

Quantification of Plasmid DNA Fragments in modRNA Injections

Andrew K. Recknagel

Research Scientist

University of South Carolina, Columbia, SC

HHMI Janelia Research Campus, Ashburn, VA

Cornell University, Ithaca, NY

Cornell University, Ithaca, NY

Cornell University, Ithaca, NY

University at Albany, Albany, NY

Cornell University, Ithaca, NY

Cornell University, Ithaca, NY

The Jackson Laboratory, Bar Harbor, ME

Research Specialist, Cancer Genetics Laboratory

Research Technician, MouseLight Project

Research Support Specialist I, Warden Lab

Research Technician V, Paszek Lab & Warden Lab

Joint Technician IV, Butcher Lab & Fischbach Lab

Teacher's Assistant, Department of Psychology

Research Technician IV, Butcher Lab

Research Technician III, Garcia Lab

Research Assistant, Eicher Lab

PUBLICATIONS

Glaser A, Chandrashekar J, Vasquez S, Arshadi C, Ouellette N, Jiang X, Baka J, Kovacs G, Woodard M, Seshamani S, Cao K, Clack N, Recknagel A, Grim A, Balaram P, Turschak E, Hooper M, Svoboda K (2025) **Expansion-assisted selective plane illumination microscopy for nanoscale imaging of centimeter-scale tissues.** eLife, 12:RP91979

Williams RM, Bloom JC, Robertus CM, Recknagel AK, Putnam D, Schimenti JC, Zipfel WR (2023) **Practical strategies for robust and inexpensive imaging of aqueous-cleared tissues.** J Microsc, 291(3):237-247.

Dean D, Weinstein H, Amin S, Karno B, McAvoy E, Hoy R, Recknagel A, Jarvis C, Deitcher D (2017) **Extending julius seizure, a bang-sensitive gene, as a model for studying epileptogenesis: Cold shock, and a new insertional mutation.** Fly, Dec 8:1-7.

Horne M, Krebsushevski K, Wells A, Tunio N, Jarvis C, Francisco G, Geiss J, Recknagel A, Deitcher DL (2017) **julius seizure, a Drosophila Mutant, Defines a Neuronal Population Underlying Epileptogenesis.** Genetics, 205(3):1261-1269.

Sung DC, Bowen CJ, Vaidya KA, Zhou J, Chapurin N, Recknagel A, Zhou B, Chen J, Kotlikoff M, Butcher JT (2016) **Cadherin-11 Overexpression Induces Extracellular Matrix Remodeling and Calcification in Mature Aortic Valves.** Arteriosclerosis, Thrombosis, and Vascular Biology, 36(8):1627-37.

Gregg CL, Recknagel AK, Butcher JT (2015) **Micro / nano-computed tomography technology for quantitative dynamic, multi-scale imaging of morphogenesis.** Methods in Molecular Biology, 1189:47-61.

Zhou J, Bowen C, Lu G, Knapp IC, Recknagel A, Norris RA, Butcher JT (2013) **Cadherin-11 expression patterns in heart valves associate with key functions during embryonic cushion formation, valve maturation and calcification.** Cells Tissues Organs, 198(4):300-10.

McNay EC, Recknagel AK (2011) **Brain insulin signaling: a key component of cognitive processes and a potential basis for cognitive impairment in type 2 diabetes.** Neurobiology of Learning and Memory, 96:432-442.

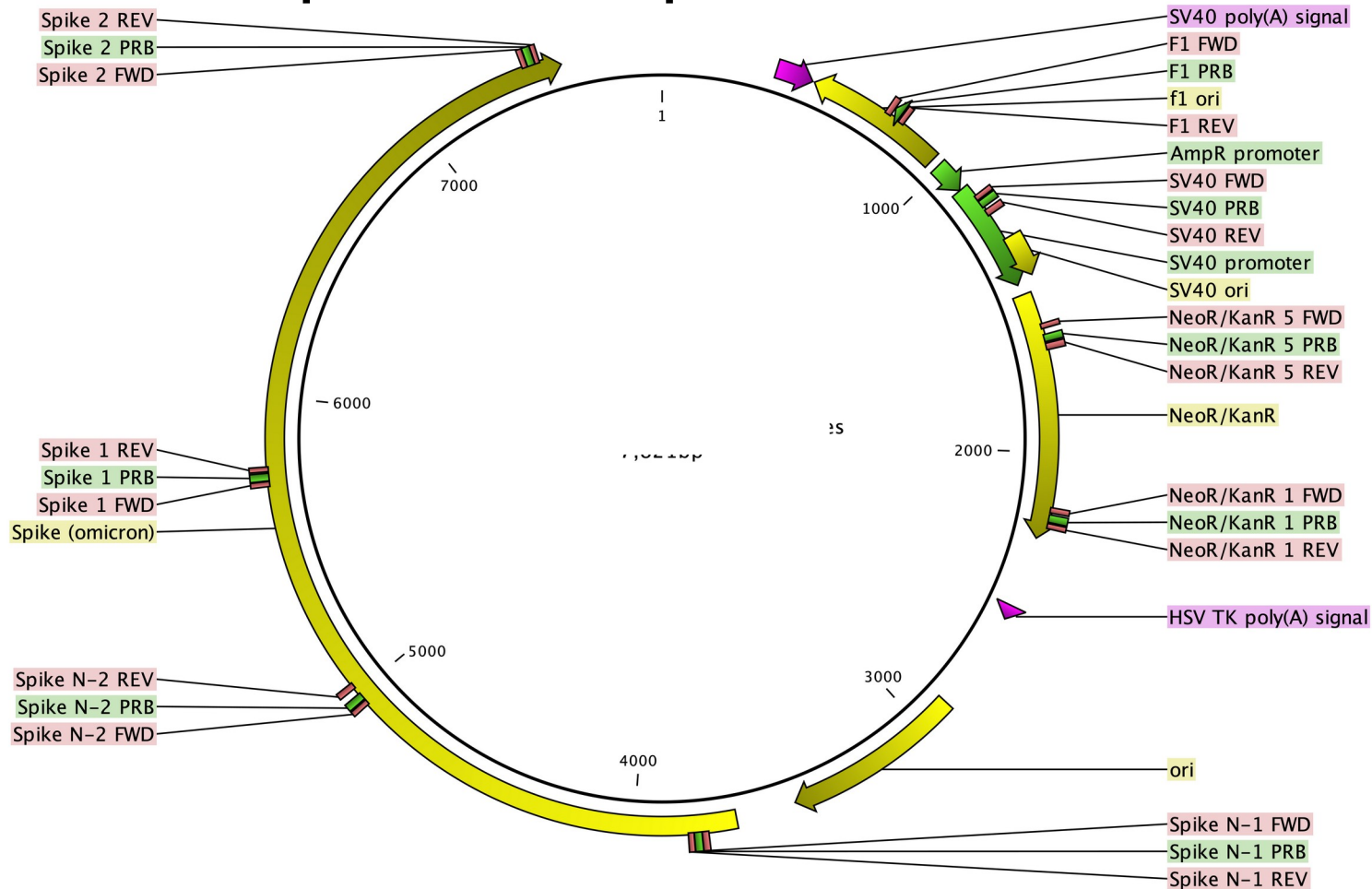
Kim JS, Min J, Recknagel AK, Riccio M, Butcher JT (2011) **Quantitative three-dimensional analysis of embryonic chick morphogenesis via microcomputed tomography.** The Anatomical Record, 294(1):1-10.

Chiu YN, Norris RA, Mahler G, Recknagel A, Butcher JT (2010) **Transforming growth factor β , bone morphogenetic protein, and vascular endothelial growth factor mediate phenotype maturation and tissue remodeling by embryonic valve progenitor cells.** Tissue Engineering Part A, 16(11):3375-83.

Bouma GJ, Albrecht KH, Washburn LL, Recknagel AK, Churchill GA, Eicher EM (2005) **Gonadal sex reversal in mutant Dax1 XY mice: A failure to up-regulate Sox9 in pre-Sertoli cells.** Development, 132(13):3045-3054.

Bouma GJ, Hart GT, Washburn LL, Recknagel AK, Eicher EM (2004) **Using real time RT-PCR analysis to determine multiple gene expression patterns during XX and XY mouse fetal gonad development.** Gene Expression Patterns, 5(1):141-149.

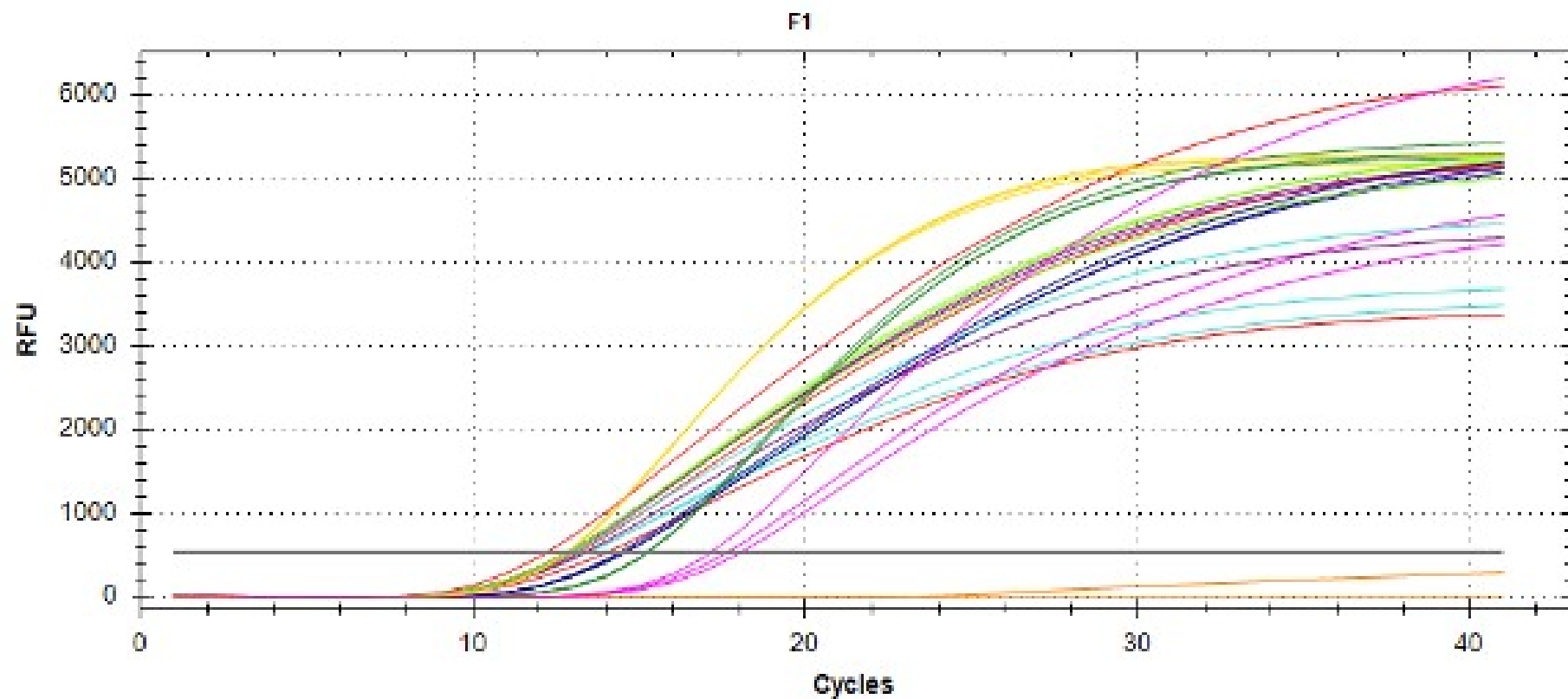
Plasmid sequence map with selected features



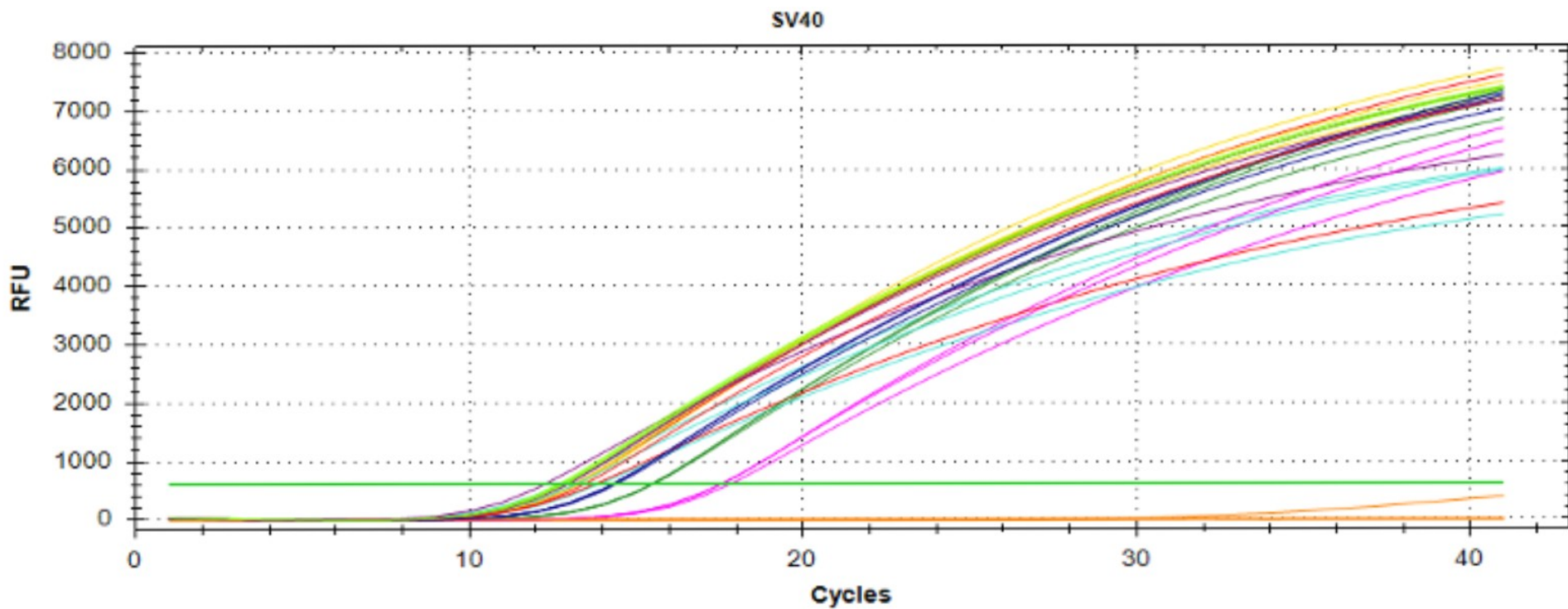
Amplification Color Code Key

Sample	Color
EL9262	Light Blue
EL9264	Red
HF9298	Dark Blue
GK0936	Purple
GK0932	Light Green
LN2588	Yellow
LM2221	Dark Green
gBlock	Magenta
Water	Orange

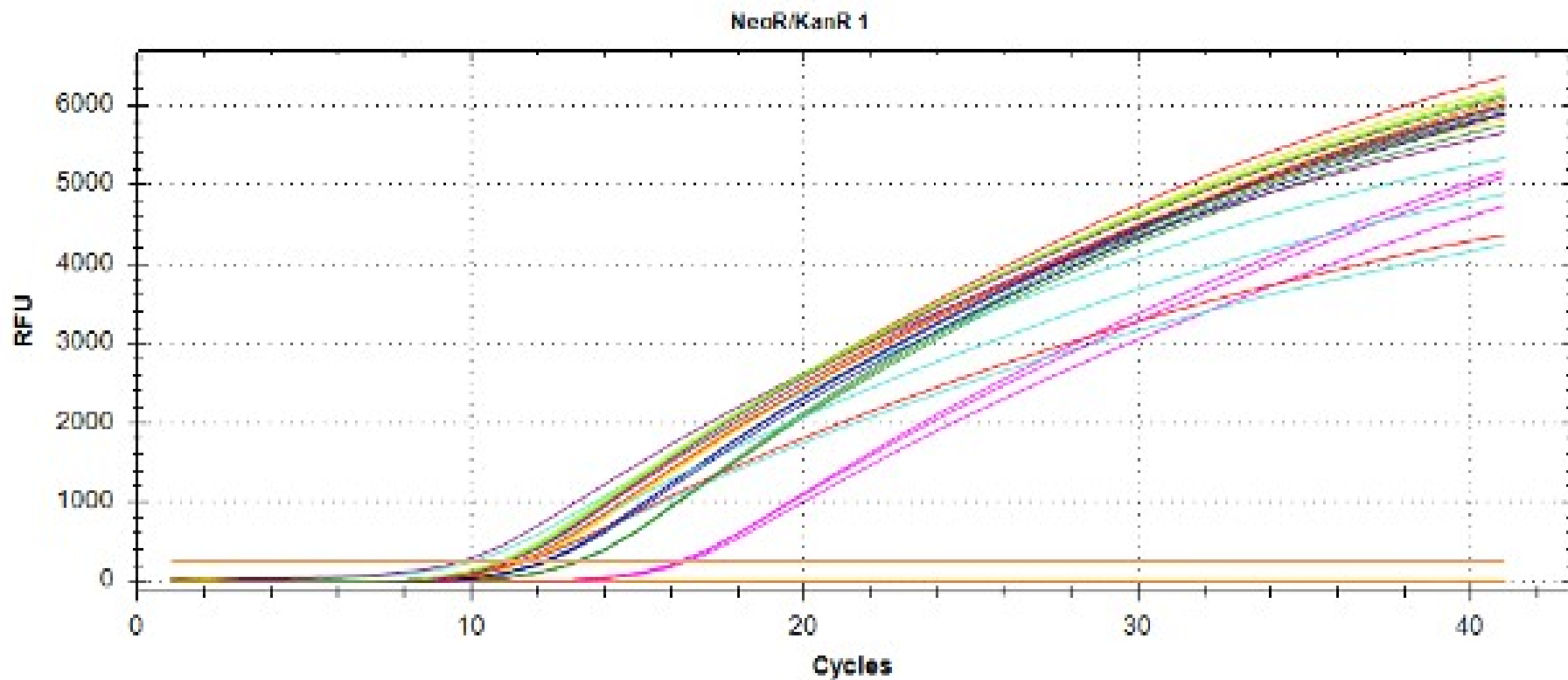
F1



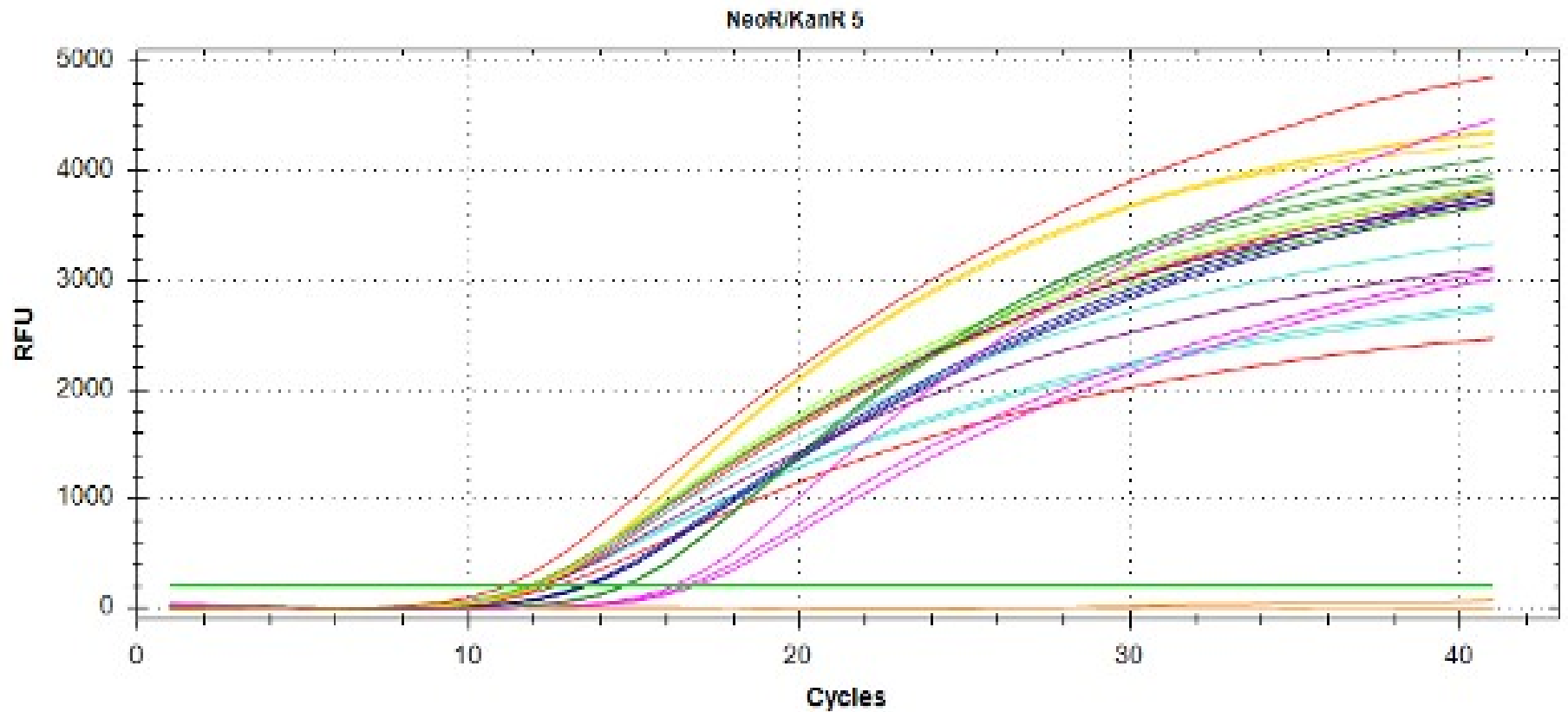
SV40



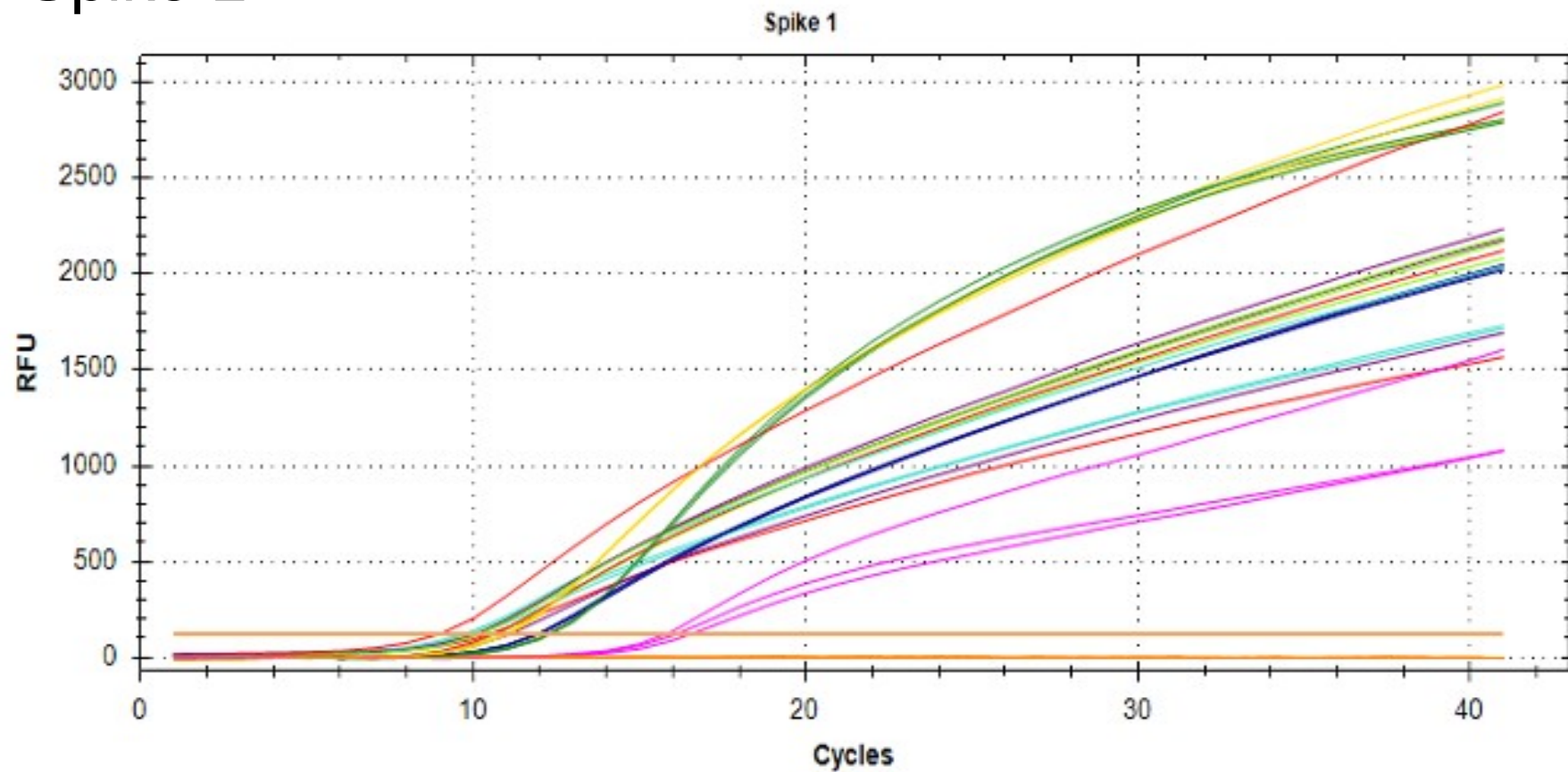
NeoR/KanR 1



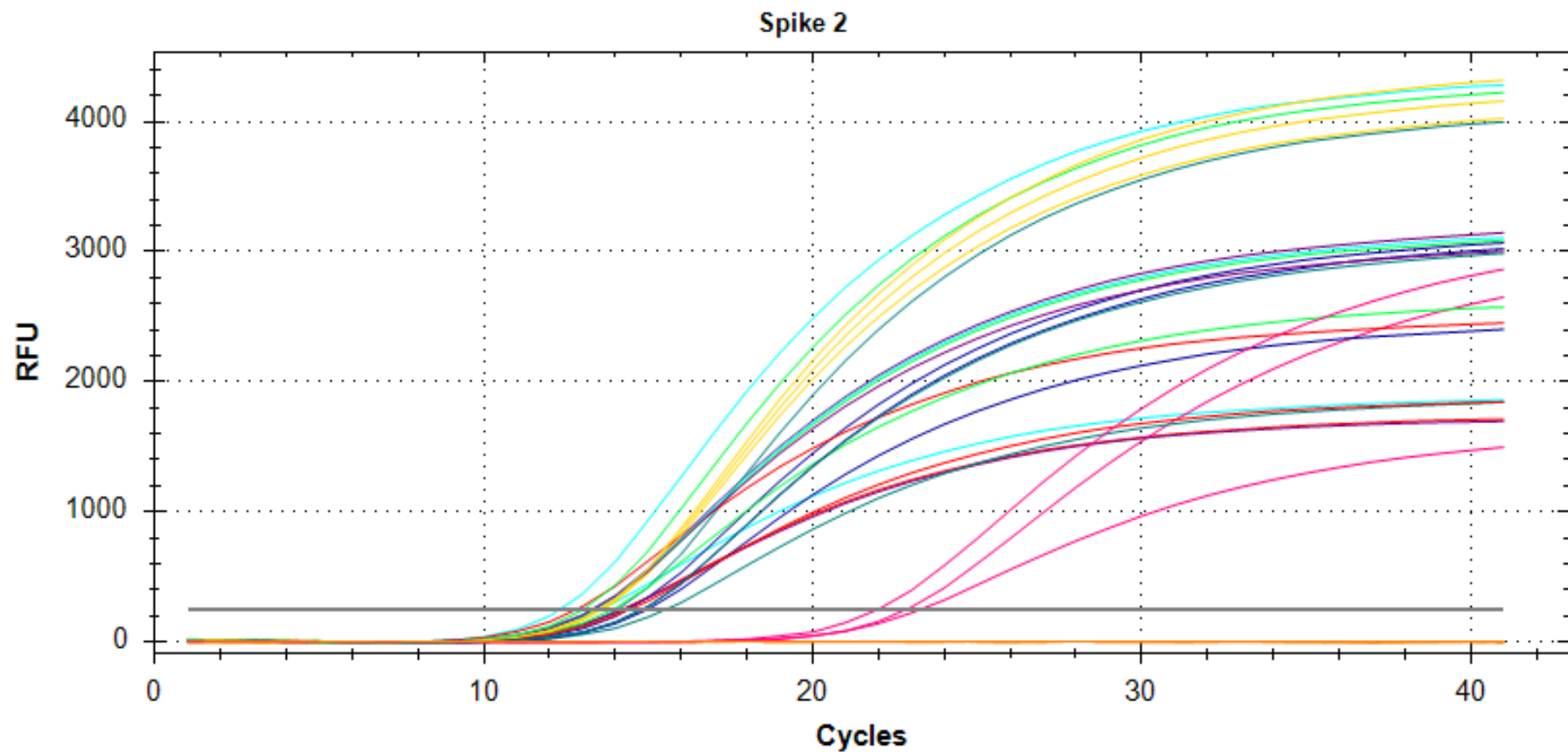
NeoR/KanR 5



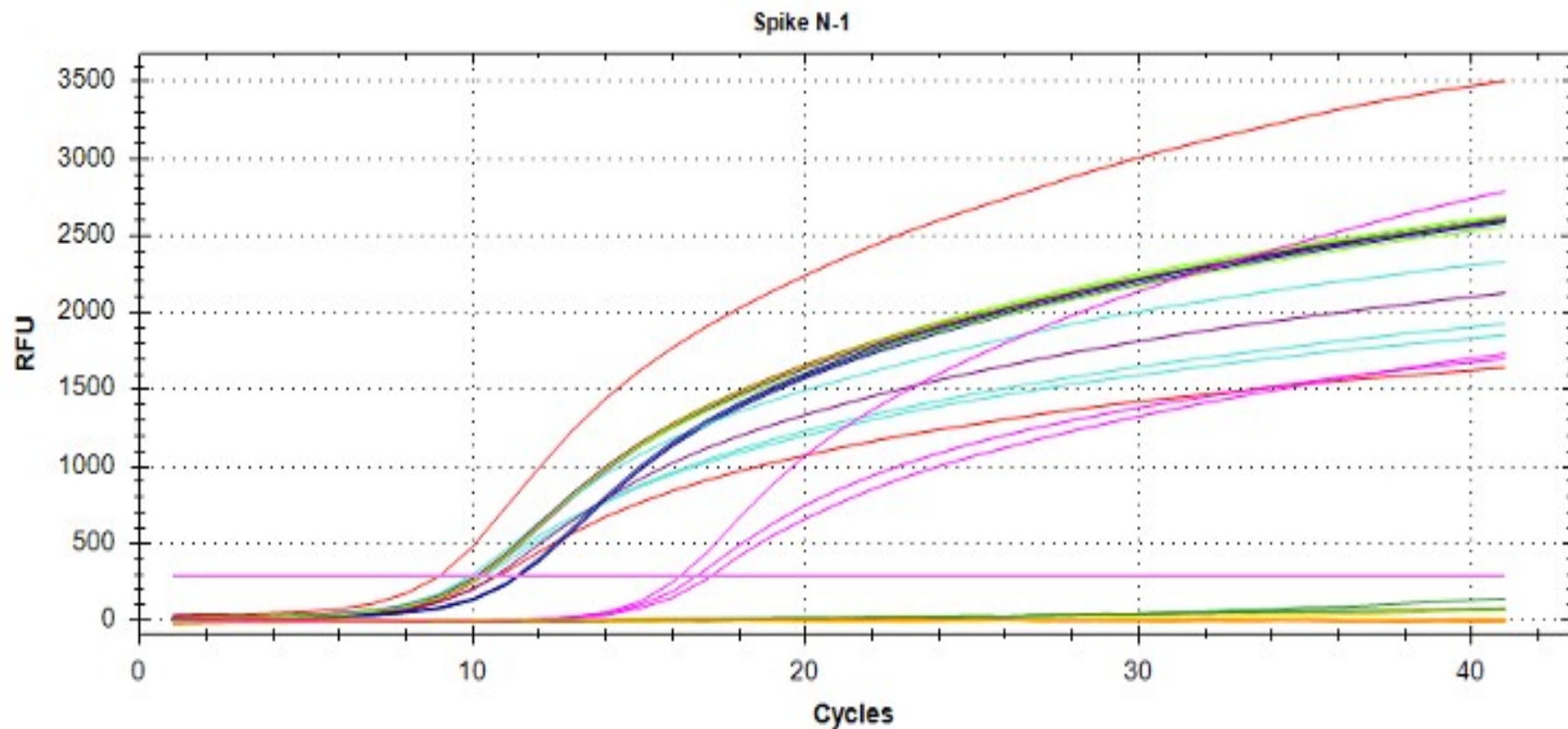
Spike 1



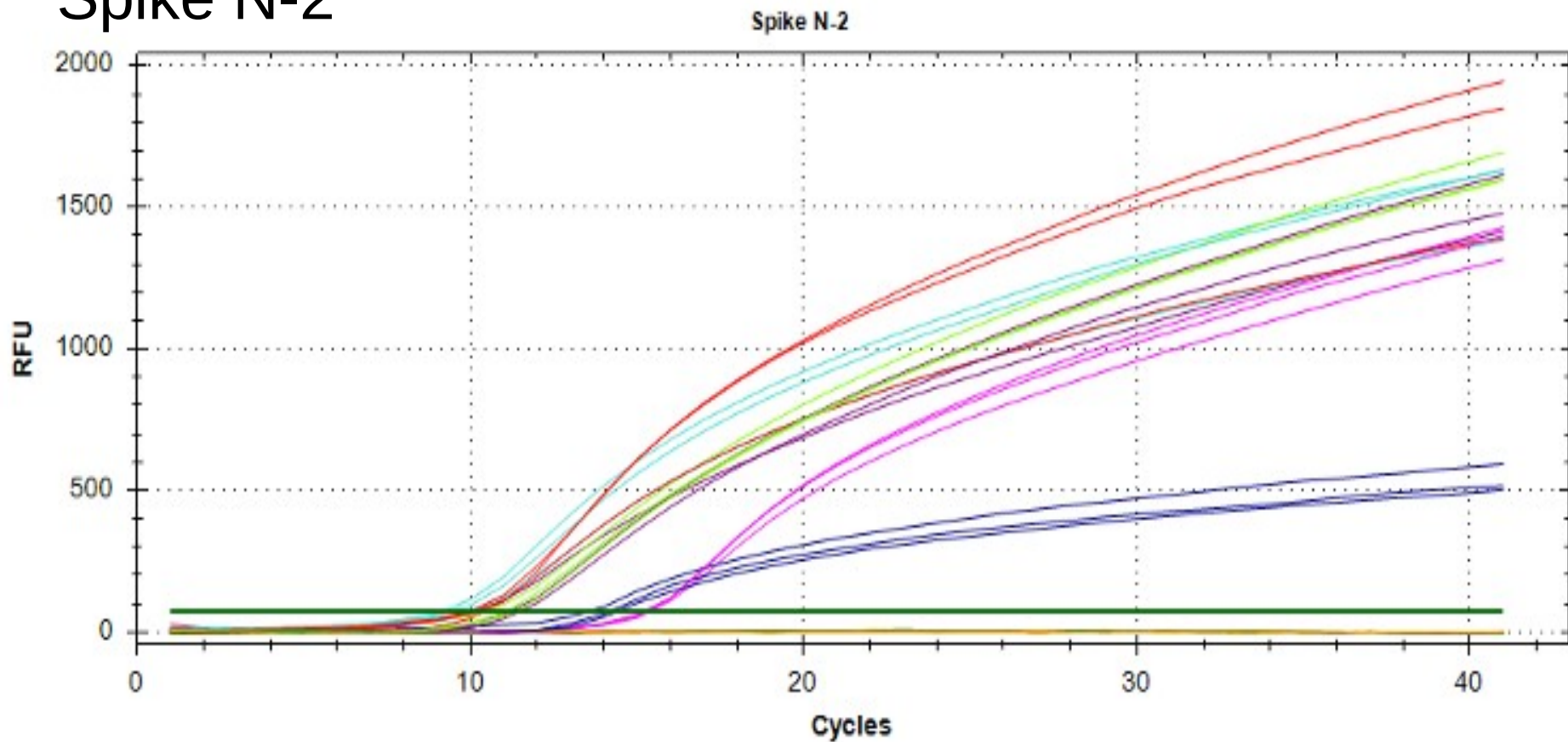
Spike 2



Spike N-1

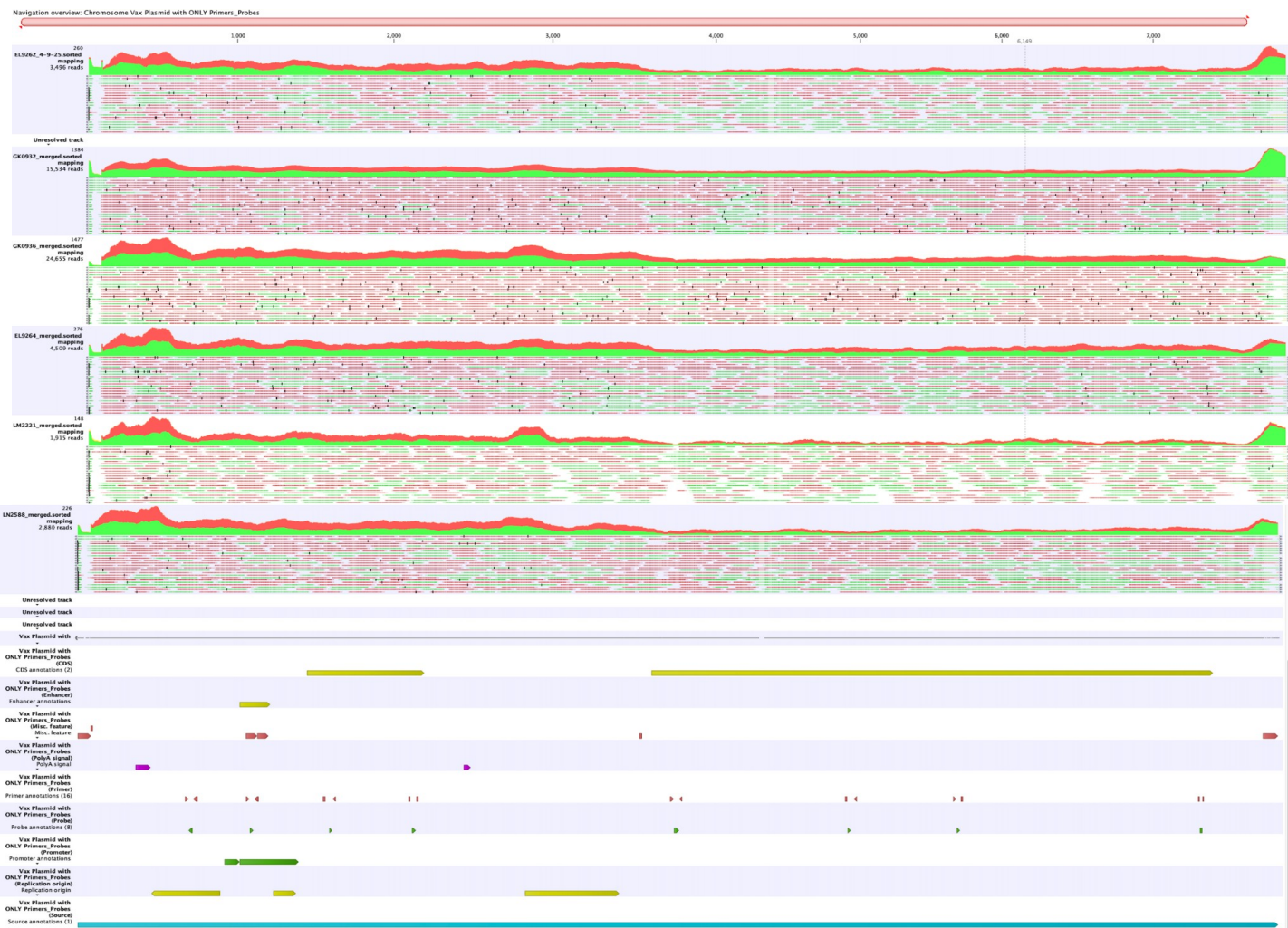


Spike N-2



Molecules/uL of target amplicons determined by qPCR

Region	EL9262	EL9264	GK0936	GK0932	LM2221	LN2588
F1	58248910	81963892	67273582	74900037	17720463	444200
NeoR/KanR 5	38443662	42004366	34100181	38943419	6903579	278299
NeoR/KanR 1	113737278	77559526	121753209	103066588	21642547	486552
SV40	54607868	53770247	81363217	88913037	17971496	579232
Spike N-1	743980839	747919246	439702710	385839500	N/A	N/A
Spike N-2	274426950	162208004	111918508	99064536	N/A	N/A
Spike 1	405952538	267616016	211571150	207407773	118294409	1880585
Spike 2	3288688433	1465156584	2357441564	2110388951	1747117428	21268798



Alignment to
the Plasmid

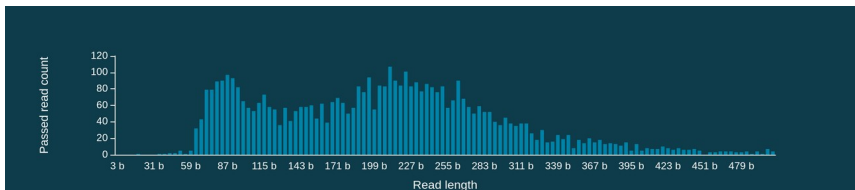
Number of reads that aligned to Plasmid

Vaccine Lot	Total Number of Reads	Number of Reads That Aligned to the Plasmid
EL9262	4.74k	3.5k
EL9264	4.91k	4.3k
GK0936	25.48k	23.8k
GK0932	16.31k	14.9k
LM2221	2.45k	1.8k
LN2588	3.03k	2.8k

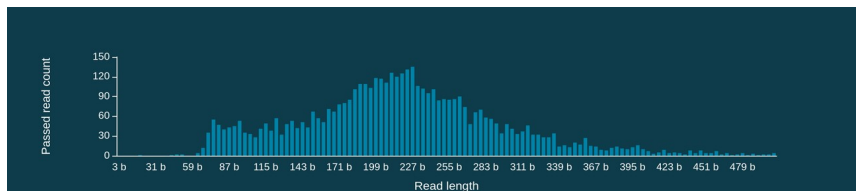
Counts of reads that span entire target amplicon (visible by qPCR)

Region	EL9262	EL9264	GK0936	GK0932	LM2221	LN2588
F1	78	71	473	297	25	77
NeoR/KanR 5	54	62	409	261	25	55
NeoR/KanR 1	64	88	530	316	39	78
SV40	69	76	440	240	23	50
Spike N-1	26	36	252	198	9	23
Spike N-2	35	48	220	161	9	14
Spike 1	33	59	305	216	12	27
Spike 2	43	73	283	212	13	39

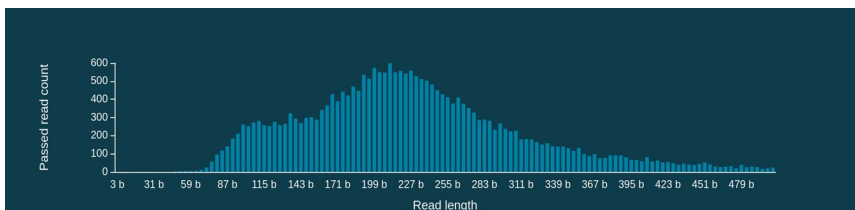
Average DNA Piece Length - Approx. 200 base pairs



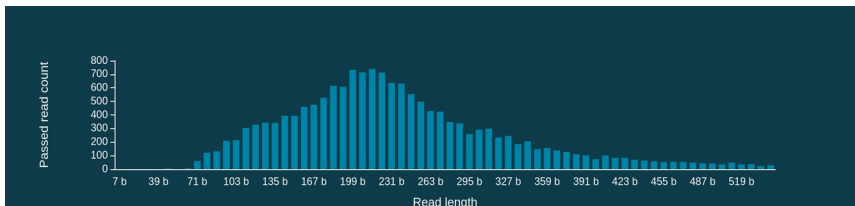
EL9262



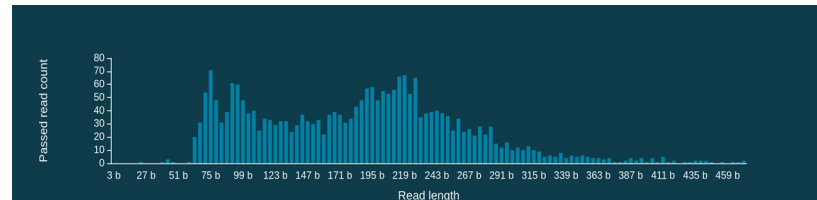
EL9264



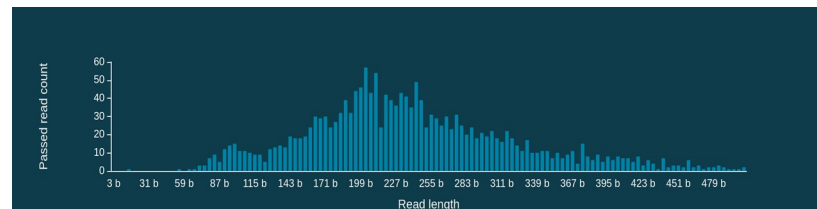
GK0936



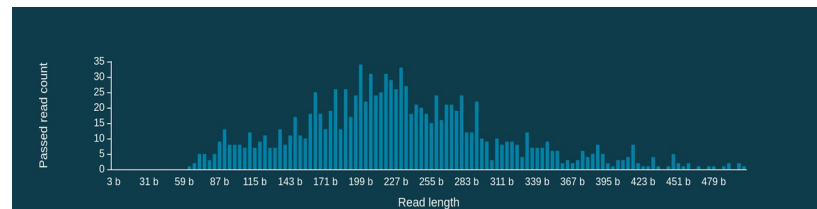
GK0932



LM2221



LN2588 - 1



LN2588 - 2

Quantification of DNA in each dose of modRNA

- The following slides contain the process of obtaining average values
 - Spike 2 was omitted from calculating the average due to unreliable amplification in PCR

	EL9262										
	Molecules per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Number of nanopore reads that assembled to the vector	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng per dose	Average estimate of ng of DNA per dose
F1	1299604	78	3496	58248910	1.75E+10	2.90E-14	200	132000	3.83E-09	3.83	15.9
NeoR/KanR 5	593809	54	3496	38443662	1.15E+10	1.92E-14	200	132000	2.53E-09	2.53	
NeoR/KanR 1	2082147	64	3496	113737278	3.41E+10	5.67E-14	200	132000	7.48E-09	7.48	
SV40	1077787	69	3496	54607868	1.64E+10	2.72E-14	200	132000	3.59E-09	3.59	
Spike N-1	5533038	26	3496	743980839	2.23E+11	3.71E-13	200	132000	4.89E-08	48.9	
Spike N-2	2747409	35	3496	274426950	8.23E+10	1.37E-13	200	132000	1.81E-08	18.1	
Spike 1	3831932	33	3496	405952538	1.22E+11	2.02E-13	200	132000	2.67E-08	26.7	
Spike 2	40450115	43	3496	3288688433	9.87E+11	1.64E-12	200	132000	2.16E-07	216	
	Molecules per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Total Number of Passed Nanopore Reads	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng per dose	Average estimate of ng of DNA per dose
F1	1299604	78	4740	78975925	2.37E+10	3.94E-14	200	132000	5.20E-09	5.2	21.5
NeoR/KanR 5	593809	54	4740	52123272	1.56E+10	2.60E-14	200	132000	3.43E-09	3.43	
NeoR/KanR 1	2082147	64	4740	154209010	4.63E+10	7.68E-14	200	132000	1.01E-08	10.1	
SV40	1077787	69	4740	74039271	2.22E+10	3.69E-14	200	132000	4.87E-09	4.87	
Spike N-1	5533038	26	4740	1008715440	3.03E+11	5.03E-13	200	132000	6.64E-08	66.4	
Spike N-2	2747409	35	4740	372077730	1.12E+11	1.85E-13	200	132000	2.45E-08	24.5	
Spike 1	3831932	33	4740	550404757	1.65E+11	2.74E-13	200	132000	3.62E-08	36.2	
Spike 2	40450115	43	4740	4458919672	1.34E+12	2.22E-12	200	132000	2.93E-07	293	

Spike 2 was omitted from calculating the average due to unreliable amplification in PCR

EL9264

	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Number of nanopore reads that assembled to the vector	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	Number of DNA molecules per dose	Number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	1290627	71	4509	81963892	2.46E+10	4.08E-14	200	132000	5.39E-09	5.39	13.47
NeoR/KanR 5	577572	62	4509	42004366	1.26E+10	2.09E-14	200	132000	2.76E-09	2.76	
NeoR/KanR 1	1513692	88	4509	77559526	2.33E+10	3.87E-14	200	132000	5.10E-09	5.10	
SV40	906307	76	4509	53770247	1.61E+10	2.68E-14	200	132000	3.54E-09	3.54	
Spike N-1	5971411	36	4509	747919246	2.24E+11	3.73E-13	200	132000	4.92E-08	49.20	
Spike N-2	1726765	48	4509	162208004	4.87E+10	8.08E-14	200	132000	1.07E-08	10.67	
Spike 1	3501740	59	4509	267616016	8.03E+10	1.33E-13	200	132000	1.76E-08	17.60	
Spike 2	23720654	73	4509	1465156584	4.40E+11	7.30E-13	200	132000	9.64E-08	96.38	
	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Total Number of Passed Nanopore Reads	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	Number of DNA molecules per dose	Number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	1290627	71	4910	89253206	2.68E+10	4.45E-14	200	132000	5.87E-09	5.87	14.66
NeoR/KanR 5	577572	62	4910	45739951	1.37E+10	2.28E-14	200	132000	3.01E-09	3.01	
NeoR/KanR 1	1513692	88	4910	84457146	2.53E+10	4.21E-14	200	132000	5.56E-09	5.56	
SV40	906307	76	4910	58552209	1.76E+10	2.92E-14	200	132000	3.85E-09	3.85	
Spike N-1	5971411	36	4910	814434131	2.44E+11	4.06E-13	200	132000	5.36E-08	53.57	
Spike N-2	1726765	48	4910	176633688	5.30E+10	8.80E-14	200	132000	1.16E-08	11.62	
Spike 1	3501740	59	4910	291415977	8.74E+10	1.45E-13	200	132000	1.92E-08	19.17	
Spike 2	23720654	73	4910	1595457712	4.79E+11	7.95E-13	200	132000	1.05E-07	104.95	

Spike 2 was omitted from calculating the average due to unreliable amplification in PCR

	GK0936										
	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Number of nanopore reads that assembled to the vector	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	1290627	473	24655	67273582	2.02E+10	3.35E-14	200	132000	4.43E-09	4.43	10.03
NeoR/KanR 5	565685	409	24655	34100181	1.02E+10	1.70E-14	200	132000	2.24E-09	2.24	
NeoR/KanR 1	2617287	530	24655	121753209	3.65E+10	6.07E-14	200	132000	8.01E-09	8.01	
SV40	1452031	440	24655	81363217	2.44E+10	4.05E-14	200	132000	5.35E-09	5.35	
Spike N-1	4494224	252	24655	439702710	1.32E+11	2.19E-13	200	132000	2.89E-08	28.92	
Spike N-2	998664	220	24655	111918508	3.36E+10	5.58E-14	200	132000	7.36E-09	7.36	
Spike 1	2617287	305	24655	211571150	6.35E+10	1.05E-13	200	132000	1.39E-08	13.92	
Spike 2	27059662	283	24655	2357441564	7.07E+11	1.17E-12	200	132000	1.55E-07	155.07	
	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Total Number of Passed Nanopore Reads	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	1290627	473	25480	69524675	2.09E+10	3.46E-14	200	132000	4.57E-09	4.57	10.37
NeoR/KanR 5	565685	409	25480	35241234	1.06E+10	1.76E-14	200	132000	2.32E-09	2.32	
NeoR/KanR 1	2617287	530	25480	125827287	3.77E+10	6.27E-14	200	132000	8.28E-09	8.28	
SV40	1452031	440	25480	84085775	2.52E+10	4.19E-14	200	132000	5.53E-09	5.53	
Spike N-1	4494224	252	25480	454415942	1.36E+11	2.26E-13	200	132000	2.99E-08	29.89	
Spike N-2	998664	220	25480	115663500	3.47E+10	5.76E-14	200	132000	7.61E-09	7.61	
Spike 1	2617287	305	25480	218650696	6.56E+10	1.09E-13	200	132000	1.44E-08	14.38	
Spike 2	27059662	283	25480	2436325737	7.31E+11	1.21E-12	200	132000	1.60E-07	160.26	

Spike 2 was omitted from calculating the average due to unreliable amplification in PCR

	GK0932										
	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Number of nanopore reads that assembled to the vector	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	1432040	297	15534	74900037	2.25E+10	3.73E-14	200	132000	4.93E-09	4.93	9.38
NeoR/KanR 5	654322	261	15534	38943419	1.17E+10	1.94E-14	200	132000	2.56E-09	2.56	
NeoR/KanR 1	2096629	316	15534	103066588	3.09E+10	5.14E-14	200	132000	6.78E-09	6.78	
SV40	1373705	240	15534	88913037	2.67E+10	4.43E-14	200	132000	5.85E-09	5.85	
Spike N-1	4918001	198	15534	385839500	1.16E+11	1.92E-13	200	132000	2.54E-08	25.38	
Spike N-2	1026741	161	15534	99064536	2.97E+10	4.94E-14	200	132000	6.52E-09	6.52	
Spike 1	2884001	216	15534	207407773	6.22E+10	1.03E-13	200	132000	1.36E-08	13.64	
Spike 2	28801497	212	15534	2110388951	6.33E+11	1.05E-12	200	132000	1.39E-07	138.82	
	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Total Number of Passed Nanopore Reads	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	1432040	297	16310	78641664	2.36E+10	3.92E-14	200	132000	5.17E-09	5.17	9.85
NeoR/KanR 5	654322	261	16310	40888835	1.23E+10	2.04E-14	200	132000	2.69E-09	2.69	
NeoR/KanR 1	2096629	316	16310	108215273	3.25E+10	5.39E-14	200	132000	7.12E-09	7.12	
SV40	1373705	240	16310	93354682	2.80E+10	4.65E-14	200	132000	6.14E-09	6.14	
Spike N-1	4918001	198	16310	405114088	1.22E+11	2.02E-13	200	132000	2.66E-08	26.65	
Spike N-2	1026741	161	16310	104013299	3.12E+10	5.18E-14	200	132000	6.84E-09	6.84	
Spike 1	2884001	216	16310	217768815	6.53E+10	1.09E-13	200	132000	1.43E-08	14.32	
Spike 2	28801497	212	16310	2215813300	6.65E+11	1.10E-12	200	132000	1.46E-07	145.76	

Spike 2 was omitted from calculating the average due to unreliable amplification in PCR

LM2221

		Number of nanopore sequencing reads that spanned the amplicon	Number of nanopore reads that assembled to the vector	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon- spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	231338	25	1915	17720463	5.32E+09	8.83E-15	200	132000	1.17E-09	1.17	2.40
NeoR/KanR 5	90125	25	1915	6903579	2.07E+09	3.44E-15	200	132000	4.54E-10	0.45	
NeoR/KanR 1	440762	39	1915	21642547	6.49E+09	1.08E-14	200	132000	1.42E-09	1.42	
SV40	215846	23	1915	17971496	5.39E+09	8.96E-15	200	132000	1.18E-09	1.18	
Spike N-1	N/A	9	1915	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike N-2	N/A	9	1915	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike 1	741270	12	1915	118294409	3.55E+10	5.90E-14	200	132000	7.78E-09	7.78	
Spike 2	11860327	13	1915	1747117428	5.24E+11	8.71E-13	200	132000	1.15E-07	114.93	
		Number of nanopore sequencing reads that spanned the amplicon	Total Number of Passed Nanopore Reads	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon- spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	231338	25	2450	22671088	6.80E+09	1.13E-14	200	132000	1.49E-09	1.49	3.07
NeoR/KanR 5	90125	25	2450	8832255	2.65E+09	4.40E-15	200	132000	5.81E-10	0.58	
NeoR/KanR 1	440762	39	2450	27688898	8.31E+09	1.38E-14	200	132000	1.82E-09	1.82	
SV40	215846	23	2450	22992254	6.90E+09	1.15E-14	200	132000	1.51E-09	1.51	
Spike N-1	N/A	9	2450	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike N-2	N/A	9	2450	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike 1	741270	12	2450	151342717	4.54E+10	7.54E-14	200	132000	9.96E-09	9.96	
Spike 2	11860327	13	2450	2235215509	6.71E+11	1.11E-12	200	132000	1.47E-07	147.03	

Spike 2 was omitted from calculating the average due to unreliable amplification in PCR

LN2588

	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Number of nanopore reads that assembled to the vector	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	11876	77	2880	444200	1.33E+08	2.21E-16	200	132000	2.92E-11	0.03	0.05
NeoR/KanR 5	5315	55	2880	278299	8.35E+07	1.39E-16	200	132000	1.83E-11	0.02	
NeoR/KanR 1	13177	78	2880	486552	1.46E+08	2.42E-16	200	132000	3.20E-11	0.03	
SV40	10056	50	2880	579232	1.74E+08	2.89E-16	200	132000	3.81E-11	0.04	
Spike N-1	N/A	23	2880	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike N-2	N/A	14	2880	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike 1	17630	27	2880	1880585	5.64E+08	9.37E-16	200	132000	1.24E-10	0.12	
Spike 2	288015	39	2880	21268798	6.38E+09	1.06E-14	200	132000	1.40E-09	1.40	

	Molecules of amplicon per ul (qPCR)	Number of nanopore sequencing reads that spanned the amplicon	Total Number of Passed Nanopore Reads	Deduced number of DNA molecules per ul (qPCR * aligned reads/amplicon-spanning reads)	number of DNA molecules per dose	number of moles of DNA/dose	Average size of each DNA molecule that assembled to vector	Molecular Weight of average DNA molecule	g/dose	ng/dose	Average estimate of ng of DNA per dose
F1	11876	77	3030	467336	1.40E+08	2.33E-16	200	132000	3.07E-11	0.03	0.05
NeoR/KanR 5	5315	55	3030	292794	8.78E+07	1.46E-16	200	132000	1.93E-11	0.02	
NeoR/KanR 1	13177	78	3030	511893	1.54E+08	2.55E-16	200	132000	3.37E-11	0.03	
SV40	10056	50	3030	609400	1.83E+08	3.04E-16	200	132000	4.01E-11	0.04	
Spike N-1	N/A	23	3030	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike N-2	N/A	14	3030	N/A	N/A	N/A	200	132000	N/A	N/A	
Spike 1	17630	27	3030	1978532	5.94E+08	9.86E-16	200	132000	1.30E-10	0.13	
Spike 2	288015	39	3030	22376548	6.71E+09	1.12E-14	200	132000	1.47E-09	1.47	

Spike 2 was omitted from calculating the average due to unreliable amplification in PCR

Estimated quantity of DNA per Dose of modRNA

Target	EL9262 ng/dose	EL9264 ng/dose	GK0936 ng/dose	GK0932 ng/dose	LM2221 ng/dose	LN2588 ng/dose
F1	5.20	5.87	4.57	5.17	1.49	0.03
NeoR/KanR 5	3.43	3.01	2.32	2.69	0.58	0.02
NeoR/KanR 1	10.10	5.56	8.28	7.12	1.82	0.03
SV40	4.87	3.85	5.53	6.14	1.51	0.04
Spike N-1	66.40	53.57	29.89	26.65	N/A (primer mismatch?)	N/A (primer mismatch?)
Spike N-2	24.50	11.62	7.61	6.84	N/A (primer mismatch?)	N/A (primer mismatch?)
Spike 1	36.20	19.17	14.38	14.32	9.96	0.13
Spike 2	293.00	104.95	160.26	145.76	147.03	1.47

Spike 2 was omitted from calculating the average due to unreliable amplification in PCR