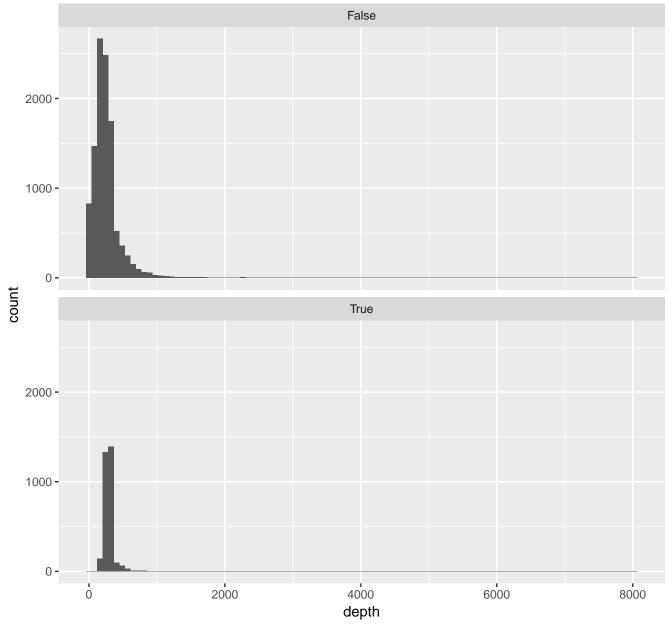
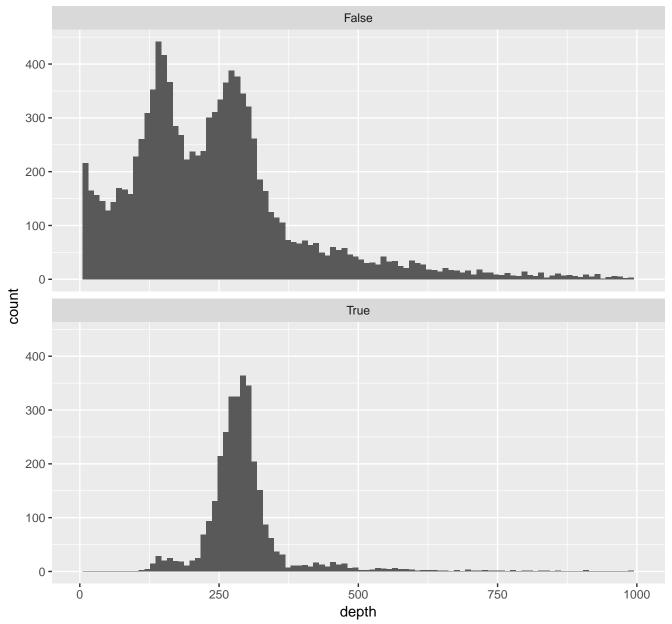
Detection rate

Coverage per site, with facets for whether or not an in-silico mutation was recovered



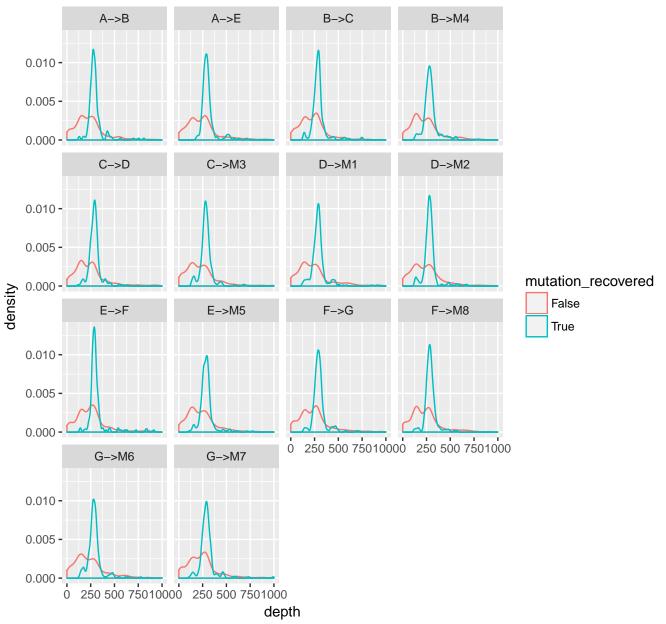
Detection rate, zoomed to x[0, 1000]

Coverage per site, with facets for whether or not an in-silico mutation was recovered



## Detection rate per branch x[0, 1000]

Coverage per site, with facets for whether or not an in-silico mutation was recovered



Detection rate per scaffold x[0, 1000] Coverage per site, with facets for whether or not an in-silico mutation was recovered scaffold\_1 scaffold\_10 scaffold\_11 scaffold\_2 0.010 scaffold\_3 scaffold\_4 scaffold\_5 scaffold\_6 mutation\_recovered False True 250 500 7501000 scaffold\_7 scaffold\_8 scaffold\_9

