

Supplemental Materials

Variable	Univariate: CD8+ T cell subset			Multivariable: CD8+ T cell subset		
	HR	95% CI	<i>P</i>	HR	95% CI	<i>P</i>
CD8+ T cell subset	1.6	0.23-11.44	0.638	0.67	0.07-6.15	0.713
Purity	-	-	-	0.6	0.16-2.22	0.443
Age	-	-	-	1.03	1.00-1.05	0.026
Male sex	-	-	-	1.37	0.78-2.42	0.273
White race	-	-	-	0.78	0.17-3.56	0.735
Stage 2	-	-	-	1.6	0.46-5.62	0.46
Stage 3	-	-	-	2.9	0.85-9.92	0.091
Stage 4	-	-	-	9.43	2.72-32.67	<0.001
¹ HR: hazards ratio; CI: confidence interval. Boldface type indicates statistical significance.						

Table S1: Relationship between CD8+ T cell and other clinical variables associated with overall survival in 458 patients with CRC whose sequencing data were available in The Cancer Genome Atlas.

Variable	Univariate: Neutrophil cell subset			Multivariable: Neutrophil cell subset		
	HR	95% CI	<i>P</i>	HR	95% CI	<i>P</i>
Neutrophil cell subset	1.08	0.12-9.73	0.945	0.75	0.03-17.29	0.855
Purity	-	-	-	0.61	0.16-2.36	0.471
Age	-	-	-	1.03	1.00-1.06	0.027
Male sex	-	-	-	1.38	0.78-2.42	0.271
White race	-	-	-	0.77	0.17-3.60	0.74
Stage 2	-	-	-	1.65	0.48-5.75	0.429
Stage 3	-	-	-	2.93	0.86-10.03	0.086
Stage 4	-	-	-	9.55	2.76-33.09	<0.001
¹ HR: hazards ratio; CI: confidence interval. Boldface type indicates statistical significance. HR for Tregs and NK cell subset not estimable.						

Table S2: The relationship between Neutrophil cell and other clinical variables associated with overall survival in 458 patients with CRC whose sequencing data were available in The Cancer Genome Atlas.

Variable	Univariate: Macrophage cell subset			Multivariable: Macrophage cell subset		
	HR	95% CI	<i>P</i>	HR	95% CI	<i>P</i>
Macrophage cell subset	4.42	0.59-33.12	0.148	4.3	0.26-71.93	0.311
Purity	-	-	-	0.73	0.20-2.74	0.643
Age	-	-	-	1.03	1.01-1.06	0.02
Male sex	-	-	-	1.4	0.80-2.48	0.242
White race	-	-	-	0.71	0.15-3.29	0.661
Stage 2	-	-	-	1.6	0.46-5.57	0.461
Stage 3	-	-	-	2.86	0.84-9.80	0.094
Stage 4	-	-	-	9.64	2.79-33.35	<0.001
¹ HR: hazards ratio; CI: confidence interval. Boldface type indicates statistical significance.						

Table S3: The relationship between Macrophage and other clinical variables associated with overall survival in 458 patients with CRC whose sequencing data were available in The Cancer Genome Atlas.

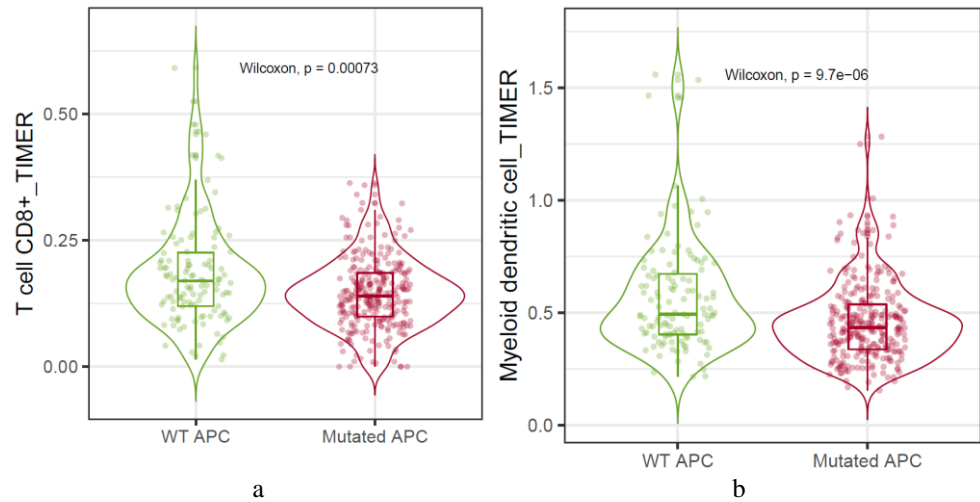
Variable	Univariate: DC cell subset			Multivariable: DC cell subset		
	HR	95% CI	<i>P</i>	HR	95% CI	<i>P</i>
DC cell subset	1.12	0.38-3.25	0.842	0.99	0.25-3.96	0.991
Purity	-	-	-	0.63	0.17-2.42	0.504
Age	-	-	-	1.03	1.00-1.05	0.027
Male sex	-	-	-	1.38	0.78-2.44	0.269
White race	-	-	-	0.76	0.16-3.55	0.726
Stage 2	-	-	-	1.65	0.47-5.73	0.432
Stage 3	-	-	-	2.93	0.86-10.03	0.087
Stage 4	-	-	-	9.63	2.76-33.57	<0.001
¹ HR: hazards ratio; CI: confidence interval. Boldface type indicates statistical significance.						

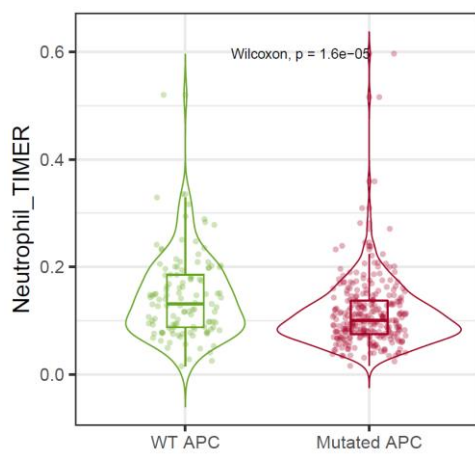
Table S4: The relationship between DC cell and other clinical variables associated with overall survival in 458 patients with CRC whose sequencing data were available in The Cancer Genome Atlas.

Variable	Univariate: CAF cell subset			Multivariable: CAF cell subset		
	HR	95% CI	<i>P</i>	HR	95% CI	<i>P</i>
CAF cell subset	1.57	0.25-9.86	0.479	1.26	0-19.76	0.871
Purity	-	-	-	0.66	0.17-2.49	0.534
Age	-	-	-	1.03	1.00-1.05	0.027
Male sex	-	-	-	1.39	0.79-2.46	0.259
White race	-	-	-	0.75	0.16-3.49	0.709
Stage 2	-	-	-	1.64	0.47-5.71	0.436
Stage 3	-	-	-	2.93	0.86-10.01	0.087
Stage 4	-	-	-	9.63	2.79-33.25	<0.001

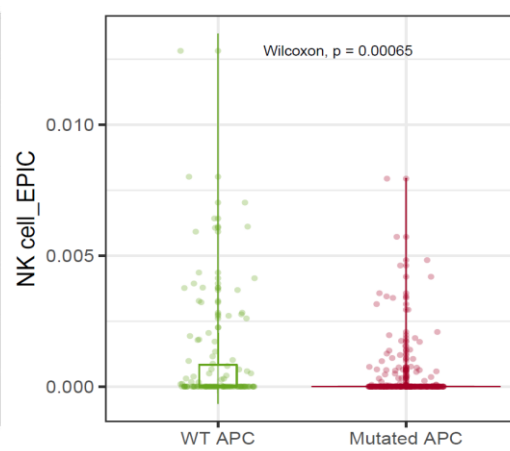
¹HR: hazards ratio; CI: confidence interval. Boldface type indicates statistical significance.

Table S5: The relationship between CAF cell and other clinical variables associated with overall survival in 458 patients with CRC whose sequencing data were available in The Cancer Genome Atlas.

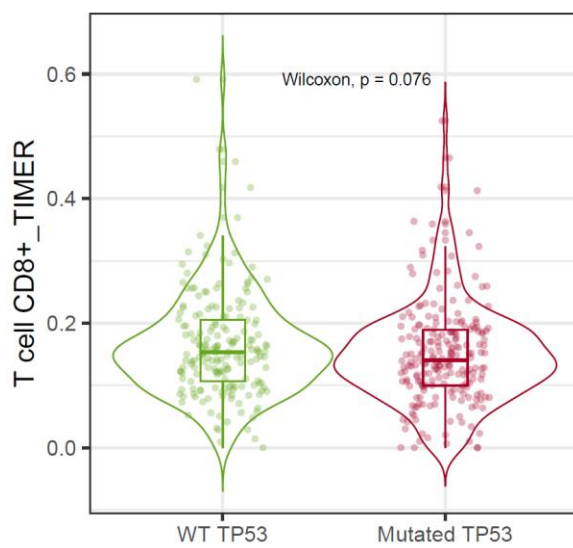




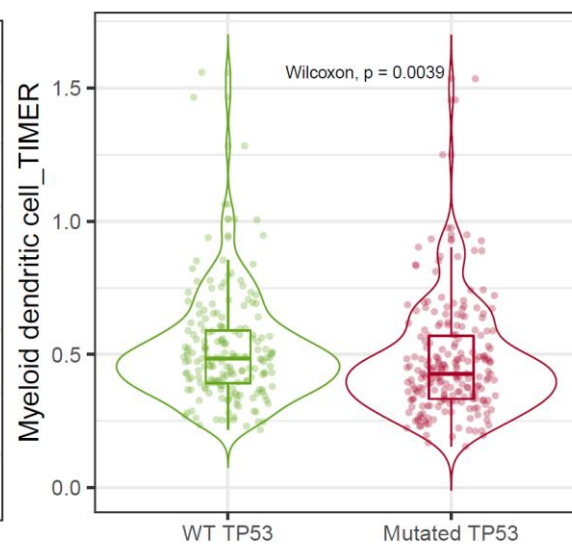
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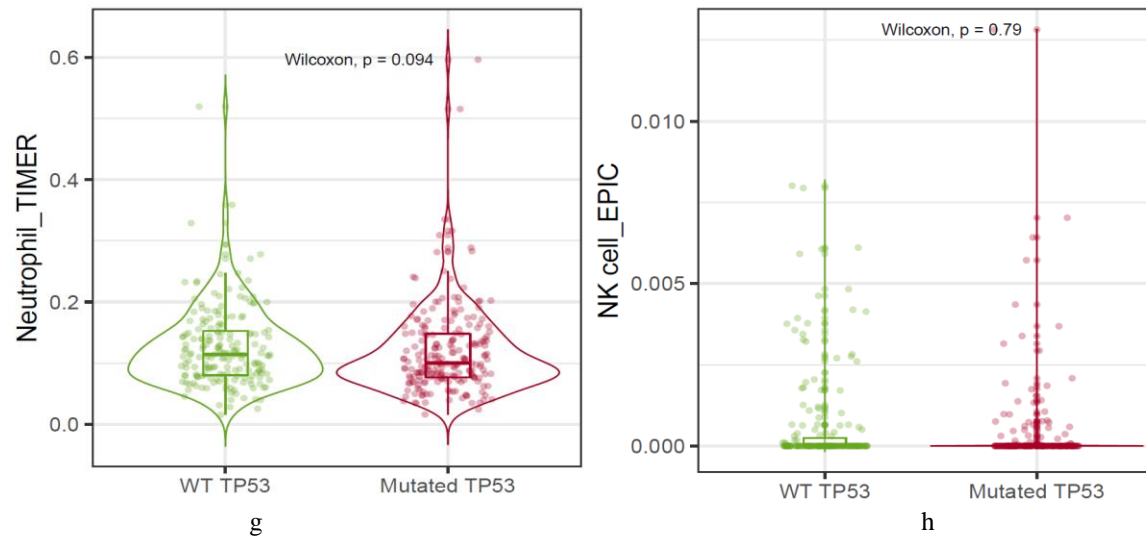
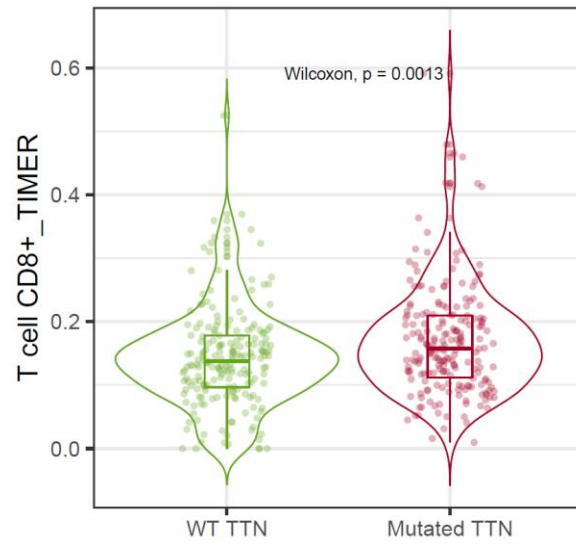
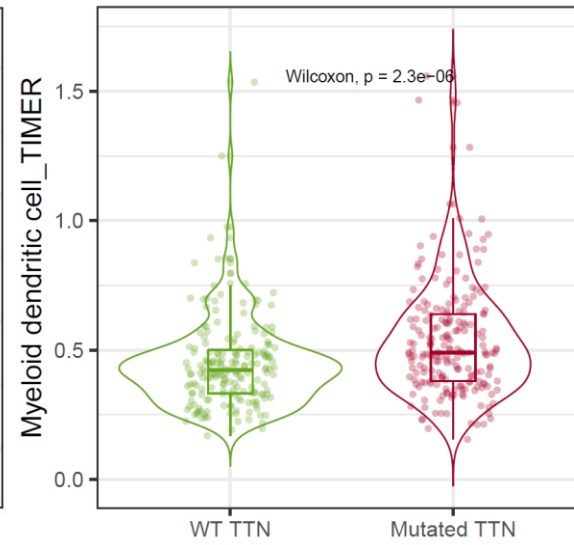


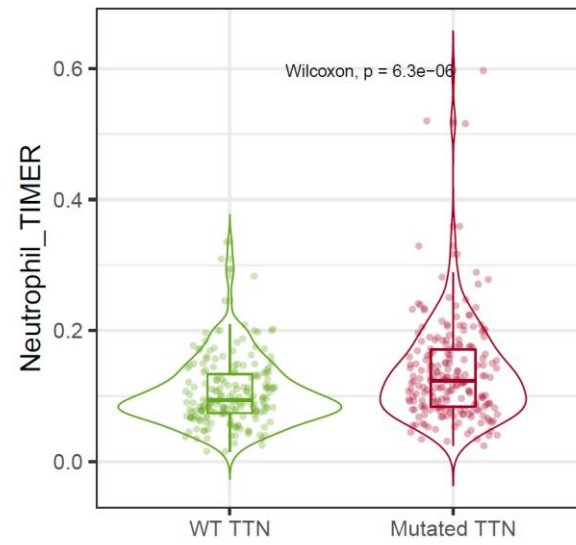
Figure S1: Immune cell subsets in COAD samples with mutated tumor suppressor genes and in those with wild-type genes. a). CD8+ in samples with mutated APC vs wild-type; b). DC in samples with mutated APC vs wild-type; c). Neutrophil in samples with mutated APC vs wild-type; d). NK in samples with mutated APC vs wild-type; e). CD8+ in samples with mutated TP53 vs wild-type; f). DC in samples with mutated TP53 vs wild-type; g). Neutrophil in samples with mutated TP53 vs wild-type; h). NK in samples with mutated TP53 vs wild-type.



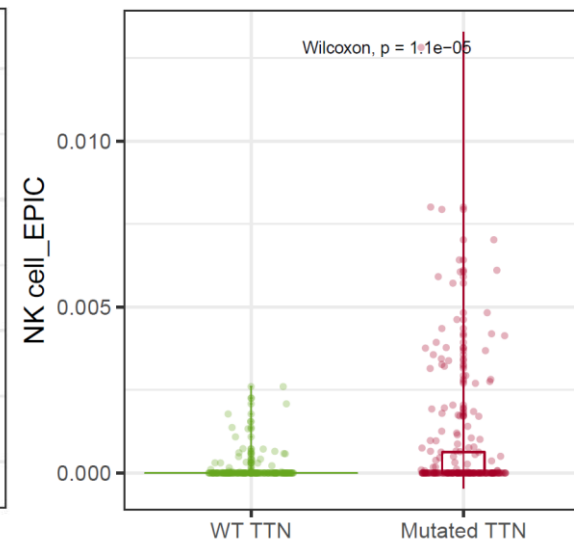
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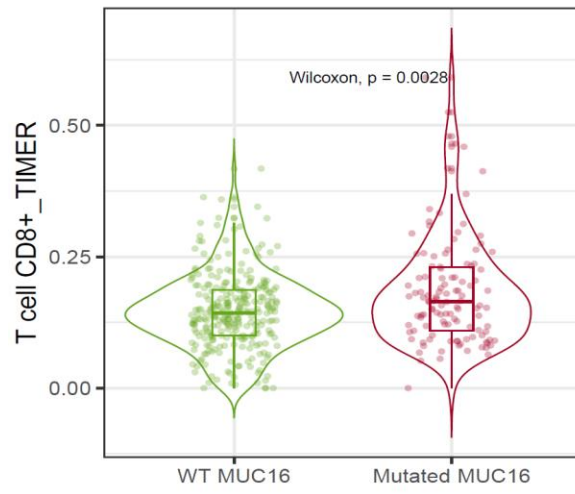
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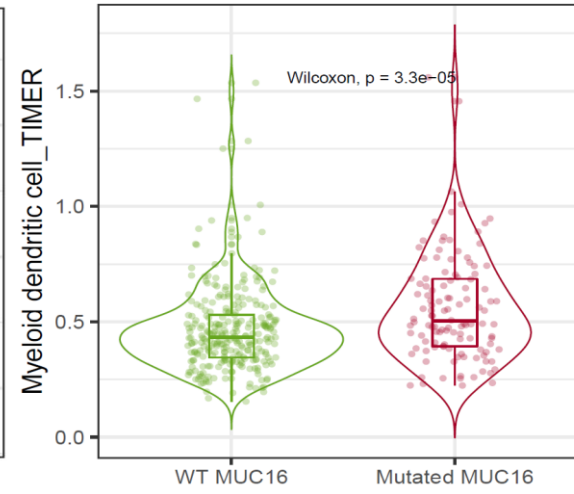
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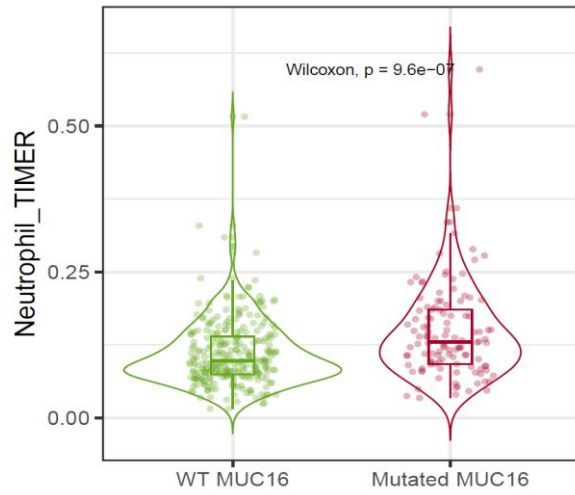
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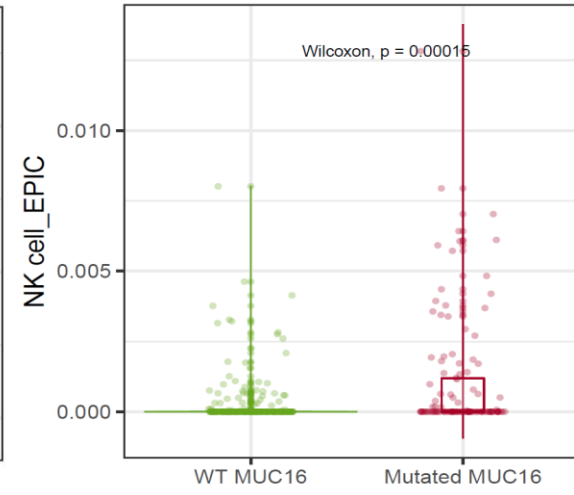
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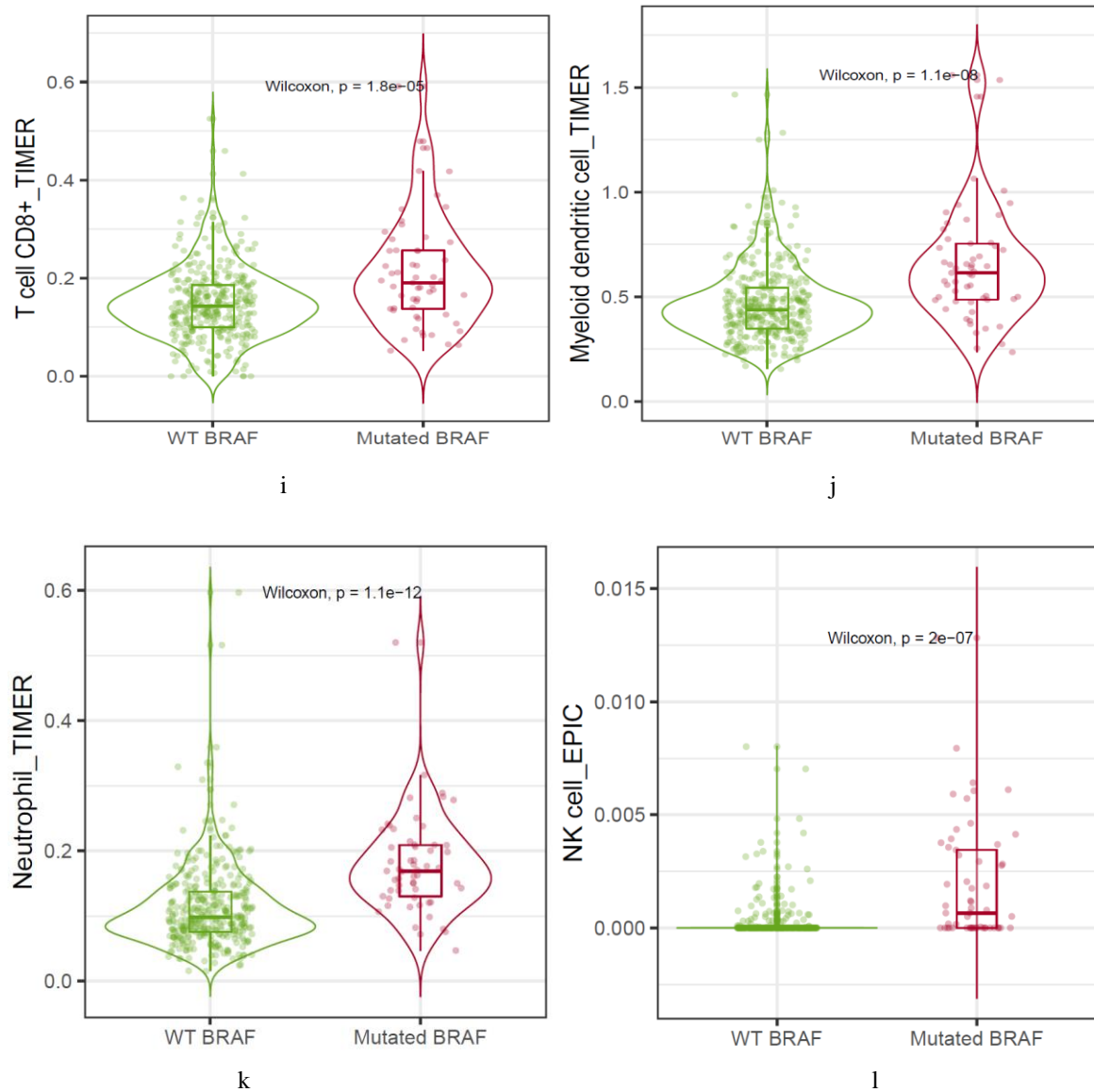
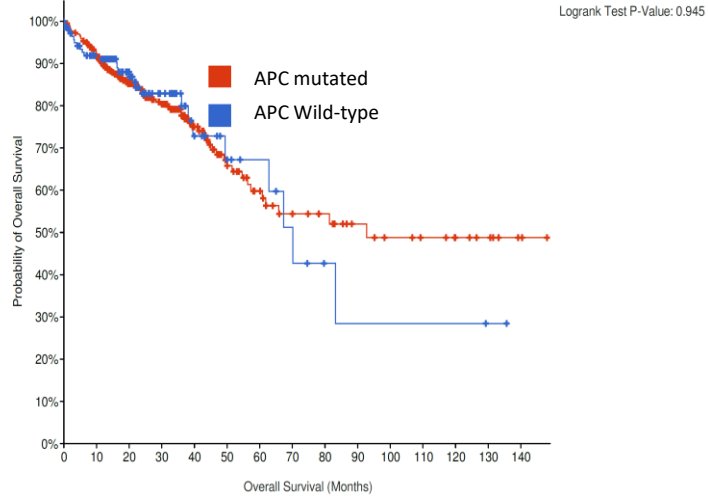
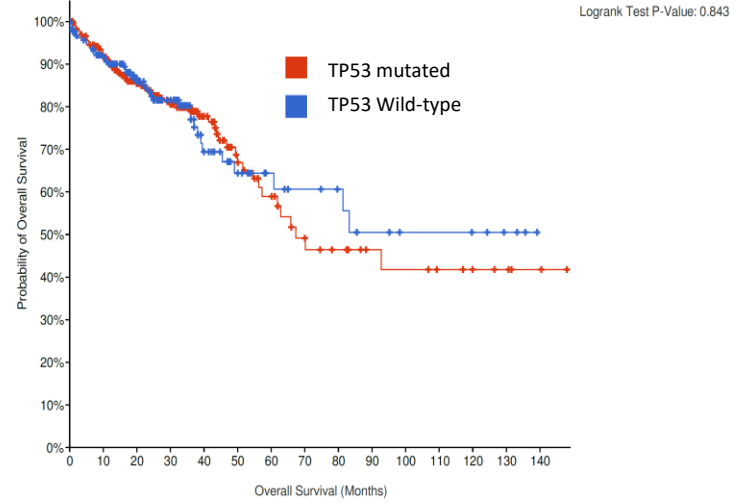


Figure S2: Immune cell subsets in COAD patients with tumor oncogenes mutated and in those with wild-type genes. a). CD8+ in samples with mutated TTN vs wild-type; b). DC in samples with mutated TTN vs wild-type; c). Neutrophil in samples with mutated TTN vs wild-type; d). NK in samples with mutated TTN vs

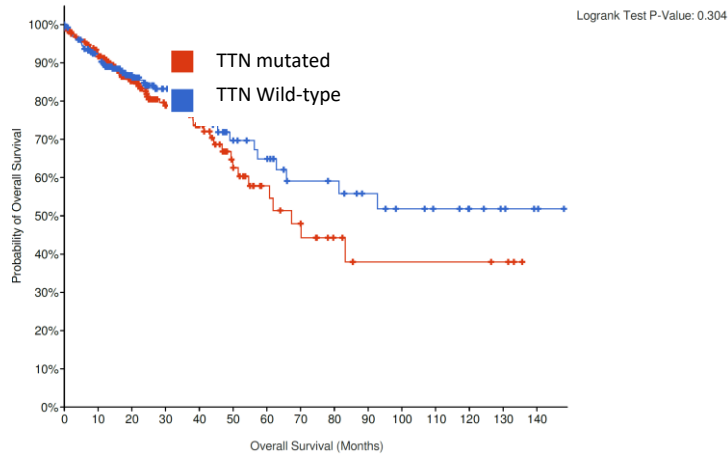
wild-type; e). CD8+ in samples with mutated MUC16 vs wild-type; f). DC in samples with mutated MUC16 vs wild-type; g). Neutrophil in samples with mutated MUC16 vs wild-type; h). NK in samples with mutated MUC16 vs wild-type; i). CD8+ in samples with mutated BRAF vs wild-type; j). DC in samples with mutated BRAF vs wild-type; k). Neutrophil in samples with mutated BRAF vs wild-type; l). NK in samples with mutated BRAF vs wild-type.



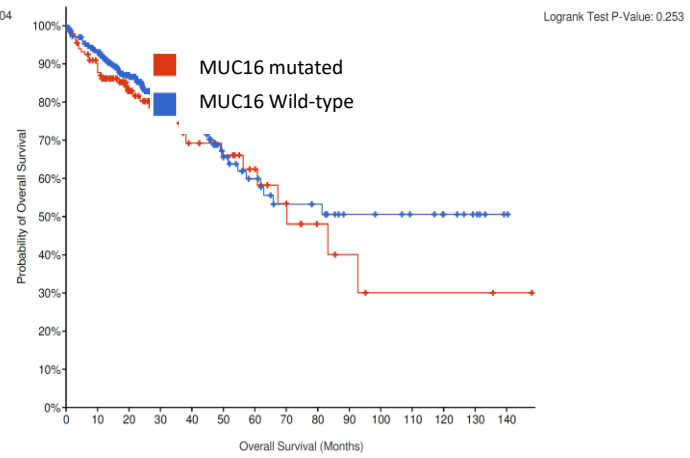
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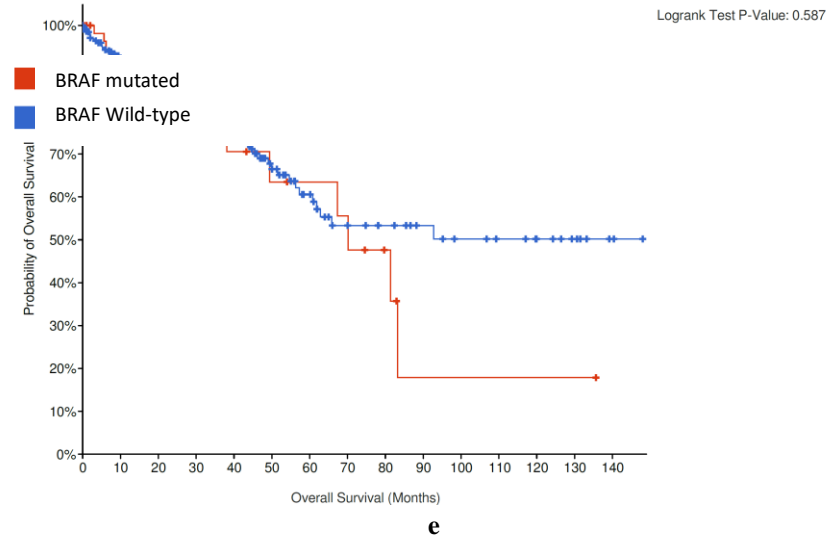


Figure S3: Genetic mutation and overall survival. Log-rank test none was significant ($P > 0.05$). a. APC mutation status and OS; b. TP53 mutation status and OS; c. TTN mutation status and OS; d. MUC16 mutation status and OS; e. BRAF mutation status and OS.