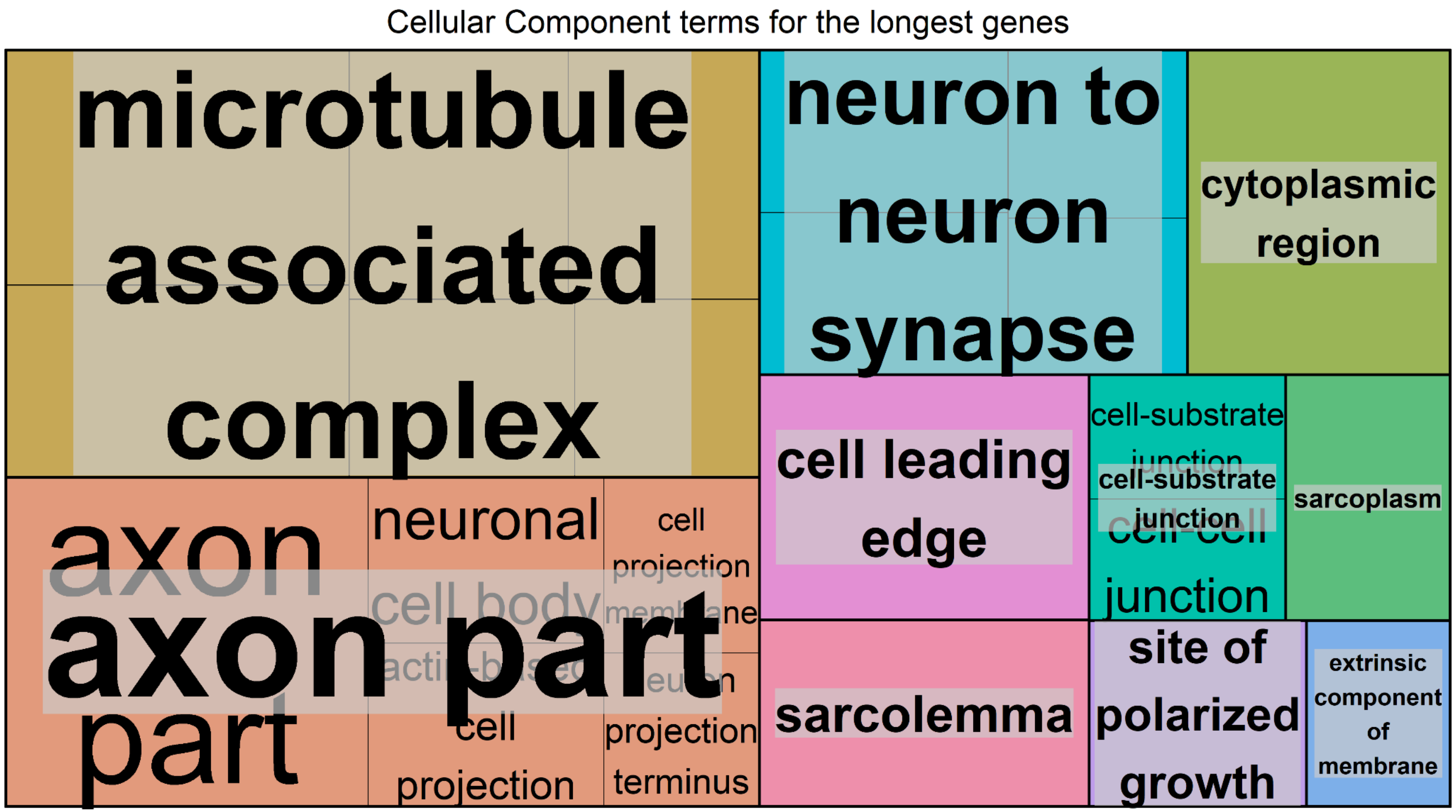
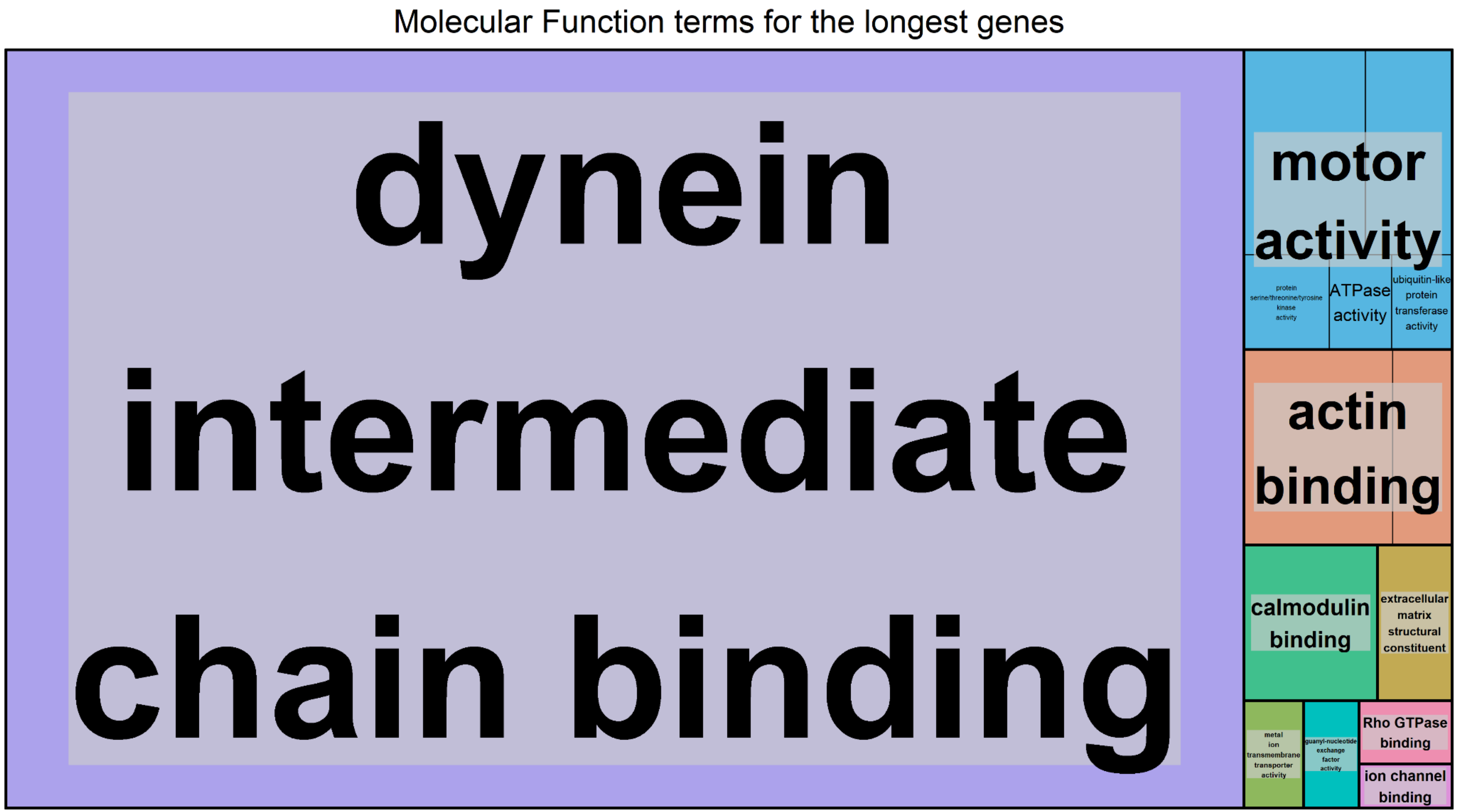
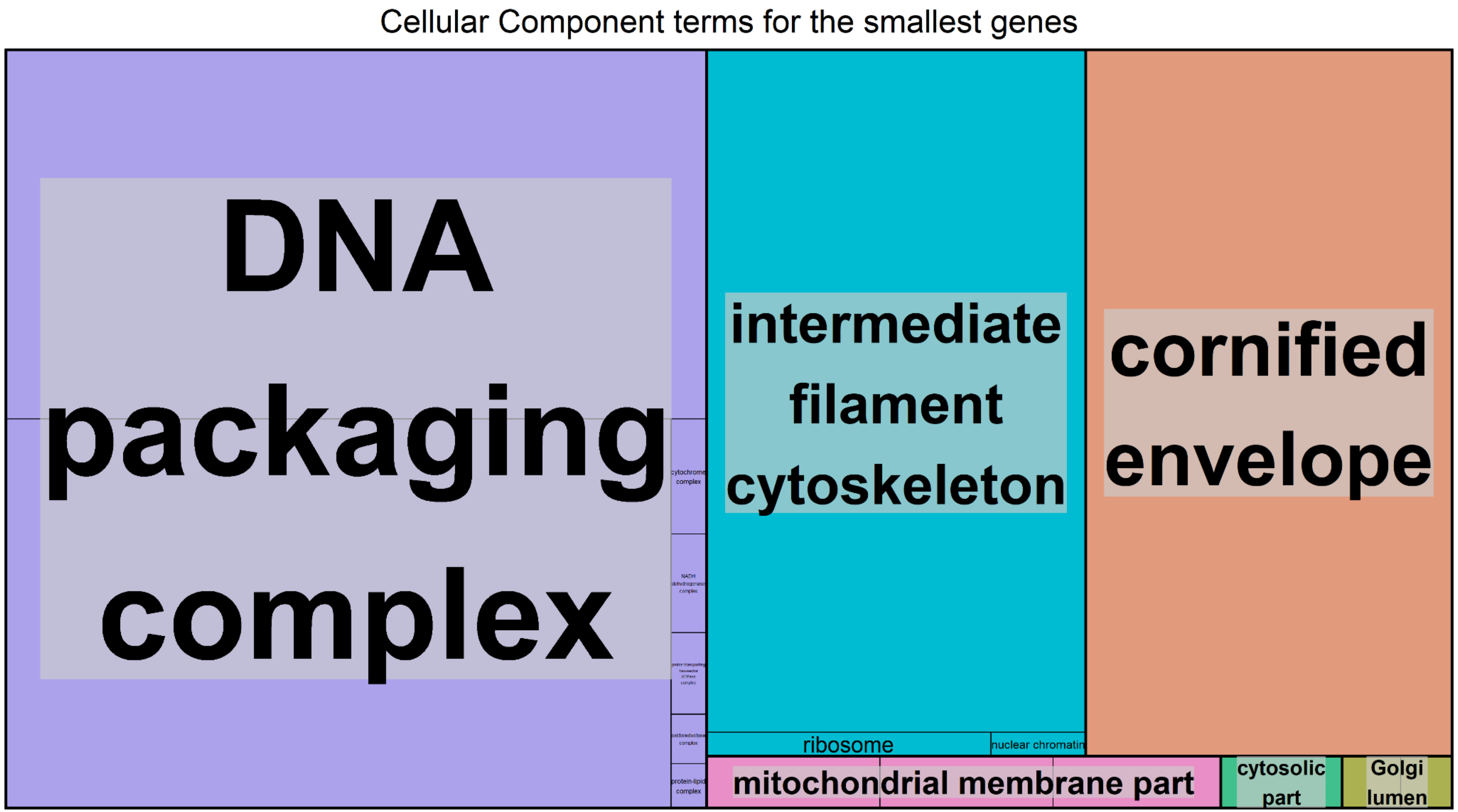


Supplementary Figure 3A.

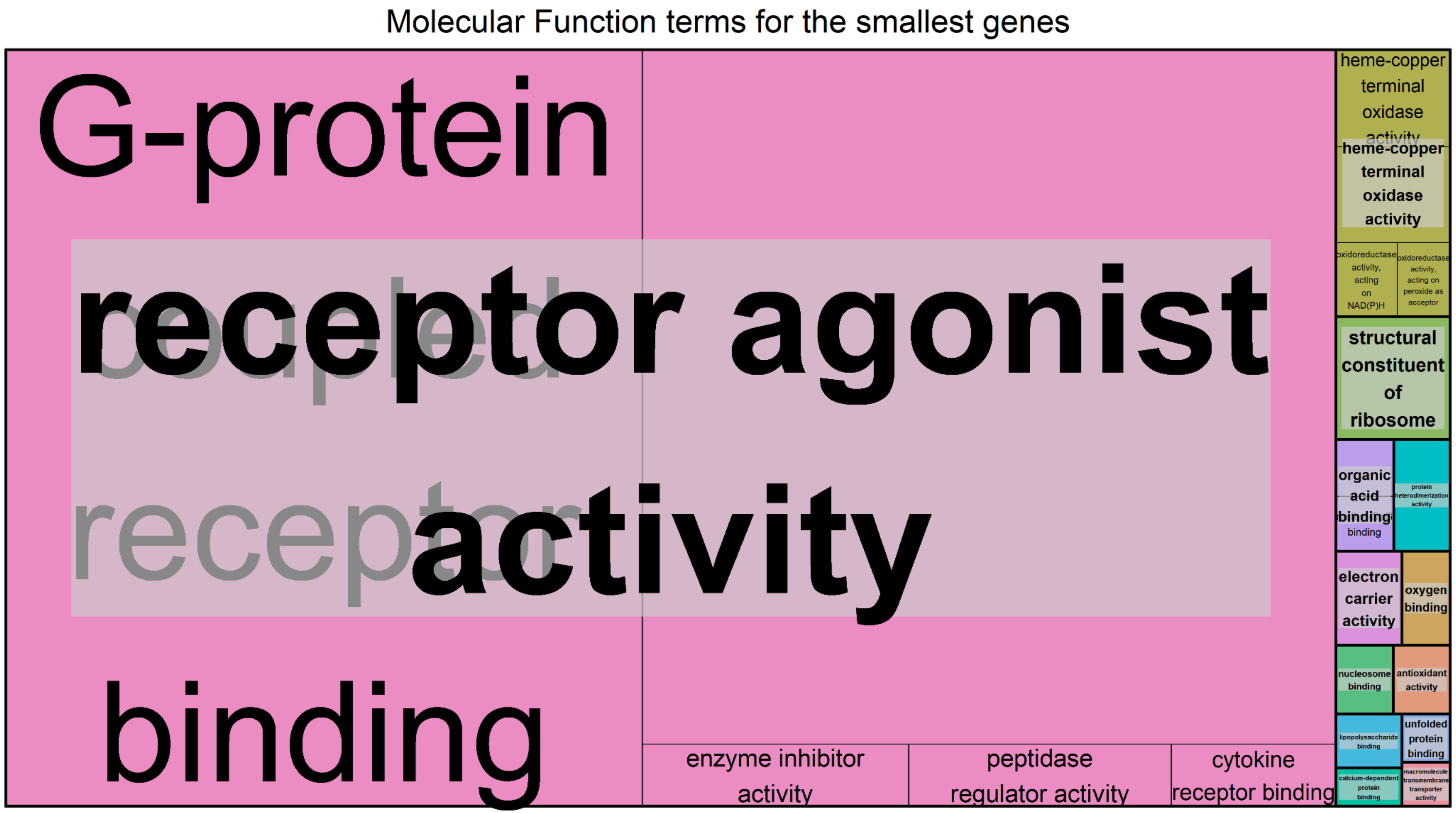
Cellular Component terms found associated to genes with the longest transcript length (5%). The significance level was $p<0.05$ and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.



Supplementary Figure 3B.
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.

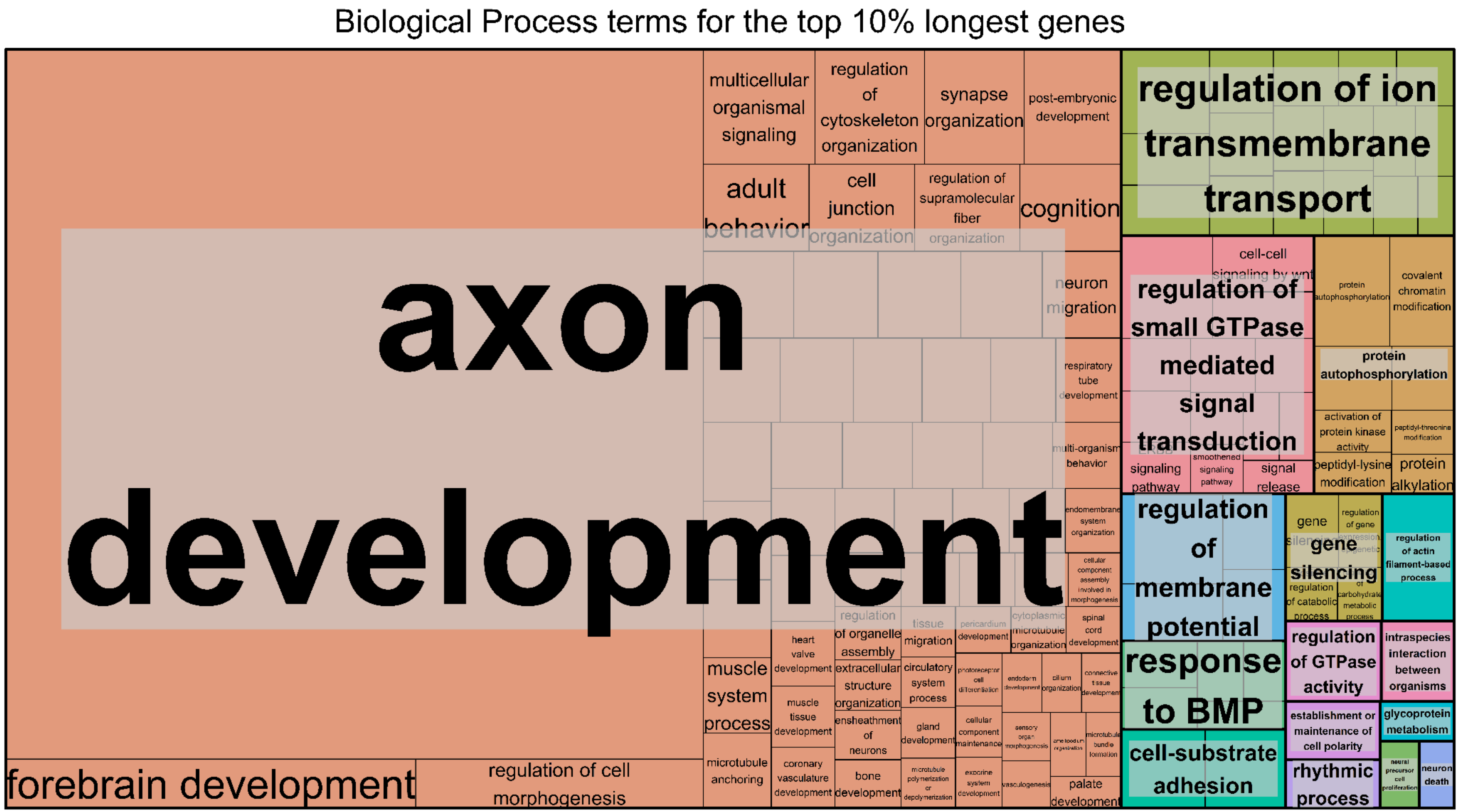


Supplementary Figure 3C.
Cellular Component terms found associated to genes with the smallest transcript length (5%). The significance level was $p<0.05$ and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.



Supplementary Figure 3D.

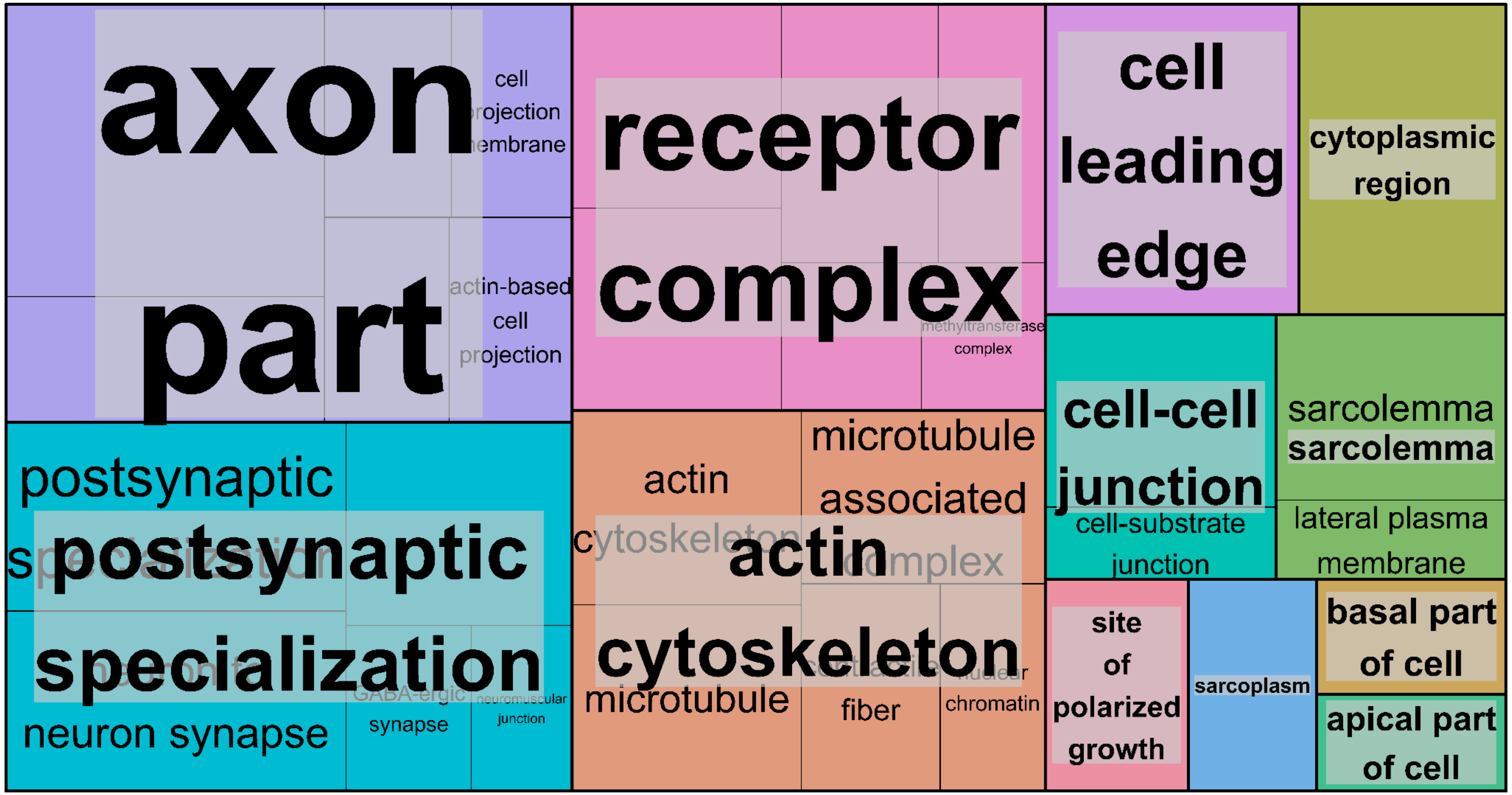
Molecular Function terms found associated to genes with the smallest transcript length (5%). The significance level was $p<0.05$ and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.



Biological Process terms for the top 10% longest genes

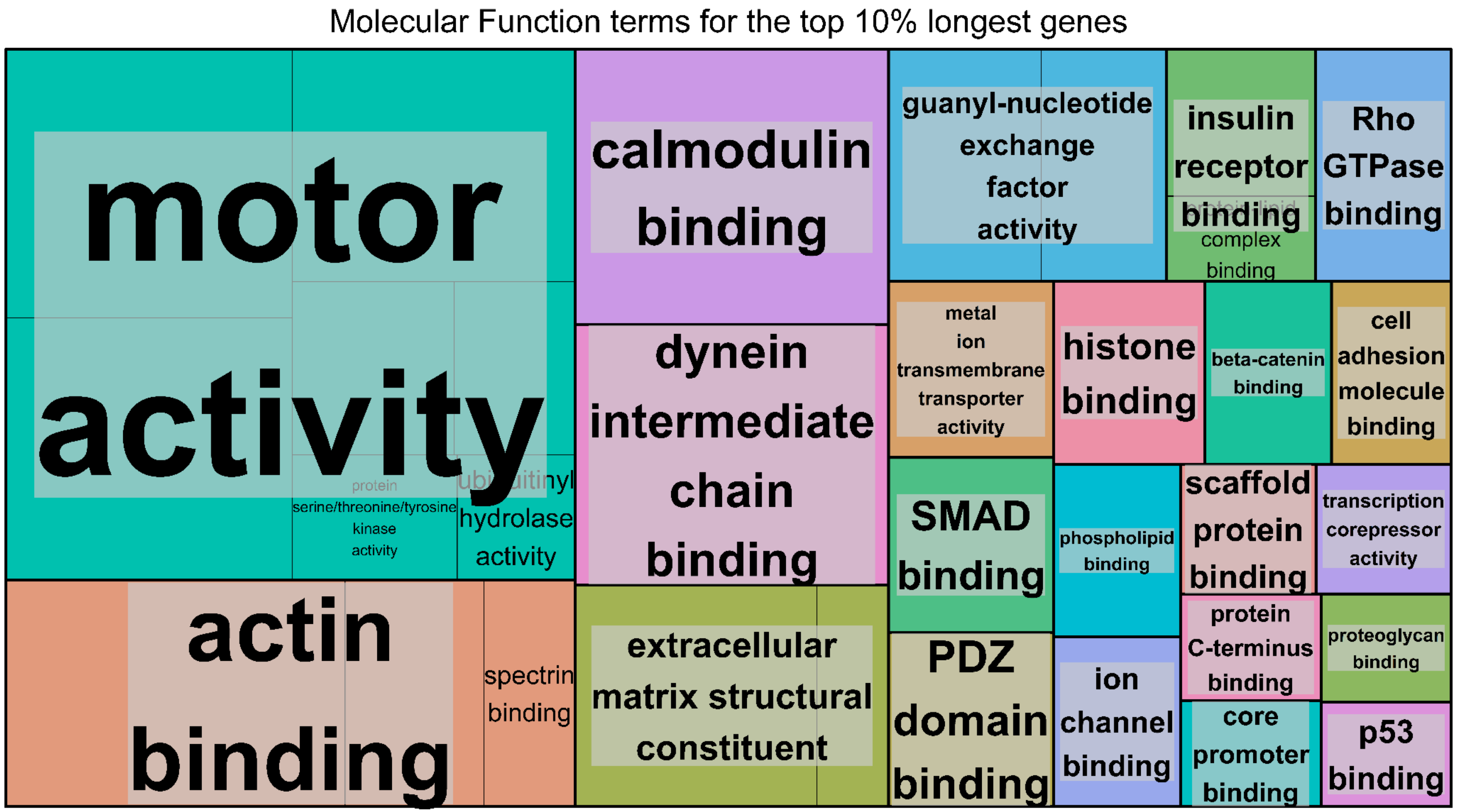
Supplementary Figure 3E.
Biological Process terms found associated to genes with the longest transcript length (10%). The significance level was $p<0.05$ and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Cellular Component terms for the top 10% longest genes



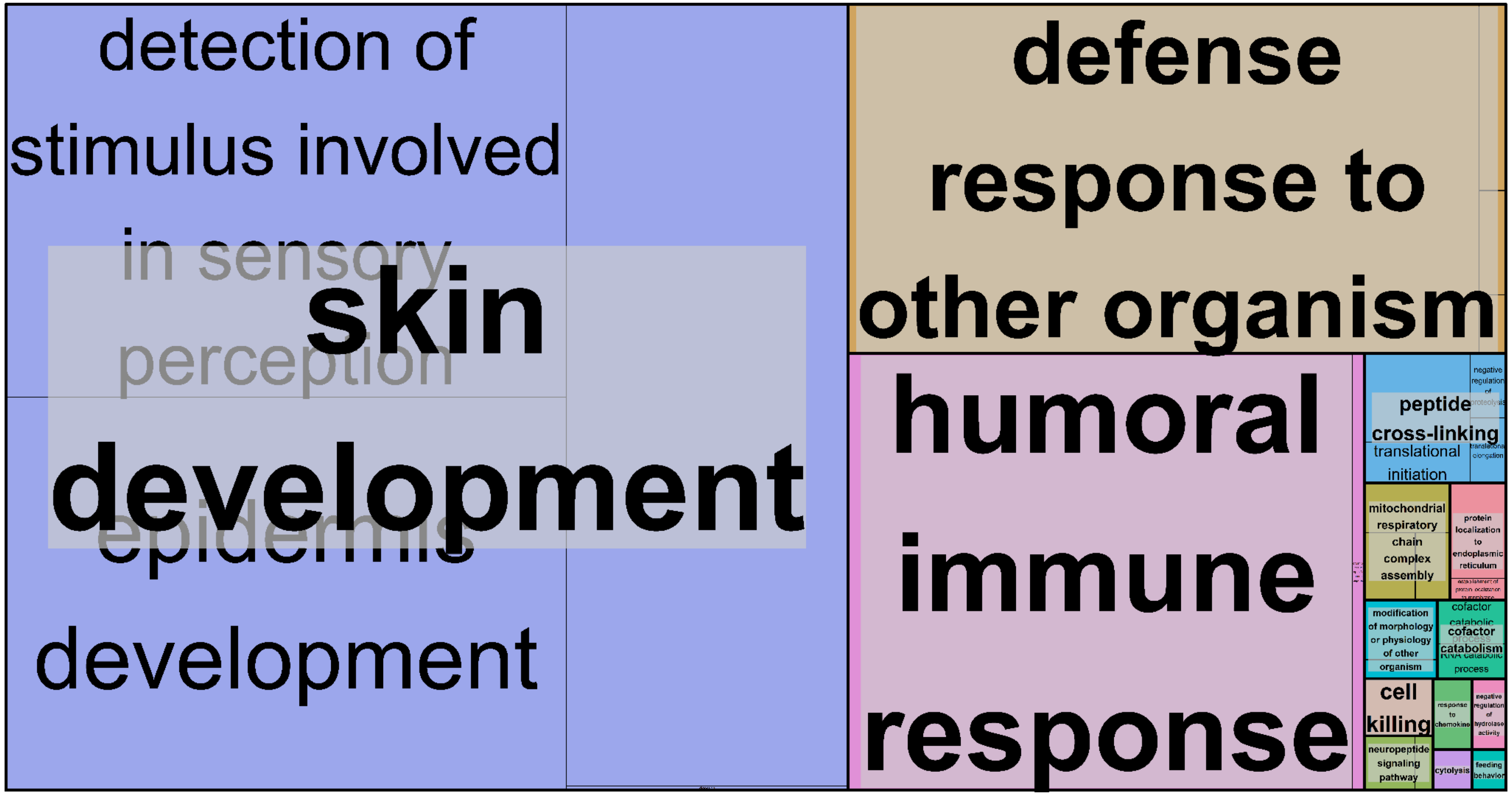
Supplementary Figure 3F.

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.

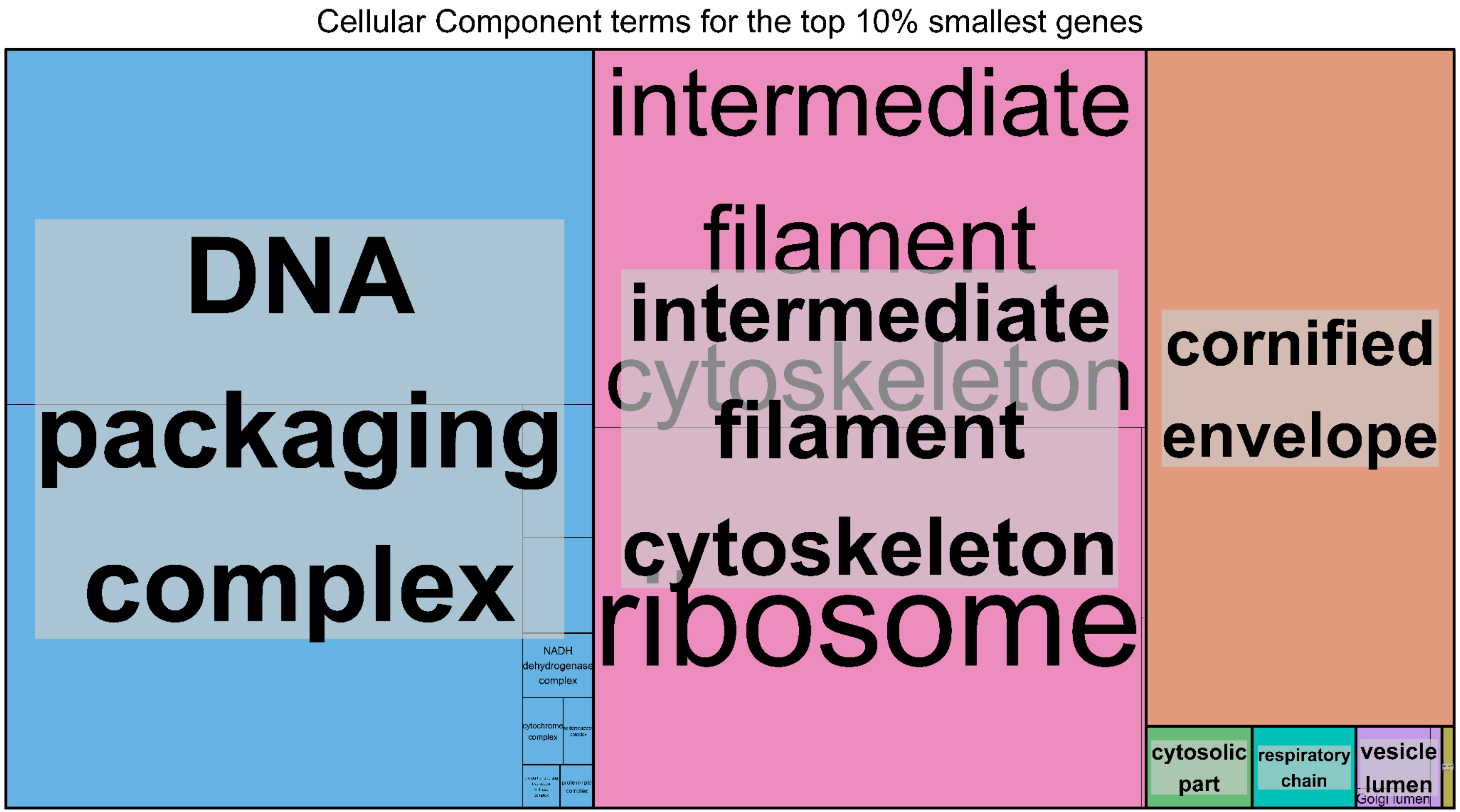


Supplementary Figure 3G.
Molecular Function terms found associated to genes with the longest transcript length (10%). The significance level was $p<0.05$ and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

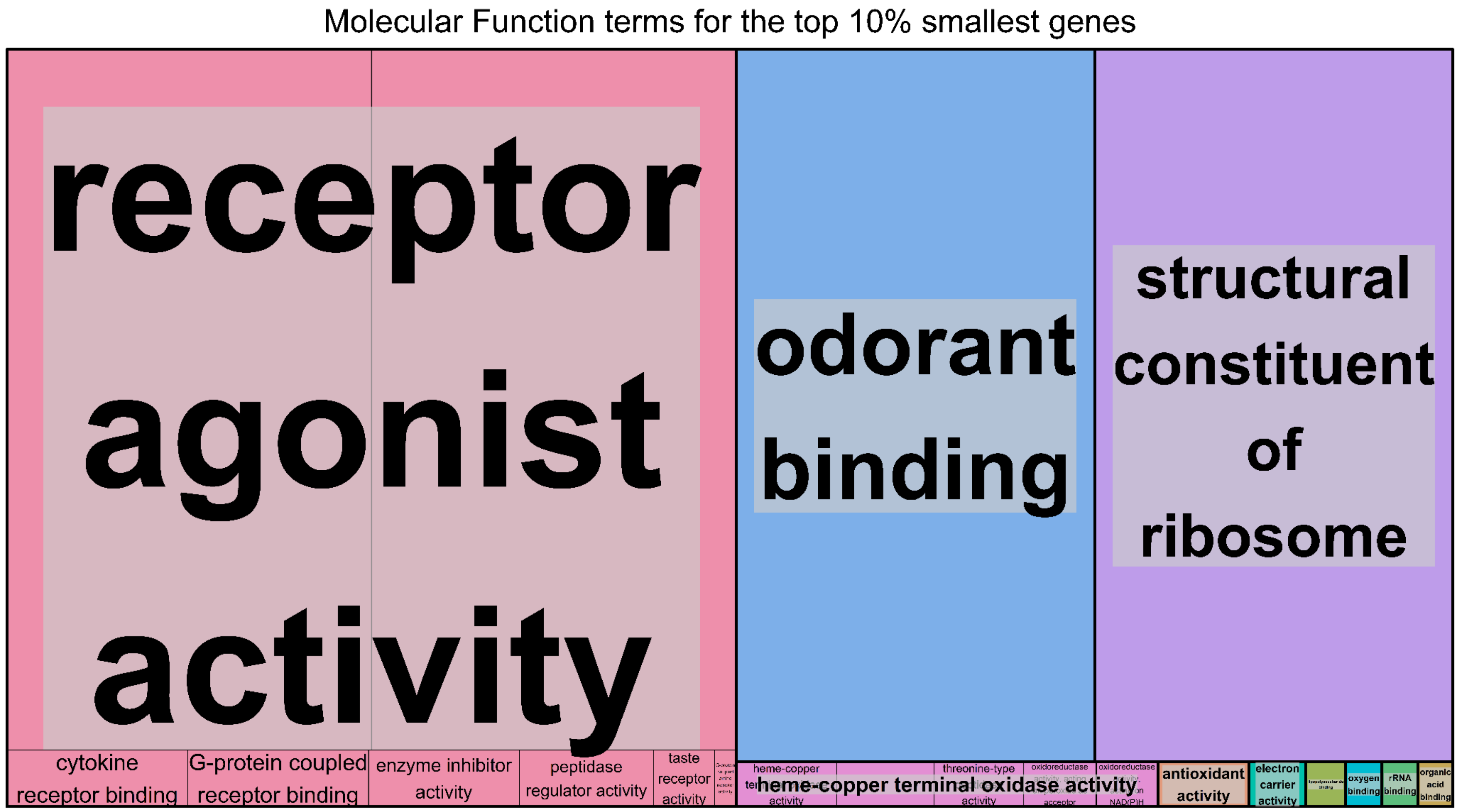
Biological Process terms for the top 10% smallest genes



Supplementary Figure 3H.
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.



Supplementary Figure 3I.
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.



Supplementary Figure 3J.

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.