Distant Metastasis-Free Survival Results From the Randomized, Phase 2 mRNA-4157-P201/ KEYNOTE-942 Trial

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Forward Looking Statement and Disclaimer

This presentation contains forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995, as amended, including statements regarding: the development by Moderna and Merck of an individualized neoantigen therapy (INT) to target an induvial patient's unique tumor mutations; the potential for therapies targeting neoantigens to produce long-term disease control for patients; the safety and tolerability profile for mRNA-4157 (V940); the potential for mRNA-4157 (V940) to improve distant metastasis-free survival (DMFS) in patients with high-risk stage III/IV melanoma; the potential for mRNA-4157 (V940) to improve recurrence-free survival (RFS) rates in stage III/IV melanoma patients; next steps for the mRNA-4157-P201/KEYNOTE-942 trial; and plans to initiate a Phase 3 study in patients with high-risk resected melanoma in 2023 and to expand to additional tumor types, including non-small cell lung cancer. In some cases, forward-looking statements can be identified by terminology such as "will," "may," "should," "could," "expects," "intends," "plans," "aims," "anticipates," "believes," "estimates," "predicts," "potential," "continue," or the negative of these terms or other comparable terminology, although not all forward-looking statements contain these words. The forward-looking statements in this presentation are neither promises nor guarantees, and you should not place undue reliance on these forward-looking statements because they involve known and unknown risks, uncertainties, and other factors, many of which are beyond Moderna's control and which could cause actual results to differ materially from those expressed or implied by these forward-looking statements. These risks, uncertainties, and other factors include, among others, those risks and uncertainties described under the heading "Risk Factors" in Moderna's Annual Report on Form 10-K for the fiscal year ended December 31, 2022, filed with the U.S. Securities and Exchange Commission (SEC), and in subsequent filings made by Moderna with the SEC, which are available on the SEC's website at www.sec.gov. Except as required by law, Moderna disclaims any intention or responsibility for updating or revising any forward-looking statements contained in this presentation in the event of new information, future developments or otherwise. These forward-looking statements are based on Moderna's current expectations and speak only as of the date of this presentation.

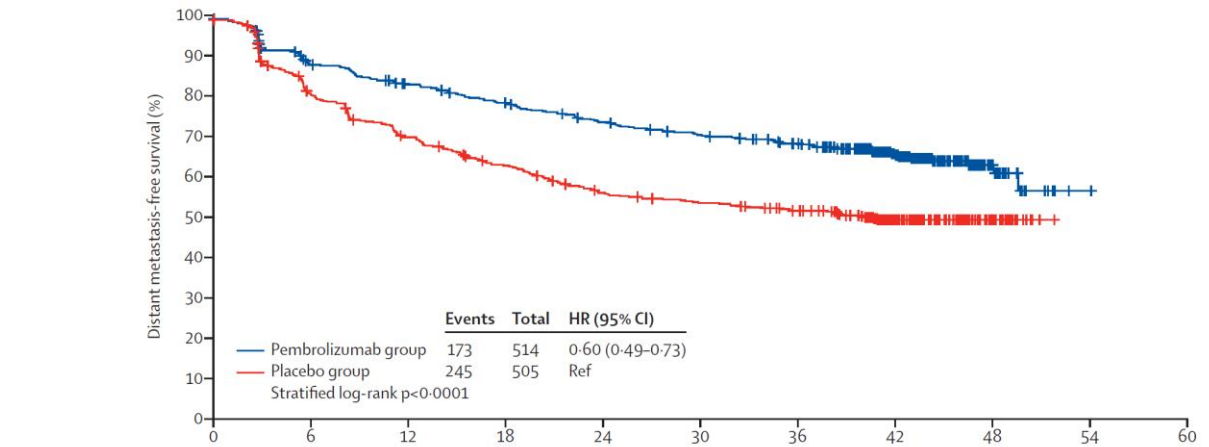
Adjuvant Immune Checkpoint Inhibitor Therapy and DMFS in High-risk Melanoma

- **Both RFS and DMFS** have been evaluated as surrogates for overall survival. **DMFS** captures patients whose **relapse is associated with a worse prognosis** and who may need further systemic treatment[1]

- The **KEYNOTE-054** study showed that the **3.5-year DMFS** was **significantly higher for patients receiving pembrolizumab** (65.3%) versus placebo (49.4%) in the ITT population (*P* <0.0001)[2]

- These analyses suggest an **unmet clinical need with high metastasis rates** even with effective adjuvant melanoma therapy

KEYNOTE-054: DMFS

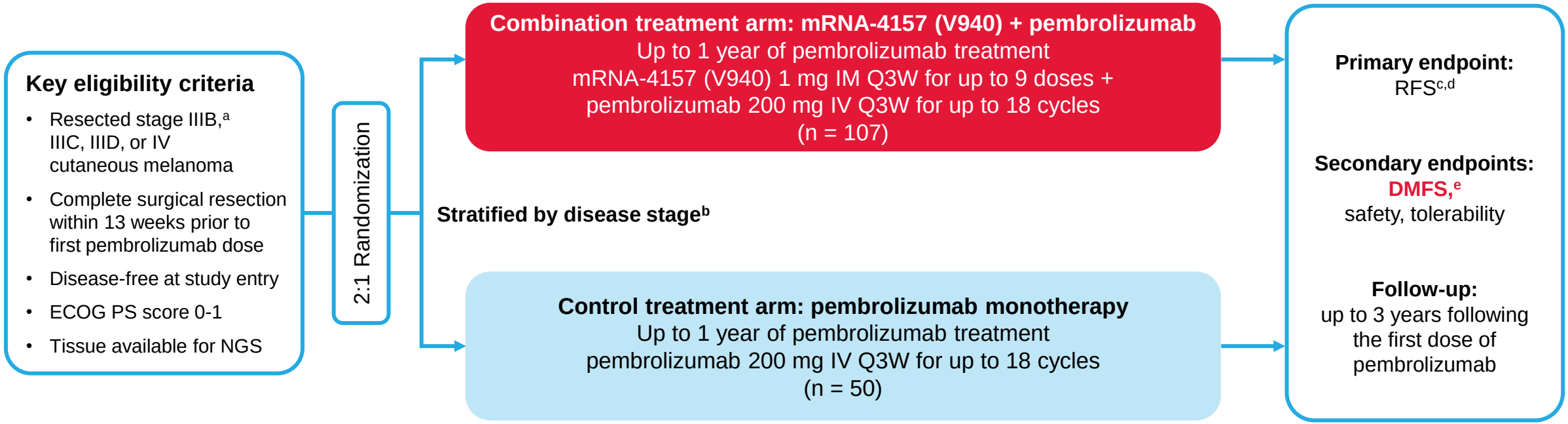


Reprinted from *Lancet Oncology,* Volume No. 22, Eggermont AMM, et al, Adjuvant pembrolizumab versus placebo in resected stage III melanoma (EORTC 1325-MG/KEYNOTE-054): distant metastasis-free survival results from a double-blind, randomised, controlled, phase 3 trial, Pages No. 643–654, Copyright 2021, with permission from Elsevier.

1. Amabile S, et al. *J Clin Med*. 2021;10:5475. 2. Eggermont AMM, et al. *Lancet Oncol.* 2021.22:643-654. 3. Khattak A, et al. Presented at the American Association for Cancer Research® (AACR) Annual Meeting; April 14-19, 2023; Orlando, FL, USA. Oral presentation CT001.

mRNA-4157-P201/KEYNOTE-942 (NCT03897881) Study Design

Randomized, phase 2, open-label study in adjuvant resected melanoma patients at high risk of recurrence

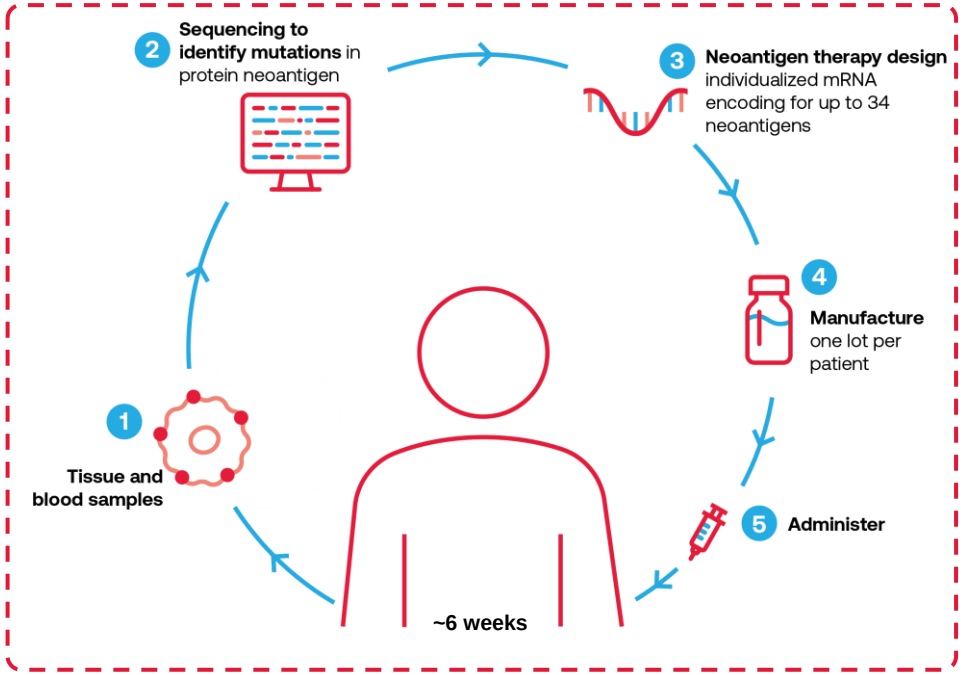


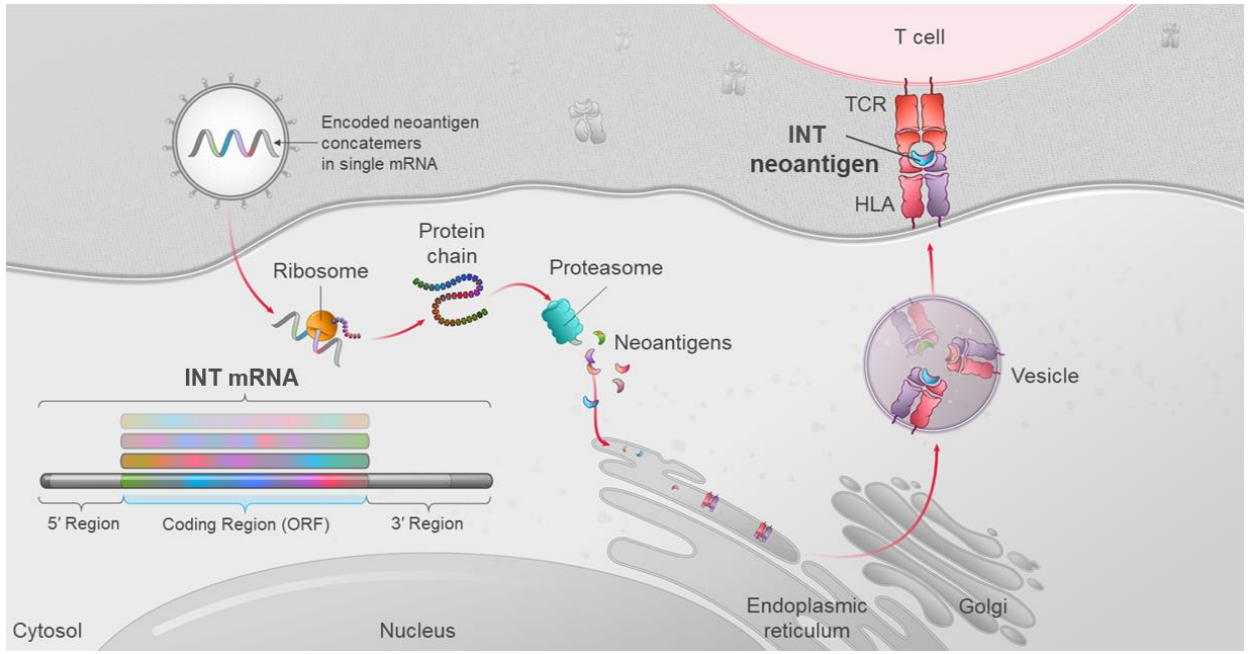
Designed with 80% power to detect an HR of 0.5 with ≥40 RFS events (with a 1-sided alpha of 0.1)
DMFS analysis was prespecified for testing following positive RFS in the ITT population[f]
Median follow-up[g]: 23 months for mRNA-4157 (V940) + pembrolizumab
24 months for pembrolizumab monotherapy

[a]Patients with stage IIIB disease were eligible only if relapse occurred within 3 months of prior surgery of curative intent. [b]According to the 8th edition of the American Joint Committee on Cancer Staging Manual. [c]The primary endpoint was investigator-assessed RFS (defined as the time from first dose of pembrolizumab until the date of first recurrence [local, regional, or distant metastasis], a new primary melanoma, or death from any cause) in the intention-to-treat population. [d]The primary analysis for RFS was specified to occur after all patients completed ≥12 months on study and ≥40 RFS events were observed. Descriptive analysis was specified to occur when ≥51 RFS events were observed. [e]Investigator-assessed DMFS was defined as the time from first dose of pembrolizumab until the date of first distant recurrence or death from any cause. [f]The stratified log-rank test was used for comparison. [g]Time of database cutoff was November 14, 2022.

mRNA-4157 (V940) Mechanism of Action

- mRNA-4157 (V940) is **an individualized neoantigen therapy** designed to target an individual patient's unique tumor mutations and encodes up to 34 neoantigens[1,2]
- Therapies targeting neoantigens can increase endogenous **neoantigen T-cell responses and induce epitope spreading** to novel antigens with the ability **to drive antitumor responses** and **maintain memory** with cytolytic properties, potentially **producing long-term disease control** for patients[3-7]





HLA, human leukocyte antigen; INT, individualized neoantigen therapy; ORF, open reading frame.

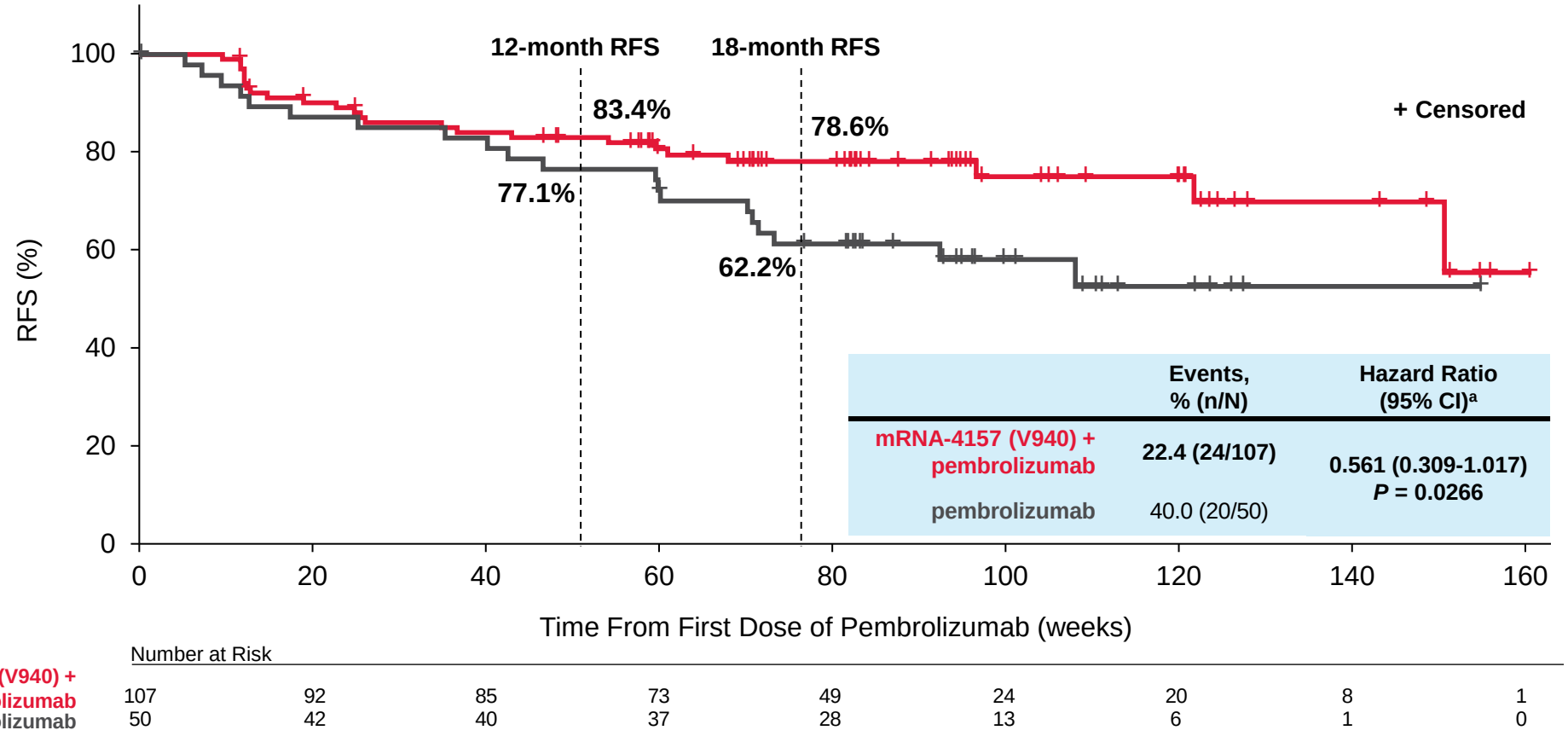
1. Burris HA, et al. *J Clin Oncol*. 2019;37(suppl 15). Abstract 2523. 2. Zhong S, et al. *Cancer Res*. 80(suppl 16). Abstract 6539. 3. Wirth TC, Kühnel F. *Front Immunol.* 2017;8:1848. 4. Ott PA, et al. *Nature*. 2017;547:217-221. 5. Hu Z, et al. *Nat Med.* 2021;27:515-525. 6. Ott PA, et al. *Cell*. 2020;183:347-362. 7. Palmer CD, et al. *Nat Med*. 2022;28:1619-1629.

mRNA-4157-P201/KEYNOTE-942 Patient Demographics

Characteristic, n (%)	mRNA-4157 (V940) + pembro (n = 107)	Pembro (n = 50)
Sex		
Male	70 (65.4)	31 (62.0)
Female	37 (34.6)	19 (38.0)
Age, years		
Mean (SD)	61.3 (13.50)	59.4 (14.25)
Range (median)	63 (26-83)	61.5 (24-89)
Age group		
<65 years	59 (55.1)	28 (56.0)
≥65 years	48 (44.9)	22 (44.0)
ECOG PS score[a]		
0	90 (84.1)	40 (80.0)
1	15 (14.0)	9 (18.0)
Stage[b]		
Stage IIIC	89 (83.2)	42 (84.0)
Stage IIID	2 (1.9)	2 (4.0)
Stage IV	16 (15.0)	6 (12.0)
LDH, U/L		
Median (range)	189.5 (118-528)	185.5 (113-1180)
>ULN	5 (4.7)	3 (6.0)
Lymph node dissection	34 (31.8)	15 (30.0)
PD-L1 status		
Positive	69 (64.5)	27 (54.0)
Negative	13 (12.1)	5 (10.0)
Indeterminant[c]	25 (23.4)	18 (36.0)
***BRAF*[d]**		
V600K or V600E mutation	41 (38.3)	20 (40.0)
WT[e]	66 (61.7)	30 (60.0)
Tumor mutational burden[f]		
<10 mutations/Mb	26 (24.3)	19 (38.0)
≥10 mutations/Mb	79 (73.8)	30 (60.0)

[a]Three patients were not treated and therefore, had no baseline ECOG PS. [b]According to the 8th edition of the American Joint Committee on Cancer staging manual. [c]Patients for whom there was no sample to send for PD-L1 evaluation or for whom sample quality or quantity was too low to perform the assay. [d]*BRAF* status determined by WES on baseline tumor samples. [e]WT refers to position 600 on BRAF gene. [f]Available for 154 patients. WES, whole exome sequencing; WT, wild type.

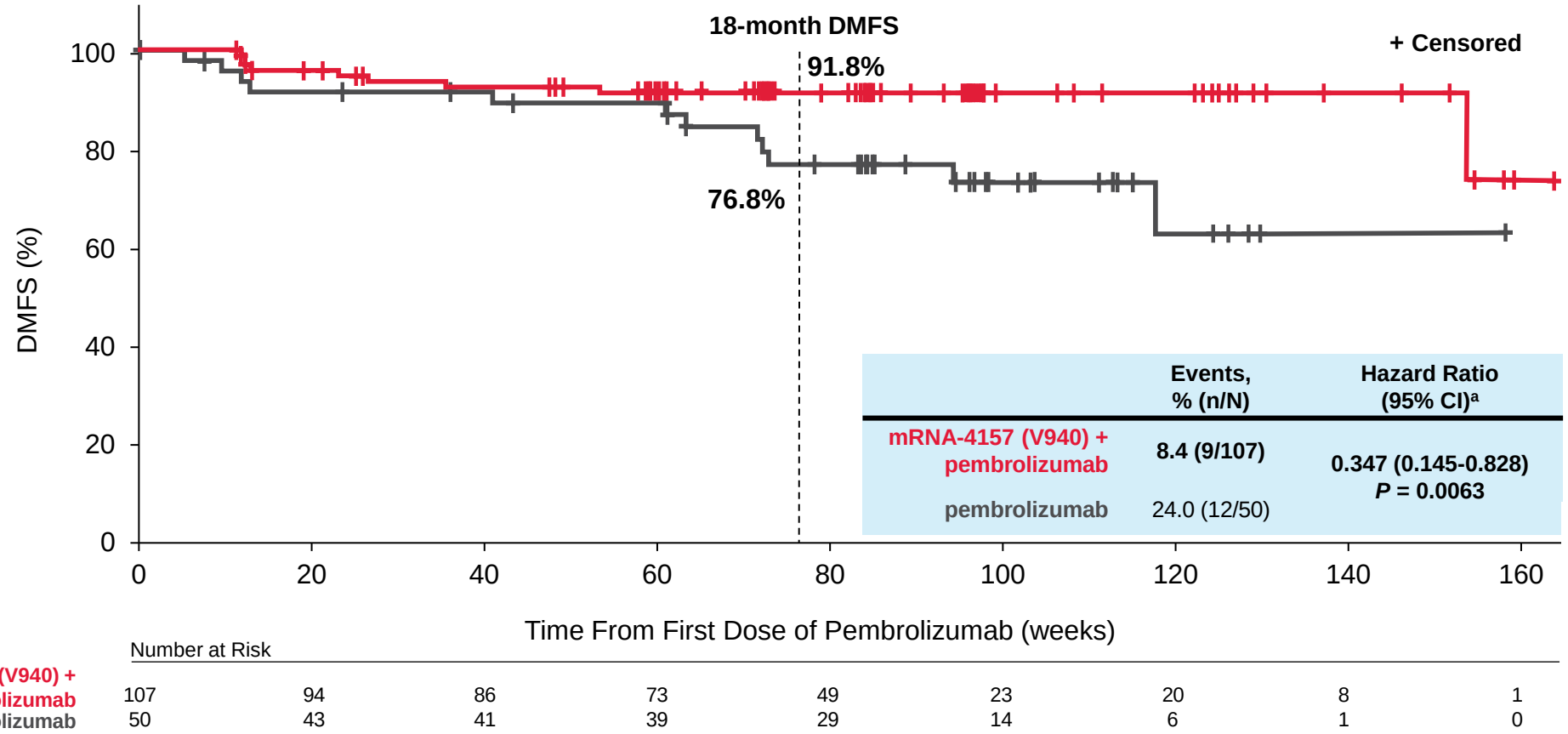
Primary Efficacy Endpoint: RFS[1]



[a]The hazard ratio and 95% CI for mRNA-4157 (V940) plus pembrolizumab versus pembrolizumab is estimated using a Cox proportional hazards model with treatment group as a covariate, stratified by disease stage (stages IIIB or IIIC or IIID vs stage IV) used for randomization. The *P* value is based on a 1-sided log-rank test stratified by disease stage (stages IIIB or IIIC or IIID vs stage IV) used for randomization.

1. Khattak A, et al. Presented at the American Association for Cancer Research® (AACR) Annual Meeting; April 14-19, 2023; Orlando, FL, USA. Oral presentation CT001.

Secondary Efficacy Endpoint: DMFS

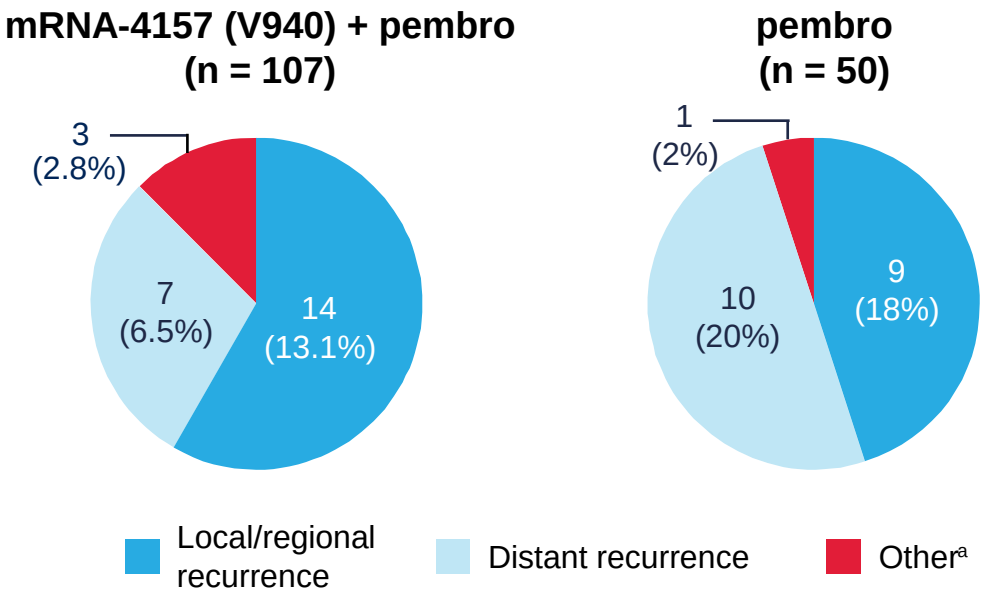


[a]The hazard ratio and 95% CI for mRNA-4157 (V940) plus pembrolizumab versus pembrolizumab is estimated using a Cox proportional hazards model with treatment group as a covariate, stratified by disease stage (stages IIIB or IIIC or IIID vs stage IV) used for randomization. The *P* value is based on a 1-sided log-rank test stratified by disease stage (stages IIIB or IIIC or IIID vs stage IV) used for randomization. At 18-months, the estimated DMFS rates were 91.8% (95% CI, 84.2-95.8) versus 76.8% (95% CI, 61.0-86.8) in the combination and monotherapy arm, respectively.

Recurrence Type and Distant Recurrence Location

24/107 (22.4%) patients in the mRNA-4157 (V940) + pembro arm versus 20/50 (40.0%) in the pembro monotherapy arm experienced an RFS event

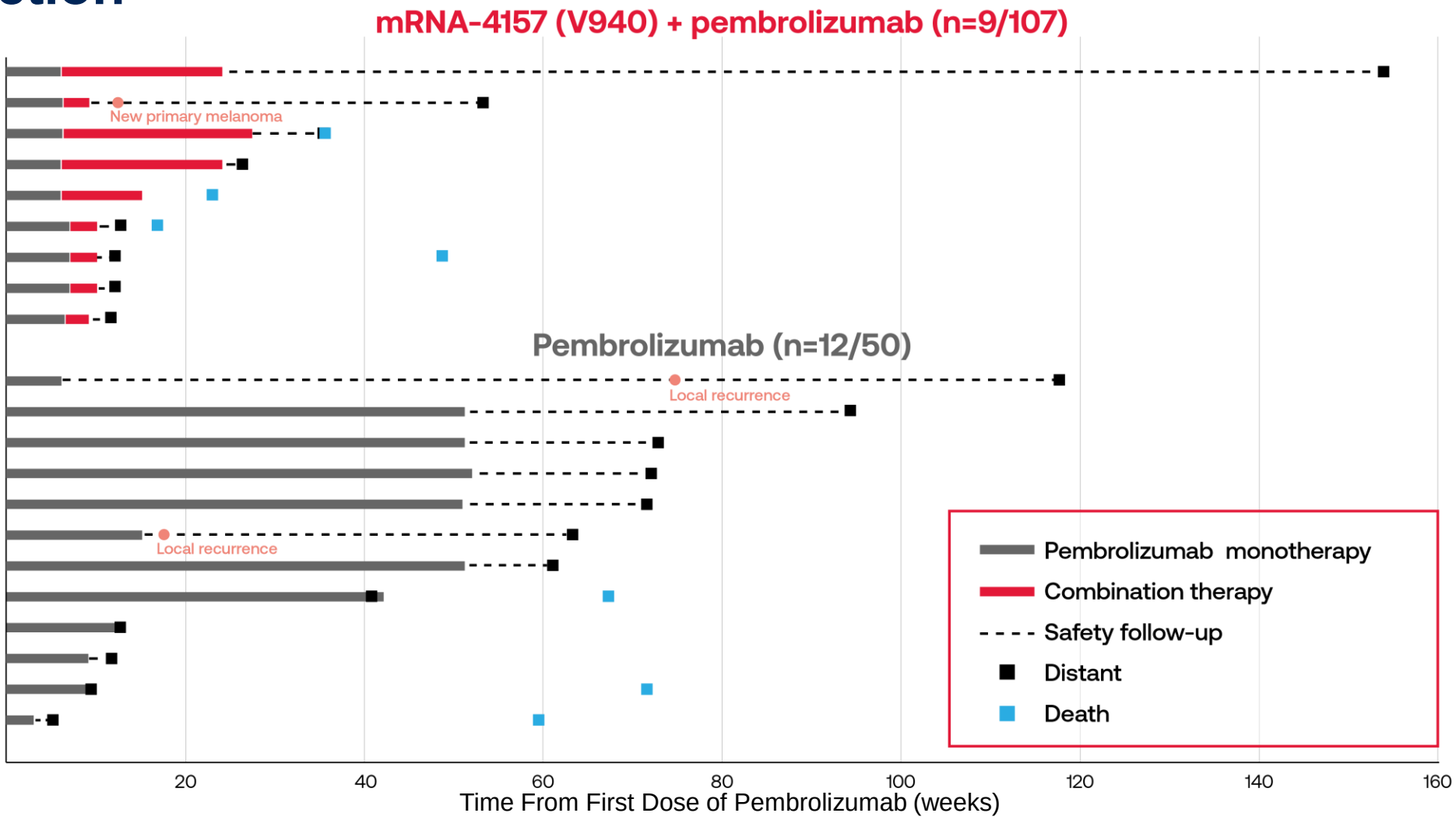
Type of RFS Event



	mRNA-4157 (V940) + pembro (n = 107)	pembro (n = 50)
Patients with distant recurrence (with or without prior recurrence) or death, n (%)	**9 (8.4)**	**12 (24.0)**
Site of distant recurrence, n (%)		
Lymph node	2 (1.9)	4 (8.0)
Lung	2 (1.9)	4 (8.0)
Liver	3 (2.8)	1 (2.0)
Bone	1 (0.9)	2 (4.0)
Brain	1 (0.9)	3 (6.0)
Skin	0	4 (8.0)
Colon	1 (0.9)	1 (2.0)
Spleen	0	1 (2.0)
Soft tissue	1 (0.9)	0
Other site	2 (1.9)	1 (2.0)
Death not due to melanoma	1 (0.9)[b]	0

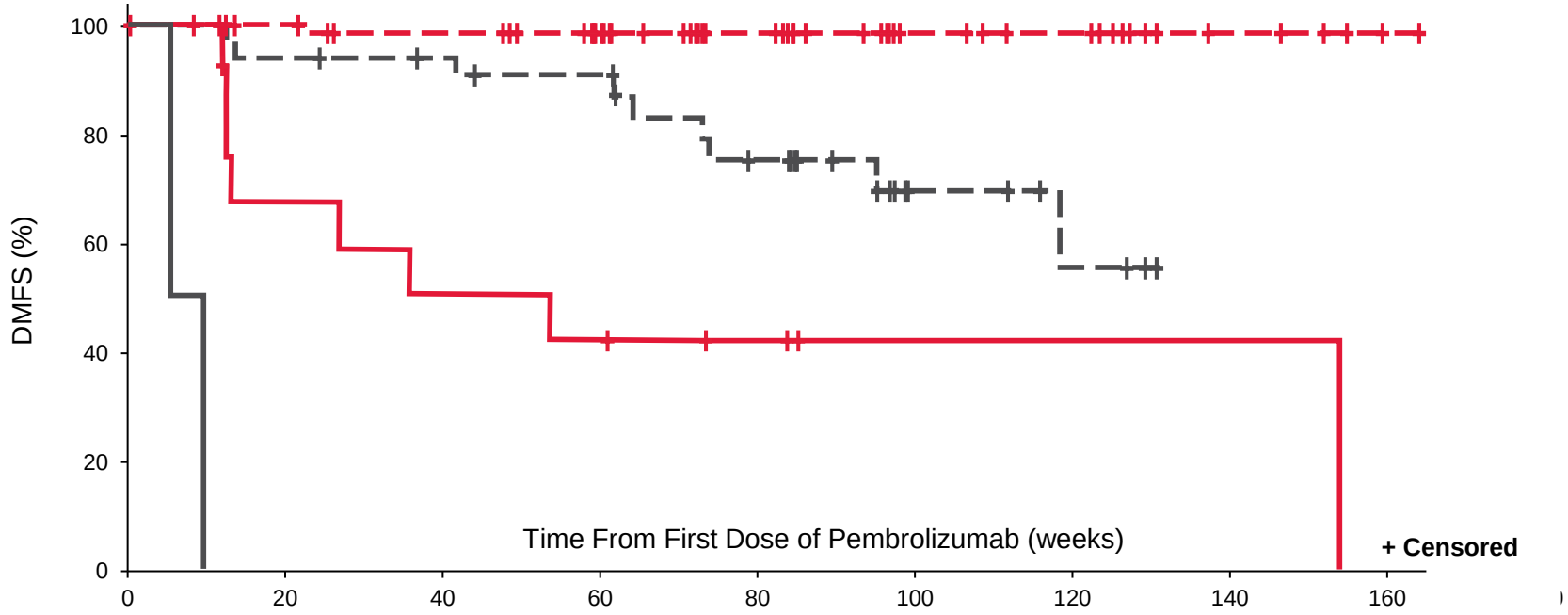
[a]Other: new primary cutaneous melanoma or death (n = 1). [b]Death from sepsis, unrelated to mRNA-4157 (V940) or pembro.

Longitudinal Pattern of DMFS Events During and After Treatment Completion



Reasons for death were disease progression (n = 2), unrelated AE (n = 1, without distant recurrence, from sepsis), and unknown (n = 1) in the mRNA-4157 (V940) + pembrolizumab arm and disease progression (n = 3) in the pembrolizumab monotherapy arm.

DMFS by ctDNA Status at Baseline



Number at Risk

ctDNA-neg: mRNA−4157 (V940) + pembrolizumab	77	73	69	57	38	18	15	6	1
ctDNA-neg: pembrolizumab	33	30	28	26	18	7	4	0	0
ctDNA-pos: mRNA−4157 (V940) + pembrolizumab	13	8	6	5	3	1	1	1	0
ctDNA-pos: pembrolizumab	2	0	0	0	0	0	0	0	0

	mRNA-4157 (V940) + pembro vs pembro HR (95% CI)[a]	mRNA-4157 (V940) + pembro Events, % (n/N)	pembro Events, % (n/N)
ctDNA-neg	0.048 (0.006, 0.380)	1.3 (1/77)	27.3 (9/33)
ctDNA-pos	NE	61.5 (8/13)	100 (2/2)

See LBA9515 presented by Matteo S. Carlino on 03Jun

Minimal residual disease by circulating tumor DNA as a biomarker of recurrence free survival in resected high-risk melanoma patients treated with mRNA-4157 (V940), a personalized cancer vaccine, and pembrolizumab.

ctDNA was NE at baseline for 20.4% (32/157) patients from this study due to unavailability of the sample at baseline (mRNA-4157 (V940) + pembrolizumab, n = 15; pembrolizumab monotherapy, n = 14) or insufficient number of RaDaR® variants identified by WES (quality control flag: mRNA-4157 (V940) + pembrolizumab, n = 2; pembrolizumab monotherapy, n = 1). Results limited by small sample size and event number. ctDNA, circulating tumor DNA.

mRNA-4157-P201/KEYNOTE-942 Safety and Tolerability[1]

	mRNA-4157 (V940) + pembro (n = 104)		pembro (n = 50)	
Event, n (%)	**Any grade**	**Grade ≥3**	**Any grade**	**Grade ≥3**
Any AE	104 (100.0)	36 (34.6)	47 (94.0)	18 (36.0)
Any treatment-related AE	104 (100.0)	26 (25.0)	41 (82.0)	9 (18.0)
Serious AE[a]	**15 (14.4)**	**13 (12.5%)**	**5 (10.0)**	**4 (8.0%)**
mRNA-4157 (V940) or combination-related AEs[b] occurring in >20% of patients				
Any	98 (94.2)	**12 (11.5)**	-	-
Fatigue	63 (60.6)	5 (4.8)	-	-
Injection site pain	58 (55.8)	0	-	-
Chills	52 (50.0)	0	-	-
Pyrexia	50 (48.1)	1 (1.0)	-	-
Headache	33 (31.7)	0	-	-
Injection site erythema	33 (31.7)	0	-	-
Influenza-like illness	32 (30.8)	0	-	-
Nausea	26 (25.0)	0	-	-
Myalgia	22 (21.2)	1 (1.0)	-	-
Pembro or combination related AEs[c] occurring in >20% of patients				
Any	101 (97.1)	24 (23.1)	41 (82.0)	9 (18.0)
Fatigue	72 (69.2)	6 (5.8)	20 (40.0)	0
Diarrhea	31 (29.8)	2 (1.9)	5 (10.0)	0
Pruritus	30 (28.8)	0	10 (20.0)	0
Nausea	23 (22.1)	0	5 (10.0)	0
Chills	22 (21.2)	0	1 (2.0)	0
Pyrexia	22 (21.2)	0	0	0

Safety analyses were conducted in the safety population, which was defined as all randomly assigned patients who received ≥1 dose of treatment. Grading per National Cancer Institute Common Terminology Criteria for Adverse Events version 5.0. [a]Serious AEs included grade 1 fever, attributed to mRNA-4157 (V940), and grade 3 muscular weakness and grade 3 autoimmune nephritis, attributed to both mRNA-4157 (V940) and pembrolizumab. [b]mRNA-4157 (V940) treatment-related AEs included events attributed by the investigator to mRNA-4157 (V940) alone as well as events attributed to both mRNA-4157 (V940) and pembrolizumab. [c]AEs related to pembrolizumab include events attributed by the investigator to pembrolizumab alone and events attributed to both pembrolizumab and mRNA-4157 (V940)..

1. Khattak A, et al. Presented at the American Association for Cancer Research® (AACR) Annual Meeting; April 14-19, 2023; Orlando, FL, USA. Oral presentation CT001.

mRNA-4157-P201/KEYNOTE-942 Safety and Tolerability

All-cause immune-mediated AEs	mRNA-4157 (V940) + pembro (n = 104)		pembro (n = 50)	
Event, n (%)	**Any grade**	**Grade ≥3[a]**	**Any grade**	**Grade ≥3[b]**
Any	**37 (35.6)**	**11 (10.6)**	**18 (36.0)**	**7 (14.0)**
Adrenal insufficiency	5 (4.8)	4 (3.8)	2 (4.0)	1 (2.0)
Colitis	6 (5.8)	3 (2.9)	2 (4.0)	0
Hepatitis	1 (1.0)	0	1 (2.0)	1 (2.0)
Hyperthyroidism	6 (5.8)	0	3 (6.0)	1 (2.0)
Hypophysitis	1 (1.0)	0	0	0
Hypothyroidism	21 (20.2)	0	8 (16.0)	0
Myositis	0	0	1 (2.0)	1 (2.0)
Nephritis	3 (2.9)	3 (2.9)	1 (2.0)	0
Pancreatitis	0	0	1 (2.0)	1 (2.0)
Pneumonitis	4 (3.8)	1 (1.0)	0	0
Sarcoidosis	0	0	1 (2.0)	0
Severe skin reaction	3 (2.9)	0	1 (2.0)	0
Thyroiditis	0	0	2 (4.0)	1 (2.0)
Type 1 diabetes mellitus	0	0	1 (2.0)	1 (2.0)
Uveitis	1 (1.0)	0	1 (2.0)	0

Safety analyses were conducted in the safety population, which was defined as all randomly assigned patients who received ≥1 dose of treatment. Grading per National Cancer Institute Common Terminology Criteria for Adverse Events version 5.0. [a]Includes grade 4 adrenal insufficiency and colitis (n = 1 each), attributed to pembro only and not mRNA-4157 (V940); no grade 5 events occurred. [b]No grade 4 or 5 events occurred.

Next Steps

- Additional analyses to include **protocol specified RFS with ≥51 events** and **other subpopulation and translational assessments including immunogenicity**
- **Longer follow-up** with mRNA-4157-P201/KEYNOTE-942 to evaluate **durability of the treatment effect**
- **A phase 3 study to confirm these results** will be initiated in patients with high-risk resected melanoma **in 2023**
- Expanded clinical studies to include **additional tumor types**, such as NSCLC

Conclusions

- mRNA-4157 (V940) and pembrolizumab demonstrated a **clinically significant improvement in RFS and DMFS** compared to standard of care pembrolizumab in high-risk resected melanoma, with a **44% reduction in the risk of recurrence or death** and a **65% reduction in the risk of distant metastasis or death** with a median of 2 years of follow-up

- mRNA-4157-P201/KEYNOTE-942 is the **first randomized trial** to **demonstrate improvement** in recurrence-free survival and distant metastasis-free survival with **an individualized neoantigen therapy approach**

- mRNA-4157 (V940) in combination with pembrolizumab was **well-tolerated without an increase in immune-mediated AEs** compared with pembrolizumab monotherapy

- mRNA-4157 (V940) in combination with pembrolizumab received **Breakthrough Therapy Designation** from FDA in February 2023 and **PRIME Designation** from EMA in April 2023

Minimal Residual Disease by Circulating Tumor DNA as a Biomarker of Recurrence-free Survival in Resected High-risk Melanoma Patients Treated With mRNA-4157 (V940), a Personalized Cancer Vaccine, and Pembrolizumab

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[1]Westmead and Blacktown Hospitals, The Melanoma Institute Australia and the University of Sydney, Sydney, Australia; [2]Hollywood Private Hospital, Nedlands, Australia; [3]Edith Cowan University, Perth, Australia; [4]NYU Langone Medical Center, New York, NY, USA; [5]Saint John of God Subiaco Hospital, Subiaco, Australia; [6]Massachusetts General Hospital, Boston, MA, USA; [7]Providence Cancer Institute, Franz Clinic, Portland, OR, USA; [8]California Pacific Medical Center Research Institute, San Francisco, CA, USA; [9]Sarah Cannon Research Institute, Nashville, TN, USA; [10]The Angeles Clinic and Research Institute, Los Angeles, CA, USA; [11]Texas Oncology, Dallas, TX, USA; [12]Lombardi Cancer Center, Washington, DC, USA; [13]UPMC Hillman Cancer Center, Pittsburgh, PA, USA; [14]Orlando Health, Orlando, FL, USA; [15]Moderna, Inc., Cambridge, MA, USA; [16]Melanoma Institute Australia, The University of Sydney, and Royal North Shore and Mater Hospitals, Sydney, Australia.

Objectives and Methods

Objectives

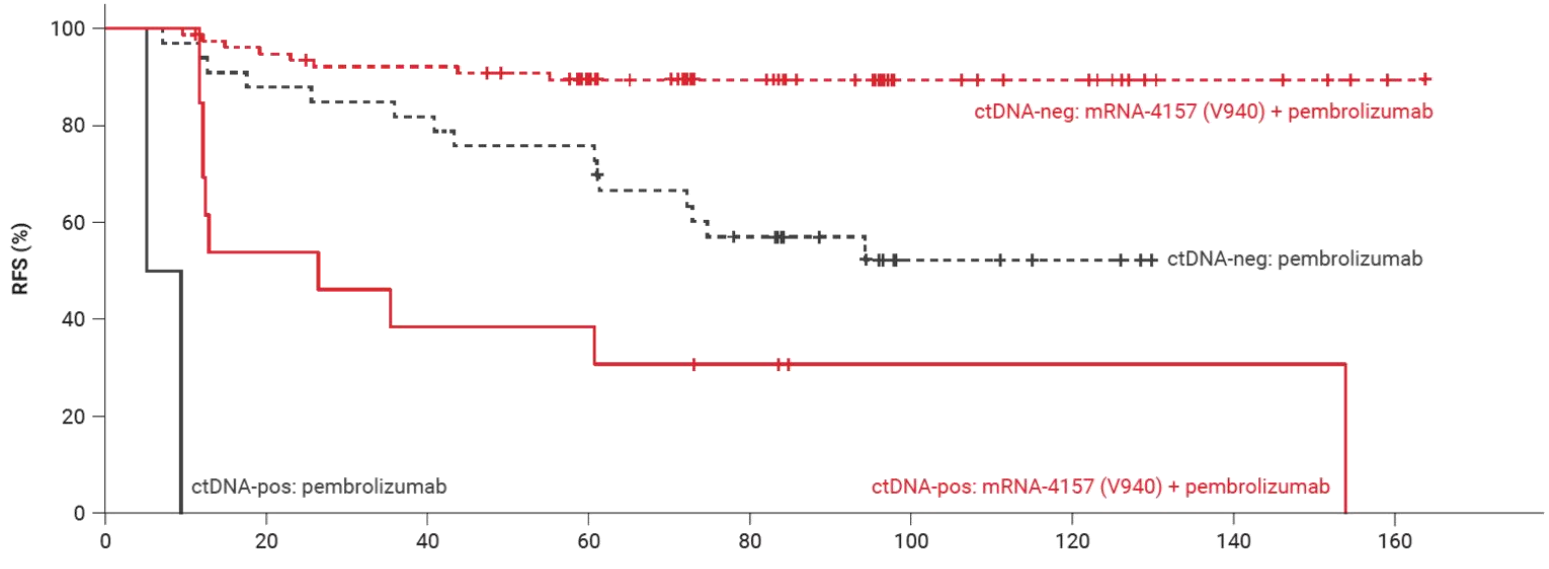
- To assess the distribution of patients with minimal residual disease (MRD) at baseline across study arms
- To assess RFS (the primary study endpoint) in patient subgroups that are ctDNA-positive or ctDNA-negative at baseline
- To assess the prognostic value of ctDNA status at baseline

Methods

- ctDNA was assessed on baseline plasma samples using the personalized amplicon-based NGS NeoGenomics (RaDaR®) assay
  - Tumor core biopsies and matched whole blood samples were subjected to whole exome sequencing (WES) to identify up to 48 patient-specific somatic variants most suitable for MRD detection
  - ctDNA was not evaluable at baseline for 20.4% (32/157) of patients from this study due to unavailability of plasma sample at baseline or insufficient number of RaDaR® variants identified in WES data
- Tumor biomarker assessments were conducted on formalin-fixed paraffin-embedded tumor core biopsies as previously described[13]
- Association of ctDNA and tumor biomarkers with the primary study endpoint RFS were evaluated with Kaplan-Meier analyses and HR with 95% CI based on an unstratified Cox proportional hazards model
- The prognostic value of ctDNA and tumor biomarkers with respect to RFS was assessed by HRs (95% CIs) comparing ctDNA and biomarker subgroups, pooled from both treatment arms, and obtained from an unstratified Cox proportional hazards model that included biomarker group as a covariate

ctDNA, circulating tumor DNA; NGS, next-generation sequencing; RFS, recurrence-free survival. For references see ASCO 2023 poster 511b, Abstract #LBA9515.

The combination of mRNA-4157 (V940) + pembrolizumab improved RFS in ctDNA-negative patients at baseline compared to pembrolizumab monotherapy



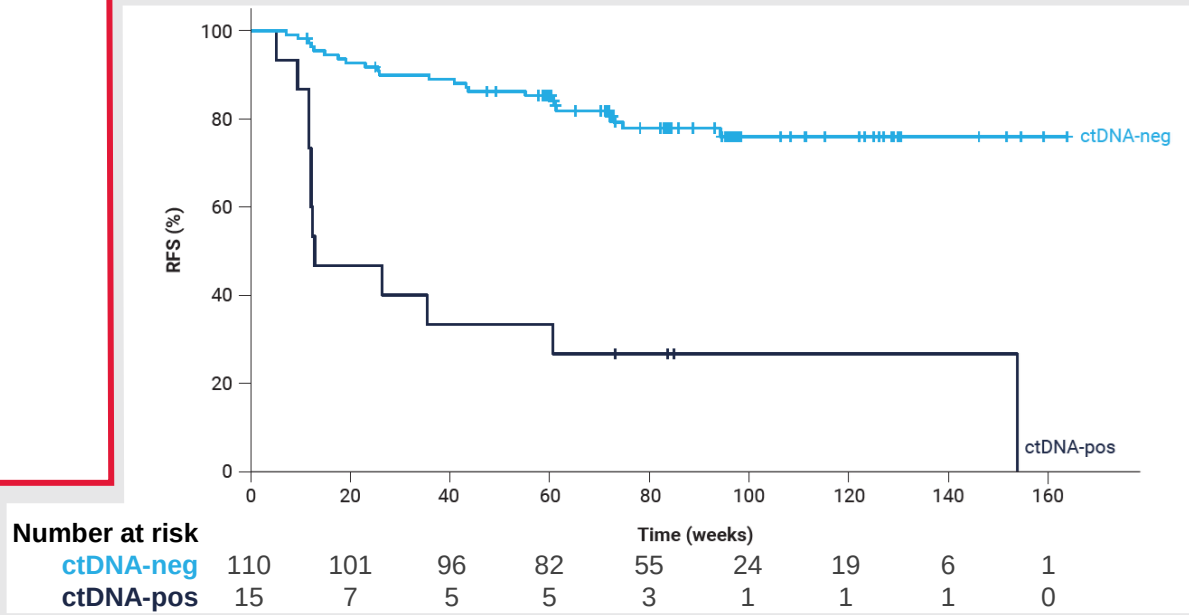
Number at risk									
ctDNA-neg: mRNA (V940) + pembrolizumab	77	72	69	57	38	18	15	6	1
ctDNA-neg: pembrolizumab	33	29	27	25	17	6	4	0	0
ctDNA-pos: mRNA (V940) + pembrolizumab	13	7	5	5	3	1	1	1	0
ctDNA-pos: pembrolizumab	2	0	0	0	0	0	0	0	0

	mRNA-4157 (V940) + pembrolizumab vs pembrolizumab HR (95% CI)	mRNA-4157 (V940) + pembrolizumab Events, n/N (%)	pembrolizumab Events, n/N (%)
ctDNA-pos	NE	10/13 (76.9)	2/2 (100)
ctDNA-neg	0.225 (0.095, 0.531)	8/77 (10.4)	15/33 (45.5)

ctDNA, circulating tumor DNA; NE, non-evaluable; neg, negative; pos, positive.

Assessments of the association of various biomarkers with RFS across study arms suggested that ctDNA status at baseline had notable negative prognostic value

Distribution of ctDNA-positive and ctDNA-negative Patients Across Study Arms			
ctDNA, n (%)	mRNA-4157 (V940) + pembrolizumab (n = 90)	Pembrolizumab (n = 35)	Total (n = 125)
Positive	13 (14.4)	2 (5.7)	**15 (12.0)**
Negative	77 (85.6)	33 (94.3)	**110 (88.0)**



RFS HR (95% CI) Comparing Biomarker Subgroups in the Biomarker-evaluable Population			
ctDNA-neg vs ctDNA-pos	TMB-high vs TMB–non-high	TIS-high vs TIS-low	PD-L1–pos vs PD-L1–neg
0.149 (0.073, 0.306) n (110 vs 15)	0.476 (0.263, 0.862) n (109 vs 45)	0.452 (0.242, 0.844) n (77 vs 77)	0.661 (0.299, 1.46) n (96 vs 18)

CI, confidence interval; ctDNA, circulating tumor DNA; HR, hazard ratio; neg, negative; PD-L1, programmed death ligand-1; pos, positive; RFS, recurrence-free survival; TIS, tumor inflammation signature; TMB, tumor mutational burden.

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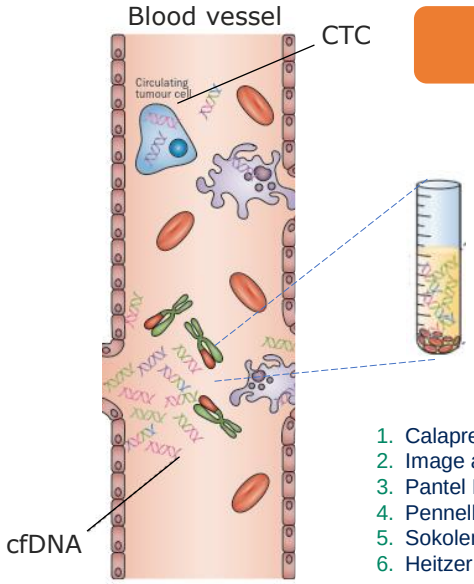
THANK YOU

Appendix

ctDNA in Cancer Detection

What Is ctDNA and How is it Collected?

- Tumor-derived circulating DNA (ctDNA) are cell free short nucleic fragments released by tumor cell apoptosis and/or necrosis[1]
- ctDNA in the blood may be obtained by a minimally invasive liquid biopsy[2,3]



LIQUID BIOPSY

Specimens	Analytes
Plasma	ctDNA

1. Calapre L et al. *Cancer Lett*. 2017 Sep 28;404:62-69.
2. Image adapted from Crowley E et al. *Nat Rev Clin Oncol*. 2013 Aug;10:472–484.
3. Pantel K et al. *Nat Rev Clin Oncol*. 2019;16:409–424.
4. Pennell et al., ASCO Educational Book. 2019 Jan;39:531-542
5. Sokolenko et al., *Front Mol Biosci*. 2018 Aug 27;5:76.
6. Heitzer E et al. *NPJ Precis Oncol*. 2017 Oct;1(1):36.

Advantages

- **Minimally invasive** (low risk, low cost)[4]
- No selection bias **can account for tumor heterogeneity** and allows a holistic view on tumor pathology[4]
- Enables **treatment monitoring for tumor evolution** of resistance mutations[5]

Limitations

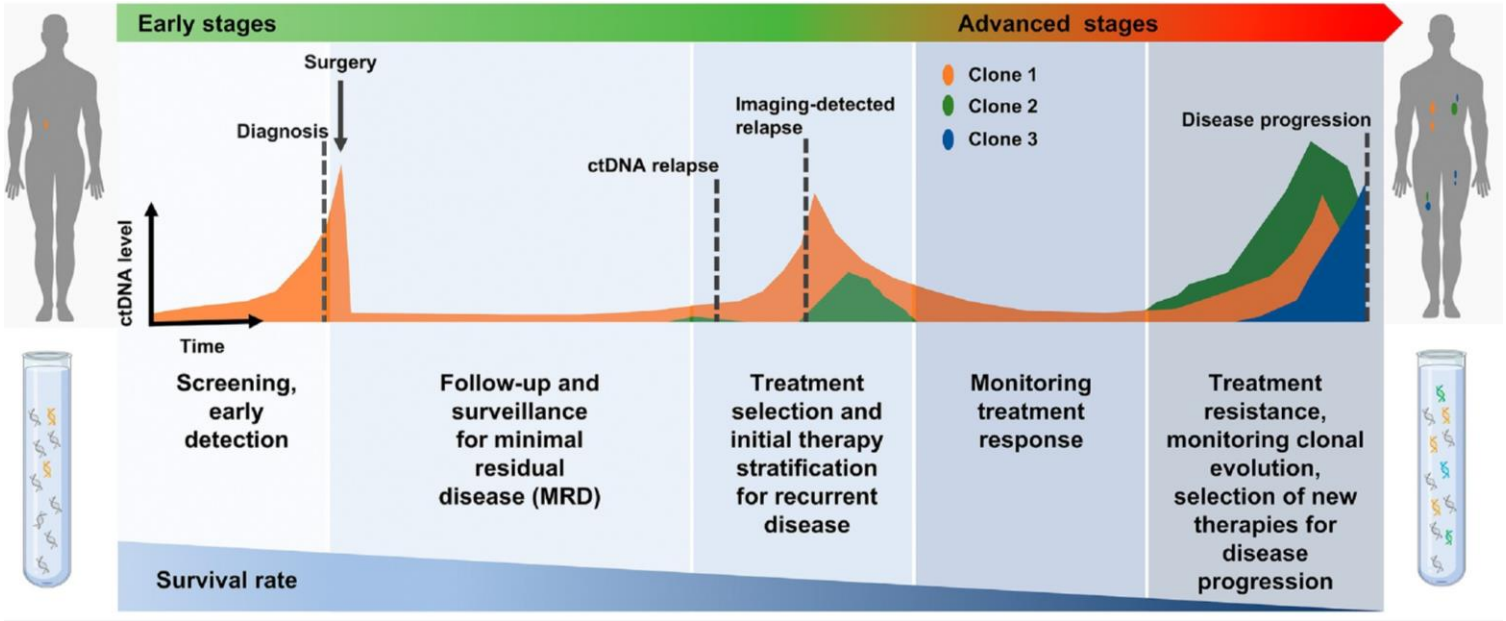
- Sensitivity is **dependent on tumor shedding**[6]
- **No protein IHC or FISH** cytology assays available

CTC, circulating tumor cell; cfDNA, cell-free DNA; ctDNA, circulating tumor DNA; FISH, fluorescent in situ hybridization; IHC, immunohistochemistry

Using ctDNA to Measure Minimal Residual Disease (MRD)

What MRD?

- **Minimal residual disease (MRD)** refers to a small number of malignant cells that remain following primary treatment that are capable of causing recurrent disease[1]
- MRD is a significant **prognostic indicator** that may help predict recurrence[2]



Measuring MRD with ctDNA

- In several solid tumor types, **ctDNA** has proven to be **effective in detecting MRD**[2]
- In early-stage cancer treatment **ctDNA can identify MRD after primary tumor resection**, thus enabling accurate risk assessment and adjuvant therapy[2]
- **ctDNA clearance** may serve as an endpoint to **assess the effectiveness in adjuvant trials** of treatment[2]

1. Dunavoelgyi R et al., *Eye*. 2021; 35:702-704
2. Peng Y et al., *Front Oncol*. 2021; 11: 763790
3. Image from Roy D et al., *Trends Mol Med*. 2021 Oct;27(10):1014-1015