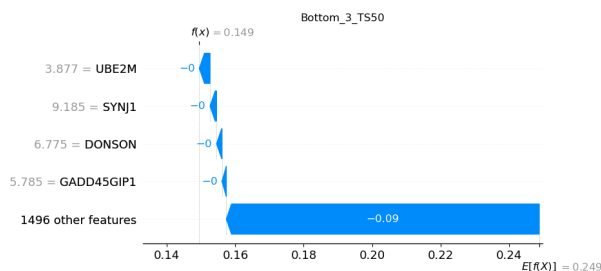


### Bottom 1 Sample: TS50

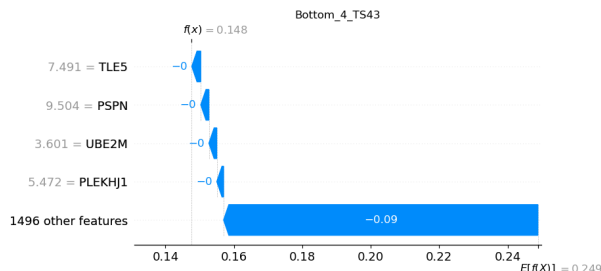


The SHAP values reveal key genetic features impacting the predicted Area Above the Curve (AAC) for erlotinib response.

- UBE2M (SHAP: -0.0031394):** Negative contribution, indicating its low expression (3.88) may be associated with reduced drug efficacy, potentially influencing the tumor's response to erlotinib.
- SYNJ1 (SHAP: -0.00190584):** Slight negative effect, suggesting its low expression (9.19) may marginally impact the drug's effectiveness.
- DONSON (SHAP: -0.001572):** Minor negative influence, reflecting its low expression (6.77) may have a limited impact on the AAC.
- GADD45GIP1 (SHAP: -0.00128787):** Slight negative effect, indicating its low expression (5.79) may contribute to reduced drug response.

In summary, the identified features suggest that low expression of UBE2M, SYNJ1, DONSON, and GADD45GIP1 may be associated with reduced erlotinib efficacy, warranting further investigation into their potential as biomarkers for personalized treatment strategies.

### Bottom 2 Sample: TS43

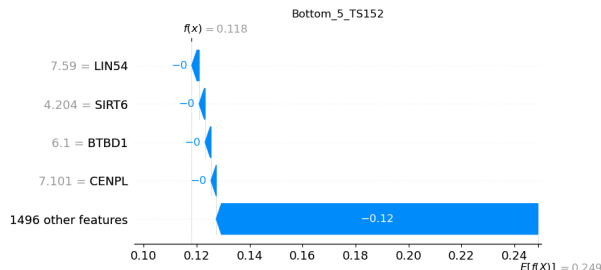


The SHAP values reveal key genetic features impacting the predicted Area Above the Curve (AAC) for erlotinib response.

- **TLE5 (SHAP: -0.00262835):** Negative contribution, indicating its low expression (7.49116) may be associated with reduced drug sensitivity.
- **PSPN (SHAP: -0.00237645):** Negative contribution, suggesting its low expression (9.50409) could be linked to decreased tumor response.
- **UBE2M (SHAP: -0.00230246):** Negative contribution, implying its low expression (3.60056) may influence the drug response in a similar manner to PSPN.
- **PLEKHJ1 (SHAP: -0.00199659):** Negative contribution, indicating its low expression (5.4724) could be related to reduced drug efficacy.

In summary, the identified features suggest that low expression of TLE5, PSPN, UBE2M, and PLEKHJ1 may be associated with reduced erlotinib response, warranting further investigation into their potential as biomarkers for personalized medicine.

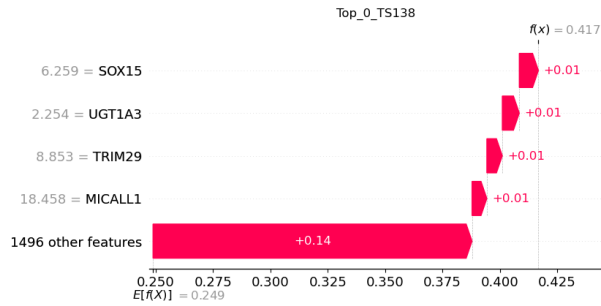
### Bottom 3 Sample: TS152



The SHAP values reveal key genetic features impacting the predicted Area Above the Curve (AAC) for erlotinib response.

- **LIN54 (SHAP: -0.00277591):** Negative contribution, indicating its low expression (7.59) may be associated with reduced drug efficacy.
- **SIRT6 (SHAP: -0.00225572):** Slightly negative effect, suggesting its low expression (4.20) could influence decreased drug response.
- **BTBD1 (SHAP: -0.00221959):** Minimal negative impact, reflecting its moderate expression (6.10) has a limited effect on drug sensitivity.
- **CENPL (SHAP: -0.00197824):** Slight negative influence, indicating its low expression (7.10) may marginally lower the AAC.

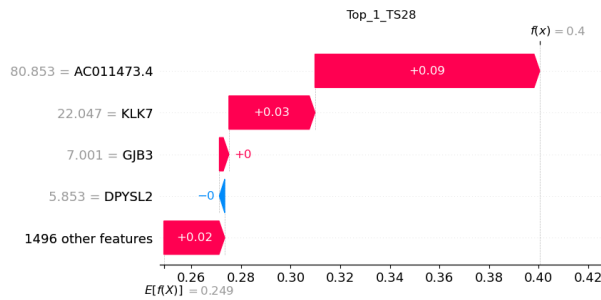
### Top 1 Sample: TS138



The SHAP values reveal key genetic features impacting the predicted Area Above the Curve (AAC) for erlotinib response.

- **SOX15 (SHAP: 0.00833636):** Moderate positive contribution, indicating its expression level (6.25921) may influence the drug's efficacy in modulating the PI3K/AKT signaling pathway, a key pathway in cancer cell proliferation.
- **UGT1A3 (SHAP: 0.00741029):** Slight positive effect, suggesting its expression level (2.25366) may impact the drug's pharmacokinetics, potentially affecting its bioavailability and efficacy.
- **TRIM29 (SHAP: 0.00673423):** Minor positive impact, reflecting its limited involvement in the regulation of cellular stress responses and apoptosis, which may influence the drug's ability to induce cancer cell death.
- **MICALL1 (SHAP: 0.00646013):** Slight positive contribution, indicating its expression level (18.4582) may play a role in modulating the cell cycle and apoptosis, potentially influencing the drug's efficacy in cancer treatment.

### Top 2 Sample: TS28

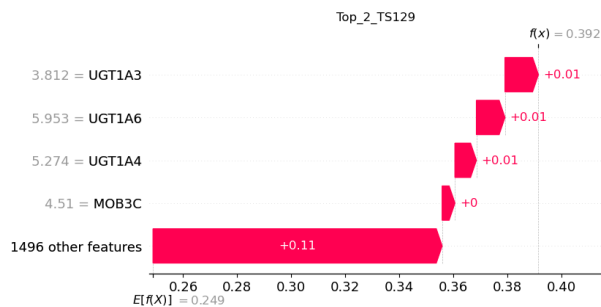


The SHAP values reveal key genetic features impacting the predicted Area Above the Curve (AAC) for erlotinib response.

- **AC011473.4 (SHAP: 0.090653):** Strong positive contribution, suggesting its high expression (80.8526) plays a key role in drug sensitivity, potentially indicating a favorable response to erlotinib.
- **KLK7 (SHAP: 0.0347236):** Moderate positive effect, with elevated expression (22.0465) potentially influencing tumor response, suggesting a possible synergistic interaction with erlotinib.
- **GJB3 (SHAP: 0.00384216):** Minor positive impact, reflecting limited involvement, and its expression (7.00119) may not significantly influence the AAC.
- **DPYSL2 (SHAP: -0.00215775):** Slight negative influence, suggesting reduced expression (5.8528) marginally lowers the AAC, indicating a potential antagonist effect on erlotinib response.

In summary, AC011473.4 is the most critical feature, highlighting its biomarker potential, and its high expression is strongly associated with a favorable response to erlotinib.

### Top 3 Sample: TS129



The SHAP values reveal key genetic features impacting the predicted Area Above the Curve (AAC) for erlotinib response.

- **UGT1A3 (SHAP: 0.0123836):** Moderate positive contribution, indicating its expression level (3.81211) may influence the efficacy of erlotinib, potentially affecting its pharmacokinetics and metabolism.
- **UGT1A6 (SHAP: 0.0105802):** Slightly positive effect, suggesting its expression level (5.95259) may contribute to the drug's pharmacokinetic profile and impact its response.
- **UGT1A4 (SHAP: 0.00793713):** Minimal positive impact, reflecting its limited involvement in the drug's metabolism and response.
- **MOB3C (SHAP: 0.0047477):** Very minor positive contribution, indicating its expression level (4.50961) has a negligible effect on the predicted AAC.