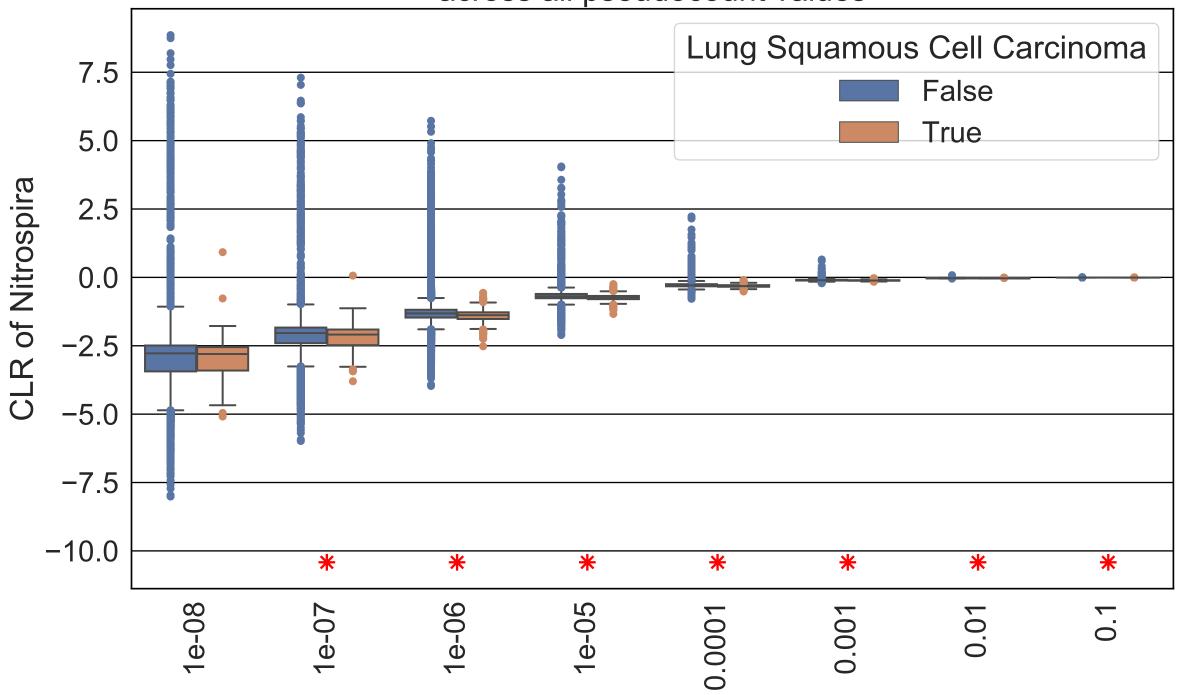
CLR introduce tumor-associated differences in TCGA sparse features across all pseudocount values



Pseudocount (added in relative abundance space)