

FIG. 1A

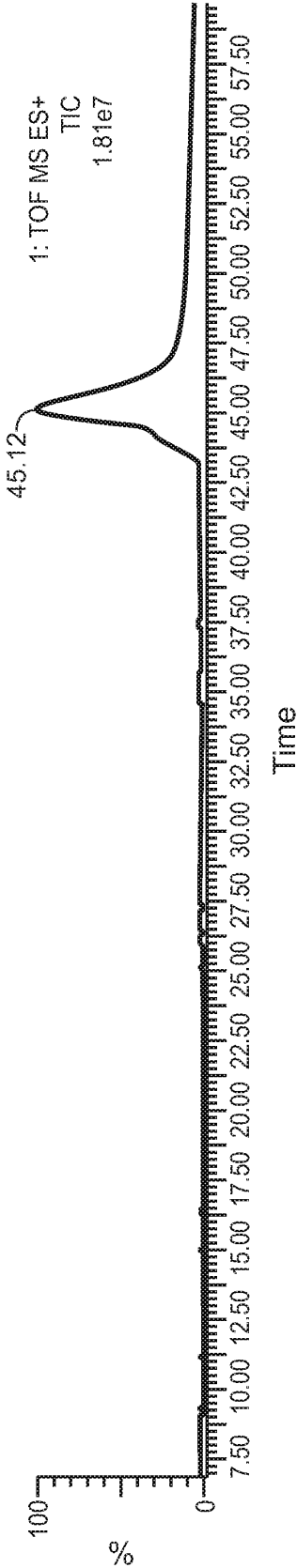


FIG. 1B

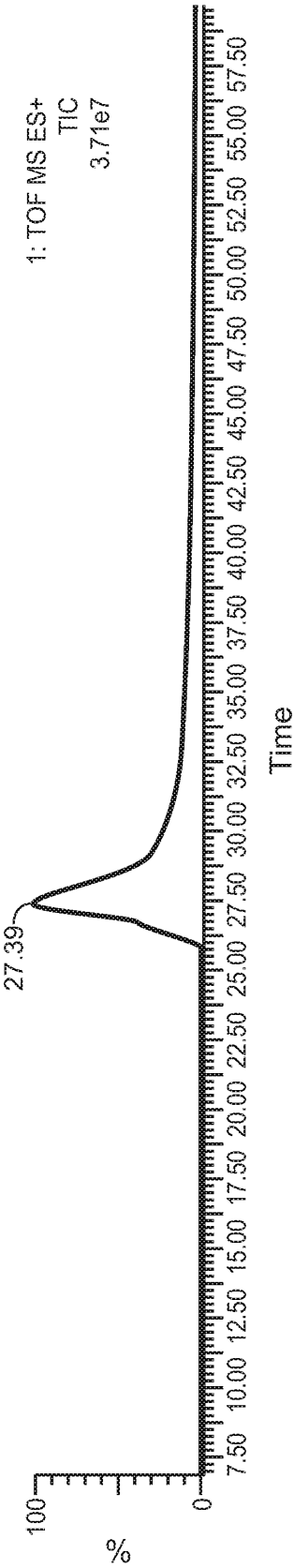


FIG. 1C

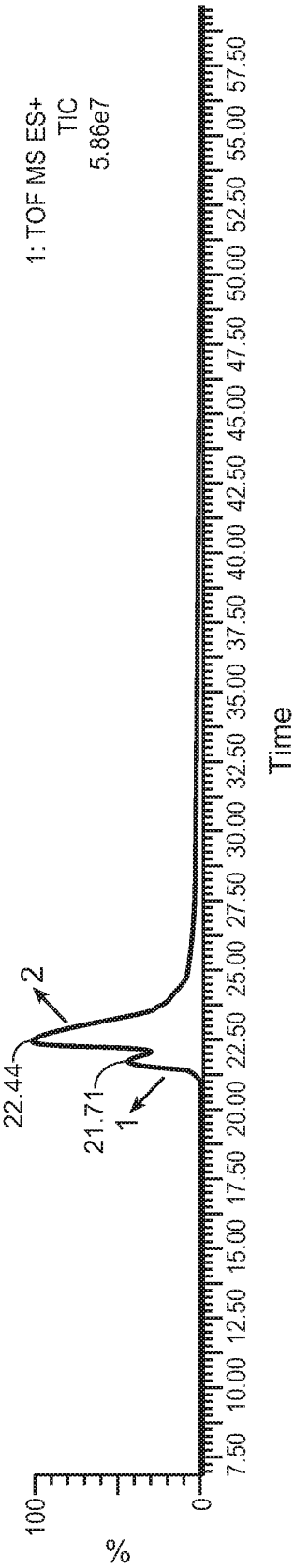
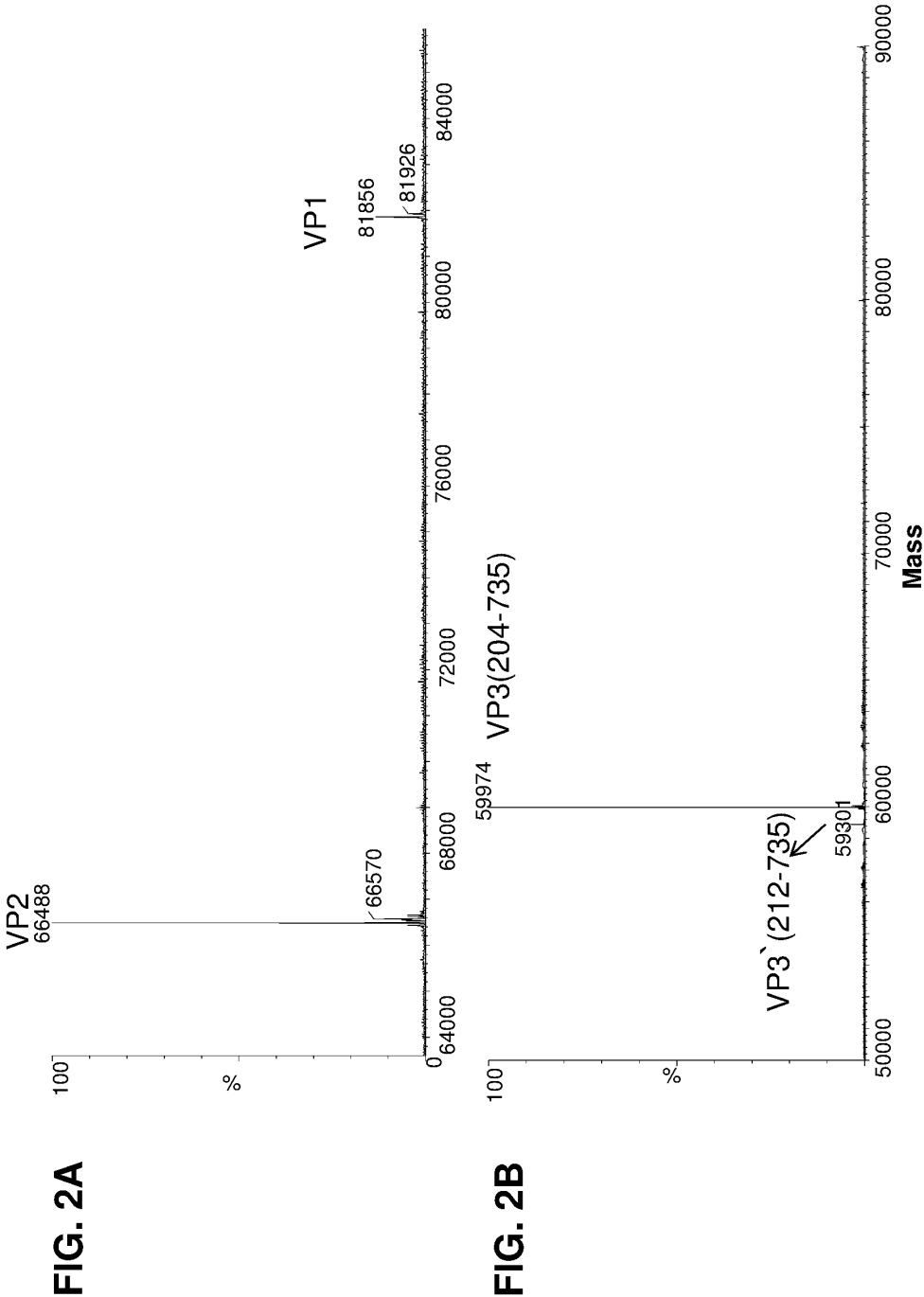


FIG. 1D



1 MAADGYLPDWLEDTLSEGIQWWKLKPGPPPPKPAERHKDDSRGLVLPGY 50
51 KYLGPFNGLDKGEFVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEF 100
101 QERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTPAGKKRPVEHSP 150
151 VEPDSSSGTGKAGQQPARKRLNFGOTGDADSVDPQPLGQPPAAPSGGLGT 200
201 NTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALP 250
251 TYNNHLYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLI 300
301 NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQL 350
351 PYVLGSAHQGCLPPFPADVFMVPQYGYLTNNQSQAVGRSSFYCLEYFPS 400
401 QMLRTGNNFTFSYTFEDVPPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNT 450
451 PSGTTTQSRLOFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEY 500
501 SWTGATKYHLNGRDSLVPNGPAMASHKDDEEKFFPQSGVLIFGKQGSEKT 550
551 NVDIEKVMITDEEEIIRTNPVATEQYGSVSTNLQRGNRQAATADVNTQGV 600
601 LPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLMGGFGLKHPPPOILIKN 650
651 TPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQENSKRWNPEIQY 700
701 TSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 735

FIG. 3

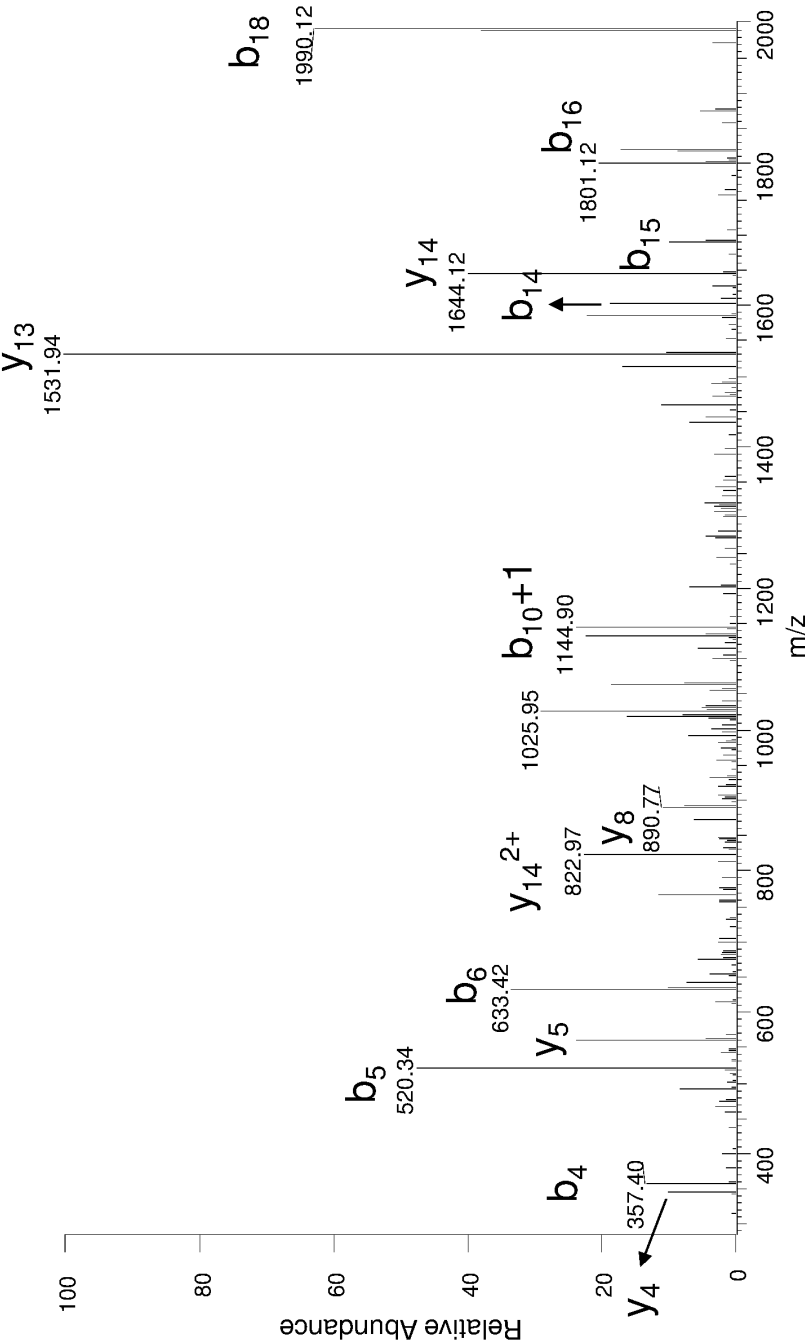


FIG. 4A

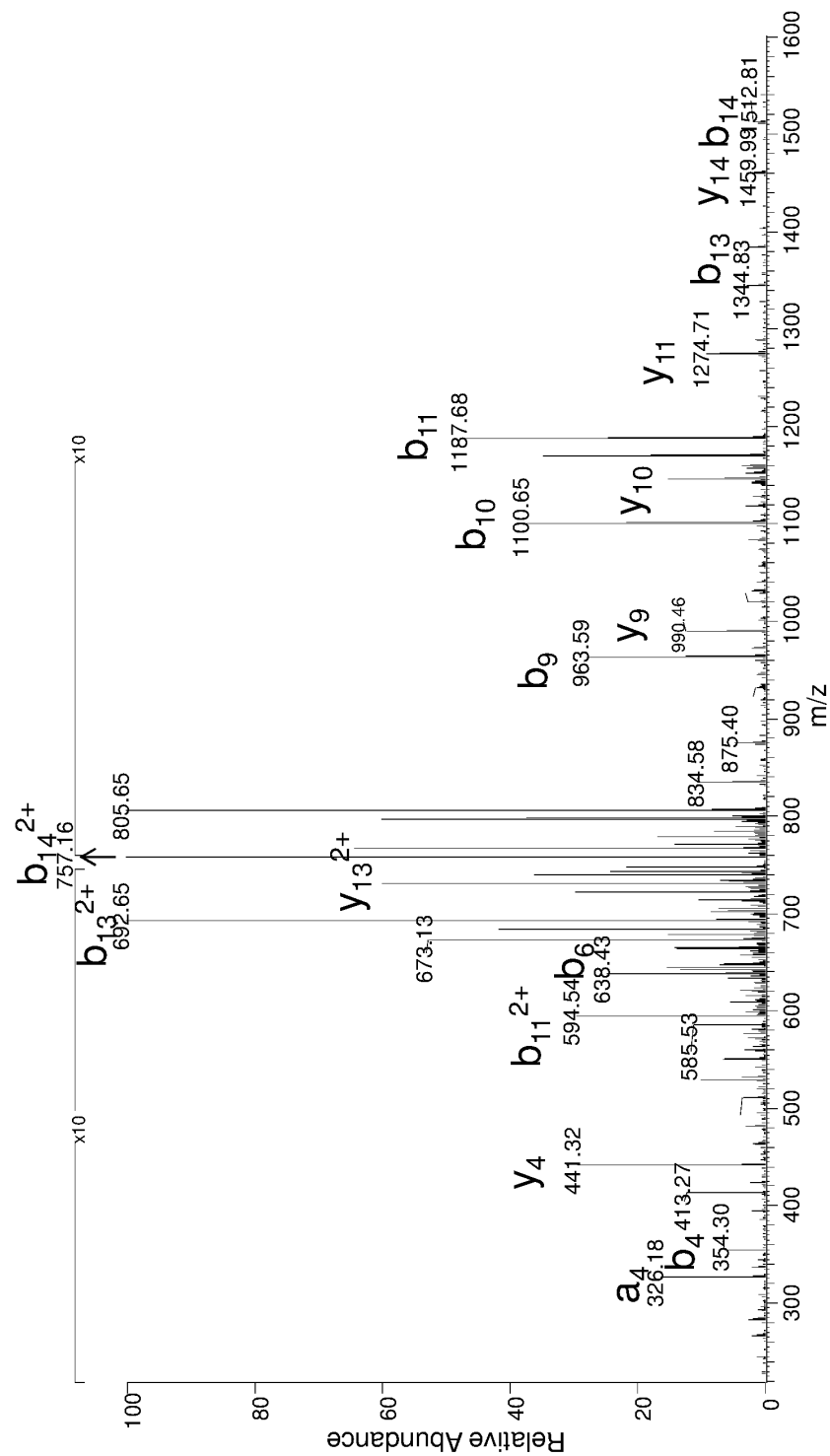


FIG. 4B

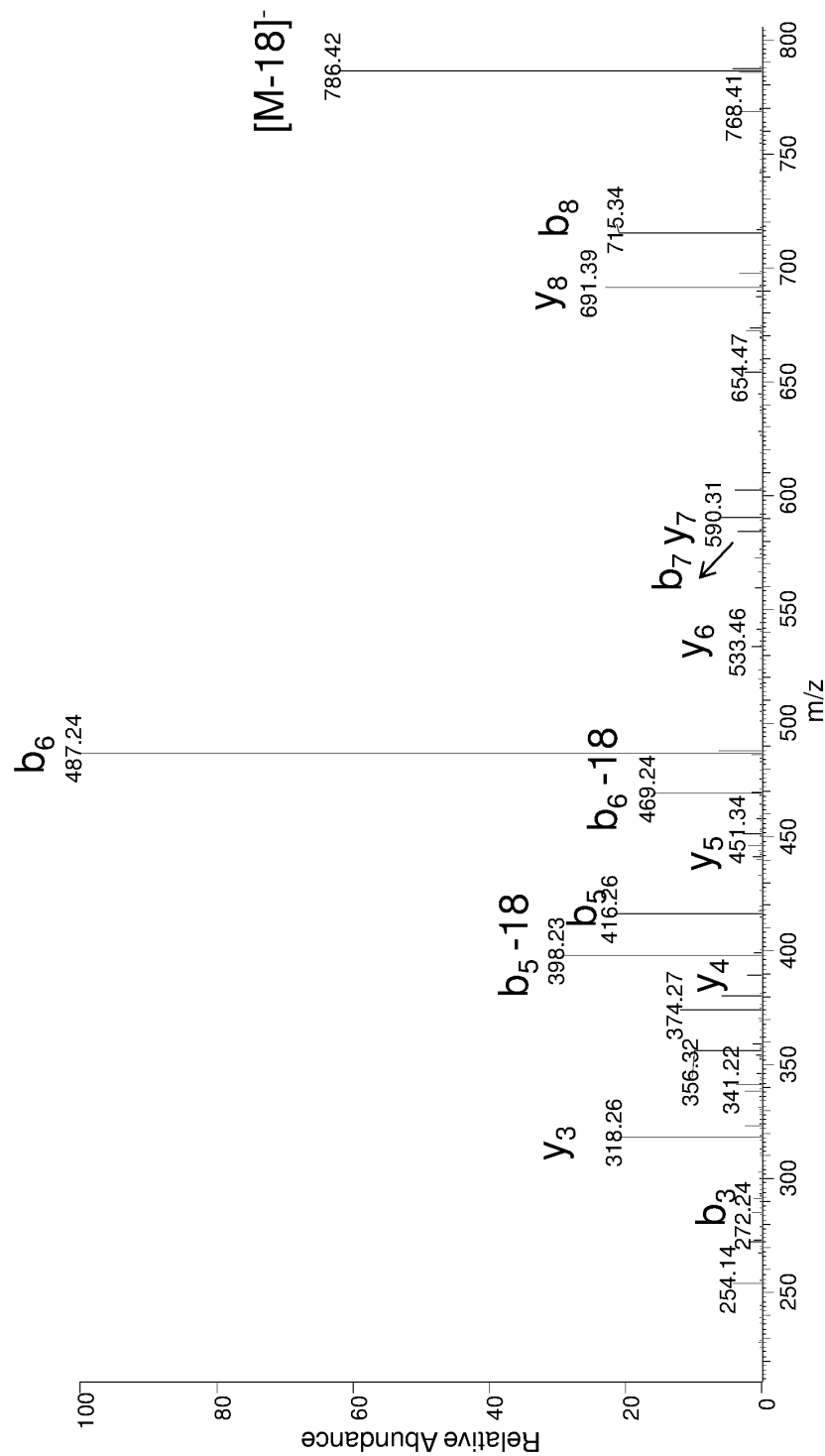


FIG. 4C

		Section 1												
		VP1												
(1)	(1)	1	10	20	30	40	50	60	70	82				
AAVRh10	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV10	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV8	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV7	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV1	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV6	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV2	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV3	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV11	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV12	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV4	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV5	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
AAV9	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD
Consensus	(1)	MAADGILPDWLE	DNLSEGI	RENN	DLKPGMPKP	KANQQKQD	GRGLVLPGYKY	LGP	FENGLDK	GEPVNAAD	AAALEHDKAYD	QD	QD	QD

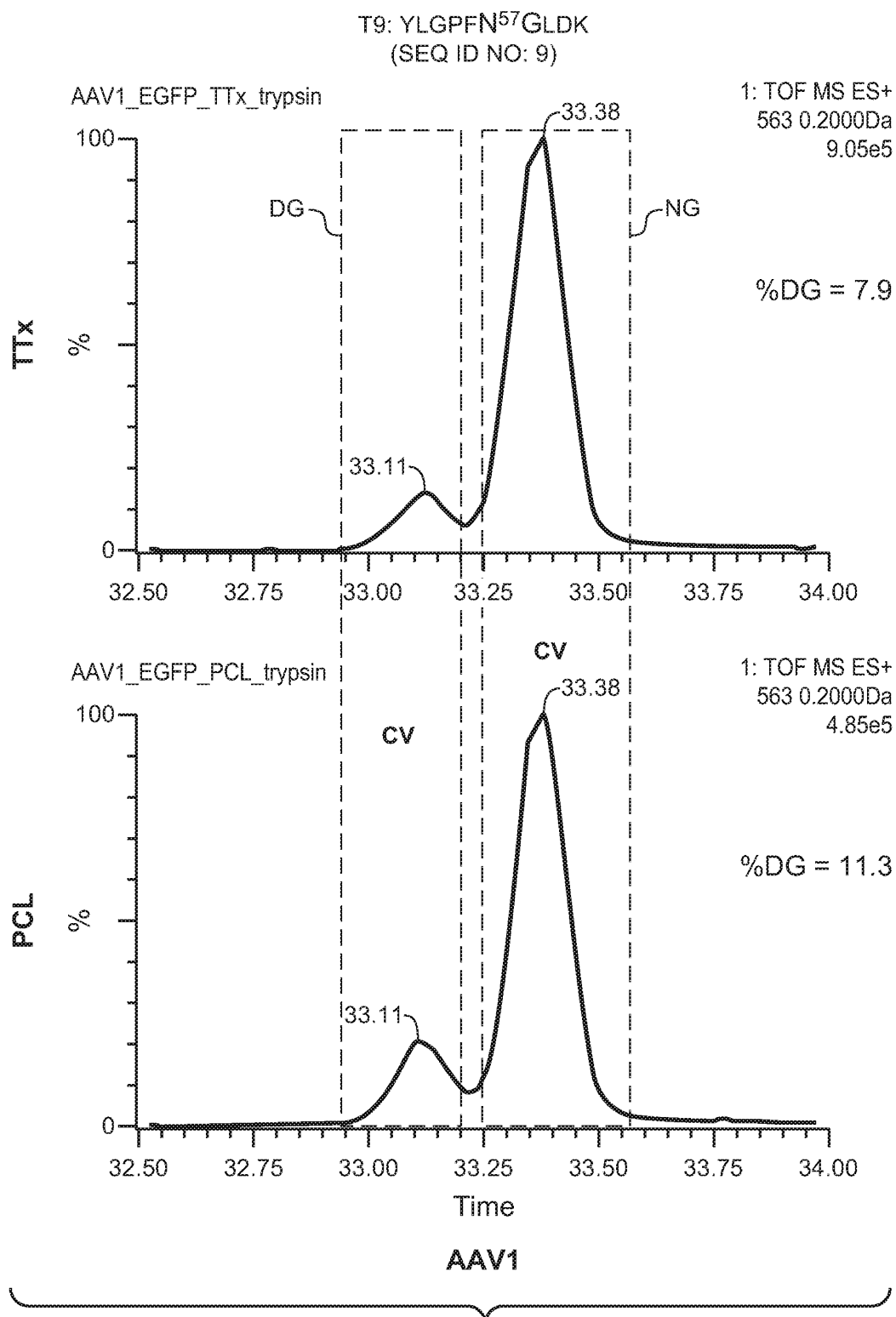
FIG. 5A

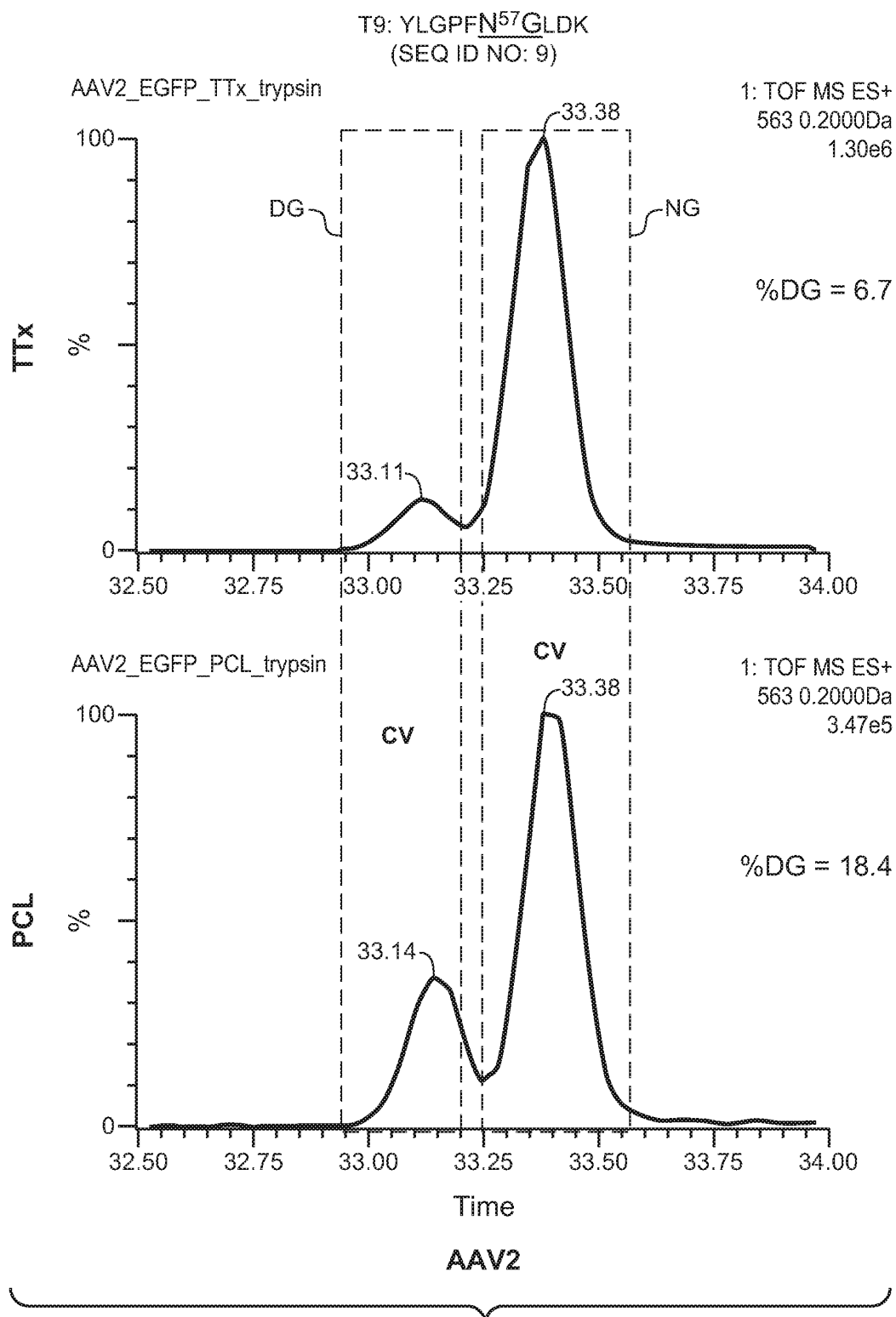
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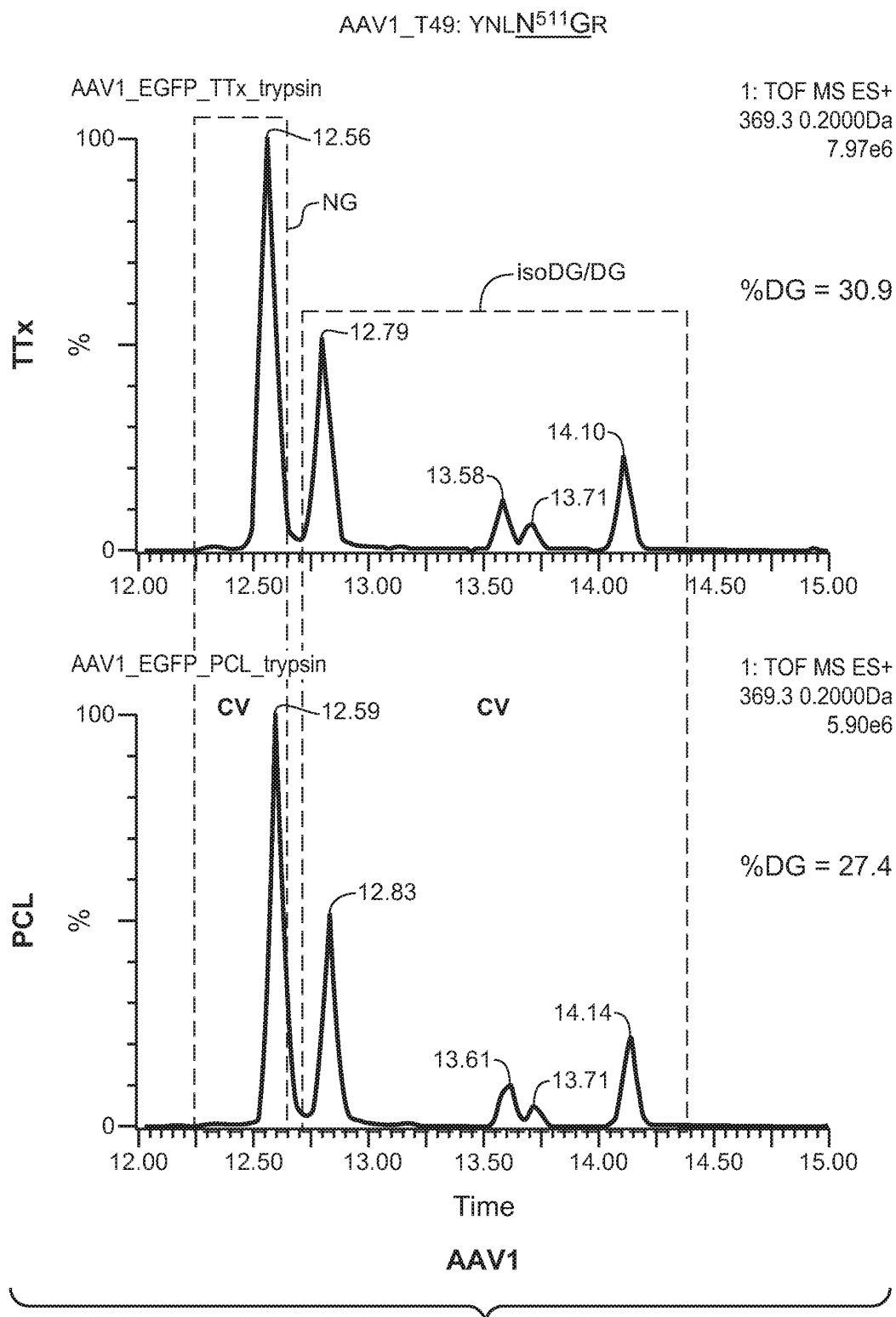
Section 3

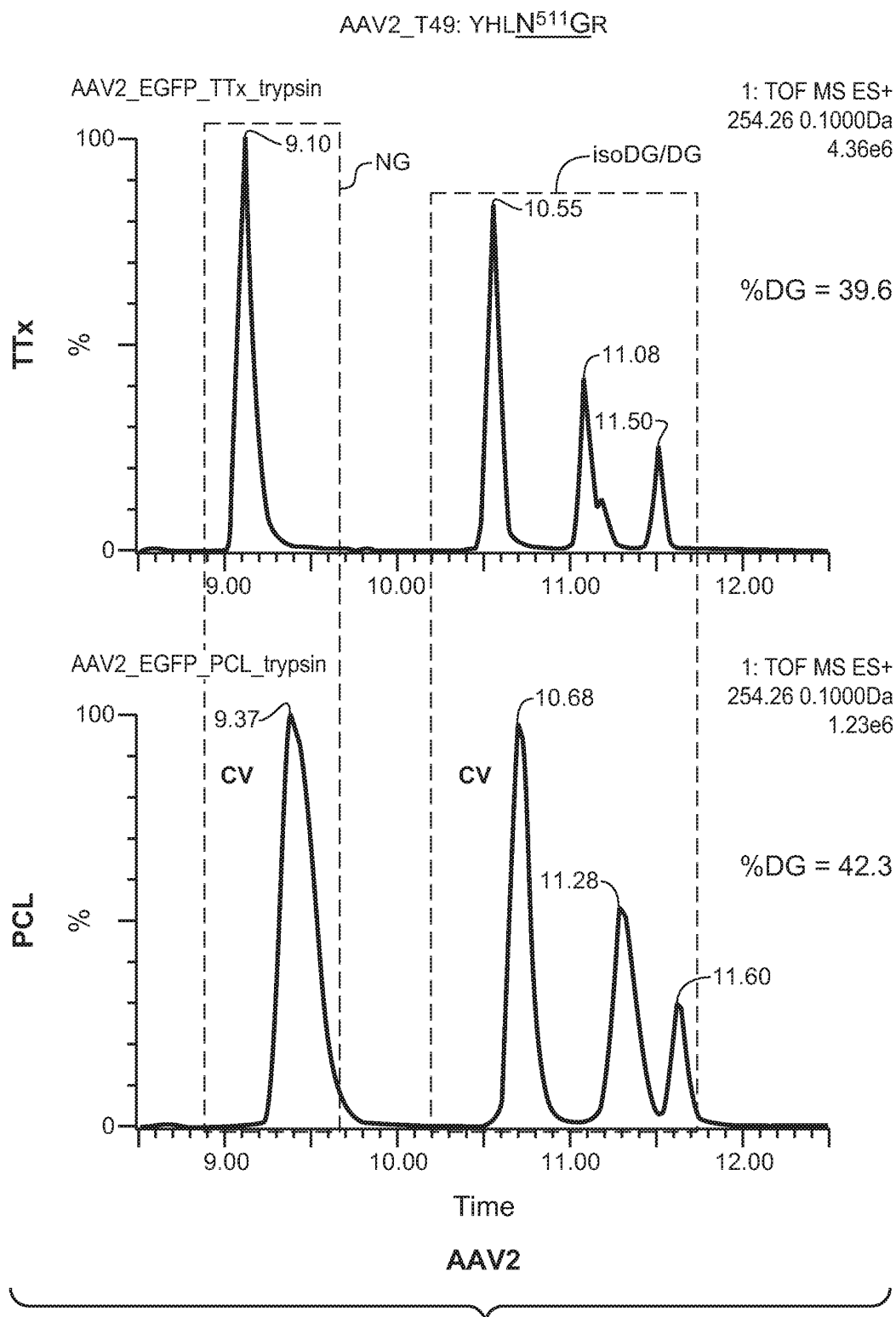
VP3																			
										210	220	230	240	250	260	270	280	290	300
AAVRh10 (163)	KGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV10 (163)	KGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV8 (163)	KGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV7 (163)	KGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV1 (162)	TGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV6 (162)	TGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV2 (162)	AGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV3 (162)	SGK	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV11 (161)	KGK	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV12 (165)	KKQ	KDGEPA	DSARR	ETLDFEDSGAG	---	DGPPEGS	SSSG	EMSHD	MEMRAAPG	GNAVEAG	---	QGDGVGN	ASGD	MWHCDSTWLGDR					
AAV4 (161)	KGK	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV5 (159)	DSK	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
AAV9 (162)	SCA	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										
Consensus (165)	KGQ	---	QPAKKRLNFGQIGDSESVDPDPQPIIGEP	PAAGPEGL	SGTMAA	GGCAPMADNNEG	DGVG	SGSG	MWHCDSTWLGDR										

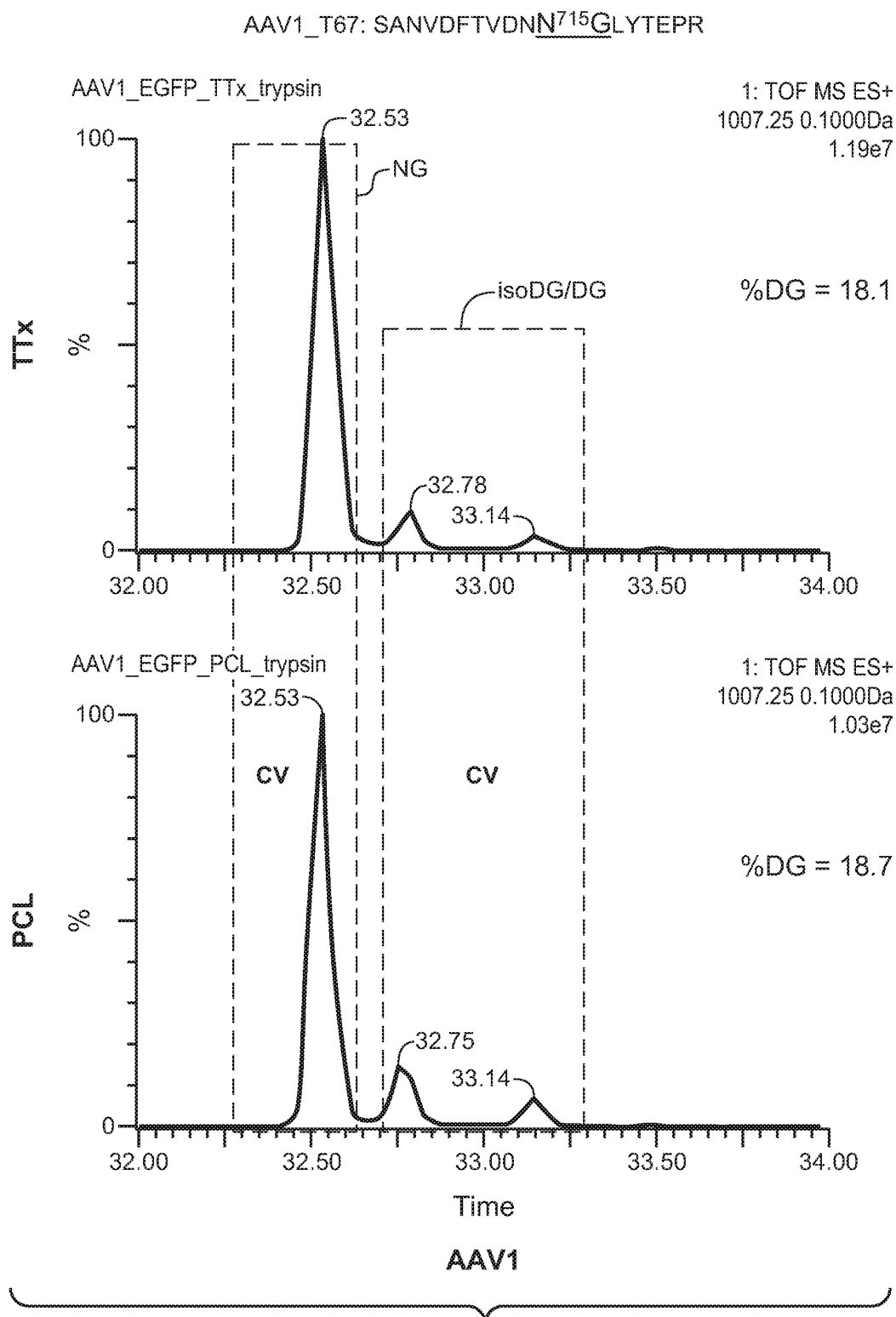
FIG. 5C

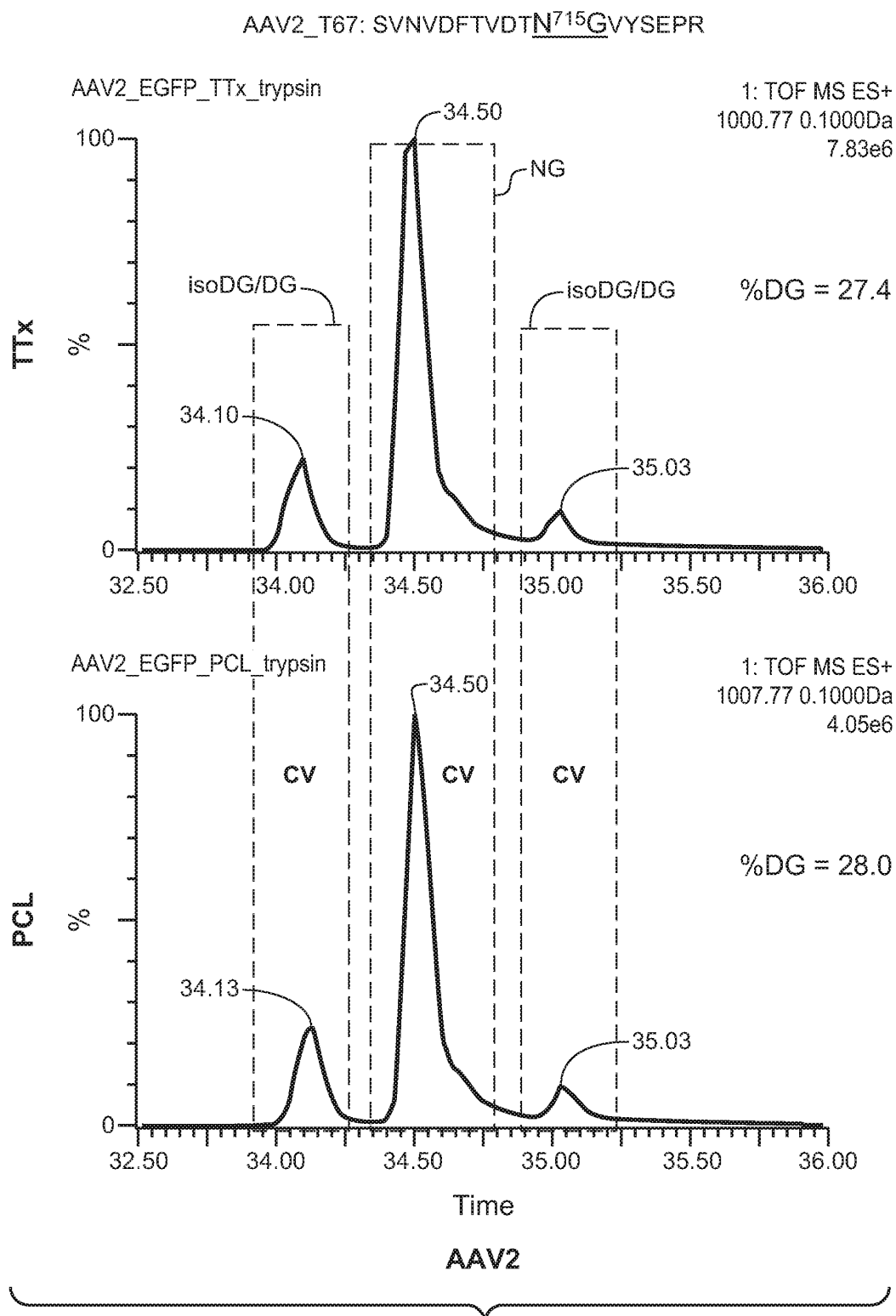
**FIG. 6A**

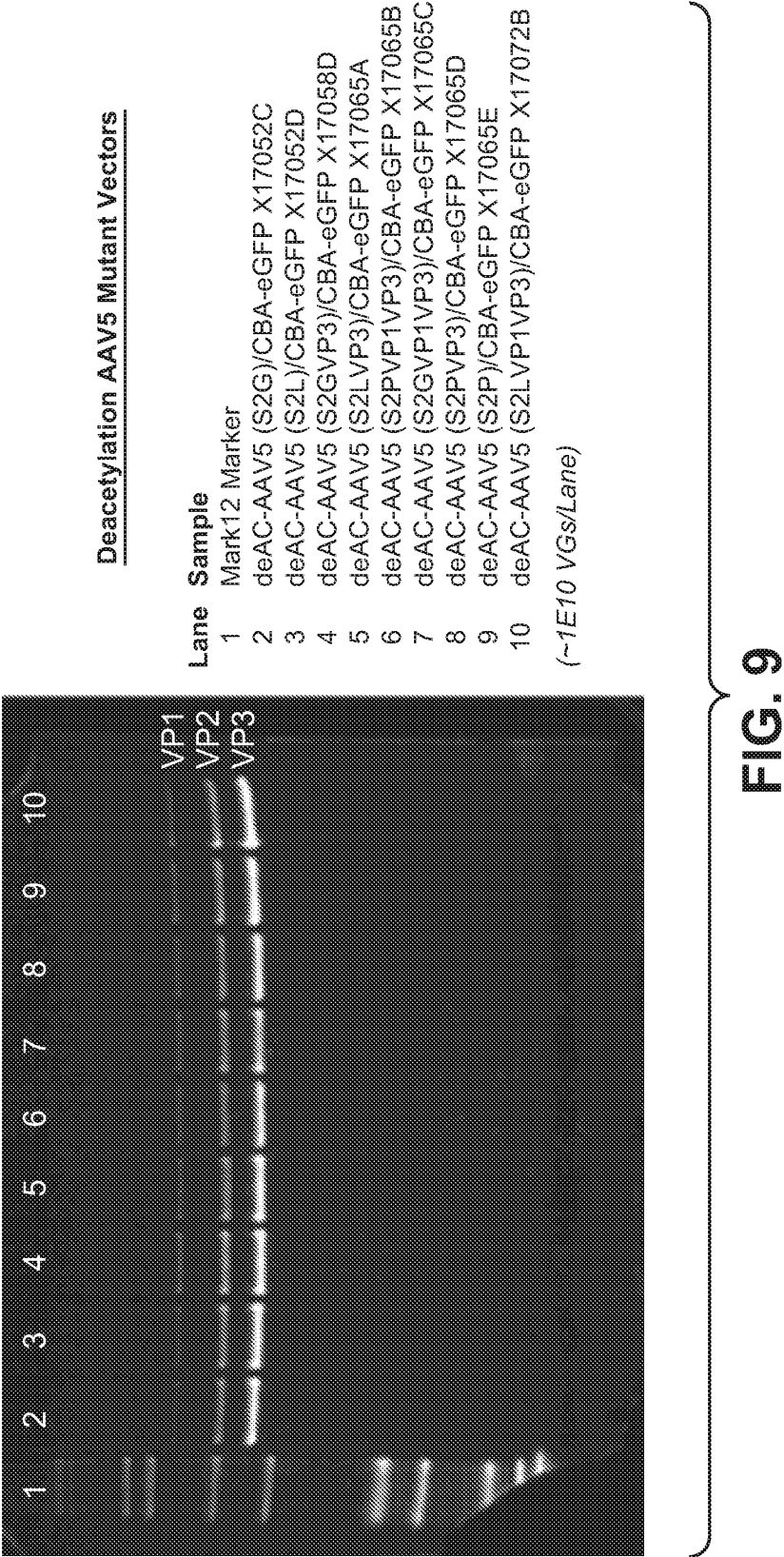
**FIG. 6B**

**FIG. 7A**

**FIG. 7B**

**FIG. 8A**

**FIG. 8B**



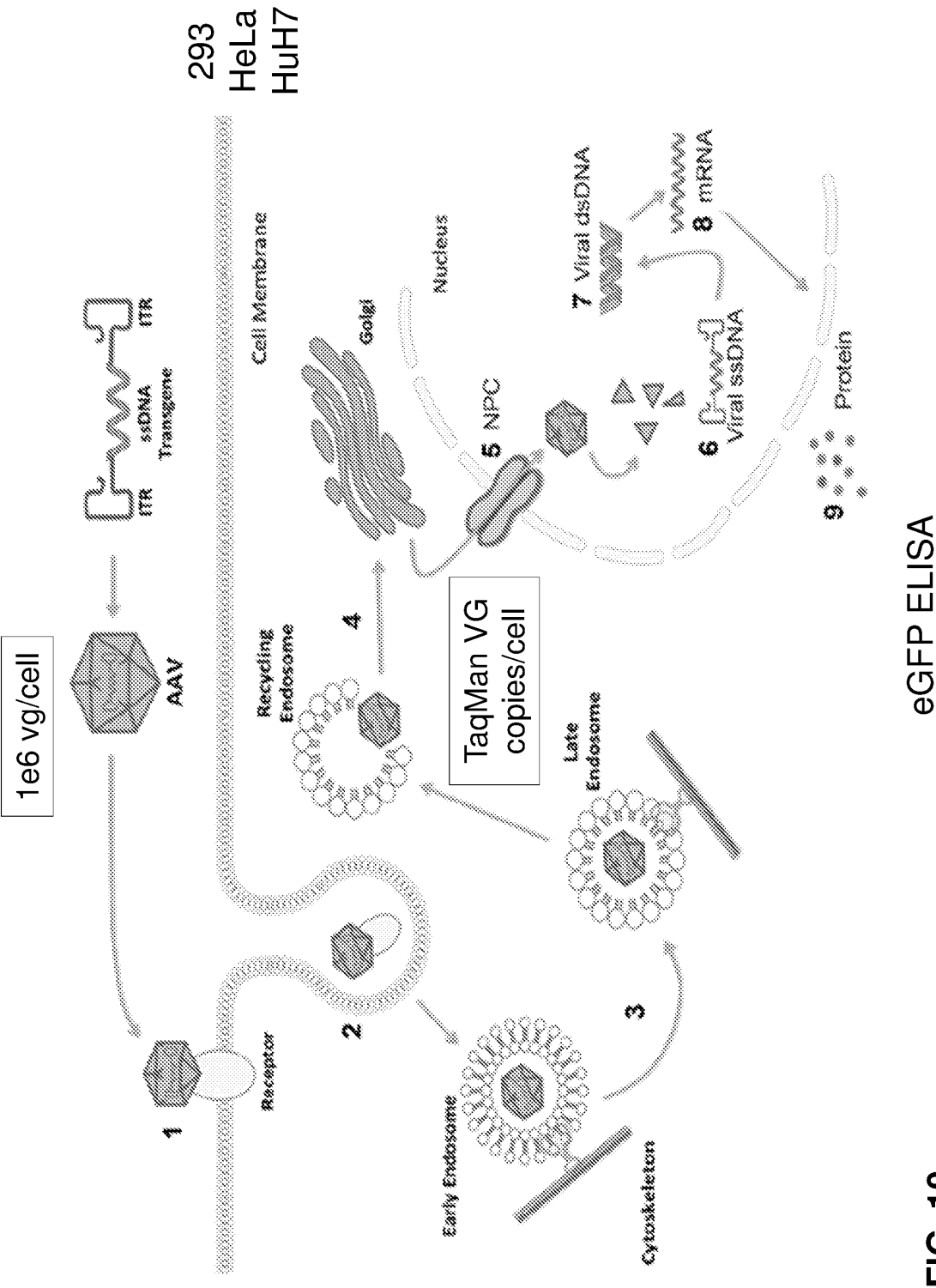


FIG. 10

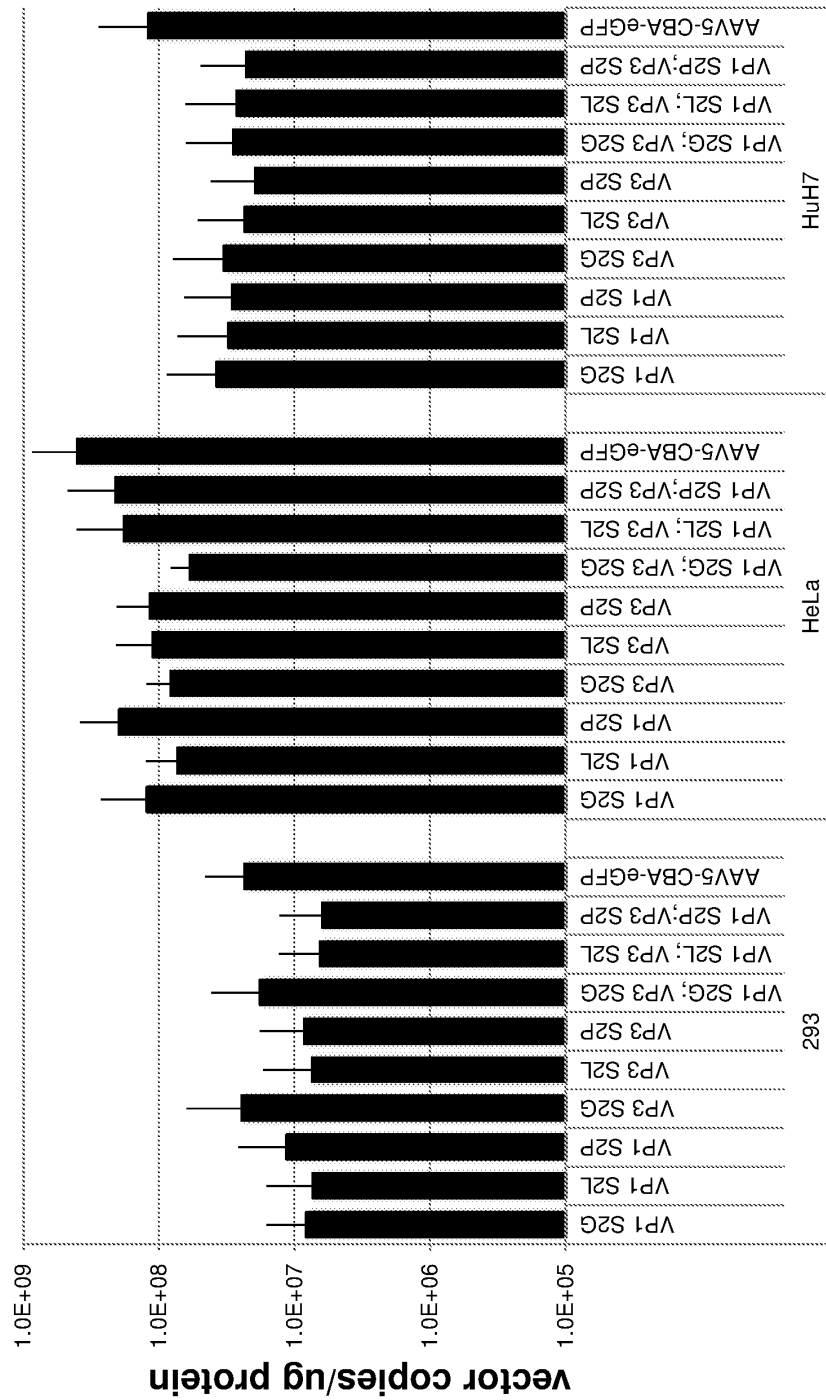
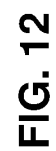


FIG. 11



	(1)	1	10	20	30	40	50	60
AAVRh10	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV10	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV8	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV7	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV1	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV6	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV2	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV3	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV11	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV12	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV4	(1)	-MTDGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV5	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
AAV9	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK
Consensus	(1)	MAADGYLPDWLE	DNLSE	GIRENWD	DLKPCG	PKPKANQQKQDD	GRGLVLPGYKYLGP	ENGLDK

FIG. 13

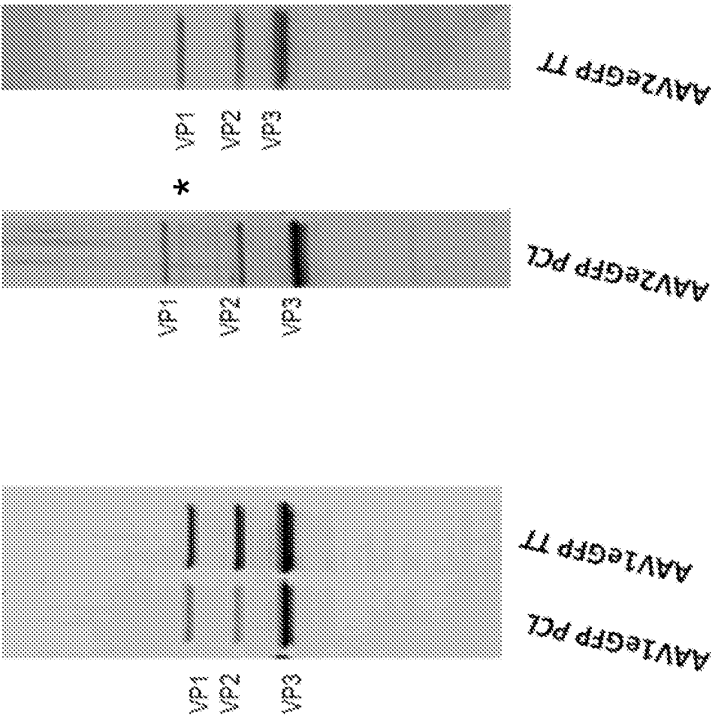


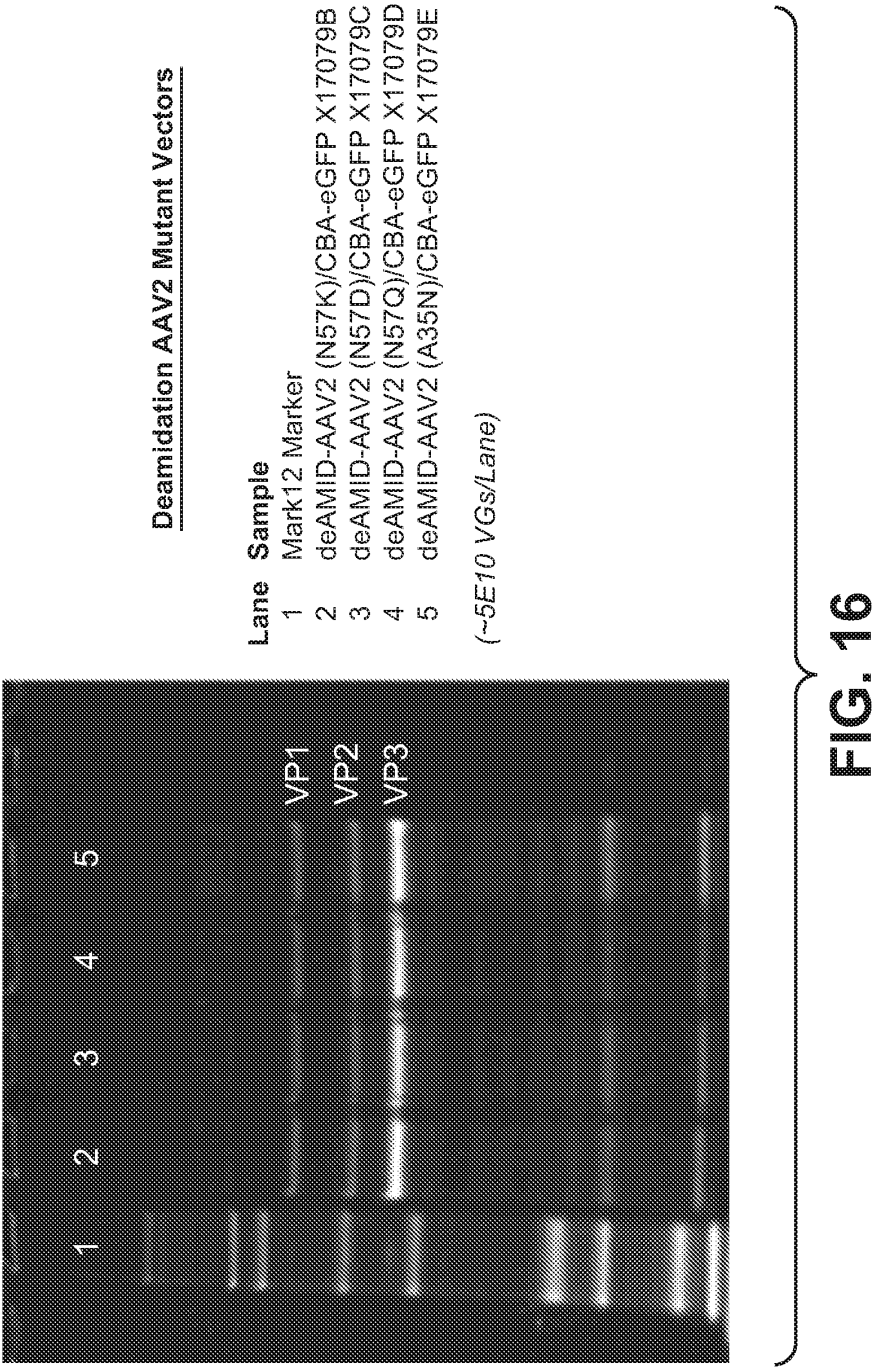
FIG. 14

Deamidation of N57(G)

	% Deamidation on N57	replicate
AAV2(A35N)	17.8	1
AAV2(G58D)	1.1	1
AAV2 control	5.7	2

AAV2(A35N) has been stored at 4C for 1 months

FIG. 15



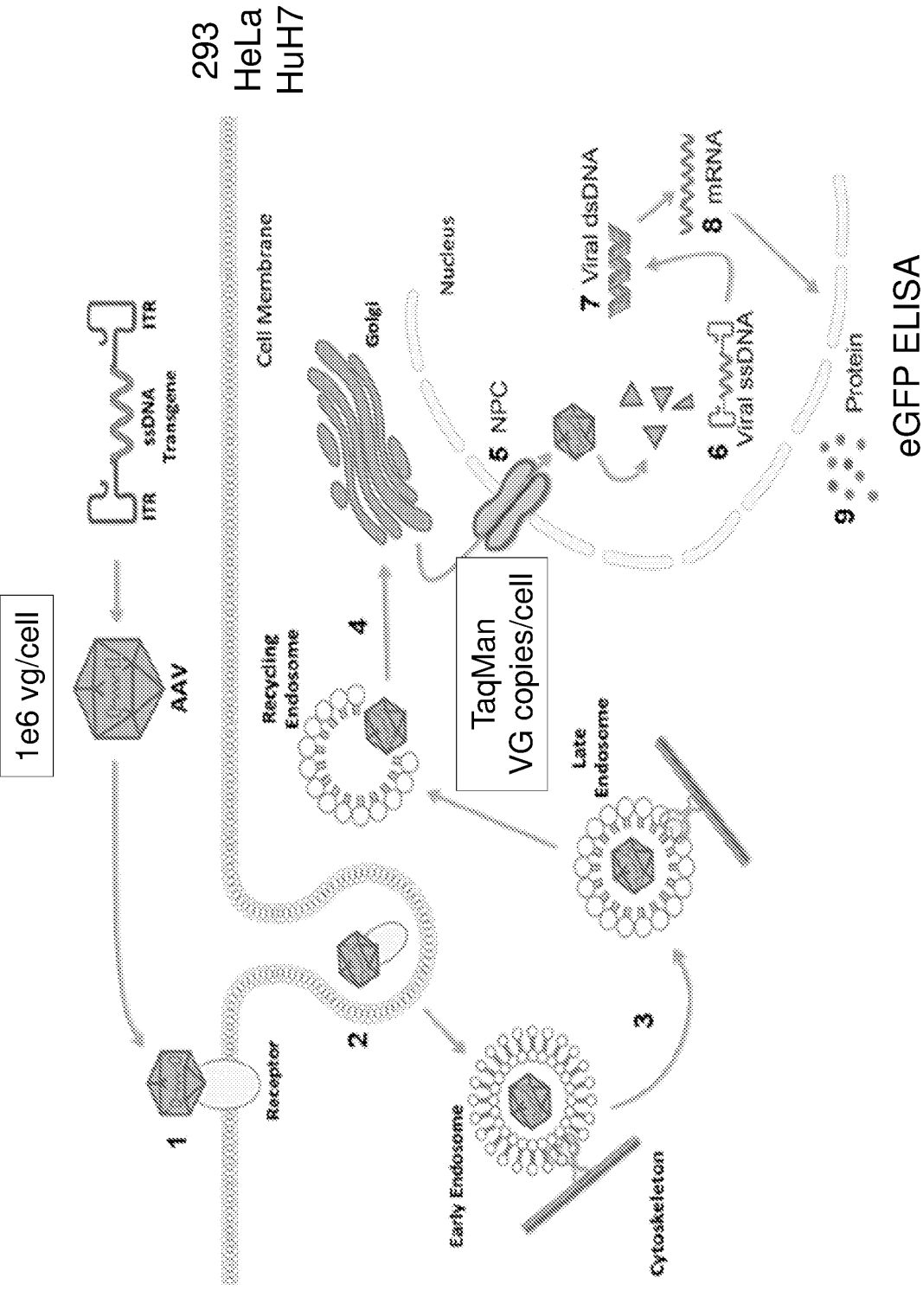


FIG. 17

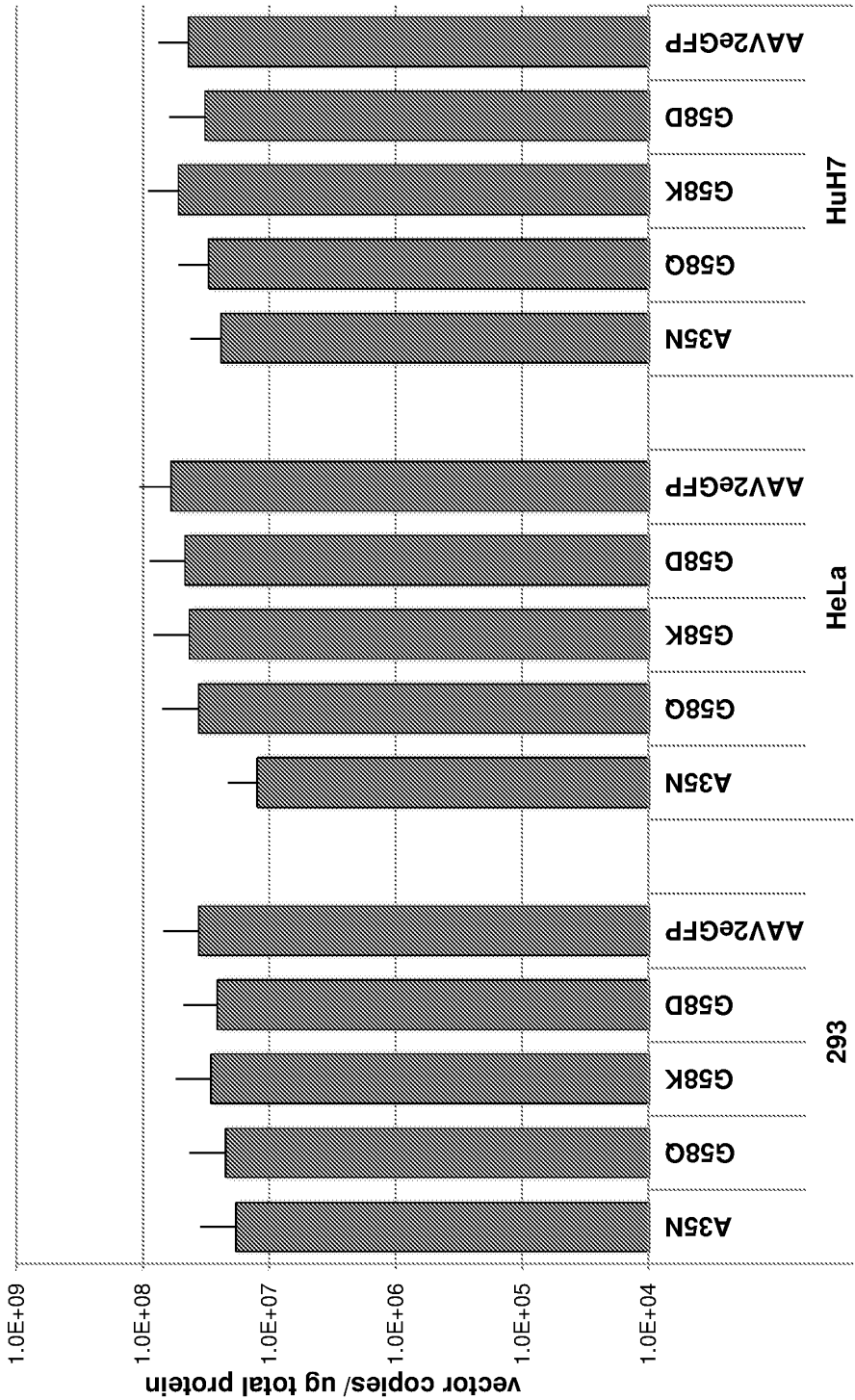


FIG. 18

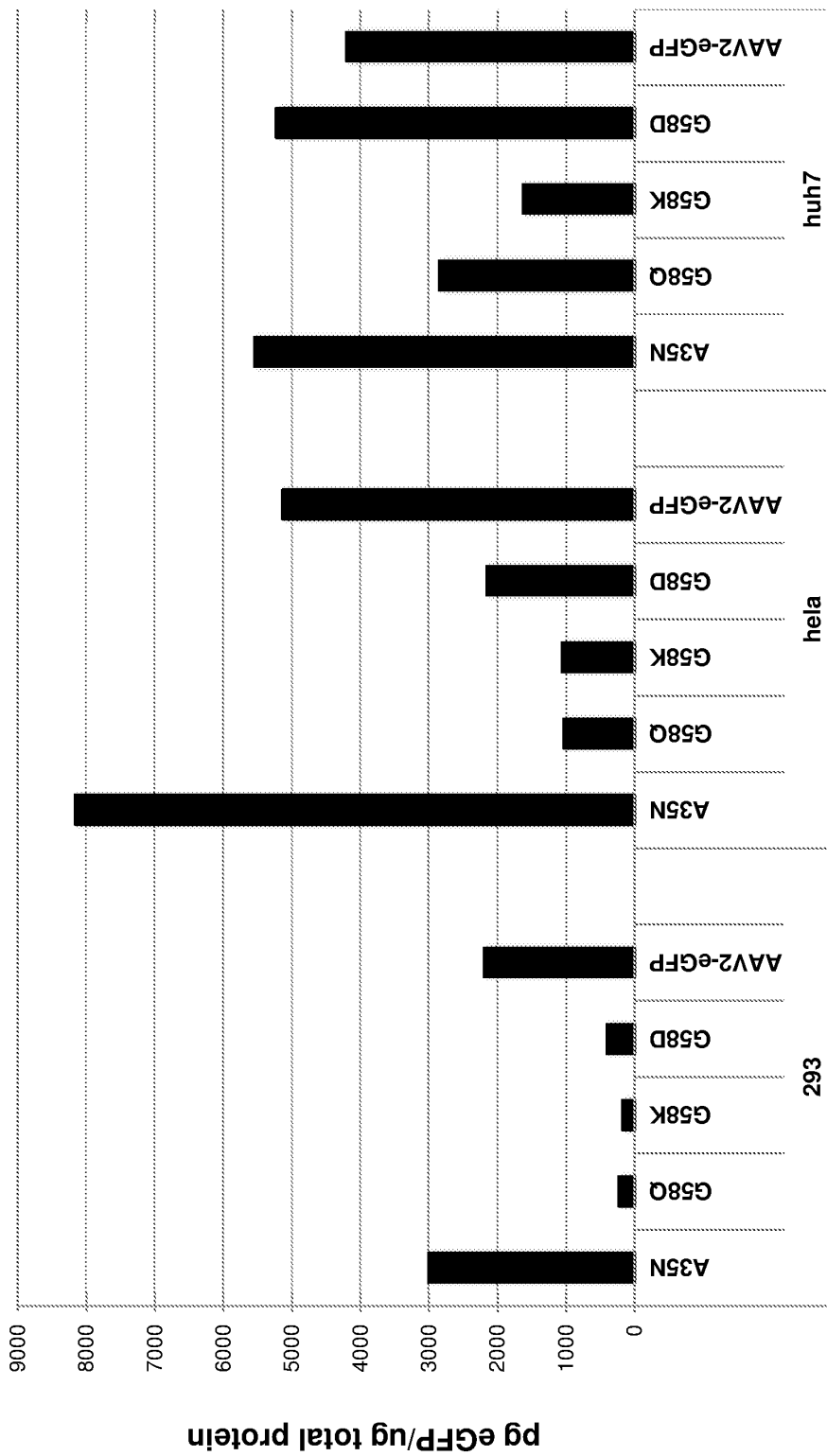


FIG. 19