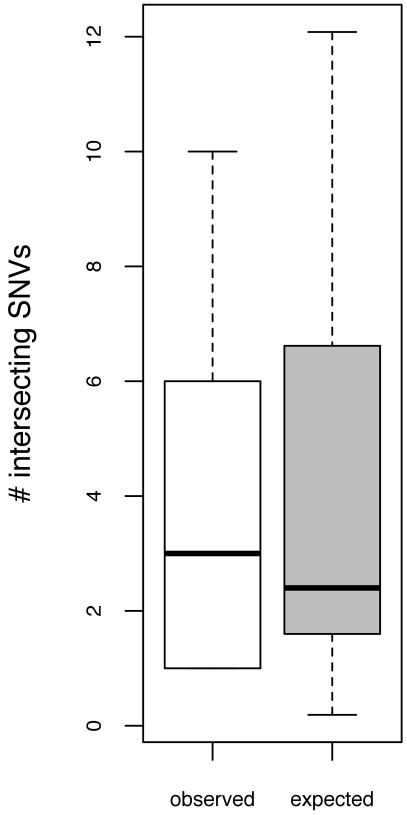
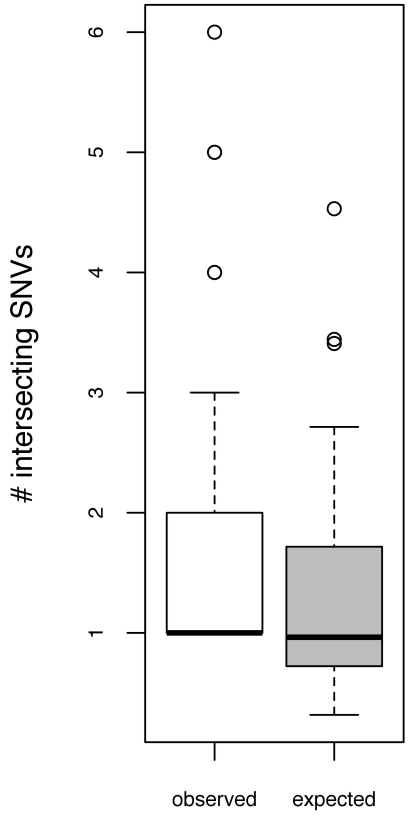
Maximally Frustr. Residues Using the Single-Residue Index

TSGs

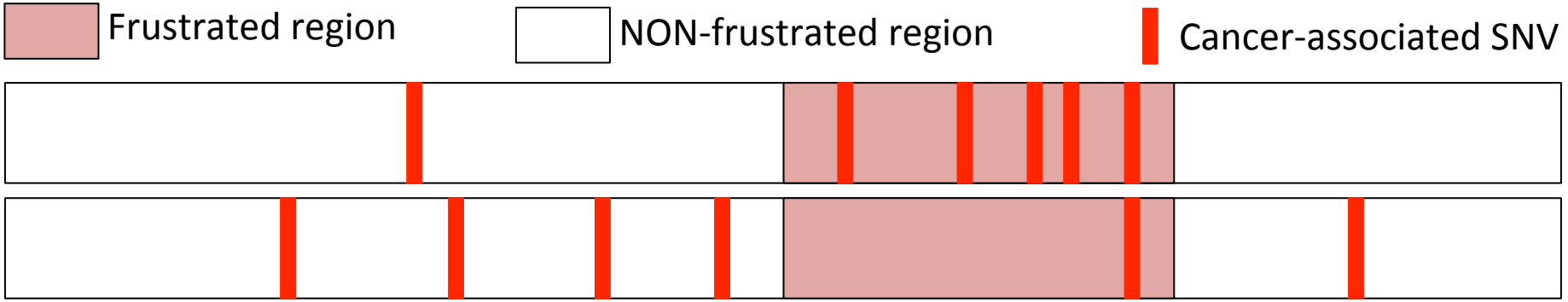
p-value = 5.5E-3
N = 28





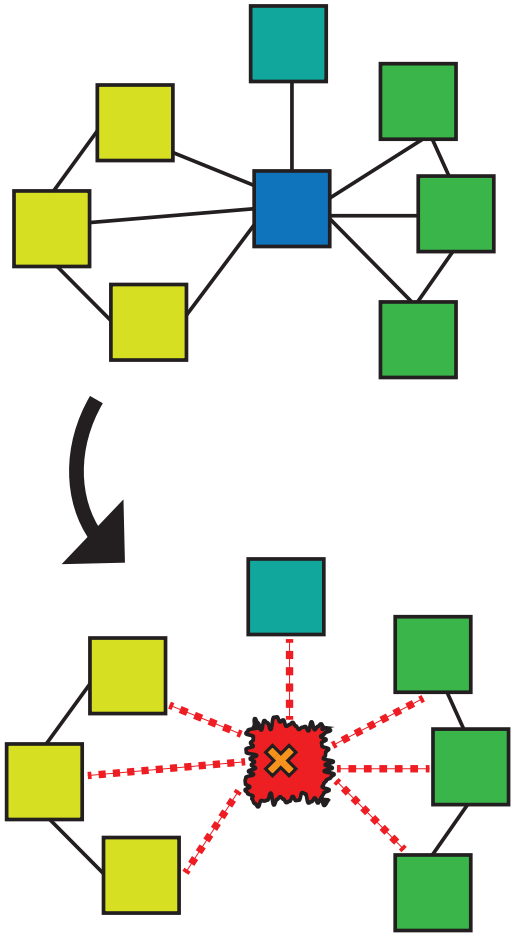
Oncogenes

p-value = 2.83E-7
N = 80

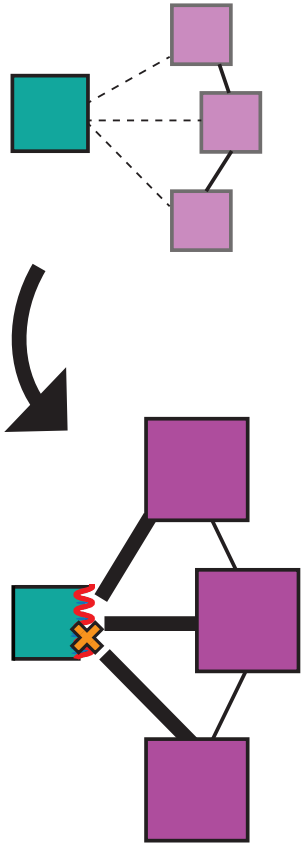


Observed: X = # of cancer-associated SNVs that intersect frustrated regions (5 in this case)
Expected: E[X] = [# frustrated residues / total # residues in protein] * [total # of cancer-associated SNVs]

Naive mechanism for the effects of many **TSG**-associated SNVs
Loss-of-Function Affects

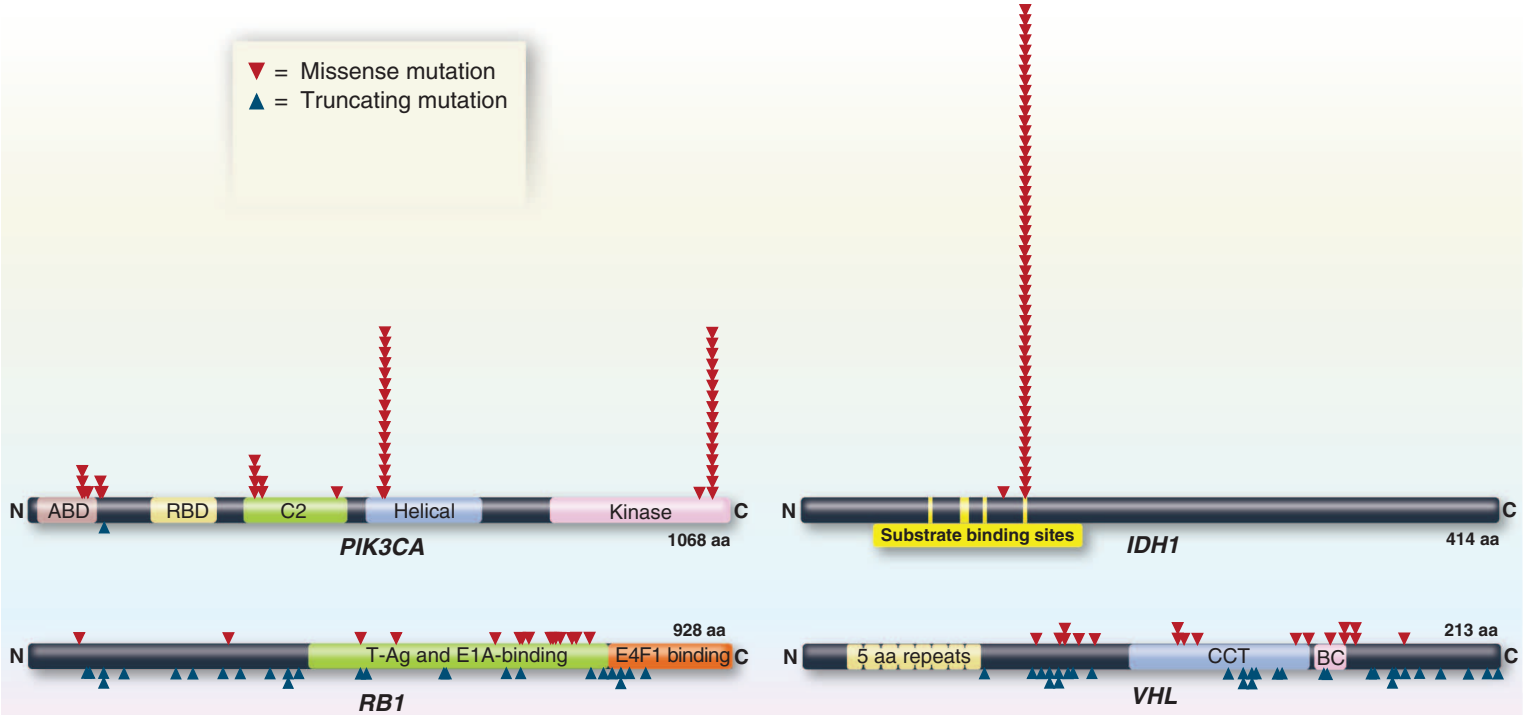


Naive mechanism for the effects of many **oncogene**-associated SNVs
Gain-of-Function Affects



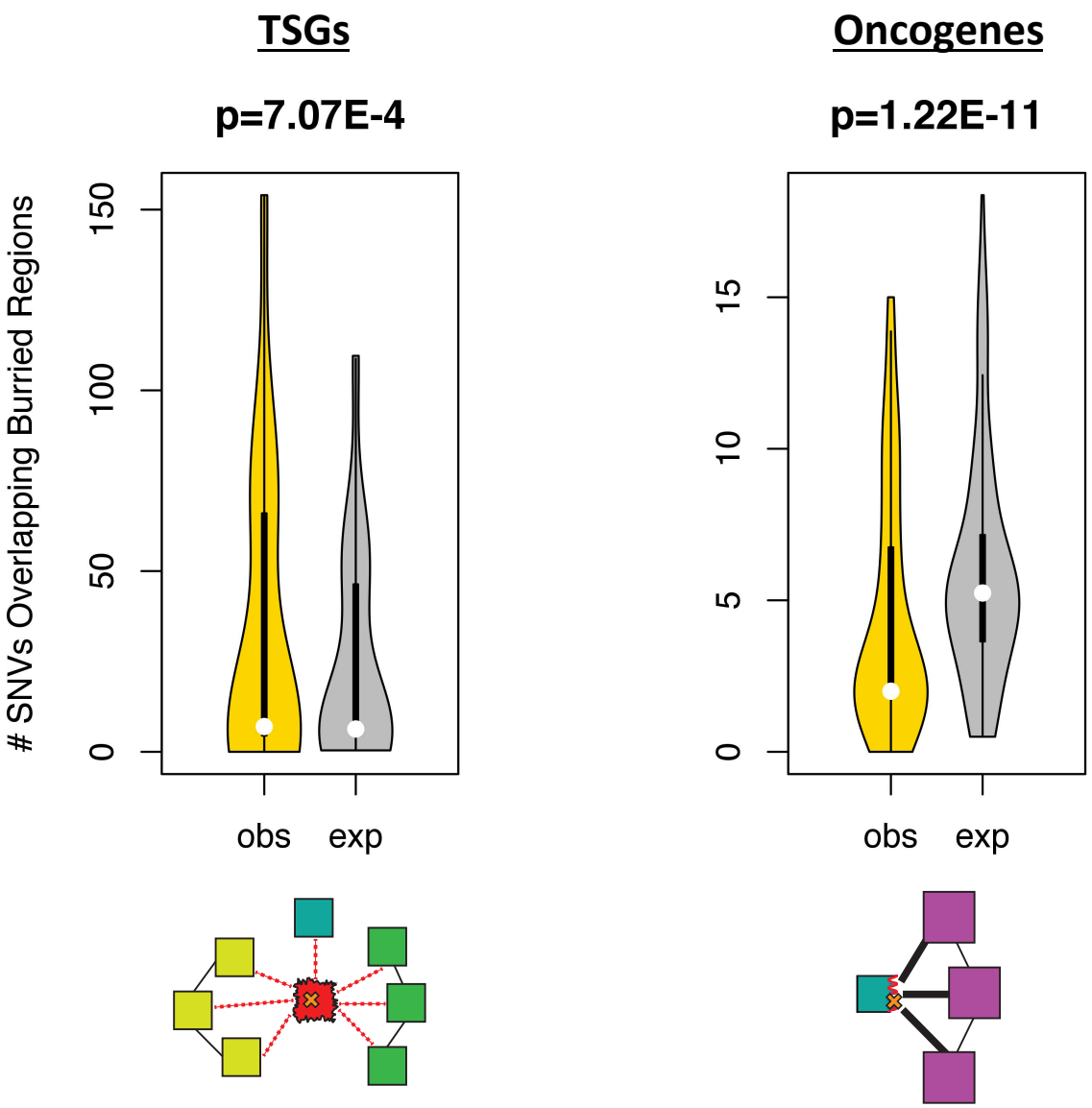
Oncogenes

TSGs



Vogelstein, Bert, et al. "Cancer genome landscapes." Science (2013)

“Redundant” model: Counting the *# of SNVs* that intersect buried regions



"Non-Redundant" model: Counting the *# of buried residues* that intersect cancer-associated SNVs