Speaker 1: BMR Insert.

We wish to be clear that we are not claiming to have developed negative binomial regression or its application to cancer genomics. We point out that a number of references have used this. A negative binomial regression is a very standard statistical technique that has been used in many contexts in genomics.

Our main point that we wish to make clear here is that the N code rollout dramatically expands the number of available cell types in tissues available for this type of regression from XXX to YYY. Furthermore, we show in our figure that this expansion is quite significant. One does not get most of the modeling of background mutation rate by including one or two features, but actually, including up to 20 or 30, or even more, does continue to incrementally give further improvement, and this is either using the features directly or principal components.

The implication here is that more data is actually useful, and that's the main point we're trying to do in highlighting the N code data. The reason we believe that the large amount of data is useful is that while it's valuable matching a cancer cell to its cell of origin, tumors, as has well been described by the referees and others, are highly heterogeneous, and so a single match is maybe not the best one, and a variety of different data sets provide the best overall fit to mutation rate.