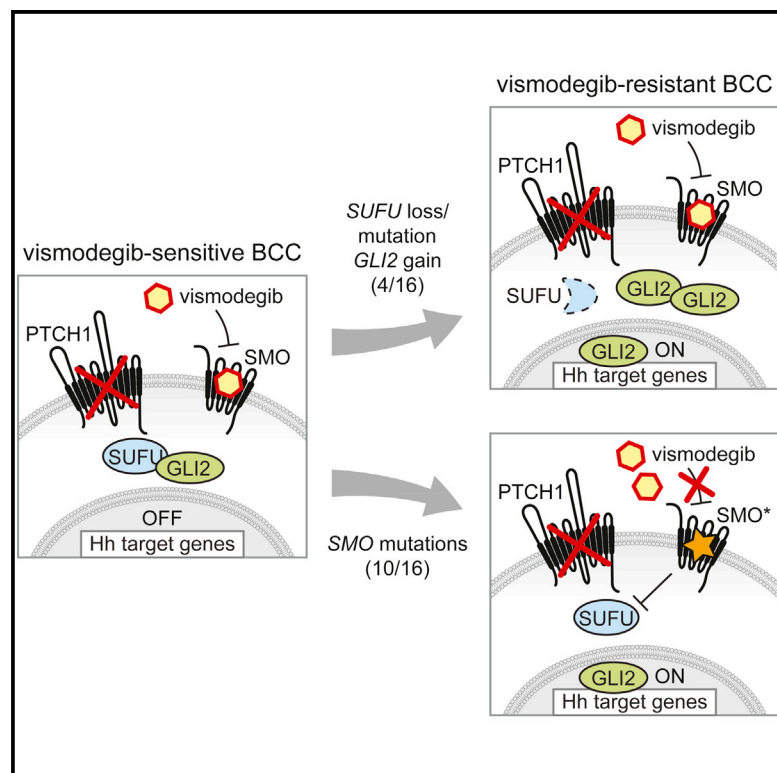


# Genomic Analysis of Smoothed Inhibitor Resistance in Basal Cell Carcinoma

## Graphical Abstract



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## In Brief

Sharpe et al. identify SMO mutations in the binding pocket for SMO inhibitors or that constitutively activate SMO in vismodegib-resistant basal cell carcinoma. They demonstrate that a single relapsed tumor can harbor clones with different resistance mutations.

## Highlights

- Recurrent mechanisms reactivate the Hh pathway in SMO inhibitor-resistant BCC
- Drug-binding pocket and activating SMO mutations reduce sensitivity to vismodegib
- Downstream *SUFU* variants co-occur with alterations predicted to increase *GLI2* levels
- A relapsed tumor can harbor multiple resistance mechanisms



# Genomic Analysis of Smoothened Inhibitor Resistance in Basal Cell Carcinoma

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## SUMMARY

Smoothened (SMO) inhibitors are under clinical investigation for the treatment of several cancers. Vismodegib is approved for the treatment of locally advanced and metastatic basal cell carcinoma (BCC). Most BCC patients experience significant clinical benefit on vismodegib, but some develop resistance. Genomic analysis of tumor biopsies revealed that vismodegib resistance is associated with Hedgehog (Hh) pathway reactivation, predominantly through mutation of the drug target SMO and to a lesser extent through concurrent copy number changes in *SUFU* and *GLI2*. SMO mutations either directly impaired drug binding or activated SMO to varying levels. Furthermore, we found evidence for intra-tumor heterogeneity, suggesting that a combination of therapies targeting components at multiple levels of the Hh pathway is required to overcome resistance.

## INTRODUCTION

Basal cell carcinoma (BCC) is the most common human cancer and is driven predominantly by hyperactivation of the Hedgehog (Hh) pathway (Oro et al., 1997; Xie et al., 1998). The association between Hh signaling and cancer was first discovered in patients with Gorlin (or basal cell nevus) syndrome, who are highly susceptible to medulloblastoma (MB) and BCC. These patients generally possess heterozygous germline mutations in the

Patched 1 gene (*PTCH1*), which encodes a receptor for Hh ligands (Hahn et al., 1996; Johnson et al., 1996). Hh ligand binding relieves *PTCH1* suppression of the serpentine transmembrane (TM) signal transducer Smoothened (SMO; see Figure 1A for a schematic of the Hh pathway). The vast majority of sporadic BCCs are driven by inactivating mutations and loss of heterozygosity (LOH) in *PTCH1*, with most of the remainder harboring activating mutations in *SMO* (Reifenberger et al., 2005). SMO promotes the activation and nuclear localization of GLI

### Significance

Acquired resistance represents a major challenge to the success of targeted cancer therapies. Therefore, understanding resistance mechanisms will help guide future therapeutic strategies. Vismodegib was approved for treatment of locally advanced and metastatic BCC and is under clinical investigation for several other cancers. We performed molecular analyses of tumor biopsies from BCC patients who initially responded but subsequently progressed on treatment. We found that vismodegib resistance is invariably linked to Hh pathway reactivation, indicating that BCC is addicted to Hh signaling. Variants occurred either in or downstream of the drug target SMO, with intra-tumor heterogeneity observed for both resistance mechanisms, suggesting that a combination of SMO and downstream targeting agents will be required to overcome vismodegib resistance in Hh-driven cancers.

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