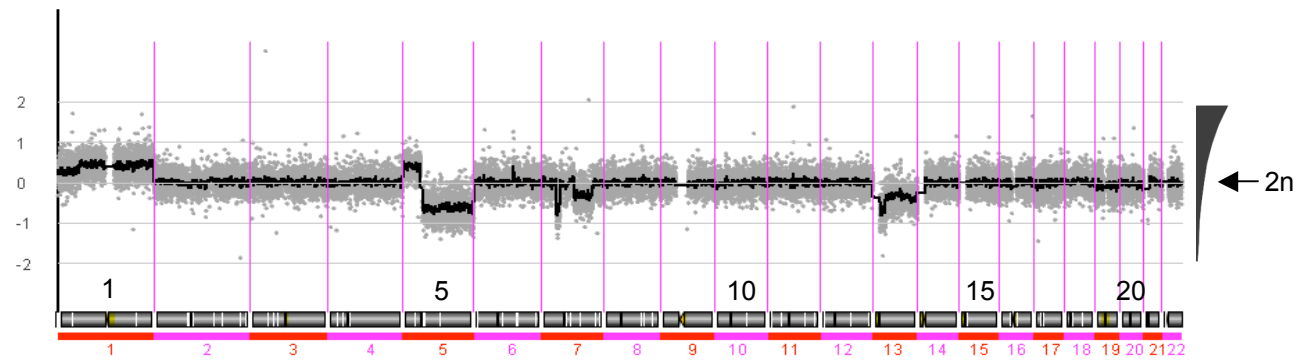


Genome-Wide Overviews of MCC Tumor Samples

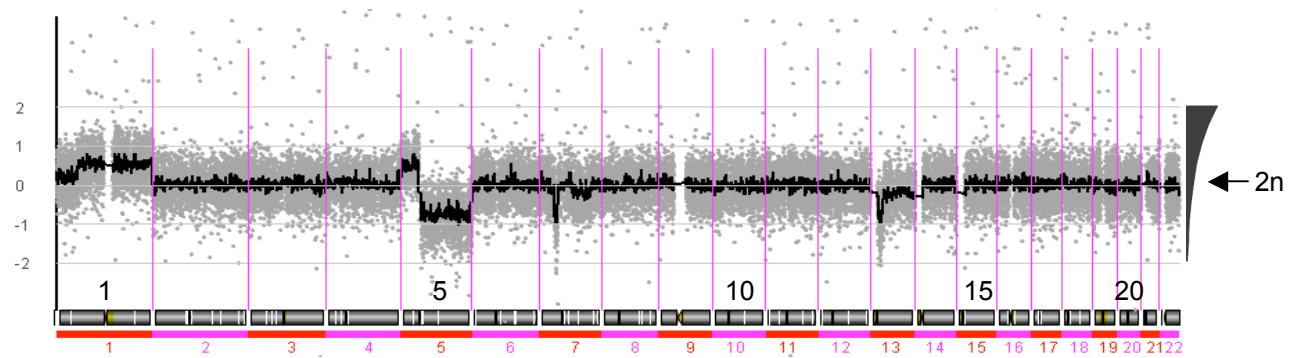
- Parameters for generating overviews:
 - CGH-explorer, version 3.1
 - Moving average fit plots
 - Neighborhood size of 29
 - Vertical plot range of -3.5 to 3.5
 - Autosomal chromosomes 1-22
 - Grid lines at 0 (2n), 1 (4n), 2 (8n), -1 (1n), -2 (0.5n)
 - Y-axis is log 2 ratio
 - Grey dots represent individual data points
 - Black line represents the line of “Moving Average Fit”

MCCd1_p



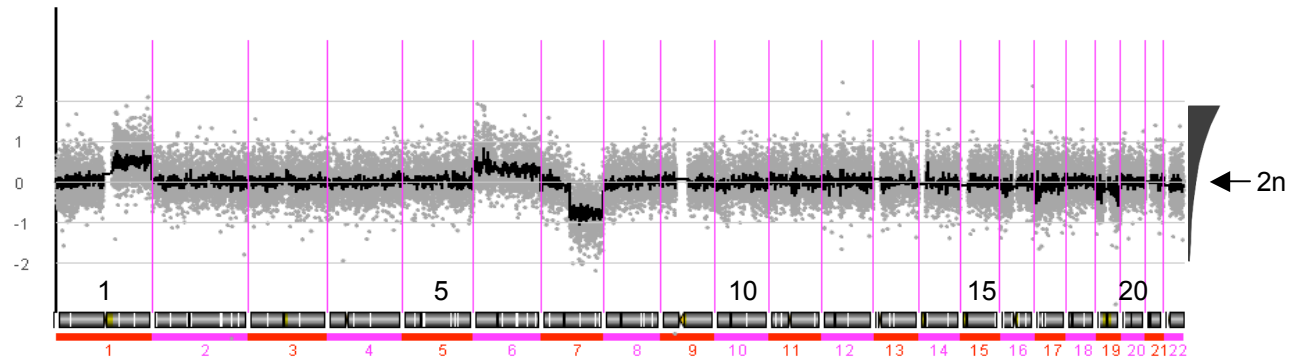
Garneski, et al.

MCCd1_m



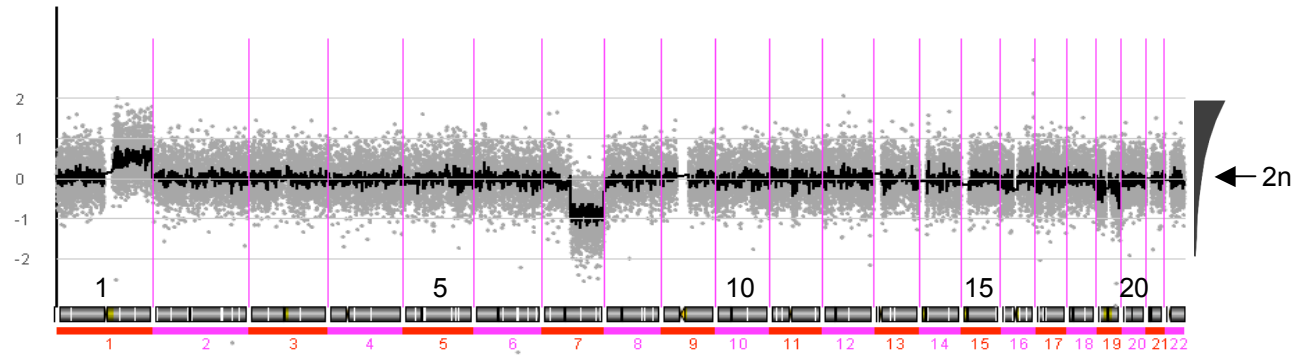
Garneski, et al.

MCCd3_p



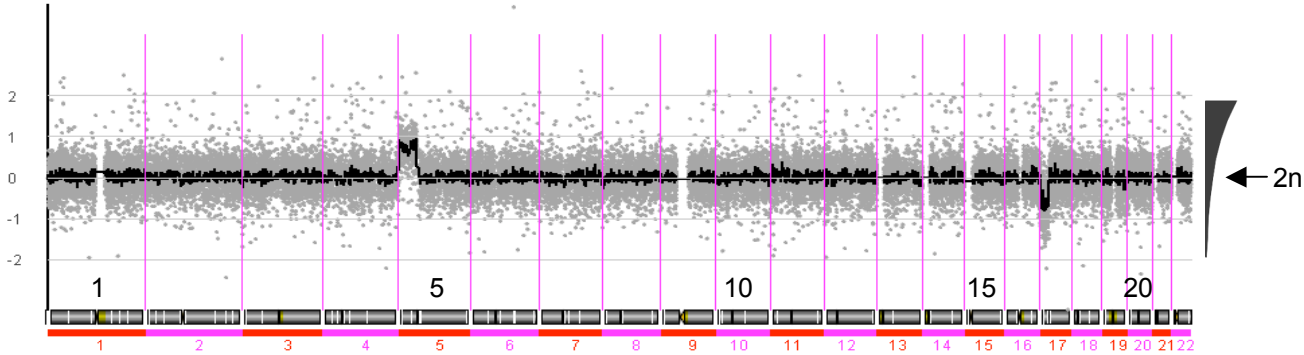
Garneski, et al.

MCCd3_m



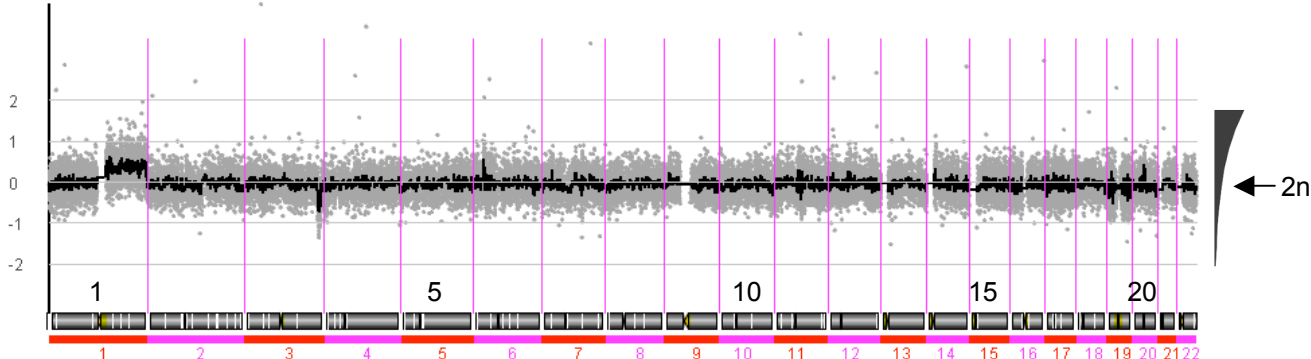
Garneski, et al.

MCCd5



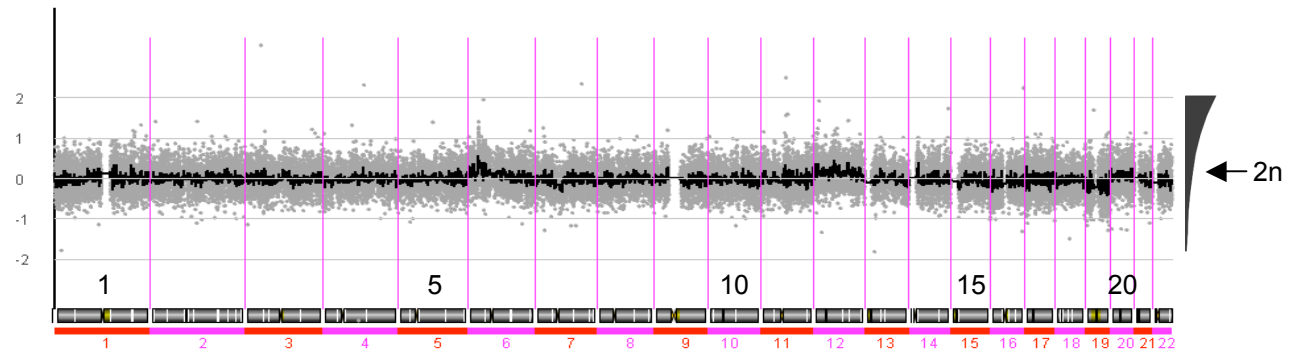
Garneski, et al.

MCCd6



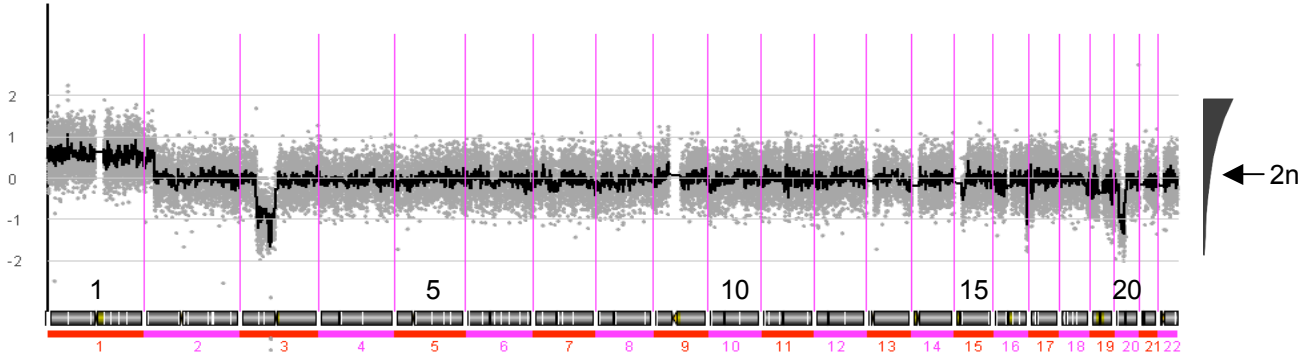
Garneski, et al.

MCCd7



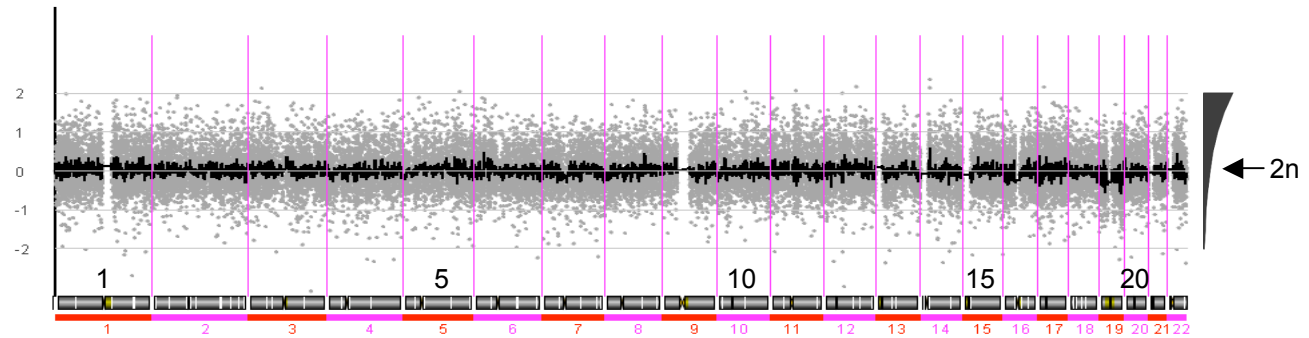
Garneski, et al.

MCCd8



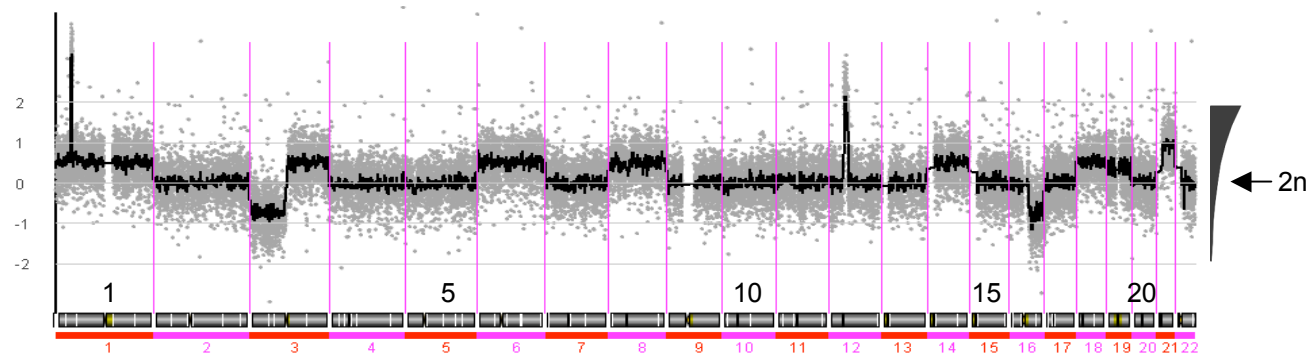
Garneski, et al.

MCCd9



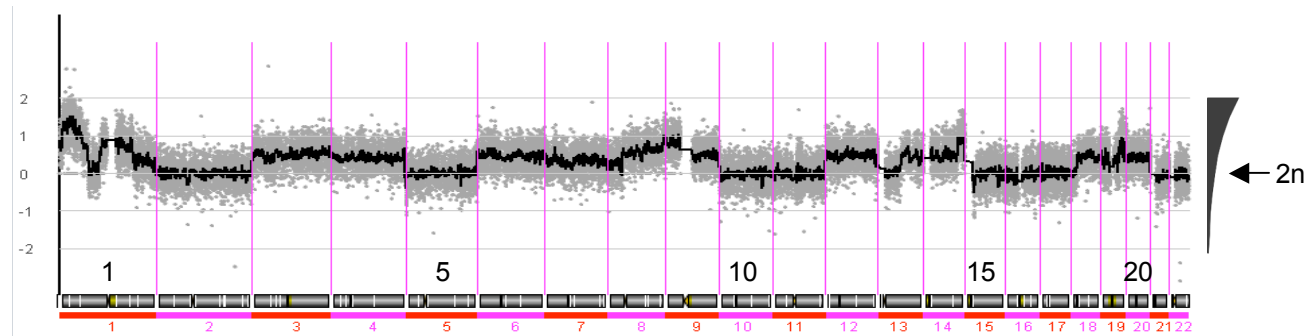
Garneski, et al.

MCCd10



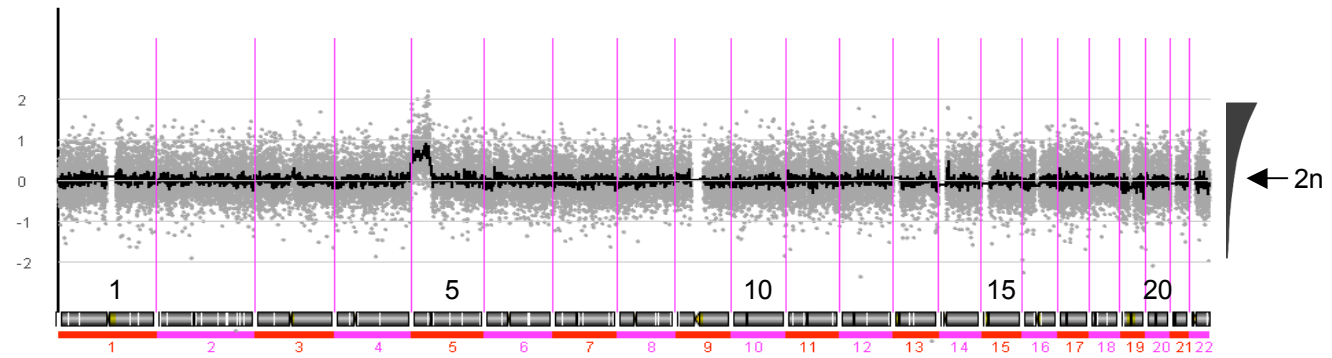
Garneski, et al.

MCCd11



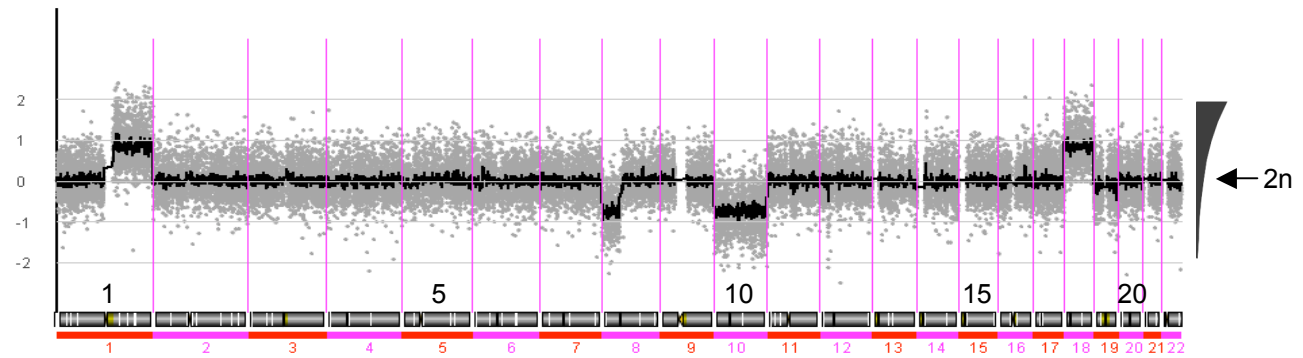
Garneski, et al.

MCCd12



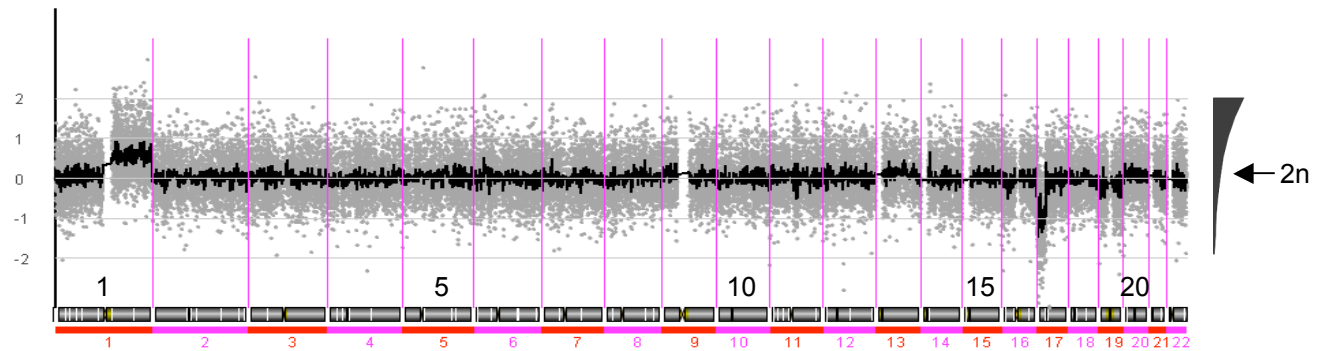
Garneski, et al.

MCCd13



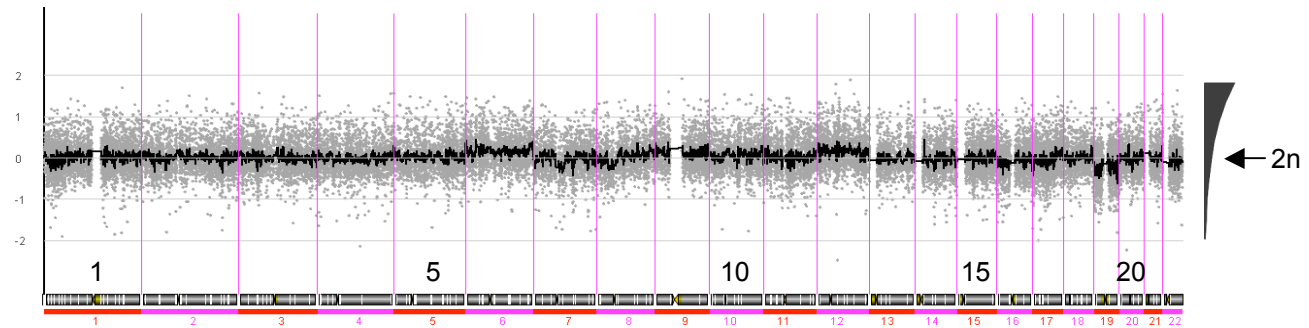
Garneski, et al.

MCCd14



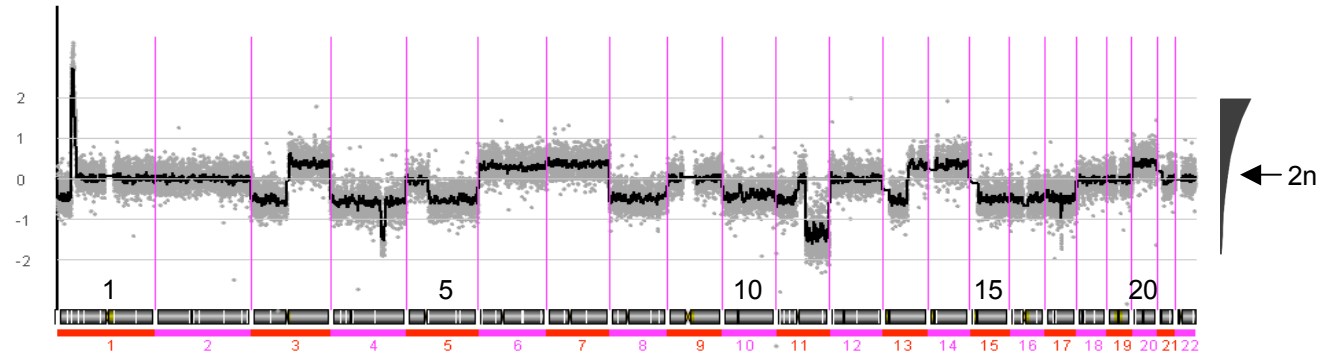
Garneski, et al.

MCCd15



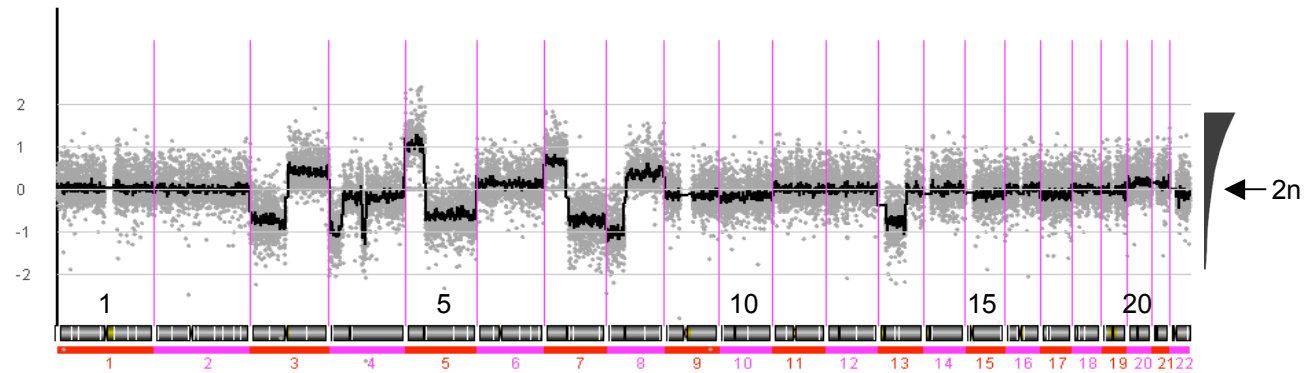
Garneski, et al.

MCCd16



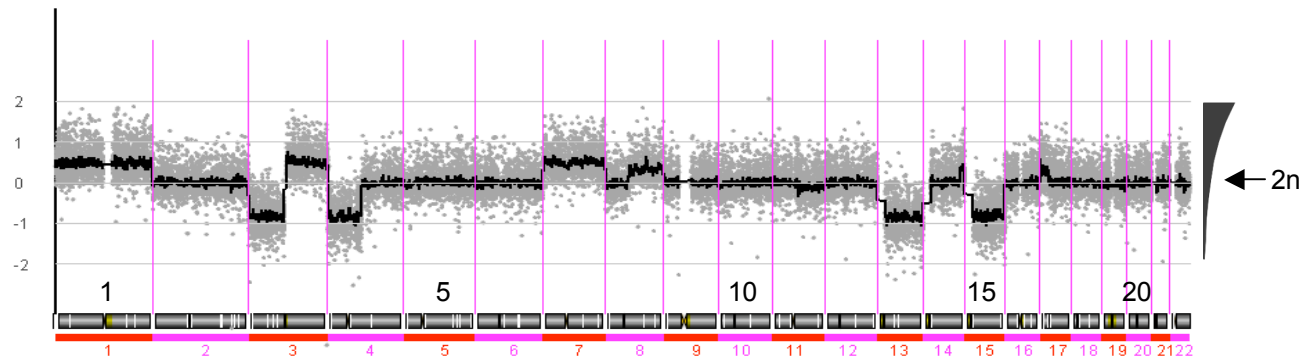
Garneski, et al.

MCC_L1T



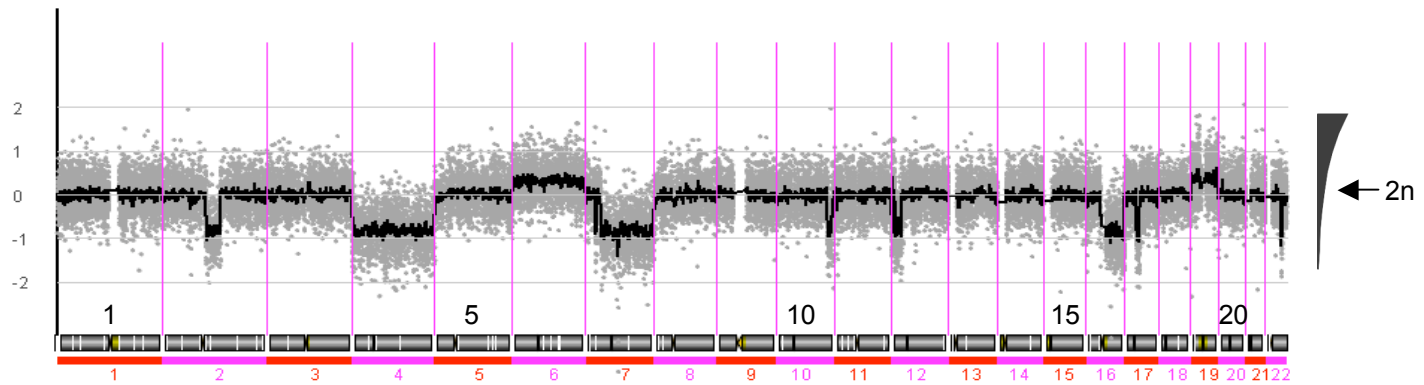
Garneski, et al.

MCC_L3T



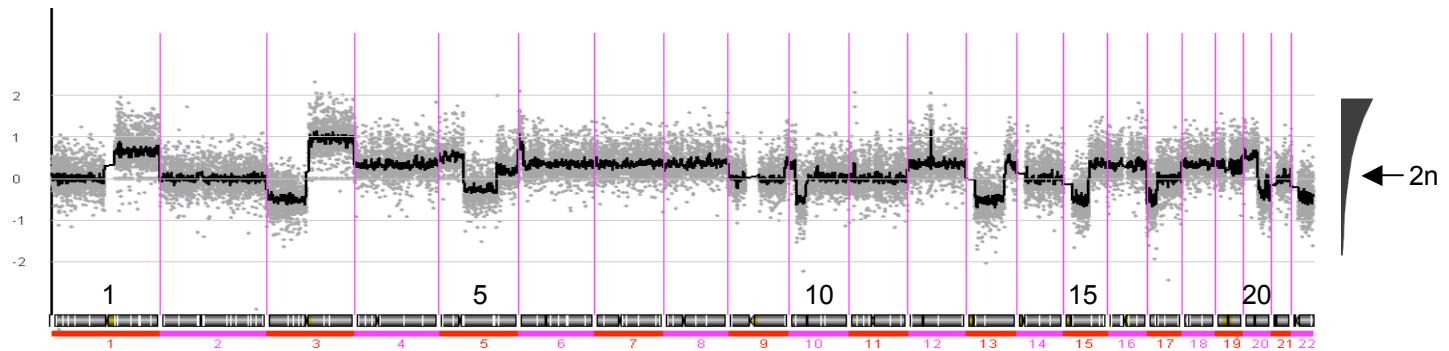
Garneski, et al.

MCC_L4T



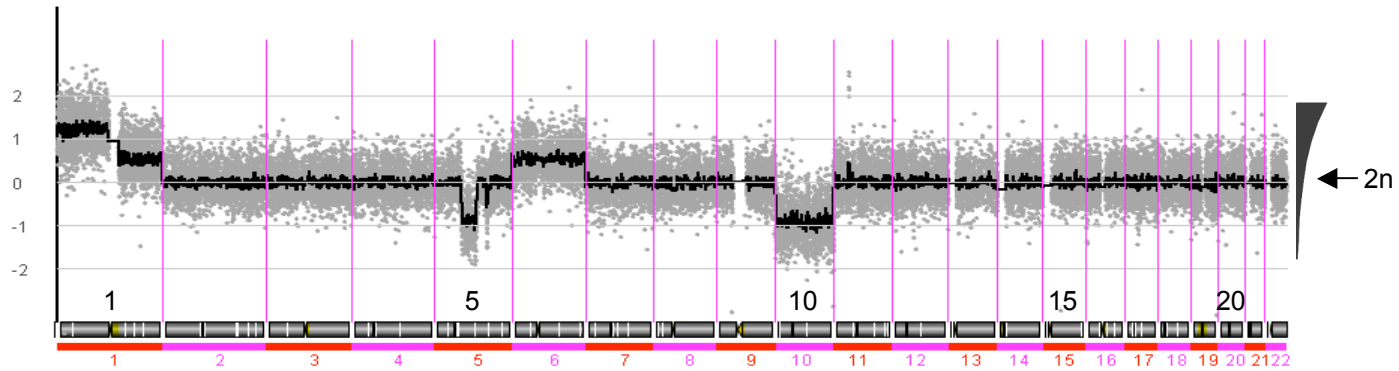
Garneski, et al.

MCC_L5T



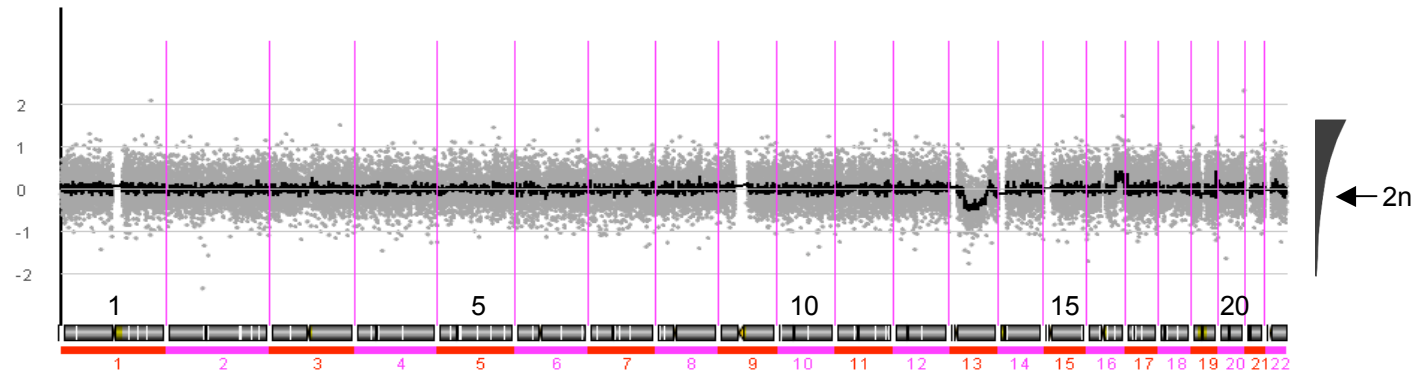
Garneski, et al.

MCC_L12T



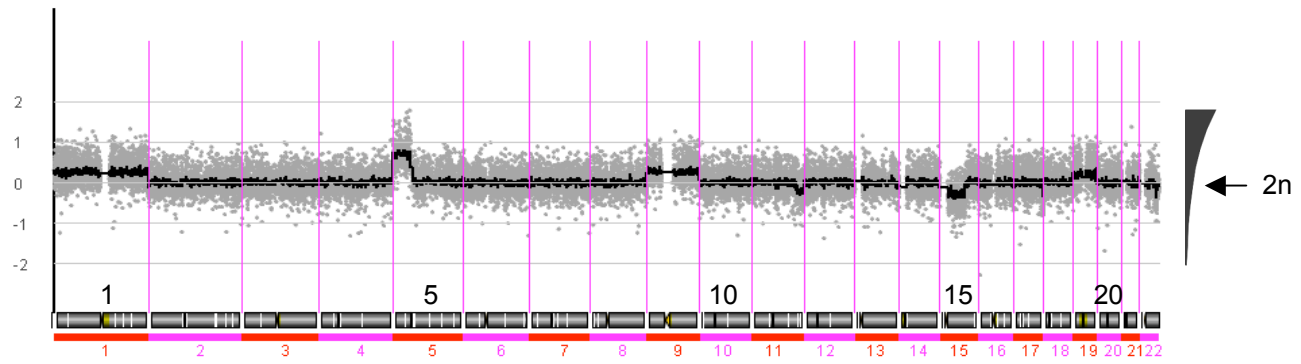
Garneski, et al.

MCC_L13T



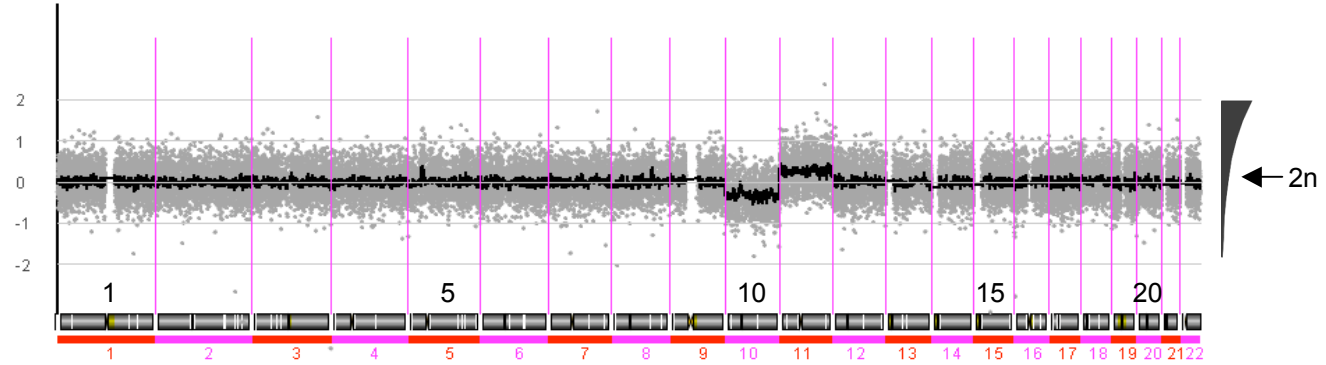
Garneski, et al.

MCC_L16T



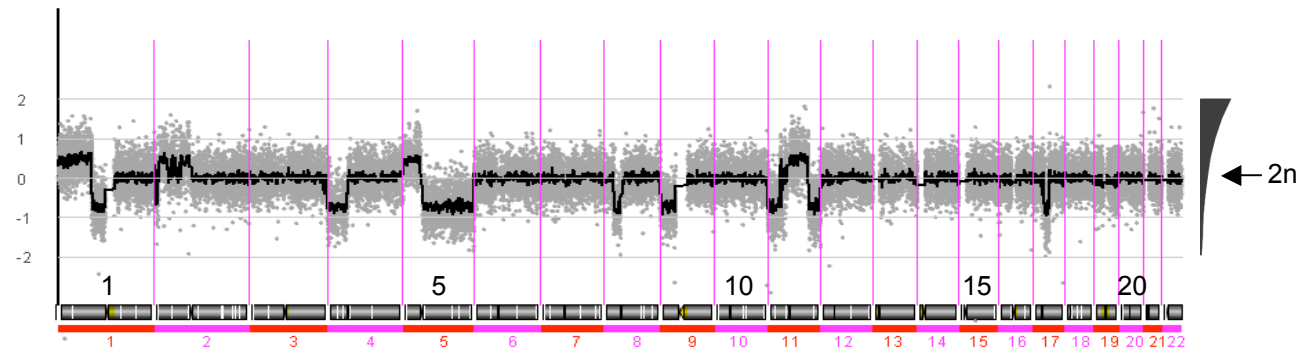
Garneski, et al.

MCC_L21T



Garneski, et al.

MCC_LSm



Garneski, et al.