

**Supplementary Note 1: Reference list data sources****Leukemia and lymphoma:**

- Andersson, A. K. *et al.* The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. *Nat. Genet.* **47**, 330-337, doi:10.1038/ng.3230 (2015).
- Bandapalli, O. R. *et al.* The activating STAT5B N642H mutation is a common abnormality in pediatric T-cell acute lymphoblastic leukemia and confers a higher risk of relapse. *Haematologica* **99**, e188-192, doi:10.3324/haematol.2014.104992 (2014).
- Faber, Z. J. *et al.* The genomic landscape of core-binding factor acute myeloid leukemias. *Nat. Genet.* **48**, 1551-1556, doi:10.1038/ng.3709 (2016).
- Gruber, T. A. *et al.* An Inv(16)(p13.3q24.3)-encoded CBFA2T3-GLIS2 fusion protein defines an aggressive subtype of pediatric acute megakaryoblastic leukemia. *Cancer Cell* **22**, 683-697, doi:10.1016/j.ccr.2012.10.007 (2012).
- Holmfeldt, L. *et al.* The genomic landscape of hypodiploid acute lymphoblastic leukemia. *Nat. Genet.* **45**, 242-252, doi:10.1038/ng.2532 (2013).
- Irving, J. *et al.* Ras pathway mutations are prevalent in relapsed childhood acute lymphoblastic leukemia and confer sensitivity to MEK inhibition. *Blood* **124**, 3420-3430, doi:10.1182/blood-2014-04-531871 (2014).
- Kunz, J. B. *et al.* Pediatric T-cell lymphoblastic leukemia evolves into relapse by clonal selection, acquisition of mutations and promoter hypomethylation. *Haematologica* **100**, 1442-1450, doi:10.3324/haematol.2015.129692 (2015).
- Li, B. *et al.* Negative feedback-defective PRPS1 mutants drive thiopurine resistance in relapsed childhood ALL. *Nat. Med.* **21**, 563-571, doi:10.1038/nm.3840 (2015).
- Lopez *et al.*, Borkhardt *et al.*, in preparation

**Ewing's sarcoma:**

- Agelopoulos, K. *et al.* Deep Sequencing in Conjunction with Expression and Functional Analyses Reveals Activation of FGFR1 in Ewing Sarcoma. *Clin. Cancer. Res.* **21**, 4935-4946, doi:10.1158/1078-0432.ccr-14-2744 (2015).

**Hepatoblastoma:**

- Eichenmuller, M. *et al.* The genomic landscape of hepatoblastoma and their progenies with HCC-like features. *Journal of hepatology* **61**, 1312-1320, doi:10.1016/j.jhep.2014.08.009 (2014).

**Osteosarcoma:**

- Chen, X. *et al.* Recurrent somatic structural variations contribute to tumorigenesis in pediatric osteosarcoma. *Cell reports* **7**, 104-112, doi:10.1016/j.celrep.2014.03.003 (2014).
- Kovac, M. *et al.* Exome sequencing of osteosarcoma reveals mutation signatures reminiscent of BRCA deficiency. *Nature communications* **6**, 8940, doi:10.1038/ncomms9940 (2015).

**Glioma:**

- Bender, S. *et al.* Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. *Nat. Med.*, doi:10.1038/nm.4204 (2016).
- Jones, D. T. *et al.* Recurrent somatic alterations of FGFR1 and NTRK2 in pilocytic astrocytoma. *Nat. Genet.* **45**, 927-932, doi:10.1038/ng.2682 (2013).
- Wu, G. *et al.* Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. *Nat. Genet.* **44**, 251-253, doi:10.1038/ng.1102 (2012).
- Wu, G. *et al.* The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. *Nat. Genet.* **46**, 444-450, doi:10.1038/ng.2938 (2014).
- Zhang, J. *et al.* Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. *Nat. Genet.* **45**, 602-612, doi:10.1038/ng.2611 (2013).

**Medulloblastoma:**

- Kool, M. *et al.* Genome sequencing of SHH medulloblastoma predicts genotype-related response to smoothed inhibition. *Cancer Cell* **25**, 393-405, doi:10.1016/j.ccr.2014.02.004 (2014).
- Northcott, P. A. *et al.* The whole-genome landscape of medulloblastoma subtypes. *Nature* **547**, 311-317, doi:10.1038/nature22973 (2017).
- Robinson, G. *et al.* Novel mutations target distinct subgroups of medulloblastoma. *Nature* **488**, 43-48, doi:10.1038/nature11213 (2012).

**Wilms' tumors:**

- Wegert, J. *et al.* Mutations in the SIX1/2 pathway and the DROSHA/DGCR8 miRNA microprocessor complex underlie high-risk blastemal type Wilms tumors. *Cancer Cell* **27**, 298-311, doi:10.1016/j.ccell.2015.01.002 (2015).

**ATRT:**

- Johann, P. D. *et al.* Atypical Teratoid/Rhabdoid Tumors Are Comprised of Three Epigenetic Subgroups with Distinct Enhancer Landscapes. *Cancer Cell* **29**, 379-393, doi:10.1016/j.ccell.2016.02.001 (2016).

**ETMR:**

- Lambo *et al.*, in preparation

**Ependymoma:**

- Mack, S. C. *et al.* Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. *Nature* **506**, 445-450, doi:10.1038/nature13108 (2014).
- Parker, M. *et al.* C11orf95-RELA fusions drive oncogenic NF-kappaB signalling in ependymoma. *Nature* **506**, 451-455, doi:10.1038/nature13109 (2014).

**Neuroblastoma:**

- Cheung, N. K. *et al.* Association of age at diagnosis and genetic mutations in patients with neuroblastoma. *Jama* **307**, 1062-1071, doi:10.1001/jama.2012.228 (2012).
- Ackermann *et al.*, in preparation

**Adrenocortical carcinoma:**

- Pinto, E. M. *et al.* Genomic landscape of paediatric adrenocortical tumours. *Nature communications* **6**, 6302, doi:10.1038/ncomms7302 (2015).

**Rhabdomyosarcoma:**

- Chen, X. *et al.* Targeting oxidative stress in embryonal rhabdomyosarcoma. *Cancer Cell* **24**, 710-724, doi:10.1016/j.ccr.2013.11.002 (2013).
- Fulda *et al.*, in preparation

**Retinoblastoma:**

- Zhang, J. *et al.* A novel retinoblastoma therapy from genomic and epigenetic analyses. *Nature* **481**, 329-334, doi:10.1038/nature10733 (2012).
- Temming *et al.*, in preparation

**Mixed:**

- Worst, B. C. *et al.* Next-generation personalised medicine for high-risk paediatric cancer patients - The INFORM pilot study. *Eur. J. Cancer* **65**, 91-101, doi:10.1016/j.ejca.2016.06.009 (2016).

**Associated accession numbers:**

European Nucleotide Archive: RP012816, PRJEB11430; European Genome Archive:  
EGAS00001001139, EGAS00001001953, EGAS00001000607, EGAS00001000381,  
EGAS00001000906, EGAS00001001297, EGAS00001000443, EGAS00001000213,  
EGAS00001000263, EGAS00001000192, EGAS00001000255, EGAS00001000254,  
EGAS00001000253, EGAS00001000256, EGAS00001000246, EGAS00001000379,  
EGAS00001000380, EGAS00001000346, EGAS00001000349, EGAS00001000347,  
EGAS00001000192