Supplementary Table 3: Complete genomic features of cases with SMARCA4 deficient undifferentiated thoracic tumor.

1. Single nucleotide variants and indels

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| --- | --- | --- | --- | --- |
| Patient ID | Gene | Nucleotide Change | Amino Acid Change | Variant Allele Fraction (%) |
| 1 | TP53 | NM\_000546.5:c.747G>T | p.Arg249Ser | 55.6 |
| 2 | TP53 | NM\_000546.5:c.764\_766del | p.Ile255del | 77.1 |
| 2 | CTNNB1 | NM\_001904.4: c.121A>G | p.Thr41Ala | 41.8 |
| 3 | TP53 | NM\_000546.5:c.672+1G>T | p.? (splice site variant) | 76.8 |
| 3 | SMARCA4 | NM\_003072.4:c.3081+1G>T | p.? (splice site variant) | 53.1 |
| 3 | APC | NM\_000038.6:c.7932\_7935del | p.Tyr2645fs | 66.1 |
| 4 | TP53 | NM\_000546.5:c.794dupT | p.Arg267fs | 75.1 |
| 4 | SMARCA4 | NM\_003072.4:c.2582\_2597del | p.Glu861fs | 72.0 |
| 4 | CDKN2A | NM\_000077.4:c.134del | p.Gly45fs | 58.3 |

1. Copy Number Changes

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| --- | --- | --- |
| Patient ID | Copy Number Loss | Copy Number Gains |
| 1 | Deep (Homozygous) deletionMTAP CDKN2A/BSMARCA4 |  |
| 2 | Deep (Homozygous) deletionMTAP CDKN2A/BSMARCA4 | FGFR1 |
| 3 | Deletion 5qDeletion 6p21.33 involving exon 5 of HLA-DRB1Deletion 8p23.2-p12Deletion of 9qDeletion 13qDeletion 14qDeletion 18q21.1-q23Monosomy 19, notably leading to loss of SMARCA4Deletion 20pMonosomy 22 | Gain of 8p11.23-8qGain of 10pGain of 11q |
| 4 | Deletion 9p24.2-21.1 | Gain of 1p36.31-34.3Gain of 1q21.1-44 Gain of 3q12.1-29Gain of 5p15.32-12Gain of 7p22.2-11.2Gain of 8p11.23-p1.21Gain of 10p15.2-11.21Trisomy 20 |