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This study retrospectively included 40 NSCLC patients harboring either EGFR or ERBB2 mutations, who had received afatinib as first-line treatment. Targeted next-generation sequencing (NGS) data on the baseline and post-treatment samples were subjected to analysis. Comparative analyses of genetic features and clinical parameters were performed.

The study identified multiple genomic characteristics associated with primary and secondary resistance to afatinib in EGFR- and ERBB2-positive subpopulations.

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**Methods**

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**Conclusions**

The study identified multiple genomic characteristics associated with primary and secondary resistance to afatinib in EGFR- and ERBB2-positive subpopulations.