Supplementary Figure 1. ALK unbalanced translocation

The ALK unbalanced translocation in Epithelioid Rhabdomyosarcoma (sample n3, table 1) was demonstrated by FISH ALK break-apart fusion. The intact ALK alleles are indicated by the yellow arrows (green plus red signals) while red arrows indicate isolated red signals corresponding to 3’ALK derivatives. ALK Break Apart Probe was purchased from Vysis (cat: o8N16-001, Abbot Park, Illinois USA) and were hybridized according to manufacturer instructions

Supplementary Table 1. Table showing the probes used for FISH experiments

<table>
<thead>
<tr>
<th>Gene</th>
<th>Company</th>
<th>Probe Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALK</td>
<td>Abbott Molecular</td>
<td>Vysis ALK  Dual Color, Break Apart FISH Probe</td>
</tr>
<tr>
<td>SS18</td>
<td>Abbott Molecular</td>
<td>Vysis SS18 Dual Color, Break Apart Probe</td>
</tr>
<tr>
<td>EWS</td>
<td>Abbott Molecular</td>
<td>Vysis EWSR1 Dual Color, Break Apart Probe</td>
</tr>
<tr>
<td>ROS1</td>
<td>Zytovision</td>
<td>Zytolight SPEC ROS1 Dual Color, Break Apart Probe</td>
</tr>
<tr>
<td>EWSR1-FLI1</td>
<td>Zytovision</td>
<td>Zytolight PEC EWSR1/FLI1 TriChec Probe</td>
</tr>
<tr>
<td>FGFR2</td>
<td>Zytovision</td>
<td>Zytolight SPEC FGFR2 Dual Color, Break Apart Probe</td>
</tr>
<tr>
<td>FUS</td>
<td>Zytovision</td>
<td>Zytolight SPEC FUS Dual Color, Break Apart Probe</td>
</tr>
<tr>
<td>RET</td>
<td>Zytovision</td>
<td>Zytolight SPEC RET Dual Color, Break Apart Probe</td>
</tr>
<tr>
<td>SS18 SSX1</td>
<td>Zytovision</td>
<td>Zytolight SPEC SS18/SSX1 TriCheck Probe</td>
</tr>
<tr>
<td>TFE3</td>
<td>Zytovision</td>
<td>Zytolight SPEC TFE3 Dual Color, Break Apart Probe</td>
</tr>
<tr>
<td>YWHAE</td>
<td>Zytovision</td>
<td>Zytolight SPEC YWHAE Dual Color, Break Apart Probe</td>
</tr>
</tbody>
</table>
**Supplementary Table 2.** Table showing the comparison between the fusions called by ADx, ARR and SFU in samples investigated by sarcoma panel

<table>
<thead>
<tr>
<th>Samples</th>
<th>Sarcoma panel ADx</th>
<th>Sarcoma panel ARR</th>
<th>Sarcoma panel SFU</th>
<th>FISH</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>ETV6-NTRK3</td>
<td>PLAG1-CHCHD7-ACACB*</td>
<td>FUS-GPT2*</td>
<td>ETV6-NTRK3 confirmed</td>
</tr>
<tr>
<td>2</td>
<td>EWSR1-PATZ1</td>
<td>EWSR1-PATZ1</td>
<td>RAB7A-MFSD4*</td>
<td>EWSR1 translocated</td>
</tr>
<tr>
<td>3</td>
<td>EWSR1-TFCP2</td>
<td>SLC3A2-ROSI1</td>
<td>SLC3A2-ROSI1</td>
<td>EWSR1 translocated</td>
</tr>
<tr>
<td></td>
<td>ALK Δ2-18</td>
<td></td>
<td></td>
<td>ALK unbalanced translocation</td>
</tr>
<tr>
<td>4</td>
<td>EWSR1-NR4A3</td>
<td>no fusions</td>
<td>no fusions</td>
<td>EWSR1-NR4A3 confirmed</td>
</tr>
<tr>
<td>5</td>
<td>EWSR1-FLI1</td>
<td>no fusions</td>
<td>FUS-MFSD4*</td>
<td>EWSR1-FLI1 confirmed</td>
</tr>
<tr>
<td>6</td>
<td>EWSR1-CREM</td>
<td>EWSR1-CREM</td>
<td>no fusions</td>
<td>EWSR1 translocated</td>
</tr>
<tr>
<td>7</td>
<td>YWHAE-NUT2</td>
<td>HMGA2-HRK*</td>
<td>no fusions</td>
<td>YWHAE translocated</td>
</tr>
<tr>
<td>8</td>
<td>SS18-SSX4</td>
<td>SS18-SSX4</td>
<td>EWSR1-MFSD4*</td>
<td>SS18 intragenic rearrangement</td>
</tr>
<tr>
<td>9</td>
<td>SS18-SSX1</td>
<td>SS18-SSX1</td>
<td>FUS-MFSD4*</td>
<td>SS18 not translocated</td>
</tr>
<tr>
<td>10</td>
<td>CIC-DUX4</td>
<td>CIC-DUX4</td>
<td>FUS-MFSD4*</td>
<td>CIC not translocated</td>
</tr>
<tr>
<td>11</td>
<td>EWSR1-CREB3L2</td>
<td>EWSR1-CREB3L2</td>
<td>no fusions</td>
<td>Not done</td>
</tr>
<tr>
<td>12</td>
<td>EWSR1-FLI1</td>
<td>EWSR1-FLI1</td>
<td>FUS-DAOA-AS1*</td>
<td>Not done</td>
</tr>
<tr>
<td>13</td>
<td>NAB2-STAT 6</td>
<td>no fusions</td>
<td>no fusions</td>
<td>Not detectable by FISH</td>
</tr>
<tr>
<td>14</td>
<td>ETV6-NTRK3</td>
<td>ETV6-NTRK3</td>
<td>ETV6-NTRK3</td>
<td>Not done</td>
</tr>
<tr>
<td>15</td>
<td>no fusions</td>
<td>no fusions</td>
<td>FUS-MFSD4*</td>
<td>SS18, EWSR1, FUS negative</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>FUS-DAOA-AS1*</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>FUS-PRPSAP1*</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>no fusions</td>
<td>no fusions</td>
<td>no fusions</td>
<td>WWTR1 negative*</td>
</tr>
<tr>
<td>17</td>
<td>no fusions</td>
<td>no fusions</td>
<td>no fusions</td>
<td>SS18, BCOR, CIC negative</td>
</tr>
<tr>
<td>18</td>
<td>no fusions</td>
<td>no fusions</td>
<td>no fusions</td>
<td>EWSR1, FUS negative*</td>
</tr>
<tr>
<td>19</td>
<td>no fusions</td>
<td>no fusions</td>
<td>FUS-PRPSAP1*</td>
<td>SS18 negative</td>
</tr>
<tr>
<td>20</td>
<td>no fusions</td>
<td>no fusions</td>
<td>FUS-PRPSAP1*</td>
<td>EWSR1, FUS, ATF1, CREB1 negative</td>
</tr>
</tbody>
</table>
21  no fusions  no fusions  no fusions  Not done
22  no fusions  no fusions  no fusions  EWSR1, BCOR, FUS, CIC, NCOA2 negative*
23  no fusions  no fusions  no fusions  Not done
24  no fusions  no fusions  no fusions  Not done
25  no fusions  no fusions  no fusions  FUS-MFSD4*  FUS negative*
26  no fusions  no fusions  no fusions  Not done
27  no fusions  no fusions  no fusions  ALK negative
28  no fusions  no fusions  no fusions  Not done
29  not evaluable  RREB1-MKL2*  RREB1-MKL2*  PHF1, FUS, CIC, BCOR, EWSR1, NR4A3 negative
30  not evaluable  CTD-HMGA2*  no fusions  EWSR1, NCOA2, CIC, SS18, BCOR negative
31  not evaluable  FUS-RP11-541P9.3*  no fusions  Not done

**Total**: 14 fusions  16 fusions  17 fusions

a: The FISH were performed on different samples respect to those used for NGS. b: The fusion was confirmed by FISH and RT-PCR that were performed after the RREB1-MKL2 fusion identification by ARR and SFU.* Unknown/unpublished

**Supplementary Table 3**: table showing the ROS1, ALK and RET FISH performed in 31 out of 121 ADx negative samples

<table>
<thead>
<tr>
<th>Samples</th>
<th>FISH</th>
<th>ROS1</th>
<th>ALK</th>
<th>RET</th>
</tr>
</thead>
<tbody>
<tr>
<td>61</td>
<td>Translocated</td>
<td>neg</td>
<td>neg</td>
<td></td>
</tr>
<tr>
<td>62</td>
<td>Translocated</td>
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<td>neg</td>
<td></td>
</tr>
<tr>
<td>63</td>
<td>neg</td>
<td>neg</td>
<td></td>
<td>Translocated</td>
</tr>
<tr>
<td>64</td>
<td>neg</td>
<td>Not done</td>
<td>neg</td>
<td></td>
</tr>
<tr>
<td>65</td>
<td>neg</td>
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<td>Not done</td>
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<td>66</td>
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<td>neg</td>
<td>Not done</td>
<td></td>
</tr>
<tr>
<td>67</td>
<td>neg</td>
<td>Not done</td>
<td>Not done</td>
<td></td>
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<tr>
<td>68</td>
<td>neg</td>
<td>Not done</td>
<td>Not done</td>
<td></td>
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<tr>
<td>69</td>
<td>neg</td>
<td>neg</td>
<td>Not done</td>
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<td>70</td>
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<td></td>
</tr>
<tr>
<td>71</td>
<td>neg</td>
<td>neg</td>
<td>neg</td>
<td></td>
</tr>
<tr>
<td>72</td>
<td>neg</td>
<td>neg</td>
<td>neg</td>
<td></td>
</tr>
<tr>
<td>73</td>
<td>neg</td>
<td>neg</td>
<td>Not done</td>
<td></td>
</tr>
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<td>74</td>
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<td>Not done</td>
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<td>75</td>
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<td>Not done</td>
<td>neg</td>
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<td>76</td>
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<td>neg</td>
<td>Not done</td>
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<td>neg</td>
<td>Not done</td>
<td>neg</td>
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</tr>
<tr>
<td>78</td>
<td>neg</td>
<td>Not done</td>
<td>Not done</td>
<td></td>
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<tr>
<td>79</td>
<td>neg</td>
<td>neg</td>
<td>Not done</td>
<td></td>
</tr>
<tr>
<td>80</td>
<td>neg</td>
<td>neg</td>
<td>Not done</td>
<td></td>
</tr>
</tbody>
</table>
All the translocation detected by FISH were unbalanced. neg: Negative; hem del: ROS1 hemizygote deletion.

**Supplementary Table 4.** Table showing the fusion genes identified by ARR and SFU in the 21 ADx positive samples

<table>
<thead>
<tr>
<th>Samples</th>
<th>Lung panel ADx</th>
<th>Lung panel ARR</th>
<th>Lung Panel SFU</th>
<th>FISH</th>
</tr>
</thead>
<tbody>
<tr>
<td>32</td>
<td>KIF5C-ALK</td>
<td>KIF5C-ALK</td>
<td>no fusions</td>
<td>ALK confirmed</td>
</tr>
<tr>
<td>33</td>
<td>EML4-ALK</td>
<td>EML4-ALK</td>
<td>no fusions</td>
<td>ALK confirmed</td>
</tr>
<tr>
<td>34</td>
<td>KIF5B-RET</td>
<td>KIF5B-RET</td>
<td>no fusions</td>
<td>RET confirmed</td>
</tr>
<tr>
<td>35</td>
<td>RET-NCOA4</td>
<td>RET-NCOA4</td>
<td>no fusions</td>
<td>RET confirmed</td>
</tr>
<tr>
<td>36</td>
<td>KIAA1468-RET</td>
<td>NTRK1- KCNK13*</td>
<td>no fusions</td>
<td>RET confirmed</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>EGFR-FAM194B*</td>
</tr>
<tr>
<td>37</td>
<td>TPM3-NTRK1</td>
<td>TPM3-NTRK1</td>
<td>TPM3-NTRK1</td>
<td>NTRK1 confirmed</td>
</tr>
<tr>
<td>38</td>
<td>FGFR2-TACC3</td>
<td>FGFR2-TACC3</td>
<td>FGFR2-TACC3</td>
<td>FGFR2 confirmed</td>
</tr>
<tr>
<td>39</td>
<td>ETV6-NTRK3</td>
<td>no fusions</td>
<td>no fusions</td>
<td>ETV6-NTRK3 confirmed</td>
</tr>
<tr>
<td>40</td>
<td>TPM3 -NTRK1</td>
<td>TPM3-NTRK1</td>
<td>EGF-TRIM13*</td>
<td>NTRK1 not confirmed</td>
</tr>
<tr>
<td>41</td>
<td>KIAA1549-BRAF</td>
<td>KIAA1549-BRAF</td>
<td>BRAF-UBE2L3*</td>
<td>Nd</td>
</tr>
<tr>
<td>42</td>
<td>KIAA1549-BRAF</td>
<td>KIAA1549-BRAF</td>
<td>no fusions</td>
<td>Nd</td>
</tr>
<tr>
<td>43</td>
<td>EML4-ALK</td>
<td>EML4-ALK</td>
<td>EML4-ALK</td>
<td>Nd</td>
</tr>
<tr>
<td>44</td>
<td>TPR-NTRK1</td>
<td>TPR-NTRK1</td>
<td>no fusions</td>
<td>Nd</td>
</tr>
<tr>
<td>45</td>
<td>EML4-ALK</td>
<td>EML4-ALK</td>
<td>no fusions</td>
<td>Nd</td>
</tr>
<tr>
<td>46</td>
<td>EML4-ALK</td>
<td>EML4-ALK</td>
<td>no fusions</td>
<td>Nd</td>
</tr>
<tr>
<td>47</td>
<td>ETV6-NTRK3</td>
<td>ETV6-NTRK3</td>
<td>ETV6-NTRK3</td>
<td>Nd</td>
</tr>
<tr>
<td>48</td>
<td>TPM3-NTRK1</td>
<td>TPM3-NTRK1</td>
<td>TPM3-NTRK1</td>
<td>Nd</td>
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<tr>
<td>49</td>
<td>TPM3-NTRK1</td>
<td>TPM3-NTRK1</td>
<td>TPM3-NTRK1</td>
<td>Nd</td>
</tr>
<tr>
<td>50</td>
<td>TPR-NTRK1</td>
<td>TPR-NTRK1</td>
<td>no fusions</td>
<td>Nd</td>
</tr>
<tr>
<td>51</td>
<td>ETV6-NTRK3</td>
<td>ETV6-NTRK3</td>
<td>ETV6-NTRK3</td>
<td>Nd</td>
</tr>
<tr>
<td>52</td>
<td>TFG-NTRK3</td>
<td>TFG-NTRK3</td>
<td>IGH-BRAFv</td>
<td>Nd</td>
</tr>
</tbody>
</table>
a: **IGH-BRAF** gene fusion was recently reported in one patient with Hairy Cells Leukemia V600E negative *(Thompson et al, Leukemia e Lymphoma 2020; 61:8, 2024-2026). ***: unknown-unpublished fusions; Nd: not done

**Supplementary Table 5.** Table showing the gene fusion called by ARR and SFU in ADx negative samples

<table>
<thead>
<tr>
<th>Samples</th>
<th>Lung panel ADx</th>
<th>Lung panel ARR</th>
<th>Lung panel SFU</th>
</tr>
</thead>
<tbody>
<tr>
<td>61 (supp. Tab2)</td>
<td>no fusions</td>
<td><em>EGFR-NTRK3</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>64 (supp. Tab2)</td>
<td>no fusions</td>
<td><em>BRAF-KIAA</em></td>
<td><em>BRAF-RASA1</em></td>
</tr>
<tr>
<td>65 (supp. Tab2)</td>
<td>no fusions</td>
<td><em>TNS3-ROSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>66 (supp. Tab2)</td>
<td>no fusions</td>
<td><em>SMARC81-PDGFR</em></td>
<td><em>FGFR3-MFSD4</em></td>
</tr>
<tr>
<td>69 (supp. Tab2)</td>
<td>no fusions</td>
<td><em>CHMP2A-&gt;CTD-UQCRFSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td></td>
<td>no fusions</td>
<td><em>SOX6-&gt;BRAF</em></td>
<td></td>
</tr>
<tr>
<td>70 (supp. Tab2)</td>
<td>no fusions</td>
<td><em>RP11-MYOZ2-&gt;ROSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>71 (supp. Tab2)</td>
<td>no fusions</td>
<td><em>PRMT3-EGFR</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>92</td>
<td>no fusions</td>
<td><em>JHDM1D-BRAF</em></td>
<td><em>JHDM1D-BRAF</em></td>
</tr>
<tr>
<td>93</td>
<td>no fusions</td>
<td><em>NRAS-BRAF</em></td>
<td><em>NRAS-BRAF</em></td>
</tr>
<tr>
<td>94</td>
<td>no fusions</td>
<td><em>SLC34A2-ROSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>95</td>
<td>no fusions</td>
<td><em>KDR - RET</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>96</td>
<td>no fusions</td>
<td><em>MET-FGFR2</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>97</td>
<td>no fusions</td>
<td><em>ATM-FGFR2</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>98</td>
<td>no fusions</td>
<td><em>FLT3 -SMAD4</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>99</td>
<td>no fusions</td>
<td><em>EGFR -MFN2</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>100</td>
<td>no fusions</td>
<td><em>MET-SEMA3A</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>101</td>
<td>no fusions</td>
<td><em>RP11- SST-BRAF</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>102</td>
<td>no fusions</td>
<td><em>CLTCL1-ALK</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>103</td>
<td>no fusions</td>
<td><em>TNS3 - ROSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>104</td>
<td>no fusions</td>
<td><em>RP11-MYOZ2-&gt;ROSI</em></td>
<td><em>BAI2-EGFR</em></td>
</tr>
<tr>
<td>105</td>
<td>no fusions</td>
<td><em>ZNF609 - KRAS</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>106</td>
<td>no fusions</td>
<td><em>RP11-MYOZ2-&gt;ROSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>107</td>
<td>no fusions</td>
<td><em>RP11-MYOZ2-&gt;ROSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>108</td>
<td>no fusions</td>
<td><em>TRIO - FGFR1</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>109</td>
<td>no fusions</td>
<td><em>DSCCI-MET</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>110</td>
<td>no fusions</td>
<td><em>RP11-FGFR2</em></td>
<td>no fusions</td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>MET-&gt;CTNND1- OR5BA1P</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>111</td>
<td>no fusions</td>
<td><em>ETV6-KRAS</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>112</td>
<td>no fusions</td>
<td><em>RP11-MYOZ2-&gt;ROSI</em></td>
<td>no fusions</td>
</tr>
<tr>
<td>113</td>
<td>no fusions</td>
<td><em>RP11- BRAF</em></td>
<td>no fusions</td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>FGFR2 - GABRG1</em></td>
<td>no fusions</td>
</tr>
</tbody>
</table>
Supplementary Table 6. Gene fusion identified by ARR and SFU in the 12 ADx not evaluable samples

<table>
<thead>
<tr>
<th>Samples</th>
<th>Lung panel ADx</th>
<th>Lung panel ARR</th>
<th>Lung panel SFU</th>
</tr>
</thead>
<tbody>
<tr>
<td>N63 (supp tab2)</td>
<td>not evaluable</td>
<td><strong>SLC34A2-ROS1</strong></td>
<td><strong>SLC34A2-ROS1</strong></td>
</tr>
<tr>
<td>N73 (supp.tab2)</td>
<td>not evaluable</td>
<td><strong>BRAF-RDX</strong></td>
<td>no fusions</td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>ABHD11-CLDN3-&gt;NTRK2</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>MET-&gt;CTD-TMEM86B</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>AL356154.1-NRG3-&gt;NTRK3</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>PLSCR4-RP11-&gt;EGFR</strong></td>
<td></td>
</tr>
<tr>
<td>N88 (supp.tab2)</td>
<td>not evaluable</td>
<td>no fusions</td>
<td></td>
</tr>
<tr>
<td>N89 (supp.tab2)</td>
<td>not evaluable</td>
<td>no fusions</td>
<td></td>
</tr>
<tr>
<td>126</td>
<td>not evaluable</td>
<td><strong>SLC34A2-ROS1</strong></td>
<td><strong>SLC34A2-ROS1</strong></td>
</tr>
<tr>
<td>127</td>
<td>not evaluable</td>
<td><strong>PSMD6,RP11-129B22.1-NRG1</strong></td>
<td>no fusions</td>
</tr>
<tr>
<td>128</td>
<td>not evaluable</td>
<td><strong>NRG1-&gt;CSNK1A1L-RNK7SKP1</strong></td>
<td>no fusions</td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>NTRK2-&gt;RP11- RP11</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td>not evaluable</td>
<td>RET-KIF5B(^a)</td>
<td>no fusions</td>
</tr>
<tr>
<td>----</td>
<td>---------------</td>
<td>-----------------</td>
<td>------------</td>
</tr>
<tr>
<td>129</td>
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<td>no fusions</td>
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<td>130</td>
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<tr>
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<tr>
<td>133</td>
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<td>no fusions</td>
<td>no fusions</td>
</tr>
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</table>

a: The RET-KIF5B translocation (case n 129) was previously published (Velcheti V et al, Thorac Oncol. 2017;12(7):e98-e99.v) in a lung adenocarcinoma patient. Supp. Tab2: sample already reported in Supplementary Table 3. *: all these fusions were previously unreported/unpublished

The parameters used for Arriba:

```bash
export version=1.8.1
event sample=$PATIENT.fastq
event folder=$PATIENT
STAR  --runThreadN 8
    --genomeDir $HOME/genome/GRCh37_genome_v19_CTAT_lib_Apr032020.plug-n-play/ctat_genome_lib_build_dir/ref_genome.fa.star.idx
    --genomeLoad NoSharedMemory
    --readFilesIn $HOME/fastq/$sample
    --outTmpDir $HOME/NGSeqINT/temp$folder
    --outStd BAM_Unsorted
    --outSAMtype BAM Unsorted
    --outSAMunmapped Within
    --outBAMcompression 0
    --outFilterMultimapNmax 1
    --outFilterMismatchNmax 3
    --chimSegmentMin 10
    --chimOutType WithinBAM SoftClip
    --chimJunctionOverhangMin 10
    --chimScoreMin 1
    --chimScoreDropMax 30
    --chimScoreJunctionNonGTAG 0
    --chimScoreSeparation 1
    --alignSJstitchMismatchNmax 5 -1 5 5
    --chimSegmentReadGapMax 3 |
arriba  -x /dev/stdin
    -o $HOME/analysis/$folder/ARRIBA.fusions.tsv
    -O $HOME/analysis/$folder/ARRIBA.fusions.discriminated.tsv
```
-a
$HOME/genome/GRCh37_gencode_v19_CTAT_lib_Apr032020.plug-n-play/ctat_genome_lib_build_dir/ref_genome.fa
-g
$HOME/genome/GRCh37_gencode_v19_CTAT_lib_Apr032020.plug-n-play/ctat_genome_lib_build_dir/ref_annot.gtf
-b
$HOME/arriba/arriba_v2.0.0/database/blacklist_hg19_hs37d5_GRCh37_v2.0.0.tsv.gz