

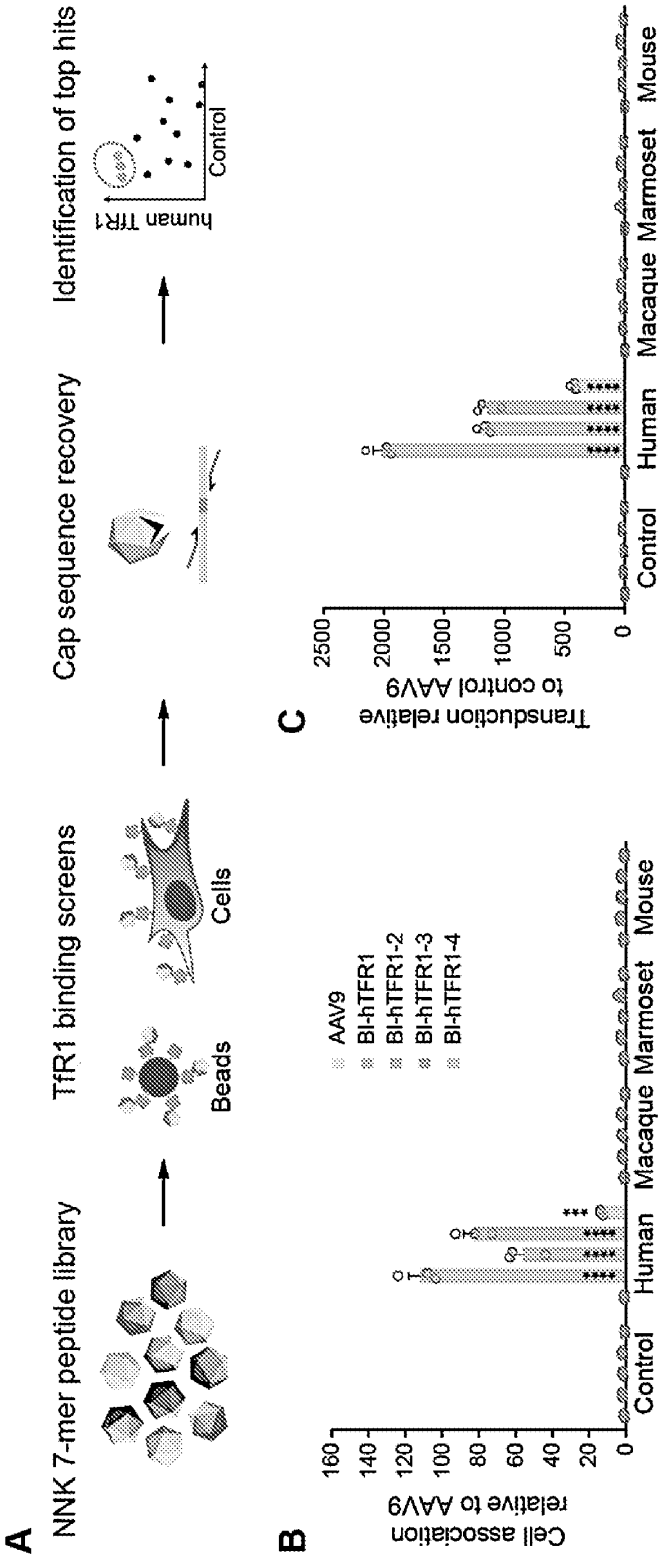
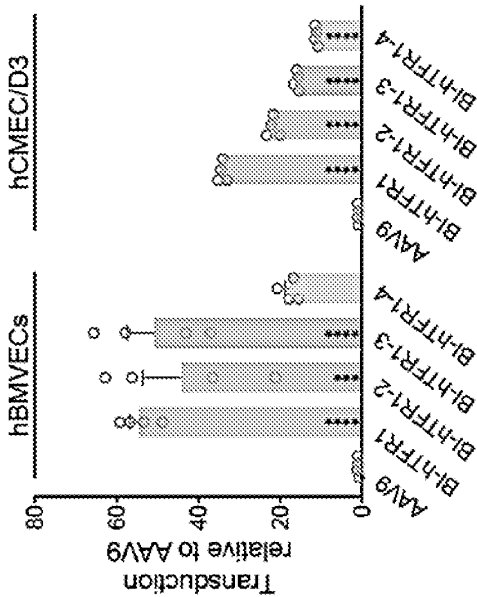
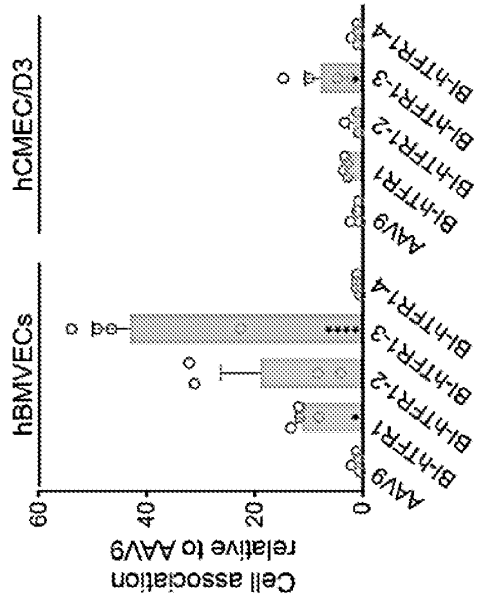


FIG. 1A-1C



E



D

FIG. 1D-1E

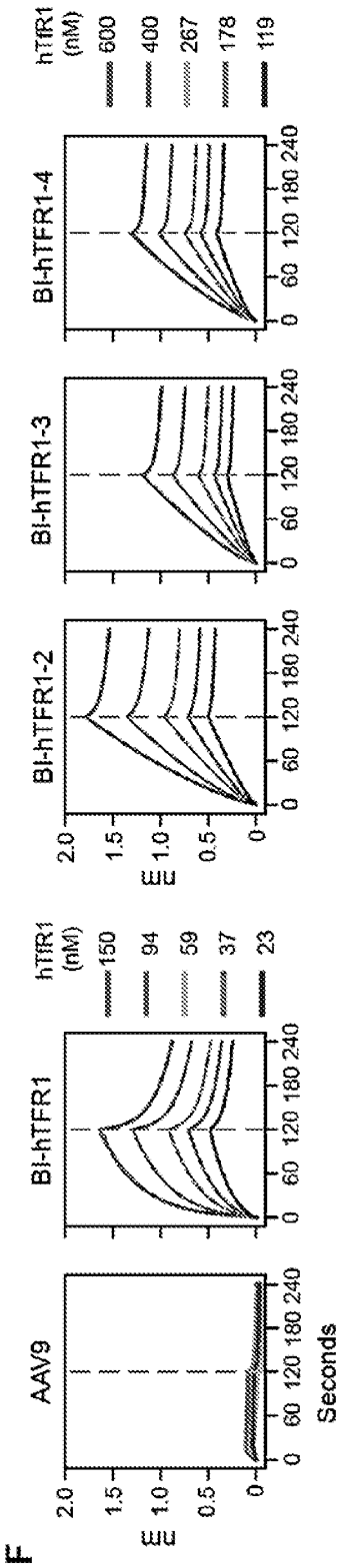


FIG. 1F

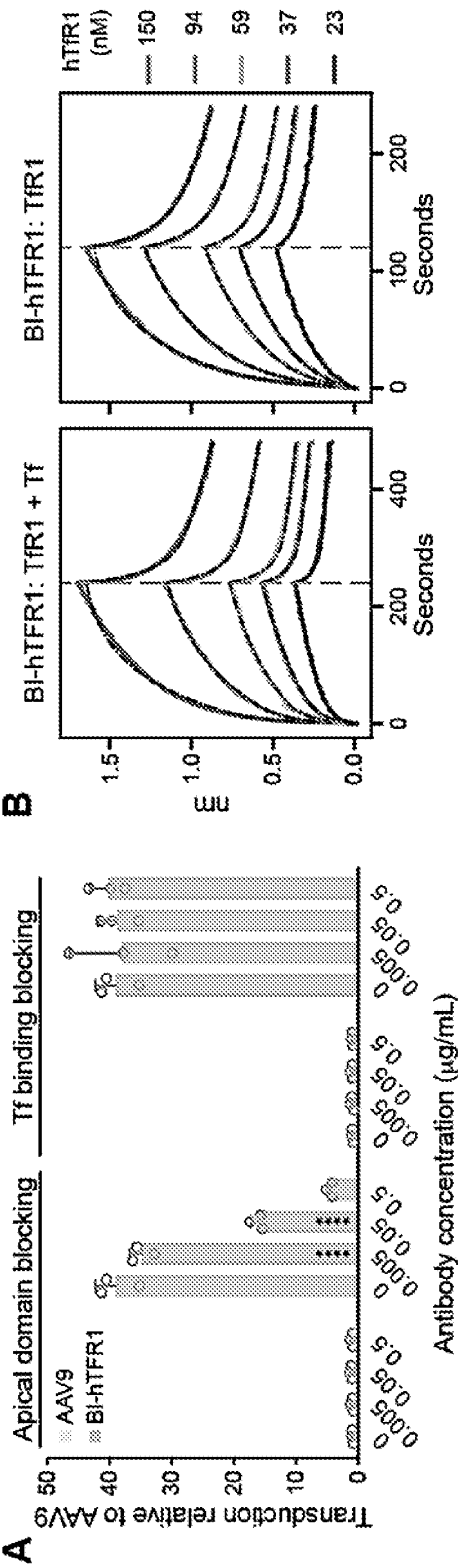


FIG. 2A-2B

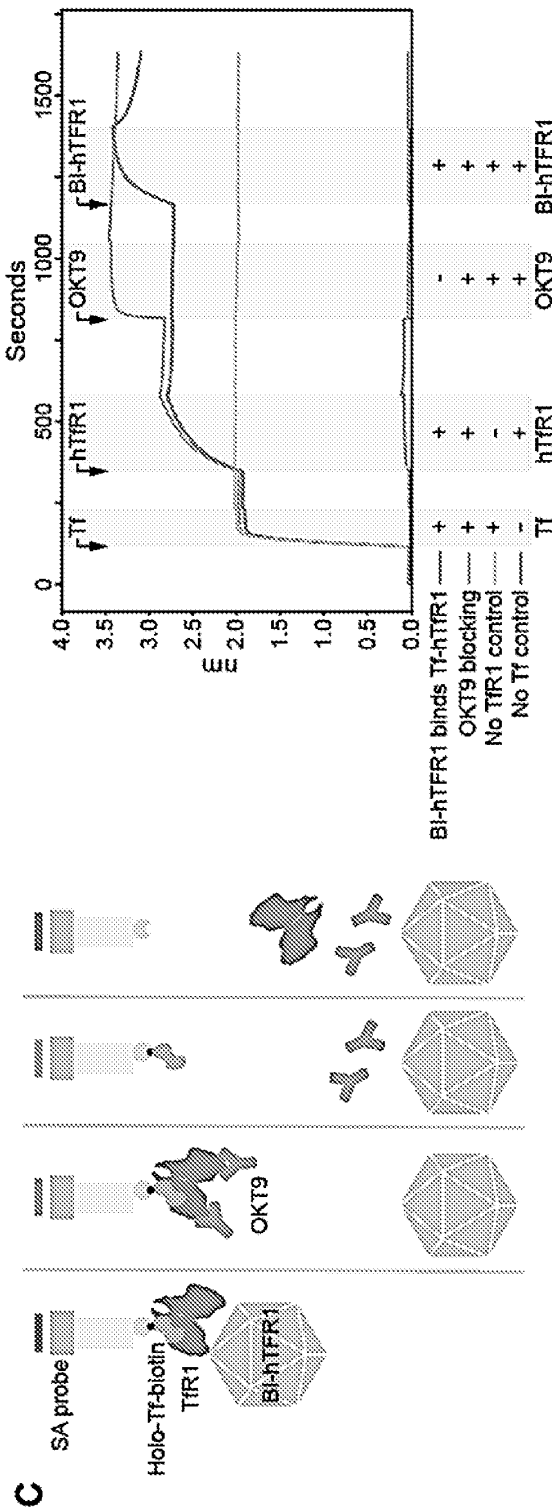


FIG. 2C

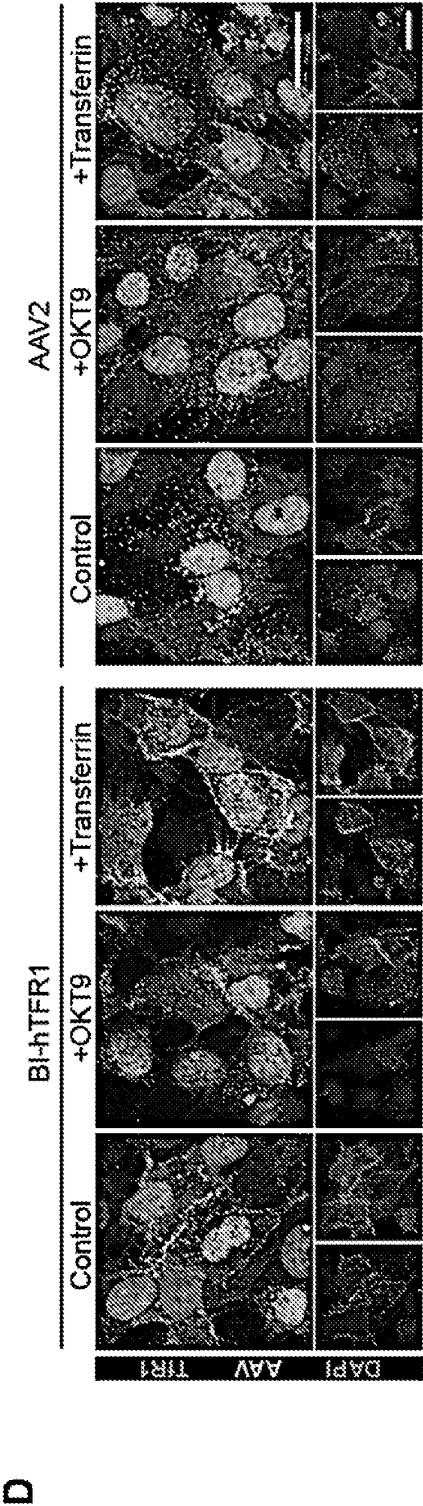


FIG. 2D

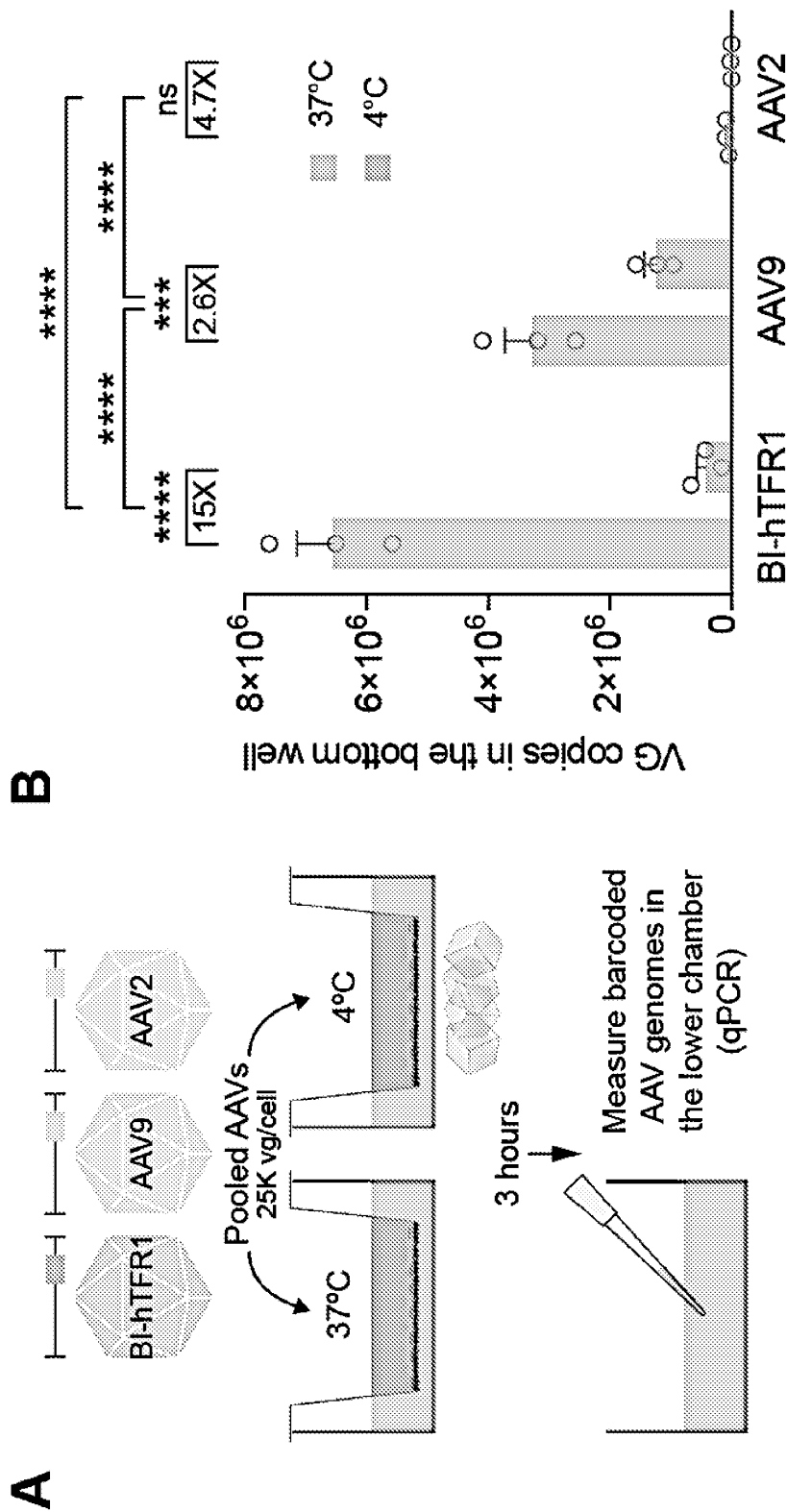


FIG. 3A-3B

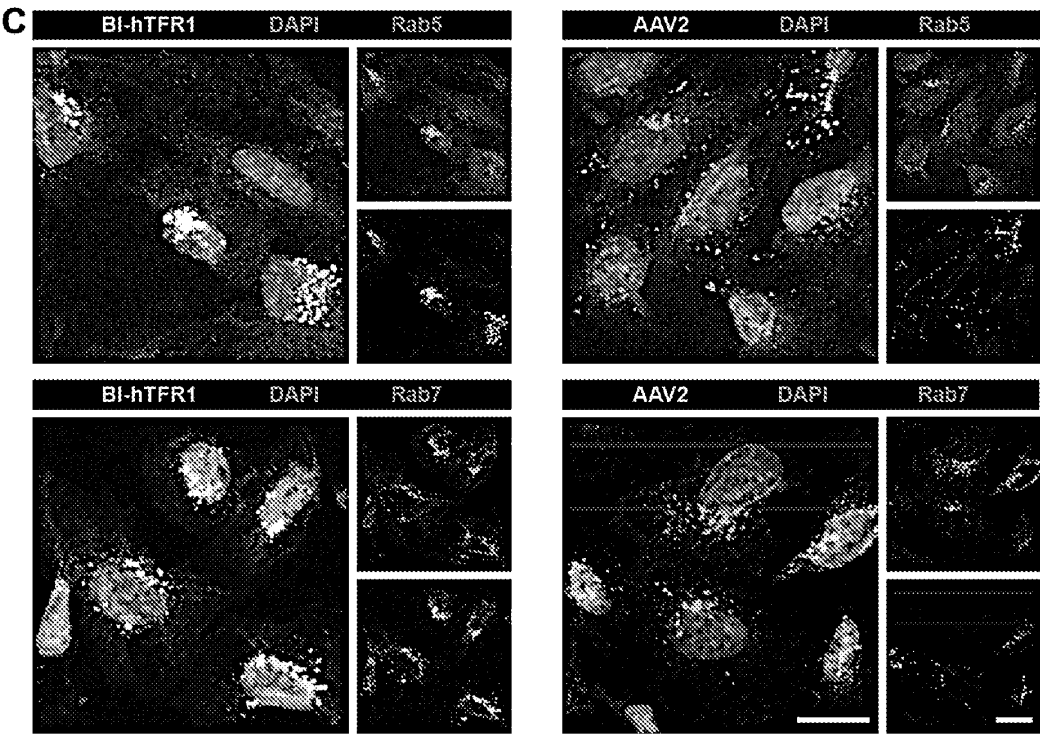
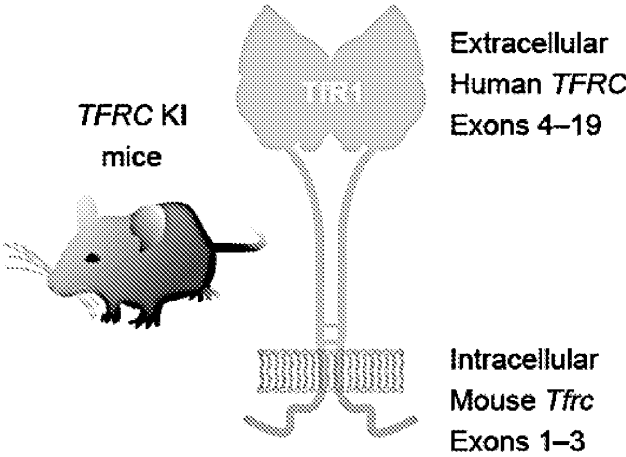


FIG. 3C

A



B

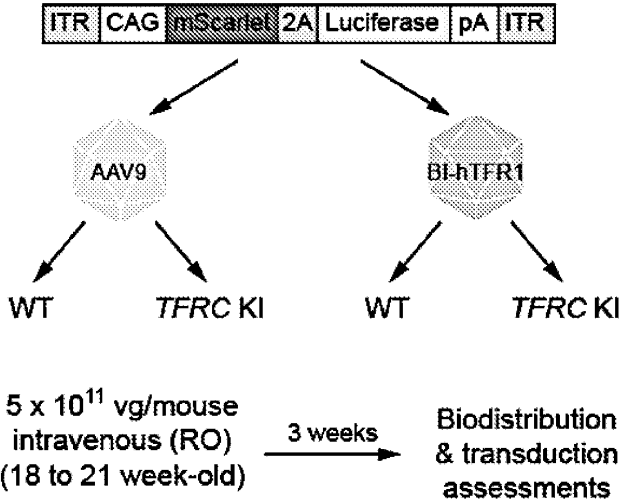


FIG. 4A-4B

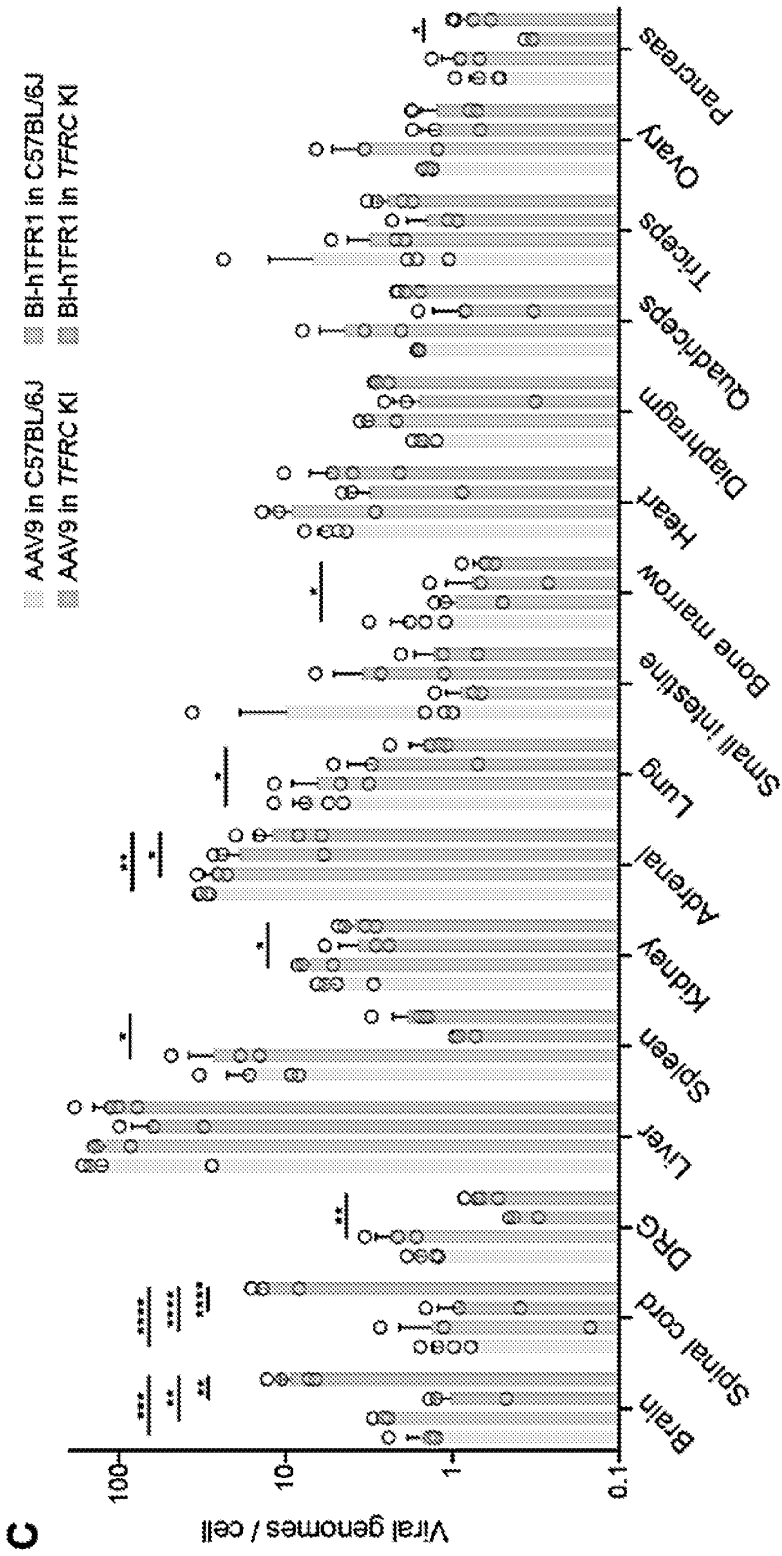


FIG. 4C

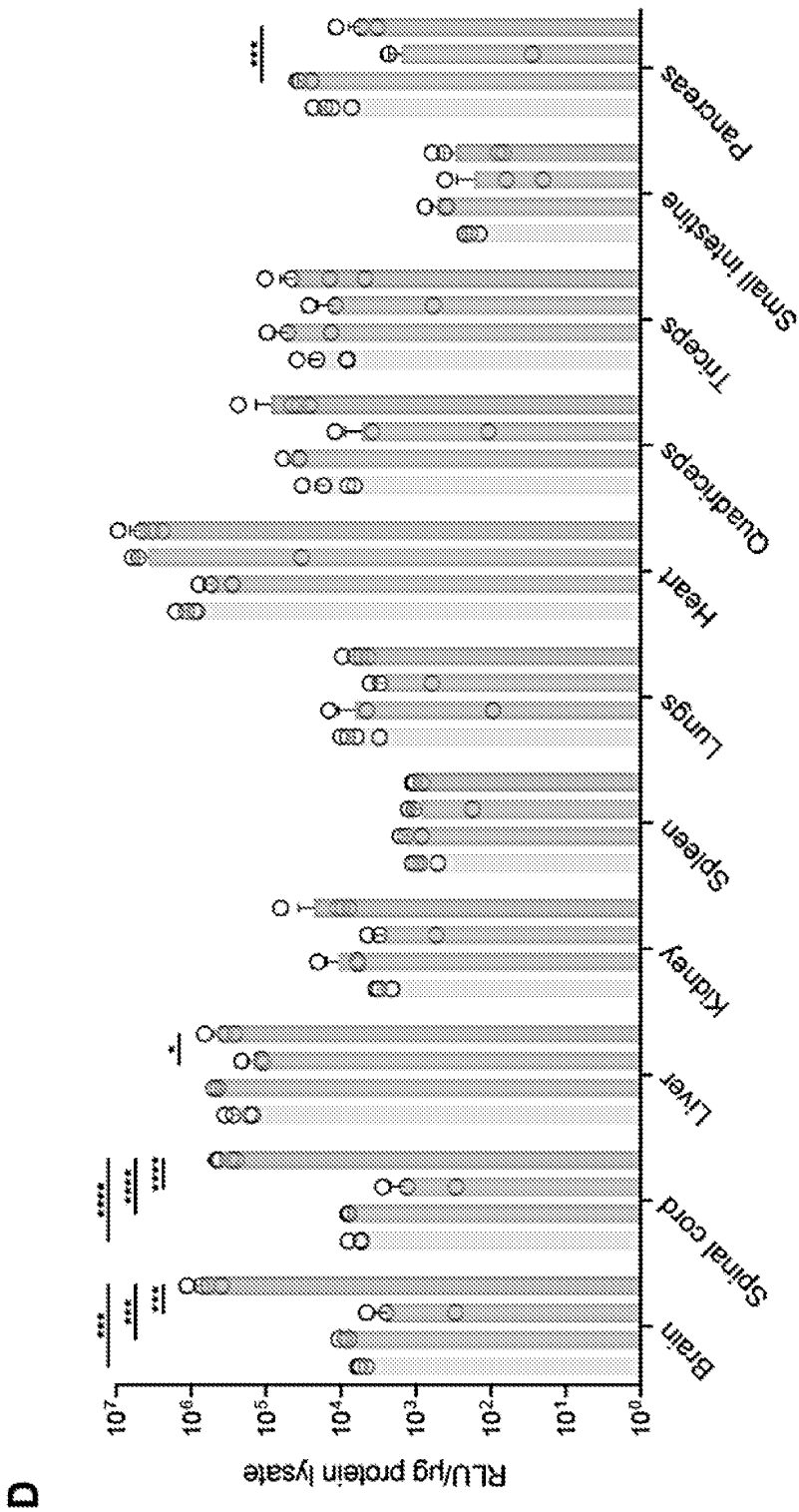


FIG. 4D

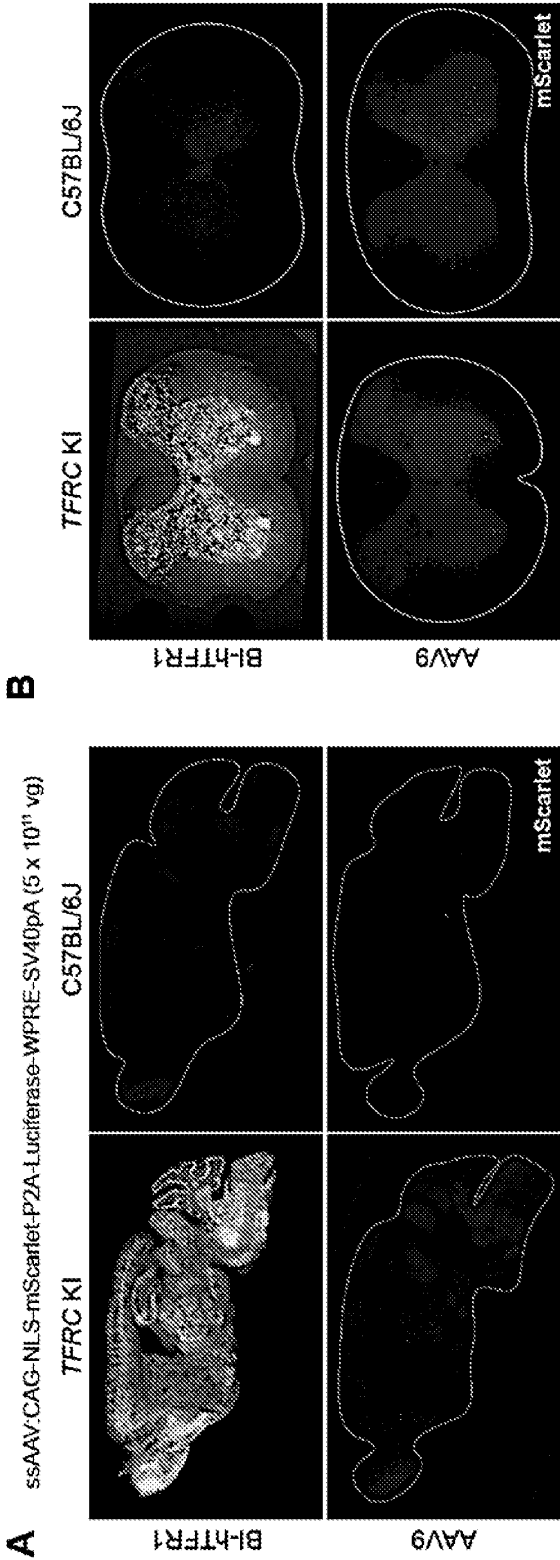


FIG. 5A-5B

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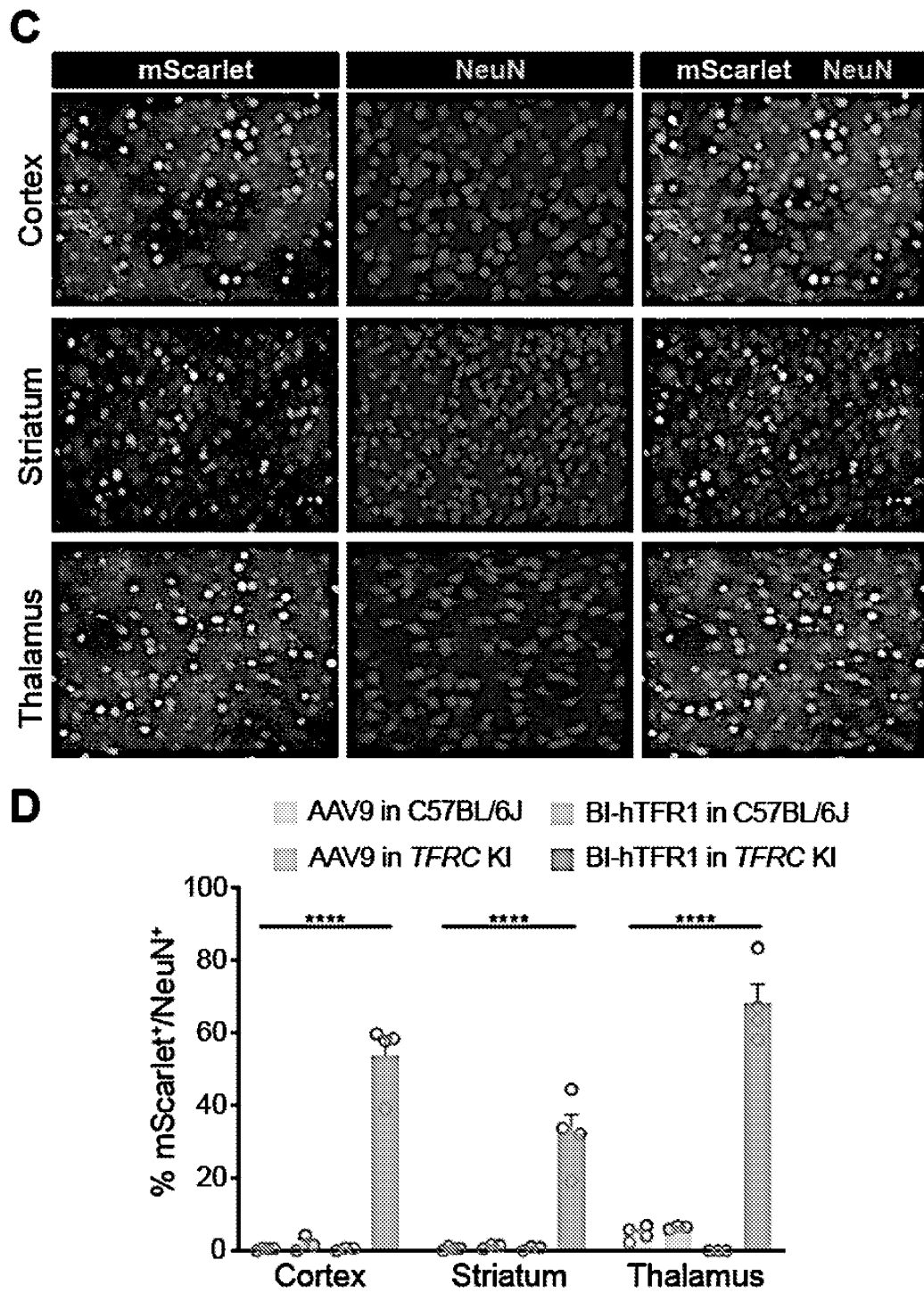


FIG. 5C-5D

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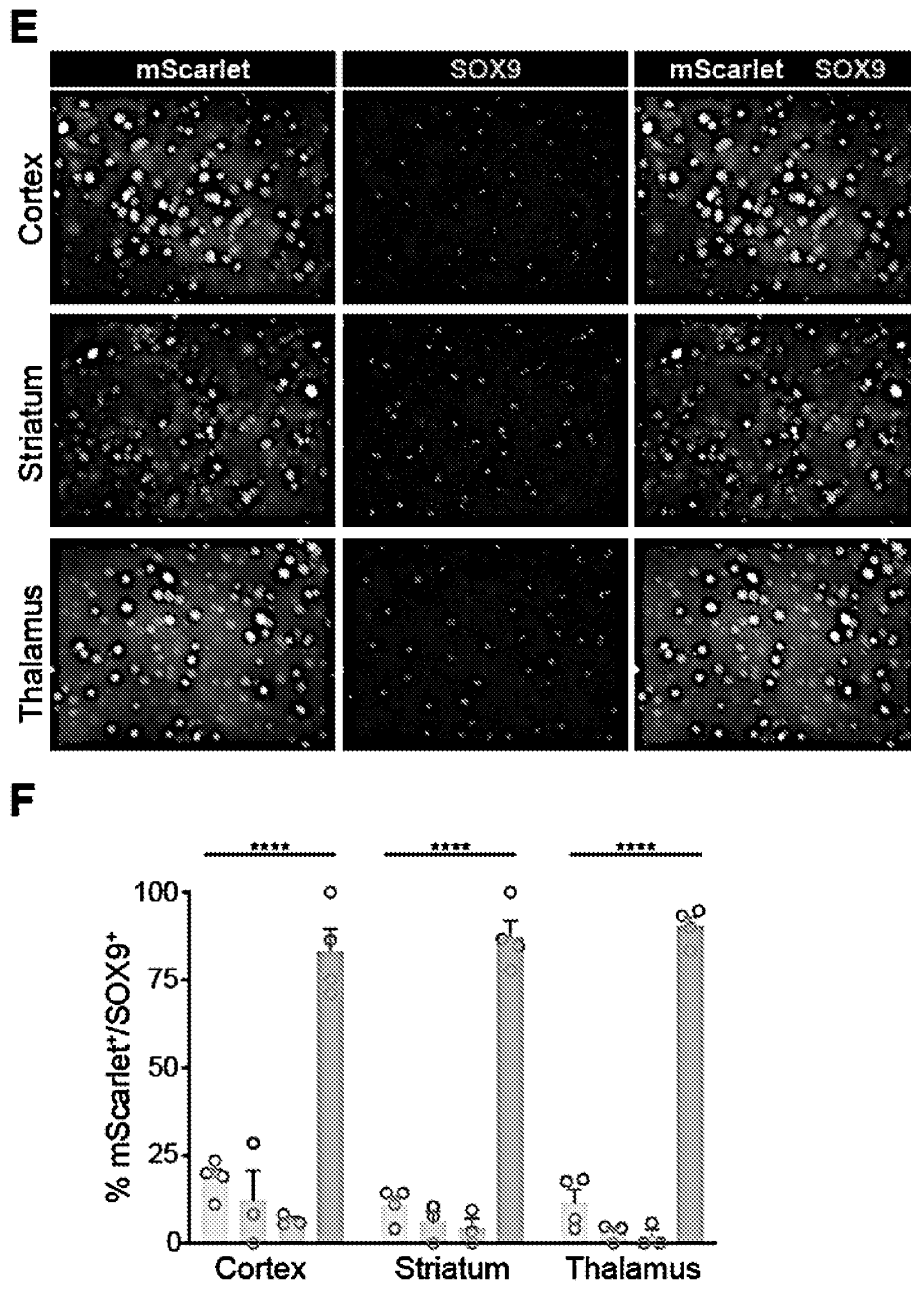


FIG. 5E-5F

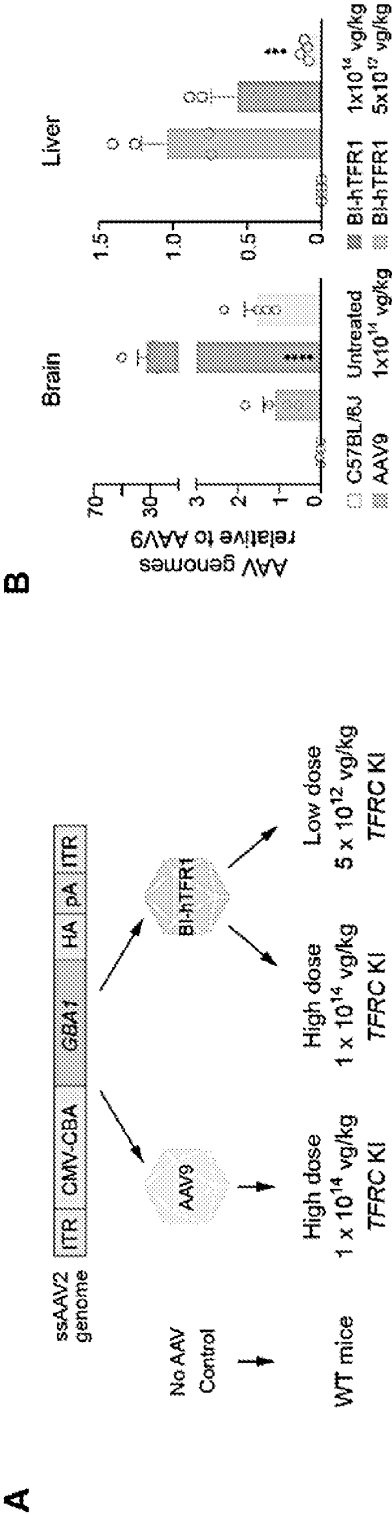


FIG. 6A-6B

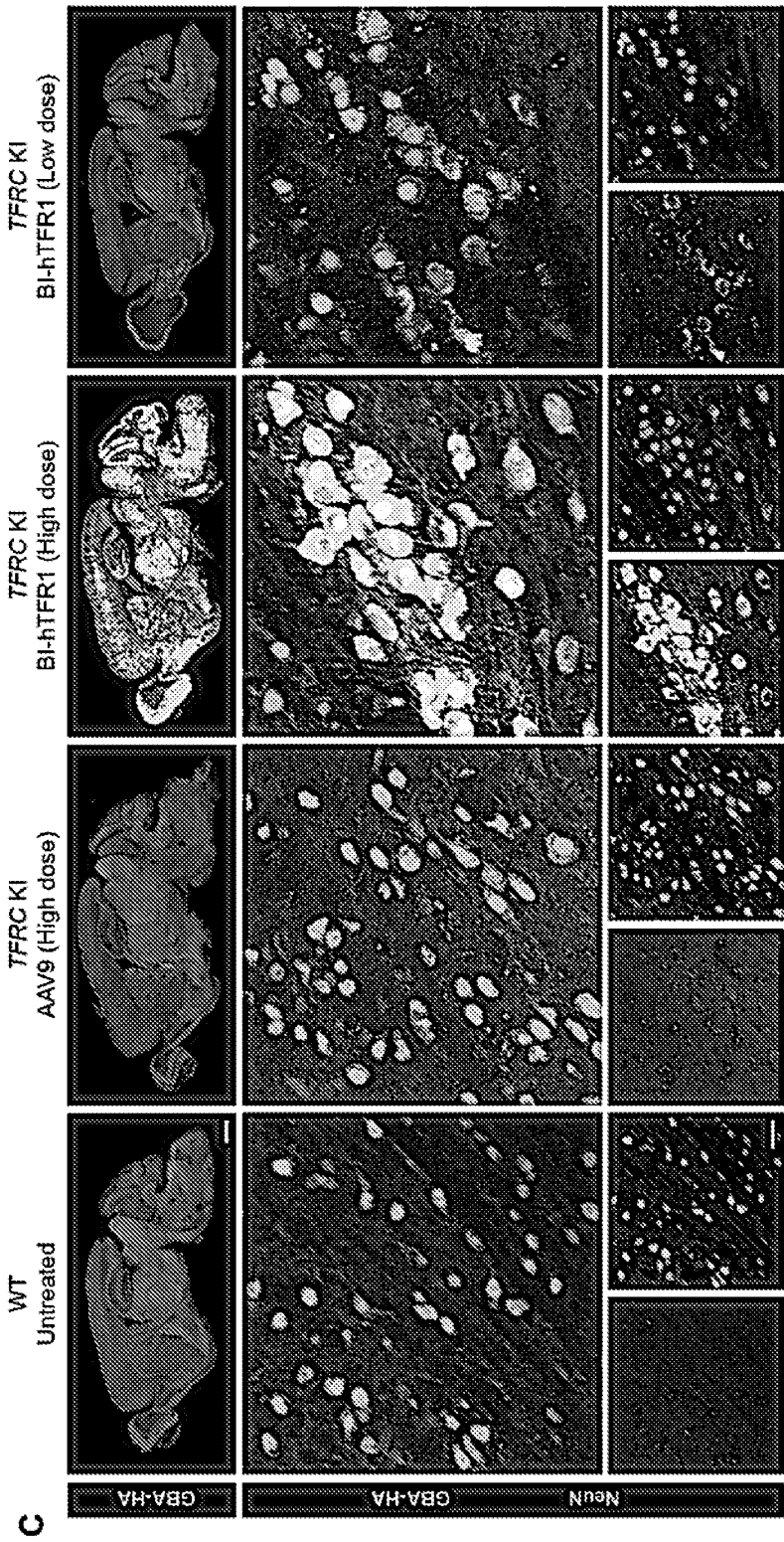


FIG. 6C

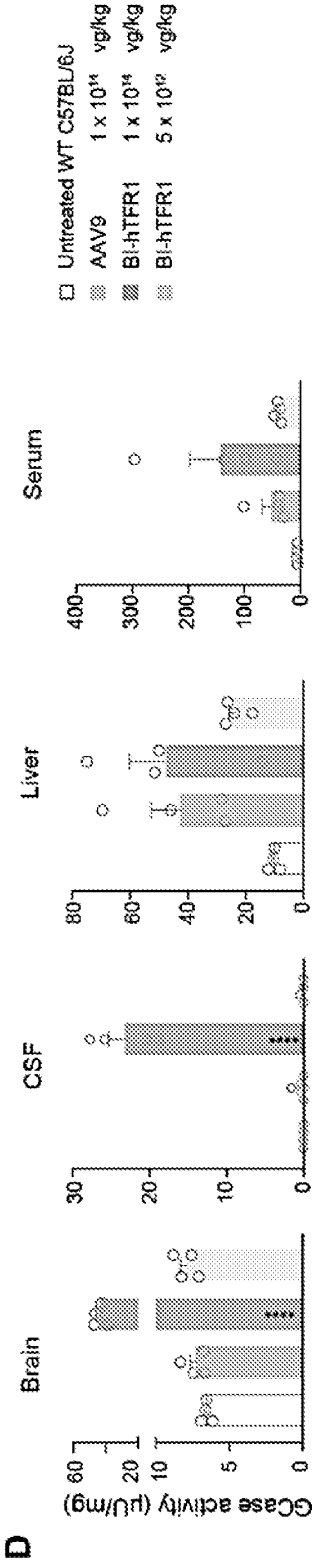


FIG. 6D

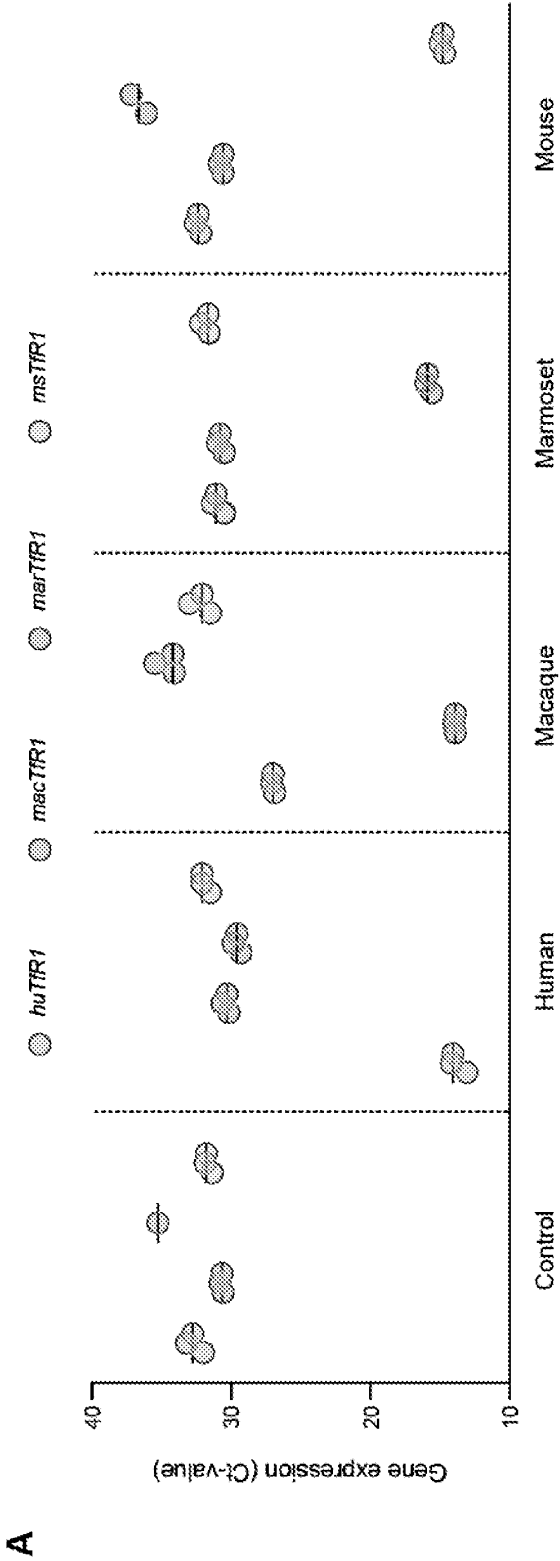


FIG. 7A

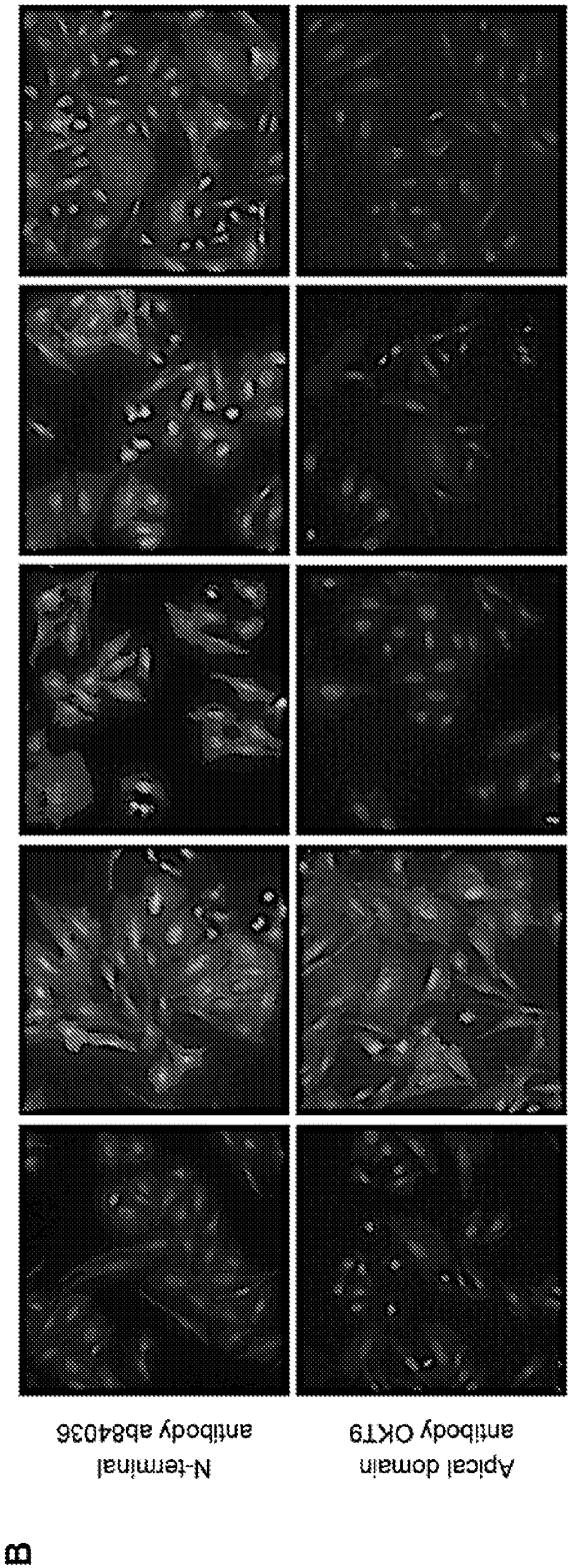


FIG. 7B

A

Capsid	K _D 1 (nM)	K _D 2 (nM)	k _{on} 1 (M ⁻¹ s ⁻¹)	k _{on} 2 (M ⁻¹ s ⁻¹)	k _{off} 1 (s ⁻¹)	k _{off} 2 (s ⁻¹)	Average R ²
AAV9				no binding			
BI-hTFR1	61.4 ± 12.1	14.6 ± 2.54	9.35 ± 0.45 x 10 ⁵	1.14 ± 0.22 x 10 ⁵	5.70 ± 1.07 x 10 ⁻²	1.76 ± 0.55 x 10 ⁻³	0.998
BI-hTFR1-2	485 ± 78.9	77.8 ± 6.56	1.26 ± 0.12 x 10 ⁵	7.66 ± 0.21 x 10 ³	5.93 ± 0.69 x 10 ⁻²	5.93 ± 0.36 x 10 ⁻⁴	0.997
BI-hTFR1-3*	568 ± 71.0	132 ± 23.0	1.60 ± 0.06 x 10 ⁵	4.41 ± 0.48 x 10 ³	9.04 ± 0.79 x 10 ⁻²	5.72 ± 0.39 x 10 ⁻⁴	0.997
BI-hTFR1-4*	904 ± 467	58.8 ± 7.10	1.34 ± 0.67 x 10 ⁵	8.80 ± 0.71 x 10 ³	8.97 ± 0.23 x 10 ⁻²	5.13 ± 0.21 x 10 ⁻⁴	0.997

FIG. 8A

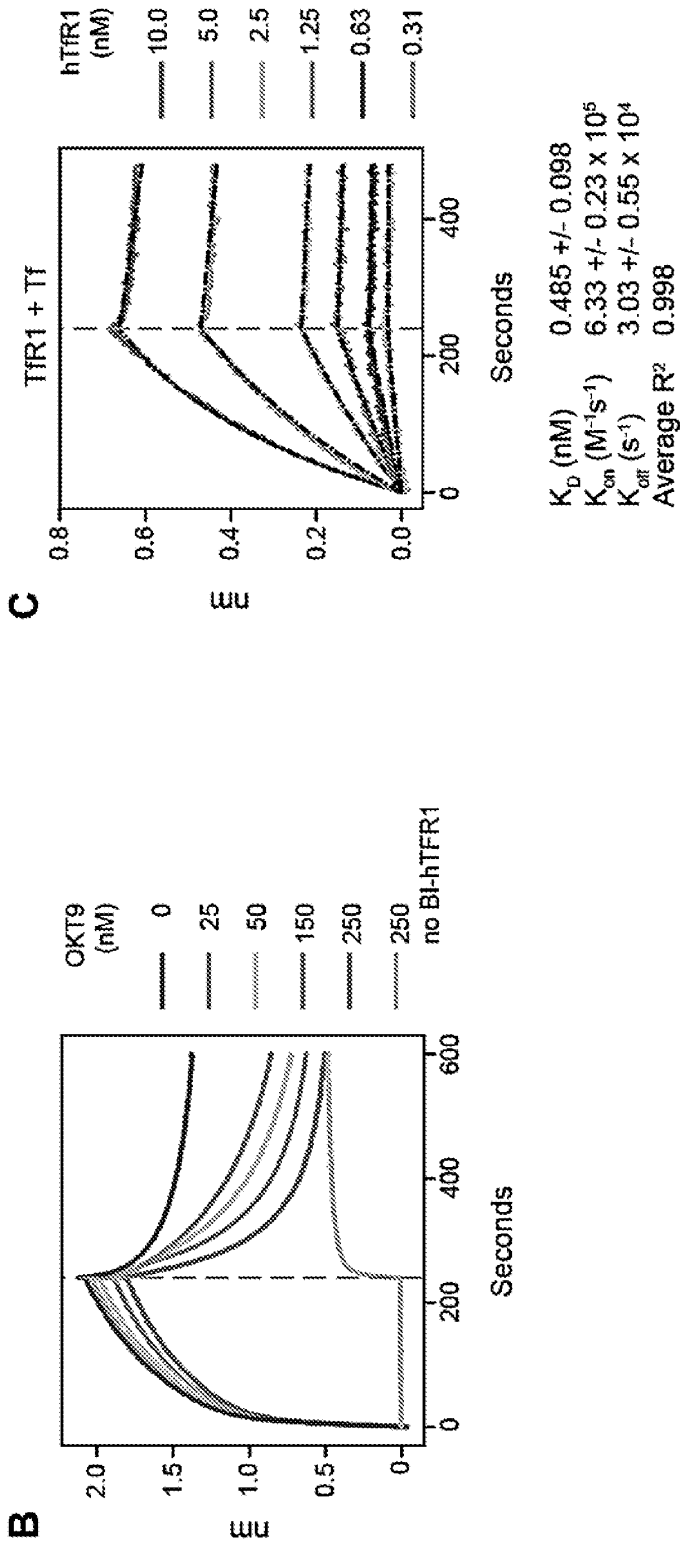


FIG. 8B-8C

D

Ligand	Analyte	K_D1 (nM)	K_D2 (nM)	$k_{on}1$ ($M^{-1}s^{-1}$)	$k_{off}2$ ($M^{-1}s^{-1}$)	$k_{off}1$ (s^{-1})	$k_{off}2$ (s^{-1})	Average R^2
AAV9	TfR1 + Tf				no binding			
BI-hTFR1	TfR1 + Tf	40.3 ± 3.4	14.8 ± 2.0	$1.40 \pm 0.08 \times 10^8$	$7.78 \pm 0.37 \times 10^4$	$5.66 \pm 0.66 \times 10^{-2}$	$1.14 \pm 0.10 \times 10^{-3}$	0.998
BI-hTFR1	TfR1	61.4 ± 12.1	14.6 ± 2.54	$9.35 \pm 0.45 \times 10^5$	$1.14 \pm 0.22 \times 10^5$	$5.70 \pm 1.07 \times 10^{-2}$	$1.76 \pm 0.55 \times 10^{-3}$	0.998

FIG. 8D

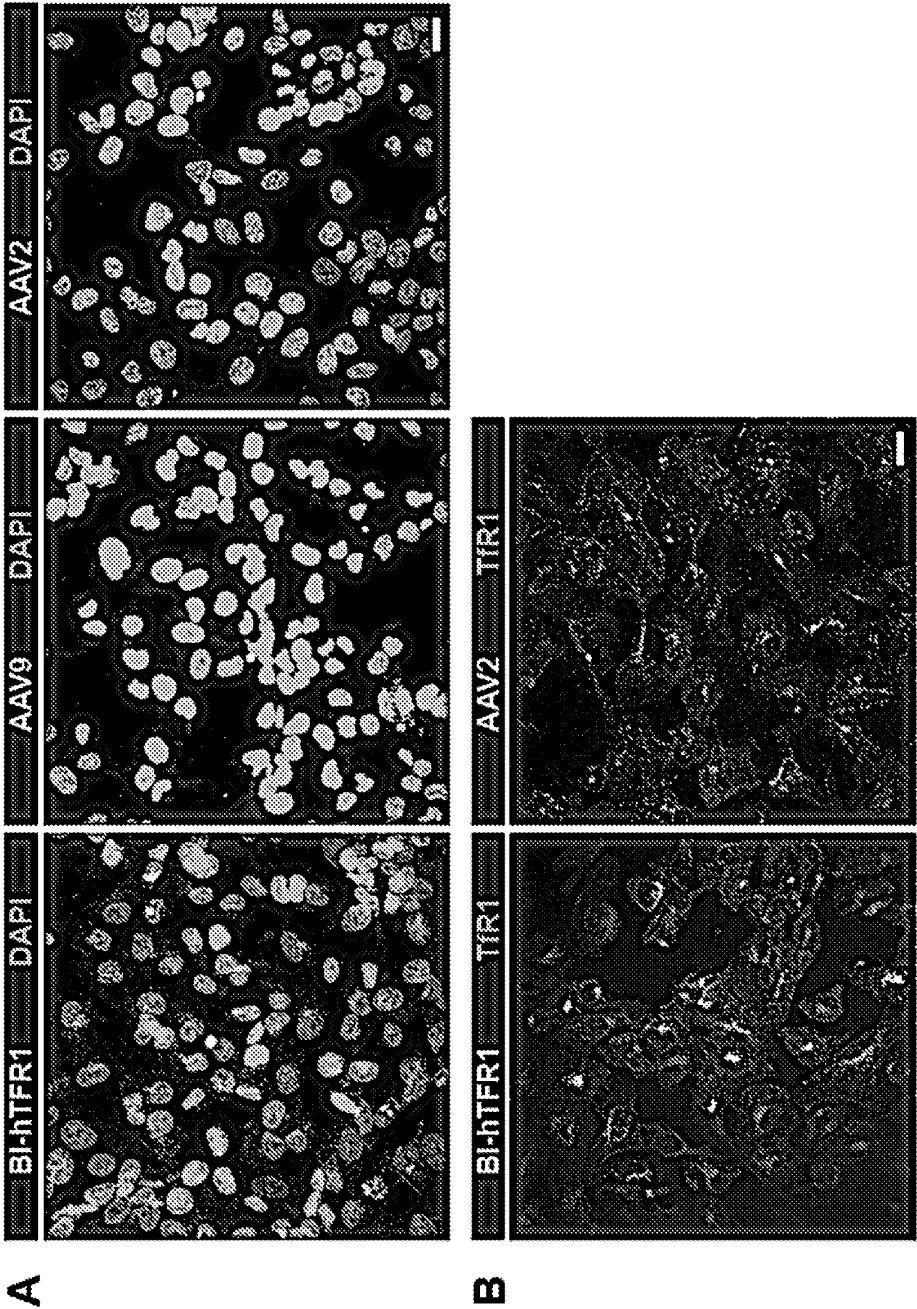


FIG. 9A-9B

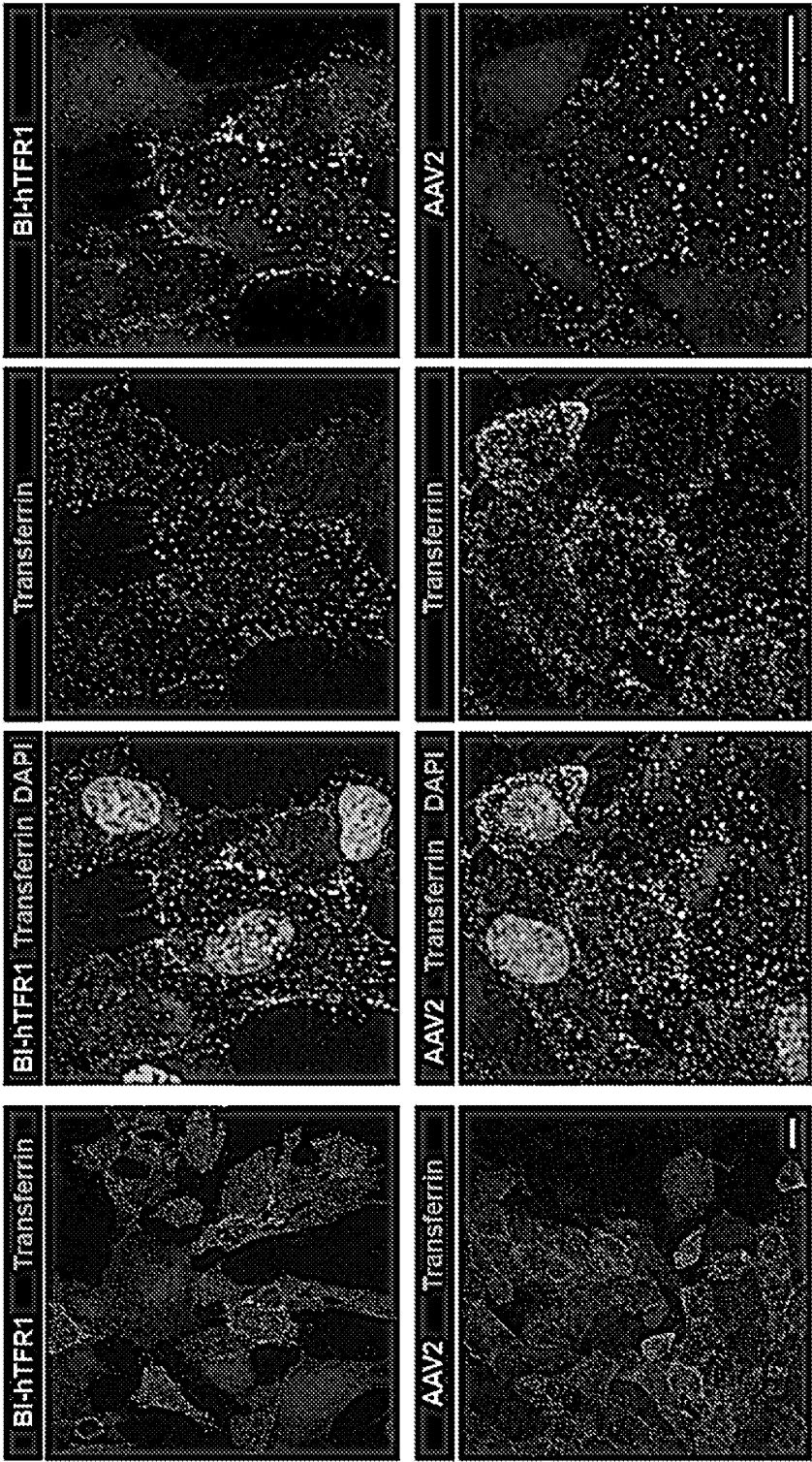


FIG. 9C

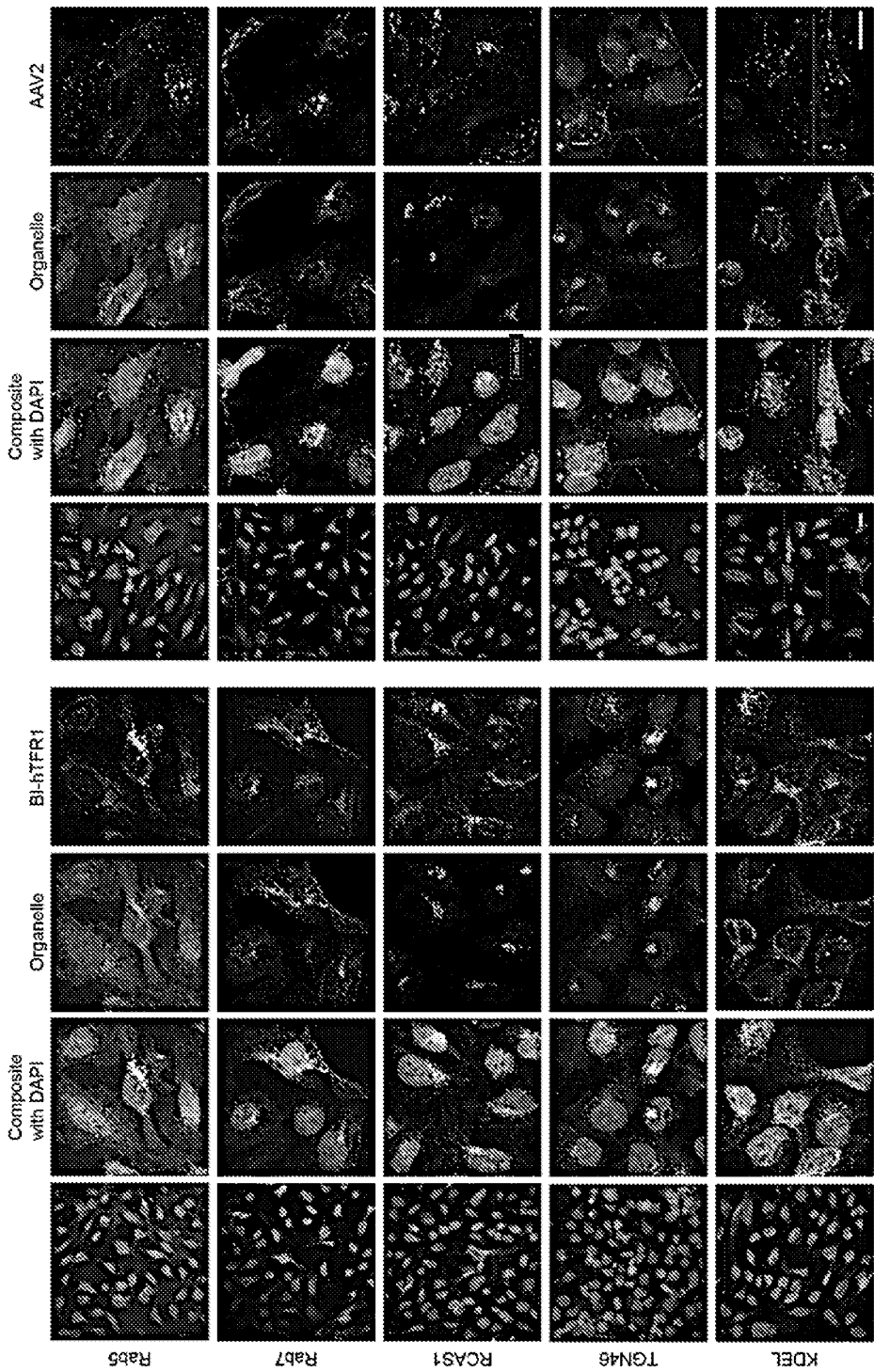


FIG. 10

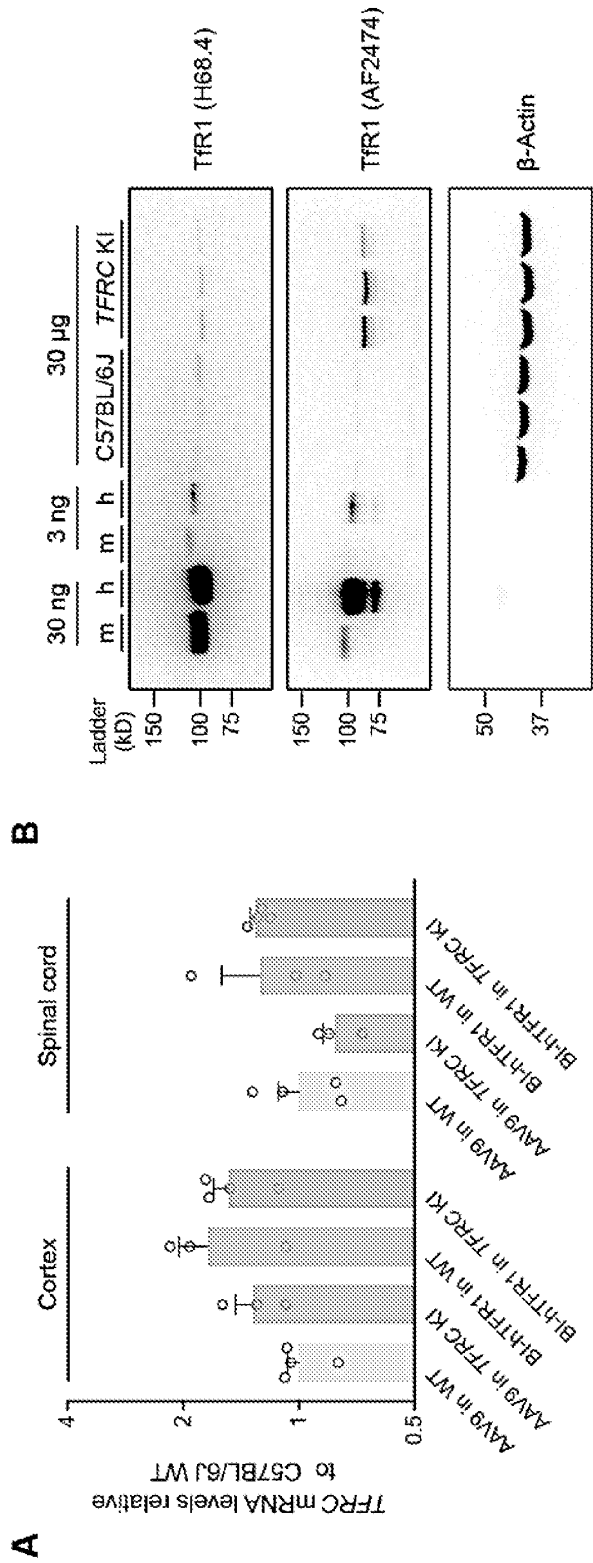


FIG. 11A-11B

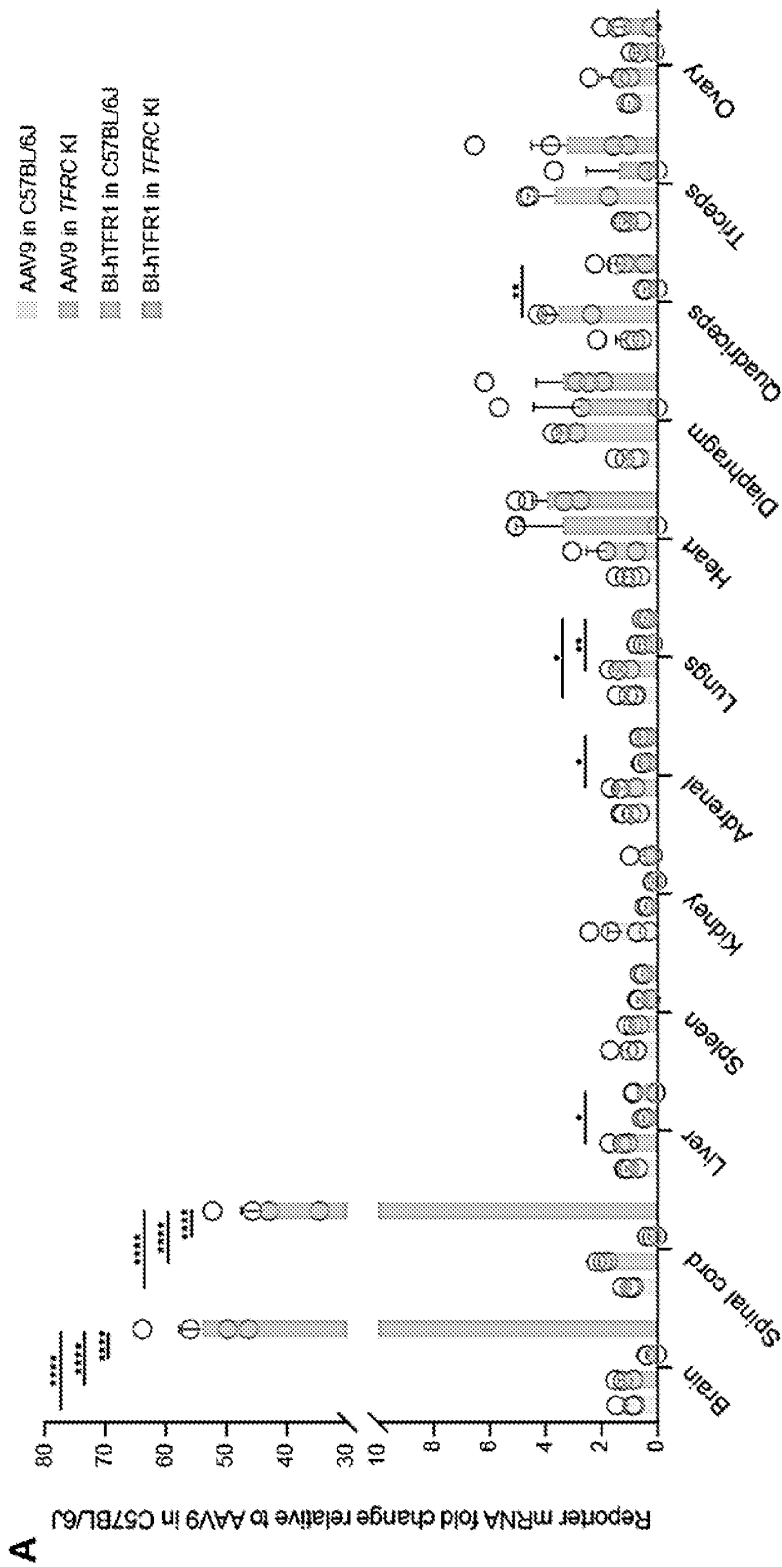


FIG. 12A

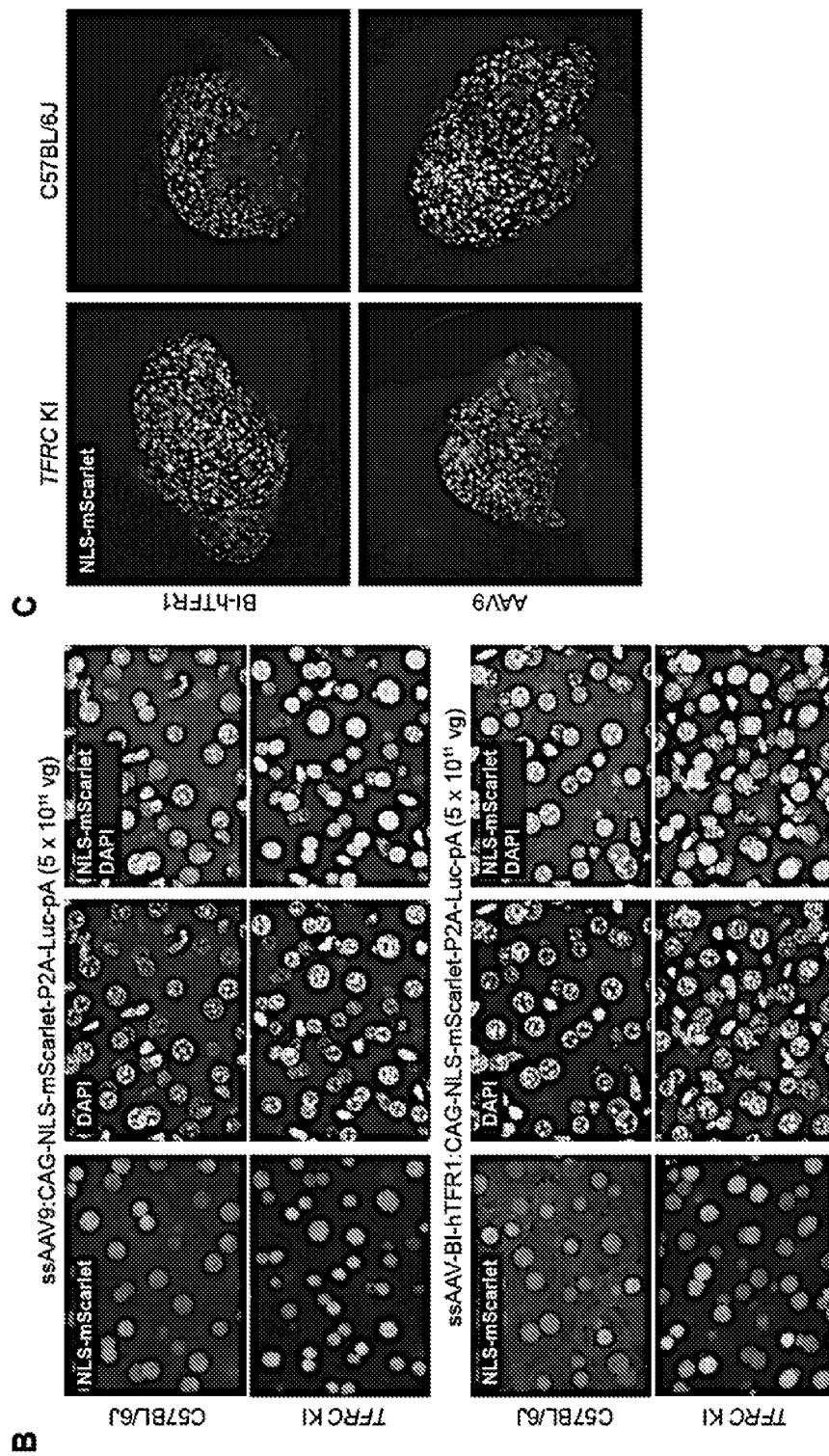


FIG. 12B-12C

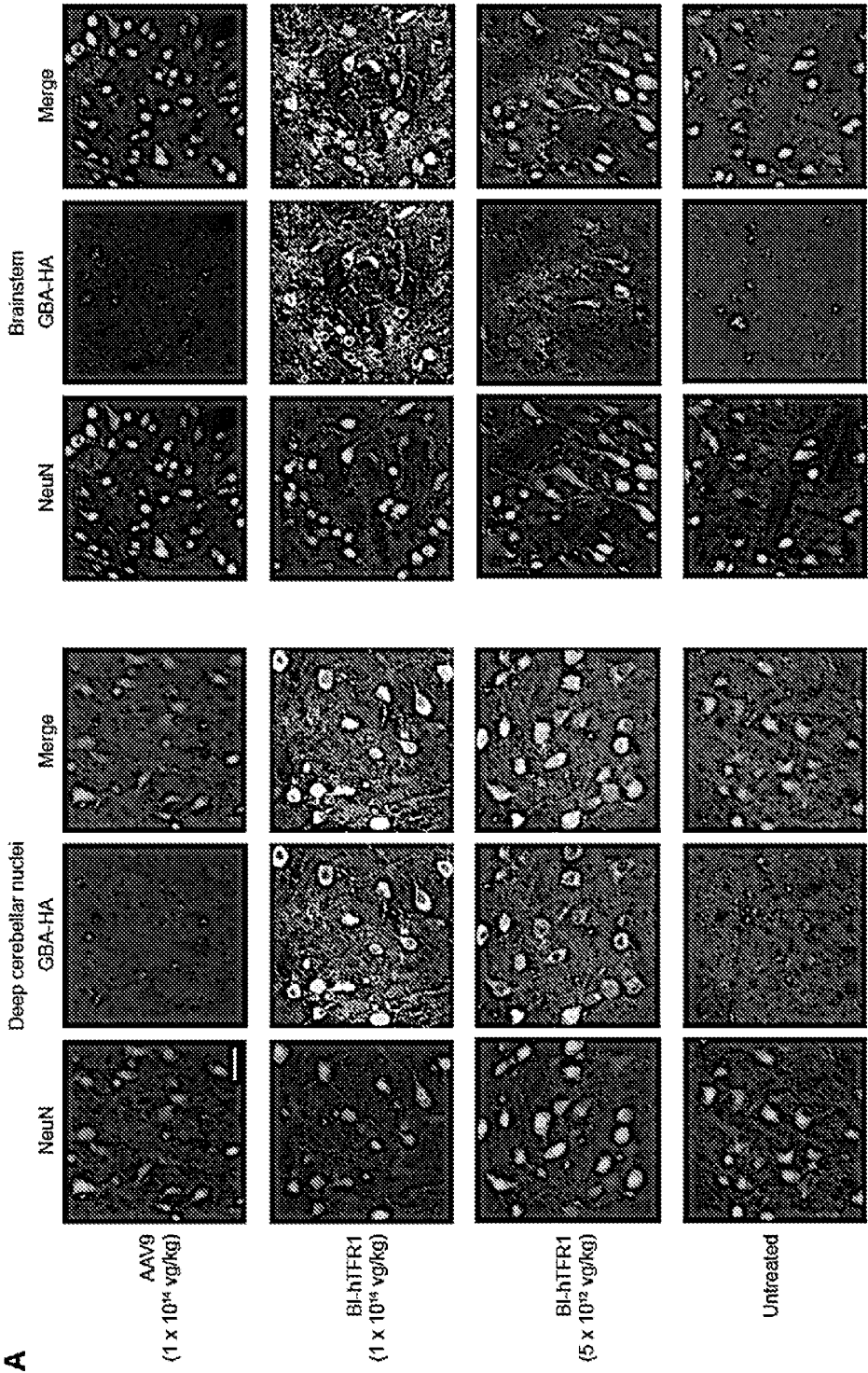


FIG. 13A

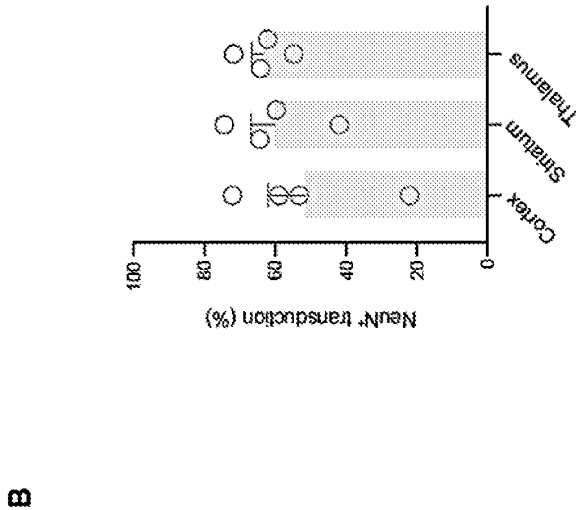
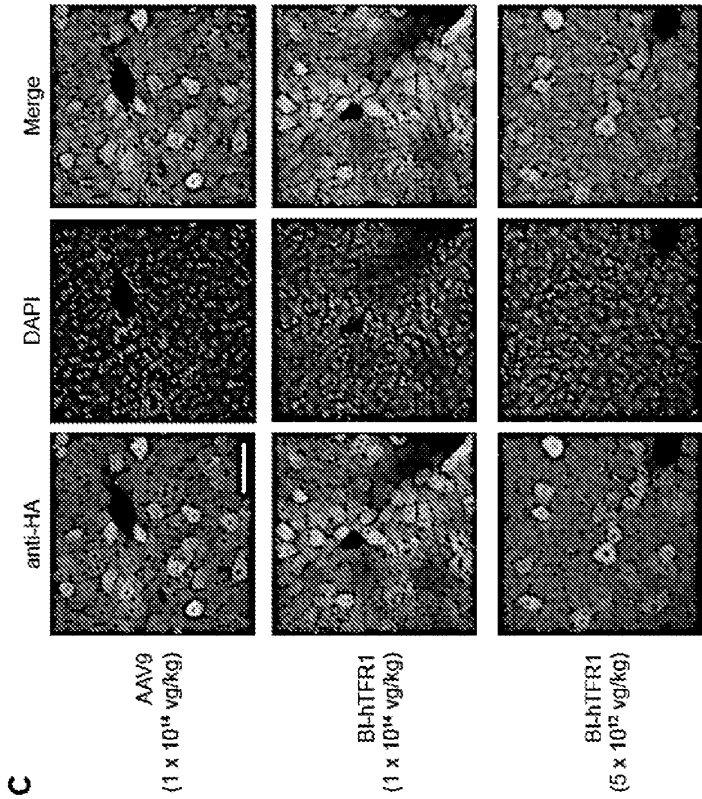


FIG. 13B-13C

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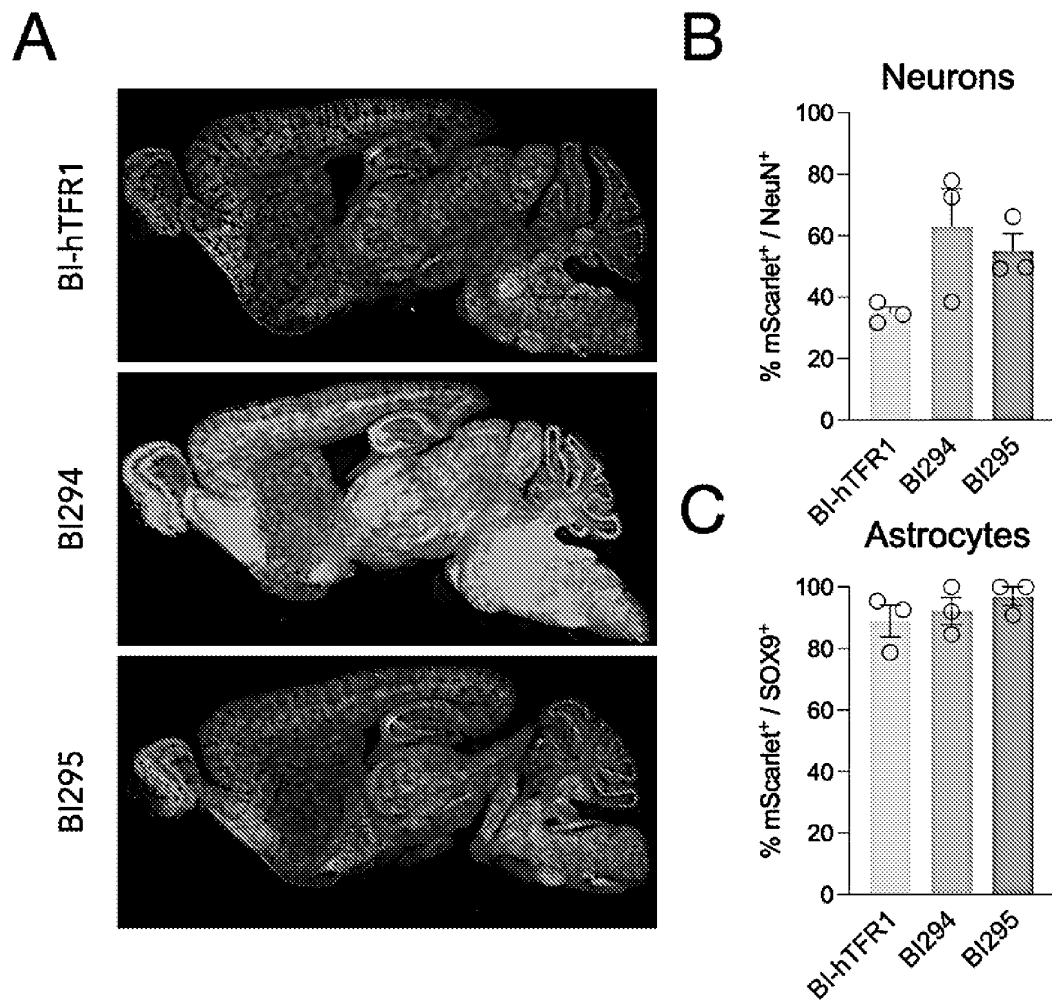


FIG. 14A-14C

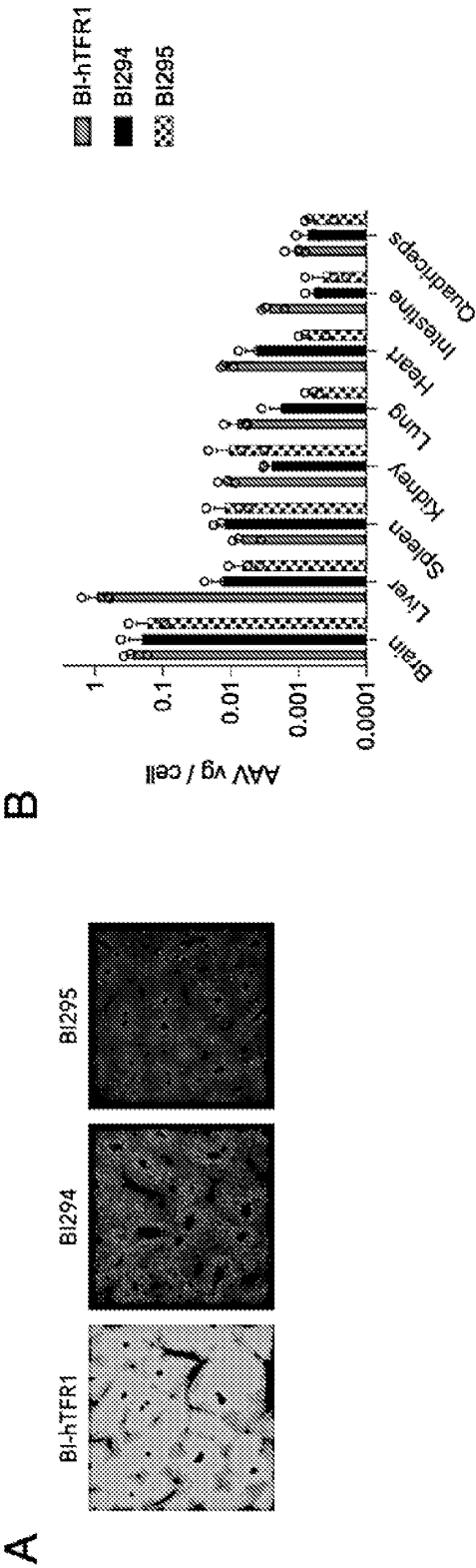


FIG. 15A-15B

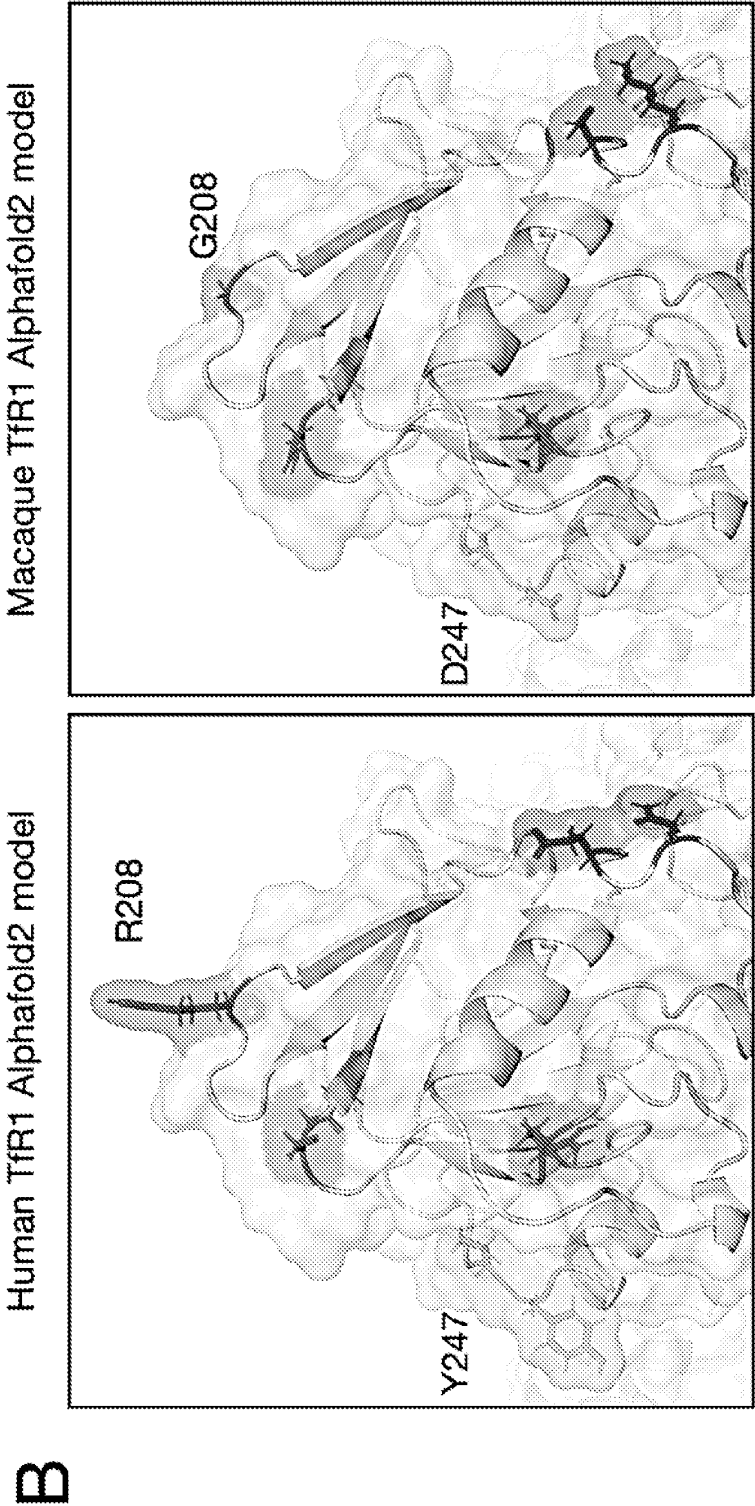


FIG. 16B

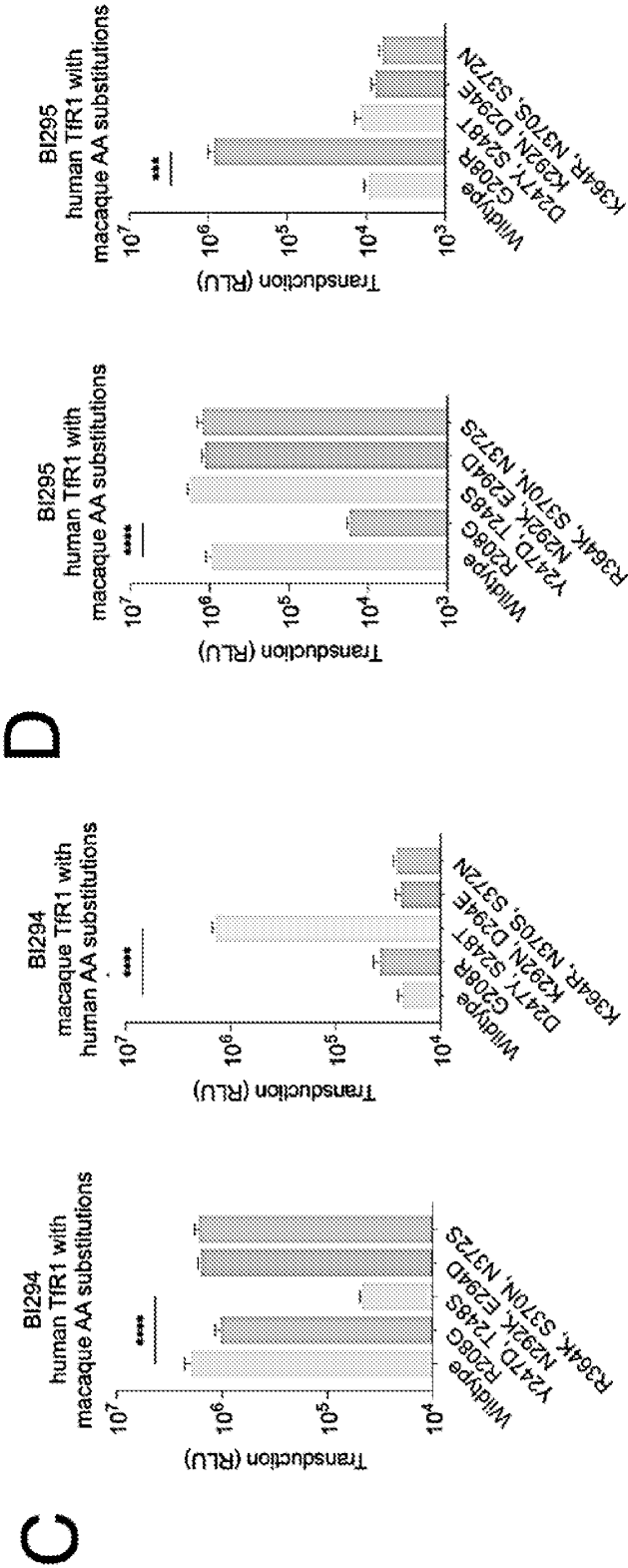


FIG. 16C-16D

7-mer insertion

► AAV9	GSLIFGKQGTG---	RDNVADKVMITNEEEIKTTNPVATESYGVQVATNHQSAQAQAQTGWVQVQNQGILP	605
► AAV1	GVMIFGKESAG---	ASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALP	605
► AAV2	GVLIFGKQGSE---	KTNVDIEKVMITDEEEIRITNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLP	604
► AAV3	GNLIFGKEGTT---	ASNAELDNVMITDEEEIRITNPVATEQYGTVANNLQSSNTAPTGTGVNHQ6GALP	605
► AAV3B	GNLIFGKEGTT---	ASNAELDNVMITDEEEIRITNPVATEQYGTVANNLQSSNTAPTTRTVNDQ6GALP	605
► AAV4	QLIFAGKQKNG---	NTATVPGTLIFTSEELAAATNATDTDMWGNLPGGDQSSNSLPTVDRLTALGA	603
► AAV5	NTMIFNSQPANPGT	TATYLEGNMLITSESETQPNRVAYNVFGQMATTNQSSTTAPATGTYNLQEIVPG	594
► AAV6	GVMIFGKESAG---	ASNTALDNVMITDEEEIKATNPVATERFGTVAVNLQSSSTDPATGDVHVNMGALP	605
► AAV7	GVLIFGKTGAT---	NK-TLENVLMTNEEEIRITNPVATEEYGISSNLQAANTAAQTQVVNVNQ6ALP	606
► AAV8	GILIFGKQNAA---	RDNADYSVMLTSEEEIKITNPVATEEYGIADVNLQDNTAPQIIGTVNSQ6ALP	607
► rh.8	GVLIFGKQGAG---	NDGVDSQVLTIDEEEEKATNPVATEEYGAIVANNQAANTQAQITGLVHNQGVIP	605
► rh.10	GVLMF6KQGAG---	KDNVDYSVMLTSEEEIKITNPVATEQYGVVADNLQDMAPIINGAVNSQ6ALP	607
► rh32.33	QLIFPGPSVTG---	NTTTSANNLLFTSEEEIAATNPRDITDMFGQIADNNQNTAPTITGNVTAMGVLP	602
► AAVrh74	GVLMF6KQGAG---	KDNVDYSVMLTSEEEIKITNPVATEQYGVVADNLQDMAAPIINGAVNSQ6ALP	607
► AAV10	GVLMF6KQGAG---	RDNVDSVMLTSEEEIKITNPVATEQYGVVADNLQDANTGPIVGNVNSQ6ALP	607
► AAV11	QLIFPGPSVTG---	NTTTSANNLLFTSEEEIAATNPRDITDMFGQIADNNQNTAPTITGNVTAMGVLP	602
► AAV12	QLIFAGPNPSG---	NTTTSANNLLFTSEEEIAATNPRDITDMFGQIADNNQNTAPTITANLDMGVIP	611
► AAV13	GTLIFGKEGTN---	ANNADLENVMITDEEEIRITNPVATEQYGTVANNLQNSNAGPTGTGVNHQ6ALP	602
► LK03	GNLIFGKEGTT---	ASNAELDNVMITDEEEIRITNPVATEQYGTVANNLQSSNTAPTTRTVNDQ6ALP	605
► AAV-D1	GVLIFGKQ6SE---	KTNVDIEKVMITDEEEIRITNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLP	606

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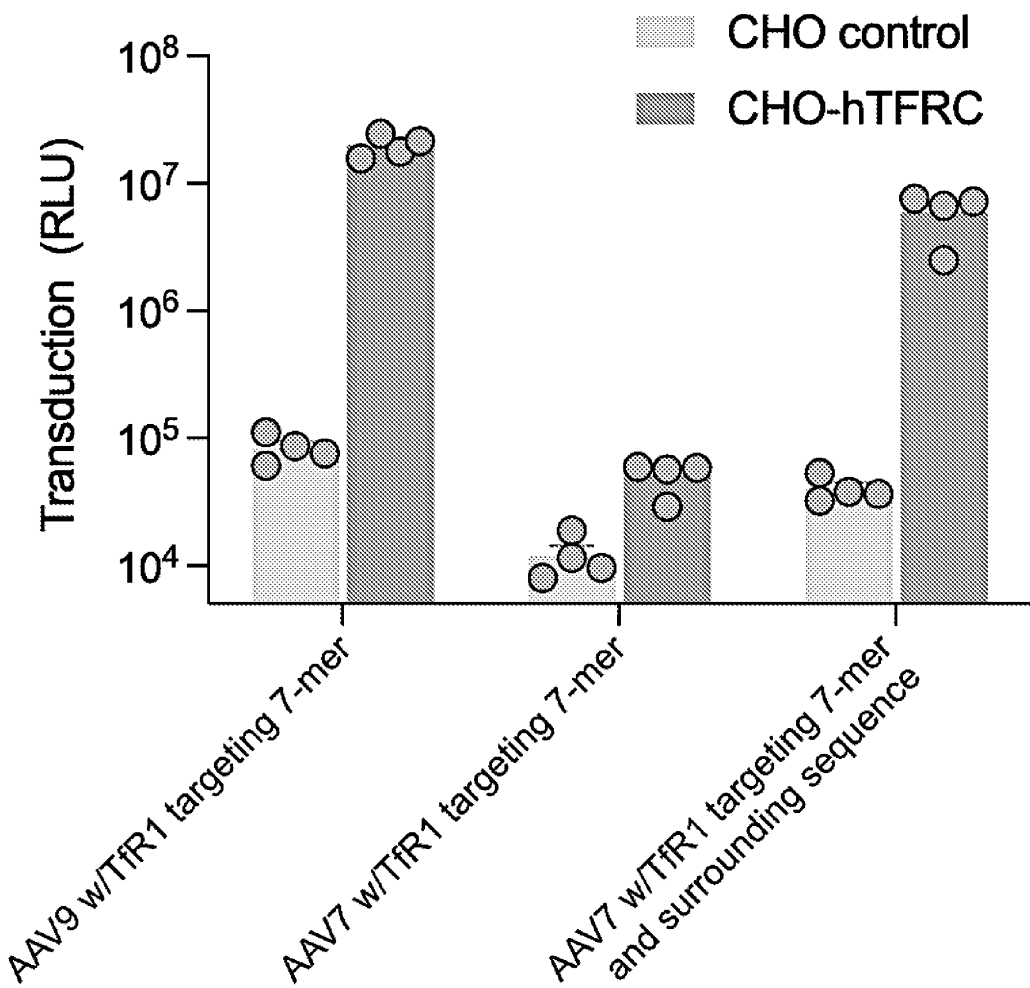


FIG. 18

AAV1	NP_049542.1	540	VMIFGKESAGASNTAL-----DNVMIITDEEEIKATNPVATERFGTVA	616
AAV2	YP_680426.1	539	VLIFGKQGSEKTNVDI-----EKVMIITDEEEIRITNPVATEQYGS	615
AAV3	NP_043394.1	540	NLIFGKEGTTASNAEL-----DNVMIITDEEEIRITNPVATEQYGT	616
AAV4	NP_044927.1	539	IFA-GPKQNGNTATVP-----GTLIFTSEEEELAAATNATDIDMGN	614
AAV5	YP_068409.1	526	TMIFNSQPANPGTTATyleGNWLIITSESEIQPWRVAYNVGGQMATN	605
AAV6	AAB95450.1	540	VMIFGKESAGASNTAL-----DNVMIITDEEEIKATNPVATERFGT	616
AAV7	YP_077178.1	542	VLIFGKTGATNKT-L-----ENVLNTNEEEIRITNPVATEEYGI	617
AAV8	YP_077180.1	542	ILIFGKONAARDNADY-----SDVMLTSEEEIKITNPVATEEYGI	618
AAV9	AAS99264.1	540	SLIFGKQGTGRDNVDA-----DKVMIITNEEEIKITNPVATESY	616
AAV10	AAT46337.1	542	VLMFGKQGAGRDNDY-----SSVMLTSEEEIKITNPVATEEYGM	618
AAV11	AAT46339.1	538	IFP-GPSVTGNTTISA-----NWLLFTSEEEIAATNPRTDIDMFG	613
AAV12	ABI16639.1	547	IFA-GPNPSONTITSS-----NWLLFTSEEEIAATNPRTDIDMFG	622
AAV13	ABZ10812.1	537	TLIFGKEGTLNNVADL-----ENVMIITDEEEIRITNPVATEQYGT	613

* AAV9 558

FIG. 19

SEROTYPE	AAV VP1 AMINO ACID SEQUENCE ALIGNMENT															
AAV1	NP_049542.1	1	MAADGYLPDML	EDNL	SEGIREWDL	KPGAPKPKANQ	QDDGRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	80				
AAV2	YP_680426.1	1	MAADGYLPDML	EDTL	SEGIRQWKL	KPGPPPKPAERHKDD	SRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NEADAAALEHDKAYD	80				
AAV3	NP_043941.1	1	MAADGYLPDML	EDNL	SEGIREWAL	KPGVPKPKANQ	QHQDNRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NEADAAALEHDKAYD	80				
AAV4	NP_044927.1	1	MT-DGYLPDML	EDNL	SEGIREWAL	KPGAPKPKANQ	QHQDNRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	79				
AAV5	YP_068409.1	1	MSFVDHPDML	EE-V	GEGLREF	LGL	EAGPPKPNQHQD	QARGLVLP	PGWYLG	PGNGLDRGEPV	NRADAVAREHDSYN	79				
AAV6	AAB95450.1	1	MAADGYLPDML	EDNL	SEGIREWDL	KPGAPKPKANQ	QDDGRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	80				
AAV7	YP_077178.1	1	MAADGYLPDML	EDNL	SEGIREWDL	KPGAPKPKANQ	QDNGRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	80				
AAV8	YP_077180.1	1	MAADGYLPDML	EDNL	SEGIREWAL	KPGAPKPKANQ	QDDGRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	80				
AAV9	AAS99264.1	1	MAADGYLPDML	EDNL	SEGIREWAL	KPGAPKPKANQ	QHQDNRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	80				
AAV10	AAT46337.1	1	MAADGYLPDML	EDNL	SEGIREWDL	KPGAPKPKANQ	QDDGRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	80				
AAV11	AAT46339.1	1	MAADGYLPDML	EDNL	SEGIREWDL	KPGAPKPKANQ	QDDGRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	80				
AAV12	ABI16639.1	1	MAADGYLPDML	EDNL	SEGIREWAL	KPGAPQPKANQ	QHQDNGRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NEADAAALEHDKAYD	80				
AAV13	ABZ10812.1	1	MT-DGYLPDML	EDNL	SEGIREWAL	KPGAPKPKANQ	QHQDNRGLVLP	PGYKYL	GPFGNGL	DKGEPV	NAADAAALEHDKAYD	79				
	NP_049542.1	81	QQLKAGDNPYL	RYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEGAKT	APGKKRPVEQSPQE-P----	DSS	156	
	YP_680426.1	81	ROLDSG	DNPYL	KYNHADA	E	FQERL	KEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEPVKT	APGKKRPVEHSPVE-P----	DSS	156
	NP_043941.1	81	QQLKAGDNPYL	KYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEAAKT	APGKKGAVDQSPQE-P----	DSS	156	
	NP_044927.1	80	QQLKAGDNPYL	KYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEQAGET	APGKKRPLIESPQQ-P----	DSS	155	
	YP_068409.1	80	EQLEAG	DNPYL	KYNHADA	E	FQERL	ADDT	TS	FGGNL	GKAV	FQAKKRV	LEPLGL	VEEGAKT	APTKRIDHFPKRKKar----	155
	AAB95450.1	81	QQLKAGDNPYL	RYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEGAKT	APGKKRPVEQSPQE-P----	DSS	156	
	YP_077178.1	81	QQLKAGDNPYL	RYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEGAKT	APGKKRPVEPSPQSP-P----	DSS	157	
	YP_077180.1	81	QQLKAGDNPYL	RYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEGAKT	APGKKRPVEPSPQSP-P----	DSS	157	
	AAS99264.1	81	QQLKAGDNPYL	RYNHADA	E	FQERL	KEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEAAKT	APGKKRPVEQSPQE-P----	DSS	156	
	AAT46337.1	81	QQLKAGDNPYL	RYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEAAKT	APGKKRPVEPSPQSP-P----	DSS	157	
	AAT46339.1	81	QQLKAGDNPYL	RYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEAAKT	APGKKRPVEPSPQSP-P----	DSS	155	
	ABI16639.1	81	KQLEQ	QGNPYL	KYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEGVKT	APGKKRPLEKT	PNR-P	159
	ABZ10812.1	80	QQLKAGDNPYL	KYNHADA	E	FQERL	QEDTS	FGGNL	GRAV	FQAKKRV	LEPLGL	VEEAAKT	APGKKRPVEQSPAE-P----	DSS	155	

FIG. 20

SEROTYPE		SEQUENCE ALIGNMENT	
AAV1	NP_049542.1	157	SGIGKTGQQP-----AKKRLNFGQTGDSESVDPQPPLGEPATP-AAVGPTTMTASGGGAPMADNNEGADGVGNASGNWH
	YP_680426.1	157	SGTGKAGQQP-----ARKRLNFGQTGDADSVDPQPPLGPPAAP-SGLGTNTMTATGSGAPMADNNEGADGVGNSSGNWH
	NP_043941.1	157	SGVGKSGKQP-----ARKRLNFGQTGDSESVDPQPPLGEPAP--TSLGSNTMTASGGGAPMADNNEGADGVGNSSGNWH
	NP_044927.1	156	TGIGKKGKQP-----DETGAGDPPPEGSTSGAM-SDDSEHRAAAGGAA---VEGGQGDGVGNASGDWH
	YP_068409.1	156	---TEEDSKP-----STSDAEAGPSGSQQLQIPAQPaSLGADMTSAGGGPLGDNVQGDGVGNASGDWH
	AA895450.1	157	SGIGKTGQQP-----AKKRLNFGQTGDSESVDPQPPLGEPATP-AAVGPTTMTASGGGAPMADNNEGADGVGNASGNWH
	YP_077178.1	158	TGIGKKGQQP-----ARKRLNFGQTGDSESVDPQPPLGEPAP--SSVSGTVAAGGAPMADNNEGADGVGNASGNWH
	YP_077180.1	158	TGIGKKGQQP-----ARKRLNFGQTGDSESVDPQPPLGEPAP--SGVGNPTMAAGGAPMADNNEGADGVSSSGNWH
	AAS99264.1	157	AGIGKSGAQP-----AKKRLNFGQTGDSESVDPQPPIGEPAP--SGVGSILTMASGGGAPVADNNEGADGVSSSGNWH
	AAT46337.1	158	TGIGKKGQQP-----AKKRLNFGQTGESESVDPQPPIGEPAGP-SGLSGTMTAAGGAPMADNNEGADGVSSSGNWH
	AAT46339.1	156	SGIGKKGKQP-----ARKRLNFE---EDTGAGDPPPEGSDTSAM-SSDIENRAAPGGNA---VDAGQGSDGVGNASGDWH
	ABI16639.1	160	KAPAKKKQKQgepadsARRTLDFE---D-SGAGDPPPEGSSGEM-SHDAENRAAPGGNA---VEAGQGADGVGNASGDWH
	ABZ10812.1	156	SGIGKSGQQP-----ARKRLNFGQTGDTEVPDPQPPLGPPAAP-SGVGSTTMTASGGGAPMADNNEGADGVGNSSGNWH
	NP_049542.1	230	CDSTWLGDRVITTTSTRTWALPTYNNHLKYQISSASTG-ASNDNHYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	YP_680426.1	230	CDSTWNGDRVITTTSTRTWALPTYNNHLKYQISSQ5-G-ASNDNHYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	NP_043941.1	230	CDSQWLGDRVITTTSTRTWALPTYNNHLKYQISSQ5-G-ASNDNHYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	NP_044927.1	224	CDSTWSEGHVITTTSTRTWLPTYNNHLKYKRLGESLQ5-----NTYNGFSTPMGYFDNRFHCHFSPRDWQRLINNHWGMR
	YP_068409.1	220	CDSTWNGDRVVTKSTRTWLPSYNNHQVREIKSG5VD-GSNANAYFGYSTPMGYFDNRFHSHWSPRDWQRLINNHWGFR
	AA895450.1	230	CDSTWLGDRVITTTSTRTWALPTYNNHLKYQISSASTG-ASNDNHYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	YP_077178.1	231	CDSTWLGDRVITTTSTRTWALPTYNNHLKYQISSSETAG-STNDNTYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	YP_077180.1	231	CDSTWLGDRVITTTSTRTWALPTYNNHLKYQISNGTSGgATNDNTYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	AAS99264.1	230	CDSQWLGDRVITTTSTRTWALPTYNNHLKYQISNSTSGgSSNDNAYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	AAT46337.1	231	CDSTWLGDRVITTTSTRTWALPTYNNHLKYQISNGTSGgSTNDNTYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR
	AAT46339.1	224	CDSTWSEKVTITTTSTRTWLPTYNNHLYLRLGTTSS5-----NTYNGFSTPMGYFDNRFHCHFSPRDWQRLINNHWGLR
	ABI16639.1	233	CDSTWSEGRVITTTSTRTWLPTYNNHLYLRLGTTANS-----NTYNGFSTPMGYFDNRFHCHFSPRDWQRLINNHWGLR
	ABZ10812.1	229	CDSQWLGDRVITTTSTRTWALPTYNNHLKYQISSQ5-G-ATNDNHYFGYSTPMGYFDNRFHCHFSPRDWQRLINNHWGFR

FIG. 20 cont.

SEROTYPE		SEQUENCE ALIGNMENT	
AAV1	NP_049542.1	309	PKRLNFKLFNIQVKEVTNDGVTIIANNLTSTVQVFSDEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYLTINNGS----
	YP_680426.1	308	PKRLNFKLFNIQVKEVTQNDGTTIIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTINNGS----
	NP_043941.1	308	PKKLSFKLFNIQVRGVTQNDGTTIIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTINNGS----
	NP_044927.1	299	PKAMRVKIFNIQVKEVTTSGEITVANNLTSTVQIFADSSYELPYVMDAQEGSLPPFPNDVFMPQYGYCGLVTGNTsq
	YP_068409.1	299	PRSLRVKIFNIQVKEVTQDSTTTIANNLTSTVQVFTDDYQLPYVVVNGTEGCLPAFPQVFTLPQYGYATLNRDN--te
	AAB95450.1	309	PKRLNFKLFNIQVKEVTNDGVTIIANNLTSTVQVFSDEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYLTINNGS-----
	YP_077178.1	310	PKKLRFKLFNIQVKEVTNDGVTIIANNLTSTVQVFSDEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYLTINNGS----
	YP_077180.1	311	PKRLSFKLFNIQVKEVTQNEGKTIIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYLTINNGS----
	AAS99264.1	310	PKRLNFKLFNIQVKEVTNDGVTIIANNLTSTVQVFTDSDYQLPYVLGSAHQGCLPPFPADVFMIPOYGYLTINNGS----
	AAT46337.1	311	PKRLSFKLFNIQVKEVTQNEGKTIIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYLTINNGS----
	AAT46339.1	299	PKAMRVKIFNIQVKEVTTSGEITVANNLTSTVQIFADSSYELPYVMDAQEGSLPPFPNDVFMPQYGYCGLVTGE--nq
	ABI16639.1	308	PKSMRVKIFNIQVKEVTTSGEITVANNLTSTVQIFADSTYELPYVMDAQEGSFPPFPNDVFMPQYGYCGVTK--nq
	ABZ10812.1	307	PKRLNFKLFNIQVKEVTQNDGTTIIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTINNGS-----
AAV2	NP_049542.1	386	QAVGRSSFYCLEYFPQSMLRTGNNTFTSYTFEEVPFHSSYAHQSGLDRLMNPLIDQLYYYLNRTQ--NQS GSAQNKDLLFS
	YP_680426.1	385	QAVGRSSFYCLEYFPQSMLRTGNNTFTSYTFEDVPFHSSYAHQSGLDRLMNPLIDQLYYYLSRTN--TPSGTTTQSRLLQFS
	NP_043941.1	385	QAVGRSSFYCLEYFPQSMLRTGNMFQSYTFEDVPFHSSYAHQSGLDRLMNPLIDQLYYYLNRTQGTTS GTTNQSRLLFS
	NP_044927.1	379	QQTDRNAFYCLEYFPQSMLRTGNNTFTSYTFEKPVPFHSSYAHQSGLDRLMNPLIDQYLVGLQSTTTTGTTLNAGTATTNFT
	YP_068409.1	378	NPTERRSSFFCLEYFPQSKMLRTGNNTFTSYTFEVPFHSSYAHQSGLDRLMNPLIDQYLVQVLYRFSVN-----NTGGVQFN
	AAB95450.1	386	QAVGRSSFYCLEYFPQSMLRTGNNTFTSYTFEDVPFHSSYAHQSGLDRLMNPLIDQLYYYLNRTQ--NQS GSAQNKDLLFS
	YP_077178.1	387	QSVGRSSFYCLEYFPQSMLRTGNNTFTSYTFEDVPFHSSYAHQSGLDRLMNPLIDQLYYYLARTQSNPGGTAGNRELQFY
	YP_077180.1	388	QAVGRSSFYCLEYFPQSMLRTGNMFQSYTFEDVPFHSSYAHQSGLDRLMNPLIDQLYYYLSRTQT--TGGTANTQTILGFS
	AAS99264.1	387	QAVGRSSFYCLEYFPQSMLRTGNMFQSYEFENVPFHSSYAHQSGLDRLMNPLIDQLYYYLSKTI--NGSGQ--NQOTLKFS
	AAT46337.1	388	QAVGRSSFYCLEYFPQSMLRTGNNTFTSYTFEDVPFHSSYAHQSGLDRLMNPLIDQLYYYLSRTQS--TGGTGTGQTQLLFS
	AAT46339.1	378	NQTDNRNAFYCLEYFPQSMLRTGNNTFTSYTFEKPVPFHSSYAHQSGLDRLMNPLIDQYLVHLSQSTTSGETLNQGNAAATTFG
	ABI16639.1	387	NQTDNRNAFYCLEYFPQSMLRTGNNTFTSYTFEKPVPFHSSYAHQSGLDRLMNPLIDQYLVHLSQSTTTTGNLSNQGTATTTYG
	ABZ10812.1	384	QAVGRSSFYCLEYFPQSMLRTGNNTFTSYTFEDVPFHSSYAHQSGLDRLMNPLIDQLYYYLNRTQ--TASGT--QQSRLLFS

FIG. 20 cont.

SEROTYPE		SEQUENCE ALIGNMENT	
AAV1	NP_049542.1	465	RGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIIINPGTAMASHKDDDEKFFPMSG
	YP_680426.1	464	QAGASDIRQSRNWLPGPCYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSL VNP GPAMASHKDDDEKFFPQSG
	NP_043941.1	465	QAGPQMSLQARNWLPGPCYRQQRVSKTANDN-----NNSNFPWTAAASKYHLNGRDSL VNP GPAMASHKDDDEKFFPMHG
	NP_044927.1	459	KL RPTNFSNFKKNWLPGPSIKQGGFKTANQNYKIPaTGSDSL IKYETHISTLDGRWSAL TPGPPMATAGPADSKFSNSQL
	YP_068409.1	451	KNLAGRYANTYKNWFP GPMGRITQGNL GSGVN-----RASVSFAFATTNRMELEGASYQVPPQPNGMGTNNL QGSENTYALEN
	AAB95450.1	465	RGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIIINPGTAMASHKDDKDKFFPMSG
	YP_077178.1	467	QGGPSTMAEQAKNWLPGPCYRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSG
	YP_077180.1	467	QGGPNTMANQAKNWLPGPCYRQQRVSTTTGQN-----NNSNFAWTAGTKYHLNGRNSLVNPGIAMATHKDDDEERFFPSNG
	AAS99264.1	465	VAGPSNMAVQGRNYIPGPSYRQQRVSTTTVTON-----NNSEFAWPGASSWALNGRNSLVNPGAMASHKEGEDRFFPLSG
	AAT46337.1	467	QAGPANMSAQAKNWLPGPCYRQQRVSTTTLSQN-----NNSNFAWTGATKYHLNGRDSL VNP GPAMATHKDDDEERFFPSSG
	AAT46339.1	458	KIRSGDFAFYRKNNWLPGPCVKQQRFSKTASQNYKIPaSGGNALLKYDTHYTLNNRWSNIAPGPPMATAGPSDGDFFSMAOL
	ABI16639.1	467	KITTGDFAYYRKNNWLPGACIKQKQKFSKMANQNYKIPaSGGDALLKYDTHYTLNGRWSNMAPGPPMATAGAGDSDFSNSQL
	ABZ10812.1	462	QAGPMSLSLQAKNWLPGPCYRQQRVSKQANDN-----NNSNFPWTGATKYHLNGRDSL VNP GPAMASHKDDKEKFFPMHG
AAV2	NP_049542.1	540	VMIFGKESAGASNTAL-----DNVMITDEEEIKATNPVATERFGTVAVNFQSSSTD PATGDVHMGALPGMWQDRD VYLOG
	YP_680426.1	539	VLIFGKQGSEKTNVDI-----EKVMITDEEEIIRTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRD VYLOG
	NP_043941.1	540	NLIFGKEGTTASNAEL-----DNVMITDEEEIIRTNPVATEQYGTVANNLQSSNTAPTTGT VNHQ GALPGMWQDRD VYLOG
	NP_044927.1	539	IFA--GPKQNGNTATVP-----GTLIFTSEEEAATNATDTDMWGNLPGGDQSSNSLPTVDRLTALGAVPGMWQNRDIYYOG
	YP_068409.1	526	TMIFNSQPANPGTTATyLeGNMLITSESETQPVNRVAVNVGGQMATNNQSSTTAPATGTYNLQEIIVPGSVMMERD VYLOG
	AAB95450.1	540	VMIFGKESAGASNTAL-----DNVMITDEEEIKATNPVATERFGTVAVNLQSSSTD PATGDVHMGALPGMWQDRD VYLOG
	YP_077178.1	542	VLIFGKTGATNKT--L-----ENVLMTNEEEIIRTNPVATEEYGISSNLQAANTAQTQVNNQ GALPGMWQNRD VYLOG
	YP_077180.1	542	ILIFGKQNAARDNADY-----SDVMLTSEEEIKITNPVATEEYGIADVNLQQNTPAQIGTVNSQ GALPGMWQNRD VYLOG
	AAS99264.1	540	SLIFGKQGTGRDNVDA-----DKVMITNEEEIIRTNPVATESYGVVADNLQQAQADTGWVQNGILPGMWQDRD VYLOG
	AAT46337.1	542	VLMFGKQAGRONVDY-----SSVMLTSEEEIKITNPVATEQYGVVADNLQQAANTGPIVGNVNSQ GALPGMWQNRD VYLOG
	AAT46339.1	538	IFP--GPSVTGNITTSa-----NNLLFTSEEEIAATNPRTDMFGQIADNNQNTATTITGNVTAMGVLPGMWQNRDIYYOG
	ABI16639.1	547	IFA--GPNPSGNITTS-----NNLLFTSEEEIATNPRTDMFGQIADNNQNTATTAPHIANLDAMGIVPGMWQNRDIYYOG
	ABZ10812.1	537	TLIFGKEGTNANNADL-----ENVMITDEEEIIRTNPVATEQYGTVSNNLQNSNAGPTTGT VNHQ GALPGMWQDRD VYLOG

FIG. 20 cont.

SEROTYPE		SEQUENCE ALIGNMENT	
AAV1	NP_049542.1	617	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQILIKNTVPANPPAEFSATKFASFIQYSTGQVSVEIEWELOKENS
AAV2	YP_680426.1	616	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQILIKNTVPANPSITFSAAKFASFIQYSTGQVSVEIEWELOKENS
AAV3	NP_043941.1	617	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQIMIKNTVPANPPITFSPAKFASFIQYSTGQVSVEIEWELOKENS
AAV4	NP_044927.1	615	PIWAKIPHTDGHFSPPLIGGFGLKHPPPQIFIKNTVPANPATTFSSTPVNSFIQYSTGQVSQIDWEIQERS
AAV5	YP_068409.1	606	PIWAKIPETGAHFSPSPAMGGFGLKHPPPMILIKNTVPQGN-ITSFSDVPVSSFIQYSTGQVTMEMELKKENS
AAV6	AAB95450.1	617	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQILIKNTVPANPPAEFSATKFASFIQYSTGQVSVEIEWELOKENS
AAV7	YP_077178.1	618	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQILIKNTVPANPEVFTPAKFASFIQYSTGQVSVEIEWELOKENS
AAV8	YP_077180.1	619	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFIQYSTGQVSVEIEWELOKENS
AAV9	AAS99264.1	617	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQILIKNTVPADPPTAFNKKLNSFIQYSTGQVSVEIEWELOKENS
AAV10	AAT46337.1	619	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQILIKNTVPADPPTTFSQAKLASFIQYSTGQVSVEIEWELOKENS
AAV11	AAT46339.1	614	PIWAKIPHADGHFSPPLIGGFGLKHPPPQIFIKNTVPANPATTTFAARVDSFIQYSTGQVAVQIEWEIEKERS
AAV12	ABI16639.1	623	PIWAKVPHTDGHFSPPLMGGFGLKHPPPQIFIKNTVPANPNITTFSAARINSFLIQYSTGQVAVQIDWEIQEHS
AAV13	ABZ10812.1	614	PIWAKIPHTDGHFSPPLMGGFGLKHPPPQIMIKNTVPANPPTNFSAAKFASFIQYSTGQVSVEIEWELOKENS
	NP_049542.1	697	PEVQYTSNYAKSANVDFTVDNGLYTEPRPIGTRYLTRPL (SEQ ID NO: 3) AAV1
	YP_680426.1	696	PEIQYTSNYAKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL (SEQ ID NO: 4) AAV2
	NP_043941.1	697	PEIQYTSNYAKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL (SEQ ID NO: 5) AAV3
	NP_044927.1	695	PEVQFTSNYGGQNSLLWAPDAAGKYTEPRPIGTRYLTRNL (SEQ ID NO: 7) AAV4
	YP_068409.1	685	PEIQYTNVNDPQVDFAPDSTGEVTRTPRPIGTRYLTRPL (SEQ ID NO: 8) AAV5
	AAB95450.1	697	PEVQYTSNYAKSANVDFTVDNGLYTEPRPIGTRYLTRPL (SEQ ID NO: 9) AAV6
	YP_077178.1	698	PEIQYTSNFEKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL (SEQ ID NO: 10) AAV7
	YP_077180.1	699	PEIQYTSNYKSTSVDFAVNTEGVYSEPRPIGTRYLTRNL (SEQ ID NO: 11) AAV8
	AAS99264.1	697	PEIQYTSNYKSNVFEAVNTEGVYSEPRPIGTRYLTRNL (SEQ ID NO: 1) AAV9
	AAT46337.1	699	PEIQYTSNYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL (SEQ ID NO: 15) AAV10
	AAT46339.1	694	PEVQFTSNYGNQSSMLWAPDITGKYTEPRVIGSRYLTRNL (SEQ ID NO: 11) AAV11
	ABI16639.1	703	PEVQFTSNYGTQNSMLWAPDNAGNYHELRAIGSRFLTHHL (SEQ ID NO: 17) AAV12
	ABZ10812.1	694	PEIQYTSNYKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL (SEQ ID NO: 18) AAV13

FIG. 20 cont.

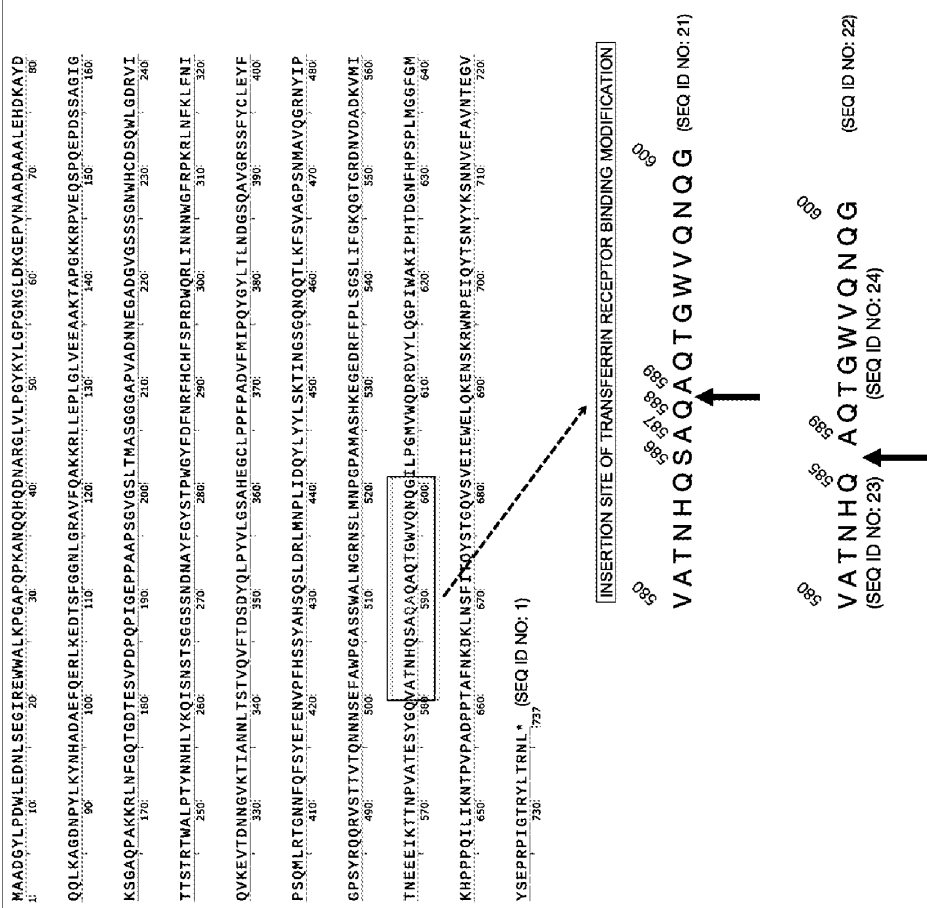


FIG. 21

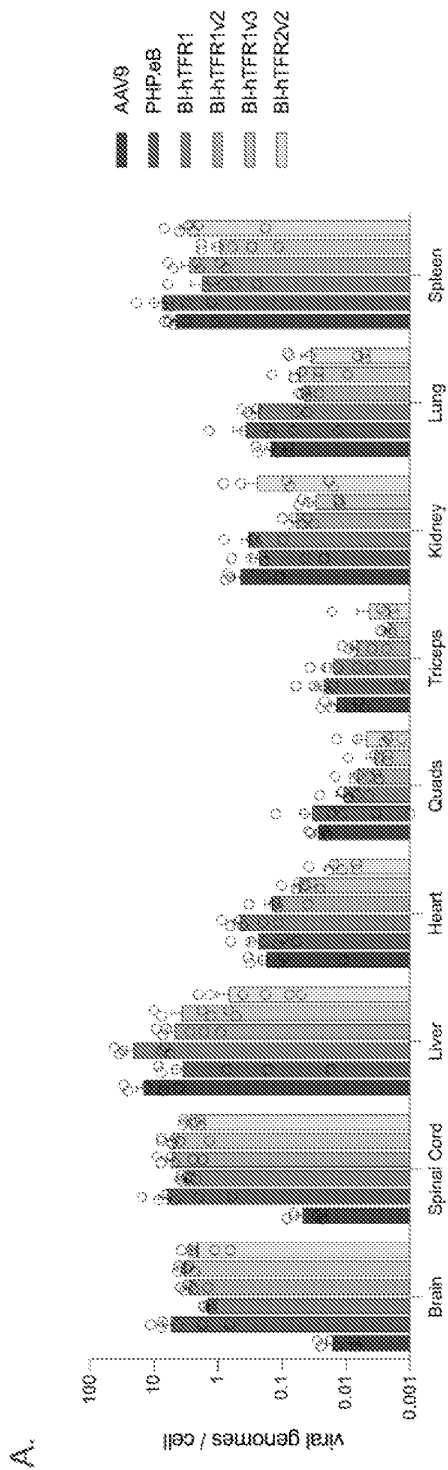


FIG. 22A

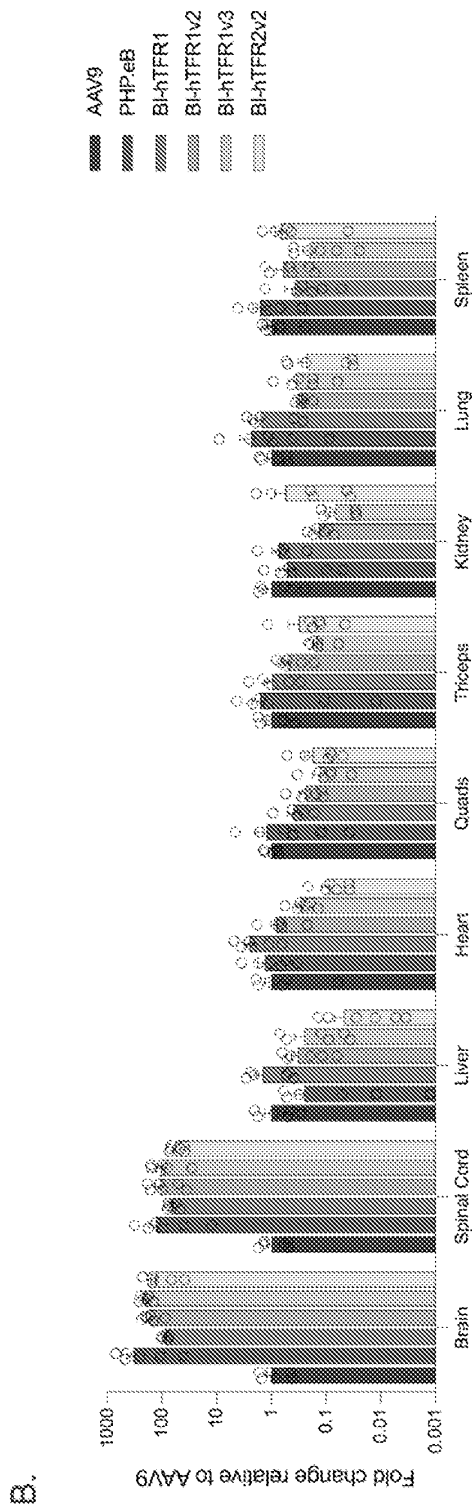


FIG. 22B

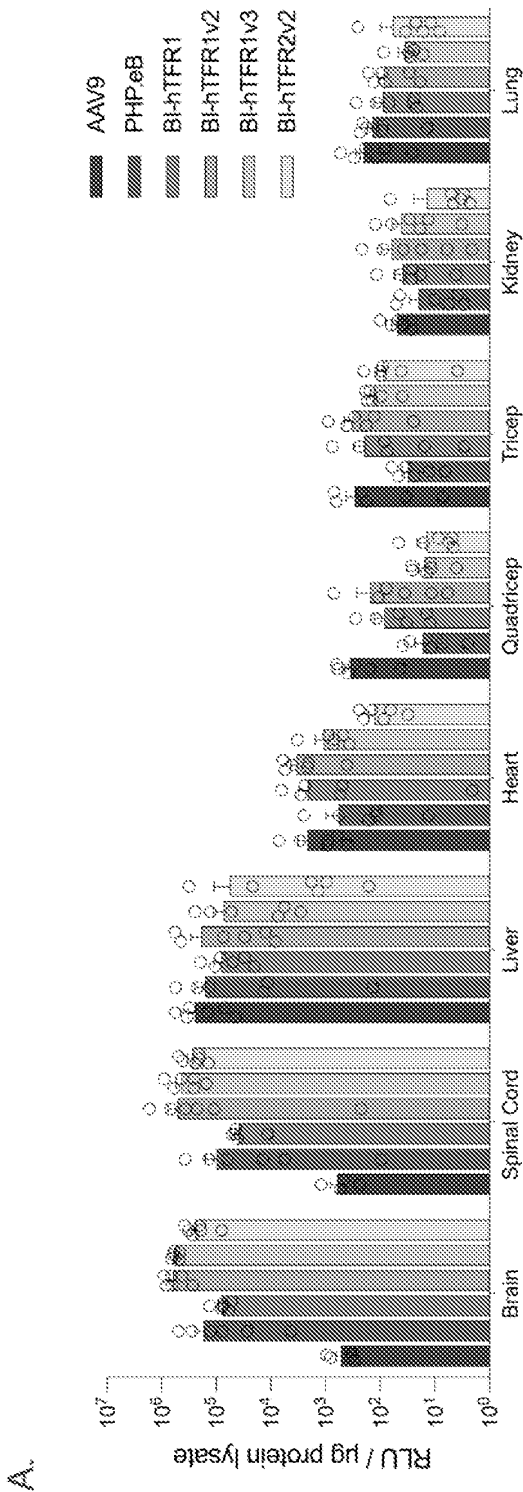


FIG. 23A

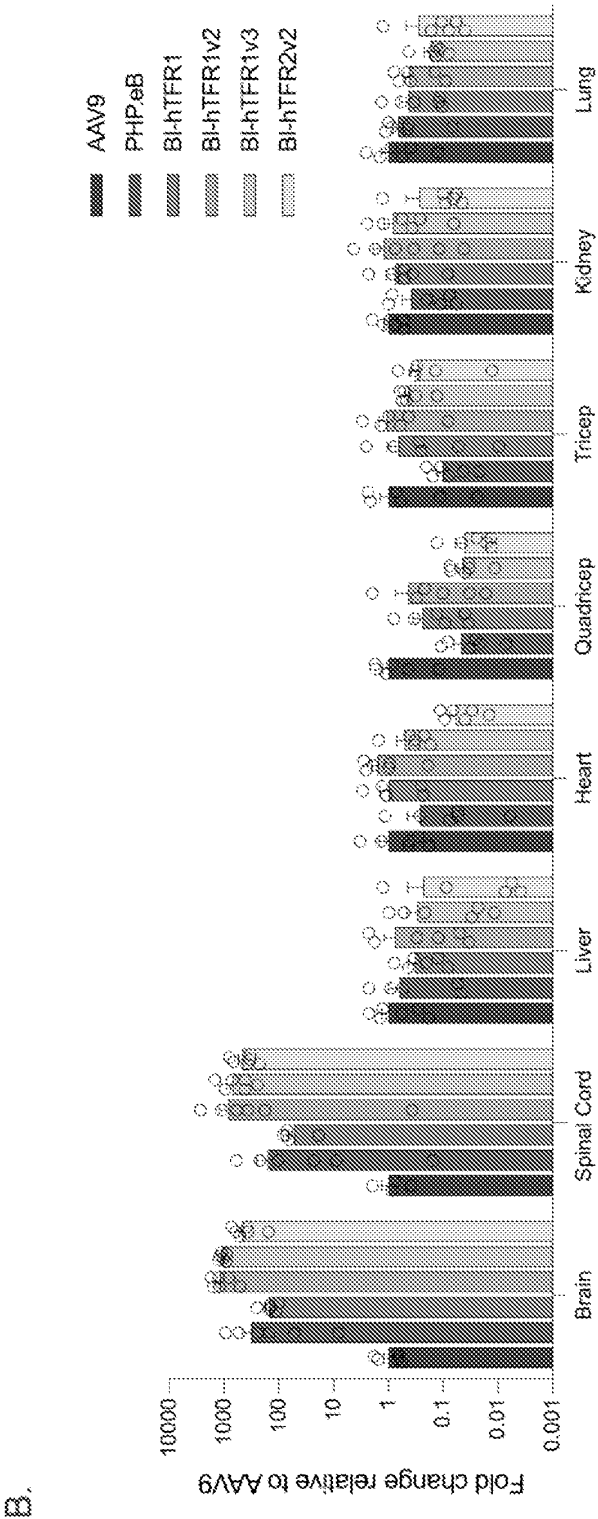


FIG. 23B

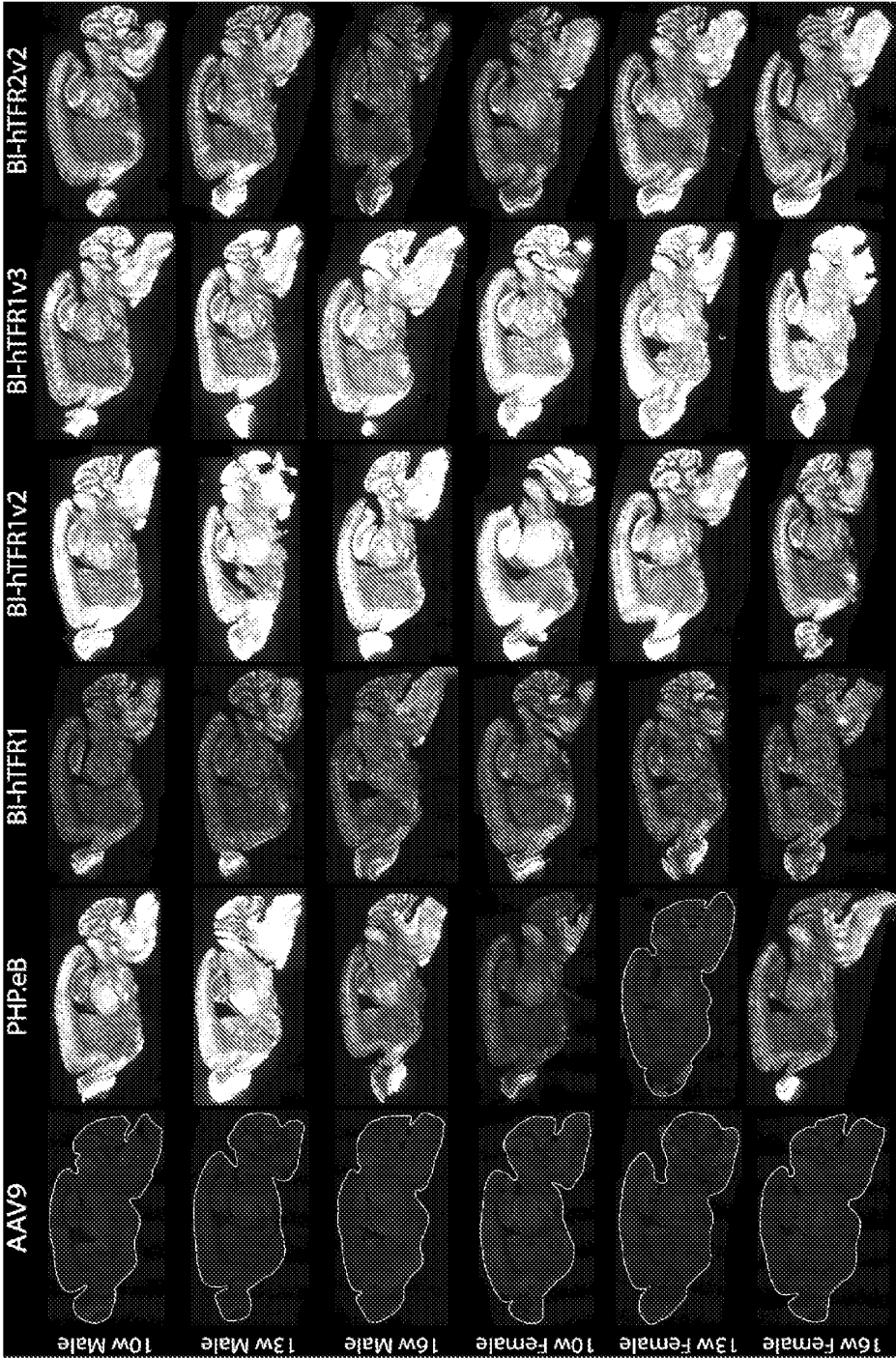


FIG. 24

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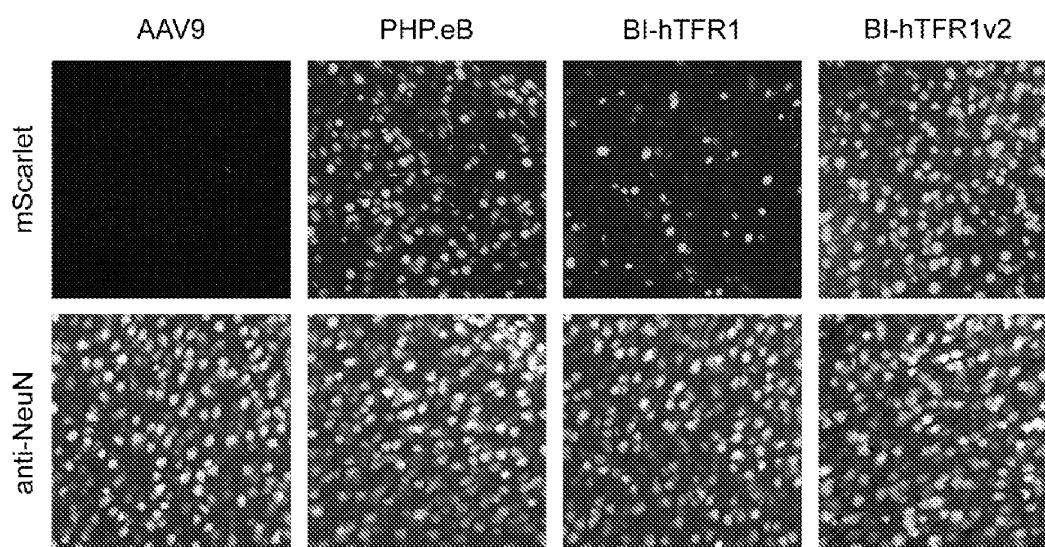


FIG. 25

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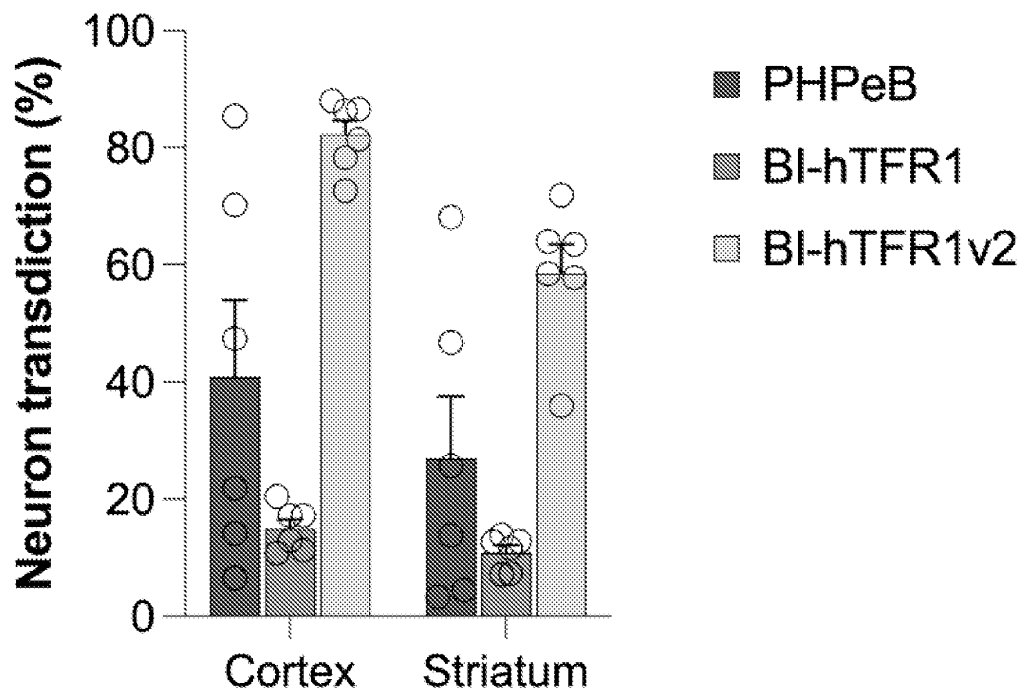


FIG. 26