Table 2. Somatic gene mutations, sequence variants and their frequencies determined in the six individual tumors by next-generation sequencing. Clinical significance was determined according to COSMIC database.

Gene symbol	Gene name	Nucleotid change	Amino acid change	S1	S2	S3	S4	S5	S6	Clinical significance
				Variant allele frequency (%)						
ALK	Anaplastic lymphoma tyrosine kinase	c.3823C>T	p.Arg1275Ter	0	20.3	0	0	0	0	pathogenic
APC	Adenomatous polyposis coli	c.7610C>T	p.Ser2537Phe	0	20	0	0	0	0	uncertain
CDH1	Cadherin-1	c.1417G>A	p.Glu473Lys	0	20.8	0	0	0	0	pathogenic
CTNNB1	Catenin beta-1	c.59C>T	p.Ala20Val	15	0	0	0	0	0	pathogenic
ERBB4	Receptor tyrosine-protein kinase erbB-4	c.493G>A	p.Asp165Asn	0	0	0	8.8	0	0	pathogenic
EZH2	Enhancer of zeste homolog 2	c.1837-6C>T	splice region	53	48.6	21.4	63.6	61.3	51.6	uncertain
FOXL2	Forkhead box protein L2	c.761C>T	p.Ser254Leu	0	15	0	0	0	0	pathogenic
HRAS	Transforming protein p21	c.290+8C>T	splice region	0	0	0	9.2	0	0	uncertain
SMAD4	SMAD family member 4	c.1487G>A	p.Arg496His	0	0	0	0	0	35.5	pathogenic
TP53	Tumor protein p53	c.-29+1G>A	splice region	0	0	0	66	69	38.4	pathogenic