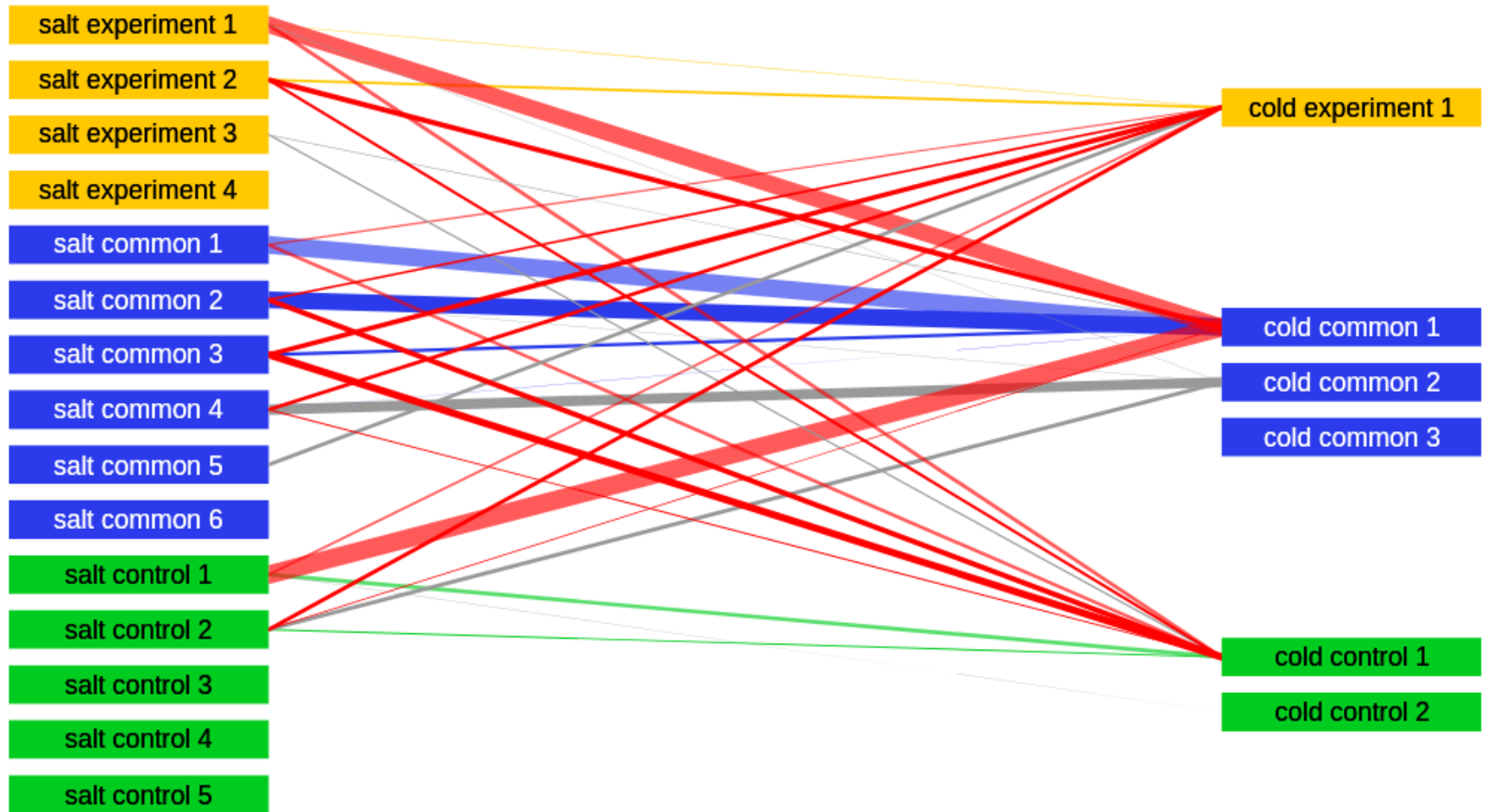
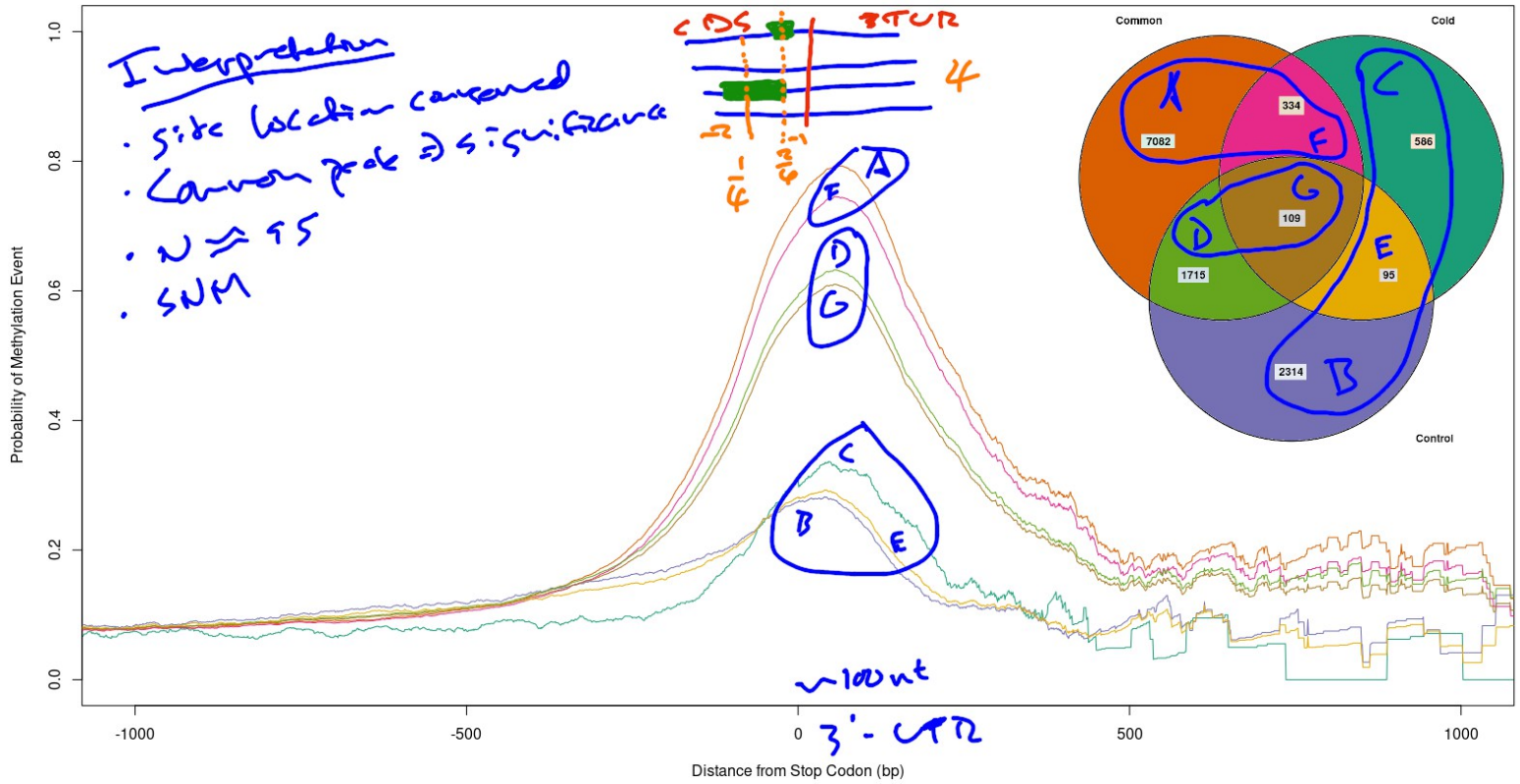
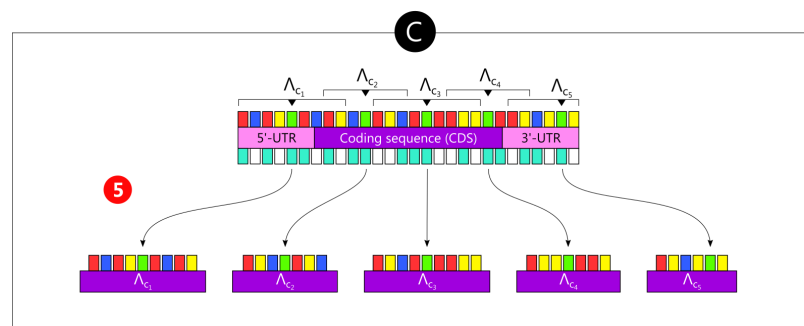
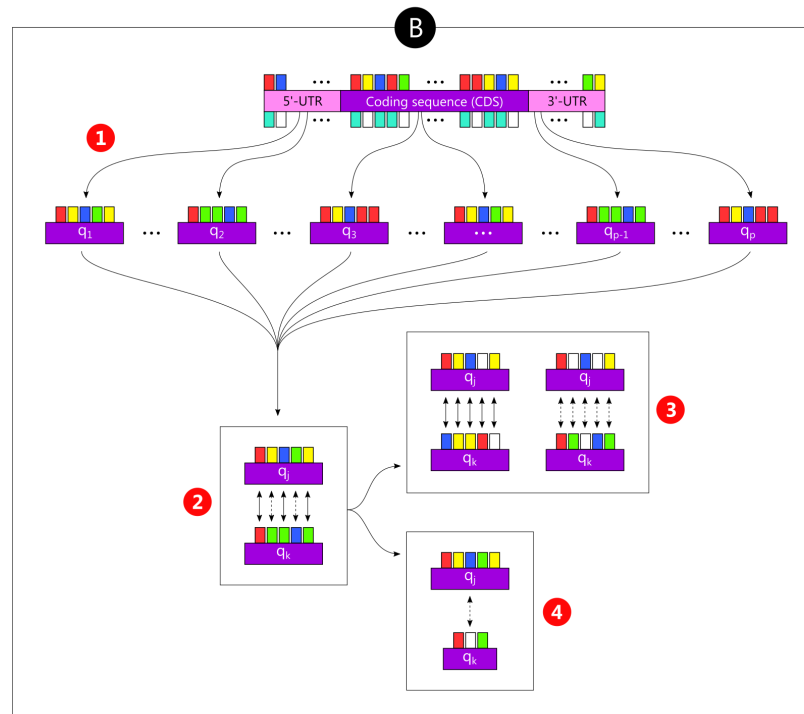
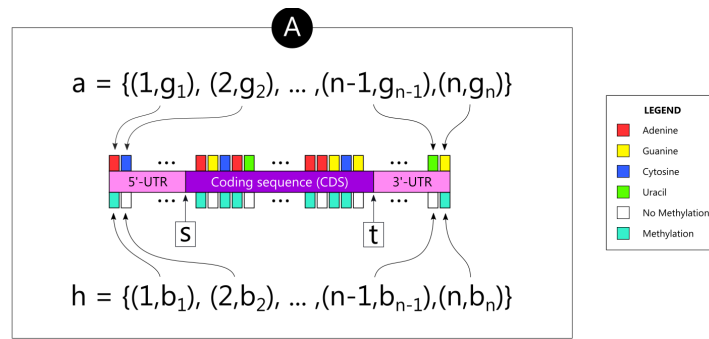


# RESEARCH SAMPLES

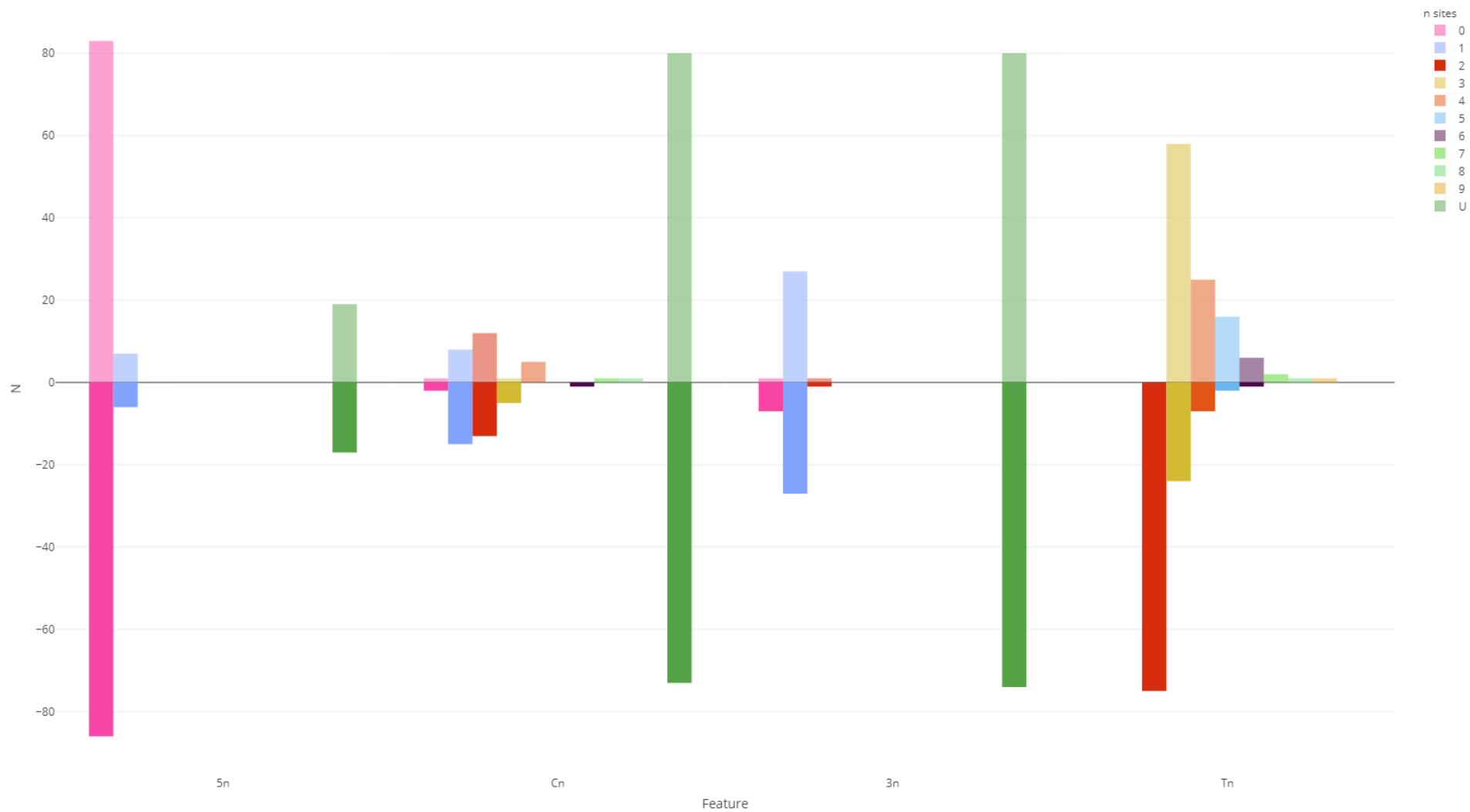






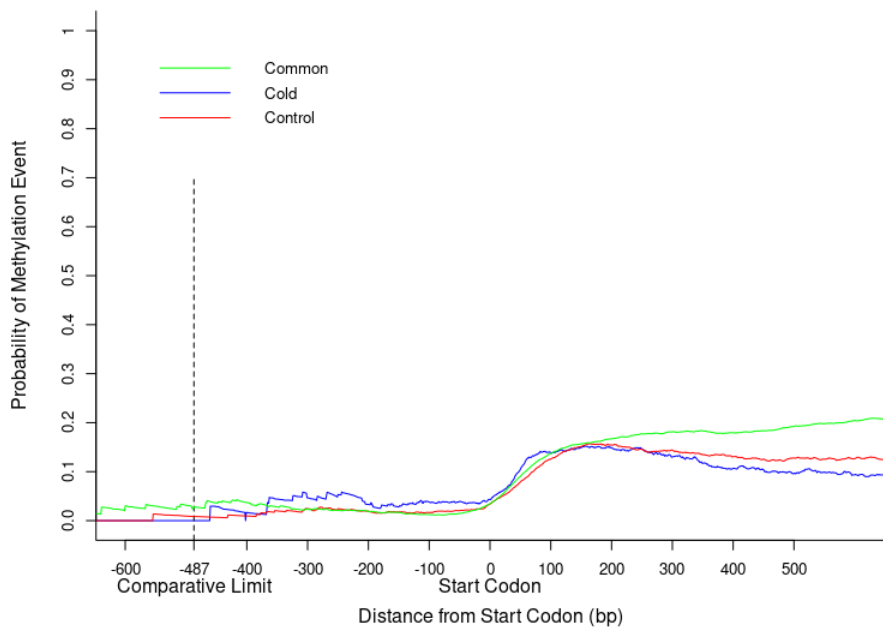


Common/Cold/Control-only  $\Delta n$



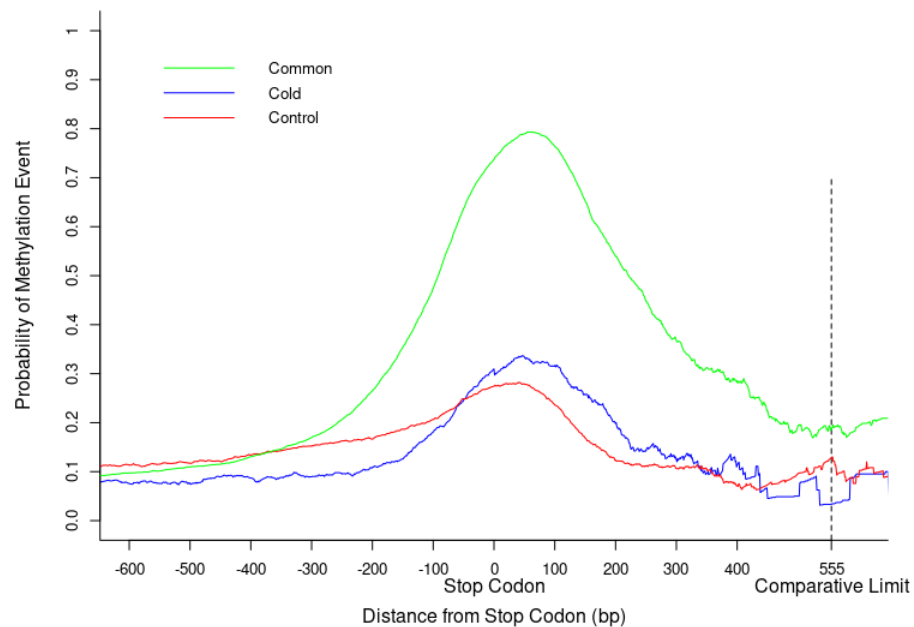
### Probability vs. Normalized Distance

5'-UTR/CDS Interface (Methylated Transcripts Only)



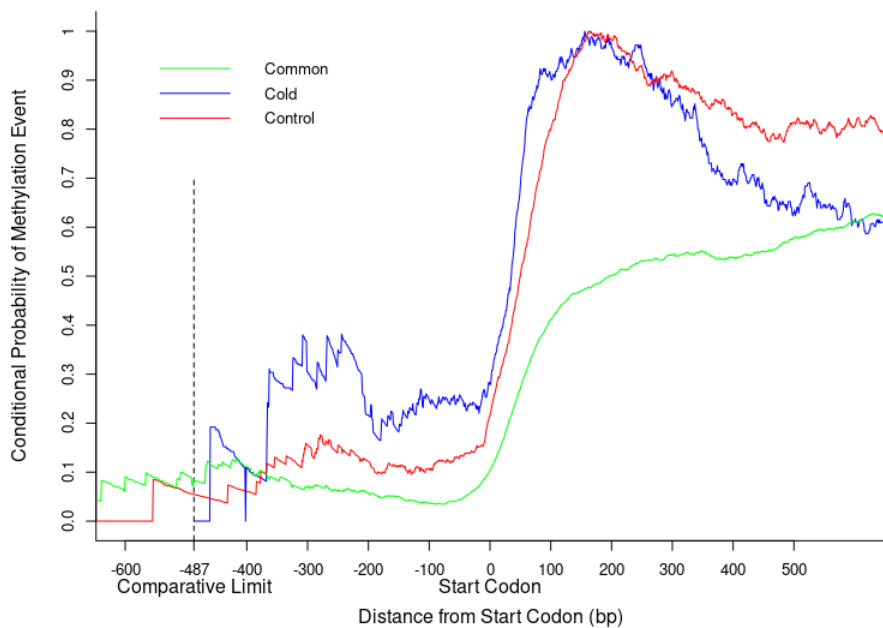
### Probability vs. Normalized Distance

CDS/3'-UTR Interface (Methylated Transcripts Only)



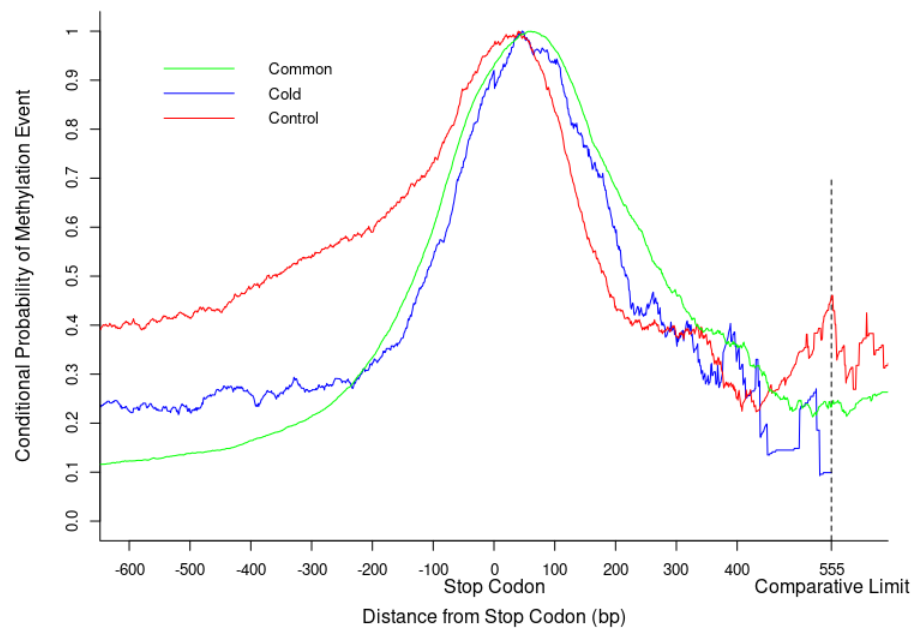
### Conditional Probability vs. Normalized Distance

5'-UTR/CDS Interface (Methylated Transcripts Only)

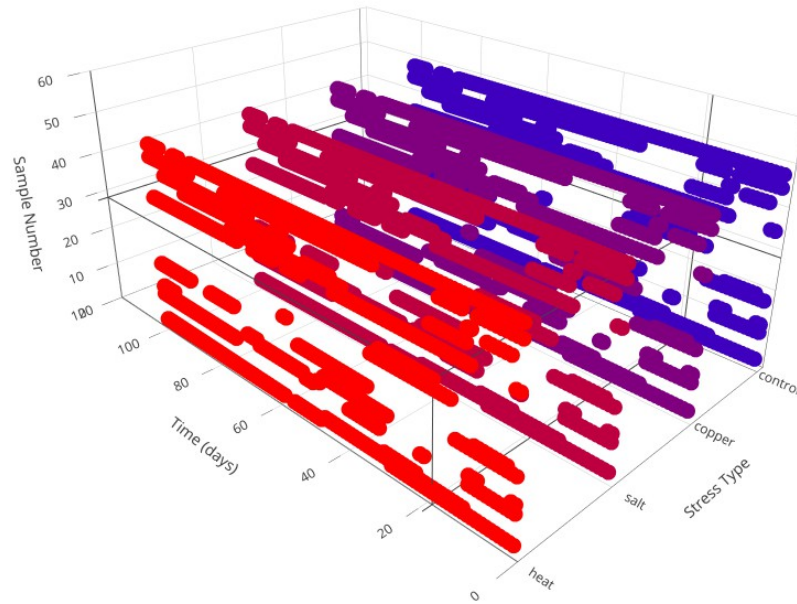


### Conditional Probability vs. Normalized Distance

CDS/3'-UTR Interface (Methylated Transcripts Only)

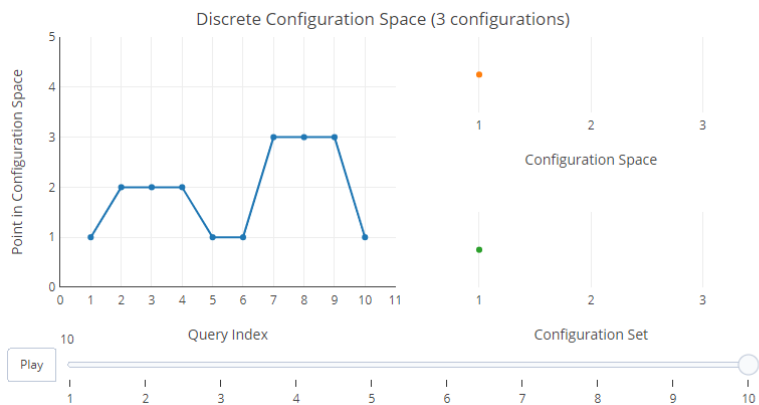
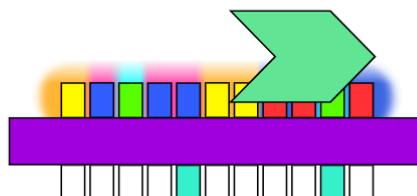


# Factorial Stability





## Memory-having Protein, 1 DOF, 3 Configurations



### Example Equivalence Classes

~ = "Induces conformation change"



~ = "Conformation allows methylation"

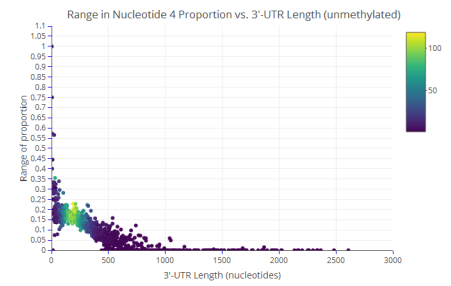
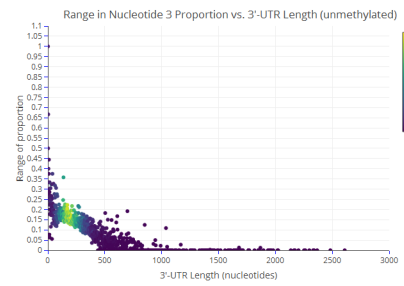
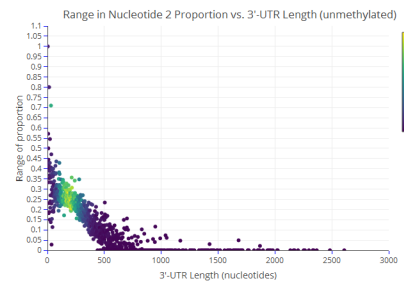
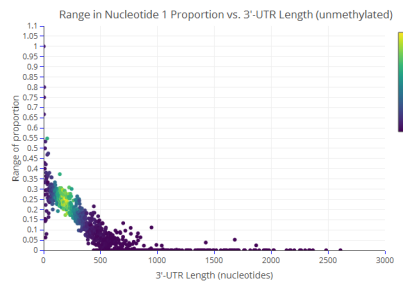
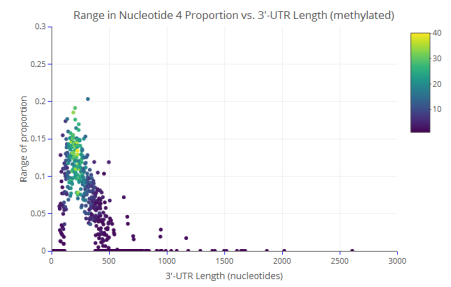
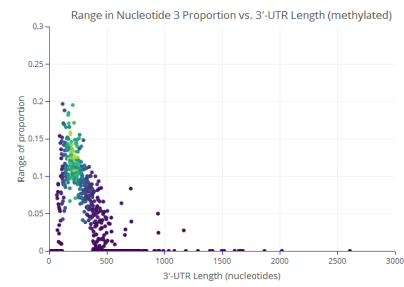
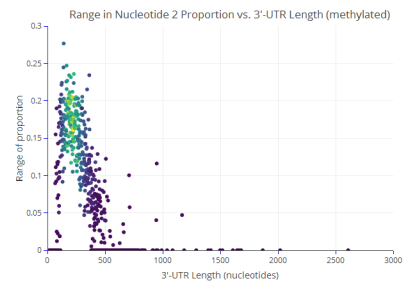
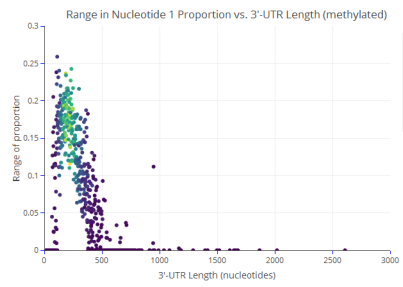


~ = "Does not induce conformation change"



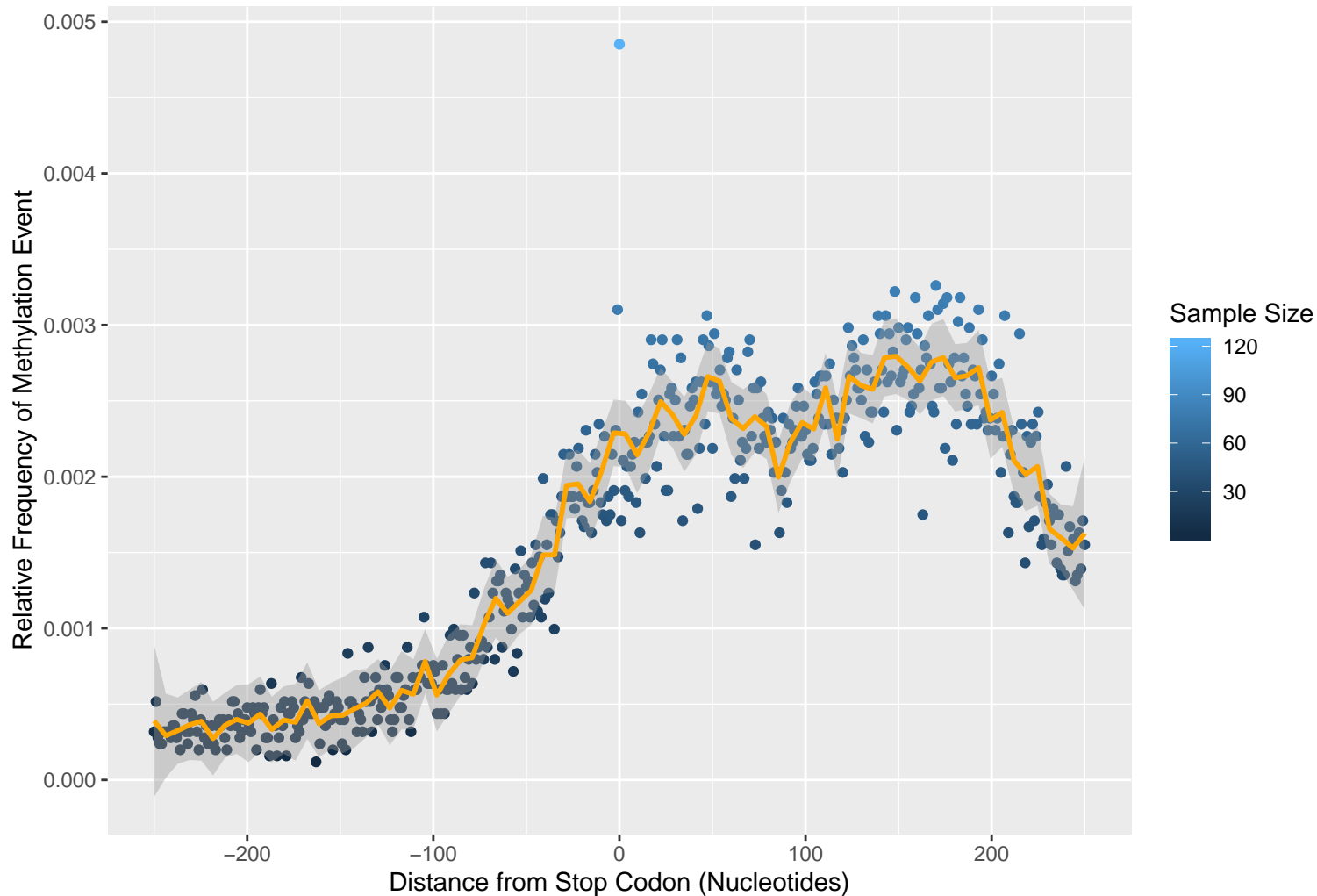
~ = "Conformation does not allow methylation"



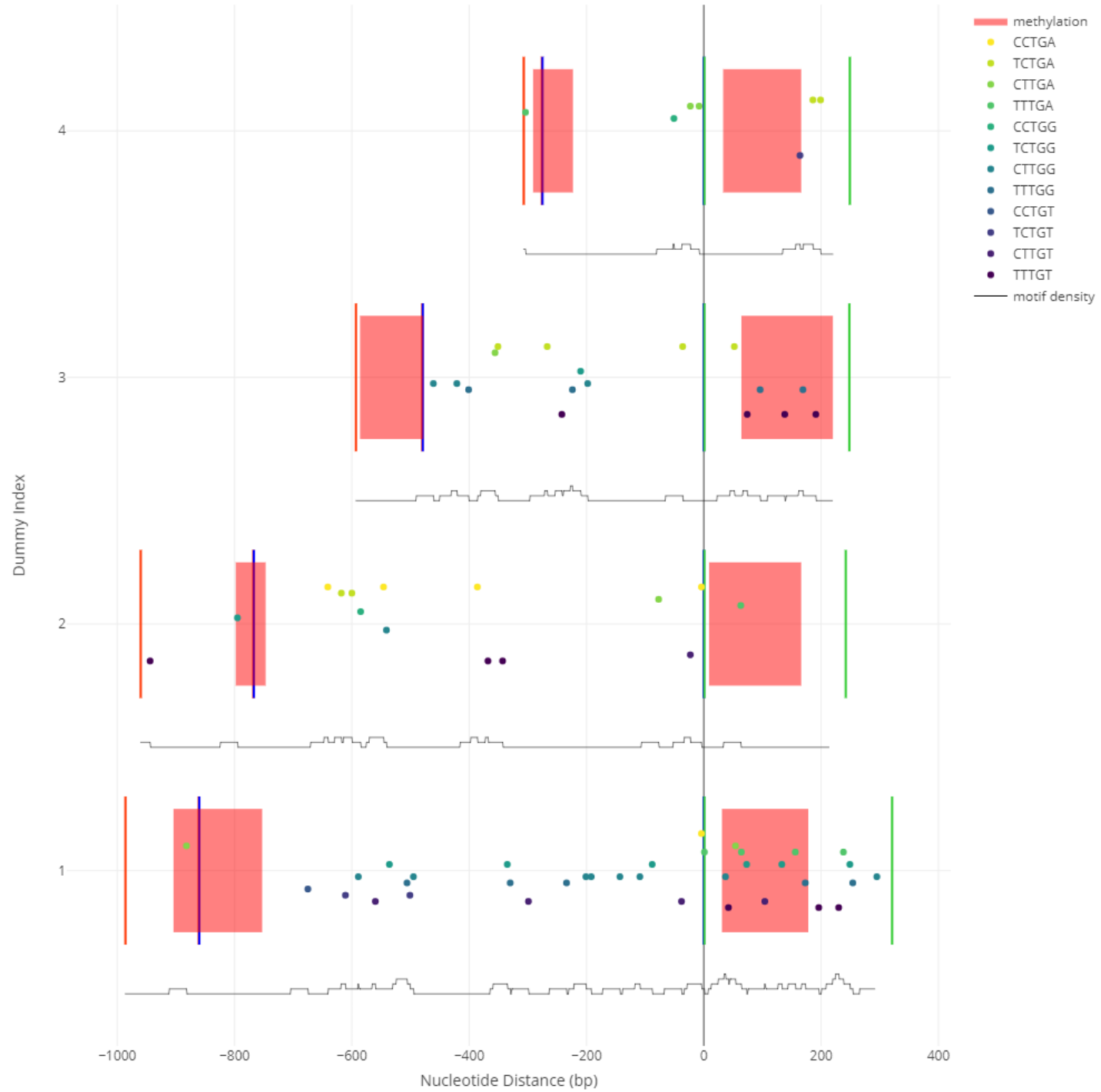


# Relative Frequency of Methylation Event vs. Distance from Stop Codon (Salt Common)

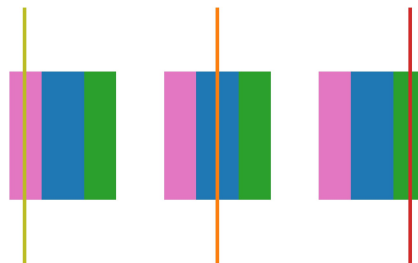
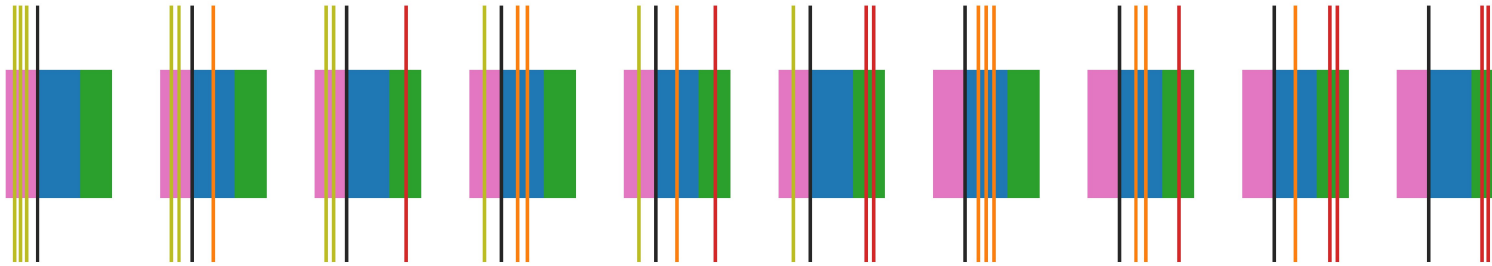
Measurement resolution of 100 nucleotides



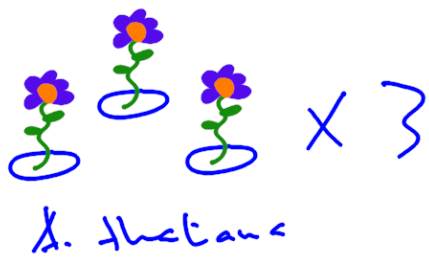
salt\_common\_Y\_5\_Y\_C\_Y\_3\_Y\_5C\_Y\_C3\_N\_5n\_U\_Cn\_U\_3n\_1\_Tn\_2 - (1 of 1)



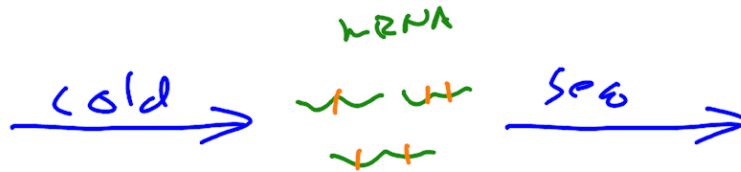
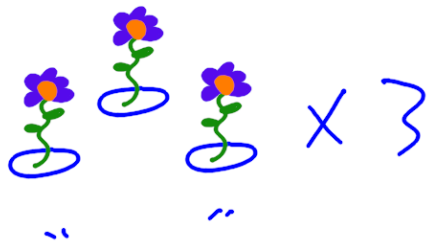
(4) U\_U\_0 → 0\_1\_0 (1)



- Legend
- 5'-UTR
  - 5'-UTR site
  - 5'-UTR/CDS straddle
  - CDS
  - CDS site
  - CDS/3'-UTR straddle
  - 3'-UTR
  - 3'-UTR site



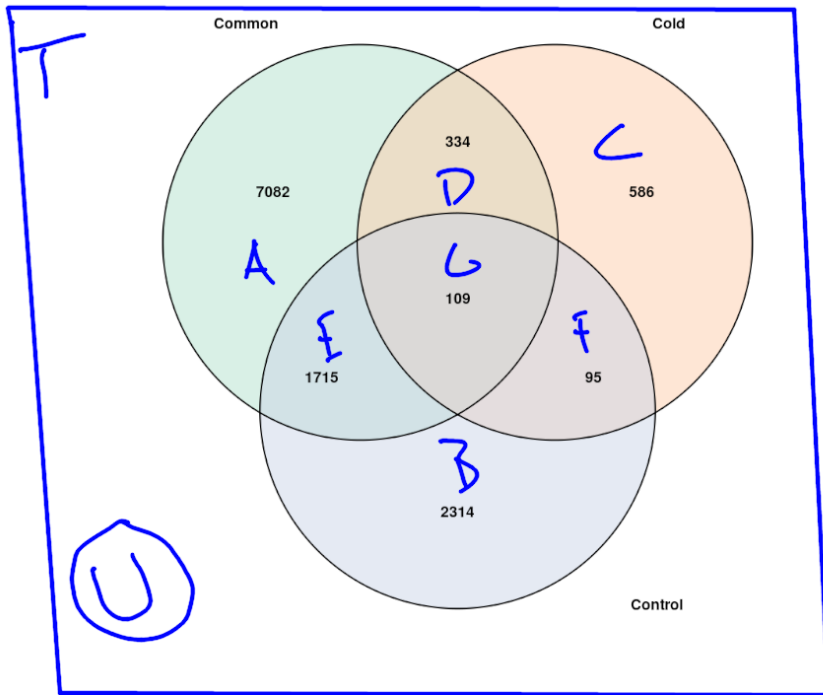
ID	index	TABLE	
		AC GT	mGA
G1	1	A	Y
G1	2	A	Y
G2	1	C	N
G2	2	T	Y
⋮			



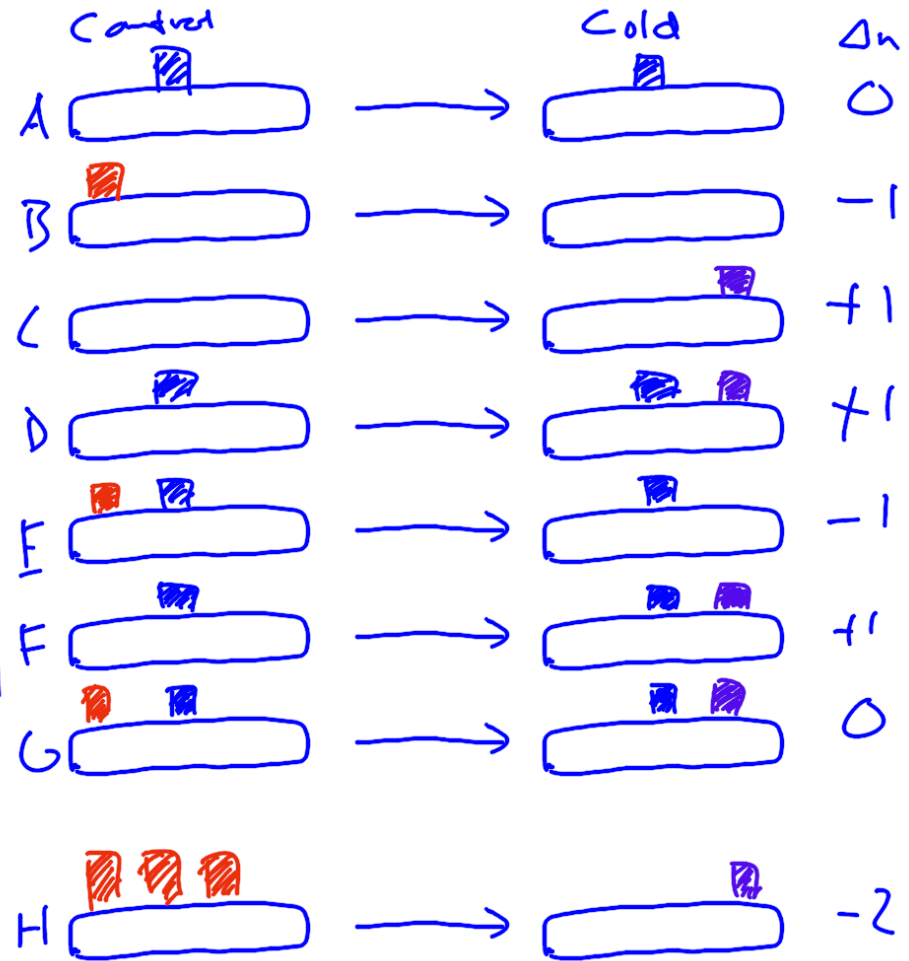
ID	index	TABLE	
		AC GT	mGA
G1	1	A	N
G1	2	A	N
G2	1	C	Y
G2	2	T	Y

etc...

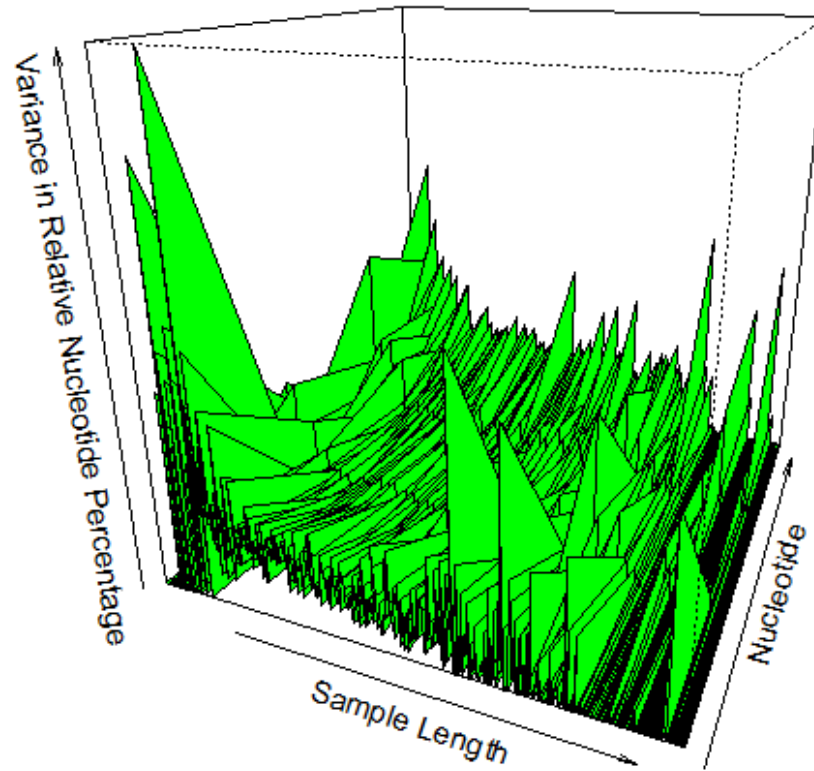




- $\pi \sim 100$  wt
- High-confidence (Anderson et al.)
- unGen

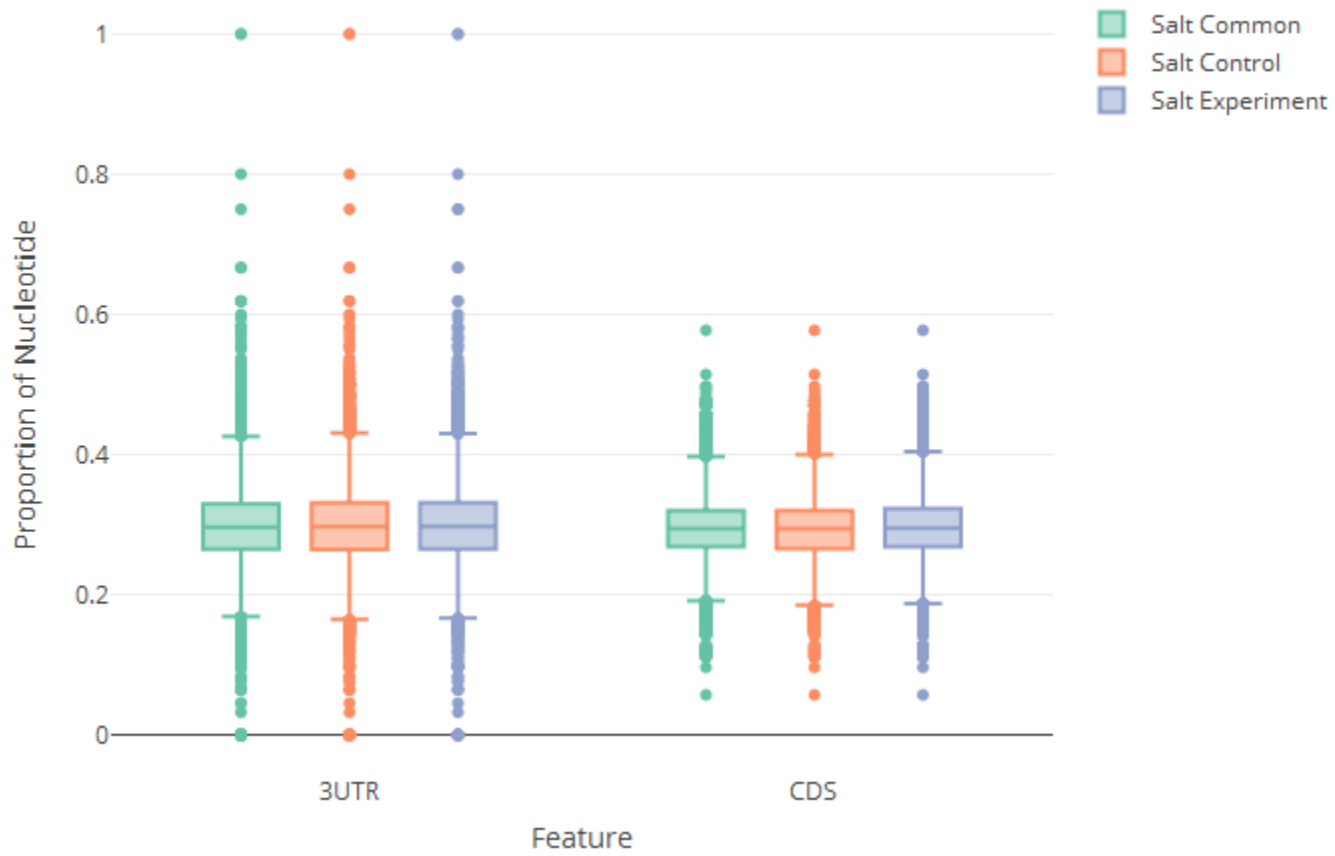


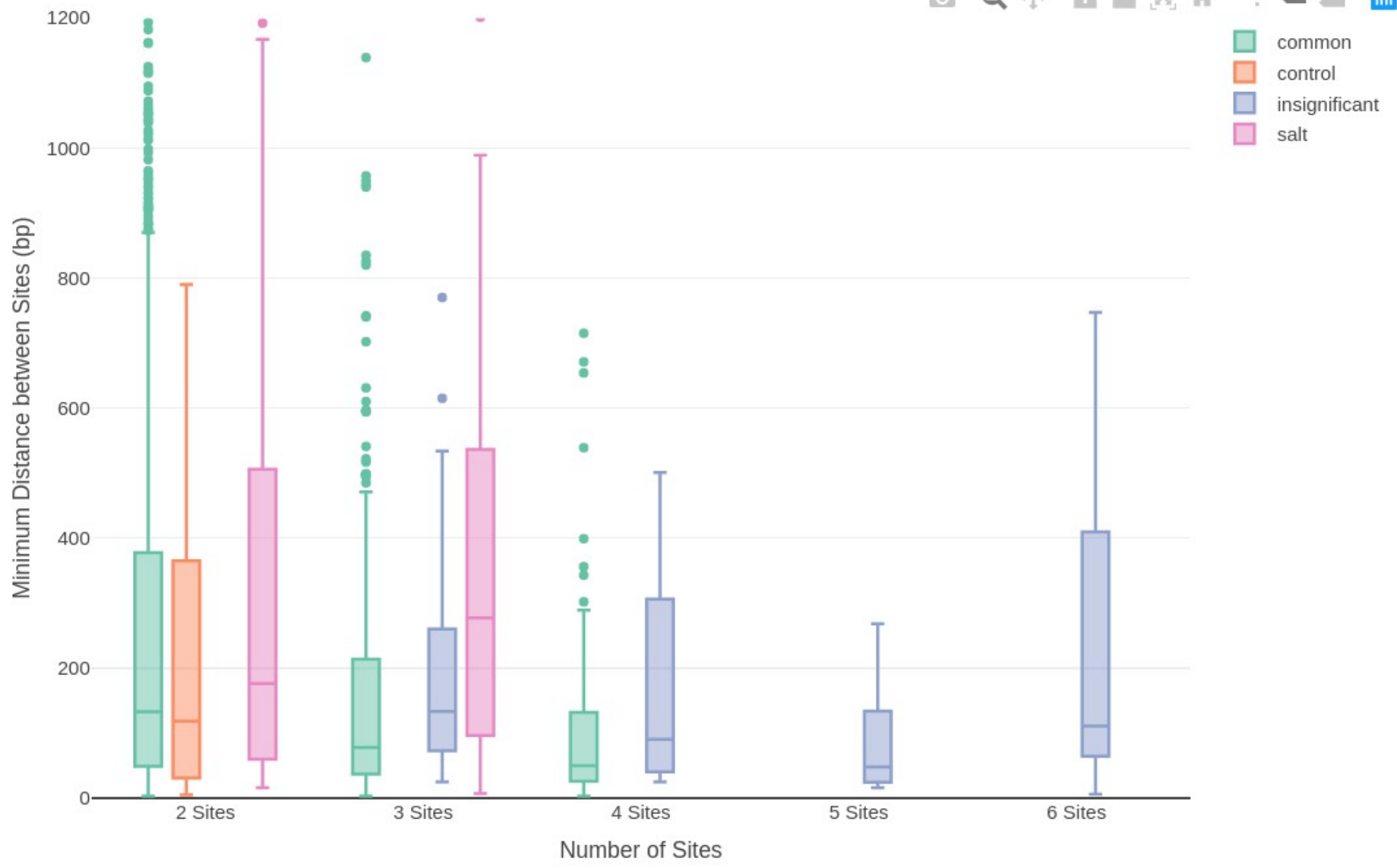
## Variance in Relative Nucleotide Proportion - Methylated Samples - 3'-UTR



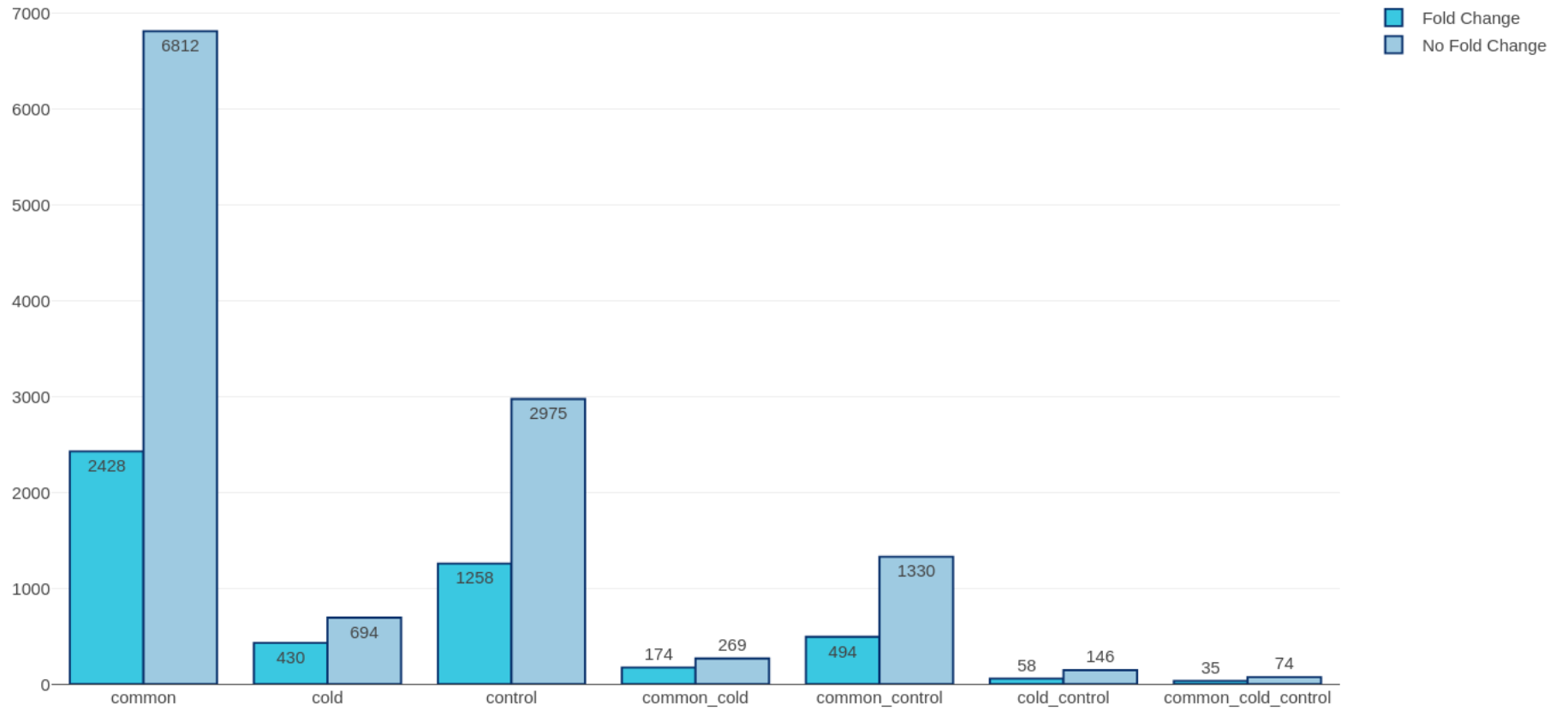


Proportion of Nucleotides in Sample by Feature - Adenine

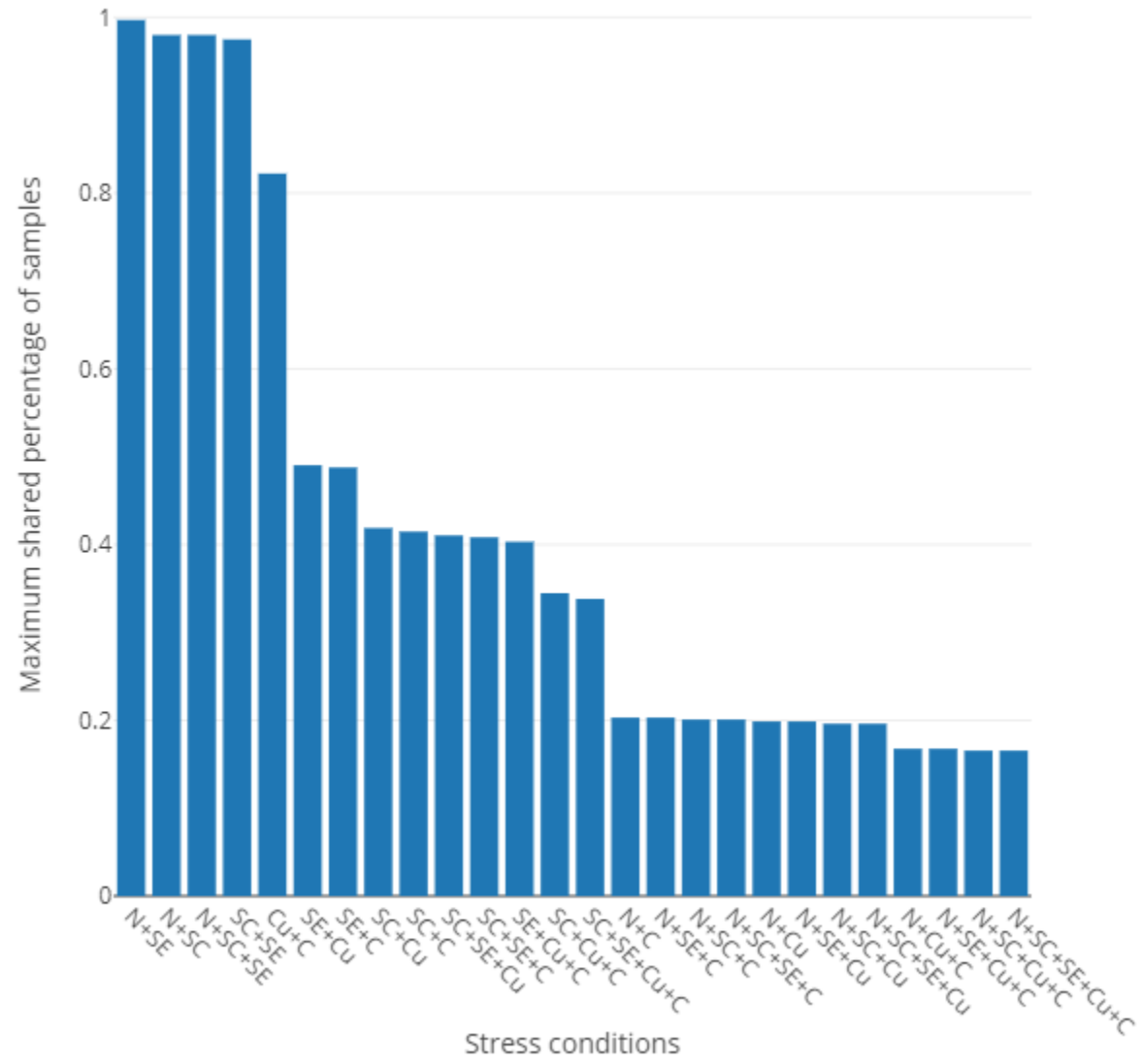




Number of Expressed Transcripts Relative to Category



Maximum shared percentage of methylated samples vs. Stress conditions



common\_cold

