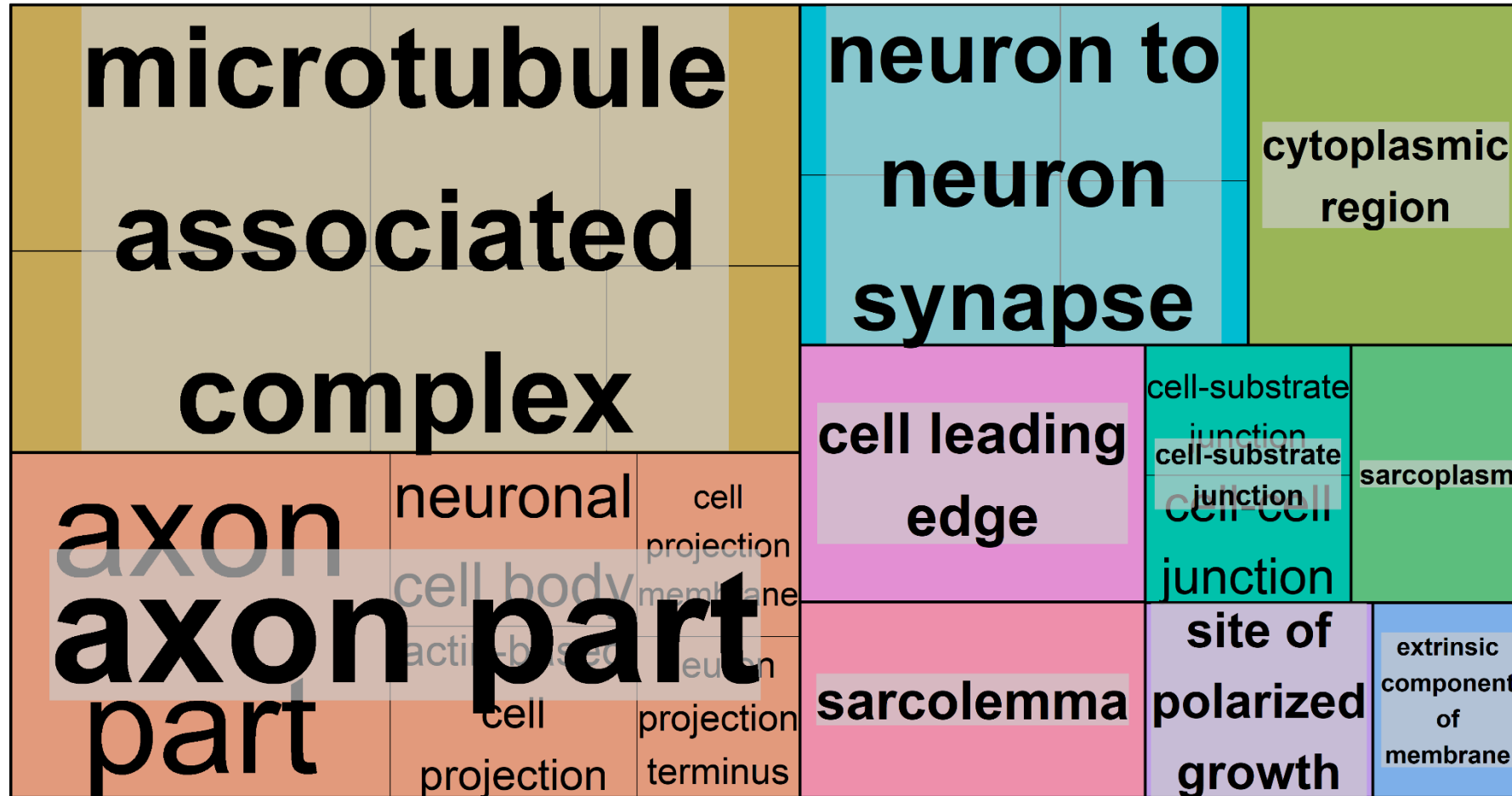


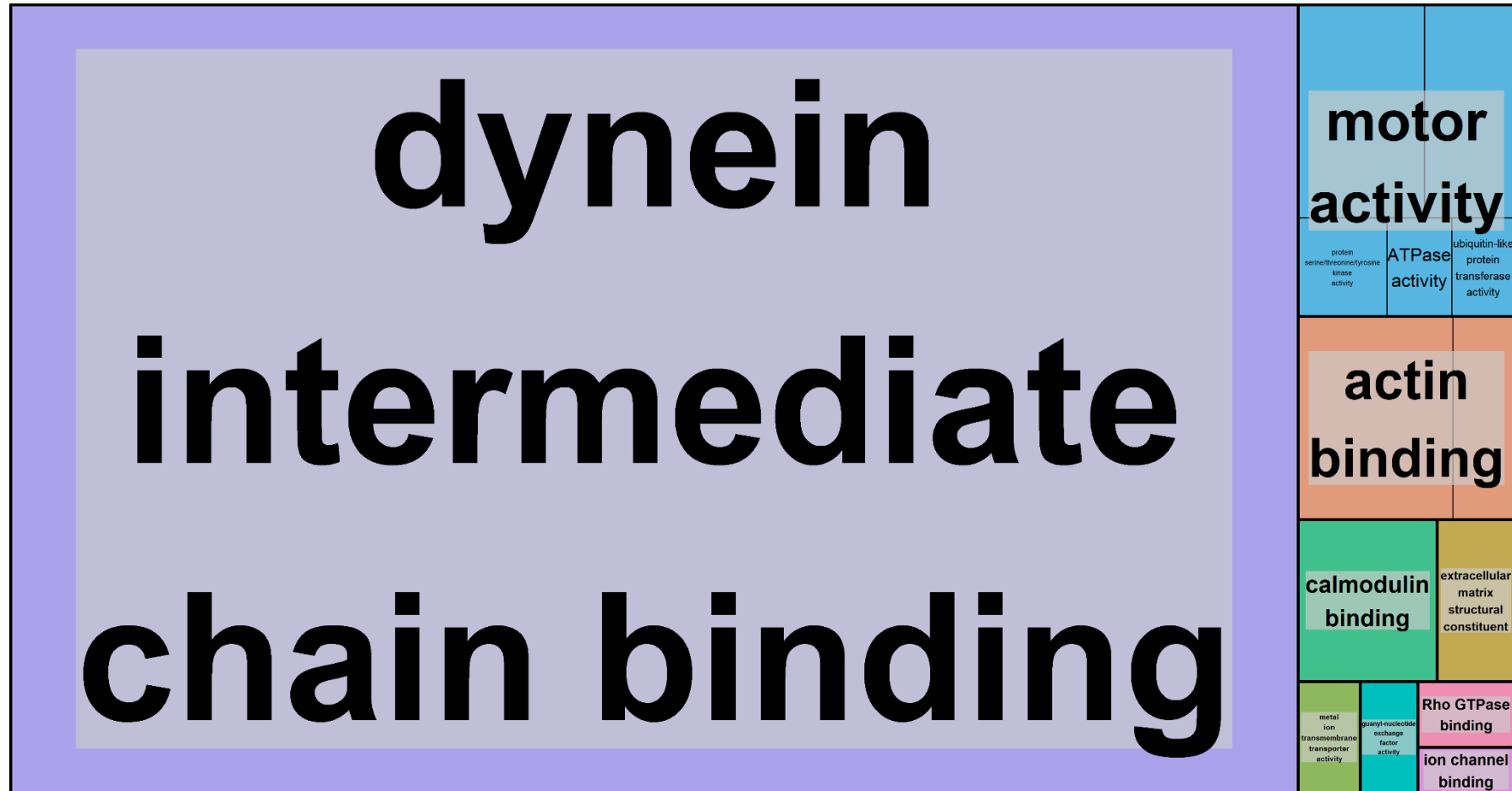
Cellular Component terms for the longest genes



**Supplementary Figure 2A.**

Cellular Component terms found associated to genes with the longest transcript length (5%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

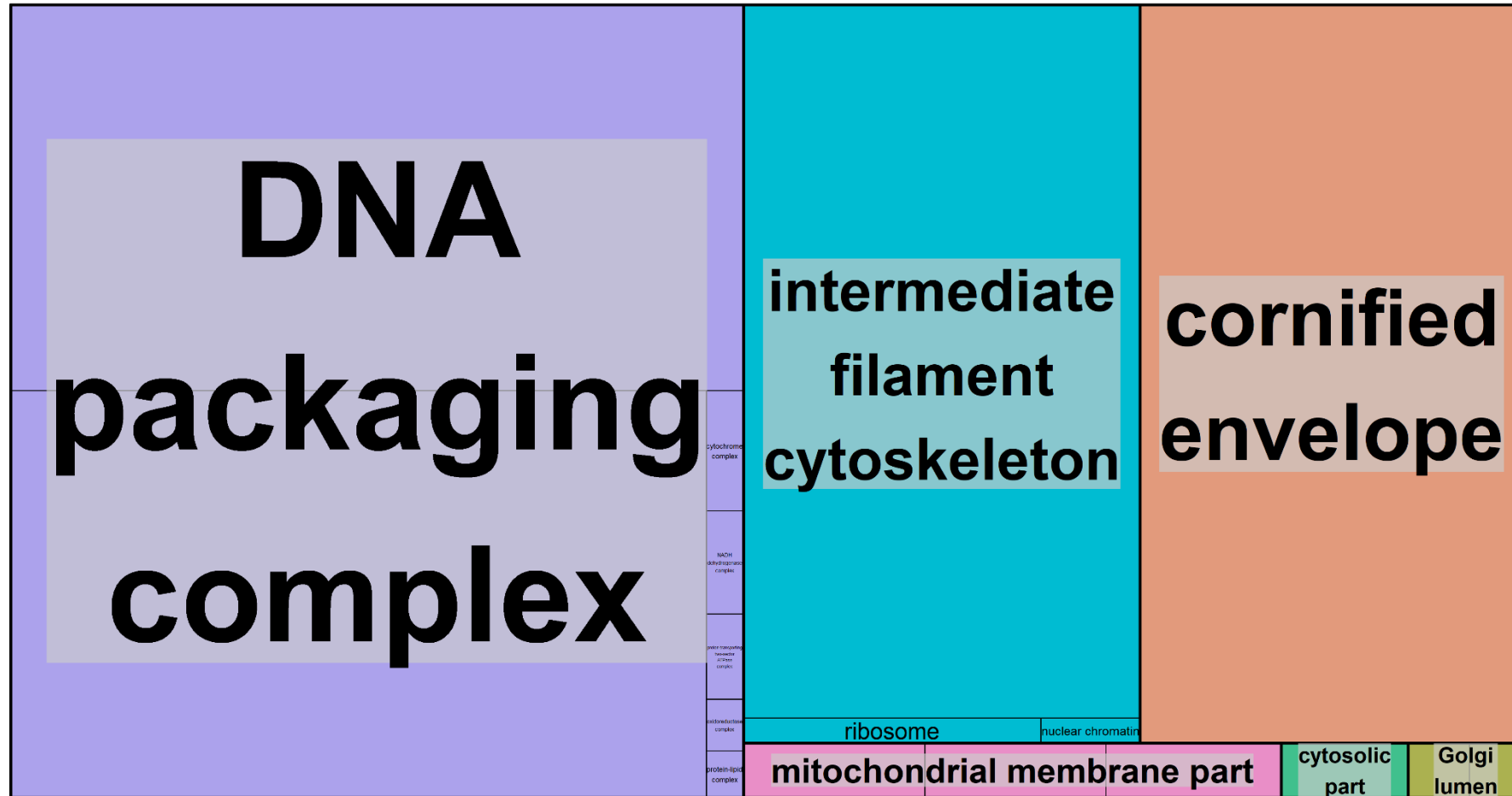
## Molecular Function terms for the longest genes



### Supplementary Figure 2B.

Molecular Function terms found associated to genes with the longest transcript length (5%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini-Hochberg method.

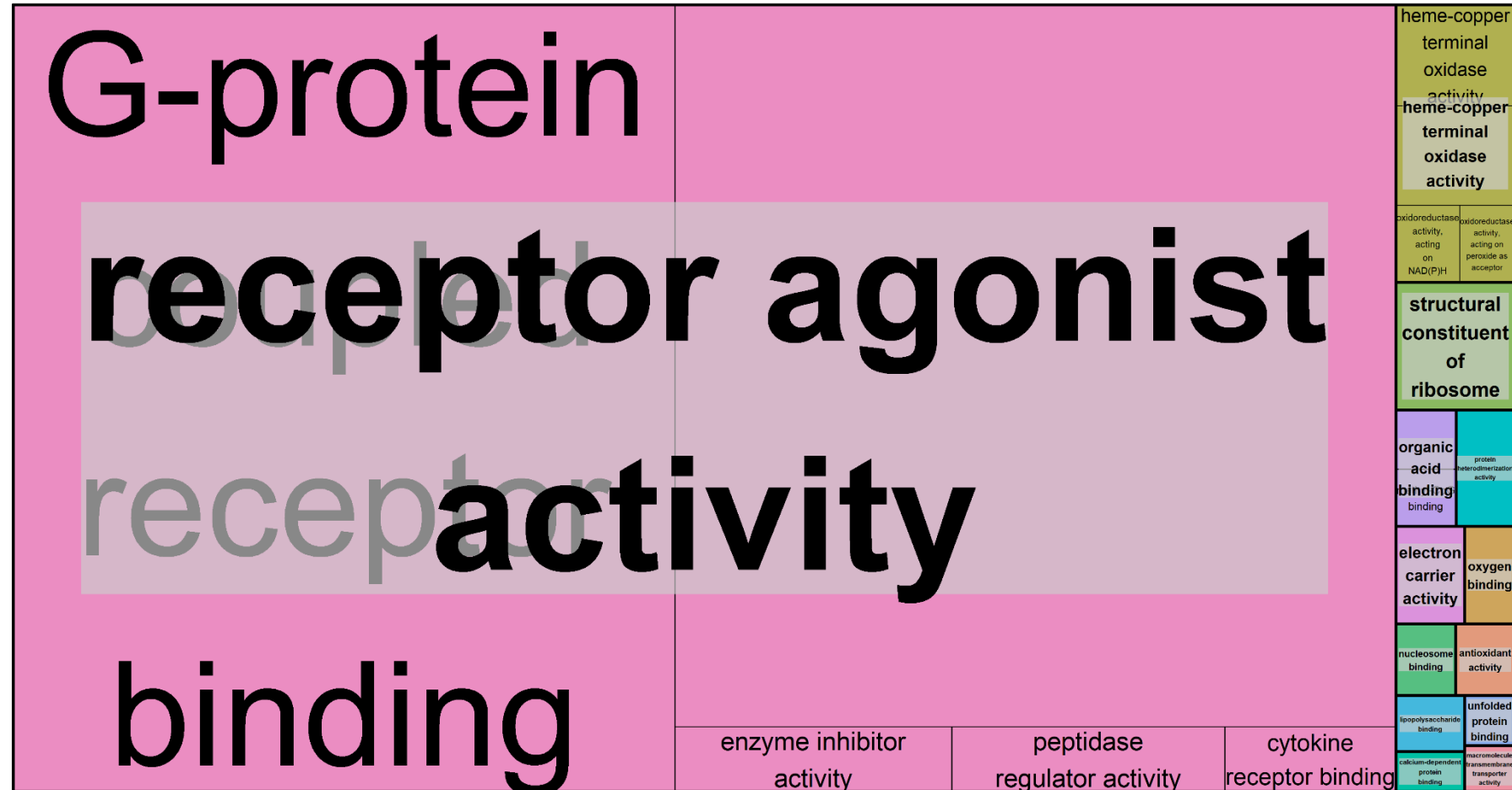
## Cellular Component terms for the smallest genes



### Supplementary Figure 2C.

Cellular Component terms found associated to genes with the smallest transcript length (5%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini-Hochberg method.

## Molecular Function terms for the smallest genes



### Supplementary Figure 2D.

Molecular Function terms found associated to genes with the smallest transcript length (5%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

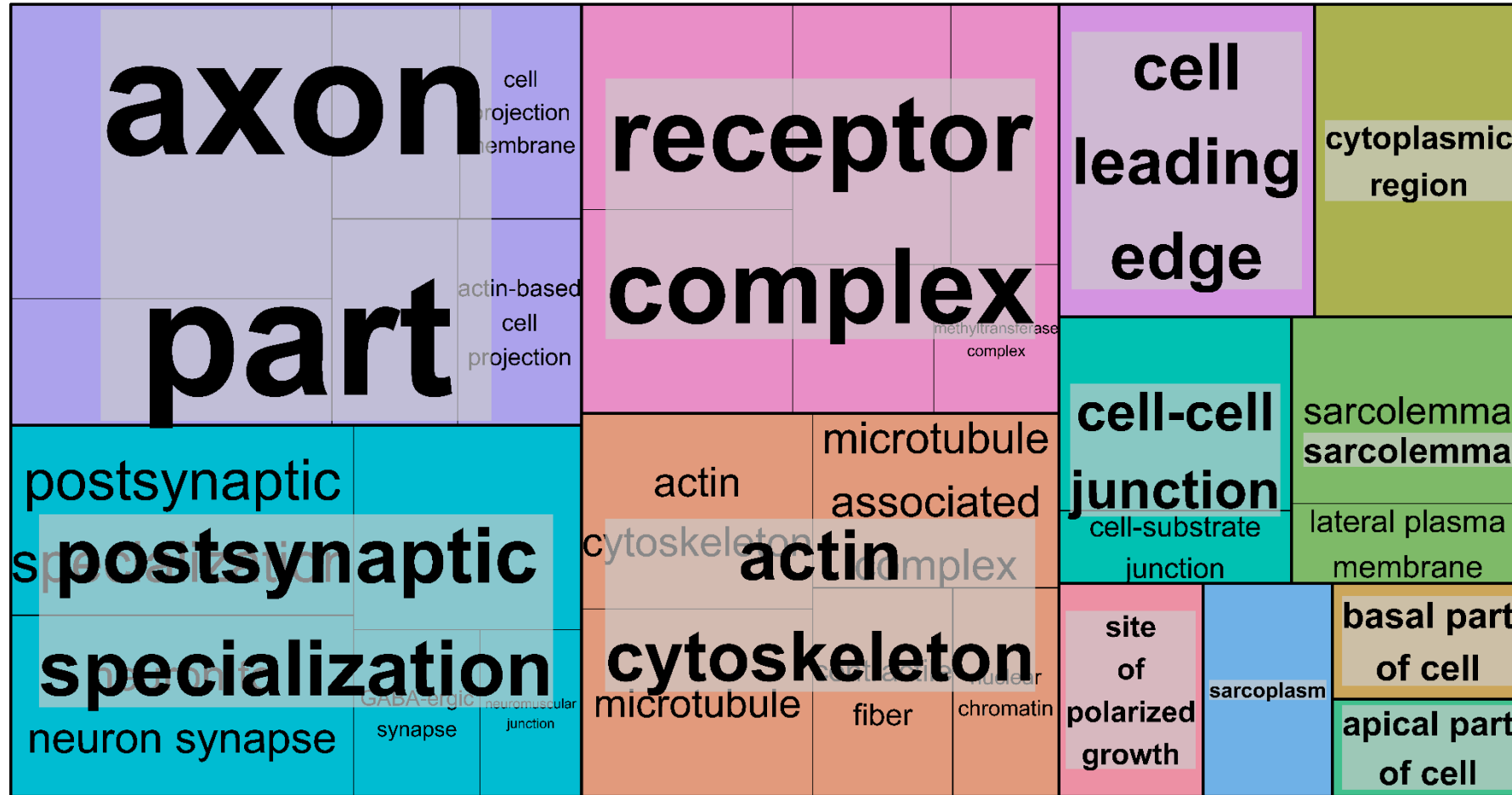
## Biological Process terms for the top 10% longest genes



### Supplementary Figure 2E.

Biological Process terms found associated to genes with the longest transcript length (10%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

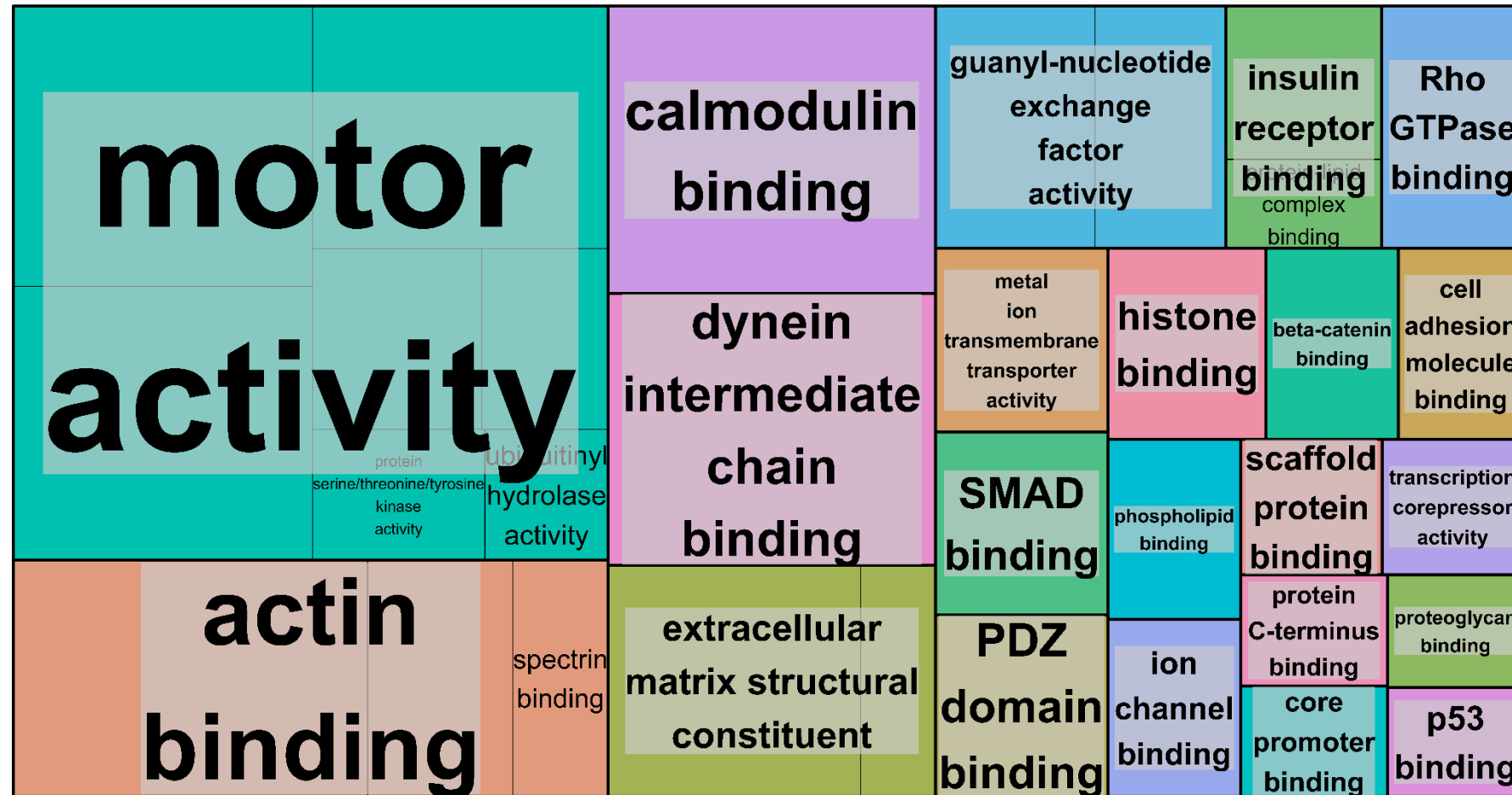
Cellular Component terms for the top 10% longest genes



**Supplementary Figure 2F.**

Cellular Component terms found associated to genes with the longest transcript length (10%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

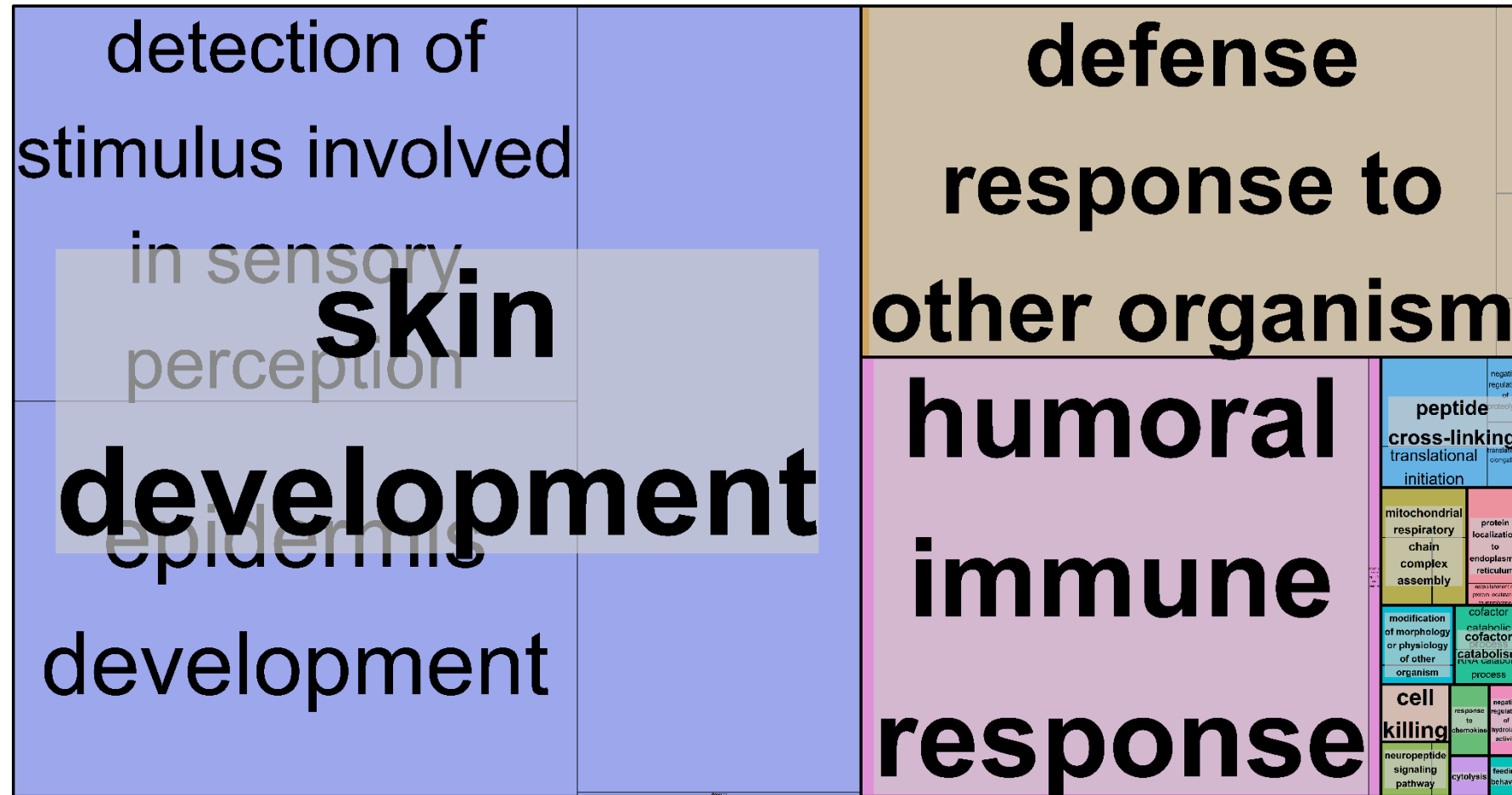
Molecular Function terms for the top 10% longest genes



**Supplementary Figure 2G.**

Molecular Function terms found associated to genes with the longest transcript length (10%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Biological Process terms for the top 10% smallest genes



### Supplementary Figure 2H.

Biological Process terms found associated to genes with the smallest transcript length (10%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

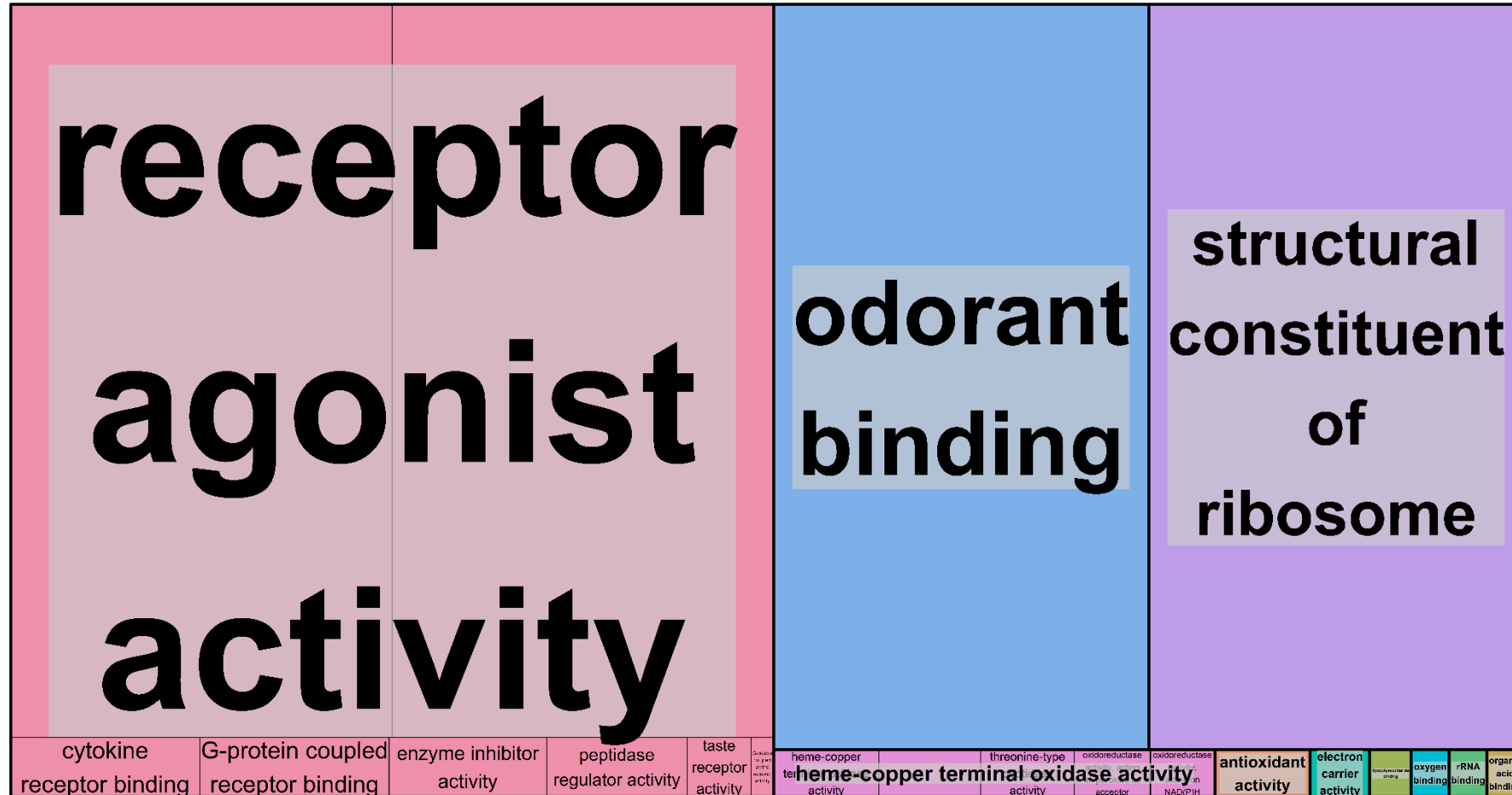


The treemap visualization displays the hierarchical structure of a cell, with the following components and their relative sizes:

- Intermediate filament cytoskeleton (pink area):** The largest area, containing:
  - intermediate filament** (large text)
  - cytoskeleton** (medium text)
  - ribosome** (large text)
- DNA packaging complex (light blue box within the blue area):** A large box containing the text **DNA packaging complex**.
- cornified envelope (orange area):** A large area on the right side.
- cytosolic part (green area):** A small area at the bottom left.
- respiratory chain (teal area):** A small area at the bottom center.
- vesicle lumen (purple area):** A small area at the bottom right.
- Other components (small boxes at the bottom left):**
  - NADH dehydrogenase complex**
  - cytochrome complex**
  - cytochrome b5**
  - cytochrome c**
  - cytochrome c1**
  - cytochrome c2**
  - cytochrome c3**
  - cytochrome c4**
  - cytochrome c5**
  - cytochrome c6**
  - cytochrome c7**
  - cytochrome c8**
  - cytochrome c9**
  - cytochrome c10**
  - cytochrome c11**
  - cytochrome c12**
  - cytochrome c13**
  - cytochrome c14**
  - cytochrome c15**
  - cytochrome c16**
  - cytochrome c17**
  - cytochrome c18**
  - cytochrome c19**
  - cytochrome c20**
  - cytochrome c21**
  - cytochrome c22**
  - cytochrome c23**
  - cytochrome c24**
  - cytochrome c25**
  - cytochrome c26**
  - cytochrome c27**
  - cytochrome c28**
  - cytochrome c29**
  - cytochrome c30**
  - cytochrome c31**
  - cytochrome c32**
  - cytochrome c33**
  - cytochrome c34**
  - cytochrome c35**
  - cytochrome c36**
  - cytochrome c37**
  - cytochrome c38**
  - cytochrome c39**
  - cytochrome c40**
  - cytochrome c41**
  - cytochrome c42**
  - cytochrome c43**
  - cytochrome c44**
  - cytochrome c45**
  - cytochrome c46**
  - cytochrome c47**
  - cytochrome c48**
  - cytochrome c49**
  - cytochrome c50**
  - cytochrome c51**
  - cytochrome c52**
  - cytochrome c53**
  - cytochrome c54**
  - cytochrome c55**
  - cytochrome c56**
  - cytochrome c57**
  - cytochrome c58**
  - cytochrome c59**
  - cytochrome c60**
  - cytochrome c61**
  - cytochrome c62**
  - cytochrome c63**
  - cytochrome c64**
  - cytochrome c65**
  - cytochrome c66**
  - cytochrome c67**
  - cytochrome c68**
  - cytochrome c69**
  - cytochrome c70**
  - cytochrome c71**
  - cytochrome c72**
  - cytochrome c73**
  - cytochrome c74**
  - cytochrome c75**
  - cytochrome c76**
  - cytochrome c77**
  - cytochrome c78**
  - cytochrome c79**
  - cytochrome c80**
  - cytochrome c81**
  - cytochrome c82**
  - cytochrome c83**
  - cytochrome c84**
  - cytochrome c85**
  - cytochrome c86**
  - cytochrome c87**
  - cytochrome c88**
  - cytochrome c89**
  - cytochrome c90**
  - cytochrome c91**
  - cytochrome c92**
  - cytochrome c93**
  - cytochrome c94**
  - cytochrome c95**
  - cytochrome c96**
  - cytochrome c97**
  - cytochrome c98**
  - cytochrome c99**
  - cytochrome c100**

Cellular Component terms found associated to genes with the smallest transcript length (10%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

# Molecular Function terms for the top 10% smallest genes



## Supplementary Figure 2J.

Molecular Function terms found associated to genes with the smallest transcript length (10%). The significance level was  $p < 0.05$  and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.