Update for figures:

Figure 3:

Figure 4:

* Ray is updating

**Figure 5:**

* Simple updates to the colours of the IDH-non-codel patients ids.
* Colours for the mouse cluster 1-4
* Panel B: methylation PCA update colours similar to color shades to the LGr 1-4 cluster from panel A.
  + Greenish colour for LGm4-6
  + Reddish for LGm1
  + Purplish for LGm2
  + Bluelish for LGm3
* Maybe we add the updated TUMOR MAP with the highlighting of the mouse cluster 1-4 and triple mutant patients

Figure 7:

* Patient classification as C1a, C1b, third group as we discussed with Maria (mixed signature, or no clear c1a or c1b characterization.
  + Using the reduced list of the genes.
  + But using the entire list of genes that were used to derive the GSVA scores for this 3 group classification.
  + Fix cut off for all 3 mutant IDH patients cohorts:
* Combining the patient annotations with immune scores.
* Look at the Methylation profile of the C1a c1b annotated patients.

**PCA and GBM**

* Turcan Machine Learning Run analysis
* Check methylation levels C1A/C1B