

	<b>R1-1</b>	<b>R1-2</b>	<b>R2-1</b>	<b>R2-2</b>	<b>R3-1</b>	<b>R3-2</b>
<b>WG1-1</b>	CN1	CN2	CN3	CN4	CN5	CN6
<b>WG1-2</b>	CN7	CN8	CN9	CN10	CN11	CN12
<b>WG2-1</b>	CN13	CN14	CN15	CN16	CN17	CN18
<b>WG2-2</b>	CN19	CN20	CN21	CN22	CN23	CN24
<b>WG3-1</b>	CN25	CN26	CN27	CN28	CN29	CN30
<b>WG3-2</b>	CN31	CN32	CN33	CN34	CN35	CN36

**Supplementary Figure 2. Schematic showing how rDNA copy number is calculated from the three highest frequency coverage bins from both the whole genome and the rDNA.** The three highest (peak) coverage bins for both rDNA and whole genome are determined. R represents the three highest peak values for rDNA, WG the three highest peak values for whole genome. The -1 and -2 designations refer to the upper and lower values of the coverage bin range, respectively. This produces a total of 36 ratios of values, as indicated by CN. The estimated copy number is then the mean of these 36 CN values.