Supplementary Table 1: List of request/changes from the users and the status of its implementation				
#	Requested feature	No of user requests	Status	
1	Implement miRNA enrichment analysis	33	✓	Completed
2	Venn diagram between Vesiclepedia and my dataset(s)	26	✓	Completed
3	Generate heatmaps for input datasets	24	✓	Completed
4	Improved coverage of UniProt IDs	24	✓	Completed
5	Mac or linux compatitbility or web based FunRich version	21	♻	In progress
6	Real time database update	20	✓	Completed
7	Compare more than two input datasets for enrichment analysis	19	✓	Completed
8	Option to customize the color of charts/graphs	18	✓	Completed
9	Download proteins/RNA identified in extracellular vesicles isolated from a specific sample	16	✓	Completed
10	Download proteins/RNA identified exclusively in a subtype of extracellular vesicle	16	✓	Completed
11	Regular update of background databases	16	✓	Completed
12	Download top 100 proteins identified in extracellular vesicles	14	✓	Completed
13	Allow users to control the databases	14	✓	Completed

14	Download all proteins/RNA identified in a subtype of extracellular vesicle	13	✔	**Completed**
15	Enrichment of genes in different cancer types using COSMIC data	13	✔	**Completed**
16	Save workspace or session feature	12	✔	**Completed**
17	Option to upload miRNA gene name or miRbase acession number	12	✔	**Completed**
18	Quantitative expression profile based enrichment analysis	11	✔	**Completed**
19	Implement metabolomic enrichment analysis	10	🔄	**In progress**
20	Update Vesiclepedia data automatically	10	✔	**Completed**
21	Mapping and conversion of acession IDs to different databases	10	✔	**Completed**
22	Venn diagram of the Vesiclepedia would benefit from displaying distribution of the sample genes by EV subtypes	9	✔	**Completed**
23	Description of the Vesiclepedia section in the manual	8	✔	**Completed**
24	For each protein resulting shared using Venn diagram tool to specify type of experiment through which it was identified in exosomes and provide the link to PubMed references supporting its identification	8	✔	**Completed**
25	Description or full name that can appear on mouse click or as a pop up window for terms/domains	7	✔	**Completed**
26	Option to choose more databases to use as background for heatmaps	7	✔	**Completed**
27	For each protein in the lists derived from Venn diagram report in which type of sample it was identified	7	✔	**Completed**
28	Ability to download the top hits (protein/ mRNA/ miRNA/ lipids)	7	✔	**Completed**

29	Ability to search for proteins that are being currently used. Especially important if you are looking for a protein / bunch of proteins amongst	7	✓	Completed
30	Edit font of all charts/graphs	7	✓	Completed
31	Refer the nature or source of the interaction in interaction maps (text mining or experimental)	6	♻	In progress
32	Ability to find the references of filtered dataset when comparing custom dataset with the filtered dataset from Vesiclepedia	6	✓	Completed
33	Identify upregulated and downregulated proteins for specific biological process from heatmap data	6	✓	Completed
34	Suggestions for the manual: for a first-time user, a description of the input data (examples would suffice) would be necessary	6	✓	Completed
35	Upload data from an Excel sheet	6	✓	Completed
36	For each protein list from the Venn diagram, provide, if available, the link to its interactome	5	✓	Completed
37	More cancer types under the cell lines tab	5	✓	Completed
38	Content types should also include other molecules including lncRNAs, piRNA, snoRNA or can be listed as other RNA molecules.	5	♻	In progress
39	Set a default output option which allows to export a summary report including excel files, image files and a summary text	5	✓	Completed
40	Clustered heatmap	5	✓	Completed
41	Under the tissue/cell types include CSF	4	✓	Completed
42	Reflect the fragmentation status of the vesicular RNAs (fragmented vs. intact)	4	♻	In progress
43	Implement quantitative Venn diagram of differentially expressed genes/proteins	3	✓	Completed
44	Include videos for custom database upload	3	✓	Completed

45	Implement Recatome pathway enrichment and automatic download of database	3	✓	Completed
46	Implement Gene Ontology enrichment and automatic download of database	3	✓	Completed
47	Display graphs/charts in Excel sheet automatically	3	✓	Completed
48	Find targets for miRNA	3	✓	Completed
49	Heatmap of interested genes (not clustered)	2	✓	Completed
50	Enrichment analysis using quantitative values	2	✓	Completed
51	Convert Gene Symbol to UniProt IDs	2	✓	Completed
52	Find which miRNA will bind to my gene list	1	✓	Completed
53	Implement q value method (Storey and Tibshirani)	1	✓	Completed
54	Protein-protein interaction for other species (non human)	1	✓	Completed