Whole genome sequencing and quantitative proteomics reveal HPV integration and HER2 overexpression in a patient with cervical cancer: Comprehensive omics analysis driving clinical treatment decisions


Introduction: Detection of drugs to treat patients with cancer is typically based on the anatomical site at which the tumor is located. Here we report a treatment decision for a patient with (HPV 18). Mutations more rearrangements and reads mapping to human level.

Methods: The patient was a 64-year-old female whose disease had progressed following surgery and more than a brain of chemotherapy. WGS was performed on the patient's formalin-fixed, paraffin-embedded (FFPE) cervical tumor and a matched-normal reference sample. Quantitative proteomics was performed on the FFPE tumor sample by Selected Reaction Monitoring Mass Spectrometry and was quantified at the atom level.

Results: WGS found scenario mutations and rearrangements and reads mapping to human papillomavirus type 18 (HPV 18). Deleterious more commonly found in breast cancer (HER2-CD73, CD74, and DT173, were noted. The HPV 18 genome was integrated chromosome 17 (a close proximity to a 3 fusion of the ERBB2 gene). Proteomic analysis of the FFPE tumor validated and quantitated overexpression of HER2 protein resulting from HPV18 integration.

Case Details

Sequencing Analysis Pipeline

Academic Collaborations, Research Consortiums (TGA)

Sequencing Centers

Alignment & Post-Process Alignment

Relative Copy Number

Allele Fraction, LOH

Annotated Germline & Somatic Small Variants

Structural Variants with Split Read Refinement

RNA Expression of Mutant Alleles

Simultaneous Analysis of Tumor DNA, RNA and Normal DNA

Aligned Tumor & Normal, RNA

Sequence

Alignment

Reference

Figure 1: Intron-exon regions were analyzed with intron-exon-specific molecular barcodes.

Figure 2: Genomic location of low-level copy number change regions detected by microdissection analysis and high-resolution genomic analysis (confirmed by sequencing) is plotted in four adjacent regions of known or potential susceptibility.

Table 1: Specific quantitative proteomic metrics were calculated for the clinical practice setting.

Table 2: HER2 and amplified forms of HER2 protein levels observed in each round of patient treatment.

Table 3: Amplification and overexpression analysis was conducted by flow cytometry with CEA detection.

Figure 3: A: The combined proteomics and genomics data are integrated in the CANCERBASE database.

Figure 4: Potential predictive markers for cancer treatment are indicated by red color.

Figure 5: The results of integrated analysis are shown in a color scale.

Table 6: Parameters for all selected kinase inhibitors are shown.

Table 7: The results of gene expression analysis are shown.

Figure 6: a) Heat map showing the expression levels of selected genes in the tumor.

Figure 7: b) Expression levels of selected genes in the tumor.

Figure 8: c) Expression levels of selected genes in the tumor.

Figure 9: d) Heat map showing the expression levels of selected genes in the tumor.

Figure 10: e) Heat map showing the expression levels of selected genes in the tumor.

Figure 11: f) Heat map showing the expression levels of selected genes in the tumor.

Figure 12: g) Heat map showing the expression levels of selected genes in the tumor.

Figure 13: h) Heat map showing the expression levels of selected genes in the tumor.

Figure 14: i) Heat map showing the expression levels of selected genes in the tumor.

Figure 15: j) Heat map showing the expression levels of selected genes in the tumor.

Figure 16: k) Heat map showing the expression levels of selected genes in the tumor.

Figure 17: l) Heat map showing the expression levels of selected genes in the tumor.

Figure 18: m) Heat map showing the expression levels of selected genes in the tumor.

Figure 19: n) Heat map showing the expression levels of selected genes in the tumor.

Figure 20: o) Heat map showing the expression levels of selected genes in the tumor.

Figure 21: p) Heat map showing the expression levels of selected genes in the tumor.

Figure 22: q) Heat map showing the expression levels of selected genes in the tumor.

Figure 23: r) Heat map showing the expression levels of selected genes in the tumor.

Figure 24: s) Heat map showing the expression levels of selected genes in the tumor.

Figure 25: t) Heat map showing the expression levels of selected genes in the tumor.

Figure 26: u) Heat map showing the expression levels of selected genes in the tumor.

Figure 27: v) Heat map showing the expression levels of selected genes in the tumor.

Figure 28: w) Heat map showing the expression levels of selected genes in the tumor.

Figure 29: x) Heat map showing the expression levels of selected genes in the tumor.

Figure 30: y) Heat map showing the expression levels of selected genes in the tumor.

Figure 31: z) Heat map showing the expression levels of selected genes in the tumor.