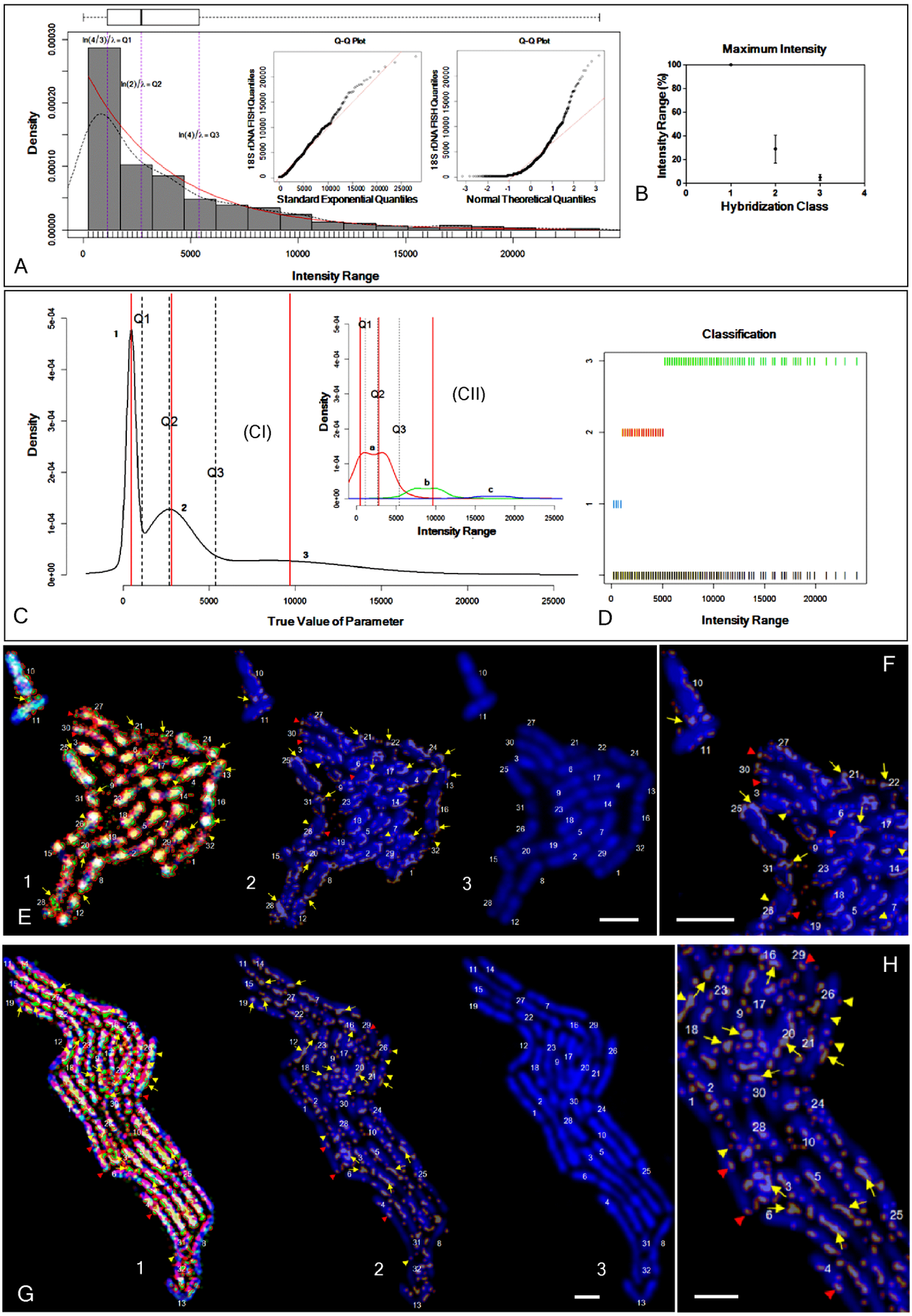

Figure S2. The intensity distribution of combined data points of 18S rDNA FISH binding sites from spreads sl48cl06 (n=343) and sl99cl49 (n=312) is shown in **A**. The purple vertical broken lines mark the components of the boxplot: lower hinge (Q1 = ln(4/3)/λ) or the 25th percentile, middle line or median (Q2 = ln(2)/λ), upper hinge (Q3 = ln(4)/λ) or the 75th percentile. The dotted curve plotted along the solid red exponential curve represents the density of the distribution. The black vertical lines below the histogram bars represent 18S rDNA data points. Two Q-Q plots (Normal Theoretical Quantiles and Standard Exponential Quantiles) are shown. **B** shows normalized averaged intensities (normalized to the average of major 18S rDNA signals = 100%) of major, medium and minor signals numbered according to decreasing intensity. **C** shows the output of model-based clustering procedures: **CI** (parametric) and **CII** (semiparametric symmetrical). Corresponding sample mean (μ) of the major, medium and minor classes of 18S rDNA FISH signals in **CI** and **C2** are indicated by solid red vertical lines. **D** is the resulting classification output of the clustering procedure parameterized for Gaussian distribution for **CI**. **E1 to E3** and **G1 to G3** show 18S rDNA probe hybridization signals as indicated by green fluorescence (Alexa 488) with orange outline in two chromosomal spreads of *C magus* sl48cl06 and sl99cl49, respectively. Examples of major, medium and minor sites are indicated by the yellow arrows, red arrow heads and yellow arrow heads, respectively. A 3D surface plot (**E2 and G2**) of the green fluorescence (Alexa 488) signals **(E1 and G1)** was depicted in the DAPI counterstained chromosomes using fire LUT. **E3 and G3** show DAPI counterstained chromosomes. **F and H** are enlarged portions of **E2 and G2**. Scale bars = 1 μm.