Secreted and Transmembrane

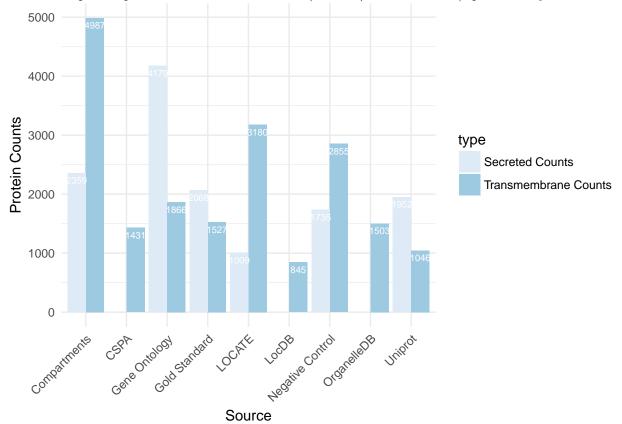
Maggie Shaw, Temple University 5/3/2018

Objective:

Analyze the database results for each protein (indicated by the corresponding protein coding gene hgnc_symbol) to determine a final comprehensive list of "transmembrane" and "secreted" proteins.

Summary of each source

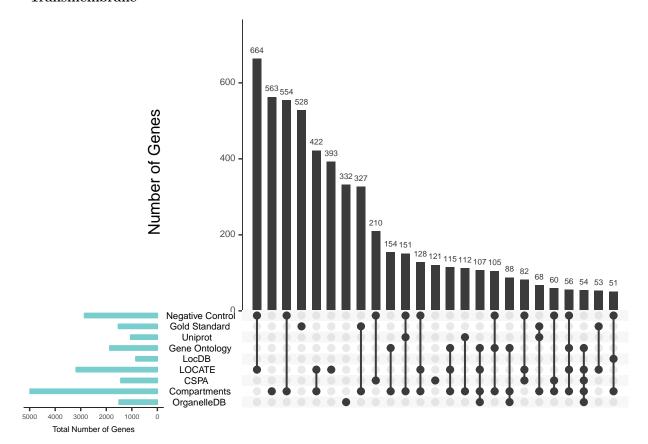
Paired bar plot depicts the number of results (secreted/transmembrane) provided by each source.



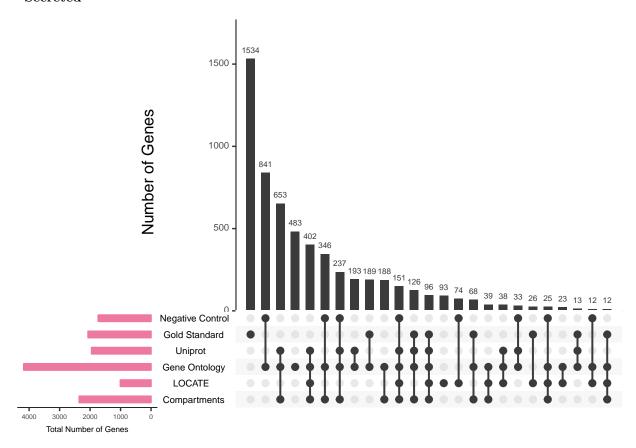
Upset Plots as a Comparison Figure

Upset plots are used to compare all the overlapping proteins between sources.

"Transmembrane"



"Secreted"



Sum Scores to Produce Final Lists

Sum the scores from each source (including "gold standard", excluding "negative control"), and only include those which occur in at least half of the sources, to produce the final lists. Remove the other columns except the number of sources the protein occured in and the hgnc_symbol.

Warning: package 'bindrcpp' was built under R version 3.4.4

##		${\tt HGNC}$	Symbol	${\tt Number}$	of	Databases	${\tt Confirmed}$
##	1		ABCB11				5
##	2		ABCB4				6
##	3		ABCC1				6
##	4		ABCC2				6
##	5		ABCC3				5
##	6		ABCC6				4
##		HGNC	Symbol	Number	of	Databases	Confirmed
## ##	1	HGNC	Symbol FUCA2	Number	of	Databases	Confirmed 4
		HGNC	•	Number	of	Databases	
##	2	HGNC	FUCA2	Number	of	Databases	4
## ##	2 3	HGNC	FUCA2 SEMA3F	Number	of	Databases	4 3
## ## ##	2 3 4	HGNC	FUCA2 SEMA3F HSPB6	Number	of	Databases	4 3 3