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This question is based on your analysis of the gene list that I gave you to compare against the Reactome database:

1. Based on the gene sets that were enriched, what kind of samples do you think were used to generate this list of differentially expressed genes? Hint: this was a disease study. What kind of disease was it? Just give your best guess.

The Voronoi diagram when set for P-values seemed to indicate that the genes were likely involved with the following: O-linked glycosylation of mucins, beta-defensins, disease associated with O-linked glycosylation of proteins (specifically "Defective LARGE causes MDDGA6 and MDDGB6"), hemophilia, passive transport by aquaporins, and transport of fatty acids. My best guess is that the O-linked glycosylation genes were used to generate the list, as both this process and a disease associated with it show up as strong hits on the Voronoi diagram and the overrepresentation analysis. Therefore, I would conclude that the disease used to generate this gene list was likely "Defective LARGE causes MDDGA6 and MDDGB6."

1. Attach your screenshots showing your analysis of the gene list. THERE SHOULD BE MANY DIFFERENT SCREENSHOTS SHOWING REAL RESULTS.

There are 15 screenshots. Please see attached files!