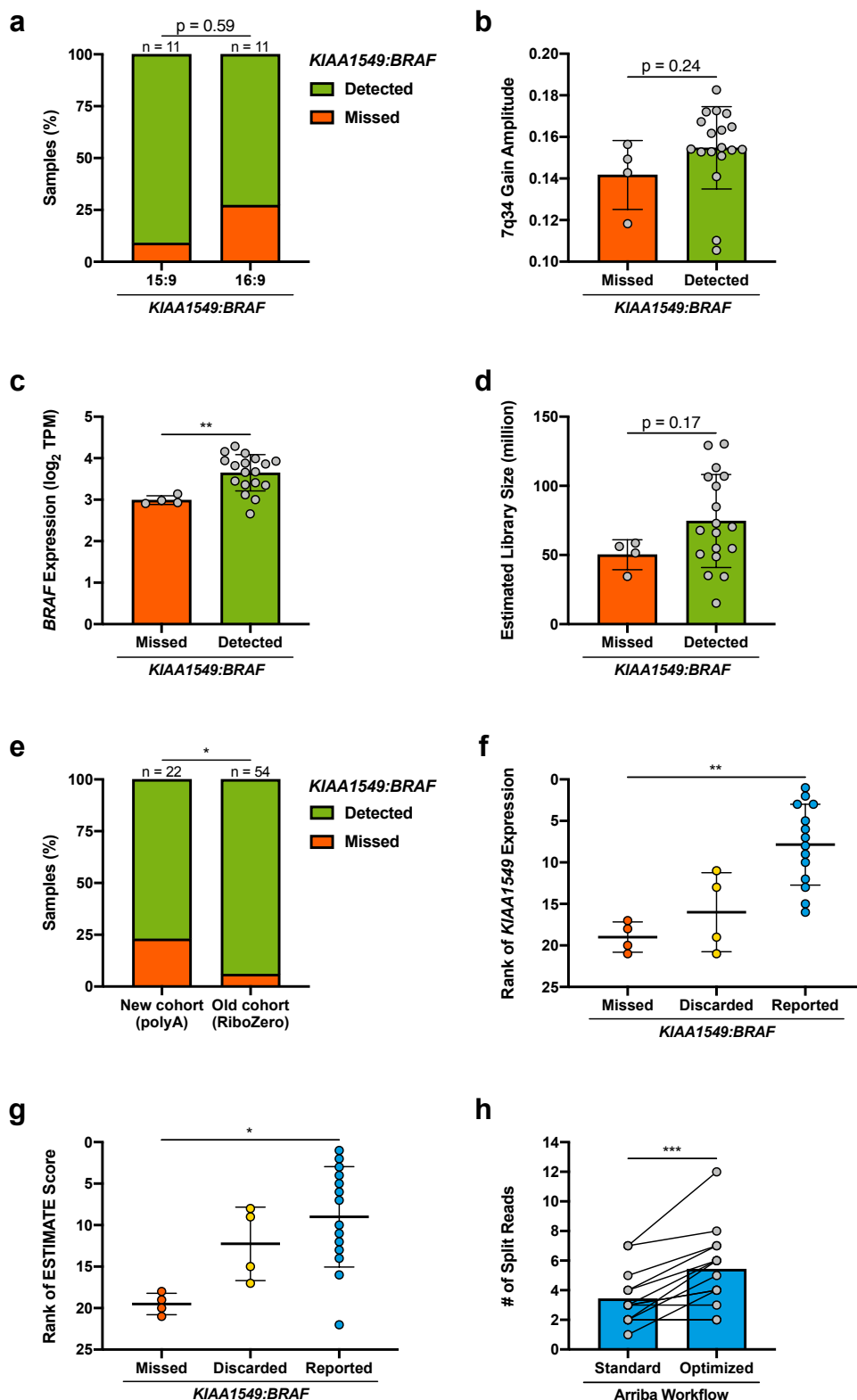
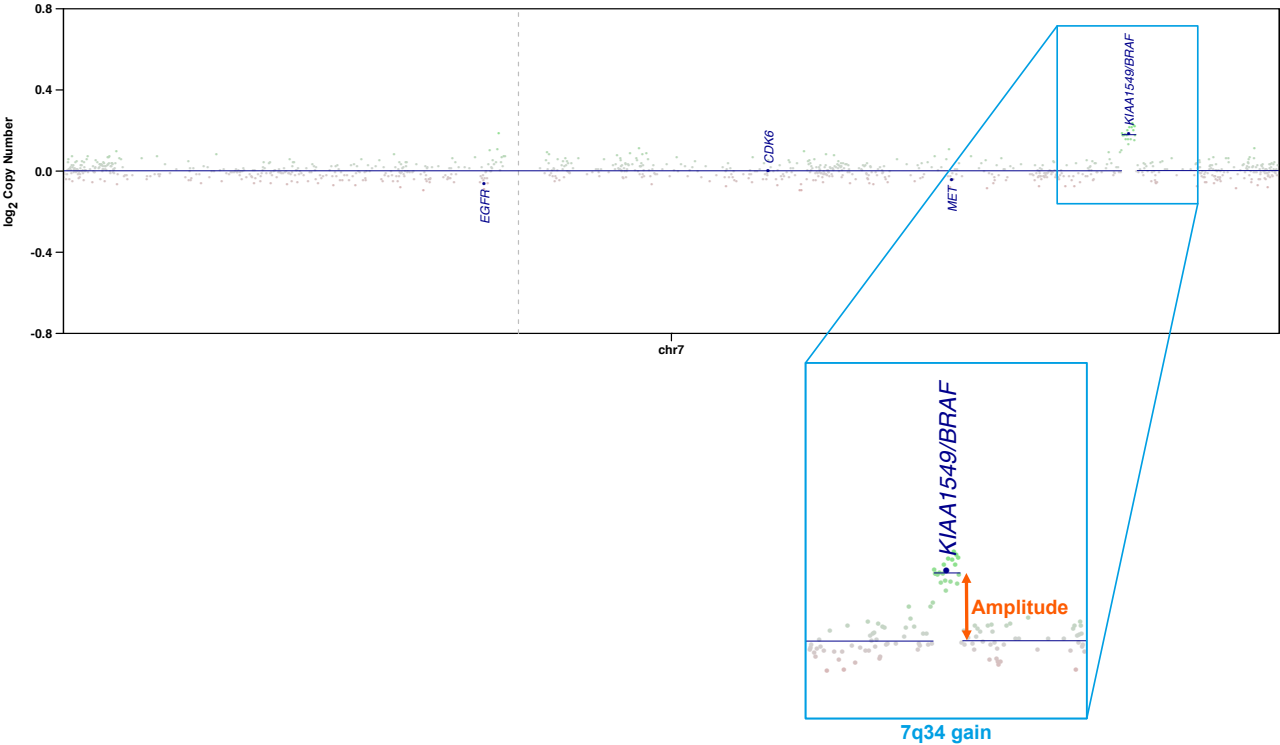




Online Resource Fig. 1 **a** Relative frequency of detected and missed *KIAA1549:BRAF* fusions in samples with known *KIAA1549:BRAF* 15:9 or 16:9 fusions. Fisher's exact test on the underlying absolute values. **b** Amplitude of the fusion-characteristic 7q34 gain extracted from methylation array-derived copy number data as an indicator of tumor cell content in samples with a missed or detected *KIAA1549:BRAF* fusion. Mean $\pm$ SD. Unpaired *t* test. **c** Expression of *BRAF* in samples with a missed or detected *KIAA1549:BRAF* fusion. Mean $\pm$ SD. Unpaired *t* test. **d** Estimated library size of samples with a missed or detected *KIAA1549:BRAF* fusion as calculated by RNA-SeQC (<https://github.com/broadinstitute/rnaseqc>). Mean $\pm$ SD. Unpaired *t* test. **e** Relative frequency of detected and missed *KIAA1549:BRAF* fusions in the presented cohort (polyA capture library preparation protocol) compared to an older cohort (RiboZero library preparation protocol). Fisher's exact test on the underlying absolute values. **f** Samples ranked by their *KIAA1549* expression with the highest-ranked sample having the highest expression. Mean $\pm$ SD. Kruskal-Wallis test followed by Dunn's multiple comparisons test. **g** Samples ranked by their ESTIMATE immune score with the highest-ranked sample having the lowest immune score. Mean $\pm$ SD. Kruskal-Wallis test followed by Dunn's multiple comparisons test. **h** Number of split reads identified by Arriba in the standard and optimized workflow for all samples that were initially reported. Paired *t* test. For all panels: $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$, n.s.: not significant



Online Resource Fig. 2 Typical copy number plot of a PA with a *KIAA1549:BRAF* fusion. The characteristic focal tandem duplication at 7q34 is magnified. The gain amplitude is measured between gain and baseline.

ID	Expected Fusion	Initial Sequencing		Re-sequencing				
		Total Read Count	Arriba v1.1.0	Total Read Count	Arriba v1.1.0	FusionCatcher v1.20	grep	Optimized Arriba Workflow
1	<i>KIAA1549:BRAF</i> 16:9	194,850,910		676,743,058			X	
2	<i>KIAA1549:BRAF</i> 16:9	207,683,590		576,945,684			X	X
3	<i>KIAA1549:BRAF</i> 15:9	163,650,066		507,411,706		X	X	X
4	<i>KIAA1549:BRAF</i> 16:9	192,301,908		631,106,492			X	X
5	<i>KIAA1549:BRAF</i> 15:9	181,693,284		605,518,510	discarded	X	X	X
6	<i>KIAA1549:BRAF</i> 15:9	213,976,502	discarded	213,976,502	discarded		X	X
7	<i>KIAA1549:BRAF</i> 15:9	246,750,814	discarded	246,750,814	discarded	X	X	X
8	<i>KIAA1549:BRAF</i> 16:9	154,956,306	discarded	154,956,306	discarded	X	X	X
9	<i>KIAA1549:BRAF</i> 15:9	248,395,826	X	248,395,826	X	X	X	X
10	<i>KIAA1549:BRAF</i> 15:9	224,107,348	X	224,107,348	X	X	X	X
11	<i>KIAA1549:BRAF</i> 15:9	258,025,596	X	258,025,596	X	X	X	X
12	<i>KIAA1549:BRAF</i> 15:9	259,592,144	X	259,592,144	X	X	X	X
13	<i>KIAA1549:BRAF</i> 15:9	222,007,910	X	222,007,910	X	X	X	X
14	<i>KIAA1549:BRAF</i> 16:9	250,453,818	X	250,453,818	X		X	X
15	<i>KIAA1549:BRAF</i> 16:9	221,572,204	X	221,572,204	X	X	X	X
16	<i>KIAA1549:BRAF</i> 16:9	212,747,662	X	212,747,662	X	X	X	X
17	<i>KIAA1549:BRAF</i> 16:9	233,864,126	X	233,864,126	X	X	X	X
18	<i>KIAA1549:BRAF</i> 15:9	201,634,092	X	201,634,092	X	X	X	X
19	<i>KIAA1549:BRAF</i> 16:9	198,666,870	X	198,666,870	X	X	X	X
20	<i>KIAA1549:BRAF</i> 16:9	179,082,272	X	179,082,272	X	X	X	X
21	<i>KIAA1549:BRAF</i> 15:9	208,710,688	X	208,710,688	X	X	X	X
22	<i>KIAA1549:BRAF</i> 16:9	187,958,056	X	187,958,056	X		X	X
		14+3		14+4		16	22	21

Online Resource Table 1 Overview of fusion detection results from RNA-Seq data of the presented cohort of fresh-frozen pediatric PA tumor samples. The higher total read counts after re-sequencing are marked in bold. X = detected