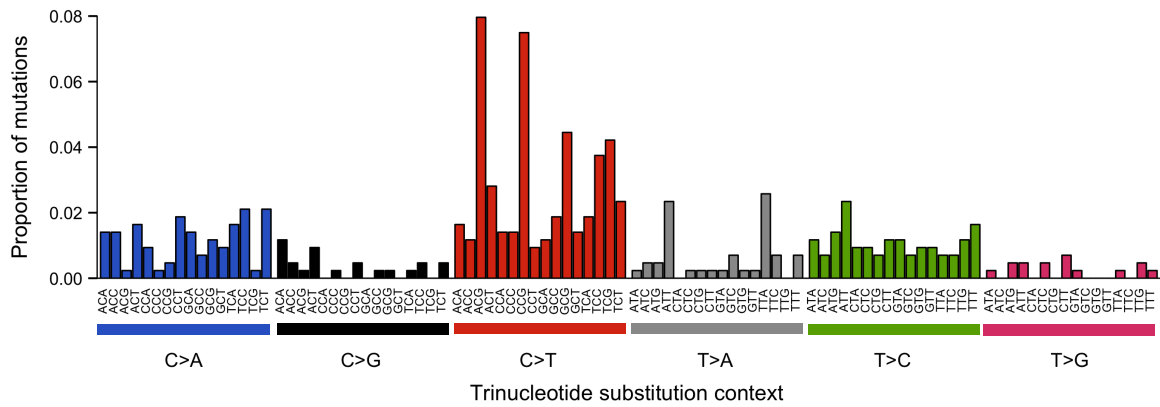


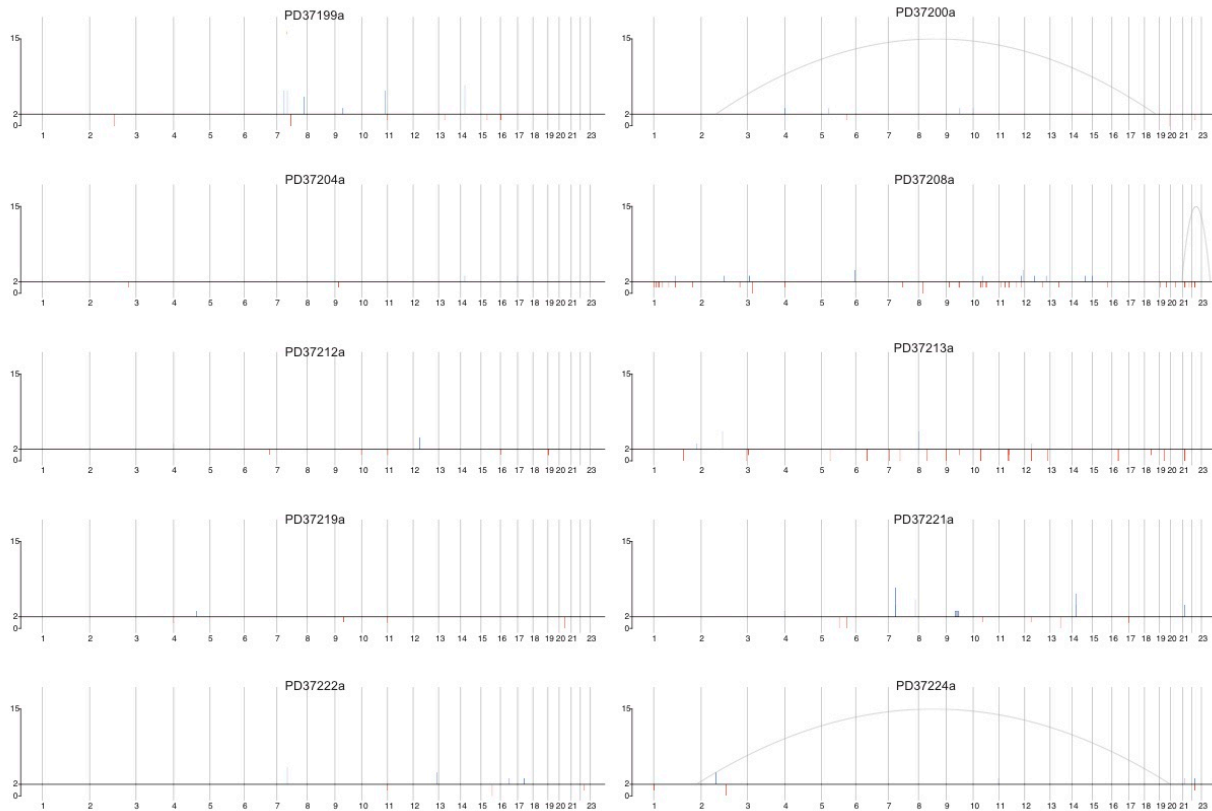
## Supplementary Information

Recurrent intragenic rearrangements of *EGFR* and *BRAF* in soft tissue tumors of infants

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**Supplementary Figure 1 | Trinucleotide context of substitution mutations in 10 classical congenital mesoblastic nephroma genomes.** The x-axis indicates the 96 classes of substitution according to trinucleotide context; proportion of substitution mutations in each class is shown on the y-axis.



**Supplementary Figure 2 | Structural changes in 10 congenital mesoblastic nephroma genomes.** Copy number profile and rearrangements are shown for 10 classical histology CMN lacking the canonical *ETV6-NTRK3* fusion. Absolute copy number is represented on the y-axis; chromosomes are indicated on the x-axis. Blue and red horizontal segments represent copy number gains and losses, respectively. Grey lines indicate start and end of translocations.

**Supplementary Table 1 | Primer sequences**

<b>Target</b>	<b>Primer name</b>	<b>Sequence</b>
<b>EGFR-ITD</b>	hEGFR-ITD1 <sup>1,3</sup>	CGACGAGTACCTCATCCCAC
	hEGFR-D2 <sup>1</sup>	AGCTTGGTTGGGAGCTTCTC
	hEGFR-D3 <sup>1,2</sup>	GCTGTATCGCTGCAAGAAGC
	hEGFR-D1 <sup>2,3</sup>	CGAGTACCTCATCCCACAGC
	hEGFR-ITD2 <sup>2</sup>	CTGGGTGTAAGAGGCTCCAC
<b>BRAF-ID</b>	BRAF-c1 <sup>1,3</sup>	GTGGGGAGCATAATCCACCA
	BRAF-c2 <sup>1</sup>	GGGCCTCTATATGTTCTGTGT
	BRAF-c4 <sup>1</sup>	GTTGATCCTCCATCACCACGA
	BRAF-c5 <sup>1,2</sup>	TCAGTTCCGTTCCCCAGAGA
	BRAF-c1b <sup>2,3</sup>	GGGAGCATAATCCACCATCAATATATC
	BRAF-c4b <sup>2</sup>	ACCACGAAATCCTTGGTCTCTAAT
<b>KIAA1549-BRAF fusion</b>	KIAA1549-e15 <sup>1</sup>	CTCAGCCTACATCGGATGCC
	KIAA1549-e16 <sup>1</sup>	AGACGGCCAACAATCCCTG
	BRAF-e9 <sup>1</sup>	GGGGGTAGCAGACAAACCTG
	BRAF-e11 <sup>1</sup>	CTGCCCATCAGGAATCTCCC
	KIAA1549-contr <sup>1</sup>	AGTAGATCCCTCTGGCAGCA
<b>LMNA-NTRK1</b>	LMNA-e2 <sup>1</sup>	TCTCAGTGAGAAGCGCACGC
	NTRK1-e13 <sup>1</sup>	GATGTCCCGGCGCTTGATGT
	LMNA-e7 <sup>1</sup>	AGGAGGTGGATGAGGAGGGC
<b>ETV6-NTRK3</b>	ETV6-3 <sup>1,3</sup>	TCATGGTCTCTGTCTCCCCG
	NTRK3-2 <sup>1</sup>	TCGCTTCAGCACGATGTCTC
	ETV6-6 <sup>1,2</sup>	CGGCTGTGAGAAAGCAACTG
	ETV6-5 <sup>2</sup>	GCCTGAAGAGCACGCCAT
	NTRK3-3 <sup>2</sup>	TCTCTCTCTTAATGTGCTGCA

<sup>1</sup> used for RT-PCR

<sup>2</sup> used for subsequent nested RT-PCR of FFPE derived RNA

<sup>3</sup> used for sequencing