**Resolving missing protein problems using functional class scoring**

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# Supplementary Figures

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**Supplementary Figure 1** **Abundance levels alone are not a sufficient explanation for missing proteins**. X-axis: Scaled mean expression values. Y-axis: Number of missing values across samples. The red hashed lines indicated the medians of each axis.



**Supplementary Figure 2** **Corresponding gene expressions of proteins specific to kidney and liver tissues tends to be discriminatory while proteins found in shared complexes have no such effects.**

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**Supplementary Figure 3** **A:** **Recovery based on protein lists is very modest. B: Recovery based on shared FCS-predicted complexes is extremely high suggesting despite different protein lists, they point back to essentially similar complexes**