

Supplementary Material S2. Reanalysis of the individual-level survival data published by USDA for Canine Melanoma Vaccine, DNA

S2.1 Data source

The data analysed here are those published by the United States Department of Agriculture, Animal and Plant Health Inspection Service, Center for Veterinary Biologics in *Summary of Studies Supporting USDA Product Licensure: Canine Melanoma Vaccine, DNA*, establishment 124, product code 9240.D0, compiled 16 May 2024. That document reports, for each of the 53 dogs in the efficacy study, the study day of first administration, the survival time in days measured from the date of surgery, and an outcome classification. No other data source was used and no value was imputed.

Two USDA compilations of this study are publicly available and they differ in one value. The melanoma-attributable survival time of dog 12158 is given as 320 days in the 2024 compilation used here and as 90 days in the Merial compilation of 13 January 2020. The 2024 compilation was adopted because it gives per-dog identifiers, which allows each record to be traced.

S2.2 Outcome classifications and event definitions

Two endpoints are analysed. The melanoma-specific endpoint follows the classification USDA applies, under which only death attributed to melanoma is an event. The overall-survival endpoint treats death from any cause as an event; USDA does not report this quantity.

USDA outcome classification	n	Melanoma-specific survival	Overall survival
Died or euthanized for melanoma	13	Event	Event
Died or euthanized, unrelated cause	9	Censored	Event
Alive at end of observation	19	Censored	Censored
Removed from study	7	Censored	Censored
Lost to follow-up	5	Censored	Censored
Total	53	13 events	22 events

Six of the seven dogs removed from study were removed by the owner or the attending veterinarian in order to pursue an alternative treatment for melanoma. Censoring in the melanoma-specific analysis may therefore be informative, as noted in Section 3.2 of the manuscript.

Each endpoint is estimated with two time origins. The first is the date of surgery, as in the analysis USDA reports. The second is the date of first vaccination, which removes the interval a dog had to survive in order to enter the vaccinated cohort. The interval between surgery and first vaccination had a median of 36 days and a range of 0 to 380 days, and five dogs were first vaccinated more than 90 days after surgery.

S2.3 Dataset

Survival time from first vaccination is the survival time from surgery less the study day of first administration. The outcome codes are those of S2.2: **disease**, death attributed to melanoma; **unrel**, death from an unrelated cause; **alive**, alive at the end of observation; **rem**, removed from study; **ltf**, lost to follow-up.

Dog	Study day of first vaccination	Survival from surgery (d)	Survival from first vaccination (d)	USDA outcome
12361	13	435	422	alive
11887	15	723	708	alive
28067	14	476	462	alive
135382	36	332	296	alive
58163	53	475	422	alive
25239	28	528	500	alive
12299	25	426	401	alive
865023	28	679	651	alive
50710	9	380	371	alive
3751	38	437	399	alive
28644	46	442	396	alive
27254	38	481	443	alive

Dog	Study day of first vaccination	Survival from surgery (d)	Survival from first vaccination (d)	USDA outcome
11978	20	685	665	alive
135756	40	314	274	alive
3741	63	633	570	alive
24239	207	736	529	alive
26189	18	455	437	alive
3740	38	625	587	alive
136371	15	267	252	alive
874398	7	235	228	disease
3739	22	100	78	disease
3742	32	52	20	disease
28077	41	464	423	disease
12158	71	320	249	disease
27134	9	475	466	disease
28018	40	199	159	disease
57456	45	177	132	disease
12285	380	583	203	disease
3748	115	181	66	disease
3749	81	290	209	disease
133349	48	293	245	disease
26456	62	165	103	disease
26105	22	550	528	unrel
861225	37	267	230	unrel
860776	41	293	252	unrel
20872	38	470	432	unrel
25403	51	87	36	unrel

Dog	Study day of first vaccination	Survival from surgery (d)	Survival from first vaccination (d)	USDA outcome
12157	26	62	36	unrel
864280	4	307	303	unrel
132409	15	274	259	unrel
27190	107	304	197	unrel
864332	20	62	42	ltf
3746	40	139	99	ltf
3750	47	200	153	ltf
12310	150	557	407	ltf
3747	33	245	212	ltf
857655	0	280	280	rem
11989	61	525	464	rem
3743	35	510	475	rem
28036	36	178	142	rem
58070	13	411	398	rem
102674	29	57	28	rem
3745	14	84	70	rem

S2.4 Results

Endpoint	Time origin	Median	25th percentile
Melanoma-specific survival	Date of surgery	Not reached	464 d
Melanoma-specific survival	Date of first vaccination	Not reached	423 d

Endpoint	Time origin	Median	25th percentile
Overall survival	Date of surgery	550 d (95% CI, 307 d to not reached)	290 d
Overall survival	Date of first vaccination	466 d (95% CI, 259 d to not reached)	230 d

The 25th percentile of 464 days obtained for melanoma-specific survival from the date of surgery reproduces the value USDA reports for this study, which confirms that the reconstruction recovers the analysis USDA performed. The remaining quantities are not reported by USDA.

S2.5 Analysis code

Kaplan-Meier estimates were computed in Python 3.12 with lifelines 0.30 and numpy. The confidence interval for a median is taken as the set of times at which 0.5 lies within the confidence band: the lower bound is the first time at which the lower confidence limit of the survival function reaches 0.5, and the upper bound the first time at which the upper limit does.

```
import csv
import numpy as np
from lifelines import KaplanMeierFitter

rows = list(csv.DictReader(open("S2_ONCEPT_dataset.csv")))
t_surg = np.array([float(r["survival_days_from_surgery"]) for r in rows])
t_vacc = np.array([float(r["survival_days_from_vaccination"]) for r in rows])
e_dis = np.array([int(r["event_melanoma_specific"]) for r in rows])
e_any = np.array([int(r["event_any_cause"]) for r in rows])

for name, event in (("melanoma-specific", e_dis), ("overall", e_any)):
    for origin, time in (("surgery", t_surg), ("first vaccination", t_vacc)):
        f = KaplanMeierFitter()
        f.fit(time, event)
        median = f.median_survival_time_
        ci = f.confidence_interval_
        low = ci[ci.iloc[:, 0] <= 0.5].index.min()
        upp = ci[ci.iloc[:, 1] <= 0.5].index.min()
        print(name, origin, median, low, upp, f.percentile(0.75))
```

Two files accompany this document. `S2_ONCEPT_dataset.csv` contains the dataset of S2.3 in machine-readable form, with the two event indicators already derived. `S2_ONCEPT_reanalysis.py` is the complete script: it holds the transcribed per-dog table, prints the quantities of S2.4, writes the CSV, and regenerates Figure 2 of the manuscript. Running that script reproduces Figure 2 exactly as submitted.