

	TRBV: human TRBV6-5					TRAV: human TRAV8-6				
FR1-IMGT	1	1	aat	ASN	N	1	0	agc	ALA	A
	2	2	gct	ALA	A	2	1	cag	GLN	Q
	3	3	ggt	GLY	G	3	2	tct	SER	S
	4	4	gtc	VAL	V	4	3	gtg	VAL	V
	5	5	act	THR	T	5	4	acc	THR	T
	6	6	cag	GLN	Q	6	5	cag	GLN	Q
	7	7	acc	THR	T	7	6	ctt	LEU	L
	8	8	cca	PRO	P	8	7	gac	ASP	D
	9	9	aaa	LYS	K	9	8	agc	SER	S
	10	10	ttc	PHE	F	10	9	caa	GLN	Q
	11	11	cag	GLN	Q	11	10	gtc	VAL	V
	12	12	gtc	VAL	V	12	11	cct	PRO	P
	13	13	ctg	LEU	L	13	12	gtc	VAL	V
	14	14	aag	LYS	K	14	13	ttt	PHE	F
	15	15	aca	THR	T	15	14	gaa	GLU	E
	16	16	gga	GLY	G	16	15	gaa	GLU	E
	17	17	cag	GLN	Q	17	16	gcc	ALA	A
	18	18	agc	SER	S	18	17	cct	PRO	P
	19	19	atg	MET	M	19	18	gtg	VAL	V
	20	20	aca	THR	T	20	19	gag	GLU	E
	21	21	ctg	LEU	L	21	20	ctg	LEU	L
	22	22	cag	GLN	Q	22	21	agg	ARG	R
	23	23	tgt	CYS	C	23	22	tgc	CYS	C
	24	24	gcc	ALA	A	24	23	aac	ASN	N
	25	25	cag	GLN	Q	25	24	tac	TYR	Y
CDR1-IMGT	26	26	gat	ASP	D	26	25	tca	SER	S
	27	27	atg	MET	M	27	26	tcg	SER	S
	28	28	aac	ASN	N	28	27	tct	SER	S
	29	29	cat	HIS	H	29	28	gtt	VAL	V
	30	30	gaa	GLU	E	30	29	tca	SER	S
	31	* 31	tac	TYR	Y	31	30	gtg	VAL	V
	32	*	—	—	—	32	* 31	tat	TYR	Y
	33		—	—	—	33	*	—	—	—
	34		—	—	—	34	*	—	—	—
	35		—	—	—	35		—	—	—
	36		—	—	—	36		—	—	—
	37		—	—	—	37		—	—	—
	38		—	—	—	38		—	—	—

Fig. 1A

TRBV: human TRBV6-5						TRAV: human TRAV8-6				
FR2-IMGT	39	32	atg	MET	M	39	32	ctc	LEU	L
	40	33	tcc	SER	S	40	33	ttc	PHE	F
	41	34	tgg	TRP	W	41	34	tgg	TRP	W
	42	35	tat	TYR	Y	42	35	tat	TYR	Y
	43	36	cga	ARG	R	43	36	gtg	VAL	V
	44	37	caa	GLN	Q	44	37	caa	GLN	Q
	45	38	gac	ASP	D	45	38	tac	TYR	Y
	46	39	cca	PRO	P	46	39	ccc	PRO	P
	47	40	ggc	GLY	G	47	40	aac	ASN	N
	48	41	atg	MET	M	48	41	caa	GLN	Q
	49	42	ggg	GLY	G	49	42	gga	GLY	G
	50	43	ctg	LEU	L	50	43	ctc	LEU	L
	51	44	agg	ARG	R	51	44	cag	GLN	Q
	52	45	ctg	LEU	L	52	45	ctt	LEU	L
	53	46	att	ILE	I	53	46	ctc	LEU	L
	54	47	cat	HIS	H	54	47	ctg	LEU	L
	55	48	tac	TYR	Y	55	48	aag	LYS	K
CDR2-IMGT	56	49	tca	SER	S	56	* 49	tat	TYR	Y
	57	50	gtt	VAL	V	57	* 50	tta	LEU	L
	58	51	ggt	GLY	G	58	* 51	tca	SER	S
	59	52	gct	ALA	A	59	* 52	gga	GLY	G
	60	53	ggt	GLY	G	60		—	—	—
	61	54	atc	ILE	I	61		—	—	—
	62		—	—	—	62		—	—	—
	63		—	—	—	63		—	—	—
	64		—	—	—	64		—	—	—
	65		—	—	—	65		—	—	—
FR3-IMGT	66	55	act	THR	T	66	* 53	tcc	SER	S
	67	56	gac	ASP	D	67	* 54	acc	THR	T
	68	57	caa	GLN	Q	68	* 55	ctg	LEU	L
	69	58	gga	GLY	G	69	* 56	gtt	VAL	V
	70	59	gaa	GLU	E	70	* 57	gaa	GLU	E
	71	60	gtc	VAL	V	71	* 58	agc	SER	S
	72	61	ccc	PRO	P	72	* 59	atc	ILE	I
	73	* 62	—	—	—	73	*	—	—	—
	74	* 63	aat	ASN	N	74	* 60	aac	ASN	N
	75	* 64	ggc	GLY	G	75	61	ggt	GLY	G
	76	65	tac	TYR	Y	76	62	ttt	PHE	F
	77	66	aat	ASN	N	77	63	gag	GLU	E

Fig. 1B

TRBV: human TRBV6-5					TRAV: human TRAV8-6					
CDR3-IMGT	78	67	gtc	VAL	V	78	64	gct	ALA	A
	79	68	tcc	SER	S	79	65	gaa	GLU	E
	80	69	aga	ARG	R	80	66	ttt	PHE	F
	81	70	tca	SER	S	81	67	aac	ASN	N
	82		—	—	—	82	68	aag	LYS	K
	83	71	acc	THR	T	83	69	agt	SER	S
	84	72	aca	THR	T	84	70	caa	GLN	Q
	85	73	gag	GLU	E	85	71	act	THR	T
	86	74	gat	ASP	D	86	72	tcc	SER	S
	87	75	ttc	PHE	F	87	73	ttc	PHE	F
	88	76	ccg	PRO	P	88	74	cac	HIS	H
	89	77	ctc	LEU	L	89	75	ttg	LEU	L
	90	78	agg	ARG	R	90	76	agg	ARG	R
	91	79	ctg	LEU	L	91	77	aaa	LYS	K
	92	80	ctg	LEU	L	92	78	ccc	PRO	P
	93	81	tcg	SER	S	93	79	tca	SER	S
	94	82	gct	ALA	A	94	80	gtc	VAL	V
	95	83	gct	ALA	A	95	81	cat	HIS	H
	96	84	ccc	PRO	P	96	82	ata	ILE	I
	97	85	tcc	SER	S	97	83	agc	SER	S
	98	86	cag	GLN	Q	98	84	gac	ASP	D
	99	87	aca	THR	T	99	85	acg	THR	T
	100	88	tct	SER	S	100	86	gct	ALA	A
	101	89	gtg	VAL	V	101	87	gag	GLU	E
	102	90	tac	TYR	Y	102	88	tac	TYR	Y
	103	91	ttc	PHE	F	103	89	ttc	PHE	F
	104	92	tgt	CYS	C	104	90	tgt	CYS	C
	105	93	gcc	ALA	A	105	91	gct	ALA	A
	106	94	agc	SER	S	106	92	gtg	VAL	V
	107	95	agt	SER	S	107	93	agt	SER	S
	108	96	tat	TYR	Y					
	109	97	—	—	—					

Fig. 1C

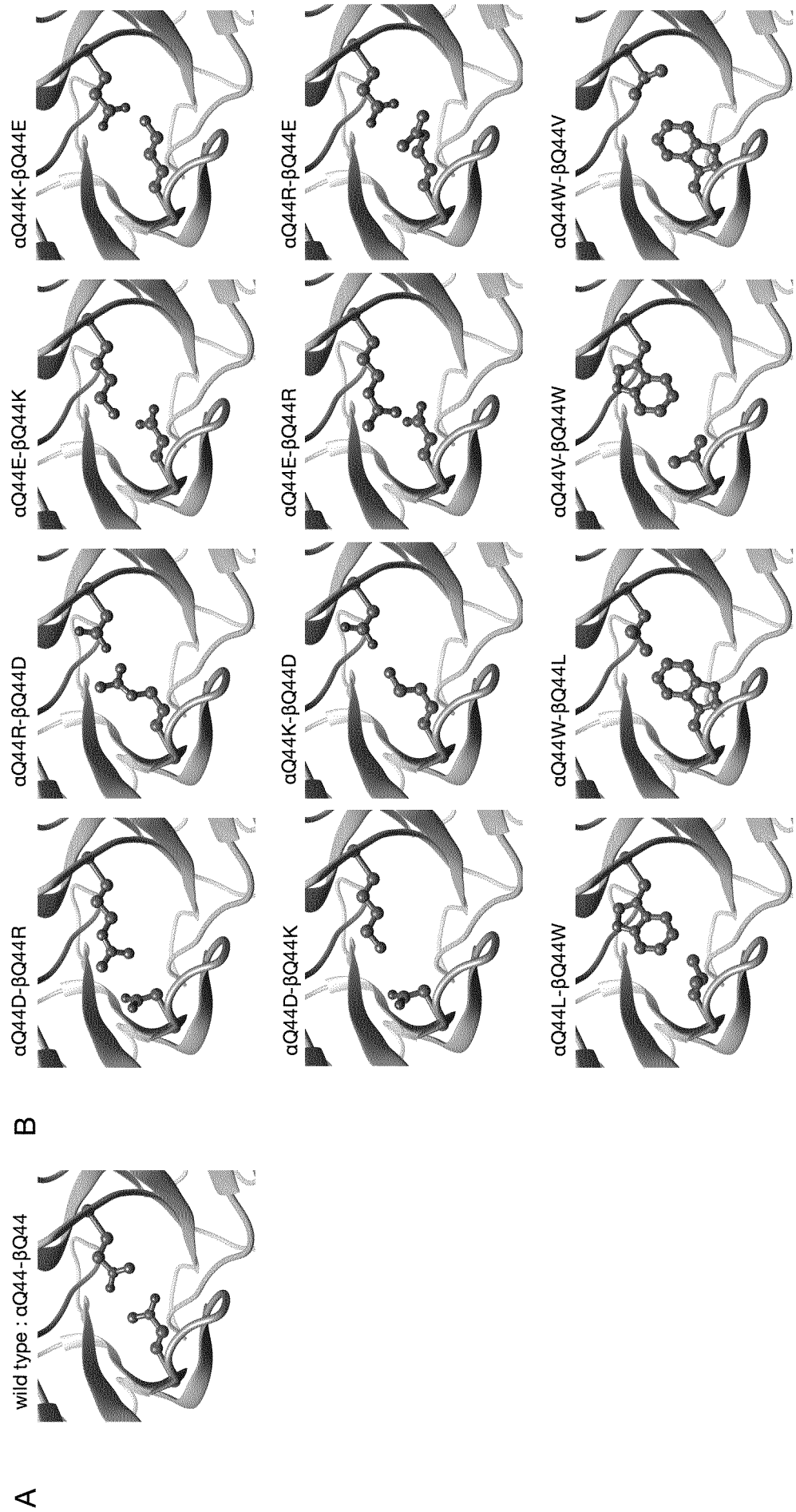
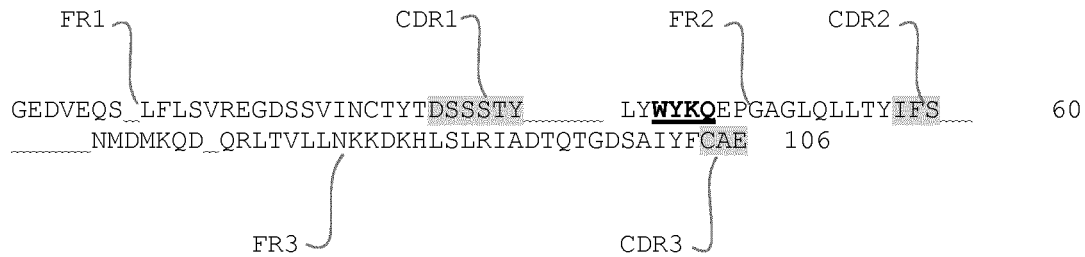


Fig. 2

SEQ ID NO 1: TCR alpha chain variable domain of R7P1D5 (TRAV5)



SEQ ID NO 2: TCR beta chain variable domain of R7P1D5 (TRBV12-4)

DAGVIQSPRHEVTEMGQEVTLRCKPISGHDY LFWYQTMMRGLELLIYFNNNV 60
P IDDSGMPEDRFSAKMP_NASFSTLKIQPSEPRDSAVYFCAS 106

SEQ ID NO 3: TCR alpha chain variable domain of TRAV 8-6

AQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSG 60
STLVESI_NGFEAEFNKSQTSFHLRKPSVHISDTAEYFCVVS 107

SEQ ID NO 4: TCR beta chain variable domain of TRBV 6-5

NAGVTQTPKFQVLKLTGQSMTLQCAQD**MNHEY**MS**WYRQ**DPGMGLRLIHYSVGAG 60
ITDQGEVP_NGYNVRS_TTEDFPLRLLSAAPSQTSVYFCASSY 108

Fig. 3

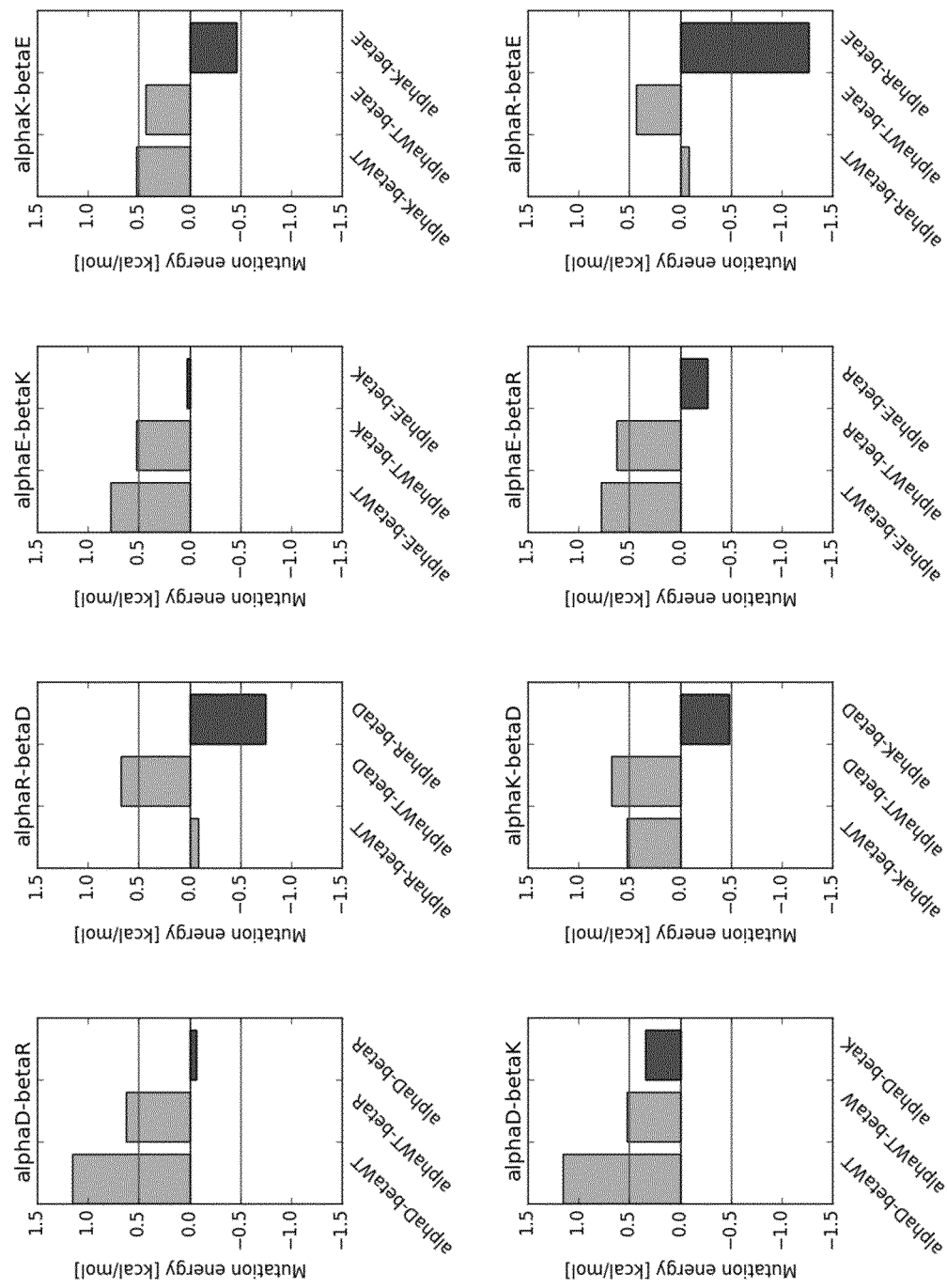
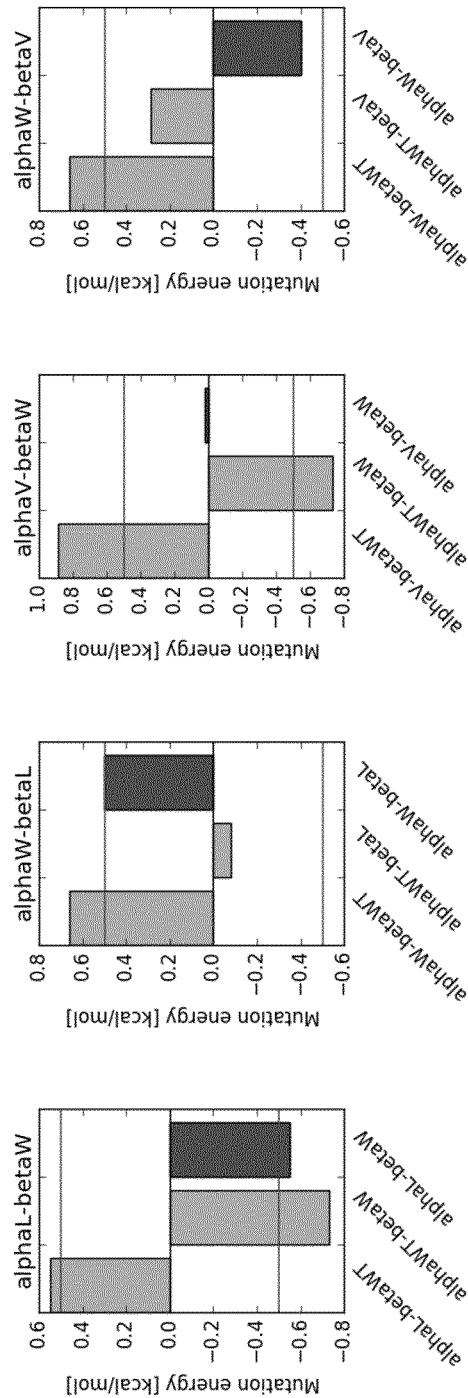


Fig. 4A



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Fig. 4B

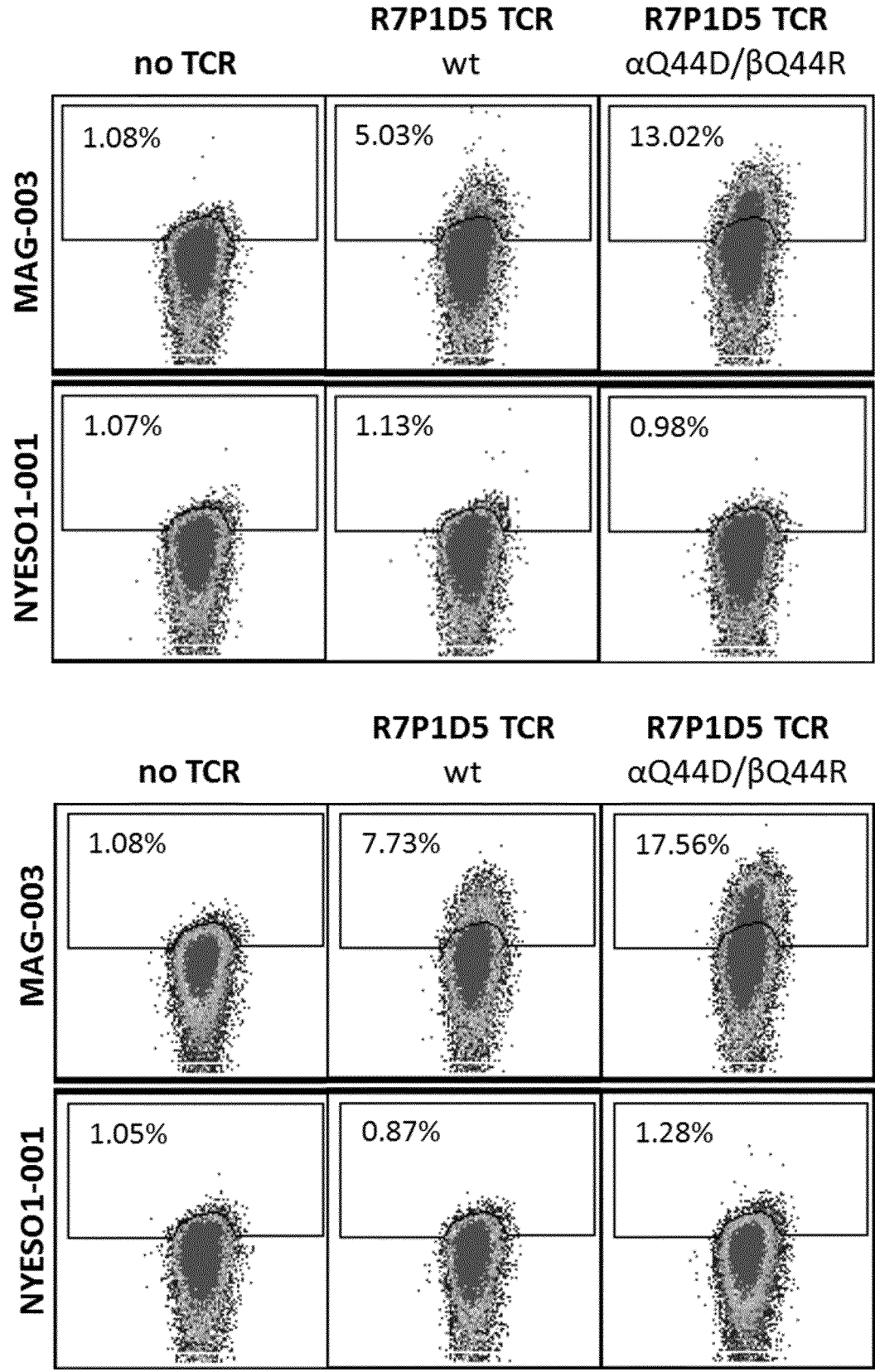
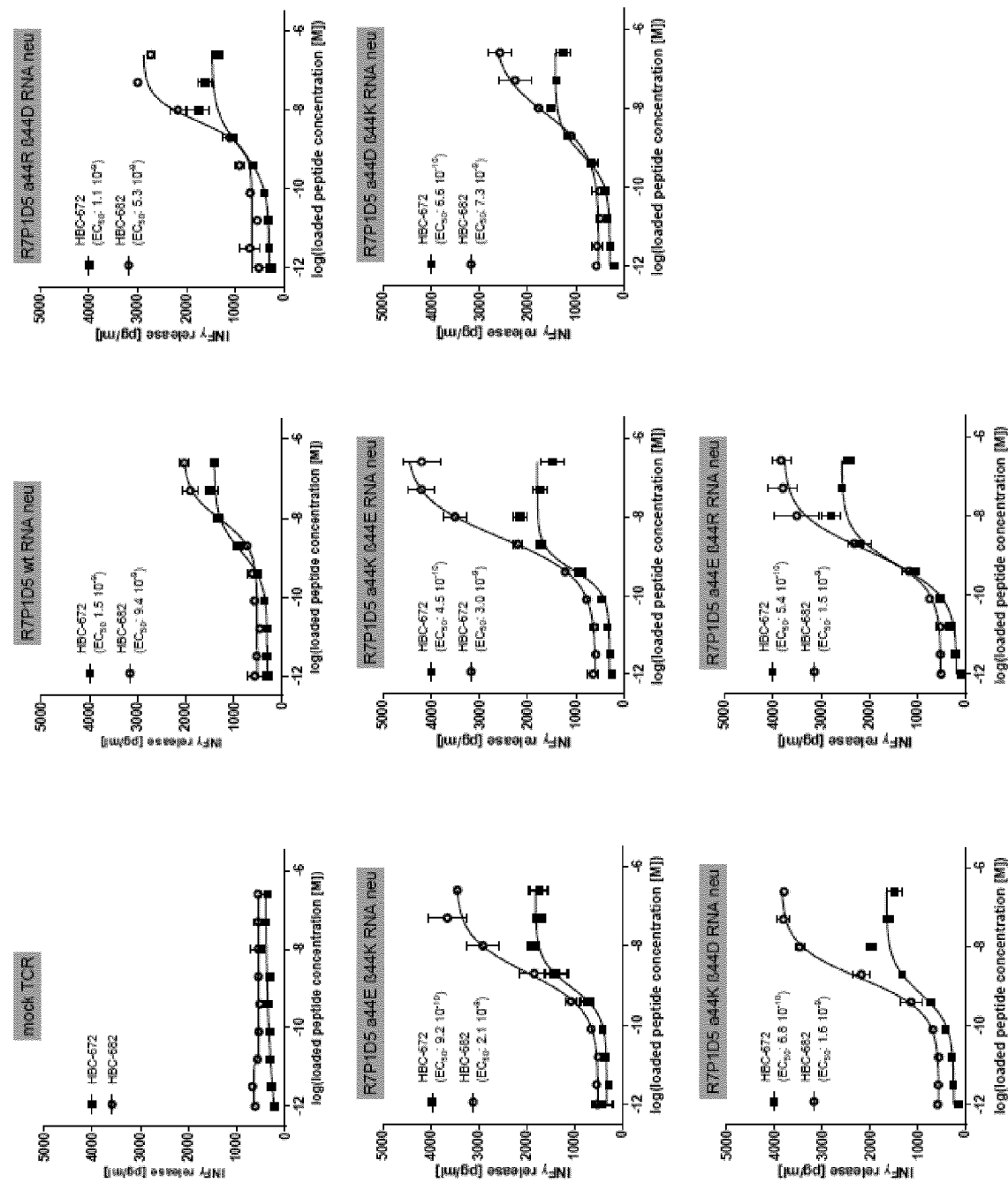


Fig. 5

Fig.6



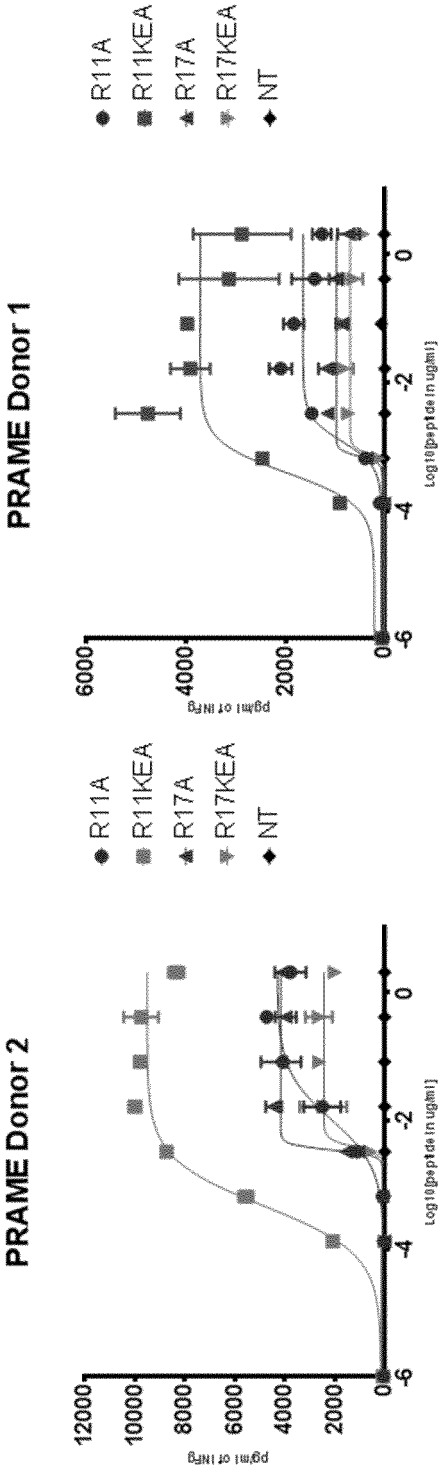


Fig.7

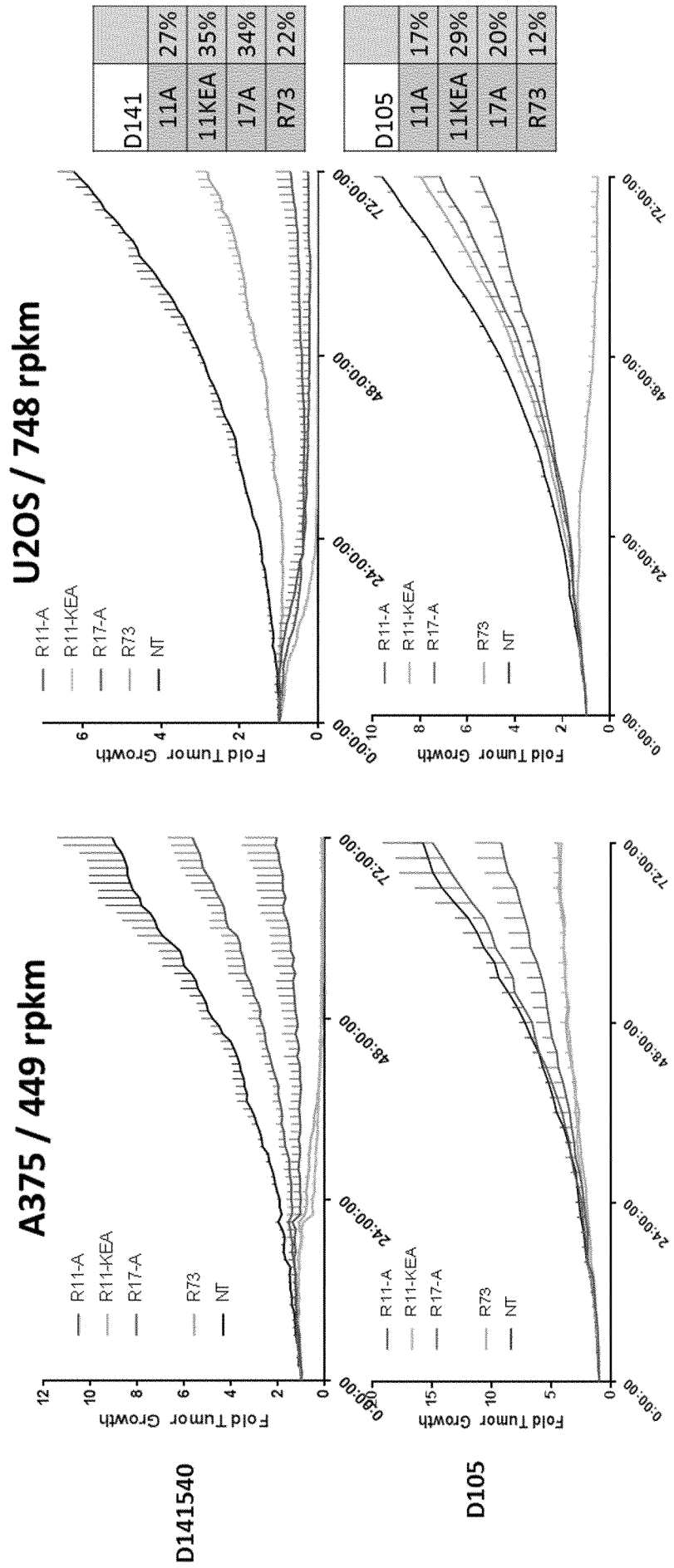


Fig.8