|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Patient** | **Gene** | **Primary Tumor** | **Pre-treatment** | **Post-treatment 1** | **Post-treatment 2** |
| **#1**  | *KRAS* | -  | - | focal amp | focal amp |
|  | *EGFR* | -  | -  | -  | -  |
|  | *ERBB2* | -  | -  | -  | -  |
|  | *MET* | -  | -  | -  | -  |
| **#2**  | *KRAS* | - | - | - | focal amp |
|  | *EGFR* | polysomy 7p | polysomy 7p | - 1 | polysomy 7p |
|  | *ERBB2* | polysomy 17 | polysomy 17 | - 1 | - 1 |
|  | *MET* | - | - | - | - |
| **#3**  | *KRAS* | - | n/a | polysomy 12p | n/a |
|  | *EGFR* | - | n/a | - | n/a |
|  | *ERBB2* | - | n/a | - | n/a |
|  | *MET* | - | n/a | - | n/a |
| **#4**  | *KRAS* | n/a2 | n/a | focal amp | n/a |
|  | *EGFR* | n/a2 | n/a | - | n/a |
|  | *ERBB2* | n/a2 | n/a | - | n/a |
|  | *MET* | n/a2 | n/a | focal amp | n/a |
| **#5** | *KRAS* | - | n/a | - | n/a |
|  | *EGFR* | polysomy 7p | n/a | polysomy 7p | n/a |
|  | *ERBB2* | amp | n/a | amp | n/a |
|  | *MET* | focal amp | n/a | focal amp | n/a |
| **#6** | *KRAS* | n/a | - | n/a3 | n/a |
|  | *EGFR* | n/a | polysomy 7p | n/a3 | n/a |
|  | *ERBB2* | n/a | polysomy 17q | n/a3 | n/a |
|  | *MET* | n/a | - | n/a3 | n/a |
| **#7** | *KRAS* | n/a4 | n/a | polysomy 12p | n/a |
|  | *EGFR* | n/a4 | n/a | polysomy 7 | n/a |
|  | *ERBB2* | amp4 | n/a | focal amp | n/a |
|  | *MET* | n/a4 | n/a | polysomy 7 | n/a |
| **#8** | *KRAS* | - 5 | - | - | n/a |
|  | *EGFR* | - 5 | polysomy 7 | polysomy 7 | n/a |
|  | *ERBB2* | - 5 | - | - | n/a |
|  | *MET* | - 5 | polysomy 7 | polysomy 7 | n/a |
| **#9** | *KRAS* | n/a | n/a | - | n/a |
|  | *EGFR* | n/a | n/a | - | n/a |
|  | *ERBB2* | n/a | n/a | - | n/a |
|  | *MET* | n/a | n/a | - | n/a |
| **#10** | *KRAS* | n/a | - | - | - |
|  | *EGFR* | n/a | - | - | - |
|  | *ERBB2* | n/a | - | - | - |
|  | *MET* | n/a | - | - | - |

**Table S4** Summary of copy number changes of *KRAS, EGFR, ERBB2*, and *MET.*

1 Polysomy was not detected owing to a low amount of tumor DNA

2 Only a biopsy was available that may not represent genetic composition of primary

3 Amount of tumor DNA in samples was too low to obtain tumor-specific copy number aberrations

4 Only biopsy was available, *ERBB2* amplification based on immunohistochemistry and silver *in situ* hybridization

5 Quality of plasma-Seq data did not allow reliable z-score calculation