S3 Table. Pathogenic non–small cell lung cancer driver mutations in *EGFR*, *KRAS*, and *MET* found by whole exome sequencing in PSC

Gene	Case	Sample	SNP/indel	VAF	Pathogenicity
EGFR	SC07	TCD	c.T2573G:p.L858R	0.368	Known pathogenic
		TSD	c.T2573G:p.L858R	0.569	Known pathogenic
	SC18	TD	c.T2573G:p.L858R, amplification	0.822	Known pathogenic
	SC28	TCD	c.G2125A:p.E709K	0.397	Known pathogenic
			c.G2156C:p.G719A	0.308	Known pathogenic
	SC37	TSD	c.G1217T:p.X406L	0.062	Neutral by function predictor
			c.G1802T:p.G601V	0.035	Pathogenic by function predictor
			c.G2892T:p.L964F	0.042	Pathogenic by function predictor
	SC14	TCD	c.2316_2321dup:p.H773_V774dup	0.529	Likely pathogenic (ClinVar)
		TSD		0.460	
		MD		0.035	
	SC19	TCD	c.G661T:p.G221W	0.096	Neutral by function predictor
		TSD		0.102	
	SC21	TCD	c.2620delG:p.G874fs	0.212	Nonpathogenic by function predictor
		TSD		0.110	
KRAS	SC29	TSD	G12C	0.250	Known pathogenic
	SC33	TCD	G12V	0.518	Known pathogenic
		TSD		0.313	
		MD		0.031	
MET	SC22	TSD	D1010N	0.292	Known pathogenic
	SC27	TCD	D1010N	0.473	Known pathogenic
	SC08	TCD	c.2901_2911del:p.E967fs	0.081	Never reported
	SC17	TSD	c.3028+2T>C (splice site mutation)	0.601	Reported in literature [23,24]
	SC25	TCD	D1010H	0.692	Known pathogenic
		TSD		0.862	
		MD		0.029	

Pathogenicity was evaluated as known pathogenic if reported in any of the following databases: www.cbioportal.org, oncokb.org, and clinvar. If not reported, published studies were searched. Unreported *EGFR* mutations were analyzed for functional prediction by FATHMM-MKL in SNPs and SIFT in Indels. All *MET*-mutated cases were tested by ddPCR to be confirmed as *MET* exon 14 skipping mutation. Three of the five *MET*-mutated cases were known pathogenic mutations and the splicing mutation was reported previously in literature. A small deletion in *MET* that caused frameshift mutation (c.2901_2011del) was a novel finding. EGFR, epidermal growth factor receptor; Indel, insertion and deletion; MD, metastatic tumor; PSC, pulmonary sarcomatoid carcinoma; SNP, single nucleotide pleomorphism; TCD, primary carcinomatous component; TD, primary tumor; TSD, primary sarcomatous component; VAF, variable allelic frequency.