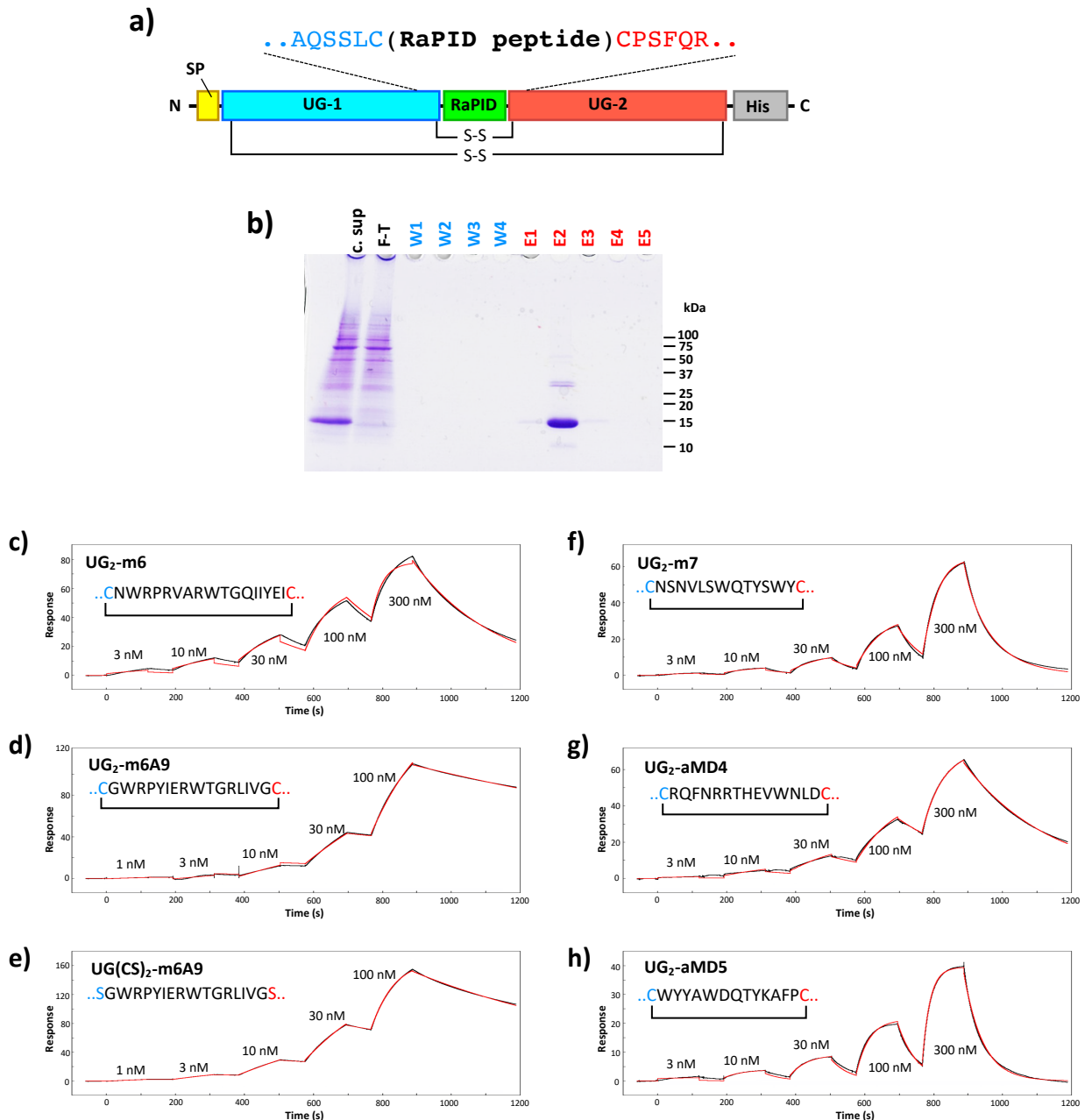


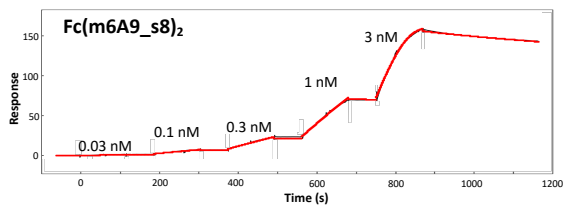
## **Supplementary Information**

# Supplementary Figures

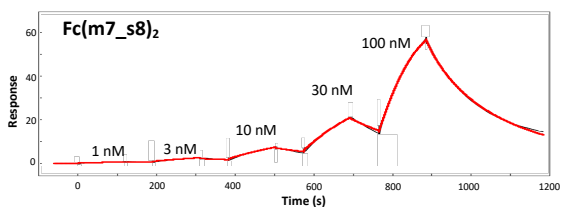


**Supplementary Figure S1.** Peptide grafting onto homodimeric uteroglobin. **a**, Construct design of peptide grafts onto UG. The construct is comprised of a signal peptide (SP), the first UG subunit (UG-1), the grafted RaPID-derived peptide, the second UG subunit (UG-2), and a (His)<sub>6</sub> tag. Disulfide bonding patterns are indicated by brackets. **b**, Purification of peptide-grafted UG tandem dimers using Ni-NTA-agarose chromatography. A representative nonreducing SDS-PAGE (15-25% gradient gel) is shown for samples taken during the purification of m6-grafted UG (UG<sub>2</sub>-m6). Samples include the original culture supernatant (c. sup), the flow-through fraction (F-T), TBS wash fractions (W1-W4), and 0.25 M imidazole elution fractions (E1-E5). **c-h**, Biacore sensorgrams from kinetic binding analyses of peptide-grafted UGs. Samples were serially diluted to the indicated concentrations and successively flowed over sensorchips with immobilized ectodomain fragments of PlxnB1 (**c-f**) or MET (**g, h**) in the “single-cycle kinetics” mode to derive kinetic rate constants shown in Fig. 1c. The actual amino acid sequences of the grafted peptide is shown below each sample name. Note that the peptide-flanking cysteines are mutated to serines in UG(CS)<sub>2</sub>-m6A9 (**e**). The sensorgrams and the fitted curves are shown in black and red lines, respectively.

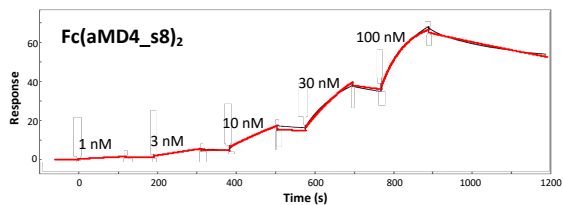
a)



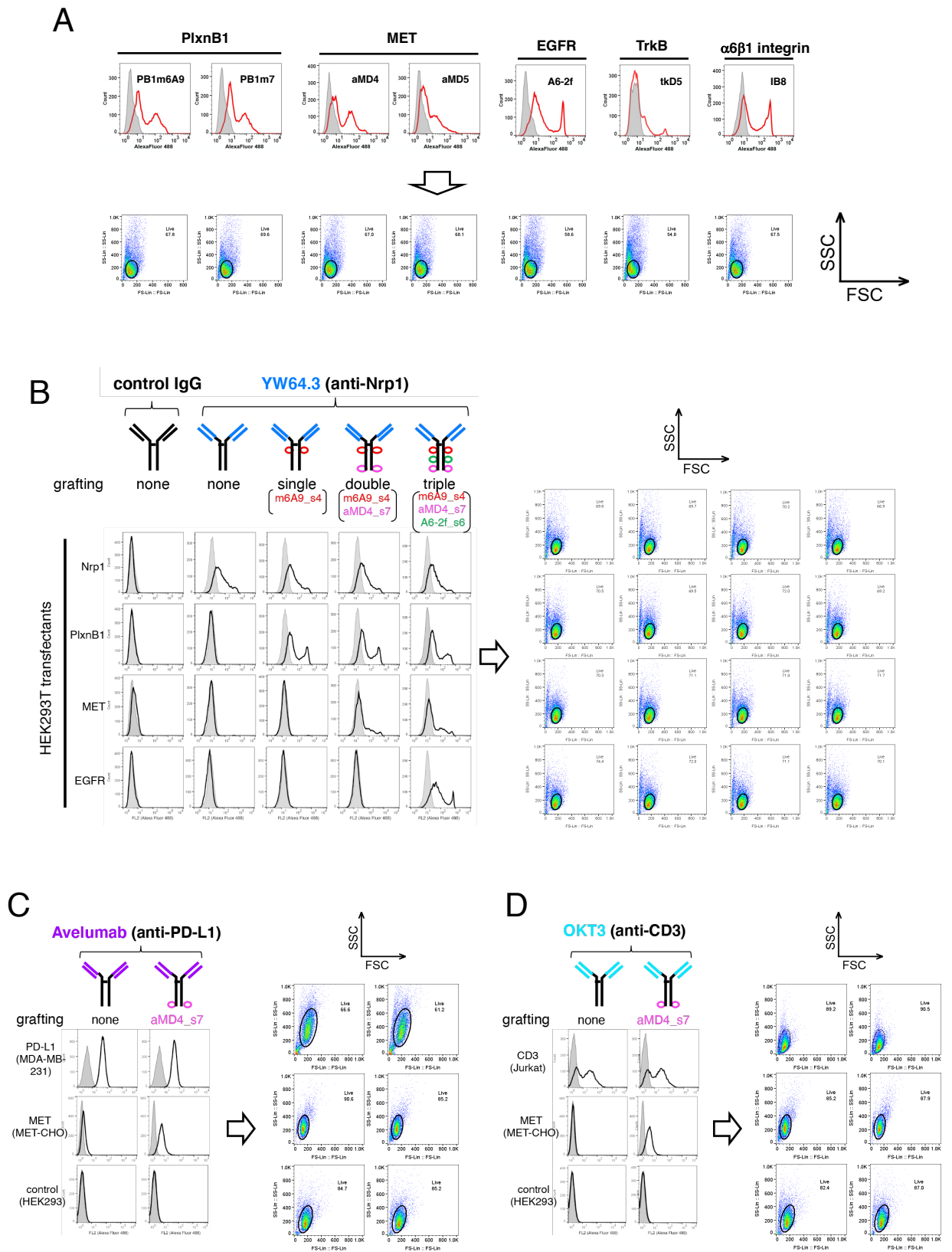
b)



c)



**Supplementary Figure S2.** Binding ability of peptide-grafted Fc proteins. **a-c**, Biacore sensorgrams for the kinetic binding analyses of the indicated peptide-grafted Fcs. Samples were serially diluted to the indicated concentrations and successively flowed over sensorchips with immobilized ectodomain fragments of PlxnB1 (**a,b**) or MET (**c**) in "single-cycle kinetics" mode to derive the kinetic rate constants shown in Fig. 1c. Note that the kinetic constants derived from these curve fitting do not reflect true 1:1 affinity due to the divalent nature of the Fc grafts.



**Supplementary Fig. S3. Flow cytometry gating strategies**

Scatterplots showing live cell gating (black ovals) for each histogram panel in (A) peptide-grafted Fc binding to receptor-expressing 293T cells (relating to Fig.4) and (B-D) antibody binding to transfected HEK cell, MDA-MB-231 cells, MET-CHO cells, and Jurkat cells, respectively (relating to Fig.5a-c).

# Supplementary Tables

Supplementary Table S1. Amino acid sequences of the peptides used in the grafting

name	target	original RaPID peptide <sup>a</sup>	sequence used for grafting <sup>b</sup>	Ref
PB1m6	Plexin B1	Ac-wRPRVARWTGQIIYC	WRPRVARWTGQIIY	(1)
PB1m6A9	Plexin B1	Ac-wRPYIERWTGRLIVC	WRPYIERWTGRLIV	(2)
PB1m7	Plexin B1	Ac-wNSNVLSWQTYSWYC	(C)NSNVLSWQTYSWY(C)	(1)
aMD4	MET	Ac-yRQFNRRTHEVWNLD	YRQFNRRTHEVWNLD	(3)
aMD5	MET	Ac-yWYYAWDQTYKAFPC	YWYYAWDQTYKAFP	(3)
A6-2f	EGFR	Ac-BASFPEELDEWYVAYGC	(C)ASFPEELDEWYVAYG(C)	this study
tkD5	TrkB	Ac-yRQASPKFTFWSC	(C)YRQASPKFTFWS(C)	this study
IB8	integrin $\alpha6\beta1$	Ac-YLVKRSGLYTVDC	YLVKRSGLYTVDC	this study
PA tag	NZ-1 antibody	n/a	GVAMPGAEDDVV	(4)

<sup>a</sup> By convention, RaPID peptides are cyclized via the *N*-chloroacetyl group of the initiator amino acid and the sulfhydryl group of the terminal Cys. The small letter indicates *D*-amino acids, and B represents an unnatural amino acid *L*-boronophenylalanine.

<sup>b</sup> Flanking Cys residues (parenthesis) were added in some peptides to increase the binding capacity of the grafted proteins.

(1) Matsunaga et al., *Cell Chem. Biol.*, 23, 1341-1350 (2016)

(2) Bashiruddin et al., *Proc. Natl. Acad. Sci. U.S.A.*, 117, 31070-31077 (2020)

(3) Ito et al. *Nature Commun.*, 6, 6373 (2015)

(4) Fujii et al., *Protein Exp. Purif.*, 95, 240 (2014)

## Supplementary Table S2. Scaffold proteins and insertion sites used for the peptide grafting

protein	length	SCOP domain(fold)	graft site	flanking sequence <sup>a</sup>
Fn10	93	Fn3( $\beta$ -sandwich)	s1	...ISWDAP//VTVRY..
			s2	...YAVTGR//SPASSK....
VHH	115	IgV( $\beta$ -sandwich)	s1	...WVAGMS//RSSYED...
			s2	...YCNVNV//FEYWGQ...
SIRP $\alpha$	118	IgV( $\beta$ -sandwich)	s1	...ELIYNQ//KEGHFP...
			s2	...KFRKG//PDTEFK...
CEA	108	IgV( $\beta$ -sandwich)	s1	...IIGYVI//QQATPG...
			s2	...TLHVIK//LVNEEA...
Fc	227	IgC( $\beta$ -sandwich)	s1	...VVDVSH//DPEVKF...
			s2	...PREEQY//NSTYRV...
			s3	...SNKALP//PIEKTI...
			s4	...TISKAK//QPREPQ...
			s5	...PPVLDS//GSFFLY...
			s6	...RDELTK//QVSLTC...
			s7	...AVEWES//GQPENN...
			s8	...KSRWQQ//NVFSCS...
HSA	590	albumin(all $\alpha$ )	s1	...TCVADE//AENC DK...
			s2	...TECCQA//DKAA CL...
			s3	...EKCCAA//DPHECY...
			s4	...EKCKKA//DKETCF...
hGH	185	4-helix cytokine (helical bundle)	s1	...RLED//SPRTGQ...
			s2	...DTNSHN//DALLKN...
RBP	201	lipocalin( $\beta$ -barrel)	s1	...GRVRL//NNWDVC...
			s2	...KYWGVA//SFLQKG...
ALP	489	alkaline phosphatase-like ( $\alpha/\beta$ )	s1	...GPGYVL//GARPDV...
Cap (AAV2)	533	n/a	s1	...RTNTPS//TTQSRL...
			s2	...TNLQRG//QAATAD...
Cap (AAV1)	534	n/a	s1	...RTQNQS//AQNKDL...
			s2	...VNFQSS//DPATGD...

<sup>a</sup> RaPID-derived peptides (shown in Table S1) are inserted in the position indicated by "//", with up to 3 linker residues.

**Supplementary Table S3. Primer sequences used for extension PCR**

Relevant construct	Primer name	Strand	Sequence(5'- 3')
UG2-m6	UG-Fwd3	sense	TGGACCGGACAGATCATTACGAGATCTGCCCTTCCTCCAACGCG
	UG-Rev3(-)	antisense	TCTCGCACCCTAGGCCGCAATTACACAGTGAGCTTTGGGCTATT
UG2-m6A9	mP69-Fwd24	sense	GTGGACAGGAAGGTTGATCGTGGGTTGCCCTTCCTCCAACGCGTG
	mP69-Rev24(-)	antisense	CTCTCGATGTAAGGCCGCCAACACACAGTGAGCTTTGGGCTATTT
UG(CS)2-m6A9	mP69-Fwd23	sense	GTGGACAGGAAGGTTGATCGTGGGTAGCCCTTCCTCCAACGCG
	mP69-Rev23(-)	antisense	CTCTCGATGTAAGGCCGCCAACCGGACAGTGAGCTTTGGGCTA
UG2-m7	P7ds-Fwd10	sense	GGCAAATTACAGCTGGTATTGCGGTAGCCCTTCCTTCC
	P7ds-Rev10(-)	antisense	AGGACAGCACGTTAGAATTGCAACCGGACAGTGAGCTTTG
UG2-aMD4	MD4-Fwd21	sense	CACGAGGTGTGGAAGTTGATTGCGGTAGCCCTTCCTTCC
	MD4-Rev21(-)	antisense	CGTAGCCTGTTGAACTGCCGCAACCGGACAGTGAGCTTTG
UG2-aMD5	MD5-Fwd13	sense	AGACCTACAAAGCCTTCCGTGCGGTAGCCCTTCCTTCC
	MD5-Rev13(-)	antisense	GATCCCAAGCATAGTACCAGCAACCGGACAGTGAGCTTTG
Fn10(m6A9_s1)	Fn10-Fwd1	sense	TAGCCGTCTCGGATCTGTACAGTGAGATATTAC
	Fn10_rev1(-)	antisense	GCCGTCTCGCCCTAGGAGCATCCAGCTGATC
Fn10(aMD4_s1)	Fn10-Fwd2	sense	AGCCGTCTCGGATCTAGCCCCGAAGCAGCAAGC
	Fn10_rev2(-)	antisense	AGCCGTCTCGCCCTACGGCCAGTGACAGCATAAC
Fn10(m6A9_s2)	FnmP69-Fwd1	sense	AGGAAGGTTGATCGTAGCCCCGCAAGCAGCAAGCC
	FnmP69-Rev1(-)	antisense	GTCCACCTCTCGATGTAAGGCCGCCAACGGCCAGTGAC
Fn10(aMD4_s2)	FnMD4-Fwd1	sense	GCACGAGGTGTGGAAGTTGGATGGCAGCCCCGAAGCAGCAAGC
	FnMD4-Rev1(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCCTCCACGGCCAGTGACAGC
SIRPa(m6A9_s1)	mP69-Fwd34	sense	GGTGGACAGGAAGGTTGATCGTGGGCGGCAAAGAAGGCCACTTCCCCCG
	mP69-Rev34(-)	antisense	TCTCGATGTAAGGCCGCCAGCCTTGATTGTAGATTAATTCCC
SIRPa(m6A9_s2)	mP69-Fwd35	sense	GCTGGACAGGAAGGTTGATCGTGGGCGGCCCTGCACACGGAG
	mP69-Rev35(-)	antisense	TCTCGATGTAAGGCCGCCAGCCGCTCCCTTCCGGAAGCTTC
SIRPa(aMD4_s1)	MD4-Fwd28	sense	GCACGAGGTGTGGAAGTTGGATGGCGGATCTAAAGAAGGCCACTTCCCCCG
	MD4-Rev28(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCCGCCGCTTATTGTAGATTAATTCCC
SIRPa(aMD4_s2)	MD4-Fwd29	sense	CGTAGCCTGTTGAACTGCCTATAGCCGCCGCTCCCTTCCGGAAGCTTC
	MD4-Rev29(-)	antisense	CACGAGGTGTGGAAGTTGGATGGCGGATCTCTGCACACGGAG
CEA(m6A9_s1)	mP69-Fwd35	sense	TGGACAGGAAGGTTGATCGTGGGATCTCAACAAGCTACCCAGGG
	mP69-Rev35(-)	antisense	CCTCTCGATGTAAGGCCGCCAACGGCCGCTTATTACATATCCTATAAATTTG
CEA(m6A9_s2)	mP69-Fwd36	sense	TGGACAGGAAGGTTGATCGTGGGATCTTGTGAATGAAGAAGCAAC
	mP69-Rev36(-)	antisense	CCTCTCGATGTAAGGCCGCCAACGGCCGCTTTTATGACGTGAGGGTG
CEA(aMD4_s1)	MD4-Fwd30	sense	GCACGAGGTGTGGAAGTTGGATGGCGGATCTCAACAAGCTACCCAGGG
	MD4-Rev30(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCCGCCGCTTATTACATATCCTATAATTTG
CEA(aMD4_s2)	MD4-Fwd31	sense	GCACGAGGTGTGGAAGTTGGATGGCGGATCTTGTGAATGAAGAAGCAAC
	MD4-Rev31(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCCGCCGCTTTTATGACGTGAGGGTG
VHH(m6A9_s1)	Nb-Fwd7	sense	TGGACAGGAAGGTTGATCGTAGGTCGCTCCTACGAAGACTC
	Nb-Rev7(-)	antisense	CCTCTCGATGTAAGGCCGCCATCCCGAGGACATTCCTGCCACC
VHH(m6A9_s2)	Nb-Fwd9	sense	AGGTGGACAGGAAGGTTGATCGTGGGCTTCGAGTATTGGG
	Nb-Rev9(-)	antisense	CTCGATGTAAGGCCGCCAGCCACGTTGACGTTACAATAG
VHH(aMD4_s1)	Nb-Fwd8	sense	ACGAGGTGTGGAAGTTGGATGGAGGTCGCTCCTACGAAGACTC
	Nb-Rev8(-)	antisense	GCGTACGCCTGTTGAACTGCCTATATCCAGCCGAGGACATTCCTG
VHH(aMD4_s2)	Nb-Fwd10	sense	ACGCACGAGGTGTGGAAGTTGGATGGGGCTTCGAGTATTGGGGCC
	Nb-Rev10(-)	antisense	ACGCCTGTTGAACTGCCTATAAGAGCCACGTTGACGTTACAATAG
Fc(m6A9_s1)	mP69-Fwd4	sense	GGACAGGAAGGTTGATCGTGGGCGGAGACCCTGAGGTCAAGTTC
	mP69-Rev4(-)	antisense	ACCTCTCGATGTAAGGCCGCCAGCCGTGGCTCACGTCCACCACC
Fc(m6A9_s2)	mP69-Fwd2	sense	TGGACAGGAAGGTTGATCGTGGGCAACAGCAGTACCGGTGGG
	mP69-Rev2(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCGTAAGTCTCCTCCCGCGGC
Fc(m6A9_s3)	mP69-Fwd3	sense	TGGACAGGAAGGTTGATCGTGGGCCCCATCGAGAAAACCATCTC
	mP69-Rev3(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCGTTGGAGGGCTTTGTTGGAG
Fc(m6A9_s4)	mP69-Fwd32	sense	GGACAGGAAGGTTGATCGTGGGAGGGCAGCCCGAGAACCAC
	mP69-Rev32(-)	antisense	ACCTCTCGATGTAAGGCCGCCACCCTTTGGCTTTGGAGATGG
Fc(m6A9_s5)	mP69-Fwd33	sense	TGGACAGGAAGGTTGATCGTGGGCGGCTCCTTCTCTACAG
	mP69-Rev33(-)	antisense	CCTCTCGATGTAAGGCCGCCACCAGGAGTCCAGCAGGGAGGC
Fc(m6A9_s6)	mP69-Fwd9	sense	GGACAGGAAGGTTGATCGTGGGCGGCCAGGTCAGCCTGACCTGC
	mP69-Rev9(-)	antisense	ACCTCTCGATGTAAGGCCGCCAGCCCTTGGTCAGCTCATCCCGG
Fc(m6A9_s7)	mP69-Fwd10	sense	GGACAGGAAGGTTGATCGTGGGCGGTGGGCGAGCCGGAGAAAC
	mP69-Rev10(-)	antisense	ACCTCTCGATGTAAGGCCGCCAGCCGCTCTCCACTCCACGGCG
Fc(m6A9_s8)	mP69-Fwd11	sense	GGACAGGAAGGTTGATCGTGGGGGGAACGTCTTCTCATGC
	mP69-Rev11(-)	antisense	ACCTCTCGATGTAAGGCCGCCACCCTGCTGCCACCTGCTC
Fc(aMD4_s1)	MD4-Fwd4	sense	CGCACGAGGTGTGGAAGTTGGATGGCGGAGACCCTGAGGTCAAGTTC
	MD4-Rev4(-)	antisense	TACGCCTGTTGAACTGCCTATAGCCTCCGTGGCTCACGTCCACCACC
Fc(aMD4_s2)	MD4-Fwd2	sense	GCACGAGGTGTGGAAGTTGGATGGCAGCAACAGCAGTACCGTGTGG
	MD4-Rev2(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCCTCCGTAAGTCTCCTCCCGCGGC
Fc(aMD4_s3)	MD4-Fwd3	sense	GCACGAGGTGTGGAAGTTGGATGGCAGCCCATCGAGAAAACCATCTC
	MD4-Rev3(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCCTCCTGGGAGGGCTTTGTTGGAG

Fc(aMD4_s4)	MD4-Fwd26	sense	ACGCACGAGGTGTGGAACCTGGATGGAGGGCAGCCCCGAGAACC
	MD4-Rev26(-)	antisense	ACGCCTGTTGAACTGCCTATAGCCCCCTTTGGCTTTGGAGATGG
Fc(aMD4_s5)	MD4-Fwd27	sense	ACGCACGAGGTGTGGAACCTGGATGGCGGCTCCTTCTCTCTAC
	MD4-Rev27(-)	antisense	ACGCCTGTTGAACTGCCTATAGCCCCGGAGTCCAGCACGGGAG
Fc(aMD4_s6)	MD4-Fwd5	sense	CGCACGAGGTGTGGAACCTGGATGGCGGCCAGGTCAGCCTGACCTGC
	MD4-Rev5(-)	antisense	TACGCCTGTTGAACTGCCTATAGCTCCCTTGGTCAGCTCATCCCGG
Fc(aMD4_s7)	MD4-Fwd6	sense	CGCACGAGGTGTGGAACCTGGATGGCGGTGGGCAGCCGGAGAACAAC
	MD4-Rev6(-)	antisense	TACGCCTGTTGAACTGCCTATAGCTCCGCTCTCCCACTCCACGGCG
Fc(aMD4_s8)	MD4-Fwd7	sense	CGCACGAGGTGTGGAACCTGGATGGGGGGAACGCTTCTTCATGC
	MD4-Rev7(-)	antisense	TACGCCTGTTGAACTGCCTATATCCCCCTGCTGCCACCTGCTC
Fc(m7_s8)	P7ds-Fwd8	sense	GCAAACCTACAGCTGGTATTGTGGATCGGGGAACGCTCTTCTC
	P7ds-Rev8(-)	antisense	CAGGACAGCACGTTAGAATTGCAGCCGCTCCCTGCTGCCAC
Fc(aMD5_s8)	MD5-Fwd9	sense	CAGACCTACAAAGCCTTTCCTGATCGGGGAACGCTTCTTCATGC
	MD5-Rev9(-)	antisense	ATCCCAAGCATAGTACCAATAGCCGCTCCCTGCTGCCACCTGCTC
Fc(A6-2f_s8)	A62f-Fwd7	sense	ATGAGTGGTACGTGGCTTATGGTTGTGGATCGGGGAACGTC
	A62f-Rev7(-)	antisense	CCAGCTCTTCAGGGAAAGAGGGCGCAGCCGCTCCCTGCTGCC
Fc(tkD5_s8)	tkD5-Fwd8	sense	AAAGTTCACCTTTTGGAGTTGTGGATCGGGGAACGTC
	tkD5-Rev8(-)	antisense	GGGGAAGCCTGGCGGTAGCAGCCGCTCCCTGCTGCC
Fc(IB8_s8)	IB8-Fwd1	sense	GTGGTTGTATACCGTGGACGGGGATCTAACGCTTCTTCATG
	IB8-Rev1(-)	antisense	CCGTTCTTTTGACGAGGTATCCGCGCTCTGTGCCACCTG
Fc(A6-2f_s6)	A62f-Fwd6	sense	ATGAGTGGTACGTGGCTTATGGTTGTGGAGGCTCCAGGTCAGC
	A62f-Rev6(-)	antisense	CCAGCTCTTCAGGGAAAGAGGGCGCAGCCCTCCGCTCTTGGTCAGC
hGH(m6A9_s1)	mP69-Fwd13	sense	TGGACAGGAAGGTTGATCGTGGGCAGCCCCGGACTGGGC
	mP69-Rev13(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCATCTTCCAGCCTCTGC
hGH(m6A9_s2)	mP69-Fwd14	sense	TGGACAGGAAGGTTGATCGTGGGTGACGCACTACTCAAGAAC
	mP69-Rev14(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCGTTGTGTGAGTTTGTGTC
hGH(aMD4_s1)	MD4-Fwd40	sense	CGCACGAGGTGTGGAACCTGGACGGGGGACGCCCGGACTG
	MD4-Rev40(-)	antisense	TACGCCTGTTGAACTGCCTATATCCGGAGCCATCTTCCAGC
hGH(aMD4_s2)	MD4-Fwd41	sense	CGCACGAGGTGTGGAACCTGGACGGGGGTGACGCACTACTC
	MD4-Rev41(-)	antisense	TACGCCTGTTGAACTGCCTATATCCGGAGCCGTTGTGTGAG
HSA(m6A9_s1)	mP69-Fwd5	sense	TGGACAGGAAGGTTGATCGTGGCGGAGCTGAAAATTGTGACAAATC
	mP69-Rev5(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCCTCATCAGCAACACATGTTTTTG
HSA(m6A9_s2)	mP69-Fwd6	sense	TGGACAGGAAGGTTGATCGTGGCGGTGATAAAGCTGCCTGCCTGTTG
	mP69-Rev6(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCAGCTTGGCAACATTCTGTA AAAAG
HSA(m6A9_s3)	mP69-Fwd7	sense	TGGACAGGAAGGTTGATCGTGGCGGAGATCCTCATGAATGCTATG
	mP69-Rev7(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCAGCGGCACAGCACTTCTCTAG
HSA(m6A9_s4)	mP69-Fwd8	sense	TGGACAGGAAGGTTGATCGTGGCGGGGATAAGGAGACCTGCTTTG
	mP69-Rev8(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCAGCCTTGACGCACTTCTCTAC
HSA(aMD4_s1)	MD4-Fwd8	sense	CGCACGAGGTGTGGAACCTGGATGGGTGAGCTGAAAATTGTGAC
	MD4-Rev8(-)	antisense	TACGCCTGTTGAACTGCCTATAGCTGACTATCAGCAACACATG
HSA(aMD4_s2)	MD4-Fwd9	sense	GCACGAGGTGTGGAACCTGGATGGGCTGATAAAGCTGCCTGCCTG
	MD4-Rev9(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCCAGCAGCTTGGCAACATTCTG
HSA(aMD4_s3)	MD4-Fwd10	sense	CACGAGGTGTGGAACCTGGATGGCTCAGATCCTCATGAATGCTATG
	MD4-Rev10(-)	antisense	CGTACGCCTGTTGAACTGCCTATAGCTGCAGCGGCACAGCACTTC
HSA(aMD4_s4)	MD4-Fwd11	sense	GCACGAGGTGTGGAACCTGGATGGCGGCATAAGGAGACCTGCTTTG
	MD4-Rev11(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCTCCAGCCTTGACGCACTTCTC
RBP(m6A9_s1)	mP69-Fwd19	sense	TGGACAGGAAGGTTGATCGTGGGGAATAACTGGGACGTGTGCG
	mP69-Rev19(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCAAAAGACGGACTCGGCC
RBP(m6A9_s2)	mP69-Fwd20	sense	GGACAGGAAGGTTGATCGTGGGCTCCTTTCTCCAGAAAGGAAATG
	mP69-Rev20(-)	antisense	ACCTCTCGATGTAAGGCCGCCAGCCGGCTACGCCCAAGTACTTC
RBP(aMD4_s1)	MD4-Fwd42	sense	CGCACGAGGTGTGGAACCTGGACGGGGGAATAACTGGGACGTG
	MD4-Rev42(-)	antisense	TACGCCTGTTGAACTGCCTATATCCGCCAAAAGACGGACTCGGC
RBP(aMD4_s2)	MD4-Fwd43	sense	CGCACGAGGTGTGGAACCTGGACGGGCTCCTTTCTCCAGAAAGG
	MD4-Rev43(-)	antisense	TACGCCTGTTGAACTGCCTATATCCGCCGGTACGCCCAAGTAC
ALP(m6A9_s1)	mP69-Fwd18	sense	TGGACAGGAAGGTTGATCGTGGGAGGGACGGCGCCCGCCGGATG
	mP69-Rev18(-)	antisense	CCTCTCGATGTAAGGCCGCCAGCCCTCCCTTGGACATAGCCTGG
ALP(aMD4_s1)	MD4-Fwd16	sense	GCACGAGGTGTGGAACCTGGATGGAGGGGACGGCGCCCGGC
	MD4-Rev16(-)	antisense	GTACGCCTGTTGAACTGCCTATAGCTCCCTTGGACACATAG
PA_s2_AAV1	PAins-Fwd	sense	GCCGAAGATGATGTGGTGGGATCTGACCCTGCGAC
	PAins-Rev(-)	antisense	ACCTGGCATGGCAACGCCCGCTGCTGCTCTGAAAATTG
aMD4_s2_AAV1	MD4-Fwd40	sense	GCGCGGCTATAGGCAGTTCAACAGGGCGCACGACGAGGTGTGGAACCTGGATGGCG
	MD4-Rev40(-)	antisense	GATCCGCCATCCAAGTTCACACCTCGTGCCTGCGCCTGTTGAACTGCCTATAGCCG
PA_s1_AAV2	pa-Fwd1	sense	CCGAAGATGATGTGGTGGGCACCACGAGTCAAGGCTTC
	pa-Rev1(-)	antisense	CACCTGGCATGGCAACGCCCTCCACTGGAGTGTGTTGTTTC
PA_s2_AAV2	pa-Fwd2	sense	CCGAAGATGATGTGGTGGGACAAGCAGTACCAGCAGATG
	pa-Rev2(-)	antisense	CACCTGGCATGGCAACGCCCTCTCTGGAGGTTGGTAG
m6A9_s2_AAV2	mP69-Fwd25	sense	GGACAGGAAGGTTGATCGTGGGCACCACGAGTCAAGGCTTC
	mP69-Rev25(-)	antisense	ACCTCTCGATGTAAGGCCGCCATCCACTTGGAGTGTGTTGTTTC



**Supplementary Table S4. Primer sequences used for mutagenesis**

Relevant construct	Primer name	Strand	Sequence(5'- 3')
pRC2-mi342_AgeI	pCR2mi342mut1+	sense	GATGCTGCGTACCGGtAACAACTTTACCTTCAG
	pCR2mi342mut1-	antisense	CTGAAGGTAAAGTTGTTaCCGGTACGCAGCATC
pRC2-mi342_NheI	pCR2mi342mut2+	sense	GCGGCAAAGTTTGCTagCTTCATCACACAGTAC
	pCR2mi342mut2-	antisense	GTACTGTGTGATGAAGetAGCAAACCTTTGCCGC