



**Figure 3. Modified bases in the 22-nucleotide SL, U4 snRNA, and decapping products.** A graph of the percent of each non-standard ribonucleoside from the total detectable bases is shown with the specific moiety on the X axis and percent on the Y axis or “ND” when not detectable. The first four classes are totals for each non-standard nucleoside followed by specific moieties for which there were standards: 1-methyl adenosine (M1A), 6-methyl adenosine (M6A), 5-methyl cytosine (M5C), 1-methyl guanosine (M1G), 7-methyl guanosine (M7G), pseudouridine (Y), and 2,2,7-trimethyl guanosine (M227G). The RNase A degradation of spliced leader isolates is shown in black, the U4 snRNA isolate is shown in light grey, and the free nucleosides following decapping of the 22nt spliced leader are shown in dark grey. Error bars represent triplicate compositional analyses from a single sample. Moieties other than 7-methyl guanosine following decapping are likely contaminants from the total RNA pool bound to the Sepharose beads used in sequence enrichment.