

Table S5. Genomic analysis of CCL5 and ANXA1 neoantigens.

Gene Name	Amino acid change	Nucleotide change	Mutation: Genomic position	*Tissue Type	Exome - tumor coverage	Tumor var freq	Tumor variant reads	RNA-seq coverage	Tumor variant freq	RNA-seq tumor variant reads	Exome-Normal coverage	Normal variant freq
CCL5	p.S109L	c.C326T	17:34199413-34199413	G>A	FrTum	101	18	22	116	1	1	
					TC	123	100	123	0	-	0	
					PBMC						161	0
ANXA1	p.E87K	c.G259A	9:75774328-75774328	G>A	FrTum	ND	-	ND	ND	-	ND	
					TC	38	39	15	32	59	19	
					PBMC						48	0

*FrTum, fresh tumor; TC, tumor cell line; PBMC, peripheral blood mononuclear cells.
 ND, Not Done.