**A unique case report of infantile gliosarcoma with *TPR*-*NTRK1* fusion treated with larotrectinib**

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| **Supplementary Table 1.** Gene targets of Oncomine Childhood Cancer Research Assay  |  |  |  |
| **Comprehensive mutation coverage (86)** |  | **Full exon coverage (44)** | **CNV (28)** |  | **Fusion and expression (98)** |  |
| *ABL1* | *EGFR* | *IL7R* | *PDGFRA* |  | *APC* | *NF1* |  | *ABL2* | *MDM4* |  | *ABL1* | *FOSB* | *MYH11* | *PLAG1* | *YAP1* |
| *ABL2* | *EP300* | *JAK1* | *PDGFRB* |  | *ARID1A* | *NF2* |  | *ALK* | *MET* |  | *ABL2* | *FUS* | *MYH9* | *RAF1* | *ZMYND11* |
| *ALK* | *ERBB2* | *JAK2* | *PIK3CA*  |  | *ARID1B* | *PHF6* |  | *BRAF* | *MYC* |  | *AFF3* | *GLI1* | *NCOA2* | *RANBP17* | *ZNF384* |
| *ACVR1* | *ERBB3* | *JAK3* | *PIK3R1* |  | *ATRX* | *PRPS1* |  | *CCND1* | *MYCN* |  | *ALK* | *GLIS2* | *NCOR1* | *RARA* |  |
| *AKT1* | *ERBB4* | *KDM4C* | *PPM1D* |  | *CDKN2A* | *PSMB5* |  | *CDK4* | *PDGFRA* |  | *BCL11B* | *HMGA2* | *NOTCH1* | *RECK* | **Gene Expression** |
| *ASXL1* | *ESR1* | *KDR* | *PTPN11* |  | *CDKN2B* | *PTCH1* |  | *CDK6* | *PIK3CA* |  | *BCOR* | *JAK2* | *NOTCH2* | *RELA* | *BCL2* |
| *ASXL2* | *EZH2* | *KIT* | *RAF1* |  | *CEBPA* | *PTEN* |  | *EGFR* |  |  | *BCR* | *KAT6A* | *NOTCH4* | *RET* | *BCL6* |
| *BRAF* | *FASLG* | *KRAS* | *RET* |  | *CHD7* | *RB1* |  | *ERBB2* |  |  | *BRAF* | *KMT2A* | *NPM1* | *ROS1* | *FGFR1* |
| *CALR* | *FBXW7* | *MAP2K1* | *RHOA* |  | *CRLF1* | *RUNX1* |  | *ERBB3* |  |  | *CAMTA1* | *KMT2B* | *NR4A3* | *RUNX1* | *FGFR4* |
| *CBL* | *FGFR1* | *MAP2K2* | *SETBP1* |  | *DDX3X* | *SMARCA4* |  | *FGFR1* |  |  | *CCND1* | *KMT2C* | *NTRK1* | *SS18* | *IGF1R* |
| *CCND1* | *FGFR2* | *MET* | *SETD2* |  | *DICER1* | *SMARCB1* |  | *FGFR2* |  |  | *CIC* | *KMT2D* | *NTRK2* | *SSBP2* | *MET* |
| *CCND3* | *FGFR3* | *MPL* | *SH2B3* |  | *EBF1* | *SOCS2* |  | *FGFR3* |  |  | *CREBBP* | *LMO2* | *NTRK3* | *STAG2* | *MYCN* |
| *CCR5* | *FLT3* | *MSH6* | *SH2D1A* |  | *EED* | *SUFU* |  | *FGFR4* |  |  | *CRLF2* | *MAML2* | *NUP214* | *STAT6* | *MYC* |
| *CDK4* | *GATA2* | *MTOR* | *SMO* |  | *FAS* | *SUZ12* |  | *GLI1* |  |  | *CSF1R* | *MAN2B1* | *NUP98* | *TAL1* | *TOP2A* |
| *CIC* | *GNA11* | *MYC* | *STAT3* |  | *GATA1* | *TCF3* |  | *GLI2* |  |  | *DUSP22* | *MECOM* | *NUTM1* | *TCF3* |  |
| *CREBBP* | *GNAQ* | *MYCN* | *STAT5B* |  | *GATA3* | *TET2* |  | *IGF1R* |  |  | *EGFR* | *MEF2D* | *NUTM2B* | *TFE3* |  |
| *CRLF2* | *H3F3A* | *NCOR2* | *TERT* |  | *GNA13* | *TP53* |  | *JAK1* |  |  | *ETV6* | *MET* | *PAX3* | *TP63* |  |
| *CSF1R* | *HDAC9* | *NOTCH1* | *TPMT* |  | *ID3* | *TSC1* |  | *JAK2* |  |  | *EWSR1* | *MKL1* | *PAX5* | *TSLP* |  |
| *CSF3R* | *HIST1H3B* | *NPM1* | *USP7* |  | *IKZF1* | *TSC2* |  | *JAK3* |  |  | *FGFR1* | *MLLT10* | *PAX7* | *TSPAN4* |  |
| *CTNNB1* | *HRAS* | *NRAS* | *ZMYM3* |  | *KDM6A* | *WHSC1* |  | *KIT* |  |  | *FGFR2* | *MN1* | *PDGFB* | *UBTF* |  |
| *DAXX* | *IDH1* | *NT5C2* |  |  | *KMT2D* | *WT1* |  | *KRAS* |  |  | *FGFR3* | *MYB* | *PDGFRA* | *USP6* |  |
| *DNMT3A* | *IDH2* | *PAX5* |  |  | *MYOD1* | *XIAP* |  | *MDM2* |  |  | *FLT3* | *MYBL1* | *PDGFRB* | *WHSC1* |  |

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| **Supplementary Table 2.** Gene targets of Archer® FusionPlex® Solid Tumor Kit  |
| **Fusion splicing or exon skipping** |  | **SNV or indel** |
| *AKT3* | *ERG* | *FGFR2* | *MSMB* | *NTRK3* | *PRKCA* | *TERT* |  | *BRAF* |
| *ALK* | *ESR1* | *FGFR3* | *MYB* | *NUMBL* | *PRKCB* | *TFE3* |  | *PDGFRA* |
| *ARHGAP26* | *ETV1* | *FGR* | *MUSK* | *NUTM* | *RAF1* | *TFEB* |  |  |
| *AXL* | *ETV4* | *INSR* | *NOTCH1* | *PDGFRA* | *RELA* | *THADA*  |  |  |
| *BRAF* | *ETV5* | *MAML2* | *NOTCH2* | *PDGFRB* | *RET* | *TMPRSS2* |  |  |
| *BRD3* | *ETV6* | *MAST1* | *NRG1* | *PIK3CA* | *ROS1* |  |  |  |
| *BRD4* | *EWSR1* | *MAST2* | *NTRK1* | *PKN1* | *RSPO2* |  |  |  |
| *EGFR* | *FGFR1* | *MET* | *NTRK2* | *PPARG* | *RSPO3* |  |  |  |



**Supplementary Figure 1:** Immunohistochemical staining of integrase interactor 1 (INI1) (Magnification 200X).

**Supplementary Table 3.** List of variants identified in the infantile gliosarcoma.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| **Chromosome** | **Position** | **Gene** | **Type** | **Referece allele** | **Variant allele** | **Depth** | **VAF %** | **Location** | **Exon** | **Consequence** | **Protein** | **c.DNA** | **Transcript** | **COSMIC** | **Clinvar** | **AMP Classification** | **Gnomad** | **ABraOM** |
| 1 | 23885498 | *ID3* | SNV | T | C | 2000 | 51.50 | exonic | 2 | missense | p.Thr105Ala | c.313A>G | NM\_002167.5 | NI | NI | Tier IV | 0.7984 | 0.853038 |
| 2 | 29416366 | *ALK* | SNV | G | C | 1997 | 99.85 | exonic | 29 | missense | p.Asp1529Glu | c.4587C>G | NM\_004304.5 | Neutral | Benign | Tier IV | 0.4697 | 0.475369 |
| 2 | 29416572 | *ALK* | SNV | T | C | 1995 | 99.65 | exonic | 29 | missense | p.Ile1461Val | c.4381A>G | NM\_004304.5 | Neutral | Benign | Tier IV | 0.9968 | 0.992611 |
| 4 | 55139771 | *PDGFRA* | SNV | T | C | 1999 | 47.42 | exonic | 10 | missense | p.Ser478Pro | c.1432T>C | NM\_006206.6 | Neutral | Benign | Tier IV | 0.1534 | 0.152709 |
| 4 | 55972946 | *KDR* | SNV | A | G | 1561 | 46.70 | exonic | 11 | missense | p.Cys482Arg | c.1444T>C | NM\_002253.3 | Pathogenic | Benign | Tier IV | 0.02304 | 0.027915 |
| 4 | 106155185 | *TET2* | SNV | C | G | 1025 | 52.59 | exonic | 3 | missense | p.Pro29Arg| | c.86C>G| | NM\_001127208.2 | Pathogenic | Not povided | Tier IV | 0.06050 | 0.048440 |
| 5 | 112176756 | *APC* | SNV | T | A | 1693 | 99.47 | exonic | 16 | missense | p.Val1822Asp | c.5465T>A | NM\_000038.6 | Neutral | Benign | Tier IV | 0.7965 | 0.821018 |
| 5 | 176517797 | *FGFR4* | SNV | C | T | 751 | 98.80 | exonic | 4 | missense | p.Pro136Leu | c.407C>T | NM\_213647.3 | Neutral | Not reported | Tier IV | 0.7945 | 0.754516 |
| 6 | 41903782 | *CCND3* | SNV | A | C | 1995 | 100.00 | exonic | 5 | missense | p.Ser259Ala | c.775T>G | NM\_001760.5 | Neutral | Not reported | Tier IV | 0.5471 | 0.565789 |
| 8 | 61654298 | *CHD7* | SNV | T | A | 1649 | 51.67 | exonic | 2 | missense | p.Ser103Thr | c.307T>A | NM\_017780.4 | NI | Benign | Tier IV | 0.01231 | 0.018062 |
| 8 | 61778448 | *CHD7* | SNV | C | T | 1749 | 48.26 | exonic | 38 | missense | p.Leu2984Phe | c.8950C>T | NM\_017780.4 | NI | Benign/Likely benign | Tier IV | 0.003887 | 0.000821 |
| 9 | 98209594 | *PTCH1* | SNV | G | A | 2000 | 89.90 | exonic | 23 | missense | p.Pro1315Leu | c.3944C>T | NM\_000264.5 | Pathogenic | Benign | Tier IV | 0.3832 | 0.342365 |
| 17 | 7579472 | *TP53* | SNV | G | C | 1995 | 46.07 | exonic | 4 | missense | p.Pro72Arg | c.215C>G | NM\_000546.5 | Neutral | Likely benign | Tier IV | 0.6629 | 0.675698 |
| 20 | 31022959 | *ASXL1* | SNV | T | C | 1999 | 100.00 | exonic | 12 | missense | p.Leu815Pro | c.2444T>C | NM\_015338.6 | NI | NI | Tier IV | 1.000 | 1.000 |
| X | 76937963 | *ATRX* | SNV | G | C | 1994 | 99.95 | exonic | 9 | missense | p.Gln929Glu | c.2785C>G | NM\_000489.5 | NI | NI | Tier IV | 0.3853 | 0.444112 |

Variant Allele Frequency (VAF), Not informed (NI)