

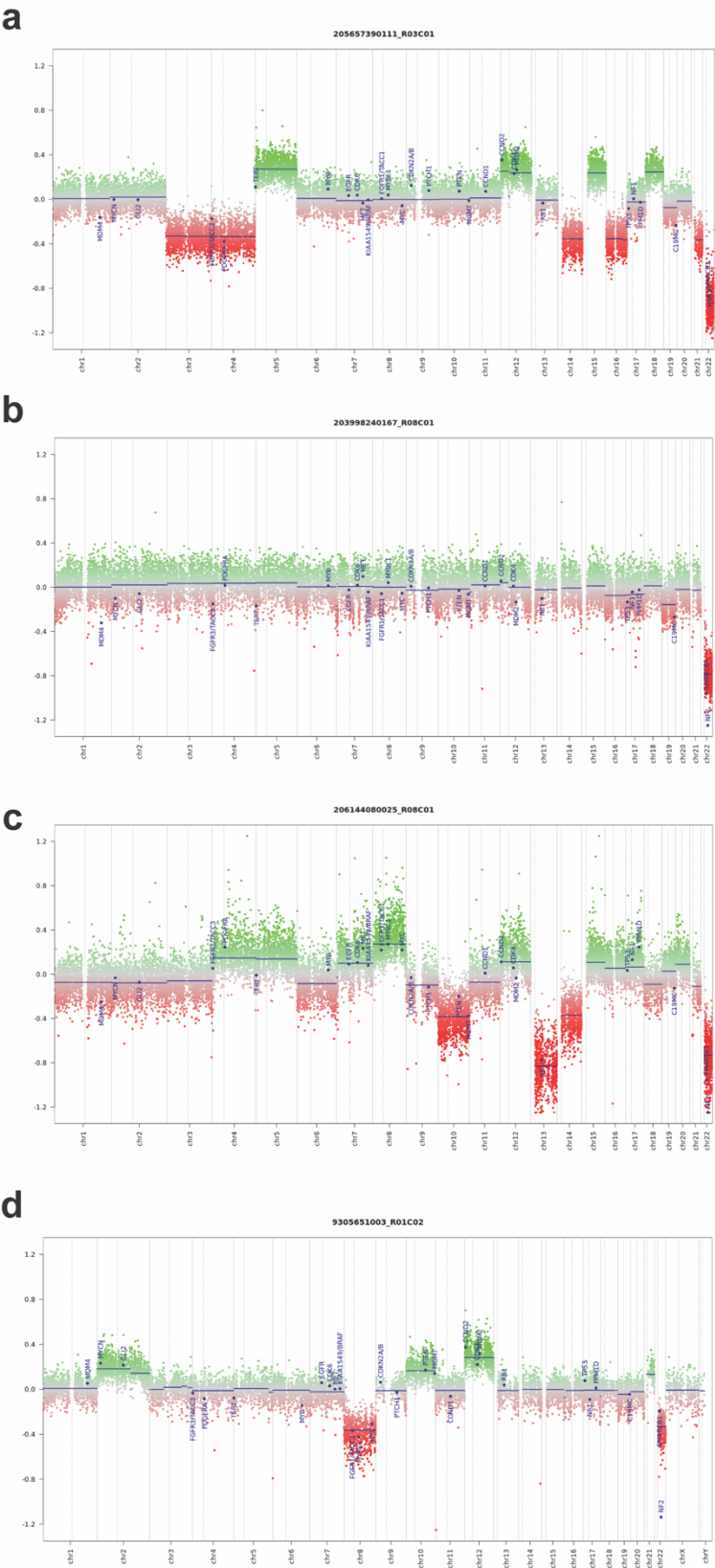
Transcriptomic and epigenetic dissection of spinal ependymoma (SP-EPN) identifies clinically relevant subtypes enriched for tumors with and without *NF2* mutation

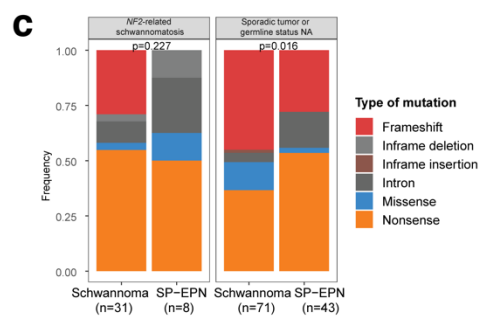
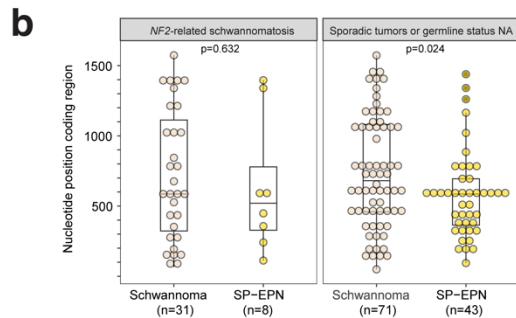
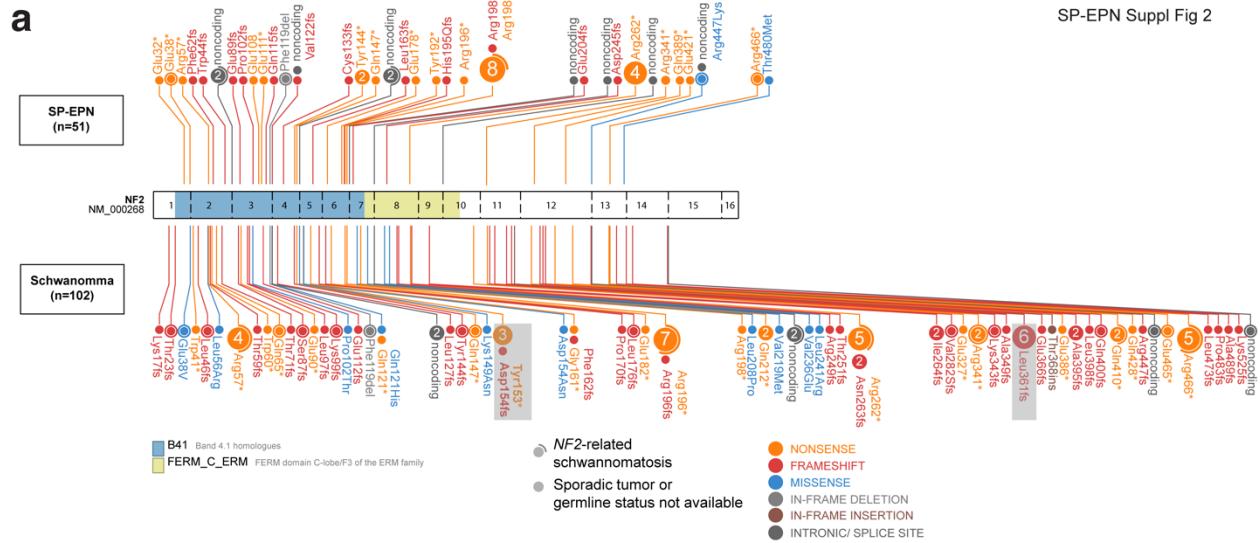
Acta Neuropathologica

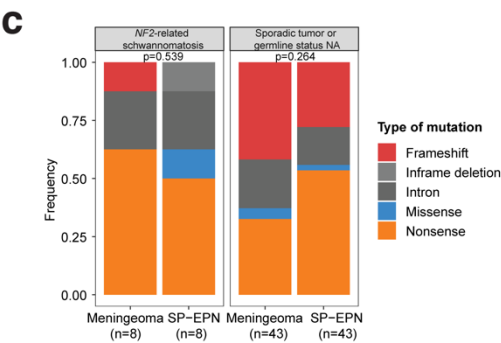
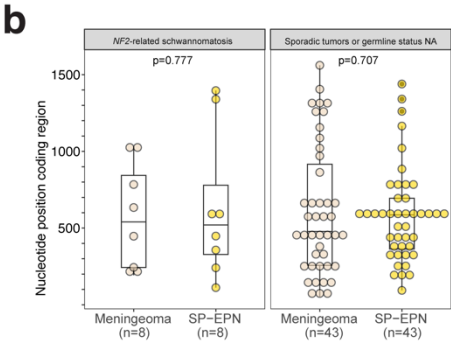
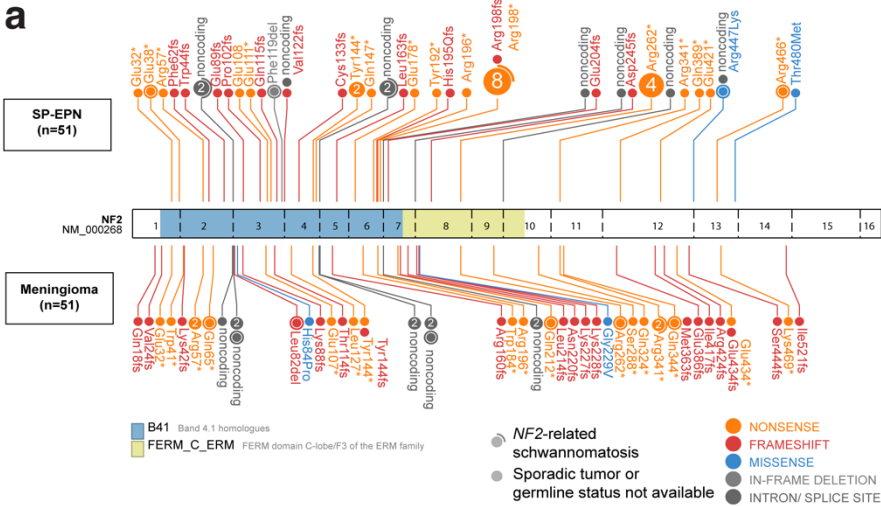
Sina Neyazi, Erika Yamazawa, Karoline Hack et al.

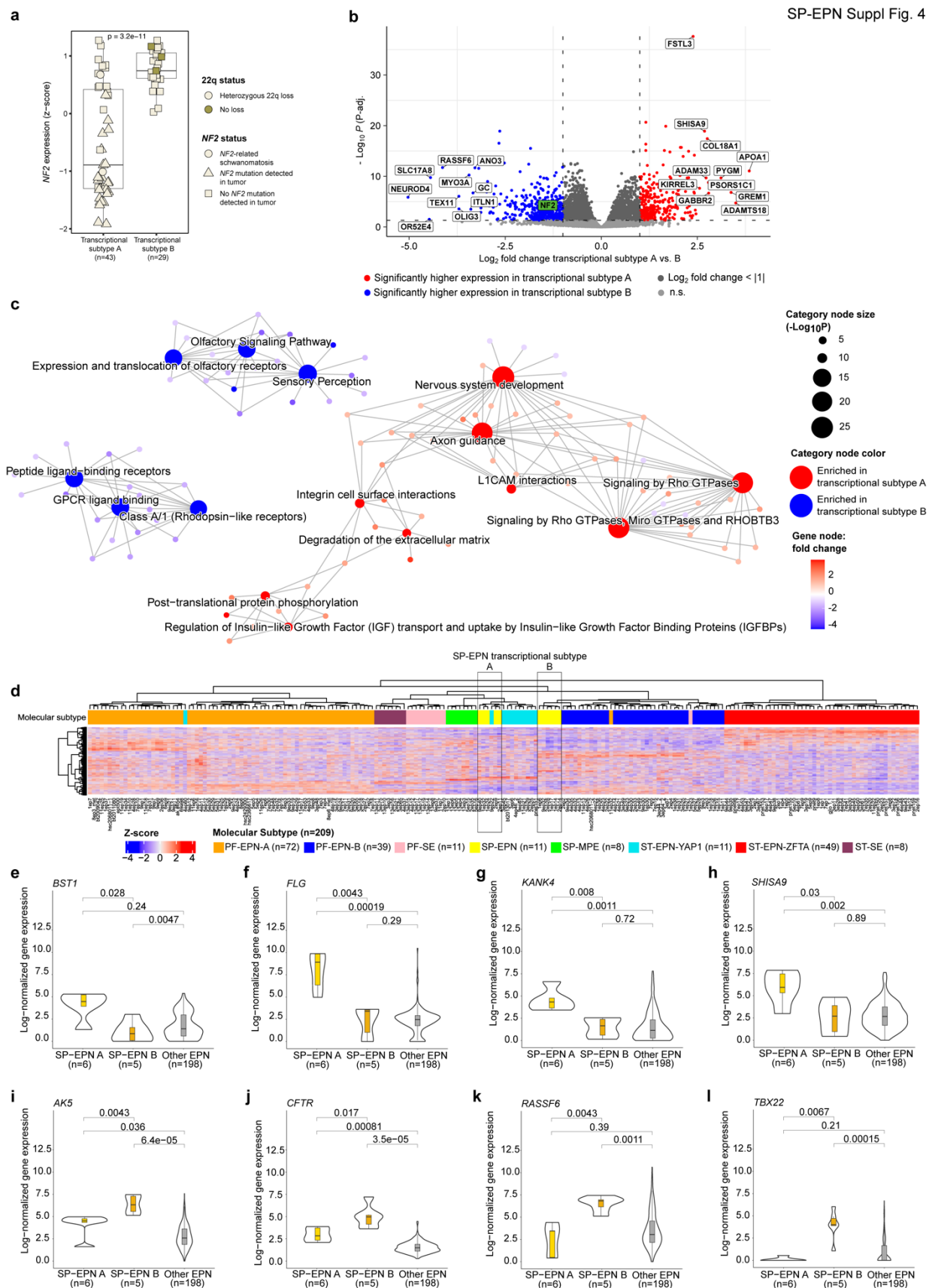
Corresponding authors: Ulrich Schüller (u.schueller@uke .de), Department of Pediatric Hematology and Oncology, University Medical Center Hamburg-Eppendorf, Germany; Shota Tanaka (stanaka@m.u-tokyo.ac.jp), Department of Neurosurgery, Graduate School of Medicine, The University of Tokyo, Japan

Supplemental figures

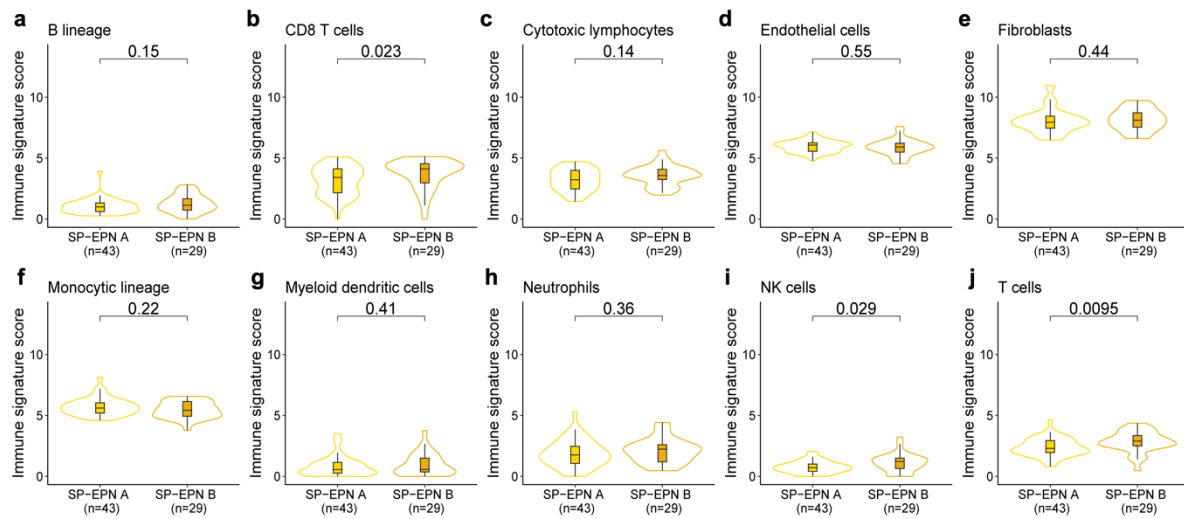


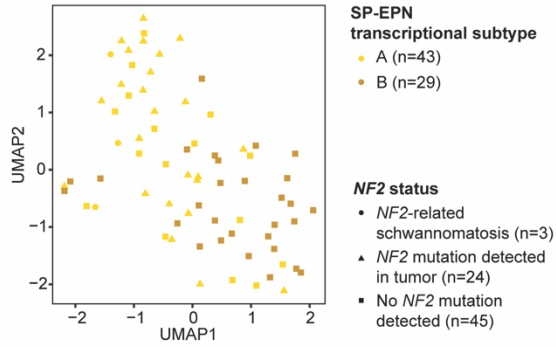
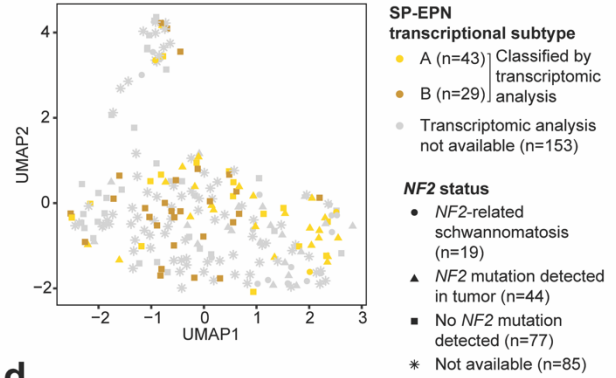
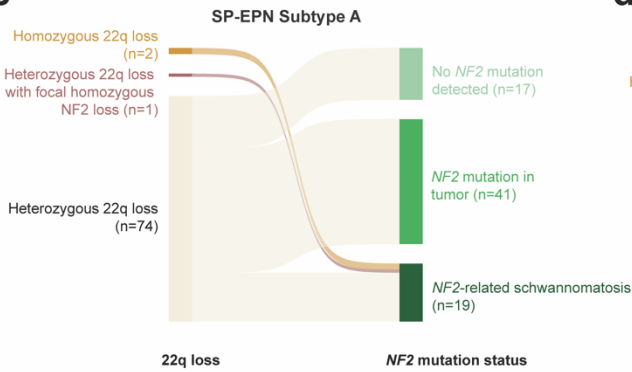
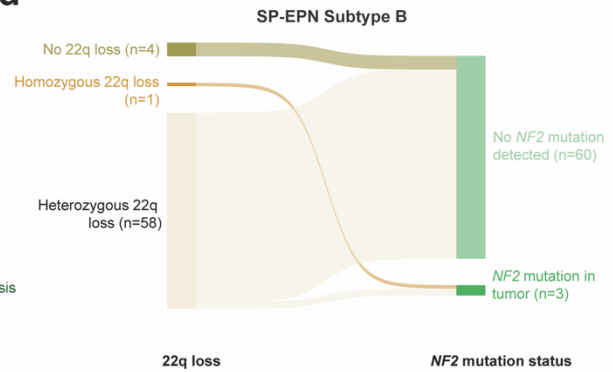
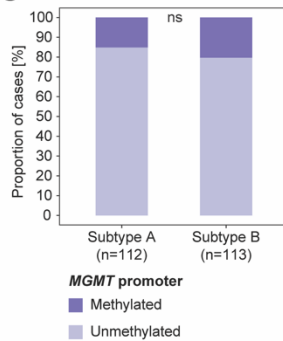
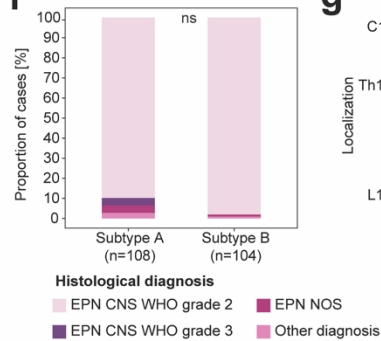
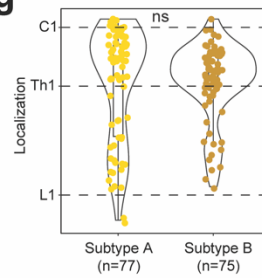
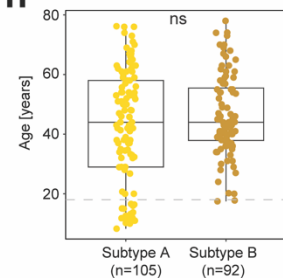
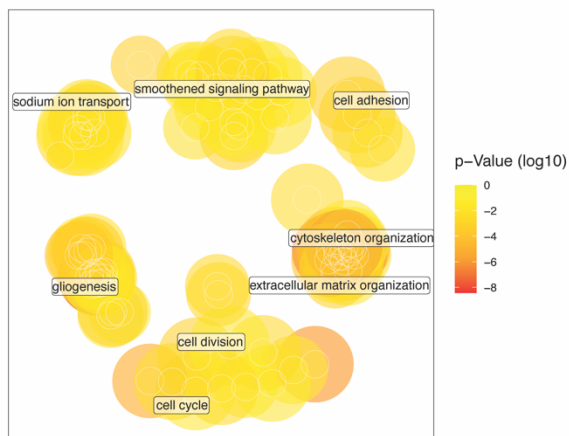






SP-EPN Suppl Fig 5



a Global methylation analysis of transcriptional subgroups**b** Global methylation analysis of all SP-EPN**c****d****e****f****g****h****i****SP-EPN Subtype A****j****SP-EPN Subtype B**