

**Table S1. DAMPs and PRRs related to chemotherapy-induced ICD**

<b>DAMPs</b>	<b>PRRs</b>
ANXA1	FPR1
ATP	P2RX7 P2RY2
CALR	LRP1
Cellular RNA	TLR3
HMGB1	TLR4

Abbreviations: DAMPs, damage-associated molecular patterns; ICD, immunogenic cell death; PRRs, pattern recognition receptors.

**Table S2. Characteristics of selected SNPs in ICD pathway**

ICD-related gene	Chromosome	SNP (rs number)	Location	MAF	Base exchange	Function
<i>CALR</i>	19	rs1049481	3'UTR	0.37	G>T	Tag SNP, transcription factor binding site
		rs1010222	5'near	0.31	G>A	Transcription factor binding site
<i>HMGB1</i>	13	rs1045411	3'UTR	0.27	C>T	Tag SNP, miRNA binding site Associated with outcome in lung cancer patients treated with platinum agent Changing the mRNA levels
		rs1412125	5'near	0.48	T>C	Transcription factor binding site Associated with platinum-based chemotherapy response in lung cancer
		rs1360485	3'near	0.31	C>T	Inversely associated with EGFR mutations among NSCLC patients who smoked
<i>ANXA1</i>	9	rs1050305	exon	0.10	A>G	Synonymous SNP, splicing regulation
<i>LRP1</i>	12	rs1799986	exon	0.15	C>T	Tag SNP, missense SNP, splicing regulation Associated with susceptibility to Alzheimer's disease
		rs11172113	intron	0.38	C>G	Tag SNP Associated with susceptibility to migraine, syncope, and stroke
<i>P2RX7</i>	12	rs208294	exon	0.44	T>C	Tag SNP, missense SNP, splicing regulation Associated with prognosis of prostate cancer patients
		rs1718119	exon	0.38	A>G	Missense SNP, splicing regulation Associated with risk of obesity, pulmonary tuberculosis, and systemic lupus erythematosus

MAF presents minor allele frequency in Caucasians in the Ensemble Genome Browser (<http://www.ensembl.org>).

Abbreviations: ICD, immunogenic cell death; MAF, minor allele frequency; miRNA, micro RNA; mRNA, messenger RNA; NSCLC, non-small-cell lung cancer; SNP, single nucleotide polymorphism; UTR, untranslated region.

**Table S3. Comparison of patient characteristics between cohorts**

Characteristics	Total N = 648	MAVERICC N = 324		TRIBE N = 324		P-value
		FOLFOX+BEV (discovery cohort) N = 161	FOLFIRI+BEV (control cohort 1) N = 163	FOLFOXIRI+BEV (validation cohort) N = 109	FOLFIRI+BEV (control cohort 2) N = 215	
Sex						0.97
Male	402	101 (62.7%)	103 (63.2%)	66 (60.6%)	132 (61.4%)	
Female	246	60 (37.3%)	60 (36.8%)	43 (39.4%)	83 (38.6%)	
Age						0.10
≤65	452	117 (72.7%)	101 (62.0%)	78 (71.6%)	156 (72.6%)	
>65	196	44 (27.3%)	62 (38.0%)	31 (28.4%)	59 (27.4%)	
Performance status						<0.001
ECOG 0	450	81 (50.3%)	97 (59.5%)	95 (87.2%)	177 (82.3%)	
ECOG 1	196	79 (49.1%)	66 (40.5%)	14 (12.8%)	37 (17.2%)	
Unknown*	2	1 (0.6%)	0 (0%)	0 (0%)	1 (0.5%)	
Primary tumor site						0.007
Right-sided	214	64 (39.8%)	67 (41.1%)	30 (27.5%)	53 (24.7%)	
Left-sided	413	97 (60.2%)	96 (58.9%)	73 (67.0%)	147 (68.4%)	
Unknown*	21	0 (0%)	0 (0%)	6 (5.5%)	15 (7.0%)	
Number of metastases						<0.001
≤2	474	101 (62.7%)	106 (65.0%)	89 (81.7%)	178 (82.8%)	
>2	174	60 (37.3%)	57 (35.0%)	20 (18.3%)	37 (17.2%)	

Unknown*	0	0 (0%)	0 (0%)	0 (0%)	0 (0%)	
Liver limited disease						0.31
No	220	NA	NA	70 (64.2%)	150 (69.8%)	
Yes	104	NA	NA	39 (35.8%)	65 (30.2%)	
Primary tumor resected						<0.001
No	412	148 (91.9%)	153 (93.9%)	31 (28.4%)	80 (37.2%)	
Yes	236	13 (8.1%)	10 (6.1%)	78 (71.6%)	135 (62.8%)	
Adjuvant chemotherapy						0.68
No	571	146 (90.7%)	143 (87.7%)	94 (86.2%)	188 (87.4%)	
Yes	77	15 (9.3%)	20 (12.3%)	15 (13.8%)	27 (12.6%)	
Unknown*	0	0 (0%)	0 (0%)	0 (0%)	0 (0%)	
RAS status						0.32
Wildtype	84	NA	NA	34 (31.2%)	50 (23.3%)	
Mutant	167	NA	NA	57 (52.3%)	110 (51.2%)	
Unknown*	73	NA	NA	18 (16.5%)	55 (25.6%)	
BRAF status						0.25
Wildtype	256	NA	NA	88 (80.7%)	168 (78.1%)	
Mutant	19	NA	NA	9 (8.3%)	10 (4.7%)	
Unknown*	49	NA	NA	12 (11.0%)	37 (17.2%)	

\*Unknown groups were not included in the analysis.

P-values was estimated by Chi-square test.

Abbreviations: BEV, bevacizumab; ECOG, Eastern Cooperative Oncology Group; NA, not assessed.

**Table S4. Follow-up and survival time in each cohort**

Time (months)	MAVERICC		TRIBE	
	N = 324		N = 324	
	FOLFOX+BEV N = 161	FOLFIRI+BEV N = 163	FOLFOXIRI+BEV N = 109	FOLFIRI+BEV N = 215
Follow-up				
Median	26.8	23.3	54.5	48.9
PFS				
Median	10.1	12.5	10.8	9.7
OS				
Median	24.7	27.4	26.0	26.2

Abbreviations: BEV, bevacizumab; OS, overall survival; PFS, progression-free survival.

**Table S5. Associations between ICD-related SNPs and clinical outcomes in MAVERICC FOLFOX+Bevacizumab arm (discovery cohort)**

Genotype	N	TR			PFS					OS				
		Yes	No	<i>P</i> <sup>a</sup>	mPFS (months)	Univariate analysis		Multivariate analysis		mOS (months)	Univariate analysis		Multivariate analysis	
						HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>		HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>
<i>CALR</i> rs1049481														
T/T	59	39 (67.2%)	19 (33.8%)	0.45	10.2	1	0.12	1	0.51	22.7	1	0.27	1	0.93
Any G	101	60 (61.2%)	38 (38.8%)		10.1	0.75 (0.52–1.08)		0.85 (0.54–1.36)		26.1	0.78 (0.50–1.21)		1.03 (0.60–1.76)	
<i>CALR</i> rs1010222														
G/G	72	47 (66.2%)	24 (33.8%)	0.48	9.0	1	<b>0.008</b>	1	0.10	22.5	1	0.07	1	0.38
Any A	87	51 (60.7%)	33 (39.3%)		11.0	0.61 (0.43–0.88)		0.67 (0.42–1.07)		28.8	0.67 (0.44–1.04)		0.78 (0.46–1.35)	
<i>HMGB1</i> rs1045411														
C/C	89	54 (63.5%)	31 (36.5%)	0.84	11.2	1	0.18	1	0.18	25.5	1	0.56	1	0.23
Any T	63	39 (61.9%)	24 (38.1%)		8.9	1.29 (0.89–1.87)		1.43 (0.85–2.41)		22.8	1.14 (0.73–1.80)		1.46 (0.79–2.69)	
<i>HMGB1</i> rs1412125														
T/T	33	19 (61.3%)	12 (38.7%)	0.76	11.8	1	0.78	1	0.29	23.2	1	0.92	1	0.48
Any C	128	81 (64.3%)	45 (35.7%)		10.1	1.07 (0.67–1.70)		0.74 (0.43–1.28)		25.5	0.97 (0.58–1.63)		0.80 (0.43–1.48)	
<i>HMGB1</i> rs1360485														
T/T	75	45 (62.5%)	27 (37.5%)	0.77	12.3	1	0.09	1	0.14	25.8	1	0.23	1	0.26
Any C	86	55 (64.7%)	30 (35.3%)		8.8	1.36 (0.95–1.95)		1.45 (0.89–2.38)		23.9	1.31 (0.84–2.03)		1.38 (0.78–2.43)	
<i>ANXA1</i> rs1050305														
A/A	138	85 (63.4%)	49 (36.6%)	0.99	11.0	1	0.26	1	0.47	25.5	1	<b>0.03</b>	1	0.10
Any G	22	14 (63.6%)	8 (36.4%)		8.8	1.33 (0.81–2.21)		1.29 (0.66–2.51)		18.7	1.87 (1.04–3.35)		1.96 (0.93–4.12)	
<i>LRP1</i> rs1799986														
C/C	111	70 (64.2%)	39 (35.8%)	0.99	11.0	1	0.22	1	0.53	25.8	1	<b>0.03</b>	1	0.14
Any T	44	27 (64.3%)	15 (35.7%)		8.5	1.30 (0.85–1.97)		1.18 (0.71–1.94)		16.9	1.69 (1.06–2.70)		1.55 (0.87–2.74)	
<i>LRP1</i> rs11172113														
T/T	51	35 (71.4%)	14 (28.6%)	0.17	10.2	1	0.50	1	0.85	23.9	1	0.78	1	0.91
Any C	110	65 (60.2%)	43 (39.8%)		10.9	1.14 (0.78–1.68)		1.05 (0.63–1.74)		25.5	0.94 (0.60–1.47)		0.97 (0.55–1.69)	
<i>P2RX7</i> rs208294														
C/C	41	29 (72.5%)	11 (27.5%)	0.18	11.0	1	0.69	1	0.80	26.1	1	0.47	1	0.14
Any T	120	71 (60.7%)	46 (39.3%)		10.2	1.09 (0.71–1.66)		0.93 (0.55–1.58)		24.8	0.83 (0.51–1.37)		0.62 (0.33–1.16)	
<i>P2RX7</i> rs1718119														
G/G	60	40 (67.8%)	19 (32.2%)	0.41	11.0	1	0.67	1	0.93	25.5	1	0.67	1	0.92
Any A	101	60 (61.2%)	38 (38.8%)		10.0	1.08 (0.75–1.57)		1.02 (0.62–1.70)		24.3	1.10 (0.71–1.72)		0.97 (0.53–1.78)	

Significant values are indicated in bold characters.

Abbreviations: CI, confidence interval; HR, hazard ratio; ICD, immunogenic cell death; mOS, median overall survival; mPFS, median progression-free survival; OS, overall survival; PFS, progression-free survival; SNP, single nucleotide polymorphism; TR, tumor response.

<sup>a</sup> *P*-values were based on Chi-square test.

<sup>b</sup> *P*-values were based on log-rank test for PFS and OS in the univariate analysis.

<sup>c</sup> *P*-values were based on Wald test in the multivariate Cox proportional hazards regression model.

**Table S6. Associations between ICD-related SNPs and clinical outcomes in TRIBE FOLFOXIRI+Bevacizumab arm (validation cohort)**

Genotype	N	TR			PFS					OS				
		Yes	No	<i>P</i> <sup>a</sup>	mPFS (months)	Univariate analysis		Multivariate analysis		mOS (months)	Univariate analysis		Multivariate analysis	
						HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>		HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>
<i>CALR</i> rs1049481														
T/T	40	27 (71.1%)	11 (28.9%)	0.41	10.3	1	0.73	1	0.19	26.7	1	0.82	1	0.26
Any G	69	41 (63.1%)	24 (36.9%)		11.0	0.92 (0.58–1.47)		0.69 (0.39–1.21)		23.6	0.95 (0.61–1.48)		0.74 (0.45–1.24)	
<i>CALR</i> rs1010222														
G/G	44	30 (71.4%)	12 (28.6%)	0.33	10.3	1	0.63	1	0.61	26.2	1	0.76	1	0.35
Any A	65	38 (62.3%)	23 (37.7%)		11.1	0.90 (0.57–1.41)		0.87 (0.52–1.46)		25.1	0.93 (0.60–1.44)		0.79 (0.49–1.29)	
<i>HMGB1</i> rs1045411														
C/C	69	41 (62.1%)	25 (37.9%)	0.39	11.9	1	0.06	1	<b>0.03</b>	28.4	1	0.99	1	0.93
Any T	34	22 (71.0%)	9 (29.0%)		9.7	1.57 (0.97–2.53)		1.93 (1.06–3.53)		23.2	1.00 (0.62–1.62)		1.03 (0.59–1.80)	
<i>HMGB1</i> rs1412125														
T/T	31	19 (65.5%)	10 (34.5%)	0.95	12.1	1	0.69	1	0.54	28.1	1	0.48	1	0.65
Any C	78	49 (66.2%)	25 (33.8%)		10.1	1.11 (0.68–1.80)		1.22 (0.64–2.30)		25.1	1.19 (0.73–1.92)		1.14 (0.64–2.01)	
<i>HMGB1</i> rs1360485														
T/T	64	39 (63.9%)	22 (36.1%)	0.59	11.9	1	0.05	1	0.07	27.4	1	0.89	1	0.80
Any C	45	29 (69.0%)	13 (31.0%)		9.6	1.56 (0.99–2.46)		1.70 (0.95–3.06)		26.1	0.97 (0.62–1.51)		0.93 (0.54–1.60)	
<i>ANXA1</i> rs1050305														
A/A	91	60 (70.6%)	25 (29.4%)	<b>0.03</b>	11.3	1	<b>0.009</b>	1	0.17	31.0	1	<b>&lt;0.001</b>	1	<b>0.04</b>
Any G	18	8 (44.4%)	10 (55.6%)		9.5	2.17 (1.20–3.92)		1.62 (0.83–3.16)		17.1	2.69 (1.56–4.61)		2.00 (1.07–3.72)	
<i>LRP1</i> rs1799986														
C/C	74	46 (63.9%)	26 (36.1%)	0.52	11.3	1	0.35	1	<b>0.005</b>	26.7	1	0.98	1	0.42
Any T	24	15 (71.4%)	6 (28.6%)		8.9	1.30 (0.75–2.25)		2.71 (1.37–5.37)		23.7	0.99 (0.58–1.71)		1.30 (0.70–2.40)	
<i>LRP1</i> rs11172113														
T/T	42	24 (60.0%)	16 (40.0%)	0.30	10.1	1	0.22	1	<b>0.04</b>	21.6	1	0.18	1	<b>0.03</b>
Any C	67	44 (69.8%)	19 (30.2%)		11.3	0.75 (0.48–1.19)		0.55 (0.31–0.98)		28.4	0.74 (0.48–1.15)		0.58 (0.34–0.96)	
<i>P2RX7</i> rs208294														
C/C	35	20 (66.7%)	10 (33.3%)	0.93	10.3	1		1	0.76	19.0	1	<b>0.004</b>	1	<b>0.02</b>
Any T	74	48 (65.8%)	25 (34.2%)		11.0	0.78 (0.49–1.25)	0.30	0.92 (0.54–1.58)		31.0	0.52 (0.33–0.82)		0.54 (0.33–0.89)	
<i>P2RX7</i> rs1718119														
G/G	44	29 (67.4%)	14 (32.6%)	0.80	10.3	1	0.67	1	0.33	26.1	1	0.34	1	0.16
Any A	65	39 (65.0%)	21 (35.0%)		10.9	0.91 (0.57–1.43)		0.77 (0.45–1.31)		26.2	0.81 (0.52–1.25)		0.69 (0.42–1.15)	

Significant values are indicated in bold characters.

Abbreviations: CI, confidence interval; HR, hazard ratio; ICD, immunogenic cell death; mOS, median overall survival; mPFS, median progression-free survival; OS, overall survival; PFS, progression-free survival; SNP, single nucleotide polymorphism; TR, tumor response.



<sup>a</sup> *P*-values were based on Chi-square test.

<sup>b</sup> *P*-values were based on log-rank test for PFS and OS in the univariate analysis.

<sup>c</sup> *P*-values were based on Wald test in the multivariate Cox proportional hazards regression model.

**Table S7. Associations between ICD-related SNPs and clinical outcomes in MAVERICC FOLFIRI+Bevacizumab arm (control cohort 1)**

Genotype	N	TR			<i>P</i> <sup>a</sup>	PFS					OS				
		Yes	No	mPFS (months)		Univariate analysis		Multivariate analysis		mOS (months)	Univariate analysis		Multivariate analysis		
						HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>		HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>	
<i>CALR</i> rs1049481															
T/T	69	46 (67.6%)	22 (32.4%)	0.97	11.2	1	0.46	1	0.70	26.5	1	0.13	1	0.80	
Any G	94	62 (67.4%)	30 (32.6%)		12.7	0.87 (0.59–1.27)		0.91 (0.54–1.51)		31.3	0.68 (0.42–1.12)		0.92 (0.47–1.78)		
<i>CALR</i> rs1010222															
G/G	81	54 (67.5%)	26 (32.5%)	1.00	12.9	1	0.98	1	0.88	26.9	1	0.41	1	0.94	
Any A	82	54 (67.5%)	26 (32.5%)		12.6	0.99 (0.69–1.44)		0.96 (0.58–1.60)		27.9	0.81 (0.49–1.34)		0.97 (0.50–1.89)		
<i>HMGB1</i> rs1045411															
C/C	109	71 (67.0%)	35 (33.0%)	0.81	11.8	1	0.39	1	0.76	27.9	1	0.97	1	0.62	
Any T	42	29 (69.0%)	13 (31.0%)		12.8	0.83 (0.54–1.27)		1.09 (0.63–1.89)		32.3	0.99 (0.56–1.75)		1.20 (0.58–2.48)		
<i>HMGB1</i> rs1412125															
T/T	50	30 (61.2%)	19 (38.8%)	0.26	12.3	1	0.63	1	0.38	32.3	1	0.32	1	0.87	
Any C	113	78 (70.3%)	33 (29.7%)		12.6	0.91 (0.61–1.34)		0.78 (0.45–1.35)		27.4	1.32 (0.76–2.30)		1.06 (0.52–2.16)		
<i>HMGB1</i> rs1360485															
T/T	98	62 (65.3%)	33 (34.7%)	0.47	11.6	1	0.13	1	0.92	27.9	1	0.75	1	0.60	
Any C	65	46 (70.8%)	19 (29.2%)		14.8	0.75 (0.51–1.09)		1.03 (0.62–1.69)		27.5	0.92 (0.56–1.53)		1.19 (0.62–2.25)		
<i>ANXA1</i> rs1050305															
A/A	128	85 (66.9%)	42 (33.1%)	0.67	12.3	1	0.72	1	0.85	27.9	1	0.82	1	0.63	
Any G	33	22 (71.0%)	9 (29.0%)		13.8	1.08 (0.70–1.67)		1.07 (0.54–2.11)		27.5	1.07 (0.60–1.92)		0.81 (0.33–1.98)		
<i>LRP1</i> rs1799986															
C/C	126	81 (65.9%)	42 (34.1%)	0.28	12.8	1	0.35	1	0.79	27.9	1	0.68	1	0.38	
Any T	33	25 (75.8%)	8 (24.2%)		12.3	1.23 (0.79–1.92)		0.93 (0.52–1.66)		25.0	1.13 (0.63–2.02)		0.71 (0.33–1.53)		
<i>LRP1</i> rs11172113															
T/T	60	36 (61.0%)	23 (39.0%)	0.18	12.9	1	0.75	1	0.45	26.9	1	0.60	1	0.21	
Any C	103	72 (71.3%)	29 (28.7%)		12.3	1.07 (0.72–1.58)		1.22 (0.72–2.06)		31.3	0.87 (0.52–1.46)		0.66 (0.34–1.26)		
<i>P2RX7</i> rs208294															
C/C	42	27 (65.9%)	14 (34.1%)	0.79	15.0	1	0.41	1	0.41	-	1	<b>0.03</b>	1	0.11	
Any T	121	81 (68.1%)	38 (31.9%)		12.3	1.20 (0.78–1.85)		1.26 (0.72–2.22)		27.5	2.07 (1.05–4.08)		1.84 (0.84–4.06)		
<i>P2RX7</i> rs1718119															
G/G	72	48 (69.6%)	21 (30.4%)	0.63	14.0	1	0.60	1	0.38	32.3	1	0.05	1	<b>0.01</b>	
Any A	91	60 (65.9%)	31 (34.1%)		11.2	1.11 (0.76–1.61)		1.26 (0.74–2.14)		23.8	1.70 (1.01–2.86)		2.57 (1.16–5.67)		

Significant values are indicated in bold characters.

Abbreviations: CI, confidence interval; HR, hazard ratio; ICD, immunogenic cell death; mOS, median overall survival; mPFS, median progression-free survival; OS, overall survival; PFS, progression-free survival; SNP, single nucleotide polymorphism; TR, tumor response.

<sup>a</sup> *P*-values were based on Chi-square test.

<sup>b</sup> *P*-values were based on log-rank test for PFS and OS in the univariate analysis.

<sup>c</sup> *P*-values were based on Wald test in the multivariate Cox proportional hazards regression model.

**Table S8. Associations between ICD-related SNPs and clinical outcomes in TRIBE FOLFIRI+Bevacizumab arm (control cohort 2)**

Genotype	N	TR		<i>P</i> <sup>a</sup>	PFS					OS				
		Yes	No		mPFS (months)	Univariate analysis		Multivariate analysis		mOS (months)	Univariate analysis		Multivariate analysis	
						HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>		HR (95% CI)	<i>P</i> <sup>b</sup>	HR (95% CI)	<i>P</i> <sup>c</sup>
<i>CALR</i> rs1049481														
T/T	81	49 (62.0%)	30 (38.0%)	0.39	10.8	1	0.40	1	0.45	28.0	1	0.94	1	0.85
Any G	131	71 (55.9%)	56 (44.1%)		9.5	1.15 (0.83–1.57)		1.14 (0.81–1.62)		26.1	1.01 (0.74–1.39)		0.97 (0.69–1.36)	
<i>CALR</i> rs1010222														
G/G	90	56 (63.6%)	32 (36.4%)	0.16	10.8	1	0.37	1	0.56	27.4	1	0.75	1	0.79
Any A	119	62 (53.9%)	53 (46.1%)		9.5	1.16 (0.84–1.58)		1.11 (0.79–1.56)		26.2	1.05 (0.77–1.44)		0.96 (1.69–1.33)	
<i>HMGB1</i> rs1045411														
C/C	138	78 (58.2%)	56 (41.8%)	0.58	9.9	1	0.87	1	0.62	25.5	1	0.51	1	0.79
Any T	59	35 (62.5%)	21 (37.5%)		9.5	0.97 (0.68–1.38)		1.11 (0.74–1.65)		29.8	0.89 (0.63–1.26)		0.95 (0.65–1.38)	
<i>HMGB1</i> rs1412125														
T/T	63	37 (60.7%)	24 (39.3%)	0.64	9.7	1	0.77	1	0.92	22.5	1	0.43	1	0.29
Any C	152	84 (57.1%)	63 (42.9%)		9.7	1.05 (0.76–1.46)		0.98 (0.69–1.40)		28.0	0.88 (0.63–1.22)		0.83 (0.58–1.17)	
<i>HMGB1</i> rs1360485														
T/T	134	76 (58.5%)	54 (41.5%)	0.91	9.9	1	0.78	1	0.76	25.8	1	0.41	1	0.89
Any C	81	45 (57.7%)	33 (42.3%)		9.7	0.95 (0.69–1.32)		1.06 (0.74–1.50)		29.8	0.88 (0.64–1.20)		0.98 (0.70–1.37)	
<i>ANXA1</i> rs1050305														
A/A	184	102 (57.6%)	75 (42.4%)	0.70	9.9	1	0.92	1	0.72	26.2	1	0.23	1	0.09
Any G	31	19 (61.3%)	12 (38.7%)		9.2	1.02 (0.66–1.58)		1.09 (0.68–1.74)		31.6	0.76 (0.48–1.19)		0.67 (0.42–1.09)	
<i>LRP1</i> rs1799986														
C/C	162	93 (58.9%)	65 (41.1%)	0.45	9.5	1	0.34	1	0.59	26.2	1	0.57	1	0.66
Any T	44	22 (52.4%)	20 (47.6%)		11.5	0.83 (0.57–1.22)		0.90 (0.60–1.34)		27.1	0.89 (0.61–1.31)		1.10 (0.73–1.66)	
<i>LRP1</i> rs11172113														
T/T	98	56 (58.9%)	39 (41.1%)	0.84	10.4	1	0.32	1	0.09	26.9	1	0.87	1	0.27
Any C	117	65 (57.5%)	48 (42.5%)		9.5	1.17 (0.86–1.59)		1.35 (0.96–1.89)		25.5	1.03 (0.76–1.39)		1.20 (0.87–1.67)	
<i>P2RX7</i> rs208294														
C/C	64	37 (59.7%)	25 (40.3%)	0.77	11.0	1	0.38	1	0.92	27.1	1	0.89	1	0.66
Any T	151	84 (57.5%)	62 (42.5%)		9.5	1.16 (0.83–1.61)		1.02 (0.71–1.47)		26.3	0.98 (0.70–1.36)		0.92 (0.64–1.32)	
<i>P2RX7</i> rs1718119														
G/G	90	48 (55.8%)	38 (44.2%)	0.56	9.5	1	0.91	1	0.41	27.1	1	0.74	1	0.26
Any A	125	73 (59.8%)	49 (40.2%)		10.6	0.98 (0.72–1.34)		0.87 (0.62–1.21)		26.3	0.95 (0.70–1.29)		0.83 (0.60–1.15)	

Significant values are indicated in bold characters.

Abbreviations: CI, confidence interval; HR, hazard ratio; ICD, immunogenic cell death; mOS, median overall survival; mPFS, median progression-free survival; OS, overall survival; PFS, progression-free survival; SNP, single nucleotide polymorphism; TR, tumor response.

<sup>a</sup> *P*-values were based on Chi-square test.

<sup>b</sup> *P*-values were based on log-rank test for PFS and OS in the univariate analysis.

<sup>c</sup> *P*-values were based on Wald test in the multivariate Cox proportional hazards regression model.