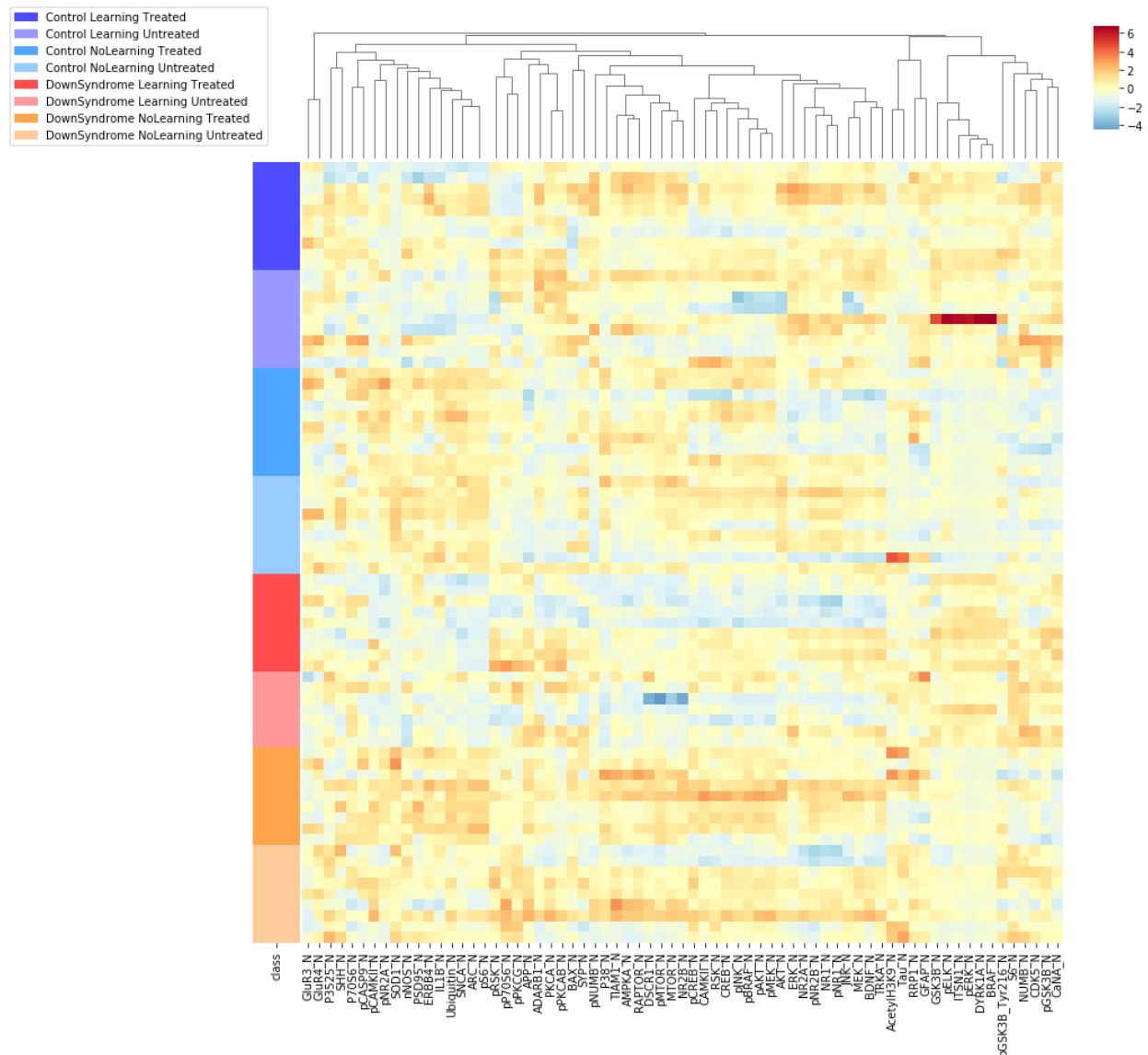


Which proteins' levels in the nucleus rise or fall with learning and/or differ between wildtype mouse brains and those of the Down Syndrome model? Which ones are affected by learning? Can I find interactions between genotype and learning that suggest ways learning differs between wildtype and Down Syndrome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

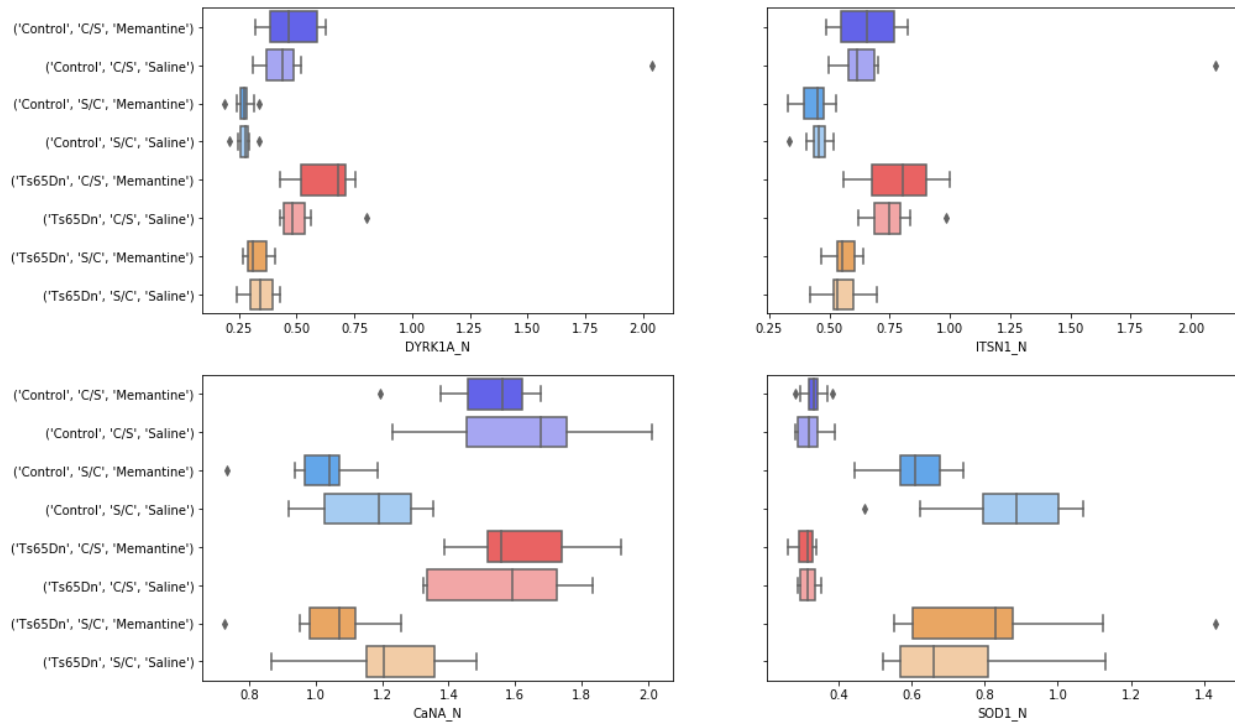
By clustering the proteins and keeping the mouse groups together, I can see that there is an obvious effect of the learning condition on the levels of many proteins:



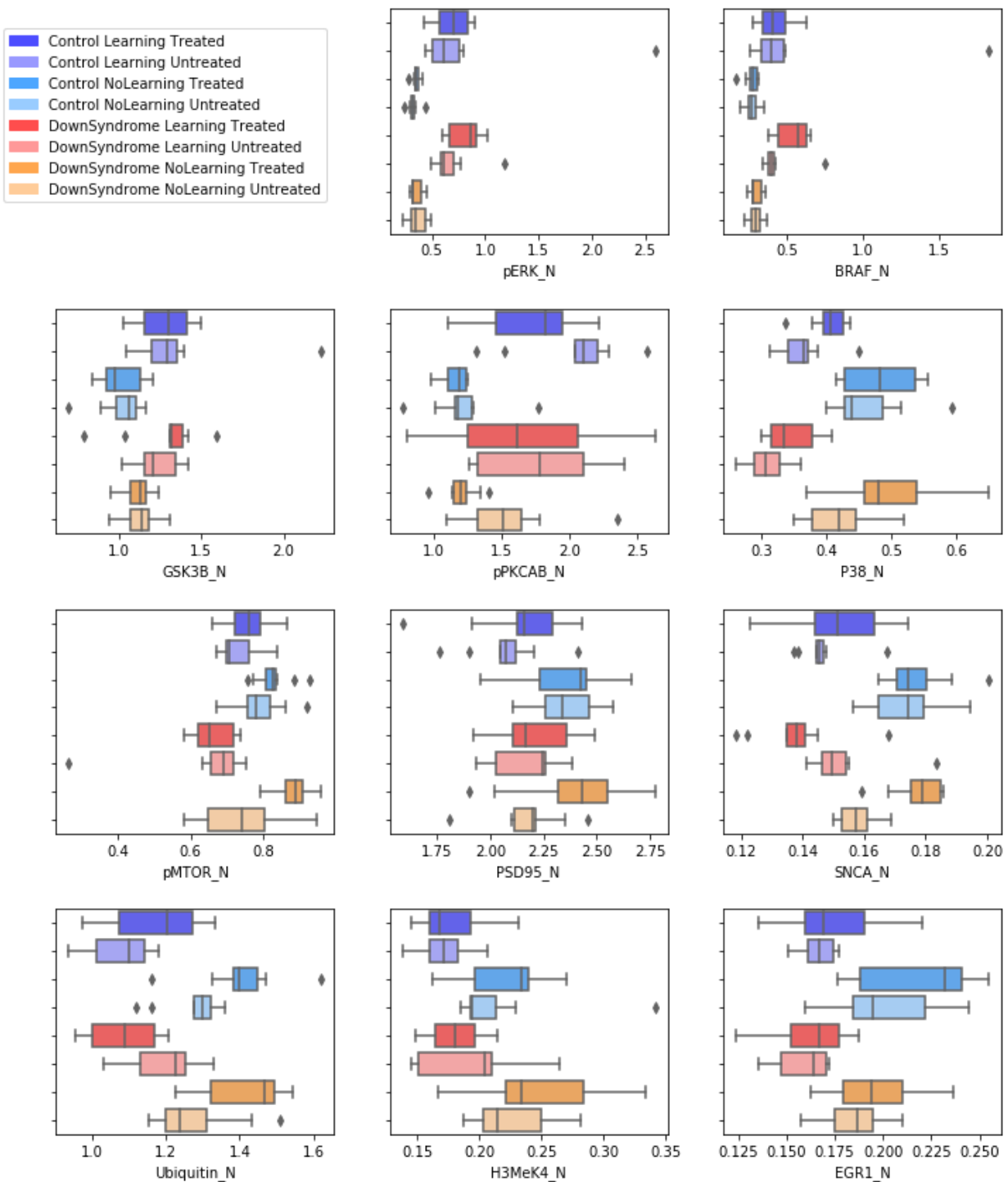
(I can also see here that there are a few mice with unusually high or low levels of some proteins, levels that may skew analysis especially based on means.)

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

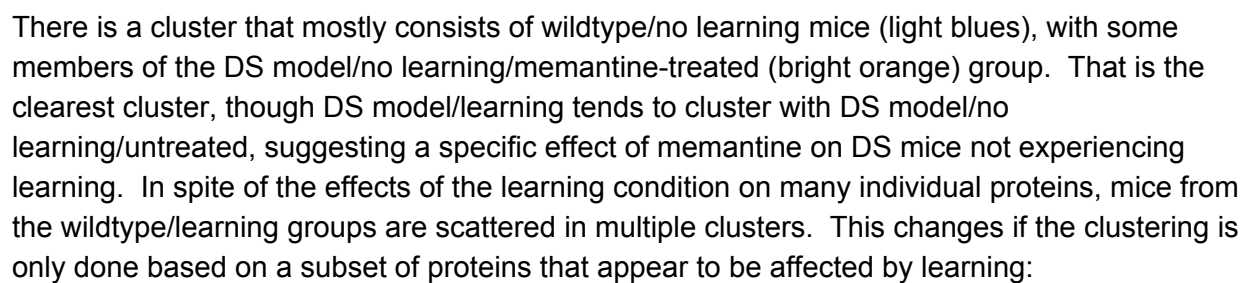
As an example, here are 3 proteins whose levels are up in mice that experienced learning and one that is down (“C/S” represents the learning condition):



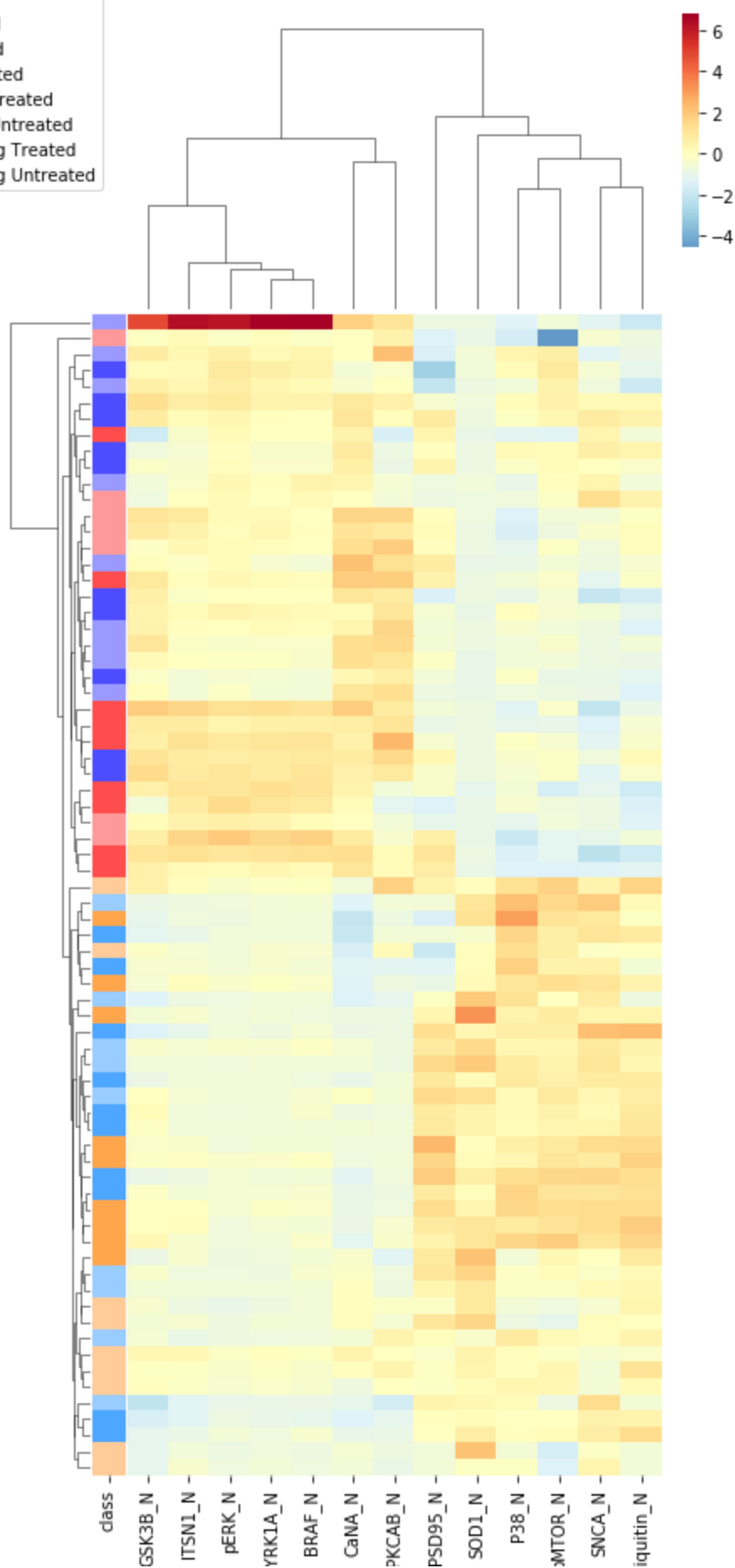
By scanning through bar graphs of every protein (see end of this document for complete set), I can visually pick out more proteins whose levels seem to be primarily affected by whether the animal experienced learning, though some may also interact with genotype or drug treatment (and some groups*proteins 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?



- Control Learning Treated
- Control Learning Untreated
- Control NoLearning Treated
- Control NoLearning Untreated
- DownSyndrome Learning Treated
- DownSyndrome Learning Untreated
- DownSyndrome NoLearning Treated
- DownSyndrome NoLearning Untreated



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

