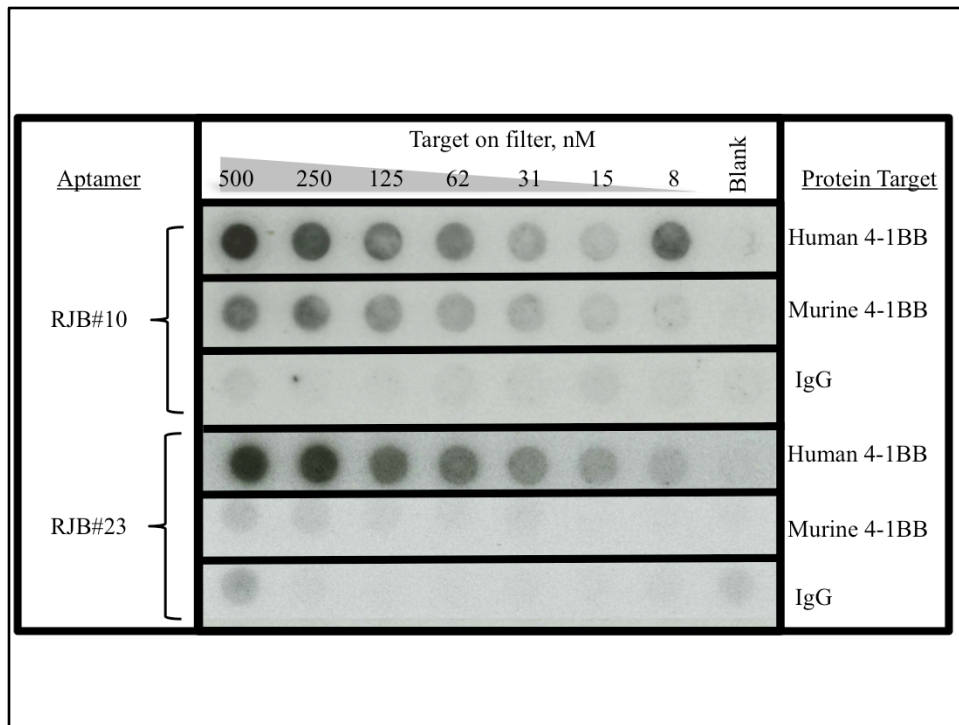


Supplementary figure 1. Nonspecific binders enriched on positively charged mIL-10RA protein.

Prevalences of aptamers from major clusters at round 5 in the pools isolated from human IL10RA protein (blue), murine IL-10RA protein (red), or IgG protein (green) were determined by high-throughput sequencing, as described in the Methods. Sequences were ranked by a specificity index that was determined as the hIL-10RA prevalence divided by the hIgG prevalence. The threshold was set at a hIL-10RA to hIgG ratio greater than 1.



Supplementary figure 2. Correlation between prevalences and binding patterns of h4-1BB aptamers.

Radiolabeled aptamers with high (RJB#10) and low (RJB#23) prevalences in the murine 4-1BB pool were incubated with decreasing concentrations of human 4-1bb protein (lanes 1 and 4), murine 4-1BB protein (lanes 2 and 5) and control (lanes 3 and 6). Binding properties were visualized by retention of the protein:RNA complex on a nitrocellulose filter.

Supplementary table S1. Conditions of hIL10-RA aptamer in vitro selection

Round	Amount of protein, ug	Amount of RNA, nM	NaCl concentration
1.	25	2	150
2.	20	1.5	150
3.	16	1	150
4.	12	1	150
5.	10	1	150

Supplementary table S2. Amplification of round 2 hIL-10RA candidate aptamers via emulsion or open PCR.

N40 sequence	GC content*	Prevalence at round 2	Prevalence at round 3		Rate of amplification R2->R3	
			ePCR	oPCR	ePCR	oPCR
CATGACACATAGTAGAACGCGCAAAAATTATTGAAGTAAA	0.325	96	109	1033	1.14	10.76
ACTATAACGCGTCAAAGTGCTTATCGAACACTATTTGTAA	0.35	615	807	463	1.31	0.75
TAGACGAGCACTTCTCTCAGTCGCATTCTATTATTTAAATT	0.35	435	565	699	1.30	1.61
CATGACACATAGAATATAACGCGCAAATCACAGTCATATG	0.375	152	239	1052	1.57	6.92
TGCAATGAGGACTTCTCTCAGTCTAACACAATGTTGTTTA	0.375	136	150	61	1.10	0.45
TATAGAGAAGCTTCTCTCAGTCGAAGCCAAAGAGCATTAAAT	0.375	135	115	75	0.85	0.56
ATGAGGACTTCTCTCAGTCGTGACCATTAAATAAGAGAAA	0.375	117	128	121	1.09	1.03
AGCAAAGTCGTCAGCAATATAAACTCGATTCTTATTGGA	0.375	84	140	280	1.67	3.33
CCACTTCAATTTTCACGTCAAAATACAGACGTGACTGAAA	0.375	37	72	36	1.95	0.97
ACGATCACTTCTCTCAGTCGGACTAATATTACGGTTAGAA	0.4	142	233	79	1.64	0.56
CATGACACATCGGATCAATAAGATCGAAAACGCGCAAGAA	0.425	59	122	61	2.07	1.03
TGTCGAGTACTTTTCTCAGTCTATTCCACAGTAGTGGAGA	0.425	58	92	17	1.59	0.29
CAAAGCGAGTTACGAAGAAGCTTGAATCTCAAGGTGCTCTT	0.425	39	36	17	0.92	0.44
ATCGACAGCTCTCAGTCCATTTCGAGGAATGTTTCATCGATA	0.45	145	186	32	1.28	0.22
TGCCCTGCTTCCCCAGTCTTGTCTCACAAGACTAATTTTA	0.45	142	207	140	1.46	0.99
TTGAGGACTTCTCTCAGTCAAAAGGACATTAGGGACCTGA	0.45	110	135	25	1.23	0.23
GTTACCTCTGCATAGGAGGCCTAGGAATAATTTAATGCGC	0.45	87	134	181	1.54	2.08
TATGTTTATCAGCGTACTTCGGGTGCTCCTGTATTGGAAC	0.45	60	84	85	1.40	1.42
TGAGAACTTCTCTCAGTCGGTGGGAGAGTACATCCTAACA	0.475	653	928	372	1.42	0.57
AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	0.475	90	192	125	2.13	1.39
TTCTCAGTCAATAACTAGTCGGATCGTGGTCCAAGAGCAG	0.475	44	165	25	3.75	0.57
ATTGAGCACTTCTCGCAGTCGCACTGTACAATAGCGTATG	0.475	34	53	15	1.56	0.44
TAGTCTCCCAAGACAGCGACTGACGAAAGCTCTGGTACTA	0.5	94	198	150	2.11	1.60
ATCATATTCTCGCGAGCCGGAAGCTCAACTTAGAGGTGCTC	0.5	67	83	22	1.24	0.33
TAAGGTCGAACGGAAGCTGGTTTAGTACCAGGTGCTCTGGT	0.5	42	33	34	0.79	0.81
TCCAGCGTAGGAAGCTAATGCATGACATACGAGGTGCTC	0.5	40	53	9	1.33	0.23
CACGCGAGGACTTCTCTCAGTCGGTACCTAACTAAGAGTT	0.5	32	46	30	1.44	0.94
CCCCTTCCAGCGATTACGATCATTGACTCTCAGTCCTGTG	0.525	320	445	68	1.39	0.21

AGAGTTAAGACCGTCGGTGCTCCATGTTCCCTCCATGGAA	0.525	128	162	32	1.27	0.25
ACACGACGAGTACAGCTCTCAGTCGAGCGTATTAGCGGAT	0.525	80	131	39	1.64	0.49
GACTCAGCAGCGCGAGAAAGACGTGGTTAGCCTCAATATG	0.525	74	128	88	1.73	1.19
TAACACTCGATTCTCCTAGCCCGCTAGAAATTCCTCTCCC	0.525	66	133	546	2.02	8.27
TGCTCCGCTGTGACGCGGAACCATCTAGACAATGCATACA	0.525	62	72	0	1.16	0.00
TCACAGTCCCGGTGCCGCACTAAAACCCATTGTTGTGCGA	0.55	1056	1372	428	1.30	0.41
TCCAAGGAACTAGGCAGGGCGTAAACCCGAATAGGTGCTC	0.55	64	47	26	0.73	0.41
CCCACGCATCACGCCGTGGTGCGATTGACACAATTGCAAT	0.55	35	18	0	0.51	0.00
CAACGAACTACAAACCTTTCATAAGCCGCCCTCGCGCA	0.55	32	59	11	1.84	0.34
CCCCCGCATCACGCCGTGGTGCGATTGACACAATTGCAAT	0.575	2572	3027	766	1.18	0.30
CTCAGCGCGTAGTCGTGTGCGAACTGCCTTTCCATGGTC	0.575	64	100	10	1.56	0.16
AATAGCTCAGCCGGTCCGGAAGTGGCAAAGTCAGGTGCTC	0.575	57	20	0	0.35	0.00
CCCCCGCATCTCGCCGTGGTGCGATTGACACAATTGCAAT	0.575	55	74	0	1.35	0.00
CTGCGTCCGGAACCTGATCCTTGATCAGGGTGCTCTAGGA	0.575	42	59	0	1.40	0.00
AATCGCTCAGCCGGTCCGGAAGTGGCAAAGTCAGGTGCTC	0.6	2171	2335	217	1.08	0.10
GTACAGCGACTCATCGGGTGCTCCCGTTGCCAAGGGAAC	0.625	68	55	20	0.81	0.29
GAGAGAACTTCTCTCAGTCGGGACCCGCCAACCGGCAACC	0.625	61	100	72	1.64	1.18
CTTATAGGGAACCGGCAGGAAGCCGGGTGCTCCCTAGACG	0.625	40	55	19	1.38	0.48
ACTCGCTCAGCCGGTCCGGAAGTGGCAAAGTCAGGTGCTC	0.625	36	25	0	0.69	0.00
TTCCCCCGACCCGCACGTCCATGGTCCGTTACACGTGTG	0.65	72	116	14	1.61	0.19
GACACGCGAGCCTGTGCGGAAGTCTTGTGCGAGGTGCTCC	0.65	33	44	48	1.33	1.45
TCCGCCGGAACCGGCCTCCGAATAGGAGTGGCGGGTGCTC	0.7	37	14	0	0.38	0.00

Supplementary table S3. Prevalence, expansion rate and binding properties of aptamers isolated in hIL-10RA selection

ID	Sequence	Round	2	3	4	5			4->5 expansion rate	Affinity to			
			hIL-10RA	hIL-10RA	hIL-10RA	hIgG (pH 7.5)	hIL-10RA	mIL-10RA	IgG (pH 6.8)	hIL-10RA Kd, nM	mIL-10RA Kd, nM	hTrkB Kd, nM	hIgG Kd, nM
401	CCCCCGCATCACGCCGTGGTGCGATTGACACAATGCAAT		620.5	1390.1	103513.1	126.5	421605.7	430594.5	232234.7	4.07	25	65	>500
402	TCACAGTCCCGGTGCCGCACTAAAACCCATTGTTGTGCGA		254.8	630.1	37630.2	91.4	149129.3	21152.9	30288.8	3.96	120		
403	TGAGAACTTCTCTCAGTCGGTGGGAGATACATCCTAACA		157.5	426.2	23423.0	38.7	6081.4	9251.0	11878.6	0.26	>500		
404	ACTATAACGCGTCAAAGTGCTTATCGAACACTATTGTGTA		148.4	370.6	20888.5	55.4	5248.7	7858.0	7808.1	0.25	50		
405	AATCGCTCAGCCGGTCCGGAACATGGCAAAGTCAGGTGCTC		523.8	1072.3	19281.9	123202.2	13084.1	21020.4	235665.7	0.68	60		120
406	TAGACGAGCACTTCTCTCAGTCGCATTATTATTTAAATT		104.9	259.5	16011.0	21.3	3058.3	3670.2	6551.4	0.19	>500		
407	CCCCCTCCAGCGATTACGATCATTGACTCTCAGTCCTGTG		77.2	204.4	11789.2	22.6	4678.9	8150.4	13777.0	0.40	>500		
408	ATCGACAGCTCTCAGTCCATTTCGAGGAATGTTTCATCGATA		35.0	85.4	5636.9	12.3	1738.1	2765.0	5184.1	0.31	>120		
409	ACACGACGAGTACAGCTCTCAGTCGAGCGTATTAGCGGAT		19.3	60.2	3479.5	14.2	376.5	608.0	740.6	0.11	>500		
410	ACGATCACTTCTCTCAGTCGGACTAATATTACGGTTAGAA		34.3	107.0	5980.7	9.3	1272.2	1896.9	3411.8	0.21	>500		
411	AGCCATGACGATGTCGTTACGTAGATGACGAGACTCCTAA		21.7	88.2	3960.6	33.3	6311.1	5817.8	1648.4	1.59	18	50	>500
412	TTCCCCCGACCCGACGTCCTAGTGGTCGTTACACGTGTG		17.4	53.3	2803.4	8.8	591.1	952.6	1570.6	0.21	>120		
413	CATGACACATAGAAATATAACGCGCAAATCACAGTCATATG		36.7	109.8	5195.9	41.9	1520.6	2821.5	2148.4	0.29	40		
414	AGCAAAGTCGTCAGCAATATAACACTCGATTCTTATTGGA		20.3	64.3	3191.9	23.0	4771.7	2005.3	1581.7	1.49	80		
415	TATAGAGAACTTCTCTCAGTCGAGCCAAAGACATTAAT		32.6	52.8	5264.0	6.4	1097.9	2366.8	3032.6	0.21	>500		
416	TGCAATGAGGACTTCTCTCAGTCTAACACAATGTTGTTTA		32.8	68.9	3954.4	10.1	1364.6	1964.2	2957.1	0.35	>500		
417	TAGTCTCCCAAGACAGCGACTGACGAAAGCTCTGGTACTA		22.7	90.9	3248.1	27.5	1045.9	1827.9	2025.9	0.32	>500		
418	GTTACCTCTCGATAGGAGGCTAGGAATAATTAATGCGC		21.0	61.5	2777.4	118.7	2604.0	9982.9	9593.7	0.94	35	80	>500
419	TGCCCTGCTTCCCCAGTCTTGTCTCACAGACTAATTTTA		34.3	95.1	4951.4	8.1	750.0	1320.0	1586.7	0.15	>500		
420	TGTCGAGTACTTTTCTCAGTCTATTCCACAGTAGTGGAGA		14.0	42.3	2125.7	6.9	1018.8	1329.2	1974.3	0.48	80		
421	TTCTCAGTCAATAACTAGTCGGATCGTGGTCCAAGAGCAG		10.6	75.8	1921.8	40.9	817.5	2334.3	700.3	0.43	20	80	>500
422	GACTCAGCAGCGCGAGAAAGACGTGGTTAGCCTCAATATG		17.9	58.8	2605.7	22.3	2466.9	948.5	1089.5	0.95	20	>250	
423	ATGAGGACTTCTCTCAGTCGTGACCATTAATAAGAGAAA		28.2	58.8	3735.4	5.9	512.3	692.5	1212.8	0.14	>500		
436	TAACACTCGATTCTCCTAGCCCCGTAGAAATCCCCCTCCC		15.9	61.1	2512.6	32.4	76373.5	7733.7	9134.3	30.40	65		
445	CCGCTAACACTCGATTCTCGGGAATGCCCCCTGAACCC		0.2	1.4	88.9	2.2	317.7	84.3	116.4	3.57	>120		
446	AAAGACCGTTTTTTAAACGCTCAATATACACGACATAAA		0.7	3.7	88.9	0.2	409.0	39.4	27.2	4.60	10	>500	>500
447	ACAGACCAAGTGTTCAAGAAAACAGTTGCTCAATATACAT		0.5	2.3	110.3	1.7	530.1	33.9	42.8	4.81	25		
454	TGAATCTCGCGCTCGTTGGTACCCTTAAAAATAAGGCATA		4.3	36.7	741.7	139.5	3147.4	3581.6	892.8	4.24	8	120	>500
455	CGTGACTCGACTCAGGTTTTGCACGGCCTCAGGGTAGCAC		5.1	25.3	811.9	640.6	1262.7	1537.2	555.9	1.56	4	120	>500
462	CTCAGCGCGTAGTCGTGTGCGAACTGCCTTTCCATGGTC		15.4	45.9	2466.3	15.7	2599.4	3263.4	3978.8	1.05	2	60	>500
463	GAGAGAACTTCTCTCAGTCGGGACCCGCGCAACCGCAACC		14.7	45.9	2579.7	5.6	1004.2	1485.6	2646.5	0.39	12		
464	CATGACACATAGTAGAACGCGCAAAAATTATTGAAGTAAA		23.2	50.1	3129.0	15.0	1131.3	2377.0	1003.1	0.36	4	80	>500
465	TTGAGGACTTCTCTCAGTCAAAAGGACATTAGGGACCTGA		26.5	62.0	3832.1	5.6	838.2	1388.0	2057.6	0.22	25		

*-sequences with high affinity to hIL-10RA (respective Kds below 20 nM) boldened in the list.

**- sequences unable to bind hIL-10RA target highlighted grey, sequence cross-reacting with a carrier protein (hIgG) highlighted red, sequence cross-reactive with murine IL-10RA highlighted green and sequence with similar abundance at hIL-10RA and hIgG and therefore considered to have significant nonspecific component in their binding to hIL-10RA highlighted blue

Supplementary table S4. *Conditions of h4-1BB aptamer in vitro selection*

Round	Amount of protein, ug	Amount of RNA, nM	NaCl concentration, nM
1.	10	1,5	50
2.	10	1	75
3.	8	1	100
4.	6	1	125
5.	5	0,75	150

Supplementary table S5. Aptamers isolated in h4-1BB selection and their properties.

ID	N25 sequence	Round 4 H4-1BB	Round 5 H4-1BB	Round 5 m4-1BB	Round 5 hIgG	R4->5 expansi on rate	Mouse to human prevale nce ratio	Mouse to human affinit y ratio	Affinit y to human 4-1BB*, nM	Affinit y to murine 4-1BB, nM	Affinit y to human IgG, nM
RJB#1	TCGAGTCCCTAAGTTTTCTCGCATATGTGC	517	8664	93	563	16.8	0.01				
RJB#15	TCGAGTCCCTATGTTGTCTTTTCGCTCTAGC	11	177	3	10	16.3	0.02				
RJB#17	TGCTCCTACTGTGGAACCATCGTTCTTGTG	241	3917	173	369	16.3	0.04	<0.09	35	>500	>1000
RJB#38	TTGAGTCCCTATGTAGTCTTGCAATGTAGC	74	1148	5	73	15.5	0.00				
RJB#54	TGCTCATTTTTGAACCATCGTTTTCTCGGCGC	171	2498	63	265	14.6	0.03		200		
RJB#19	TGCTCTATTTCCACGTCTTCATTGTCAACCG	82	1154	3	104	14.1	0.00		>500		
RJB#16	TGCTCATGTAATTTGAACCATCGTTCTGCC	31	414	13	30	13.5	0.03				
RJB#23	TGCTCACAAACGTGAACCATCGTCTTGTGC	215	2708	83	340	12.6	0.03	<0.03	30	>1000	>1000
RJB#25	TGCTCAATTAAGAACCATCGCTCTCCGGTG	119	1410	22	153	11.8	0.02	<0.02	25	>1000	>1000
RJB#18	TGCTCCATGTGGAACCATGTTCTTGTCCC	37	430	38	54	11.8	0.09				
RJB#35	TCGAGTCTCTATGTTGTCTAGCCTTACGGT	33	362	6	22	11.1	0.02				
RJB#161	TGCTCGTTTTCGAACCATCGTAACTCCTGTG	576	6188	223	994	10.7	0.04	0.13	20	150	>1000
RJB#108	AGGTGCTCATTAATGAACTCCGCTTGTCTG	19	186	9	30	9.9	0.05				
RJB#12	TCGAGTCCCATACGTAGTCTTGCTTAATGC	161	1592	8	138	9.9	0.01				
RJB#67	TGTTCTGTCACATTGAACTCGTTGTCTG	51	502	57	215	9.8	0.11				
RJB#8	TCGTCCTGACGTTTGAGACTTGTGTTCTG	59	534	464	123	9.0	0.87				
RJB#31	TGCTCATCTTGAACGCATTGTTTCTCCGTG	188	1673	41	297	8.9	0.02	<0.02	20	>1000	>500
RJB#47	TGTCCTAAATCGGAACCATCGTCTCCGG	67	583	12	54	8.7	0.02				
RJB#45	TGCTCATTTCTGAACGCTCGTTATCTCCTG	37	324	8	57	8.7	0.03		60		
RJB#44	TGTTTCATAGAAACGCGCATCTTCCTGTG	56	468	18	130	8.3	0.04	<0.06	60	>1000	>1000
RJB#2	TCCCATCTTCCCGATTCTCAACATCGTGTG	878	6868	892	2028	7.8	0.13				

RJB#10	TGCTCACATACGTGAACCATCGTCAATGGC	33	250	52	25	7.7	0.21	0.25	30	120	>1000
RJB#102	TACGTAATCGTCACTGAAGCAGCGTTTGGC	77	590	36	142	7.7	0.06				
RJB#74	TGCTCCTCATTTGGAACGCTTCGTTCGTCTG	224	1678	212	413	7.5	0.13		200		
RJB#93	TGCTCAACATTGAACCATCGTTCCAGTGGC	165	1162	26	171	7.1	0.02		120		
RJB#59	TGCTCCATGAGTGAACGCATTTTGTCTGG	149	1032	57	112	6.9	0.05		40		
RJB#3	CGTCCGTTTGGGTAACCATATATTTGGCCC	176	1133	8	181	6.5	0.01				
RJB#127	TGCTCATAATGAACCATTGTCCTCGTTGGG	20	126	2	22	6.4	0.01		>500		
RJB#75	TAACGCATCACTGAAGTGAGCCTTCAGCGA	40	254	0	17	6.3	0.00				
RJB#7	ACTATTGCGTAGCACACGCTTTCTTTGTGC	54	331	3	60	6.1	0.01				
RJB#231	TGCTCATACGAACGTATCGTCCATTTGCCG	105	629	23	170	6.0	0.04				
RJB#6	TCACGCGCTCTCTTCGTGATTATTCCTCCC	48	273	5	33	5.6	0.02				
RJB#4	GCGCTTACGTTATGCCTCTCATAGATCGTG	131	701	41	131	5.3	0.06				
RJB#294	GTCCTACGTGATGAACTTGTCGTTTGGTG	142	708	378	431	5.0	0.53				
RJB#13	CGTCTCGTCAATGCCCTACGTTTGTCTGTG	187	793	95	269	4.3	0.12		>1000	>1000	>1000
RJB#14	TTTCGTCTGTTACAAACCTCGCTCGTCTGG	88	270	79	126	3.1	0.29				
RJB#9	TAACACCATCTTCCCGATTCTCAAACCTGGC	302	921	59	405	3.0	0.06				

*-sequences with high affinity to h4-1BB boldened in the list

Supplementary table S6. Sequences belonging to cluster #411-J and their prevalence at round 5 of selection

ID	Sequence	Round 5 prevalence	Murine R5 prevalence
411	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	6311	5818
A1G	GGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	47	44
G30T	AGCCATGACGATGTCGTTACGTAGATGCATAGACTCCTAA	46	31
C4G	AGCGATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	35	24
G32T	AGCCATGACGATGTCGTTACGTAGATGCAGATACTCCTAA	29	20
A5C	AGCCCTGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	25	34
T12C	AGCCATGACGACGTCGTTACGTAGATGCAGAGACTCCTAA	25	18
G7T	AGCCATTACGATGTCGTTACGTAGATGCAGAGACTCCTAA	25	18
G10A	AGCCATGACAATGTCGTTACGTAGATGCAGAGACTCCTAA	22	25
T6C	AGCCACGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	21	16
C4A	AGCAATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	21	17
G2A	AACCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	21	17
C9T	AGCCATGATGATGTCGTTACGTAGATGCAGAGACTCCTAA	20	22
G7A	AGCCATAACGATGTCGTTACGTAGATGCAGAGACTCCTAA	20	17
G27T	AGCCATGACGATGTCGTTACGTAGATTGAGAGACTCCTAA	19	15
G13T	AGCCATGACGATTTTCGTTACGTAGATGCAGAGACTCCTAA	19	16
A8G	AGCCATGGCGATGTCGTTACGTAGATGCAGAGACTCCTAA	17	15
C28T	AGCCATGACGATGTCGTTACGTAGATGTAGAGACTCCTAA	17	15
G10C	AGCCATGACCATGTCGTTACGTAGATGCAGAGACTCCTAA	14	11
T17C	AGCCATGACGATGTCGCTACGTAGATGCAGAGACTCCTAA	13	16
T26C	AGCCATGACGATGTCGTTACGTAGACGCAGAGACTCCTAA	12	8
T38C	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCCAA	11	9
T14C	AGCCATGACGATGCCGTTACGTAGATGCAGAGACTCCTAA	11	11
A8C	AGCCATGCCGATGTCGTTACGTAGATGCAGAGACTCCTAA	11	9
T35C	AGCCATGACGATGTCGTTACGTAGATGCAGAGACCCCTAA	10	12
A29T	AGCCATGACGATGTCGTTACGTAGATGCTGAGACTCCTAA	10	10
G10T	AGCCATGACTATGTCGTTACGTAGATGCAGAGACTCCTAA	10	11
T18C	AGCCATGACGATGTCGTCACGTAGATGCAGAGACTCCTAA	10	6
T22C	AGCCATGACGATGTCGTTACGCAGATGCAGAGACTCCTAA	10	10
C15T	AGCCATGACGATGTTGTTACGTAGATGCAGAGACTCCTAA	10	7
A29G	AGCCATGACGATGTCGTTACGTAGATGCGGAGACTCCTAA	9	10
G30A	AGCCATGACGATGTCGTTACGTAGATGCAAAGACTCCTAA	9	8
A31G	AGCCATGACGATGTCGTTACGTAGATGCAGGGACTCCTAA	8	8
C36T	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTTCTAA	8	6
C4T	AGCTATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	8	7
C20T	AGCCATGACGATGTCGTTATGTAGATGCAGAGACTCCTAA	8	8
C37T	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCTTAA	8	6
A5G	AGCCGTGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	7	7

A33C	AGCCATGACGATGTCGTTACGTAGATGCAGAGCCTCCTAA	7	4
A33G	AGCCATGACGATGTCGTTACGTAGATGCAGAGGCTCCTAA	7	8
G21A	AGCCATGACGATGTCGTTACATAGATGCAGAGACTCCTAA	7	4
G24T	AGCCATGACGATGTCGTTACGTATATGCAGAGACTCCTAA	7	8
G16T	AGCCATGACGATGTCTTTACGTAGATGCAGAGACTCCTAA	7	7
C3T	AGTCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	6	6
T12G	AGCCATGACGAGGTCGTTACGTAGATGCAGAGACTCCTAA	6	4
A8T	AGCCATGTCGATGTCGTTACGTAGATGCAGAGACTCCTAA	6	4
A40G	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAG	6	6
C3A	AGACATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	6	5
C34T	AGCCATGACGATGTCGTTACGTAGATGCAGAGATTCCTAA	6	4
G27A	AGCCATGACGATGTCGTTACGTAGATACAGAGACTCCTAA	6	4
G21T	AGCCATGACGATGTCGTTACTTAGATGCAGAGACTCCTAA	6	7
A39G	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTGA	5	7
A25G	AGCCATGACGATGTCGTTACGTAGGTGCAGAGACTCCTAA	5	4
A11T	AGCCATGACGTTGTCGTTACGTAGATGCAGAGACTCCTAA	5	3
G2T	ATCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	5	9
C9A	AGCCATGAAGATGTCGTTACGTAGATGCAGAGACTCCTAA	5	4
A23G	AGCCATGACGATGTCGTTACGTGGATGCAGAGACTCCTAA	5	4
G24A	AGCCATGACGATGTCGTTACGTAAATGCAGAGACTCCTAA	5	2
A11G	AGCCATGACGGTGTCGTTACGTAGATGCAGAGACTCCTAA	4	4
C36A	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTACTAA	4	2
A1C	CGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	4	2
G13A	AGCCATGACGATATCGTTACGTAGATGCAGAGACTCCTAA	4	4
A33T	AGCCATGACGATGTCGTTACGTAGATGCAGAGTCTCCTAA	4	3
T6G	AGCCAGGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	4	4
G32A	AGCCATGACGATGTCGTTACGTAGATGCAGAAACTCCTAA	4	4
A31T	AGCCATGACGATGTCGTTACGTAGATGCAGTGACTCCTAA	4	3
G16A	AGCCATGACGATGTCATTACGTAGATGCAGAGACTCCTAA	3	3
A5T	AGCCTTGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	3	2
A19G	AGCCATGACGATGTCGTTGCGTAGATGCAGAGACTCCTAA	3	3
G7C	AGCCATCACGATGTCGTTACGTAGATGCAGAGACTCCTAA	3	3
T12A	AGCCATGACGAAGTCGTTACGTAGATGCAGAGACTCCTAA	3	2
G2C	ACCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAA	3	4
G30C	AGCCATGACGATGTCGTTACGTAGATGCACAGACTCCTAA	3	1
T14A	AGCCATGACGATGACGTTACGTAGATGCAGAGACTCCTAA	3	2
A40T	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAT	3	2
T38A	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCAAA	3	2
T14G	AGCCATGACGATGGCGTTACGTAGATGCAGAGACTCCTAA	2	3
A19T	AGCCATGACGATGTCGTTTCGTAGATGCAGAGACTCCTAA	2	2
A40C	AGCCATGACGATGTCGTTACGTAGATGCAGAGACTCCTAC	2	1