

Sequenza output files

Files	Description
Test_alternative_fit.pdf	Alternative solution fir to the segments. One solution per slide
Test_alternative_solutions.txt	List of all ploidy/cellularity alternative solution
Test_chromosome_depths.pdf	Visualization of sequencing coverage in the normal and in the tumor samples, before and after normalization
Test_chromosome_view.pdf	Visualization per chromosome of depth.ratio, B-allele frequency and mutations, using the selected or estimated solution. One chromosome per slide
Test_CN_bars.pdf	Bar plot representing the percentage of genome in the detected copy number states
Test_confints_CP.txt	Table of the confidence interval of the best solution from the model
Test_CP_contours.pdf	Visualization of the likelihood density for each pair of cellularity/ploidy solution. The local maximum-likelihood points and confidence interval of the best estimate are also visualized
Test_gc_plots.pdf	Visualization of the GC correction in the normal and in the tumor sample
Test_genome_view.pdf	Genome-whide visualization of the allele-specific and absolute copy number results, and raw profile of the depth ratio and allele frequency
Test_model_fit.pdf	model_fit.pdf
Test_mutations.txt	Table with mutation and estimated number of mutated alleles (Mt)
Test_segments.txt	Table listing the detected segments, with estimated copy number state at each sement
Test_sequenza_cp_table.RData	RData object dump of the maxima a posteriori computation
Test_sequenza_extract.RData	RData object dump of all the sample information
Test_sequenza_log.txt	Log with version and time information