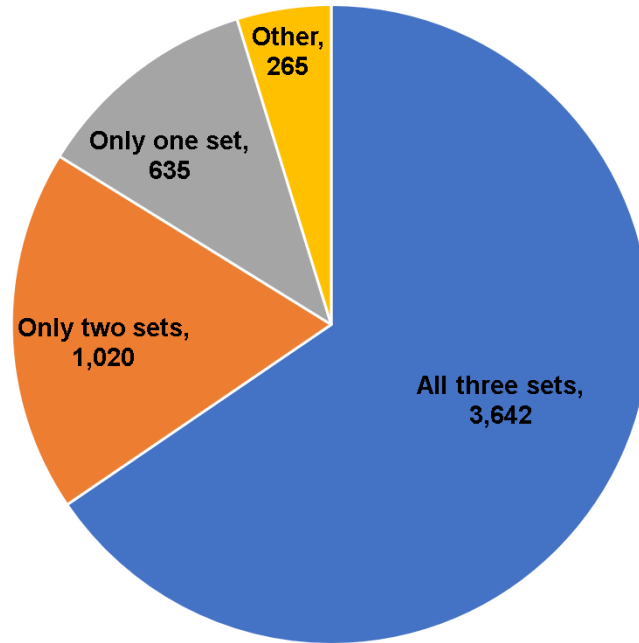


**Supplementary Figures for**  
**Quantitative Proteomic Analysis of Prostate Tissue Specimens Identifies Deregulated Protein**  
**Complexes in Primary Prostate Cancer**

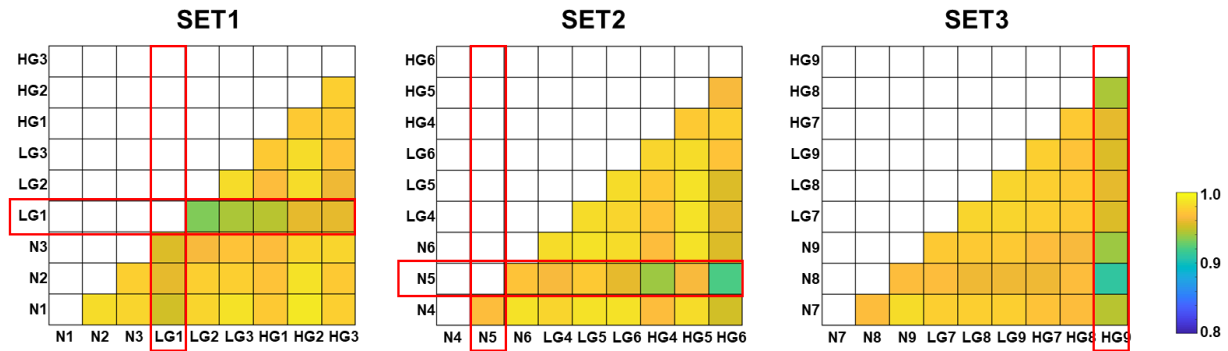
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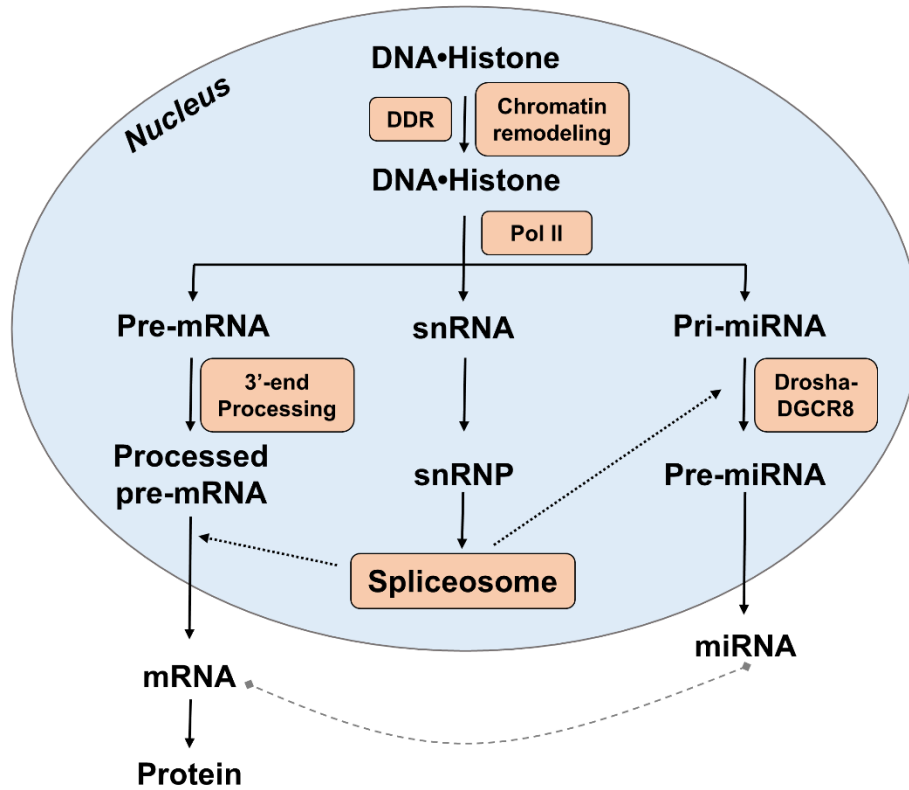
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**Figure S1. Pie chart of protein groups quantified in different TMT10plex sets.** Of all the 5,562 identified protein groups, 3,642 protein groups were quantified in all the three sets (30 samples), 4,662 (3,642 + 1,020) protein groups were quantified in at least two sets, and 5,297 (4,662 + 635) protein groups were quantified in at least one TMT set.



**Figure S2. Detection and removal of outlier samples.** The outlier samples were detected in each set using the SuperHirn, followed by visual inspection. Red box indicates similarity pattern of outlier samples with other samples in the same set. The samples LG1, N5, and HG9 were identified as outlier samples and were thus removed prior to further analysis.



**Figure S3. Biological processes involving the protein complexes with increased assembly levels in low-grade prostate cancer, compared with normal prostate.** See Table 1 for specific protein complexes belonging to each class, which was shown in light orange box in this figure.