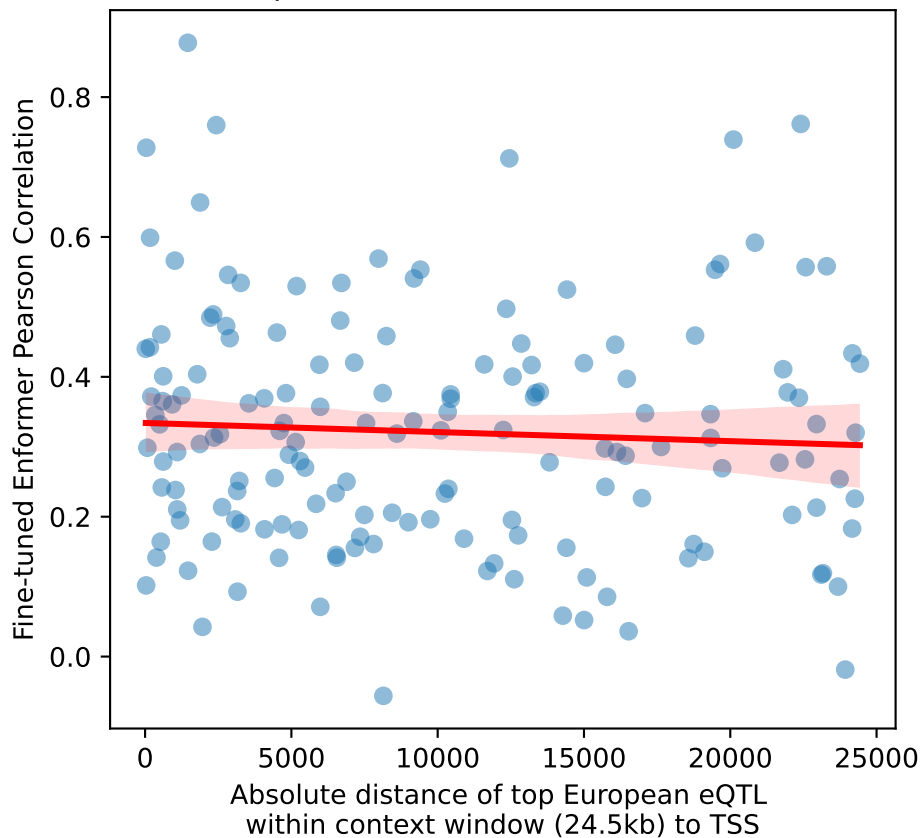
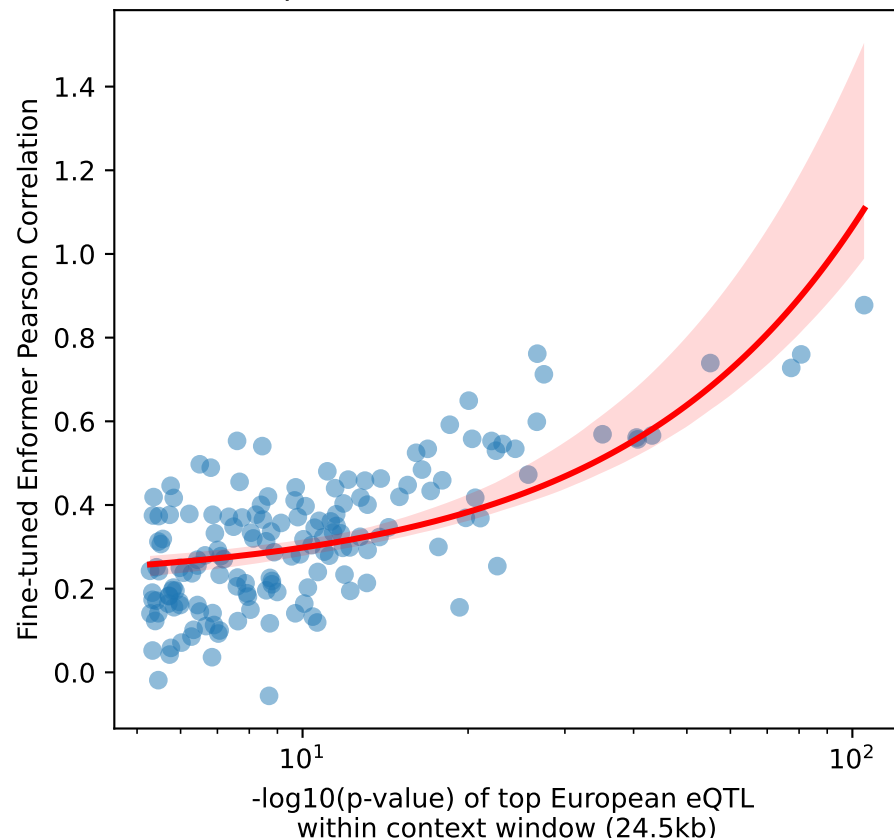


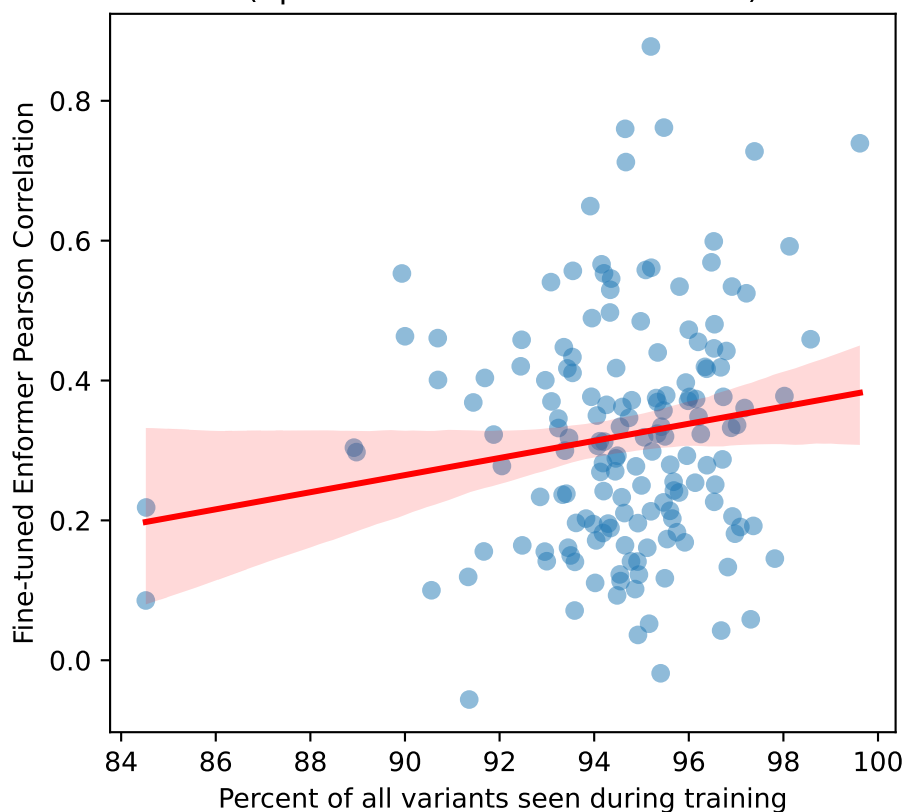
Fine-tuned model performance  
on random-split genes vs.  
the distance of the top European eQTL to the TSS  
(Spearman Correlation = -0.073)



Fine-tuned model performance  
on random-split genes vs.  
the p-value of top European eQTL within context window  
(Spearman Correlation = 0.602)



Random-split genes  
(Spearman Correlation = 0.112)



Population-split genes  
(Spearman Correlation = 0.102)

