

Figure S1. Isoform switching event of the MALRD1 gene. There is no difference in the gene expression of MALRD1 between the CTRL and OMWW samples (bottom left), meaning that a standard gene-level analysis would not pick up any changes to MALRD1. Next, we see the large and highly significant switch in isoform usage across conditions (bottom right). By comparing which isoforms are changing (bottom right) to the isoform structure (top), it can be inferred that in the CTRL samples, it is primarily the two short isoforms that are used

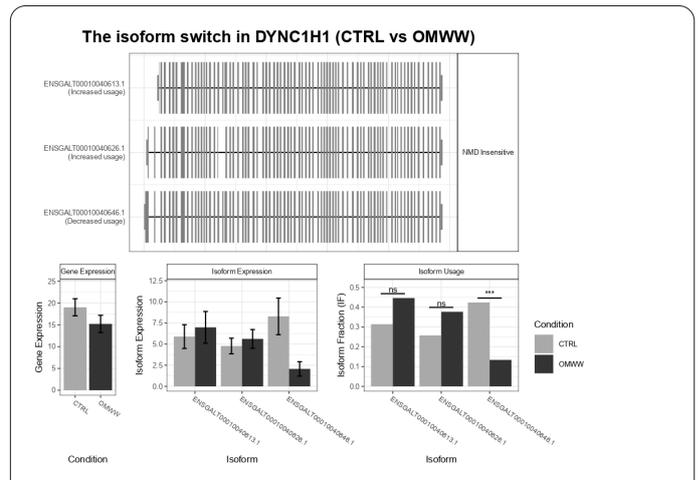


Figure S2. Isoform switching event of the DYNC1H1 gene. There is no difference in the gene expression of DYNC1H1 between the CTRL and OMWW samples (bottom left), meaning that a standard gene level analysis would not pick up any changes to DYNC1H1. Next, we see the large and highly significant switch in isoform usage across conditions (bottom right). By comparing which isoforms are changing (bottom right) to the isoform structure (top), it can be inferred that in the CTRL samples it is decreased in two short isoforms and increased in one that is used.

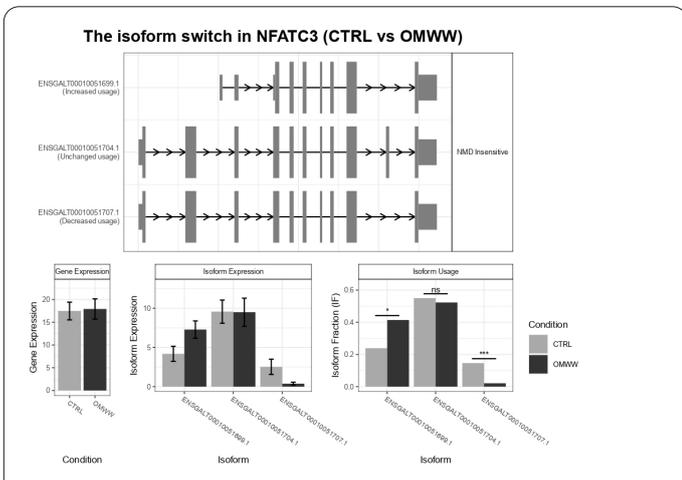


Figure S3. Isoform switching event of the NFATC3 gene. There is no difference in the gene expression of NFATC3 between the CTRL and OMWW samples (bottom left), meaning that a standard gene-level analysis would not pick up any changes to NFATC3. Next, we see the large and highly significant switch in isoform usage across conditions (bottom right). By comparing which isoforms are changing (bottom right) to the isoform structure (top), it can be inferred that in the CTRL samples, it is primarily the short isoforms that are used.

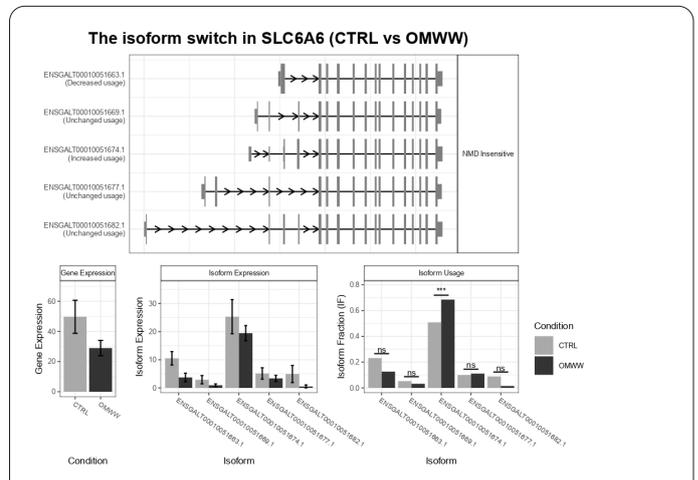


Figure S4. Isoform switching event of the SLC6A6 gene. There is no difference in the gene expression of SLC6A6 between the CTRL and OMWW samples (bottom left), meaning that a standard gene-level analysis would not pick up any changes to SLC6A6. Next, we see the large and highly significant switch in isoform usage across conditions (bottom right). By comparing which isoforms are changing (bottom right) to the isoform structure (top), it can be inferred that in the CTRL samples it is primarily the short isoforms that are used.

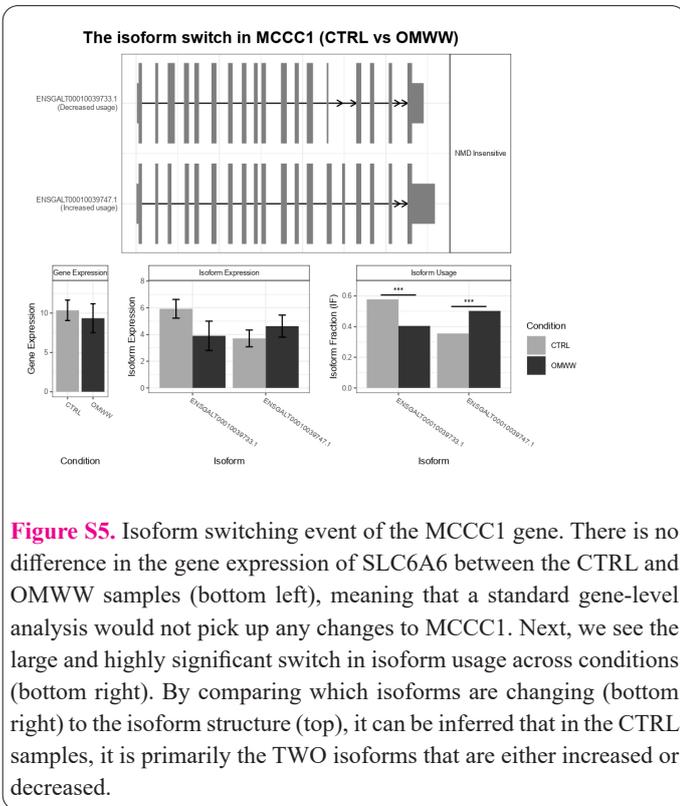


Figure S5. Isoform switching event of the MCCC1 gene. There is no difference in the gene expression of SLC6A6 between the CTRL and OMWW samples (bottom left), meaning that a standard gene-level analysis would not pick up any changes to MCCC1. Next, we see the large and highly significant switch in isoform usage across conditions (bottom right). By comparing which isoforms are changing (bottom right) to the isoform structure (top), it can be inferred that in the CTRL samples, it is primarily the TWO isoforms that are either increased or decreased.

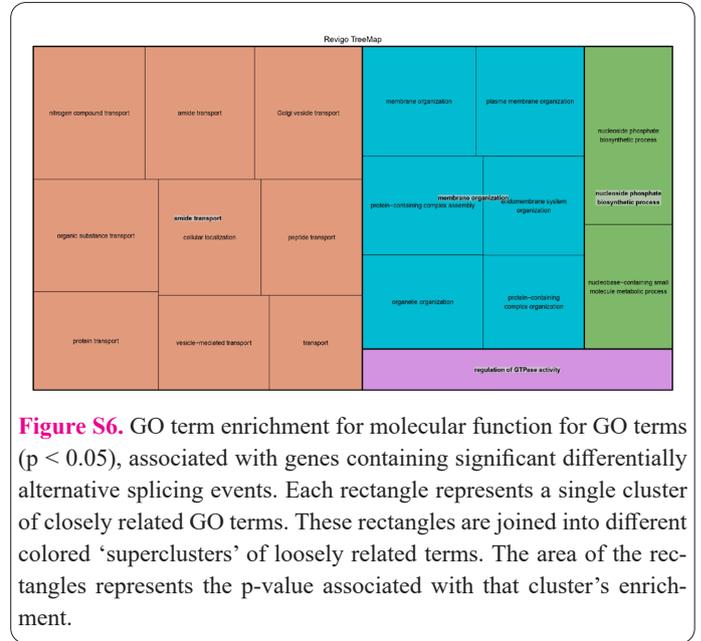


Figure S6. GO term enrichment for molecular function for GO terms ($p < 0.05$), associated with genes containing significant differentially alternative splicing events. Each rectangle represents a single cluster of closely related GO terms. These rectangles are joined into different colored ‘superclusters’ of loosely related terms. The area of the rectangles represents the p-value associated with that cluster’s enrichment.

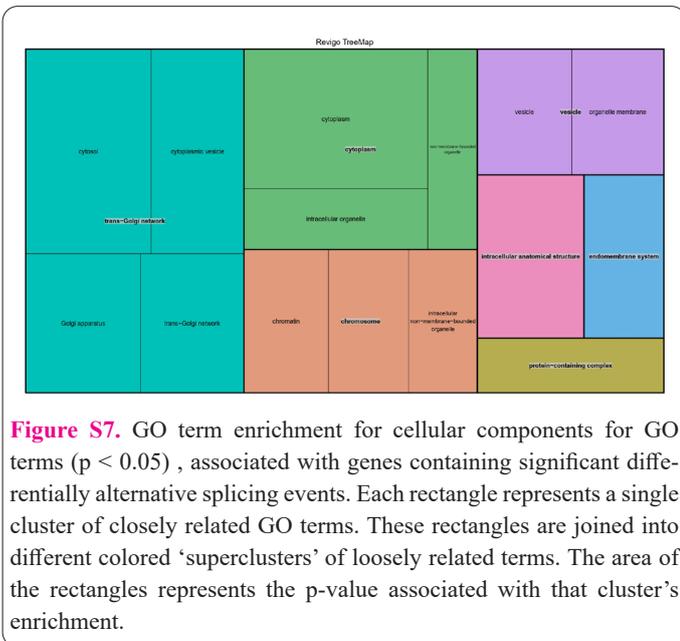


Figure S7. GO term enrichment for cellular components for GO terms ($p < 0.05$), associated with genes containing significant differentially alternative splicing events. Each rectangle represents a single cluster of closely related GO terms. These rectangles are joined into different colored ‘superclusters’ of loosely related terms. The area of the rectangles represents the p-value associated with that cluster’s enrichment.

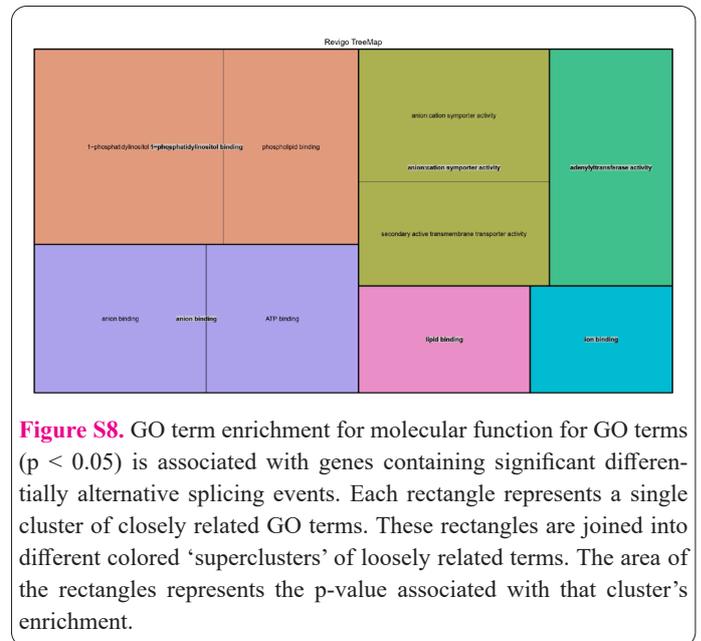


Figure S8. GO term enrichment for molecular function for GO terms ($p < 0.05$) is associated with genes containing significant differentially alternative splicing events. Each rectangle represents a single cluster of closely related GO terms. These rectangles are joined into different colored ‘superclusters’ of loosely related terms. The area of the rectangles represents the p-value associated with that cluster’s enrichment.