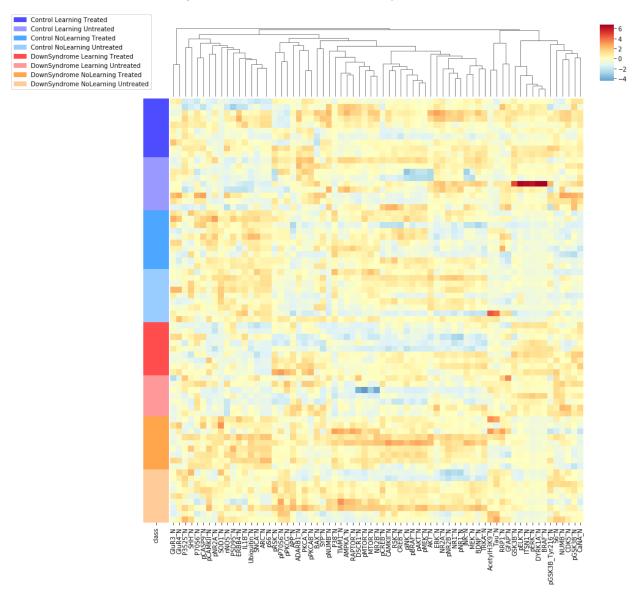
Introduction:

Which proteins' levels in the nucleus rise or fall with learning and/or differ between wildtype mouse brains and those of the Down Syndrome model? Which ones are affected by learning? Can I find interactions between genotype and learning that suggest ways learning differs between wildtype and Down Syndrome mics?

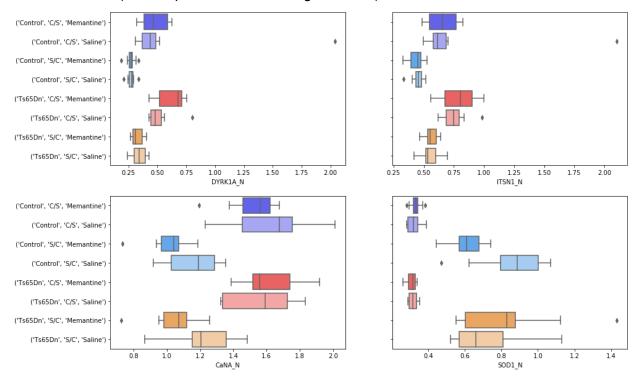
By clustering the proteins and keeping the mouse groups together, I can see that there is an obvious effect of the learning condition on the levels of many proteins:



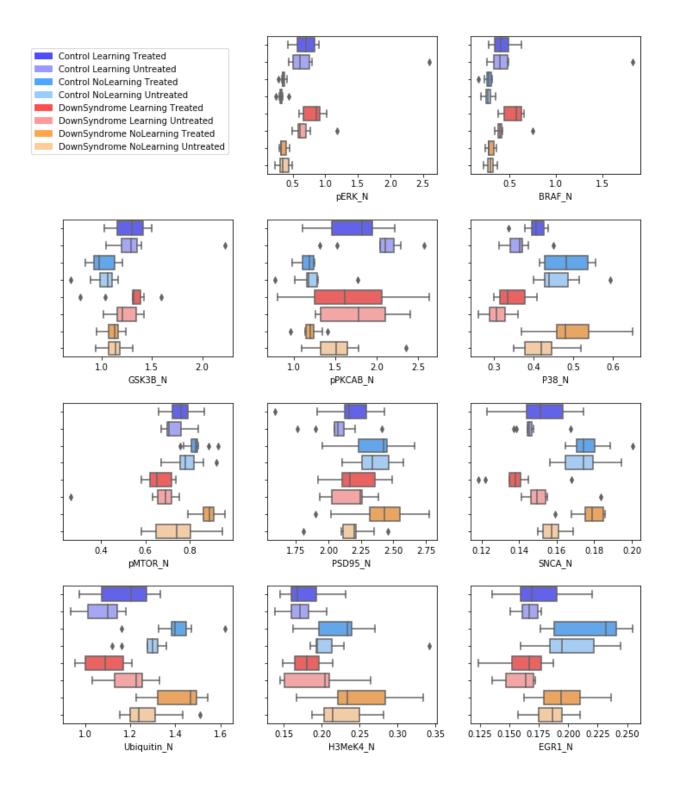
(I can also see here that there are a few mice with unusually high or low levels of some proteins, levels that may skew analysis especially based on means.)

Note that proteins with missing data points (8/76 proteins) are not compatible with this cluster map and are left out.

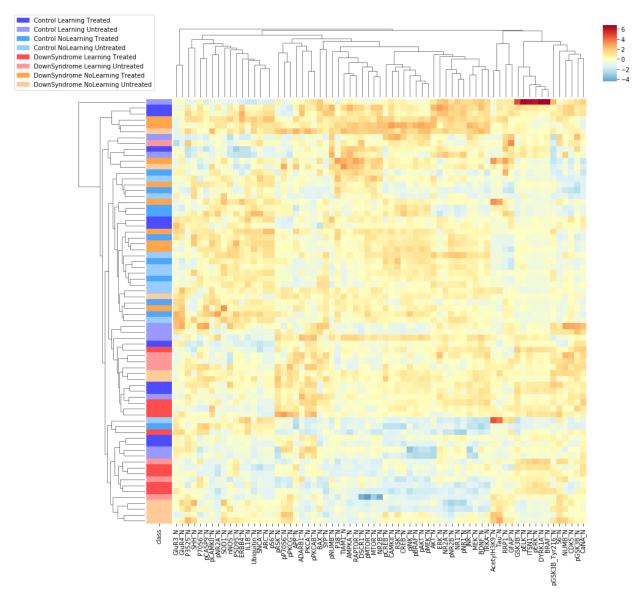
As an example, here are 3 proteins whose levels are up in mice that experienced learning and one that is down ("C/S" represents the learning condition):



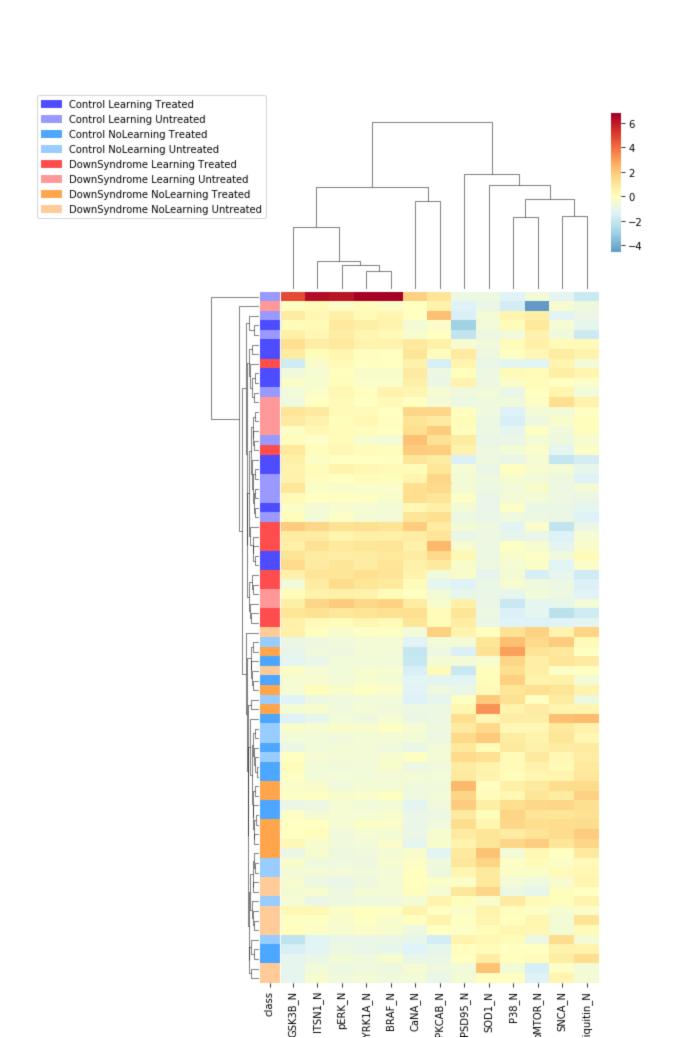
By scanning through bar graphs of every protein (see end of this document for complete set), I can visually pick out more proteins whose levels seem to be primarily affected by whether the animal experienced learning, though some may also interact with genotype or drug treatment (and some groups*proteins have means that are not the best measure due to the effect of outliers).



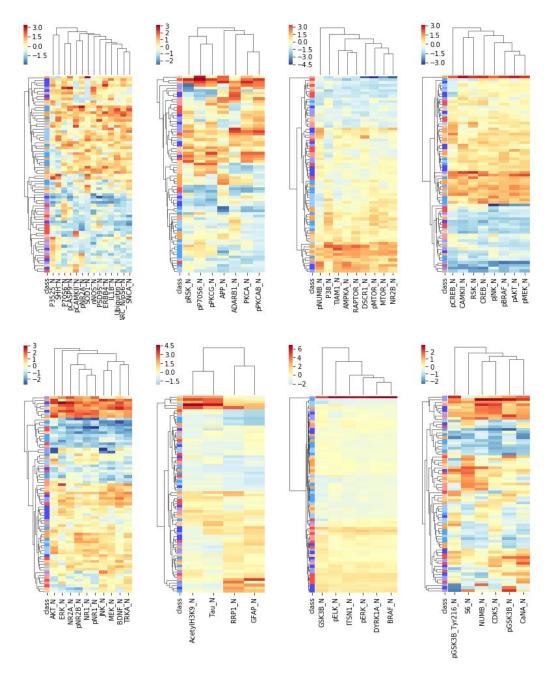
What about the other variables, treatment and genotype? I didn't see visually obvious clusters of proteins that distinguished them, but do they contribute to distinguishing the mice when I cluster both proteins and mice?



There is a cluster that mostly consists of wildtype/no learning mice (light blues), with some members of the DS model/no learning/memantine-treated (bright orange) group. That is the clearest cluster, though DS model/learning tends to cluster with DS model/no learning/untreated, suggesting a specific effect of memantine on DS mice not experiencing learning. In spite of the effects of the learning condition on many individual proteins, mice from the wildtype/learning groups are scattered in multiple clusters. This changes if the clustering is only done based on a subset of proteins that appear to be affected by learning:



Dividing proteins into clusters and then clustering samples based on those subsets does not clearly identify groups of proteins whose levels are specific to genotype (which would be seen by dark and light blues clustering away from reds and oranges):



It looks like learning has a stronger effect on the nuclear levels of this subset of proteins than does genotype or treatment; I will need other methods to identify these effects and the interactions between variables.

Appendix: bar graphs of all proteins by group, mean ± s.e.m.:

