

Supplemental Information

**Integrating Ligand-Receptor Interactions
and *In Vitro* Evolution for Streamlined
Discovery of Artificial Nucleic Acid Ligands**

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Integrating Ligand-receptor Interactions and *In Vitro* Evolution for Streamlined Discovery of Artificial Nucleic Acid Ligands

Supporting Information

Hasan E. Zumrut^{1,2}, Sana Batoon¹, Kimon V. Argyropoulos⁴, Nicole Williams³, Roksana Azad², and Prabodhika R. Mallikaratchy^{1,2,3 *}

¹Department of Chemistry, Lehman College, The City University of New York,
250 Bedford Park Blvd., West, Bronx, NY 10468, USA

²Ph.D. Program in Chemistry and Biochemistry, CUNY Graduate Center
365 Fifth Avenue, New York, NY 10016, USA

³Ph.D. Program in Molecular, Cellular and Developmental Biology, CUNY Graduate Center
365 Fifth Avenue, New York, NY 10016, USA

⁴Immunology Program, Memorial Sloan Kettering Cancer Center, 408 E 69th St., New York, NY,
10021

*To whom correspondence should be addressed: Prabodhika Mallikaratchy, Department of Chemistry, Lehman College, The City University of New York, 250 Bedford Park West, Bronx New York, NY 10468; prabodhika.mallikaratchy@lehman.cuny.edu; Phone: 347-577-4082.

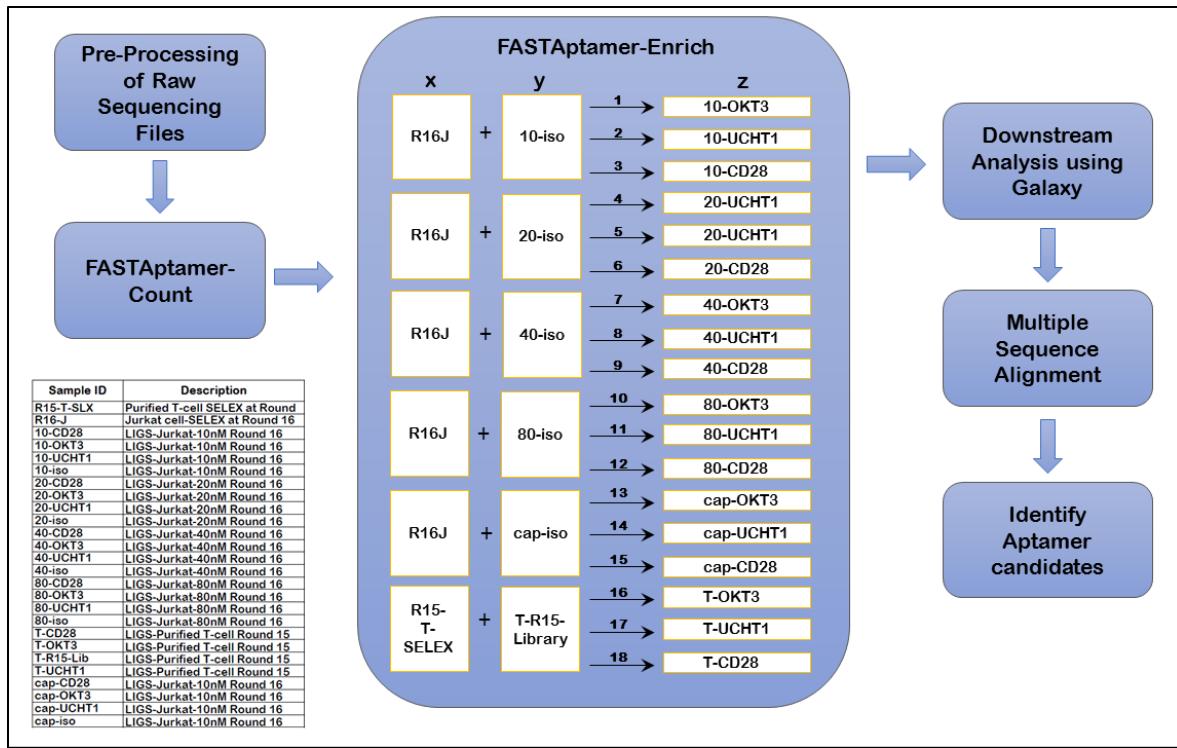


Figure S1. Flowchart describing the steps involved in bioinformatics analysis of LIGS sequencing data. First, raw sequencing data was pre-processed to remove two types of reads: 1) Low-quality reads ($Q < 20$ at a single position) and the reads without intact SELEX primer regions, 2) The reads that are not within 20% range of the randomized SELEX region. Second, FASTAptamer-Count tool was used to obtain read counts and normalized read counts, RPM (reads per million), of each unique sequence (see Table S2 for a summary of FASTAptamer-Count results). These data were then analyzed with FASTAptamer-Enrich tool to obtain fold-enrichment values. Inputs for each FASTAptamer-Enrich run were defined as: x= final enriched cell-SELEX library (i.e., Round 16), y= LIGS pool from isotype control antibody, and z= the specific monoclonal antibodies (OKT3, UCHT1 or anti-CD28). A total of 18 tabular FASTAptamer Enrich files as listed in Table S3 were generated using the combinations as outlined by the numbered arrows. Then the downstream analysis was performed on the tabular FASTAptamer-Enrich files using GALAXY server. Analysis of sequences in GALAXY server included following steps: first, the filter tool was applied as $RPM \geq 1$ to x. Then a second filter was applied as $RPM(z/y) \geq 4$ to identify sequences enriched in mAb eluted pools compared to the isotype control. This filter was used as $RPM(z/y) > 1$ for positive control antibody (anti-CD28) to eliminate sequences eluted by anti-CD28 binding to cells. Finally, the compare tool was used to remove matching sequences between CD3 specific sequences and the sequences identified as hits for anti-CD28. The resulting sequences were converted to FASTA format, concatenated and aligned using ClustalW. Finally, the aptamer candidates were picked based on the multiple sequence alignment results.

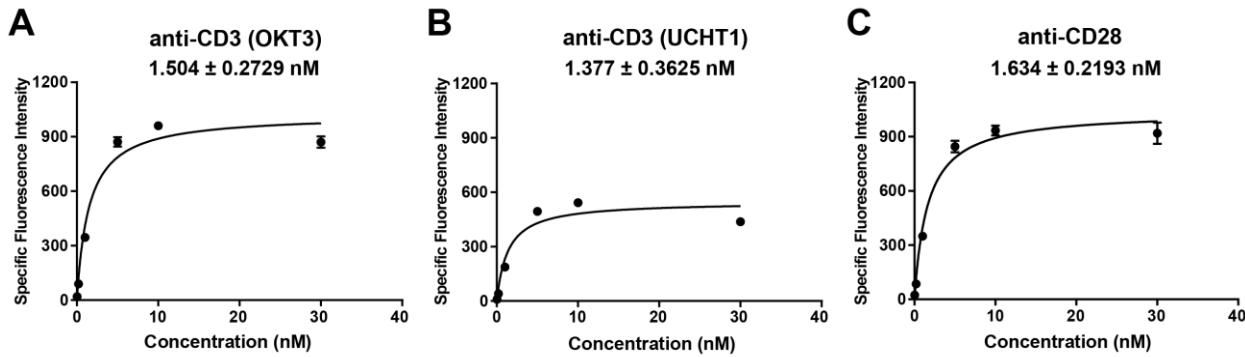


Figure S2. Affinity analysis of OKT3, UCHT1 and anti-CD28 antibodies against Jurkat.E6 cells at 25 °C.

Binding curves are shown for each monoclonal antibody used during LIGS; (A) OKT3, (B) UCHT1 (C) anti-CD28. Affinity analyses were performed by incubating 2.0×10^5 Jurkat.E6 cells with a serially diluted unlabeled antibody for 45 min at 25 °C in cell suspension buffer used in SELEX. For each mAb the following final concentrations were used: 0.04 nM, 0.2 nM, 1 nM, 5 nM 10 nM and 30 nM. The assay was performed in triplicates. The isotype control antibody was used at 30 nM. After the incubation with primary antibodies, the cells were washed twice using 2 mL of RPMI, followed by secondary antibody staining using Alexa Fluor 647®-conjugated Goat Anti-Mouse IgG at a final concentration of 5 µg/mL for 30 min. on ice. The cells were then washed again twice with 2 mL RPMI and reconstituted in 300 µL of RPMI. And the binding events were analyzed using flow cytometry (BD FACScan). The specific binding of mAbs was calculated by subtracting the median fluorescence intensity obtained by isotype control from that of mAbs at each concentration. The binding curves were constructed by plotting the specific median fluorescence intensity values for each concentration as a function of mAb concentration on GraphPad Prism software using one-site specific binding. The Kd values were calculated by GraphPad Prism software using the formula: $Y = \frac{B_{\max} * X}{(K_d + X)}$.

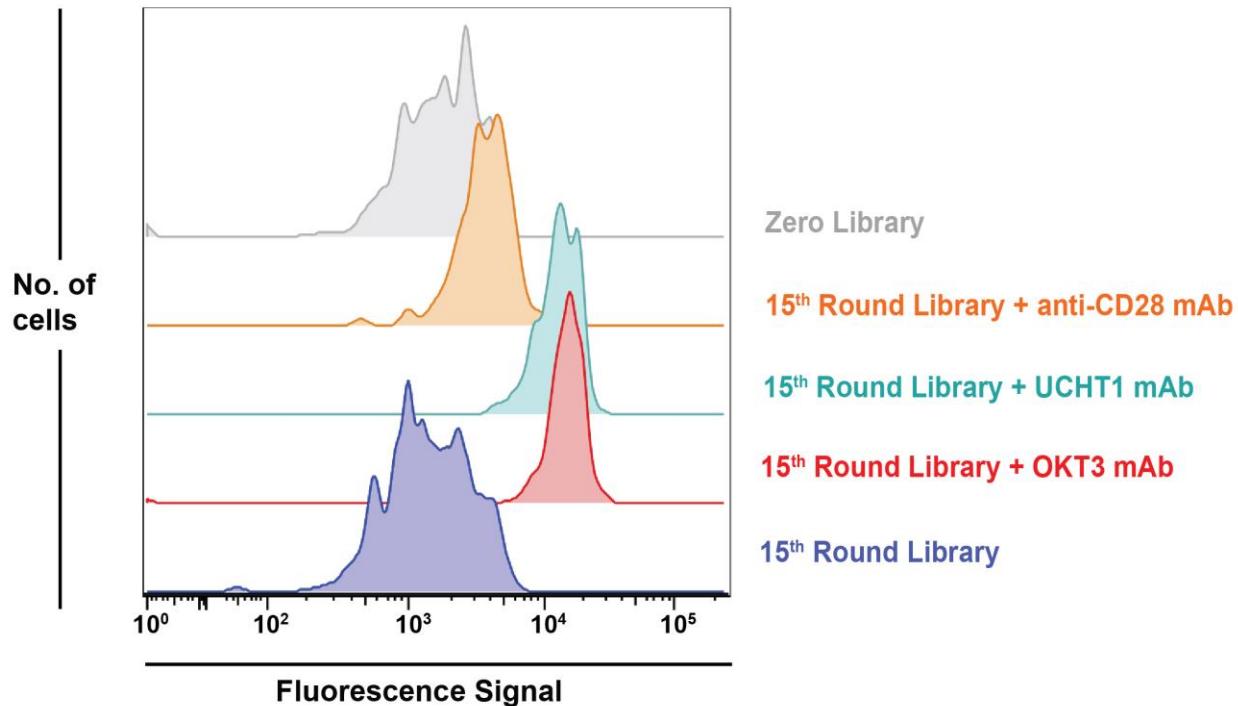


Figure S3. Flow cytometric analysis of CD3 and CD28 expression of T-cells isolated from PBMCs. Following LIGS, the PBMCs were subjected to secondary antibody staining. The Alexa Fluor 647®-conjugated goat anti-mouse IgG at 5 µg/mL incubated for 30 min on ice, washed and analyzed by flow cytometry to evaluate the binding of mAbs. Histograms obtained at round 0 library (gray) and 15th round library (purple) did not contain any primary mAbs, hence they represent the background fluorescence signal. Red, green and orange histograms corresponds to samples incubated with OKT3, UCHT1 and anti-CD28 mAbs during LIGS respectively. Increased fluorescence signal after secondary antibody staining is observed for all samples with OKT3 and UCHT1 mAbs (red and green histograms) and to a lesser degree with anti-CD28 mAb (orange histogram) compared to the background signal, confirming the CD3 and the CD28 receptor expression on T cells isolated from PMBCs, which was used during LIGS.

Table S1. List of all sequencing library pools with sample names and descriptions.

Sample No.	Description	Sample ID	Barcode Sequence (Illumina)	PF Clusters	% of Lane	% Perfect Barcode	% One Mismatch Barcode	Yield (Mbases)	% PF Clusters	% ≥ Q30 Bases	Mean Quality Score
1	Jurkat cell-SELEX at Round 7	R7	CGTACTAG	22,088,216	7.34	96	3.96	2,231	63.28	89.69	37.8
2	Jurkat cell-SELEX at Round 9	R9	AGGCAGAA	45,124,139	15	95	5.42	4,558	63.17	90.16	37.92
3	Jurkat cell-SELEX at Round 12	R12	TCC TGAGC	25,771,275	8.57	96.72	3.28	2,603	63.38	90.54	38.01
4	Jurkat cell-SELEX at Round 13	R13	GGACTCCT	44,046,358	14.64	96	3.78	4,449	63.33	90.54	38.02
5	Jurkat cell-SELEX at Round 14	R14-J	GGACTCCT+TATCCTCT	10,652,725	3.04	95.03	4.97	1,076	100	97.02	39.76
6	Jurkat cell-SELEX at Round 15	R15-J	TAGGCATG+TATCCTCT	18,591,191	5.31	95.51	4.49	1,878	100	96.85	39.7
7	Purified T-cell SELEX at Round 15	R15-T-SLX	GGACTCCT+TATCCTCT	11,340,437	3.18	94.93	5.07	1,145	100	97.12	39.77
8	Jurkat cell-SELEX at Round 16	R16-J	GGACTCCT+GCCGAAGA	9,994,449	2.82	95.53	4.47	1,009	100	96.82	39.61
9	LIGS-Jurkat-10nM Round 16 Library	10-CD28	TCCTGAGC+TATCCTCT	10,586,615	2.98	95.33	4.67	1,069	100	96.42	39.51
10	LIGS-Jurkat-10nM Round 16 Library	10-OKT3	CGTACTAG+TATCCTCT	15,339,339	4.32	95.17	4.83	1,549	100	96.26	39.46
11	LIGS-Jurkat-10nM Round 16 Library	10-UCHT1	AGGCAGAA+TATCCTCT	13,373,005	3.77	95.1	4.9	1,351	100	96.52	39.52
12	LIGS-Jurkat-10nM Round 16 Library	10-iso	TAAGGCGA+TATCCTCT	12,567,693	3.54	95.62	4.38	1,269	100	96.62	39.58
13	LIGS-Jurkat-20nM Round 16 Library	20-CD28	TCCTGAGC+AGAGTAGA	24,273,135	6.84	95.1	4.9	2,452	100	95.82	39.33
14	LIGS-Jurkat-20nM Round 16 Library	20-OKT3	CGTACTAG+AGAGTAGA	20,769,041	5.85	94.82	5.18	2,098	100	95.45	39.22
15	LIGS-Jurkat-20nM Round 16 Library	20-UCHT1	AGGCAGAA+AGAGTAGA	18,728,168	5.28	94.53	5.47	1,892	100	95.74	39.29
16	LIGS-Jurkat-20nM Round 16 Library	20-iso	TAAGGCGA+AGAGTAGA	21,420,810	6.04	95.03	4.97	2,164	100	96	39.39
17	LIGS-Jurkat-40nM Round 16 Library	40-CD28	TCCTGAGC+TATCCTCT	11,523,741	3.29	94.57	5.43	1,164	100	96.37	39.57
18	LIGS-Jurkat-40nM Round 16 Library	40-OKT3	CGTACTAG+TATCCTCT	27,773,873	7.93	95	5	2,805	100	96.54	39.61
19	LIGS-Jurkat-40nM Round 16 Library	40-UCHT1	AGGCAGAA+TATCCTCT	8,640,907	2.47	94.26	5.74	873	100	96.65	39.63
20	LIGS-Jurkat-40nM Round 16 Library	40-iso	TAAGGCGA+TATCCTCT	26,406,696	7.54	95.27	4.73	2,667	100	96.76	39.69
21	LIGS-Jurkat-80nM Round 16 Library	80-CD28	TCCTGAGC+AGAGTAGA	23,794,452	6.8	94.74	5.26	2,403	100	96.28	39.53
22	LIGS-Jurkat-80nM Round 16 Library	80-OKT3	CGTACTAG+AGAGTAGA	10,876,595	3.11	94.24	5.76	1,099	100	96.06	39.47
23	LIGS-Jurkat-80nM Round 16 Library	80-UCHT1	AGGCAGAA+AGAGTAGA	10,497,609	3	94.34	5.66	1,060	100	96.34	39.52
24	LIGS-Jurkat-80nM Round 16 Library	80-iso	TAAGGCGA+AGAGTAGA	18,732,468	5.35	94.7	5.3	1,892	100	96.37	39.56
25	LIGS-Purified T-cell Round 15 Library	T-CD28	TCCTGAGC+AGAGTAGA	18,137,402	5.09	94.72	5.28	1,832	100	96.47	39.57
26	LIGS-Purified T-cell Round 15 Library	T-OKT3	CGTACTAG+AGAGTAGA	17,532,868	4.92	94.71	5.29	1,771	100	96.07	39.45
27	LIGS-Purified T-cell Round 15 Library	T-R15-Lib	TAAGGCGA+AGAGTAGA	21,163,380	5.94	94.9	5.1	2,138	100	96.55	39.59
28	LIGS-Purified T-cell Round 15 Library	T-UCHT1	AGGCAGAA+AGAGTAGA	16,736,291	4.7	94.43	5.57	1,690	100	96.42	39.53
29	LIGS-Jurkat-10nM Round 16 Library	cap-CD28	TCCTGAGC+TATCCTCT	17,057,479	4.79	95.11	4.89	1,723	100	96.53	39.61
30	LIGS-Jurkat-10nM Round 16 Library	cap-OKT3	CGTACTAG+TATCCTCT	18,305,330	5.14	95.06	4.94	1,849	100	96.31	39.54
31	LIGS-Jurkat-10nM Round 16 Library	cap-UCHT1	AGGCAGAA+TATCCTCT	17,650,650	4.95	94.89	5.11	1,783	100	96.58	39.59
32	LIGS-Jurkat-10nM Round 16 Library	cap-iso	TAAGGCGA+TATCCTCT	13,914,585	3.91	95.16	4.84	1,405	100	96.54	39.61

Table S2. Summary of results from FASTAptamer-Count for each library that has been sequenced.

Sample No.	Sample ID	Number of Unique Reads	Number of Total Reads	Diversity (unique/total)	Enrichment (1-diversity)	Percent Enrichment
1	R7	14,041,300	18,944,225	0.741	0.259	25.9
2	R9	12,892,067	37,677,052	0.342	0.658	65.8
3	R12	3,950,975	22,260,603	0.177	0.823	82.3
4	R13	6,214,461	38,328,982	0.162	0.838	83.8
5	R14-J	1,604,366	9,422,736	0.17	0.83	83
6	R15-J	2,521,223	16,225,266	0.155	0.845	84.5
7	R15-T-SLX	1,303,190	9,948,080	0.13	0.87	87
8	R16-J	1,568,058	8,508,383	0.184	0.816	81.6
9	10-iso	1,824,881	10,710,622	0.17	0.83	83
10	10-OKT3	2,117,980	12,859,911	0.164	0.836	83.6
11	10-UCHT1	1,888,849	11,339,221	0.166	0.834	83.4
12	10-CD28	1,609,903	8,947,893	0.179	0.821	82.1
13	20-iso	3,080,936	17,767,962	0.173	0.827	82.7
14	20-OKT3	3,007,195	16,818,767	0.178	0.822	82.2
15	20-UCHT1	2,806,662	15,286,542	0.183	0.817	81.7
16	20-CD28	3,446,074	19,985,695	0.172	0.828	82.8
17	40-iso	2,407,824	23,132,091	0.104	0.896	89.6
18	40-OKT3	2,461,688	24,053,144	0.102	0.898	89.8
19	40-UCHT1	1,104,291	7,496,012	0.147	0.853	85.3
20	40-CD28	1,372,050	9,946,198	0.137	0.863	86.3
21	80-iso	2,308,687	16,105,522	0.143	0.857	85.7
22	80-OKT3	1,565,887	9,210,755	0.17	0.83	83
23	80-UCHT1	1,501,662	8,956,696	0.167	0.833	83.3
24	80-CD28	2,749,145	20,412,920	0.134	0.866	86.6
25	cap-iso	2,001,019	12,006,585	0.166	0.834	83.4
26	cap-OKT3	2,157,541	15,651,603	0.137	0.863	86.3
27	cap-UCHT1	2,558,769	15,225,696	0.168	0.832	83.2
28	cap-CD28	2,280,739	14,719,989	0.154	0.846	84.6
29	T-R15-Lib	1,872,596	18,020,697	0.103	0.897	89.7
30	T-OKT3	1,633,305	14,634,645	0.111	0.889	88.9
31	T-UCHT1	1,381,965	14,045,508	0.098	0.902	90.2
32	T-CD28	1,351,403	15,486,441	0.087	0.913	91.3

Table S3. List of 18 files obtained by FASTAptamer-Enrich and the summary of results obtained after filtering sequences on GALAXY.

Sample No.	File Name	No. of Total Lines	No. Kept After Filter ≥ 1 RPM (x)	No. of Reads ≥ 4 (z/y)
1	R16-J_vs_10-iso_vs_10-OKT3	4,235,909	65,085	675
2	R16-J_vs_10-iso_vs_10-UCHT1	4,063,069	65,085	558
3	R16-J_vs_10-iso_vs_10-CD28	3,854,386	65,085	791
4	R16-J_vs_20-iso_vs_20-OKT3	5,829,736	65,085	180
5	R16-J_vs_20-iso_vs_20-UCHT1	5,683,346	65,085	231
6	R16-J_vs_20-iso_vs_20-CD28	6,178,433	65,085	189
7	R16-J_vs_40-iso_vs_40-OKT3	4,861,996	65,085	277
8	R16-J_vs_40-iso_vs_40-UCHT1	3,915,304	65,085	433
9	R16-J_vs_40-iso_vs_40-CD28	4,086,579	65,085	260
10	R16-J_vs_80-iso_vs_80-OKT3	4,137,852	65,085	309
11	R16-J_vs_80-iso_vs_80-UCHT1	4,093,159	65,085	337
12	R16-J_vs_80-iso_vs_80-CD28	5,012,917	65,085	238
13	R16-J_vs_cap-iso_vs_cap-OKT3	4,461,677	65,085	151
14	R16-J_vs_cap-iso_vs_cap-UCHT1	4,738,828	65,085	1,366
15	R16-J_vs_cap-iso_vs_cap-CD28	4,524,612	65,085	590
16	R15-T-SLX_vs_T-R15-Lib_vs_T-OKT3	3,694,766	42,182	130
17	R15-T-SLX_vs_T-R15-Lib_vs_T-UCHT1	3,513,520	42,182	81
18	R15-T-SLX_vs_T-R15-Lib_vs_T-CD28	3,489,135	42,182	110

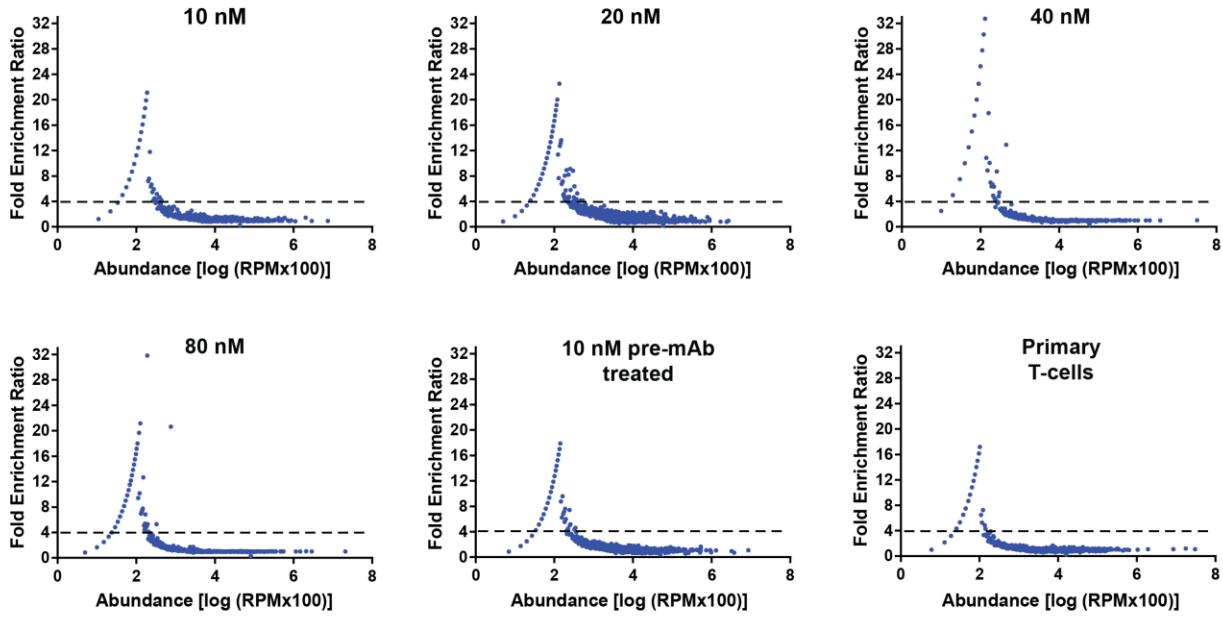


Figure S4. Fold enrichment ratio vs. abundance plots for LIGS using anti-CD28 mAb.

Fold enrichment ratios were obtained using the formula: $(\text{RPM}_z/\text{RPM}_y)$ where $z = \text{anti-CD28 mAb}$ and $y = \text{isotype control}$, and abundance values were obtained using: $\log (\text{RPM} \times 100)$ for each sequence. A distinct population of sequences were observed above the fold enrichment value of 4 as shown by the dashed line.

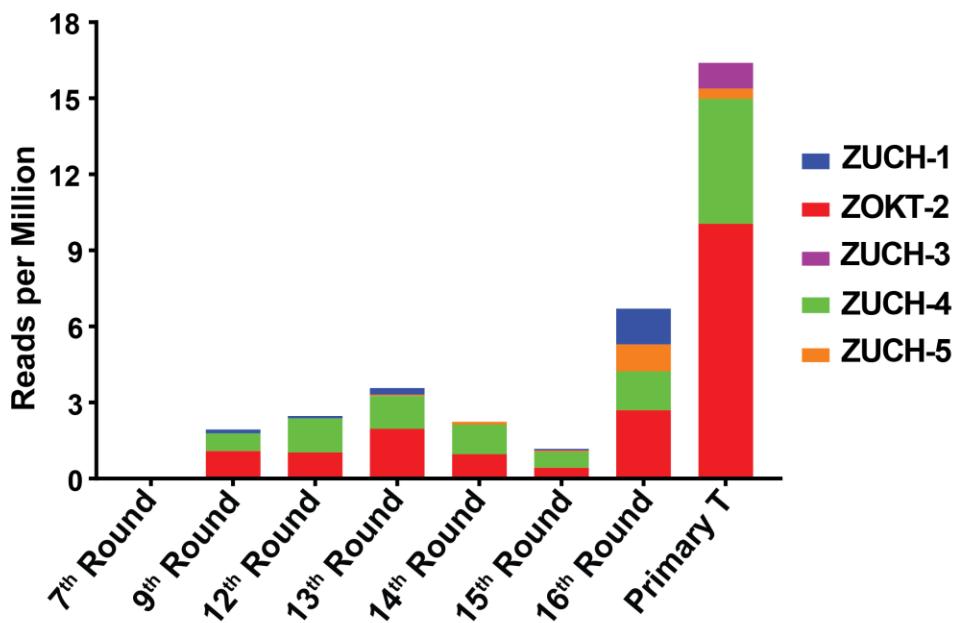


Figure S5. The appearance of five aptamers during the progress of selection.

Appearance of five aptamer sequences that are identified by LIGS were evaluated in each round of cell-SELEX that was sequenced. Normalized read counts (Reads per Million) on the Y-axis of each aptamer were obtained from FASTAptamer-Count data corresponding to each round of cell-SELEX. Starting from 9th round members of this family started to appear, and at 13th round of SELEX, all the members of this family were present with the exception of the ZUCH-3 aptamer. ZUCH-3 aptamer was identified from the LIGS experiment using primary T-cells and this sequence only appeared in the SELEX round after primary-T cells were incorporated.

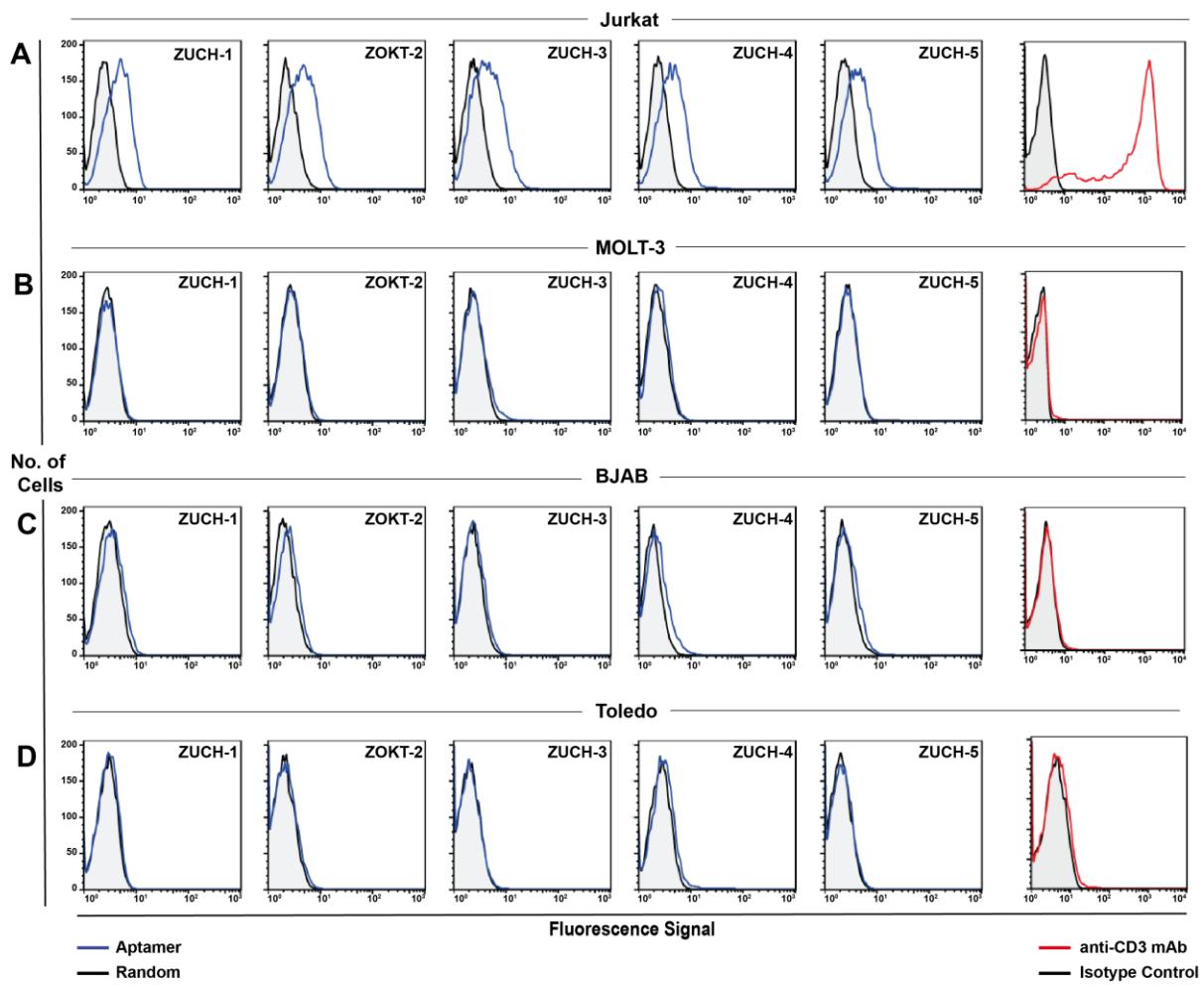


Figure S6. Individual histograms from flow cytometric analysis of ZUCH-1, ZOKT-2, ZUCH-3, and ZUCH-4 and ZUCH-5 aptamers from figure 4A. Binding of each aptamer (blue histograms) is evaluated against Jurkat.E6 (A), MOLT-3 (B), BJAB (C) and Toledo (D) cells. These assays were performed by incubating fluorophore-labeled aptamers or random ssDNA molecules with 2.0×10^5 cells in a total volume of 100 μL at 25 °C for 1 hr. After washing twice with 3 mL of RPMI, cells were reconstituted in 250 μL of RPMI, and binding events were analyzed using flow cytometry (BD FACScan). Red histograms show anti-CD3 mAb staining for each cell line. All five aptamers showed specific binding against Jurkat.E6 cells (A) that express CD3 receptor (A, red histogram). No significant binding was observed against the control cell lines negative for CD3 (red histograms for B, C and D).

Table S4. Summary of the LIGS conditions used to identify each aptamer discovered by LIGS along with the antibody that eluted each sequence and their apparent affinity values towards target Jurkat.E6 cells.

Aptamer Name	LIGS Condition	The Antibody used during LIGS	Apparent Dissociation Constant (K _d)
ZUCH-1	40 nM Round 16 Library without free ligands	UCHT1	3.0 ± 0.48 nM
ZOKT-2	10 nM Round 16 Library with free ligands	OKT3	16.1 ± 3.71 nM
ZUCH-3	LIGS against primary T cells	UCHT1	27.5 ± 5.86 nM
ZUCH-4	20 nM Round 16 Library with free ligands	UCHT1	52.5. ± 11.6 nM
ZUCH-5	10 nM Round 16 Library against pre-mAb treated (capped) cells	UCHT1	325 ± 62.7 nM
ZOKT-6	LIGS against primary T cells	OKT3	NA
ZUCH-7	LIGS against primary T cells	UCHT1	NA
ZUCH-8	20 nM Round 16 Library with free ligands	UCHT1	NA

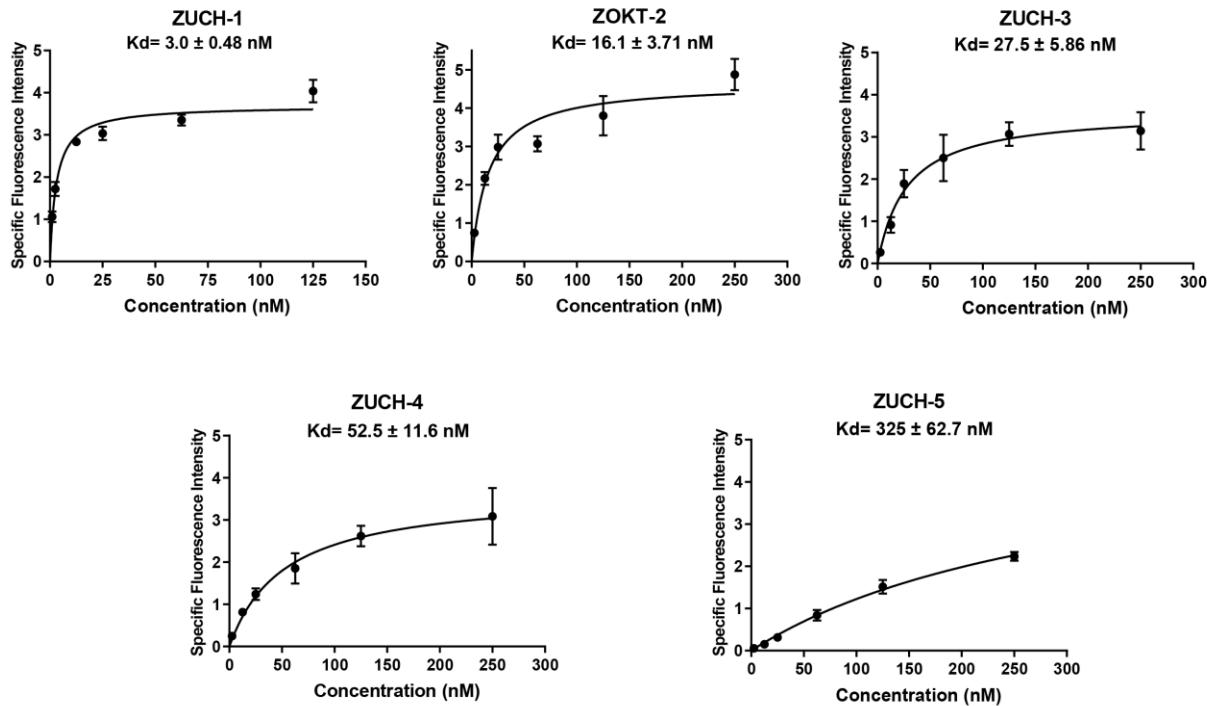


Figure S7. Affinity analysis of ZUCH-1, ZOKT-2, ZUCH-3, ZUCH-4 and ZUCH-5 against Jurkat.E6 cells at 25 °C. A range of fluorophore labeled aptamer and random DNA concentrations (1 nM to 250 nM) were incubated with 2.0×10^5 Jurkat.E6 cells at 25 °C for 1 hr. Cells were then washed once using 3 mL of RPMI, and binding events were analyzed by flow cytometry (BD FACScan). These experiments were performed in triplicates for each aptamer. Apparent affinity values were obtained by plotting the specific median fluorescence intensities (Aptamer fluorescence intensity – Random DNA fluorescence intensity) against each concentration value on GraphPad Prism software based on the one-site specific binding model using the formula: $Y = \frac{B_{max} * X}{(K_d + X)}$.

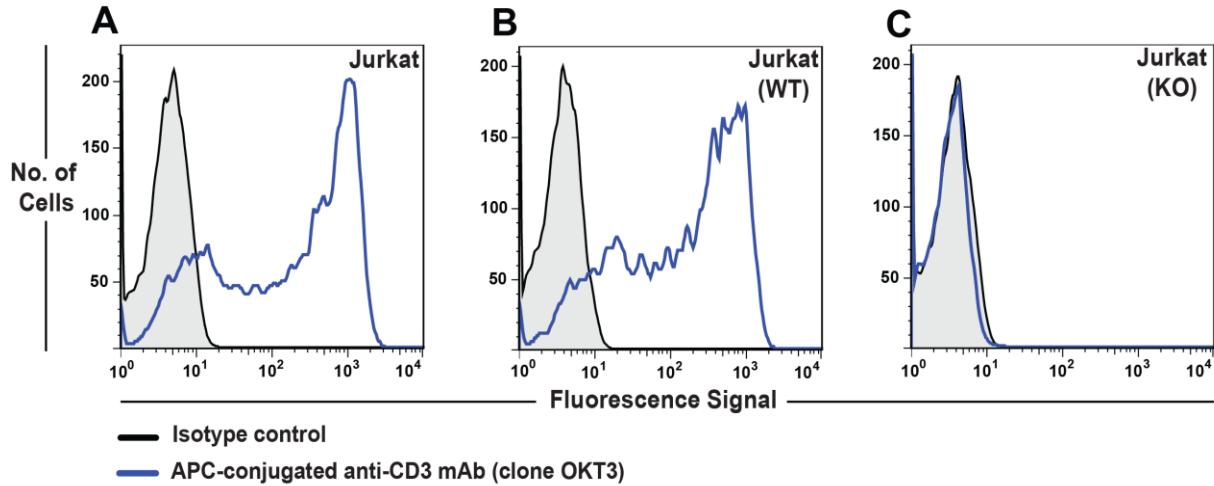


Figure S8. Flow cytometry analysis of CD3 expression of cells used in specificity experiments involving knockout cells in Fig. 5A. The Jurkat E.6 cells used in SELEX (A) and wild-type Jurkat cells used for generating CRISPR knockout cell lines (B) are positive for TCR-CD3 complex while the double knockout Jurkat cells obtained from Synthego do not express TCR-CD3 complex (C). These assays were performed by incubating 1.0×10^5 of each cell type with 5 μL of APC-conjugated anti-CD3 mAb (clone OKT3, eBioscienceTM, 17-0037-41) in a total volume of 100 μL at 25 °C for 30 min. The cells were then washed once with 3 mL RPMI, and the binding events were analyzed using flow cytometry (BD FACScan).

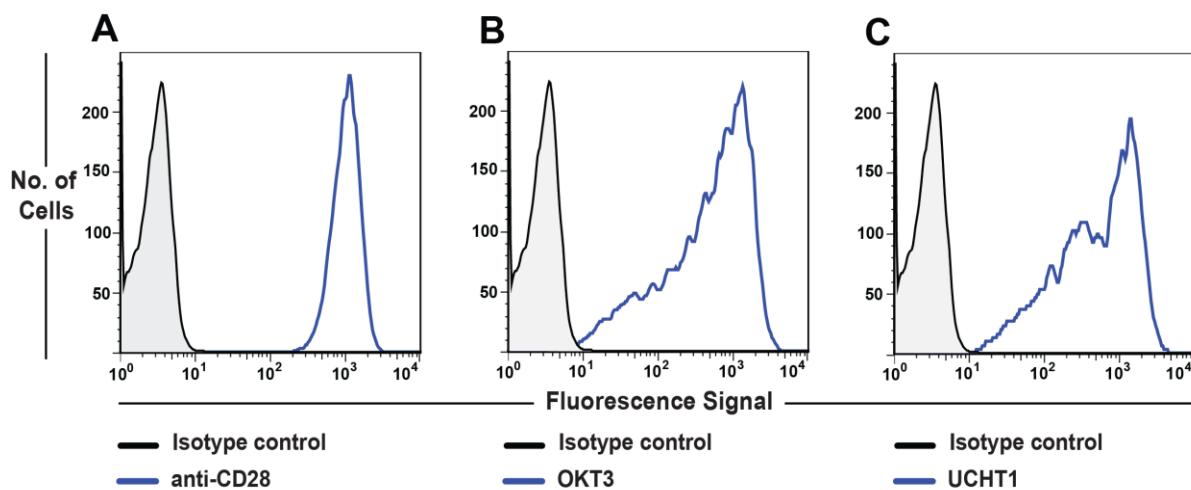


Figure S9. Secondary antibody staining of Jurkat.E6 cells used for competitive binding assays in Fig. 5B. Following the competitive binding assays, the same cells were secondary antibody stained using Alexa Fluor 647[®]-conjugated goat anti-mouse IgG at 5 $\mu\text{g}/\text{mL}$ final concentration for 30 min on ice and the binding was analyzed by flow cytometry (BD FACScan). Blue histograms showing binding of anti-CD28 mAb (A), OKT3 mAb (B) and the UCHT1 mAb (C) towards Jurkat.E6 cells.

Multiple Sequence Alignment (CLUSTALW) of 485 Sequences Identified Based on Bioinformatics Analysis.

10-UC-1.3_524	-----GGTCCCCCGTTACATTATTC-CATTGGCTGTCTTGGG-----	37
40-UC-1.3_410	-----AGACCCCCCCTGCATTATAGGTATTGGCCG-CTTGTG-----	37
40-OK-1.3_253	-----ACCCCCCGTCGTCT-TATCTTTGGCCC-CGTGGATTG-----	37
80-OK-1.3_199	-----TGTGTTTTTACGTTTGCCCCCTTGTCTGTCTTGG-----	37
80-UC-1.3_290	-----TGTGTTTTTACGTTTGCCCCCTTGTCTGTCTTGG-----	37
cap-UC-1.3_1228	-----TGTGTGTGTCTCGTTGGGCCCTTGTTCAGTGTGTG-----	37
40-OK-1.3_167	-----TGTCCACCCCCAGCGTAT-TGGTCTTCCTTG-CCCTTG-----	37
40-UC-1.3_157	-----TGTCCACCCCCAGCGTAT-TGGTCTTCCTTG-CCCTTG-----	37
cap-OK-1.3_68	-----TGTCC-CGCCGTTCGTAT-TCTCCTTCCTTGGTCCTTGG-----	38
T-OK-1.3_87	-----AGTAGTTCACCCCCCGTTCGTATGTTCTTTCTTGTTC-----	38
cap-CD-1.3_160	-----TCGATGCCCCCCCCGTTCCCGTCTTCTGGTTGGT-----	37
cap-OK-1.3_129	-----TCCCCCGTGAGTATTTCGCCCTTTTGTCTGTGTG-----	36
cap-UC-1.3_1275	-----TCCCCCGTGAGTATTTCGCCCTTTTGTCTGTGTG-----	36
40-UC-1.3_203	-----CGTCCCCCTAATTGGTCTTGTGTTAGCC-TGGTTGC-----	37
10-UC-1.3_226	-----TCCCTTGGTCGG-TTGTGT-TTGTGGTTGGCGCTGTGTG-----	37
40-UC-1.3_64	-----GTCCCCCTTACCG-TTTCGTATTGTTGTGGCAGCTGCG-----	37
cap-UC-1.3_1311	-----GGCCCTTCATTGCGGGTTTGGTTCTTGTCAAGCTGG-----	37
cap-CD-1.3_434	-----TGTGCCCTCAGTCG-GCTTGTGTTGTTTTGCTGG-----	37
40-UC-1.3_166	-----GCGCTGTCCCCCGTTAATGTAATTGGAGTTCGAATTG-----	37
cap-UC-1.3_82	-----TGTTCCCCCTGTCAAGTTGGTGTGATTTCGAATGGTGTGG-----	38
80-UC-1.3_236	-----CGTCCCCCTTATGTTGGCGAATGGACTTGGTTGTTG-----	38
cap-UC-1.3_695	-----TTGTCCCCGTCTGTTCG-GCCCGGGTTGGTTCTGC-----	37
cap-UC-1.3_37	-----TCGGTCCCCATGTGCGTTGATGGCTGTCTTGGTGG-----	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_1043	-----TGTGCGTCCCCCTCCGTGTGTTGGTTGGTTGGT-----	37
10-OK-1.3_173	-----TGGTGT-CTGTTTCCCCCTGTCC-GCTTGGTCTTATGTG-----	37
cap-UC-1.3_168	-----TGGTGT-CTGTTTCCCCCTGTCC-GCTTGGTCTTATGTG-----	37
10-UC-1.3_316	-----TTGGTGC G C T ATTACCCCCCCCCGT-TGGTGAGCTGGTG-----	37
cap-UC-1.3_169	-----TGGTGA C TTTCC T CTCCGTTC-GTGGTGGGT-ATGGG-----	37
cap-UC-1.3_628	-----AGTGGGGGTCTATTGCC T CTTCC-GTTCTGGTTGTG-----	37
10-CD-1.3_220	-----TGTGTGGGTCTTAGCGTTCCGTGGGTATTGGTTG-----	37
10-OK-1.3_247	-----TTGGTTGAATTCTCC C TTCCAGTTGCCGGGGTG-----	37
10-UC-1.3_93	-----TTGGTTGAATTCTCC C TTCCAGTTGCCGGGGTG-----	37
40-UC-1.3_80	-----TGAGTTGGGTCTGCTTGTCCC-TTGGCGTGTGGTGG-----	37
T-OK-1.3_11	-----GTGGTTTGTCA--TTCGCTTCC T GTGTTCTGGGTGGG-----	37
T-UC-1.3_20	-----GTGGTTTGTCA--TTCGCTTCC T GTGTTCTGGGTGGG-----	37
cap-UC-1.3_1164	-----TTGGTTTGT C ATTCTGCTTCCGTGGTCCGTGGTGG-----	37
10-OK-1.3_215	-----CGAACTGGTTGGGTTAGTG-GGTTGCTAGTGGGGACG-----	37
10-UC-1.3_435	-----CGAACTGGTTGGGTTAGTG-GGTTGCTAGTGGGGACG-----	37
20-UC-1.3_183	-----CGAAC T GGGTGAGTTAGTG-GGTTGCTAGTGGGGACG-----	37
40-UC-1.3_232	-----CGAACAGTGTGGGTTAGTG-GGTTGCTAGTGGGGACG-----	37
20-OK-1.3_174	-----CGAACGGGGTTGGATTAGTG-GGTTGCTAGTGGGGACG-----	37
40-UC-1.3_329	-----CGAACGGGGTTGGTTAGTG-GGTTGCCAGTGGGGACG-----	37
cap-UC-1.3_664	-----CGAACGGGATTGGTTAGTG-GGTTGCTAGTGGGGACG-----	37
cap-UC-1.3_1339	-----CGAACGGGGTGGGTTAGCG-GGCTGCTAGTGGGGACG-----	37
cap-UC-1.3_864	-----CGAACGGGGTAGGTTAGTG-TGTTGCTAGTGGGGACG-----	37
20-UC-1.3_134	-----CAAACGGGGTGGGTTAGTG-GATTGCTAGTGGGGACG-----	37
	1.....10.....20.....30.....40.....50.....	



20-UC-1.3_176	- - - - - C T A A C C G G G G T G G G T T T A G T G - G G T T G C T A G T G C G G A C G - - - - -	37
20-UC-1.3_91	- - - - - C G A A C C G G G G C G G G T T T A G T G - G G T T T C T A G T G G G G A C G - - - - -	37
cap-UC-1.3_279	- - - - - C G A A C C G G G G C G G G T T T A T T G - G G T T G C T A G T G G G G A C G - - - - -	37
10-OK-1.3_597	- - - - - C G A A C C G G G G T G G G T T T A G T G - G G T T G C T A G T G G G G T A C T - - - - -	37
10-CD-1.3_353	- - - - - C G A A C C G G G T G G G T T T A G T G - G G T T G C T A G T G G G G A C T - - - - -	37
10-OK-1.3_121	- - - - - C G A A C C G G G G T G G G T T T A G T G - G T T T G C T A G T T G G G G A C G - - - - -	37
cap-UC-1.3_863	- - - - - C G A A C C G G G G T G G G T T T A G T G - G G T T C C T A G T G T G G G A C G - - - - -	37
cap-UC-1.3_1336	- - - - - C G A A C C G T G G G T G G G T T T A G T T - G G T T G C T A G T G T G G G A C G - - - - -	37
T-UC-1.3_21	- - - - - C G A A C C G G G G T G G G T T T A G T G - G G T T G C T A G T G G G G G G G - - - - -	37
T-UC-1.3_70	- - - - - C G A A C C G G G G T G G G T T T C A G T G - G G T T G C T A G T G G G G G C G G - - - - -	38
cap-OK-1.3_50	- - - - - C G A A C C G G G G T G G G T T T A G T G - G G T T G C T A G T G G G G G A C G - - - - -	38
T-OK-1.3_36	- - - - - C G A A C C G G G G T G G G T T T A T T G - G G T T G C T A G T G G G G C G G - - - - -	37
T-UC-1.3_44	- - - - - C G A A C C G G G G T G G G T T T A T T G - G G T T G C T A G T G G G G A C C G - - - - -	37
10-CD-1.3_563	- - - - - C G A A C C G G G G T G G G T T T A T T G - G G T T G C T A T T G G G G A C G - - - - -	37
T-UC-1.3_27	- - - - - A G G G G G G T G A G T T T A G T G - G G T T G C T A G T G G G G A C G - - - - -	35
T-CD-1.3_11	- - - - - A G G G G G G T G G G G T T T A G T G - G G T T G C T A G T G A G G A C G - - - - -	35
T-UC-1.3_24	- - - - - C C G T G G G G T G G G T T T A G T G - G A T T G C T A G T G G G G A C G - - - - -	36
T-UC-1.3_23	- - - - - C C G T G G G G T G G G T T T A G T G - G G T T G C T A G T G - G G A C G - - - - -	35
80-UC-1.3_312	- - - - - A G G G G T G T G G G T T T A G T G C G G T T G T C T A A T G G G A C C G - - - - -	37
10-CD-1.3_586	- - - - - A G G G G G G T G G G G T C T A G T G C G G T T T T C T A A G G G G A C C G - - - - -	37
20-OK-1.3_177	- - - - - A G T G G G G T G T G T T T A G T G C G G T T G T C T A A G G G G A C C G - - - - -	37
T-OK-1.3_88	- - - - - A G G G G G G T G G G T T T A G T G C T G T T G T C T A A G G G G G C G G - - - - -	37
40-OK-1.3_83	- - - - - C G C C A A G A T G G G A T T C G T G G T T G G G T A A G T G T G G A A G - - - - -	37
	1.....10.....20.....30.....40.....50.....	

40-UC-1.3_109	- - - - - CGCCAAGATGGGATTCTGGGTGGGTAAGTGTGGAAG - - - - -	37
cap-UC-1.3_1083	- - - - - CGCCAAGAGGGGATTCTGGGTGGGTAAGTGTGGAAC - - - - -	37
T-OK-1.3_80	- - - - - CGCCAAGAGGGGATTCTGGGTGGGTAAGTGGGACG - - - - -	37
20-UC-1.3_210	- - - TGGTTCTCGTCGTGTTCAAGGTTGCTTCTATTGGGG - - -	37
cap-UC-1.3_1289	- - - GTGTGTTTCCTCGTTATGTCAGG - - - CGTGTATTGGGG - - -	37
cap-UC-1.3_1346	- - - ATGGGGTTTGTGCGTTAGTG - - - GTGATATTGGCG - - -	37
cap-UC-1.3_404	- - - CGGGTTCAGTGGGGCTGCAG - - - GCTATTGGCTTTATGG - - -	37
cap-UC-1.3_1326	- - - CTGGGTTTGTGGGTGATC - - - GCTATTGGATTTCCTGG - - -	37
cap-UC-1.3_869	- - - ATCGGGTCCTT - - TCGTGC - - - TTCTGGTT-GTGTGGCTTTG - - -	37
cap-UC-1.3_1362	- - - CTCGGTTCTTCGTTGCAA - - - TATTGGTCTGGGCTTGGC - - -	37
10-OK-1.3_349	- - - CTGAGTTCGGTTCTAG - - GGGGGTATAATTGGCTGTGCG - - -	36
cap-UC-1.3_1240	- - - TGGGGTCTGTTCTTCGGGGATGTTCTGGTCTTTG - - -	37
10-UC-1.3_422	- - - GCGGTGTTCTATATTTCGGGG-GGTATTGCTTAAAGG - - -	37
cap-UC-1.3_1105	- - - TGTTCTTCTCTCGCTGGGTGGTATTGGCTTTATTGCG - - -	37
10-UC-1.3_497	- - - TTGTTTCAATTGCGTGTGGGTTTGTGGTTTTCTGC - - -	37
10-CD-1.3_207	- - - TTGGATTCTTCTGGGGGGGTTT-TGGTCGGTCATGT - - -	37
cap-UC-1.3_1175	- - - TTGGTTCATCGTCGGGTCATAGGGGTATTGGTGT - - -	37
10-CD-1.3_21	- - - TTGGTTCTCTGCTGGGCTTATTGGGTATTGGGGG - - -	37
cap-UC-1.3_721	- - - GTGTTTCAATGTCCTGGTTACGTTGGGTATTGGCTGG - - -	38
80-OK-1.3_123	- - - TGTCTTCTCTGGGT-CGTGTGGGTGGGACGC - - -	37
10-UC-1.3_311	- - - TTGTAGTCTGCGCGGGTC-GTTGGTATTGGTCAGTGTG - - -	37
cap-UC-1.3_749	- - - TTGTGTTCGCGGGT-GGTGGTATTGGGTGTTGTGCC - - -	37
40-OK-1.3_81	- - - GATCT-CTTCGTCGCGGGTA-TATGTGGTTGTCAAGTCATG - - -	38
	1.....10.....20.....30.....40.....50.....	

10-CD-1.3_629	- - - - - G A T G T A A T G T C G T C G C G G G T - - T A T - T G G T T G T - G G T C T C G - - - - -	37
20-UC-1.3_212	- - - - - T G C G T T C T T A T T C G A T G C T G - - - - G G G G C T G T T G G - - T T G G C - - - - -	37
cap-UC-1.3_1160	- - - - - T T T T G T T C G A A A A C G T G C G G G G G T T A T T G G A T T T G G - - - - -	36
80-UC-1.3_178	- - - - - T T G G T C T G T T T A T T C G T T G A A A G - - - C G G G G T A T T G G C G T - - - - -	37
cap-UC-1.3_556	- - - - - T G T C G T C T G T T T A T G C A T C G T G G - - - G G G G T A T T G G G T C G - - - - -	37
cap-OK-1.3_8	- - - - - T T G G T C T T G G A A T G C T C T G G T G - - - G G A T A T T G T G T T G C G - - - - -	37
cap-UC-1.3_1185	- - - - - T T G G T C T T G G A A T G C T C T G G T G - - - G G A T A T T G T G T T G C G - - - - -	37
cap-UC-1.3_1230	- - - - - T G T G G T C C - T T T G T T T G T G C G G G - - - G G G T G T A T T G G T C - - - - -	37
cap-UC-1.3_495	- - - - - T G G T T G A T A T T T C T G T T C G C G G G G G G T A T T G T G T G - - - - -	37
cap-UC-1.3_1166	- - - - - T T G T T G T T T A T G G - C G T C C C G G G G G A T A T T G T C G G T C - - - - -	36
20-UC-1.3_172	- - - - - G G T T A T T A G T C G C G T - - - T G T G G G G G C A A T T G T C G T C G G G - - - - -	38
cap-UC-1.3_564	- - - - - T G C T T T C G T T T C T G T T C G C G T G T G T G G G - - - G C T T G T G G - - - - -	37
cap-UC-1.3_644	- - - - - T T G T C G T T G T T C G C C G C G G G T G G G G T T G T G C T T G T T G - - - - -	37
20-UC-1.3_162	- - - - - T G A T G G T T T G T A T - - - T G C T G G G G G T - A T T G G A G G C T T G G G - - - - -	37
cap-UC-1.3_1341	- - - - - C C C G T T C G T A T C C - T A T T G G T G C T C A G T G G G G G C T G C - - - - -	37
40-UC-1.3_173	- - - - - G T T G T T T - T C C A T G C - T G T G T C C G C G T C T T T G T G G G G T G G - - - - -	37
40-UC-1.3_212	- - - - - T G G T T G A T T G G T C C G T - C - T G T G G T G G G G T A T T G G A G G T - - - - -	37
cap-UC-1.3_773	- - - - - T T G G C G C C G T T C - T G T T G A T T G - C G T G T G T G G G T T T G T G - - - - -	37
40-CD-1.3_233	- - - - - T G T T T G C G C C G T T T - T - T T G T T C G T C T T G G A T G G G T T G G - - - - -	37
cap-UC-1.3_765	- - - - - T T G G G T T T C G T T C T - G G C - T G C G T C G G G T A - - T C T G G G C G G - - - - -	37
cap-UC-1.3_1197	- - - - - T T G G C T T T C T C T T T - T G C G T G G T T C G A T T A G T T C T G G G - - - - -	37
10-OK-1.3_540	- - - - - T C C C T G G G T T G T G T T A T - G T G T G A G T G C G G T T A T T G T C - - - - -	37
cap-UC-1.3_49	- - - - - T T G G G T T T C T T T G T G A T T T G T G G G A T C T G C T T G - - - - -	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_574	-----TCTCGGTTCTTCT-TTCTGGTGGTGGTCTTGTG-----	37
cap-UC-1.3_540	-----TTCTTGCTTGGTCTGTCTTTGGGGTTTGTGGG-----	37
cap-UC-1.3_978	-----TGCTTCTCTGTCT-TCTTGTGGGATTCTGCGGGGG-----	37
cap-UC-1.3_817	-----TCGATTCTGGTTGGGGATTA-AATGGGGTG-GGTTG-----	38
cap-UC-1.3_1174	-----TTGGTTGTTGTGGCTGTGATGTGGTGTGGTCTGC-----	37
10-UC-1.3_332	-----TTGCTGTCGT-CGTCGTT-GTGGGTTGGTACCGTTG-----	37
10-UC-1.3_522	-----GTCGTCGTCGTCGTG-TCTGTGTGGTATTGTTGG-----	37
cap-UC-1.3_746	-----TTGTTGTTCACTCGTCGTC-TCTGTGGGGGTTCTGG-----	38
cap-UC-1.3_971	-----TTGTTGTTCTCATTGTCGTC-TCTGTGGGGGTTCTGG-----	38
cap-UC-1.3_585	-----GTTGGCTGTCTTCGGT-GTGTGGCGGGTATTGCGTTG-----	37
10-CD-1.3_223	-----TGTGGTCCGTCGG-GTT-GGGGCTCCGGTATTGTTGG-----	38
cap-UC-1.3_1143	-----CCCCATTGTTGGCCGGCTGTGTGTCGTTG-----	37
40-CD-1.3_193	-----CGTCCCCCTTGTGTTGTC-CTTCTTGCGTTGTTGG-----	37
cap-UC-1.3_1284	-----GTTGTCTCGGTCTGTGGT-TGTGTGGTTATGCTCTG-----	37
cap-UC-1.3_96	-----GTGCTTCTGTCCGTCTGTGTTCTGTGTCGGTGTG-----	37
cap-UC-1.3_116	-----TGTTCGTTCTTTCG-CTGGGTTT-CGTTCGGTTGTGC-----	37
cap-OK-1.3_26	-----TCTTTTCTCGTCCGGGGGT-TCTTGGGCTGTGTTCG-----	37
cap-UC-1.3_1236	-----TGTCCCTC-TCTTGTGGT-CTCCGGCGCTTGGTCCCTG-----	37
T-OK-1.3_44	-----TCCGTCGTGTGGTACTCCCCCTGTG-CCCTGCC-----	38
10-OK-1.3_49	-----TGTCGTGGGTGTGTCGTGTTCCCCTGGTATCCGG-----	37
10-OK-1.3_323	-----TAAGTCGGCTGT-GTGTGTTCTGATTGGTGTATGGG-----	36
40-OK-1.3_41	-----CCGCCCCCTGTGTAGA-TTG---TC-TGTCCGCTG-TTGGTC-----	35
40-UC-1.3_111	-----CCGCCCCCTGTGTAGA-TTG---TC-TGTCCGCTG-TTGGTC-----	35
	1.....10.....20.....30.....40.....50.....	



cap-UC-1.3_331	- - - - - TTGC GTGTGTAGTCTTG - - - TG-TGCTGTCTGGTTGGTTTG-	37
cap-UC-1.3_1293	- - - - - GTGGT-TGTGTGTAT-GTGCG - - C - TGGGGTCTGTTCTTC - -	37
cap-UC-1.3_1186	- - - - - TTGGTCTGTGTGTATTGTTCG - - TG-TGGGGTCTGTATGT - - -	37
cap-UC-1.3_1040	- - - - - TGTGTGGGTTGTTTCGGCTC - - TGTGGTCTGTTCTGT - - -	37
cap-UC-1.3_988	- - - - - GCGTGGTTCGT-TGTGTGGTTC - - TA-TGTCCCCGTGTCTG - - -	38
10-OK-1.3_330	- - - - - GTGTCTCGTGGCTTCTCTGTGTTCTGTTCCGGTGTGG - - -	37
10-UC-1.3_380	- - - - - TCGTGTTCCTGTGGCTTGTGTTCTCCGGTGGGGTGT - - -	37
cap-UC-1.3_870	- - - - - AGTCGTTCCGTGGCCCCTGTGTGTTCTGTCTGCTGG - - -	37
cap-UC-1.3_933	- - - - - GTTGTGCGTCTGTGCCGGTGTG-GTTTCTTGCTTGGG - - -	37
40-OK-1.3_188	- - - - - TGTTCTGTGTCTGGT - - TCGTGTGT-TGTTTGTGCCTG - - -	36
40-CD-1.3_142	- - - - - GTGTGTCCGTGATGATCTGTGGGT-TGTTTTTCTCTGG - - -	37
cap-UC-1.3_56	- - - - - TGTGTTGCTGTGGTTGTATGTTGGGTTGCTTCCCTGG - - -	37
T-OK-1.3_108	- - - - - CTGTTTCCGTGGTGTGCTGTTGTTCTTTCTG - - -	37
10-OK-1.3_593	- - - - - CGGTCCC-TGTGAATCCC-GTGGCG - - TTGGTTTGTGTTG - - -	37
10-UC-1.3_260	- - - - - CGGTCCC-TGTGAATCCC-GTGGCG - - TTGGTTTGTGTTG - - -	37
cap-UC-1.3_1112	- - - - - TGGTTCCGTGTCGCTTCC-GTTGTC - - GTG-TTTGTTTTG - - -	37
10-UC-1.3_183	- - - - - TTGGGGTCCGTGT - - TCTG-CTGGAG - - TGTGATTGTTGTG - - -	37
10-UC-1.3_143	- - - - - CTCTTGTGGGTTCC-TTGCGC - - CTGGGGTGGCTGTCT-CG - - -	37
cap-UC-1.3_693	- - - - - TTGTCTGTTCTGTCTGCGTCTGGGGTTGTCTTTGCG - - -	37
cap-UC-1.3_539	- - - - - TTGCGGGTTCG-TTGGTGCCTGGTGTCTGGCG - - -	36
cap-UC-1.3_936	- - - - - GTGTGTTCTCCTTCACTGCGGTGGGTTCTGTTGTGG - - -	37
cap-UC-1.3_1044	- - - - - TGTGAAGTGTGTGCTCTCCGGTC-TGTGGT - - - TTCCGGTTGA - - -	38
10-UC-1.3_478	- - - - - ATGCATACTCACCGCGTCGGGGTCCCGTAGTCAGGTGG - - -	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_566	-TGCTCTTGGTCCGTGATTGGGTTGTCTTTGGG-----	37
cap-CD-1.3_102	-TCCGTTGGTCCCGTTCGTCATTGGGGTTCCGTATTG-----	37
cap-UC-1.3_871	-AGGATTGTCCACGCG-GTATTGGGTATGCATTGATGGG-----	37
cap-UC-1.3_1202	-TTGGATCGTCCGTGTGCAATGTGGGGCTGCTTTTG-----	37
20-OK-1.3_137	-TTGGCTATGTGGTTCGTGTCGTGTCGGGGTTGTTG-----	37
40-UC-1.3_40	-TTGGATAAAGTG-TGGGTGTTGGCTGTTAGTTGTTG-----	37
cap-UC-1.3_815	-TCTGGGTT-CGTGGGTCTTGTTC-CTTTGGGGTGTG-----	37
10-CD-1.3_408	-TTGGGTTGCTGTGGGTTGTCGTGCGTTGGGCTGG-----	37
cap-UC-1.3_522	-TTGGGTTACTGTTGC-TCTGGGTCGGCTGTGTTG-----	37
cap-UC-1.3_1190	-TTGGGTTCTGTGGGG-TATGTGGTGTCTCATCGTGTG-----	37
cap-UC-1.3_323	-TTGGGTCCTGTGTG-GTTCTGTCGGTTCTTATTTGG-----	37
10-OK-1.3_159	-TGTGTTCTTTTGCTGC-GGGTGTGTTCTTGCGGG-----	37
10-UC-1.3_347	-TGTGTTCTTTTGCTGC-GGGTGTGTTCTTGCGGG-----	37
cap-OK-1.3_107	-TGTTGTGTTCTGTGTTG-GGGTGTG-TCTTTGTTGGCT-----	37
cap-UC-1.3_546	-TGTTGTGTTCTGTGTTG-GGGTGTG-TCTTTGTTGGCT-----	37
80-OK-1.3_127	-TCTCTGTGGTTCCCTGGATTG-GGGGTTTCTTTTG-----	37
80-UC-1.3_72	-TCTCTGTGGTTCCCTGGATTG-GGGGTTTCTTTTG-----	37
20-UC-1.3_27	-GTTGGGGTTGTCGTGTTCTGGGGCGTCTTTTG-----	37
10-UC-1.3_463	-GCGCTGTGGTGTGTTCCAATTG-CGGGGTCCTGTTTG-----	38
cap-UC-1.3_1235	-TGTCTGTGTTG-CTGTTAC-CGGGGTCGTTGTATTGCTGG-----	37
20-UC-1.3_221	-CGTGCTCTG-TTCGGGGTCTTGTGTTCTTGCGGGGG-----	37
T-UC-1.3_81	-TTGCT-TG-TGGTGGGTTCTAGTTCTTGTGTTCGTTGGG-----	36
cap-UC-1.3_837	-GTGCTGTG-TTGTGTTCGTTATTGGTGTGCCTGGGG-----	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_613	- - - - -	CTGTGGGTCTGATTGTGGGTTGTAT	- TCC	TGGCGGG	- - - - -	36		
cap-UC-1.3_812	- - - - -	TCTTCTA	TGGTTCTG- TTT	CGCGGGGGAT	- TTTGGCG	- - - - -	37	
cap-UC-1.3_1053	- - - - -	TGC	GGTTGTGTT	C	GGGGGTTTTTGTC	TTGGTTGGG	- - - - -	37
10-OK-1.3_482	- - - - -	TGTTCTCTT	GCTGGGTGTTGGTTTCTGTTGGTTGC	- - - - -			37	
10-UC-1.3_344	- - - - -	TGTTCTCTT	GCTGGGTGTTGGTTTCTGTTGGTTGC	- - - - -			37	
40-OK-1.3_189	- - - - -	TGTGCTT	CGTGGTGCGTTTCTGTC	TGGTGGCTGGG	- - - - -		37	
cap-UC-1.3_594	- - - - -	GTCTCGTTT	TGTGG- GTGTTTTT	TCTGGTGGCTGGG	- - - - -		36	
80-OK-1.3_140	- - - - -	TTGTGTGTT	CGTGC	GGTGTGT	CCTTTCA	AGTGGC	- - - - -	37
cap-UC-1.3_1206	- - - - -	TTGCGGGTGG	TTGTTGGGTGTTGGGTGTTTTGATGTGGC	- - - - -			37	
40-UC-1.3_364	- - - - -	GTTCTGTGCTT	TGGTGGT-TGTTGTCTTGATGTGGG	- - - - -			37	
40-UC-1.3_121	- - - - -	TTATGTTCTGTTG	TGTTGTGTT-GTGCTGGATGTGCTTG	- - - - -			37	
cap-UC-1.3_783	- - - - -	TTATGTTCTGTTG	TGTTGTGTT-GTGCTGGATGTGCTTG	- - - - -			37	
T-OK-1.3_106	- - - - -	GGTTGTTCTGTG	CTGC	TGGTGTGTTCTGGATGTGG	- - - - -		37	
cap-UC-1.3_653	- - - - -	TGGTTGTCTGTT	CTG-TGTGGGTATTGTTATTGGT	- - - - -			37	
cap-UC-1.3_339	- - - - -	TGTTTCTGGT	ATCTGG-TGTTGTGTTATTGCTGTGG	- - - - -			37	
cap-UC-1.3_782	- - - - -	TTCC	TGGTTCTCGGTTGTGCGT-TGGGTTCTGTTG	- - - - -			37	
cap-UC-1.3_468	- - - - -	TCTCTGCTT	ATCTT-TGTTGGGGGTCTA-TTGTGCTG	- - - - -			37	
cap-UC-1.3_537	- - - - -	TTGCTTGT	TTCTGTGCCGGGTGT-TTACTTTGTTGG	- - - - -			37	
20-OK-1.3_62	- - - - -	TTGGTGTCTACCTGTA	TCGCTTCTTGTC	TGTGGCGGG	- - - - -		38	
cap-UC-1.3_181	- - - - -	TCTGGTTGTT	ATC- ATGTCGCGCTGTCTTGTTGGGG	- - - - -			37	
10-UC-1.3_196	- - - - -	TGTTGCT	- GTGTCG-CGGGTGTTACTAATGTTGTG	TGGG	- - - - -		37	
cap-UC-1.3_1147	- - - - -	TGTTGCT	- GTGTTATCCGTTCTCATTTTCTGTTGGGG	- - - - -			37	
cap-UC-1.3_1037	- - - - -	TGTGTTGTTGTT	CGATCGG-GTCTTCTTTGTTGG	- - - - -			37	
	1.....	10.....	20.....	30.....	40.....	50.....		



10-OK-1.3_609	- - - - - A T G C G T G T T G T G T G C T T C T - G C T T T T T C G G G G T G G G - - - - -	37
cap-UC-1.3_1242	- - - - - T G C T T G T T C G C T G T G T G T C T C G T T T G T G G G G G C G G G - - - - -	37
10-OK-1.3_449	- - - - - T T G G T G A T - T A G T T G T T G T T C T C G G G T T T C T T G C G G G - - - - -	37
cap-UC-1.3_1301	- - - - - G T G A T G T T A T T G T T T - T G T G T G G G T T A T T G G C G G C G G G - - - - -	37
10-UC-1.3_337	- - - - - T T C G - G G T - G T G T G T G T G T G G T C T C T T C T G T T A T G - - - - -	37
cap-UC-1.3_541	- - - - - T T C G T G G T - G T G T G T T T C G G G - A G T G T T T C T G G T T T T G - - - - -	37
cap-OK-1.3_117	- - - - - T G G T - G T G T T G T A T G T G T G T C T - T G G C T G G T A T T G T G T C - - - - -	37
cap-UC-1.3_1114	- - - - - T C T G G T - G T T T C G T G C T C A A G G G T G T C T C T G G T G T T T G - - - - -	38
cap-UC-1.3_1315	- - - - - G C G C G T T C G G G G T - G T G T C T T G T G T G G G T A T A T T G T C C - - - - -	37
cap-UC-1.3_1213	- - - - - T T C G T G G G T T G T G T C T G T G G G G G T C T A T T T C A A G G - - - - -	36
cap-UC-1.3_780	- - - - - T T C G T G G G G T G T G T T C - - - T G G G T C T A T T G T C G C T C T G G G - - - - -	37
20-UC-1.3_12	- - - - - C T G T G T T C T G T G A T G T C T G C C T T G T G G G T T T T G G G G - - - - -	37
10-UC-1.3_529	- - - - - G C G A G T G T T G T A G T G C T T T C T C C T T G G T C T T T G T G G G - - - - -	37
cap-UC-1.3_946	- - - - - C T A G T T G - T G T - G T G T G T - T A T G T C T G T C T T A T G G G G G G - - - - -	37
T-UC-1.3_28	- - - - - T T G T T G C T G A - T T G T G T C T G T G T C T T T T C A T T G T G G - - - - -	37
40-OK-1.3_272	- - - - - A T G T G T G T G T T G T G G G G T G T G T A T T G G G T C T C T G T C - - - - -	37
cap-UC-1.3_1308	- - - - - G G T A T T G T G T T T C T T T G C G G T - - - A T T G G G T - T C A T G T G C - - - - -	37
cap-UC-1.3_241	- - - - - T G T C C T G T G G C G C G G G T T T T T C T T G G C T G T G T G G G - - - - -	37
cap-UC-1.3_1262	- - - - - T C T G C G G C G T T G T G G A T T G T C T A T T G G T C - T A T T G G G T - - - - -	37
T-OK-1.3_73	- - - - - T G T G T G T G T C C G T T T G T C G T T C T T G G G T T T T G T G G C - - - - -	37
T-UC-1.3_12	- - - - - T G T G T G T G T C C G T T T G T C G T T C T T G G G T T T T G T G G C - - - - -	37
cap-UC-1.3_159	- - - - - T G T G T G T G - - - G T C T G G C G T - C T T G T G T T T T G T C G T G T T G - - - - -	37
cap-UC-1.3_1305	- - - - - G T A T G T - C G T G T C T C T C T T G C G T - G G G G T G T T T G G T C G - - - - -	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_1217	-TTATGTGTGTGGCTGTCTTCGT-	ATTGGGTGCTTCTC	37
cap-UC-1.3_277	-CTCTGGGGCTGGCTTCTTGTTTGTTCGGG-	-	35
cap-UC-1.3_1321	-CTTCTGTGGGCCG--TTTATTGGTGTGTTCGGGTG	-	37
cap-UC-1.3_1168	--TTGTGTGGGGTG-TG-AATAAGCTTTGGTTGGGTCGG-	-	38
10-CD-1.3_211	--TTGCCTGGGGTT-TCTGGTGGCTCTGGTTCCGTC	-	37
20-OK-1.3_54	--GTTAGTTGGTGCTGTGGGTTATTGGTTCTTGCGG-	-	37
20-UC-1.3_73	--GTTAGTTGGTGCTGTGGGTTATTGGTTCTTGCGG-	-	37
40-OK-1.3_28	--TGGGCTCTGTGTTGTCT-TG--TTCTGCTGGGTTCTGG-	-	37
cap-UC-1.3_1260	--TCTGGCGCTCTGTTCT-TGGTTTCCCTGCTGGGTTGGG-	-	37
cap-UC-1.3_301	--GTC A TTTGTGCTCTGGGTT-GTTG--TTCTTTTGTTG-	-	37
cap-UC-1.3_677	--TC G TGACCCGGGTTGTTG--TTTGGCTGTGTTCCCC	-	37
10-OK-1.3_492	--TGTGGT A TCCCTGGG-TTG-TCTG--CGTC G TTTATGGGTG-	-	37
cap-UC-1.3_179	--TGATGTCCTGGG-TCT-TATGGTTCTTGTATTGGGGG-	-	37
20-UC-1.3_154	--TGTGTCCCTGGGGTGT-TCCTCGTTTATGGCTGGGGG-	-	37
cap-UC-1.3_1263	--TC G TTCCCTGGGTTGTTGCGCTTTTTGGGTCGG-	-	37
10-CD-1.3_376	--TTGTGTTCCCTGGGGTGT-TATG-GTTTGTTGTGCTGC-	-	37
10-OK-1.3_252	--TTGGGTTGC-ATCATGGTTGTTGTGGGTATTGTTG-	-	37
10-UC-1.3_321	--TTGGGTTGC-ATCATGGTTGTTGTGGGTATTGTTG-	-	37
10-CD-1.3_696	--TTGGGGTGTATCCTGGGCTGTGTGATTGTTGTTG-	-	37
cap-UC-1.3_396	--GCGGTGGGGTTGCCTCGTGGTTGTGATTGGCTTTG-	-	37
cap-UC-1.3_710	--TGC G GTGGGCTTCTCGGGTGTGTTG-C T TTGTTG-	-	37
10-OK-1.3_431	--TTGTGTGCTGGGGTCT-TGGGCTTTAATC C CGTGTGTTG-	-	37
cap-UC-1.3_1249	--TGC G CTGGGGTGTCTCGGGTTAGTCTGGTTTGTGTC	-	37
	1.....10.....20.....30.....40.....50.....		

40-OK-1.3_39	- - - - - TCTGGGGTCCCCTTACTCTTTATTGCGTCCTTCTTGTG- - - - -	37
T-OK-1.3_109	- - - - - CTCGGGGGTTTCTTACGGTTGGT-GCTTCTTGGTCTG- - - - -	37
cap-UC-1.3_1327	- - - - - CTCTGTGGGGCTTT-CTCGTTGGTGTGCTGGTTGTCTG- - - - -	37
10-UC-1.3_390	- - - - - TCCGGGGTCTCTTGGTTGTTTTCTCGTCTGCTG- - - - -	36
40-UC-1.3_297	- - - - - CCCCAAGCCGGTAAGTATCTCGTTGTTCT-CCTCTTCTTC- - - - -	38
40-UC-1.3_144	- - - - - CTGCGGTTTGTT-TTTGTTGGTTCCCCTGGTCTGTGGC- - - - -	37
cap-UC-1.3_593	- - - - - GTCTGC GG G C T C - - TGTGTTGGTTGTCATGGTCTGTGTG- - - - -	37
cap-UC-1.3_785	- - - - - TGTTTCCGGCTCTGGGATGTT-GTTTCTCTGTGTT-TGTGG- - - - -	37
T-OK-1.3_19	- - - - - GTTCGGGTGTCGGGTTGTTGCTGTGCTTCTGTG- - - - -	37
40-OK-1.3_75	- - - - - TTGGGTGGTGGG-TATTGGGTGTTTGCT-TGTGATGG- - - - -	37
10-OK-1.3_184	- - - - - TCGCGTGGTCCTGGCCTTGGCTTACTGGTTGTTGTC- - - - -	37
40-UC-1.3_79	- - - - - TGCTGGTCCCTTTGCGTTTTCACTGGTTGTTGTC- - - - -	37
10-UC-1.3_355	- - - - - TGTGGTTGGCTTGTGTTTTGCTTGGTTGCTGTGG- - - - -	37
10-OK-1.3_245	- - - - - TTGTGGTCTCGTTCTGTTCTTGGTTCTGGGCTGGG- - - - -	37
cap-UC-1.3_528	- - - - - TTGGGGTGTTCCTTCGTTGGGCTTTCTATGCGGGG- - - - -	37
cap-UC-1.3_750	- - - - - TTGTGTGTTGTTGTTTGGGTTGTCCTTTTTCCGG- - - - -	37
10-CD-1.3_383	- - - - - TTGTGGTGGTTCGTGTCTGGTTGGCTATTGGCTGG- - - - -	37
10-OK-1.3_171	- - - - - TGTCGTGTCTGGTTCCCTTTATTCTGCGGGTGGTGA- - - - -	37
cap-UC-1.3_1234	- - - - - TGTCTTCGTGTTG-TGCTTGTTATGGTCTGGGGTGG- - - - -	37
10-OK-1.3_527	- - - - - TCGTGTCCCTGTGGGGTTCTGTTGCTTGGTTGTG- - - - -	37
cap-UC-1.3_246	- - - - - TCTTGTGCT-TGTTGTTGTGATGGGGGGGGTTG- - - - -	36
10-OK-1.3_508	- - - - - TGCTCTGGCTGTGACCTTGTCTCTCTGGTGTGGGG- - - - -	37
cap-UC-1.3_360	- - - - - TGCTCTGGCTGTGACCTTGTCTCTCTGGTGTGGGG- - - - -	37
	1.....10.....20.....30.....40.....50.....	

cap-CD-1.3_172	-----GGGTTTGGC-GTGTCA	TGGTGTCTGTCTTGAA	TGGGGG-----	38	
20-UC-1.3_34	-----TTGGTAGTGTCC	TGTGTTGTGGTC	CGCTCGGGGG-----	37	
cap-UC-1.3_764	-----TTGGTAGTGTCC	TGTGTTGTGGTC	CGCTCGGGGG-----	37	
10-UC-1.3_313	-----TTGGTTGTGTCTCGTGA	TCTGGTAAT	TGCCGC	GGGG-----	37
40-CD-1.3_245	-----AGGTGTGTCCC	TGCTCATGTTCTT	CGTGCCCCGGGG-----	37	
10-UC-1.3_358	-----TGTGCGTGTGGC	TTTTTGCGATT	CTGGTTCTGGG-----	37	
cap-UC-1.3_691	-----TTGTG-GTGTGTCT	GTTTTTGCTGTTCTGGTTCCGTG-----	37		
20-OK-1.3_89	-----GCTGGGTGGCTT	CTTTCTCGTATTGT	-CGGTGGGG-----	36	
cap-UC-1.3_1258	-----TCTGTGGGGT	CCTTGCTTCTGGTATA	ACTGTTGTGGGG-----	37	
10-OK-1.3_649	-----TCTGGGTTATTGCT	TTTCTTGTTCTGGTTCT	CTGGTGTGG-----	37	
20-OK-1.3_150	-----TTGGTTTGTGTGATG	-TCGGTTC-CGGGGGATTGGGT	C-----	37	
cap-UC-1.3_757	-----TTGGTTTGTATGTCT	-TGTGTT-CGGGTGGATTGGCTGC-----	38		
cap-UC-1.3_479	-----GTGGGTTGTTGGCT	-TTTCTTTCTTGGGATTGGCG-----	37		
cap-UC-1.3_1187	-----TTGGCTGTGGGTTGA	ATTGGTTTCTTCTGTTGGCG-----	37		
20-CD-1.3_50	-----TTGGCTGTGGGTTGA	ATTGGTTTCTTCTGTTGGCG-----	37		
cap-UC-1.3_1198	-----TTGG-CTGTCTGTTCATT	--GTTTCTGGTATTGT	CGGATG-----	37	
10-OK-1.3_652	-----TCGTGTTGTGTTCCGGCTGTGTT	CTCCTGTGGGG-----	37		
cap-UC-1.3_223	-----TTGGTTCGTGCTCGT	-TTTCCGGGGGTGGCTG	-CCTGTGG-----	38	
cap-UC-1.3_447	-----TCGGGTTCA	TTCTCTGGTCTCTGTTGTGG-----	36		
cap-UC-1.3_501	-----TTTCGGGGTGTGGT	GTTTCGGGTCTCTGTTGTGG-----	37		
cap-UC-1.3_260	-----GTGCTCTCGGGTCCGC	-GTTCCCCTTCTCTCGGGGTGG-----	38		
cap-UC-1.3_659	-----GGGTTCTGTGGGT	-ATTGTCTCTTCTTGGGTTG-----	37		
cap-CD-1.3_415	-----TTGATCGGTTCTT	-GCCCTTCATTCTGC	GGGGTGTGG-----	37	
	1.....10.....20.....30.....40.....50.....				

cap-UC-1.3_17	-----GTGGCGTCATCGTGTGGGGTATTGCTTC-----T-CGGTCGG-----	37
cap-UC-1.3_1310	-----GGCGTCAT-----GGGGTATCTTTTC-----TTCGTTGGTGGTTG-----	37
10-OK-1.3_255	-----TTGGC-TCAT-----GGTGTACTTTTTGCCTTTGTTGGG-----	37
cap-UC-1.3_1218	---TTATGCGGTCTGGGGTCTGTGGGGTTATTTC-----TTTG-----	37
10-CD-1.3_592	-ACTAGTGGGGTCTGA-----TCTGTGGGGT-GTTCTTC-----TGTGTG-----	38
cap-UC-1.3_895	TACTCGGGGGTCCTGG-----TGTGCGCTTTTTTG-----TTTGC-----	37
40-UC-1.3_349	-----TAAGCGTCAA-TCGGGGGGCCCTGCTATT-----TTTGTTCCTGG-----	37
cap-UC-1.3_872	-----TGAA-TGGGGGTATTGGTATT-----CTTGTATCGCTTGG-----	37
cap-UC-1.3_709	-----TGCTTTCAT-TCTGTGGTTTGCTGTTA-----TTCGTTCTGG-----	37
cap-UC-1.3_1266	-----TCGTGTCAC-TCT-TGGTTGCGGGTTA-----TTC-TTCTGGGG-----	37
cap-UC-1.3_865	-----CCGTGGGGTG-----GGTCTAGTGT-----GGATGTTCGGGGACGG-----	37
T-UC-1.3_55	-----CCATGGGGTG-----GGTCTAGTGT-----GGATGTTCGGGGACCG-----	37
10-OK-1.3_598	-----CCTTGGGGTG-----GGTCTAGTGT-----GGATGTTCGGGGGCTG-----	37
T-OK-1.3_83	-----CCGTGGGGTG-----GGTCTAGTGT-----GGATGTTCTGGG-----	33
40-UC-1.3_28	-----CCGCGGGGTG-----GGTCTAGTGT-----GGATGTTAGGGGGCGG-----	37
20-UC-1.3_84	-----CTGTGGTGTG-----GGTCTAGTGT-----GGATGTTCGGGGGCGG-----	37
20-UC-1.3_185	-----CCGTGGTGTG-----GGTCTAGTGT-----GTATGTTCGGGGGCGG-----	37
T-UC-1.3_52	-----CCGTGGGGTG-----GGTCTAGTGT-----GGATGTTCGTTG-----	33
T-OK-1.3_35	-----GTGTGGGGTGTCTGGCTGGTGTATTGTATGTTTTAAG-----	37
cap-UC-1.3_1024	-----TTGGGGTT-----TGTATGGTCGGGGGTTTGTTCGTTCTGC-----	38
cap-UC-1.3_1319	-----GAGGTG-----GGTATCGTCGTGGGGTATTGGT-GTTATGTAC-----	37
20-UC-1.3_216	-----GTGTGGGGTG-----AATATTGT-----GGGTTTTGT-GTTCTGTCG-----	37
10-OK-1.3_536	-----TCGCGTGGGGTC-ATTGTAGTGGTTGTCTGATTATG-----	37
	1.....10.....20.....30.....40.....50.....	

10-CD-1.3_253	-----TCGCCTGGGGGCCATATGTTTG-TTGTCTTTGTG-----	37
cap-UC-1.3_1095	-----TTGTTCGCGGGGGGTATATTCTTCATG-TGGTTGTGG-----	37
40-OK-1.3_227	-----CAGGGGGTCCCTGCGGGTGGGCTT-ATTGTTGATGGTTCG-----	38
40-UC-1.3_17	-----CAAGGGGGTCCCTGCGGGTGGGCTT-ATTGTTGATGGTTCG-----	38
10-CD-1.3_768	-----TGTTCGCGGGGGGCTTCATTGTTG-TGCTTCTG-----	36
cap-UC-1.3_811	---TGAAGCGCTCTGGGGGGG-TA---TTGTAAGTATTAGTTG-----	37
cap-UC-1.3_1333	---CGGCCTCCGGGGGGGATA---TTGCTGT-TTTATTGTGCG-----	37
20-UC-1.3_215	-----TCCGTCCGGGGGCGTTCTGTTGTTGTTGTTGTTG-----	37
40-OK-1.3_54	-----TTTAGTTTCGCGGGGGGTTGTTGGATGTTATGCG-----	37
40-UC-1.3_11	-----TTTAGTTTCGCGGGGGGTTGTTGGATGTTATGCG-----	37
cap-UC-1.3_1036	-----TTACCGCGGGTGGGGTGTCTGGATTTATGTTTGTGCG-----	37
40-OK-1.3_82	-----CGTATCCTGGG-GGGTCTGTTCGTTCTTTCTTTG-----	37
40-UC-1.3_108	-----CGTATCCTGGG-GGGTCTGTTCGTTCTTTCTTTG-----	37
cap-UC-1.3_1074	-----GCTCGTGGG-GGGT-TGTTCGTTTTTTGTTGTCG-----	35
10-OK-1.3_513	-----TGCCTGTTGGTGGGTTG-TTAAATTGGTTTTCGTTG-----	37
cap-UC-1.3_1051	-----TGGGTGTTGTGGGTT-TGTTTGTATGGCGTTG-----	37
cap-UC-1.3_531	-----TTGGGCTGCGGTGGAATGGTCGGGTATTGGTTGTC-----	37
cap-UC-1.3_945	-----CTGCGGTGGGG-----GGCTATTGGCTTATCTAAATATGGGC-----	37
10-UC-1.3_140	-----GGGGGAGGTGGGGTTAGTATTGGCTGTCTATTG-----	37
cap-UC-1.3_604	-----GCTGGCGGGTGATTGAGTATTGGAATGTCTTGGG-----	37
20-UC-1.3_69	-----TTGGGGGTGTATTGGCTTCTCTAGTCGTGGCGG-----	37
cap-UC-1.3_1001	-----TTGGGCG-GTGT-GCTTCTTCGTATTGGCGGTCTATG-----	37
80-UC-1.3_138	-----TTGGGGTTGTGGTGGTCTCGGATTGGCCGCGTGTG-----	36
	1.....10.....20.....30.....40.....50.....	



cap-UC-1.3_390	-----GGTCGAGTTGGGGGTG-GGTATT-GGATCGCCTTCGTG-----	37
cap-OK-1.3_65	-----TTG-GCGGAATGGGGCTGTTGAACGG--ATTGGATGGTC-----	37
10-CD-1.3_510	-----TAGCGTGGAAATGTAGGGGGTATTGGC--ATTGGTTGTG-----	37
cap-UC-1.3_860	-----CTCTGAGGGGGATGTGGTGTTCGCT-ATTGGATATTCG-----	37
cap-UC-1.3_1140	-----ACG-GGGGGCATATAATTGGACTTCCTTTGCTGGTGTG-----	37
10-CD-1.3_352	-----CTAGTATGCGGGGGGGATATTGGACTA-TTTGCTGG-----	36
cap-UC-1.3_377	-----TAGCGGGGGATATTGTCTTG-TTATGGGAATGTG-----	37
cap-CD-1.3_527	-----AGTGTGGGGATATTGGTCTGTC-TTTTCGGATTG-----	37
cap-UC-1.3_349	-----TGTCTGGGGTGGGTATTGTATTCG-TGTTCTGGTGT-----	37
cap-UC-1.3_993	-----ATTCTGCTGTACGGG-GGCTATTGGATT-GTCTGGTG-----	37
10-CD-1.3_299	-----CAGCGAGATCTGGGGCTATTGGGT-TTTATTGGCGG-----	37
10-CD-1.3_399	-----TTGGTTAGGTCTGGGG-CTATTGGACT-AGTCTGGGG-----	37
10-OK-1.3_457	-----TTGGGTTCCGTCTCGCGTTCGTGGTTGCTCTGTC-----	36
10-UC-1.3_181	-----TTGGGTTCCGTCTCGCGTTCGTGGTTGCTCTGTC-----	36
cap-UC-1.3_848	-----GGGGGTCCCTCGCCCGGGT-GTATTGGTCGTTCTG-----	36
cap-UC-1.3_234	-----TTCGGGTCTCTCTGGGGGGTTGCACTTTCGTGG-----	37
cap-UC-1.3_1100	-----TTGGGCCCTCAC-GTGCGGGATTGGATCTTCGTTGGC-----	37
10-UC-1.3_322	-----TTGGGTTATTTTCGATGGGGGGTATTGTGAAGGTG-----	36
10-CD-1.3_540	-----GGGGCTATTATCGC-TGGGGGTGTTGGACTGTTCGT-----	37
20-UC-1.3_123	-----TTGGCGTATTTGTCTGGTGGGGTTGTTCATGTGGG-----	37
40-UC-1.3_87	-----TTGGCGTGTATCTCGGGGGGGAAATAGTTTTATG-----	37
cap-UC-1.3_380	-----GTTACTATGGCGCCGGTAT-TGGAGGTTATATGG-----	36
cap-UC-1.3_612	-----GATCTCTTACTTTCGCGGGGTAT-TGGGGTTAGTGC-----	37
	1.....10.....20.....30.....40.....50.....	



cap-UC-1.3_466	- - - - - TTGACGGCGGGAAATCTATGGGGGTTTGGGACTATTG - - - - -	37
cap-UC-1.3_851	- - - - - GGATTTTCGCGGGGGGTTGGGCCGA-TATTGGCGGC- - - - -	36
cap-UC-1.3_850	- - - - - GGATTTTCGCGGGGGGTTGGGCTGA-TATTGGCGGC- - - - -	36
cap-UC-1.3_1343	- - - - - CATGGCAGGGGGATTCTTGGGCTATTGGCGGCCTTA- - - - -	37
cap-UC-1.3_608	- - - - - GCGGGGGGATCGCTGGGGATTGGTTCTCTGTATCGG- - - - -	37
cap-UC-1.3_1192	- - - - - TTGGGGTCGCTTGGTCCGGGGCTTTCTCTGT-TCGG- - - - -	37
cap-UC-1.3_614	- - - - - CTGTCGCGGGGACACTGGGGGTTATTGTTCTCTGG- - - - -	37
10-UC-1.3_312	- - - - - TTGGTTTATGCG-GGGGTTATTGTTGTTCAAGTTGCGT- - - - -	37
10-CD-1.3_401	- - - - - TTGGTGTATTCGCTGGGGGGTGTGTTCTCTGACTTGC- - - - -	37
cap-UC-1.3_822	- - - - - TCGGGTCATGGGTTTATGCGGGGGTTGTTCTTCTTG- - - - -	37
cap-CD-1.3_416	- - - - - TTGATCCGGGGTTTGTGGGGGTGGTTGTCTCTGC- - - - -	37
20-UC-1.3_208	- - - - - TTCTCTGCGCTGTCTGGGGGGTGT-TTGCTTTCTCG- - - - -	37
40-OK-1.3_110	- - - - - TTGTGTTGATTCGTGGGGGGGATCTTCCCTTCTC- - - - -	37
cap-UC-1.3_555	- - - - - TGTCTGC-GCC-TGGGGTTGGGGTCTCTTATTCCTGC- - - - -	37
cap-UC-1.3_1261	- - - - - TCTGC-GGTGTGGTGTGGTGTGCTCTTCTGGG- - - - -	37
cap-UC-1.3_740	- - - - - ATGTTCCGTGGTCGCTGG-GT-CTTGGTCGTATTGGCTG- - - - -	37
cap-UC-1.3_1035	- - - - - TTCCCTGTTCTGG-CTGGCTCTGTGGTTTGGCTG- - - - -	36
10-UC-1.3_289	- - - - - TTGCCTGTGTGTTG-TGGTCCGGTAGTTCTCGTTCTGG- - - - -	37
40-OK-1.3_122	- - - - - GTTTT-TGTTTCCGGCTGGGGATTGGTTGTCGTTG- - - - -	37
40-UC-1.3_101	- - - - - GTTTT-TGTTTCCGGCTGGGGATTGGTTGTCGTTG- - - - -	37
cap-UC-1.3_1219	- - - - - TGTTTCGTGTGGCAGGGTATAAGGGGTA-TTGTCTGTG- - - - -	37
40-OK-1.3_71	- - - - - GTGTGTGCTGGTGTGTTATGGTTGTTGTC-GTATTG-GTGG- - - - -	38
cap-UC-1.3_1089	- - - - - ATGTGCTCTGGTGGTGGT-GTTGTCTGTATTGTGTGG- - - - -	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_121	- - - - - TGC GG GTGGTGGGTCAATTGGCAGTATT C - - TCTTG-GTG- - - - -	37
80-CD-1.3_132	- - - - - GGGGTGTT CGGTTGGGGCTTGCAG- - TATTG-GCGTG- - - - -	37
cap-UC-1.3_835	- - - - - GTGGGTGGGGGGATATTGGTCAGTATT - - CGTCG-TTGG- - - - -	37
cap-UC-1.3_799	- - - - - TGGTGTGGCTGGGTGGGTATTG-TTGCATTG- - CGTCG-G- - - - -	37
cap-UC-1.3_392	- - - - - GGGGGAAATGTGTGGGTATTGCGTTCTTCTT - - TGTGGG- - - - -	37
cap-UC-1.3_1231	- - - - - TGTGGGTCTGTGGGGGTATTGCTCTGTTGC- - TGTAG- - - - -	37
10-OK-1.3_510	- - - - - TGCGTGTCTGGGGTTATTGTATT-CTTGTGTATTGGGG- - - - -	37
cap-UC-1.3_676	- - - - - TGCTTGCCGTGCCCTTGTGTTCTT-TCTTCGTGCTGG- - - - -	37
cap-UC-1.3_1041	- - - - - TGTGTGCTGGGGGTGGGTTTCTTGTTCCTCTCGTGTG- - - - -	37
10-UC-1.3_421	- - - - - GCTGTGTGGGGGT-CGTGTTGCTTCCTTGTTCTCTG- - - - -	37
cap-UC-1.3_280	- - - - - CAGTGGGGGTCTCGGGGTTTGGTATTGTTGTTCTCG- - - - -	37
cap-UC-1.3_858	- - - - - CTGCATGTGGGGGCCCTTTG-TCTTTGTTATTGGG- - - - -	37
cap-CD-1.3_288	- - - - - GTGCGGGGTGGGGCTCTTGGTCTTTCTTTCTTCG- - - - -	37
10-UC-1.3_553	- - - - - TTGGTTCTGTGGGTGTTCTCGTT- - TAACCTTTCTGCTG- - - - -	36
cap-UC-1.3_1099	- - - - - TTGGGTCTGCCGTGGGTGTGGTCATTCTTCTGGCG- - - - -	37
cap-UC-1.3_582	- - - - - GTTTGGGGCTGTGG--TTCTGCTTTTTCTTCGG- - - - -	37
10-CD-1.3_748	- - - - - CGTGGGGTCCGTGGG-GTTCTGGCTATTTCGTCTGTG- - - - -	37
cap-UC-1.3_821	- - - - - TCGGGTGTCTGGTTACTCTTGTGCTTTTGAGGGGG- - - - -	37
10-CD-1.3_500	- - - - - TCGGCTGTTGTTAATCTTGTGCTTTTGAGGGGG- - - - -	37
10-UC-1.3_433	- - - - - CGTGGTTGTGGTTCTGTTCTGCTTCTGGGGTGC- - - - -	37
cap-UC-1.3_876	- - - - - CTTCCGGGGGGCTGTTGGT-TATTTCACTTATTGGG- - - - -	37
cap-UC-1.3_338	- - - - - TTAGCGGGGTGTGGTGGGTCTATT CCTCTTTTCG- - - - -	36
cap-UC-1.3_1070	- - - - - GGTGTGGTGTCCCTGGTCTGTTCTTTTCGCAGGGG- - - - -	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_1179	-----TTGGTGTGTTGGTCTTCCTCGTGGTGT-----	37
cap-UC-1.3_394	-GCTGGGTTGTCGTGTTGGGTGT-CGTCTTTCTTGG-----	37
cap-UC-1.3_1203	-TTGCTGGGTT---TGTTGTGGCTTTCGAGTTGTCCCTGGG-----	37
cap-UC-1.3_1306	-GTA G TGCCGGGTGTGTTGA T GTCTCTA T TTGCCTG-----	38
10-CD-1.3_639	-TTTGGCCCCTCGTGTGTTG-TGCTGGTCCATTTCCCGTCG-----	38
20-OK-1.3_173	-CTGCTGTTGTGTGG-GGTTCTT--ACT---TCTTCTGGGGGGG-----	37
10-CD-1.3_524	-GTGTCGTGTCGTGGTCCTT-AATA A TATTGTCTGGGGGG-----	37
cap-UC-1.3_1270	-TCGCGGGG-GGTCTTC-AAT-TATTATCCGGGGCTTT CG -----	37
cap-UC-1.3_225	-TTGGGGTCGTCTGGTTCT-TGTTCTCCTGTCCGGG-----	36
cap-UC-1.3_732	-GGTTGTCGTTCTGTGTCCCTCT-TGTTCTCCTGGTCGGG-----	37
cap-UC-1.3_802	-TGCTGTTGTGGGGTCCCTCTGTGTGCTTCCTTGTGG-----	38
cap-UC-1.3_1292	-GTGGTTTCATGGGGGTTCTCT-TGT-CTTC T GTCTGG-----	37
10-OK-1.3_314	-TCGATTCTCTGGTGTGTTGCTG-TTCGTTGTTGTGG-----	37
10-UC-1.3_388	-TCGATTCTCTGGTGTGTTGCTG-TTCGTTGTTGTGG-----	37
10-CD-1.3_235	-TGGCGTATTCTGGGGTTTTTG-TG-GTCGTTCTTGTGG-----	37
20-OK-1.3_127	-TGCTGTTGTTGCTGTTGTTCT-GTTCTG-ATGGTCTT-GTTGT CG -----	37
T-UC-1.3_79	-GTGGGTTGGTCC T CGTGTCTTTGTGTGTCGTGTG-----	37
40-OK-1.3_138	-TCGTTGTC-TCCGGGTGGTTCT-GTG-CTGTTATTGTGG-----	37
cap-UC-1.3_791	-TGTGGTTGTC C GGGTATTCTT A GTG-GTGT T GGCGTG-----	38
T-OK-1.3_76	-GTTGTTTC A CTGGGTTGTTGCG-GCTTTCTGG-----	37
10-CD-1.3_406	-TTGGGTTGTTCTGGGCTTGTGTTGGG-A-TTGTCTGGTC-----	37
cap-UC-1.3_357	-TGGGGATCTGTGGTTGTTGTGCTGTCGTGCGTGG-----	37
cap-UC-1.3_1191	-TTGGGGTGGTCTCATTG-TGGTCTTGTCC T GC G TTG-----	37
	1.....10.....20.....30.....40.....50.....	



cap-UC-1.3_370	- - - - - TCGCCC GTCT ATGTC CCC CGGTAGCT CTT GTGG TT GGG - - - - -	38
T-OK-1.3_32	- - - - - TTCCCCGGGCTGT-TACTCTGTCGTTGTTGTGTCTGG- - - - -	37
cap-UC-1.3_489	- - - - - CCCCCCGCCTGTGTGTTGC GTTGTGTCTGGTCCCGTG- - - - -	37
cap-UC-1.3_949	- - - - - CCCCCCCCCCTTGTGTTGGATTCTCCG-GTGTGTTCTTGTG- - - - -	36
10-OK-1.3_459	- - - - - TTGGGTCTTGTGTTTGC GTCGCGTGTTCGTATGTGTG- - - - -	37
cap-UC-1.3_502	- - - - - TTT CGCGGGTTTGTGTTTCG-GGGTGATCGT-TCTGTGG- - - - -	37
T-OK-1.3_93	- - - - - TTT CCTTCTGCGGGTATTGTTGGTGTGTGTTCTC- - - - -	37
40-UC-1.3_211	- - - - - TGTCTGTCTGTTGGGTCTTGTGTTGGG- - - ATTCTGGTCTTC- - - - -	37
cap-UC-1.3_1153	- - - - - GGTCTGTGT CGTTCGCTGGGTCTATGTTAGTTCTGGC- - - - -	38
cap-UC-1.3_332	- - - - - TTGCGGGCTCTGTGGGTTCTGTCTGGGTTACTCGTGG- - - - -	37
40-OK-1.3_155	- - - - - TTGTGGTTTCTGTGG-TGGTTTTGTGTCTCT-TCTGATG- - - - -	37
40-UC-1.3_82	- - - - - TTGTGGTTTCTGTGG-TGGTTTTGTGTCTCT-TCTGATG- - - - -	37
cap-UC-1.3_1171	- - - - - TTGTGGGTTTTGTGC-TGGTTTTGGATCTGTATCTGGG- - - - -	37
40-OK-1.3_194	- - - - - TCTTGTGATTCCCCGTT-GCGTTTTGG-CGGTTGTTGG- - - - -	37
cap-OK-1.3_127	- - - - - TCCTTGTGATTCCCCGTT-GCGTTTTGG-CGGTTGTTGG- - - - -	37
cap-UC-1.3_916	- - - - - TGTCTGTGATTGCCCTTC-TCGGTTTG-CTGT-GTTG- - - - -	37
cap-UC-1.3_506	- - - - - TTGTGGTTATTCTGCGTT-CGGTGGTGG-CTGTTTTTG- - - - -	37
cap-UC-1.3_549	- - - - - TGTGTGTCTCTCGTGGGTGTTACT-T-TGTCTGGTTG- - - - -	36
cap-UC-1.3_1282	- - - - - GTTGTGTTCTCGTGG-TGTTATGG-TGTCTGTTGTG- - - - -	37
cap-UC-1.3_1013	- - - - - TTTGTGGGTT-TGGTG-TGGTACTCTGTCT-TGGTCTG- - - - -	37
80-CD-1.3_137	- - - - - TGTGGTGT CGCTGGTG-TGGTATTGTATCTGGTTTG- - - - -	37
10-OK-1.3_185	- - - - - TCGCGGTGTTGTG-TGGTTCCT-TCCCTGGTTGGTTG- - - - -	37
10-UC-1.3_399	- - - - - GTGTTGTCTTTG-TGGTTCCGTGGTTGTTCTGG- - - - -	37
	1.....10.....20.....30.....40.....50.....	

cap-UC-1.3_446	- - - - - TCGTTCTTGTT -- GGTTCTTGTCCTGTGTTGGG - - - - -	37
T-OK-1.3_125	- - - - - GGCTGTTTGCCTC -- TGGTGCTCGTGTGTTGGT - - - - -	37
cap-UC-1.3_1201	- - - - - TTGGCATGTGTTGTC -- CGGGATTTTCGTTGGTGGC - - - - -	37
cap-UC-1.3_1358	- - - - - TGTGTGGGTTATGTTGTC -- GTTTTTTTGGGTGGTTG - - - - -	37
10-OK-1.3_346	- - - - - CTGTTGCTTC-GGTGTTCTGCTGGGTTGGTTGTG - - - - -	37
cap-UC-1.3_792	- - - - - TGTGGCTTACTGGGGTTTCTTCGTCTGTGGTTGAG - - - - -	37
20-UC-1.3_155	- - - - - TGTGGGGTTTTT-CGGGG -- GGTGCTTCATTGTTGTG - - - - -	37
40-UC-1.3_41	- - - - - TTCGTGGGGCCTAGTGCCTGG -- GGTG-TTCTCTGTTGTG - - - - -	37
10-OK-1.3_585	- - - - - CTCTTGTGGCTTTTCCGGGCT -- GGTTCTCGTGGTTG - - - - -	37
10-OK-1.3_630	- - - - - AGGTGTTTCCCCCCC -- GCTGTTTCGTTGATGTG - - - - -	36
cap-UC-1.3_351	- - - - - TGTTTGTGCCCGCC -- GCGTTTTG -- GTTGAATTGTGG - - - - -	37
cap-UC-1.3_973	- - - - - TTGTGCCGTGTTCCGCG -- TGTGCTTAT -- TTGGTTTG - - - - -	37
cap-UC-1.3_761	- - - - - TTGGTGCTCGTTGGTTTCTTCTCTGGCTTGGTGG - - - - -	37
cap-UC-1.3_1068	- - - - - GTCGTGCTCCATGGTTGTGTCCTCCTT-TGTGTTGGG - - - - -	37
40-UC-1.3_96	- - - - - TGTTCATTGCTTCATTCTTGCTGGTTGTGG - - - - -	35
cap-UC-1.3_731	- - - - - GTCCCCCTGT-TGTGATTCAATTCTGGCTGGTTGTG - - - - -	37
cap-UC-1.3_941	- - - - - GGCCCCCTGT-TCTATGGT-TCCCGCTGTGTTGGTGT - - - - -	37
cap-UC-1.3_1080	- - - - - CTGCGGGGTGTTCTGTTCATGGTGTTGGTGTG - - - - -	37
cap-UC-1.3_1246	- - - - - TGGGTGTTGTTAATTCTTCGGGTGGGTTGTGGC - - - - -	37
10-OK-1.3_345	- - - - - GAGTTCCCCCGGCTGTTCGTGTCTTGGTCTTGGTGG - - - - -	38
40-CD-1.3_150	- - - - - GAGTTCCCCCGGCTGTTCGTGTCTTGTCTTGGTGG - - - - -	38
cap-UC-1.3_898	- - - - - TTTGCCCGGTACGTTCGGTTGTTGCTCGTGTGG - - - - -	37
cap-UC-1.3_617	- - - - - CTCCCTTGTCTGTTGCTTGCCTCGTGGTTCGTTG - - - - -	38
	1.....10.....20.....30.....40.....50.....	

10-CD-1.3_468	- - - - - TGTCCCCGGGCTGTGGTCTGTTGTGT -- TTGGTCGCCTG - - - - -	37
10-OK-1.3_248	- - - - - TTGGTGTGTTCTGCCGGTTGAATGTTTTTACGTGGG - - - - -	37
cap-UC-1.3_526	- - - - - TTGGGTATGGTCCCCGGGGATGTCCTTGTCTTCGTGG - - - - -	37
cap-UC-1.3_879	- - - - - TTGTGTGGTCCCCAG -- TGGCTTTTCTTCGTGGTCGG - - - - -	37
cap-UC-1.3_510	- - - - - TTGTGCGTTCCCTGGG -- TGCCGTTCTTGTTGGGGTC - - - - -	37
cap-UC-1.3_1065	- - - - - GTGTCTTGCCTCCG -- TGTT - TCGTTCTGTCGTGTGTG - - - - -	36
10-OK-1.3_619	- - - - - TGGTATGTTTCCGGGGTCGAGG - TATTGGATAATTTCG - - - - -	37
cap-UC-1.3_1278	- - - - - TATGCCCTTCCGGTTCTGTGT - TTTTGGGTTCTTCGTGG - - - - -	37
cap-UC-1.3_471	- - - - - TCCGTTTCTGGCTGTCTG - GGGTGT - ATTGCTTATG - - - - -	37
cap-UC-1.3_952	- - - - - ATGTTTCTGGCC - CCGG - TGTTGG - TTGTGCGTATTGC - - - - -	37
10-UC-1.3_502	- - - - - TTCTCTCCGTGGTGTGCGT - TCTGGGGTTGTCTGTGC - - - - -	37
cap-UC-1.3_1072	- - - - - GCTTCCTGTCGTGT - TCGCGTGTCCCCGGTTGT - TGTGG - - - - -	37
40-UC-1.3_50	- - - - - ATCGTCTGGTTGTCGCGCTGGTATTG - GGTTCTCTGC - - - - -	37
cap-UC-1.3_250	- - - - - TCGTCTTCGGTCCCCGG - GGTGTTGTGGTGCTCTGG - - - - -	36
40-UC-1.3_261	- - - - - GTGTTGC - GCTTTCTCCGGGTTGTCT - TTGGGTGTAG - - - - -	37
cap-UC-1.3_1323	- - - - - CTTCGTTGC - GTCCCCCGGTTGTGTGTTCTGGGTG - - - - -	37
20-OK-1.3_169	- - - - - GTCTCGTGGTTGTGGGT - CCCGGTGTGTTTGTGTG - - - - -	37
40-UC-1.3_222	- - - - - GTCTGG - GGTCTGGTC - TCTCTCGTT - TTGTATGGTGGT - - - - -	37
40-UC-1.3_422	- - - - - TTGCTGGGCCCGAGG - TATTCTGTATTGGTTTGTCG - - - - -	37
cap-UC-1.3_806	- - - - - TCGGGGGGCCCGGC - TATCTCTCTCTGTGTTGTGG - - - - -	37
cap-UC-1.3_846	- - - - - GGTGGTCCC CGGT - TGTGCCTTTCTCTGGTTGTGG - - - - -	37
cap-UC-1.3_918	- - - - - TGGCCCCCGCTGTCT - TCTGTGTCCTGAATGGTGG - - - - -	36
40-OK-1.3_15	- - - - - TAACGTCTGGGGCCCCGGTATTGGTCTATGTCTCG - - - - -	36
	1.....10.....20.....30.....40.....50.....	

40-UC-1.3_100	-T-A-C-G-T-C-T-T-G-G-G-G-C-C-C-G-G-T-A-T-T-G-G-T-C-T-A-T-G-T-C-T-C-G-	36
cap-UC-1.3_1189	-T-T-G-G-T-A-A-T-A-C-G-G-C-T-G-G-G-G-C-T-A-T-T-G-G-T-C-G-T-A-G-T-C-	37
cap-OK-1.3_39	-T-T-G-C-C-G-G-G-T-A-C-C-T-A-T-T-G-T-T-C-G-T-C-T-C-C-T-G-T-C-T-G-T-G-G-	37
cap-UC-1.3_1207	-T-T-G-C-C-G-G-G-T-A-C-C-T-A-T-T-G-T-T-C-G-T-C-T-C-C-T-G-T-C-T-G-T-G-G-	37
cap-UC-1.3_530	-T-T-G-G-G-G-C-C-T-G-G-T-G-G-T-T-C-T-C-C-G-T-T-T-C-T-G-T-G-G-T-G-G-T-	37
T-OK-1.3_121	-T-T-G-C-T-T-C-C-T-G-G-C-G-G-C-C-T-T-G-T-T-T-C-T-A-T-T-G-T-G-T-G-T-G-	37
80-OK-1.3_46	-A-T-C-C-C-C-C-G-G-C-G-T-C-G-T-T-T-G-G-T-G-G-C-A-T-T-T-G-T-T-T-G-T-G-	37
80-UC-1.3_89	-A-T-C-C-C-C-C-G-G-C-G-T-C-G-T-T-T-G-G-T-G-G-C-A-T-T-T-G-T-T-T-G-T-G-	37
cap-CD-1.3_585	-G-T-G-C-C-C-C-C-C-G-T-C-G-T-G-T-G-T-G-T-G-T-G-G-T-T-A-T-T-G-G-A-G-T-T-G-T-T-G-	35
40-UC-1.3_432	-C-C-C-C-G-C-T-C-C-C-T-G-T-C-G-T-C-G-T-T-G-T-T-T-A-C-T-T-T-G-T-T-T-G-C-	38
cap-OK-1.3_93	-G-T-C-T-C-A-T-C-C-C-G-C-T-G-T-C-G-T-A-T-T-G-G-T-T-A-T-C-C-G-T-T-T-T-C-	37
40-UC-1.3_134	-G-G-C-C-C-C-G-T-C-A-T-C-G-A-G-T-C-C-T-G-T-A-C-T-T-T-A-C-T-G-T-T-C-G-	38
40-UC-1.3_224	-G-G-T-C-C-G-C-G-G-C-T-T-G-T-G-T-C-T-C-T-G-T-C-T-G-T-G-C-T-G-G-	38
40-UC-1.3_336	-C-G-T-C-C-C-C-C-T-G-G-T-C-T-T-T-T-A-G-T-G-C-T-T-C-G-T-A-T-G-T-T-G-G-	37
20-OK-1.3_46	-T-T-G-G-T-G-G-G-T-C-C-T-G-T-G-T-G-G-T-T-C-C-G-T-T-G-C-T-G-C-T-G-T-	37
40-OK-1.3_195	-T-A-T-G-A-T-T-C-C-T-T-G-G-C-T-T-G-T-C-T-G-T-G-T-G-G-C-G-C-T-G-T-G-	36
cap-UC-1.3_60	-T-G-G-T-T-C-C-G-T-G-G-T-C-A-T-T-G-T-G-T-T-C-C-G-T-G-C-T-G-G-G-T-T-T-G-T-G-	37
cap-UC-1.3_1064	-G-T-G-T-G-T-C-C-G-G-G-G-A-T-A-T-T-G-G-T-T-C-C-T-A-C-T-A-A-G-T-G-T-G-T-G-	37
40-OK-1.3_125	-C-G-T-C-C-A-C-C-T-T-C-G-C-G-T-T-A-T-G-T-T-G-T-C-T-G-G-A-T-A-C-T-T-G-G-G-	38
40-UC-1.3_107	-C-G-T-C-C-A-C-C-T-T-C-G-C-G-T-T-A-T-G-T-T-G-T-C-T-G-G-A-T-A-C-T-T-G-G-G-	38
cap-UC-1.3_939	-G-G-G-C-C-A-C-C-C-T-T-C-G-T-T-A-T-G-G-G-T-C-T-G-C-A-T-A-G-G-G-	37
80-OK-1.3_212	-A-C-C-C-C-C-T-T-A-C-C-A-C-G-A-T-C-G-A-T-G-C-A-T-T-T-T-G-G-A-C-G-C-G-G-C-	38
40-UC-1.3_404	-C-C-C-C-C-T-C-A-G-A-A-C-G-G-A-T-A-C-C-C-G-C-T-A-T-T-G-G-A-C-T-C-T-G-C-A-	38
	1.....10.....20.....30.....40.....50.....	

80-UC-1.3_88 -----CC1ACCGCTCGAGACATGAGACGTTAATTGCCCGGAG----- 38
40-UC-1.3_339 -----AACCCACCCGTCGGTCCACAATTCTTTTCTCGCTA----- 36
40-CD-1.3_123 -----TCTCACCCAAACCCCCAGACCGATATCTTCTCCCGATCA----- 38
40-OK-1.3_252 -----ACCTCACCAAACCATTACACATAACGTGGACGGATCTA----- 38
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