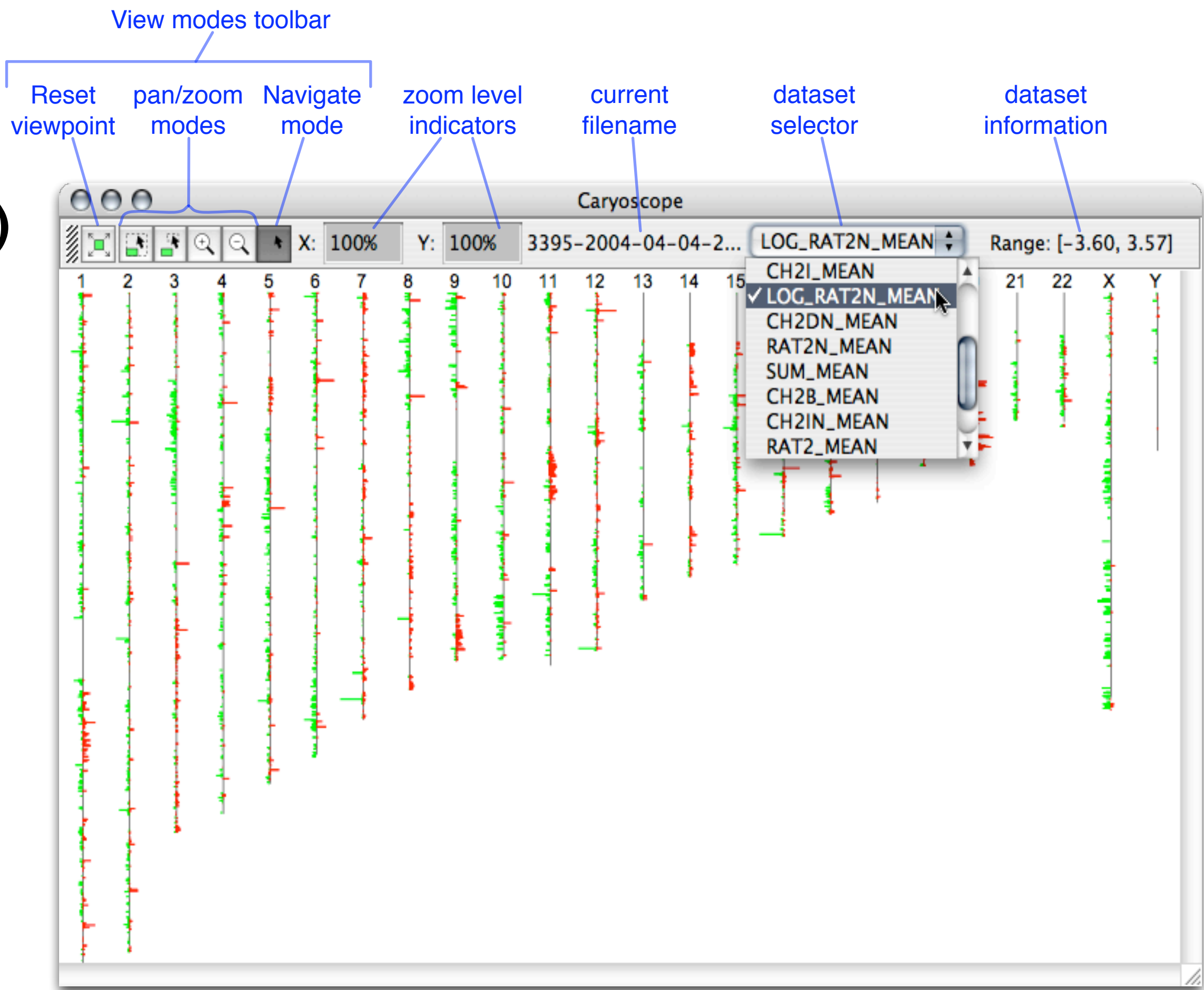


(a)



(b)

Caryoscope settings

Chromosome axis shown ☒

Data scale shown ☐

Data scale increment 2.0

Axis line thickness 0.5

Centromere shown ☒

Logarithm enabled ☐

Logarithm base 2.0

Minimum feature width 1.0

Moving average enabled ☐

Averaging half window width 3

Averaging half decay distance 100000

Feature tooltip expression \${GBACC} - \${GENE_NAME}

Feature URL expression http://genome-www5.stanford.edu,

Apply Revert Defaults

The screenshot shows the 'Caryoscope settings' dialog box. It contains a list of settings with checkboxes and input fields. The settings are: 'Chromosome axis shown' (checked), 'Data scale shown' (unchecked), 'Data scale increment' (2.0), 'Axis line thickness' (0.5), 'Centromere shown' (checked), 'Logarithm enabled' (unchecked), 'Logarithm base' (2.0), 'Minimum feature width' (1.0), 'Moving average enabled' (unchecked), 'Averaging half window width' (3), 'Averaging half decay distance' (100000), 'Feature tooltip expression' (\${GBACC} - \${GENE_NAME}), and 'Feature URL expression' (http://genome-www5.stanford.edu,). At the bottom of the dialog are three buttons: 'Apply', 'Revert', and 'Defaults'.