S4 Table. *MET* mutations detected using whole exome sequencing were confirmed to be *MET* exon 14 skipping mutations through the ddPCR

Case	Sample	WES		ddPCR		
		SNP/Indel	VAF	cMET exon14 skipping (copy number)	cMET (copy number)	Mutation index (%)
SC22	TSD	D1010N	0.292	516	692	74.57
SC27	TCD	D1010N	0.473	310	670	46.27
SC08	TCD	c.2901_2911del:p.E967fs	0.081	50	62	80.65
SC17	TSD	c.3028+2T>C	0.601	950	1,476	64.36
SC25	TCD	D1010H	0.692	4,160	7,120	58.43
	TSD		0.862			
	MD		0.029	500	804	62.19

ddPCR, digital droplet polymerase chain reaction; Indel, insertion and deletion; MD, metastatic tumor; SNP, single nucleotide pleomorphism; TCD, primary carcinomatous component; TSD, primary sarcomatous component; VAF, variable allelic frequency; WES, whole exome sequencing.