Fig. 3 Analysis Presentation by the Nexus Express OncoScan Software **a** The Nexus Express software presents Copy Number (CN) (top panel) and BAF (bottom panel) on all chromosomes of a single patient. All chromosomes are color-coded, and tracks consist of dots, which are calculated CN or BAF values at corresponding SNP positions. **b** The software also displays CN and BAF on an individual chromosome with detailed information. Blue and red bars around the chromosome image represent gain and loss, respectively. LOH is marked by orange colored bars. In the CN graph, each dot represents CN values, which are calculated from signal intensities of a sample compared to those of a normal reference. CN values from loss regions are negative, while those from gain regions are positive on the logarithm 2 graph. Consistent with the whole chromosome image, loss regions are highlighted by red, while gain regions are marked with blue color. In the BAF graph, dots are from division of minor allele signal intensities by the signal intensity sum of both minor and major alleles at each SNP position. When these dots are placed across the chromosome, they look like tracks, and normal chromosome regions have three tracks. LOH regions have only two tracks in this case because the sample is homogeneous for tumor. LOHs are marked with orange color. Gain regions generate allelic imbalance, which is presented by four tracks

Quality control

OncoScan analysis has numerous quality control (QC) metrics, some of which were developed and are being used for previous versions of array platforms. Major QC metrics include the Median of the Absolute values of all Pairwise Differences between log2 ratios (MAPD), Normal Diploid Waviness Standard Deviation (ndWavinessSD), and SNP Quality Control of Normal Diploid Markers (ndSNPQC) [22]. MAPD and ndWavinessSD represent short-range and long-range noise levels, respectively; therefore, the lower these values, the greater the quality of CNV estimation. Resolution of