Researching “non-coding DNA” to find causative risk factors in ALS

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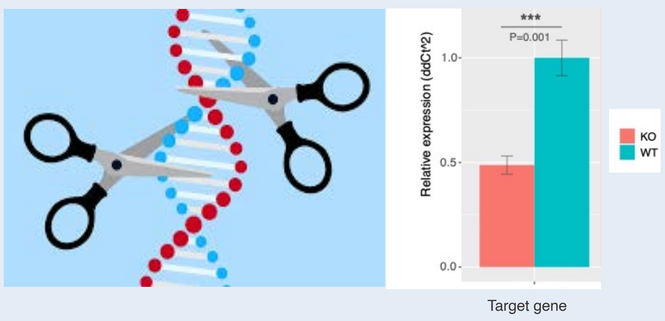
Why research “non-coding DNA” in ALS?

- We believe that hidden changes to “non-coding DNA” play a major role in ALS.
- Discovering these non-coding DNA changes will require new methodological approaches but could reveal a wealth of undiscovered genetic risk factors.
- A deeper understanding of non-coding DNA could accordingly advance efforts in both ALS drug development and genetic counselling.

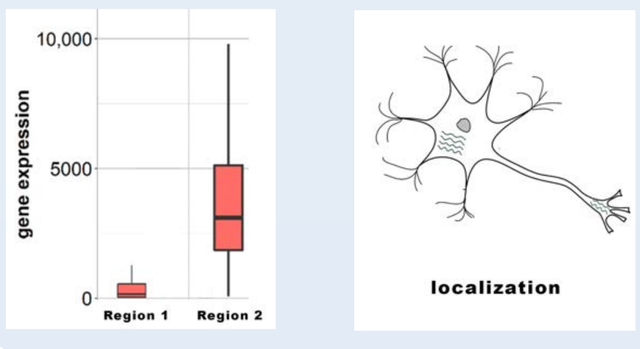
Methods

- Measure DNA activities in human brain and spinal cord tissue, link non-coding DNA mutations to abnormal DNA activities in patients.
- Measure RNA signals in brain and spinal cord tissue, link non-coding DNA mutations to abnormal RNA signals in patients.
- Characterize the effects of non-coding DNA mutations from ALS patients using lab cultured brain cells.

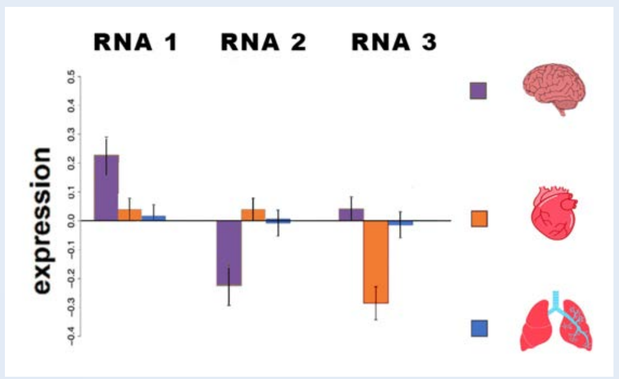
Gene editing to artificially introduce changes to non-coding DNA



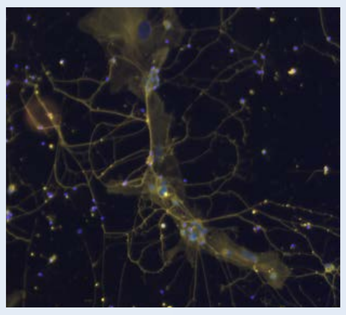
Find non-coding elements that impact RNA regulation in ALS

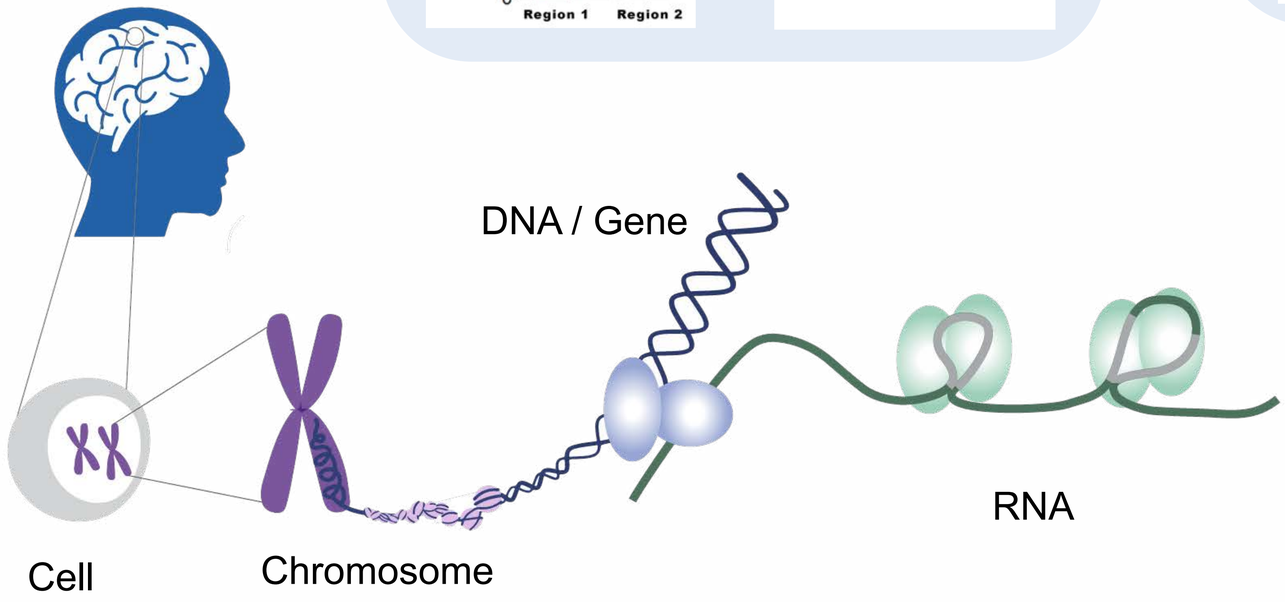


Find RNAs that are specific to the brain

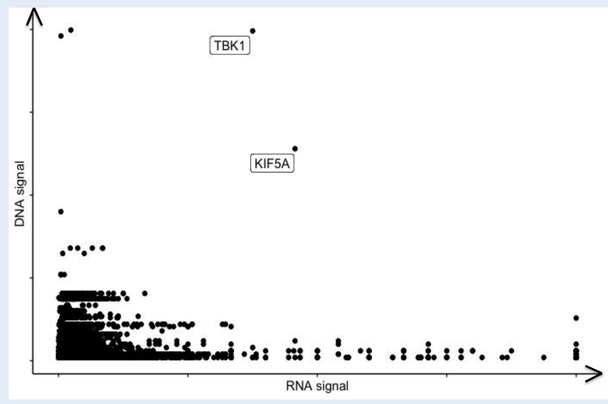


Modelling ALS in cultured brain cells





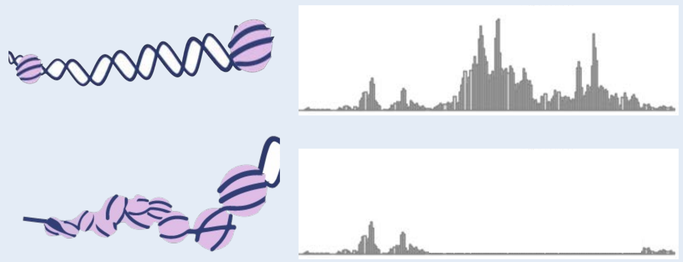
Link RNA signals to non-coding DNA signals



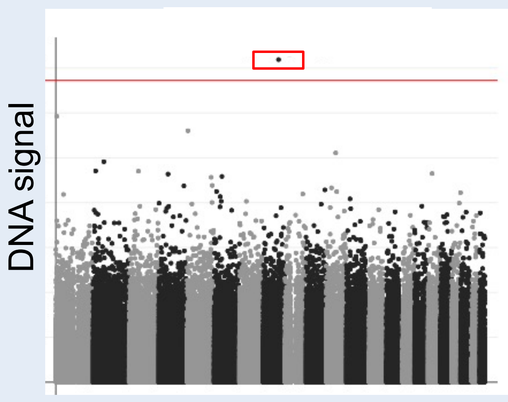
Leverage large scale genetics data from ALS patients & healthy controls

project MinE
Make it yours

Contrast non-coding DNA activity in ALS patients and healthy controls



Find abnormal non-coding DNA activity in ALS



Results

- We have identified multiple examples of novel non-coding DNA disruptions that appear to contribute to ALS risk (on-going research).
- We have been working to corroborate novel findings with independent evidence and to create online tools to support reuse of our work by others.

What’s next?

- We are conducting on-going laboratory investigations of selected non-coding DNA disruptions using artificial brain cells.
- We are working to implement new AI based strategies for deeper insights into new kinds of non-coding DNA disruptions in ALS.

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