

Supplemental Information for DNA Aptamers That Inhibit Binding to Human Interleukin-17A and Interleukin-20

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Supplemental Experimental - Dimethyl Sulfate (DMS) probing

5' TAMRA-labeled 10CZ1 was incubated with increasing concentrations of IL-20 in appropriate binding buffer for 1 h at room temperature. 200 μ L of the resulting solution was then treated with 5 μ L of 10% v/v DMS at room temperature for 5 min. Reactions were quenched with 50 μ L of a stop solution containing 1.5 M sodium acetate (pH 7.0) and 1 M beta-mercaptoethanol. Following ethanol precipitation, the methylated aptamers were treated with 1 M piperidine at 95 $^{\circ}$ C for 10 min. The resulting cleavage products were analyzed via denaturing PAGE. Changes in cleavage patterns were determined by quantifying band intensities using Image Lab (Bio-Rad, Hercules, CA, USA) and comparing to the band intensities for cleavage of the folded aptamer without added IL-20.

Supplemental Discussion - DMS Probing Analysis

In comparing the DMS cleavage patterns between folded 10CZ1 in the presence and absence of its IL-20 target, we observed pattern differences were localized to nucleotides 1 – 40 and focused our analysis on this region of the aptamer. Secondary structure prediction (shown in Figure S5) indicates nucleotides 41 – 100 can form a rather stable structure dominated an extended paired region with two loops. In future work, this region can likely be shortened. Our probing studies indicate that upon binding of IL-20, the region of the aptamer from A6 (As are also susceptible to DMS modification and cleavage, but to a lesser extent than Gs) to approximately G20 become less prone to cleavage, indicating protection from IL-20 binding. This is concurrent with the region containing G26 to approximately G37 becoming more prone to cleavage. We hypothesize that IL-20 binding disrupts the proposed structure and opens G26 – G37, with IL-20 interactions occurring with A6 – G20.

Table S1. Buffers used during SELEX

Selection Buffer	Composition
Binding buffer CS/CY	10 mM CaCl ₂ , 1X PBS pH 7.4 , 0.02% Tween 20
Binding buffer CT/CZ	10 mM MgCl ₂ , 1X PBS pH 7.4 , 0.02% Tween 20
Binding Buffer CW/DA	10 mM CaCl ₂ , 20 mM Tris pH 7.4, 5 mM KCl, 0.02% Tween 20
Binding Buffer CX/DB	10 mM MgCl ₂ , 20 mM Tris pH 7.4, 5 mM KCl, 0.02% Tween 20
PBS Elution Buffer	1X PBS pH 7.4, 3.5 M urea, 10 mM EDTA, 0.02% Tween 20
Tris Elution Buffer	20 mM Tris pH 7.4, 3.5 M urea, 10 mM EDTA, 0.02% Tween 20

Table S2. Sequencing results for cloning of IL-17 Aptamer Selections CS and CT

	GAACTAGATCGCAGC - Random Region - GGATCGAGGTAATCC
9CS2	CCAACCGGTGACGCACAGTTAGCAACGAATCCCCTAGCCTCGATATGACAGTCATACCCGTGCGATGTGG
9CS3 ^a	CTAATGCCCCGTACATAGCCACGCATACTGTTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTG
9CS5 ^b	CCACAGCATCACCGTCTATCCGGCAGTGACACTTGAACCTTGCCCTTTTCCATCTTGTG
9CS6	CCCACGAGGGTTTATCTCCTACGTGCAACAAGTCCACTATAGGATCAGAGATGAGTTTGGTCGTGCAGTG
9CS9 ^c	CCACGGGAGACGCATTAAGCCGATTCACTATCCCTACCCGTGGGACCGATCTAGGACCGGTGAGTGTGTG
9CS11	CCACCAACCAAGGACCATAAGCAGGTCCAAC TAGGGCGGGCGATAGACAGCGGCACTGTTGTG CAGTTGGG
9CS12	CCCAGCAGGTTAAAGTGTAAGTAGCAACCAAAGGATACGATGTTTCTGGTAGTCCCTCGCCTCTCGGTG
9CS14a ^d	CCACACACAATAGTCCGCTGCCACGAAACAGACCTAATGTCGTTTATAACGATTATATGTAGCTCCGTGG
9CS18	CCCACGCACCGCGGCCTCACTGACATTATCTCTAAACCAGTTGACTAAAGCACCGTGCATTCACCTTGG
9CS19b ^d	CCACGGCGGGACCCGCTAGACGGCAGGGGACTCTTGAACATATCCGTCTGACCGGTGTGGGG
9CT1 ^e	CTAATGCCCCGTACATAGCCACGCATACTGTTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTG
9CT2	CCCCCGGGTCACCGTTATAATCCGCTATCCAAAACCCGATTGACGTA CTGCTATTGAAGCCGGGAGCGTG
9CT3 ^{b, f}	CCACAGCATCACCGTCTATCCGGCAGTGACACTTGAACCTTGCCCTTTTCCATCTTGTG
9CT6	CCCAGGGACGAGTATGGCGACATGGGATGGCACTAGTCGGTTGTCCAAACACGTTGATTTGTCCCGGTG
9CT11	CCAAGGTGTTAAGAGGCGTGTGCTGGAACCTCGTTCCATCACCGGAGGTTTTGACAAGACACTCTGTTGG
9CT12	CACATCATATGAGTCCCATTCGGCAGTGA CTCTTGAACGCCGGGTCTTGATTGTGCTG
9CT13	CCACGGGAGACGCATTAAGCCGATTCACTATCCCTACCCGTGGGACCGATCTAGGACCGGTGAGTGTGTG
9CT17	CCACAGCATCACCGTTATCCGGAGTGACACTTGAACCTTGCCCTTTTCCATCTTGTG
9CT18	CCACAGTCACGACATCGCTTCGTGACATCACATACGTGATTTCACTACAATTGCTCCGTTTACCCCTTGTG
9CT19	CCACCGACACACACCGTATATCCCTAGCCCCACATGAGGCCATCTCGCAACTGGACGTTGCTTCTGGG
9CT20	CCTGTACATAGCCACGCATACTGTTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTG
9CT21	CACACCAGTATAGGCCACAGTTGTGCTATACGAGATAAACCTATGCCACATTCCAACGTTCTCGCGTGTGG

^aSequence was found in 10 additional clones (9CS4, 10, 13, 14b, 15, 16, 19a, 20, 21, and 22)

^bSequence found in CS and CT clones

^cSequence found in 1 additional clone (9CS17)

^dPlasmid contained more than one insert with different sequences, designated a and b.

^eSequence found in 1 additional clone (9CT16)

^fSequence found in 3 additional clones (9CT7, 14, and 15)

Table S3. Sequencing results for cloning of IL-20 Aptamer Selections CY and CZ

	GAACTAGATCGCAGC - Random Region - GGATCGAGGTAATCC
10CY1	CACCGGCGGAAGTGCGAAATCTGGGTTACGCAGGCACTCCTACGTCTCTCTCCCGACTGCGTTCGAGGTAACCTTGG
10CY2	CACACACGCCAGCCGACGACTCCACTTAGCTATACCAATATCTCAGCAAGTTAACGTACTACGCGGTCCC
10CY4	ACGACGCGCTTACTTTTTACGATTATGAATGCCGCTAAATACTCCGCTGTCGCGTACTGCGGAAGCGCCCG
10CY5	CGCGGGAATAGTGGCTAATACCGGGTGTATGCGACTGATGTATGCCCCGTGTACGGAAGGTCGGCGTTGTG
10CY6	ACGACGCGCTTACTTTTTACGATTATGAATGCCGCTAAATACTCCGCTGTCGCGTACTGCAAAGCGCCCA
10CY7	CACGGGAATAGGGGCTAATTCCGGGTGGAAGGCACTCAATTTGCCCCACGTACAAAGGTCGGCGGTCC
10CY8	ACCCATTGGAGTAATCCACAGAAATTCGCGGCCACCTATTTATTCGGAGCCGAACACTTCTTCCTTGCCT
10CY9	CACCCACAATCGATAAGATCTTACCTACCGACAAAGCGGTACACCAGGTATCTTGCCCTCTGCC
10CY10	CTAATGCCCGTACATAGCCACGCATACTGTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTG
10CY11	ACCACGGCCGACCATGTACAGGCGATAAACCTTCAATGTCACCTACGAGGACCGGGAACACTACTAATATG
10CY12	CCCCACAGTGTGATCTAACCCGCCGCTTCCAGGAACCACATAGATGATAAGAGTTTCCCGCTGCCCGCC
10CY13	CTAATGCCCGTACATAGCCACGCATACTGTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTG
10CY15	CCCACAGCAGCCCTTGTTCCTGACTGGGGACGAGTCAAGAATTGAAGGCCTGAGTCAGTTCCCTATCCGTGTG
10CY16	CCACGACACTATCTAGCAACTAAATGACCGACCTAAACAACCGTGTGGAGCCGTTCTCCTTCCGATATG
10CY17	CCACGGGAGACGCATTAAGCCGATTCACCTATCCCTACCCGTGGGACCGATCTAGGACCGGTCAGTGTGTG
10CY18 ^a	ACGACGTTTTCTTATACTTATCCTCCCGGGTAGTGATGCTTACCGTTCAGAGGATTGTTGGGCCACGT
10CY19	CACACCCCGACTCCCCAGATTGAAGTCTGTAGTATGTTATGACAGTGTAATCGTCTCATGGTTAGCCGT
10CZ1	GGCAGCACACGTCCAGTGTAGGCGTCATCCCTCTATCCAATCGTCGTTACAGCATTATCATGGGTTGTG
10CZ2	CCAACACTCAGTAATGGTACGTAGCGGCACGCTAAGTGAGTAAGTACATTAGCTGTTTACCTCCAGTGTG
10CZ4	CTAACGCCCGTACATAGCCACGCATACTGTTTTCTAATAAAGCTCCTCGAGGTGAACCGTCGCTGGGTG
10CZ6	CATGTGGGTTTTCTCTGAAGCAACCCATCCGATCTACCTATAATTCTTTGACTAAATGAAGTTCGCCCGG
10CZ7	CAGAAGTGGCTCGTGCTTAGTCTACCAGTGAATGTGAGATTATAGTACCGTCTACTTGGCCGTCCC
10CZ8	CTAATGCCCGTACATAGCCACGCATACTGTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTG
10CZ9	AGGGCAAAAATAGGTTTATCCGTAAGTCAACTAAGTTATAATTTCTCCGTTAGTAGGTGGGAACTTTCA
10CZ10	CTAATGCCCGTACATAGCCACGCATACTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTG
10CZ11	CCACAGGCTCAACATTCAATCCGAACGAAACCTTCCTAAGTGCATCTCTTGGCGTCAACTGCGGCC
10CZ12	CAAGCGGTGACCATGTTGGTTGGAGCTTCTTACCGCGTGTACCAGTGTGTATCTGGTCTGGAGCATGG
10CZ13	CTACCCCGTCTGGAGAGTTTTTTCAGCATGGTTACACAATACGTATAACAGCTTCCCCAGCGGGTTGCC
10CZ14 ^b	CAGAAGACAGCATTTAGTACATTGGAGCAGTCGGCCAGTTATGTAGATTCAACCATCAGTAAACGCTC
10CZ16	ACCACACTACAACGTAGCCTACAGGGCCAAAGTATAGCCATGCCGTCCGATTCGGTCTGCTTACCCC
10CZ17	CAGCAGGTATAGGTATCACTGACAGCTATTCGCGCACTAAGGAAGTTACAGCATTTATATGACGCACCCC
10CZ18	CACACCCGAGGCTACAAATGAGACAGGGTGGCAATATCCAGAAGTGTGGTGATACATTGCAGCCTAGG
10CZ20	CCACGGGAGACGCATTAAGCCGATTCACCTATCCCTACCCGTGGGACCGATCTAGGACCGGTCAGTGTGTG

^aSequence was found in 1 additional clone (10CY20)

^bSequence was found in 1 additional clone (10CZ19)

Table S4. Sequencing results for cloning of IL-20 Aptamer Selections DA and DB

	GAACTAGATCGCAGC - Random Region - GGATCGAGGTAATCC
10DA1	ATGCACGCACATGATAAAGCCCGAGGACGTATTAATGATGTGGAACCGGGAATTTGTTACAACGGCTGGG
10DA4	CCGCGCTCTCCGATCGGCGCCGTGAATAACGACGAAACCCGAGTCTTTGGGTCGAGACGTTAAGCTCGGTTCTAT
10DA6	CCGCGGATCGCTTTTGGCTAGCTGTAGCTCCGCGGAACAGCGTCTGCTTAGGGGATCTAGGCCGGGGTG
10DA7	CACCACAGTTACCGATCGACATTCCACTTGACACTCCCCCTGTATCCCGTGTGCTCCACTCGTCCTGGTG
10DA9	CACAGCACGTCCACCAGACATAAATAGTCACCAAGGAGGTCCATACGATTCGCAAGCCCAGCATTTGTCCG
10DA10	CTCCCCTGGACCTAGGGATTGCGAGGTGAATGATCTGTAGTAGCTCGTACGACGCGAGCTTATTGGCGTGA
10DA11	CACGACACCTACCACACCTTATCTCACCGTTTATTCTGATCAGCTCTCAACCAGCATGCCCGGCTATCG
10DA13	CACCAGGGTATGTAAACGGCGAGCTGAGATATCAACGGACAATTAAACATTGATGCGACTCACCCATGCA
10DA14	CACAACTACGTGATCAACGAGGAAATATAAGCAAATAGACGGAAATTCAAACTAAATCAGACTTAGTCCC
10DA16	CACAGCATCGAGGGGGTAAGACCCACGTCACAGTAACTCATGGAACCTCACACAATGATCTCCCGTCCC
10DA17	GAGCAAAGTCTAAGAGTTTCACCATGGCGGACCCCACTCACTACTCGAATATTAACCCGAGCGTATTCTCCTGCC
10DA18	CCACCCGCATAGCGCAGCATACGAACCCCGAGGATCGATACAACGGGGCTACGACATAAAGTACTATTAG
10DB1	CGGCACGAACACGATGTTCCCTCGTTAGTTTATTAGTCCGACACGAGGGCTCGCCCCGTACTATGGTCCAGTG
10DB2	CGGCACGAACACGATGTTCCCTCATTAGTTTATTAGTCCACACAGGGCTCACCCCGTACTATGGTCCAGTG
10DB5 ^a	CACACAGAACAACCTGAATACGAGGGCCGGTCCCGTATTAAATCCCTCGAGTGTGTAGATCACGATTAC
10DB6	CTACCGACAACGCACCGTCAACCAATGAATTATCCGATTCCATTCACCTCTTTGTAGACGACGTCCCC
10DB7	CCAGCGCGCGGGAACGTCATGTAAGTGTTCCTCAATCTACTAACGGATATACTTTTCGTATACGGACCAG
10DB8	CCAACCGGGTAACTAATCATGAAGAATTCGAATGCTATAACGGAGAGTCTGCCGATCACGTCGTGCTT
10DB9	ACGCAGTTACACCTCACATATTGTTCAAACCTCCACATCGTTCACCAGAACTCGCCAGTTCCTCCGGCAT
10DB10	TATACTCGCCTACGAAAAGTAAATTTTCATCACCACTTACGATTCGGGCGAACCTCACGTACATTGGGGC
10DB13	CAAACGCCACGATACCCACTATAAGTCGCCGGCCTCCCAATCAACGCCGCACGACGCTCTATACTCCCCAG
10DB14	CCACACCTACTACAGCCGTCTAAAGACACACATGGGTGAAATTCAGACACCGGGCGCCACCCCTGCGGGGGC
10DB15	CCACACACTATGAACCTAGCGGCCGTGTCTATTACGGTGCCCGAGCTCTCTCGTACTACGGACTGCCCGAGTCTCA
10DB16	CAGTAACCTGCATTTGTGAACTAAACATGCCGAGCATAGCGGATACTGTGGTCACTGTTGCCACAGTAGG
10DB17	GGAACCGGCCACCCAAATCGATTGGAAGGTCAGATCTGTGGAGGAATATGAGGGCTGCGAACGCAATAG
10DB18	CGAGCTCCCTAGTGCACATCTACACCATGTCAATACGACCTCTGCGTGTAGTTAATAAATGATCGACTA
10DB19	ACCACGACCGGCAGTGTACATCGGAGCTTAATAAGCTCTCTTCGAATGGTAATTACTATTACGTCAGTAC
10DB20	CAGCCGTGACAAACCTTCTCTGTAAACTCCCGGTCTAGTTCCTAGACACTTCGCCATTAGCTAGTG

^aSequence found in 1 additional clone (10DB11)

Table S5. Initial binding assays for IL-17 aptamer sequences

Sequence	Wash	Elution
9CS2	4	96
9CS3	7	93
9CS5	2	98
9CS6	6	94
9CS9	5	95
9CS11	6	94
9CS12	7	93
9CS14a	13	87
9CS18	2	98
9CS19b	10	90
9CT1	24	76
9CT2	37	63
9CT3	38	62
9CT6	31	69
9CT11	45	55
9CT12	15	85
9CT13	31	69
9CT17	45	55
9CT18	43	57
9CT19	30	70
9CT20	51	49
9CT21	46	54

Table S6. Initial binding assays for IL-20 aptamer sequences

Sequence ^a	Wash	Elution
10CY2	57	43
10CY5	24	76
10CY6	29	71
10CY7	21	79
10CY9	31	69
10CY10	43	57
10CY11	43	57
10CY12	35	65
10CY13	39	61
10CY16	27	73
10CY17	32	68
10CY18	30	70
10CY19	79	21
10CZ1	16	84
10CZ4	46	54
10CZ6	24	76
10CZ8	33	67
10CZ10	43	57
10CZ12	49	51
10CZ13	31	69
10CZ14	60	40
10CZ16	53	47
10CZ17	45	55
10DA1	78	22
10DA6	23	77
10DA7	5	95
10DA10	31	69
10DA11	24	76
10DA14	21	79
10DA16	26	74
10DA17	39	61
10DA18	17	83
10DB1	32	68
10DB7	51	49
10DB8	65	35
10DB10	40	60
10DB13	23	77
10DB14	58	42
10DB15	33	67
10DB16	36	64
10DB17	29	71
10DB18	32	68

^aClones that were sequenced, but not included in table failed to produce sufficient PCR product for testing.

Table S7. Oligonucleotides used for fluorescence polarization studies

	Sequence
9CS2	GAACTAGATCGCAGCCCAACCGGTGACGCACAGTTAGCAACGAATCCCCTAGCCTCGATATGACAGTCATACCCGTCGCATGTGGGGATCGAGGTAATCC
9CS3	GAACTAGATCGCAGCCTAATGCCGTACATAGCCACGCATACTGTTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTGGGATCGAGGTAATCC
9CT6	GAACTAGATCGCAGCCCCAGGGACGAGTATGGCGACATGGGATGGCACTAGTCGGTTGTCCAAACACGTTGATTTGTCCCCGGTGGGATCGAGGTAATCC
9CT19	GAACTAGATCGCAGCCACCCACACACACCCGTATATCCCCTAGCCCCACATGAGGCCATCTCGCAACTGGACGTTTCGCTTCTGGGGATCGAGGTAATCC
9CT20	GAACTAGATCGCAGCCCTGTACATAGCCACGCATACTGTTTTTCTAATAAAGCTCCTTGAGGTGAACCGTCGCTGGGTGGGATCGAGGTAATCC
9CT21	GAACTAGATCGCAGCCACACCAGTATAGGCCACAGTTGTGTATACGAGATAAACCTATGCCACATTCCAACGCTTTCGCGTGTGGGGATCGAGGTAATCC
Aptamer 1 from Ref 15	GCTGTGTGACTCCTGCAACTGGATTGTATGATCTGTCAGGAGCACCGTCTGAGGGTACACACGCCTATGACCTGTGCAGCTGTATCTTGTCTCC
Truncated Aptamer 1 from Ref 15	ATACAACCTGGATTGTAT
Aptamer 2 from Ref 15	GCTGTGTGACTCCTGCAATTAACCTGTTTTCTTTTTGTTTTTATGTTGTTGGCTTTTTCTTTTTGCAGCTGTATCTTGTCTCC
Truncated Aptamer 2 from Ref 15	CGACTAACTGTTTTCTTTTTGTTTTTAGTCG
10cy7	GAACTAGATCGCAGCCACGGGAATAGGGCTAATTCCGGGTGGAAGGCACTCAATTTGCCCCACGTACAAAGGTCGGCGGTCCGGATCGAGGTAATCC
10Cz1	GAACTAGATCGCAGCGGCAGCACACGTCCAGTGTAGGCGTCATCCCTCTATCCAATCGTCGTTACAGCATTATCATGGGTTGTGGGATCGAGGTAATCC
10DA7	GAACTAGATCGCAGCCACCACAGTTACCGATCGACATTCCACTTGACACTCCCCCTGTATCCCGTGTGCTCCACTCGTCCTGGTGGGATCGAGGTAATCC
10DA14	GAACTAGATCGCAGCCACAACCTACGTGATCAACGAGGAAATATAAGCAAATAGACGGAATTCCAAATAAATCAGACTTAGTCCCAGGATCGAGGTAATCC
10DA18	GAACTAGATCGCAGCCACCCGCATAGCGCAGCATAACGAACCCCGAGGATCGATACAACGGGCTACGACATAAAGTACTATTAGGGATCGAGGTAATCC
10DB13	GAACTAGATCGCAGCCAAACGCCACGATACCCACTATAAGTCGCCGGCCTCCAATCAACGCCGCACGCACGCTCTATACTCCCCAGGGATCGAGGTAATCC

Table S8. K_d values for aptamers determined by fluorescence polarization

Aptamer	Target	K_d
9CS2	IL-17	4.2 nM
9CS3	IL-17	9.9 nM
9CS6	IL-17	ND ^a
9CS9	IL-17	ND
9CS18	IL-17	ND
9CS19b	IL-17	ND
9CT3	IL-17	ND
9CT6	IL-17	12.5 nM
9CT11	IL-17	ND
9CT19	IL-17	5.3 nM
Aptamer 1 from Ref 15	IL-17	ND
Truncated Aptamer 1 from Ref 15	IL-17	ND
Aptamer 2 from Ref 15	IL-17	3.1 nM
Truncated Aptamer 2 from Ref 15	IL-17	2.5 nM
10CY7	IL-20	0.3 μ M
10CZ1	IL-20	0.1 μ M
10DA7	IL-20	>1.3 μ M
10DA14	IL-20	>22.0 μ M
10DA18	IL-20	0.2 μ M
10DB13	IL-20	1.0 μ M

^aND = Not determined. In these cases, aptamer binding curves were not consistent with single binding events.

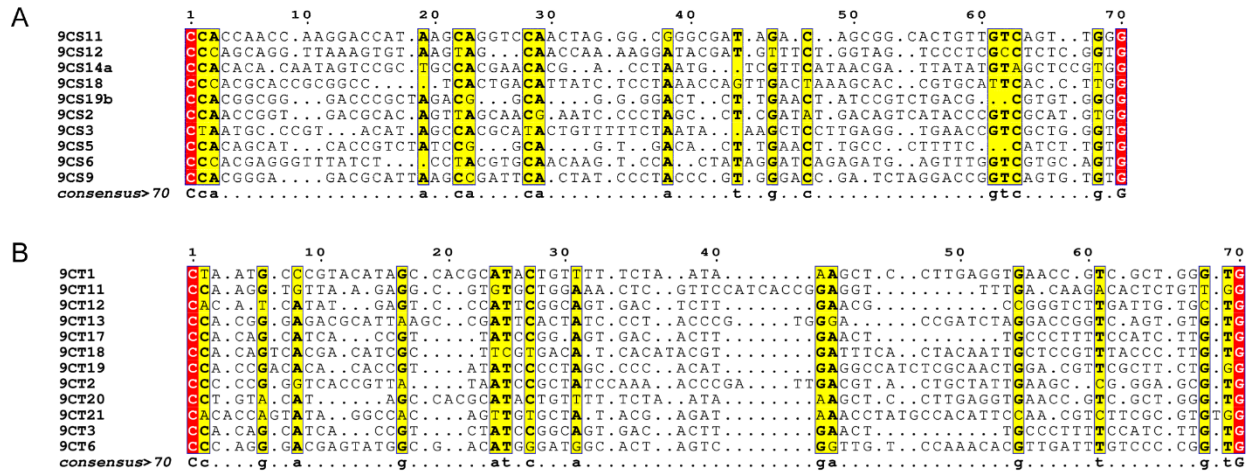


Figure S1. Sequence alignment for 9CS and 9CT clones. The unique sequence regions for the clones from selection 9CS (A) and 9CT (B) were aligned using T-Coffee^{18,19} and displayed using N*ESPRIT.²⁰ Duplicate clone sequences and the primer binding regions were not included in the alignments.

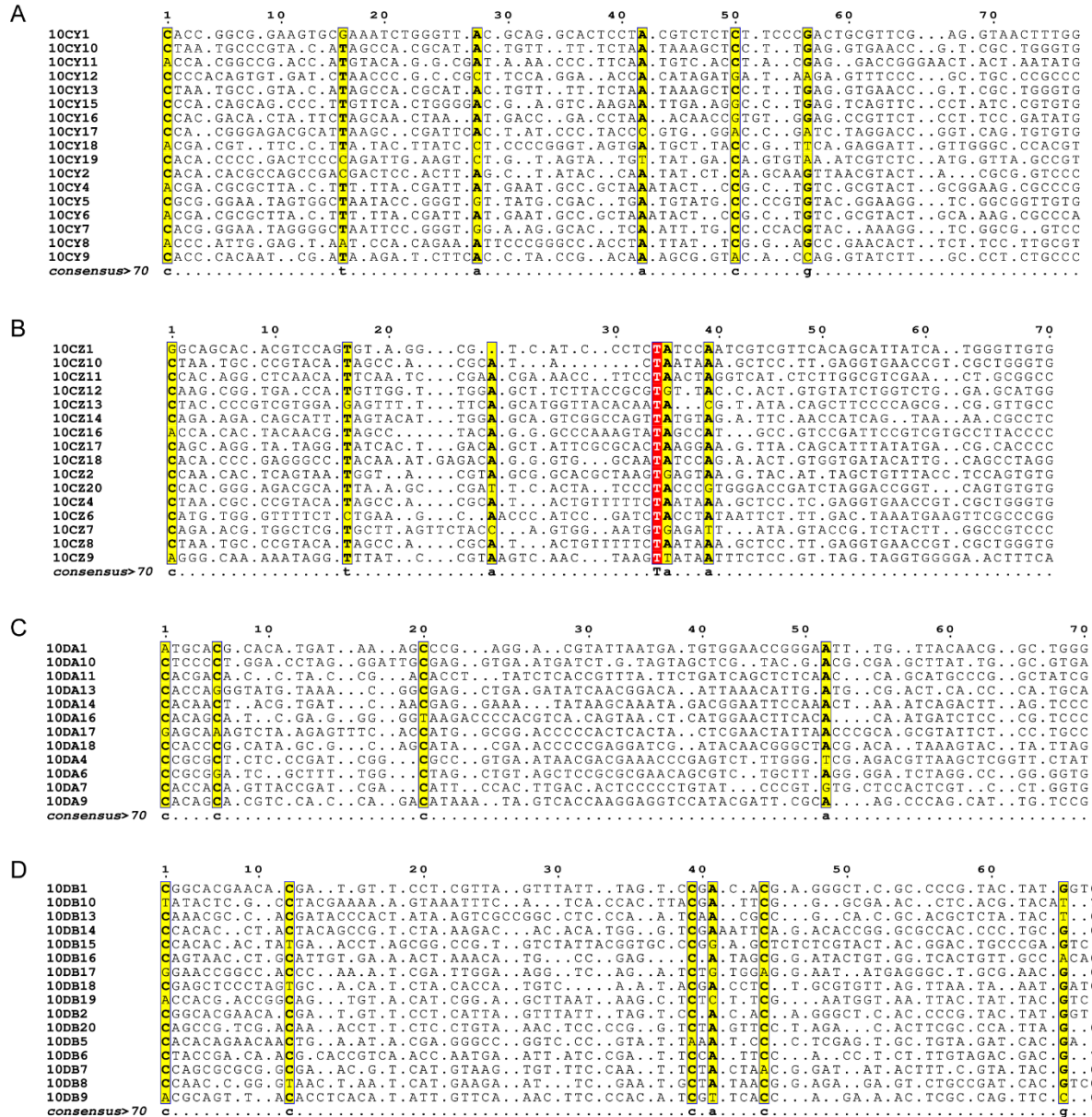


Figure S2. Sequence alignment for 10CY, 10CZ, 10DA and 10DB clones. The unique sequence regions of the clones sequenced from selection 10CY (A), 10CZ (B), 10DA (C) and 10DB (D) were aligned using T-Coffee^{18,19} and displayed using N*ESPRIT²⁰. Duplicate clone sequences and the primer binding regions were not included in the alignments.

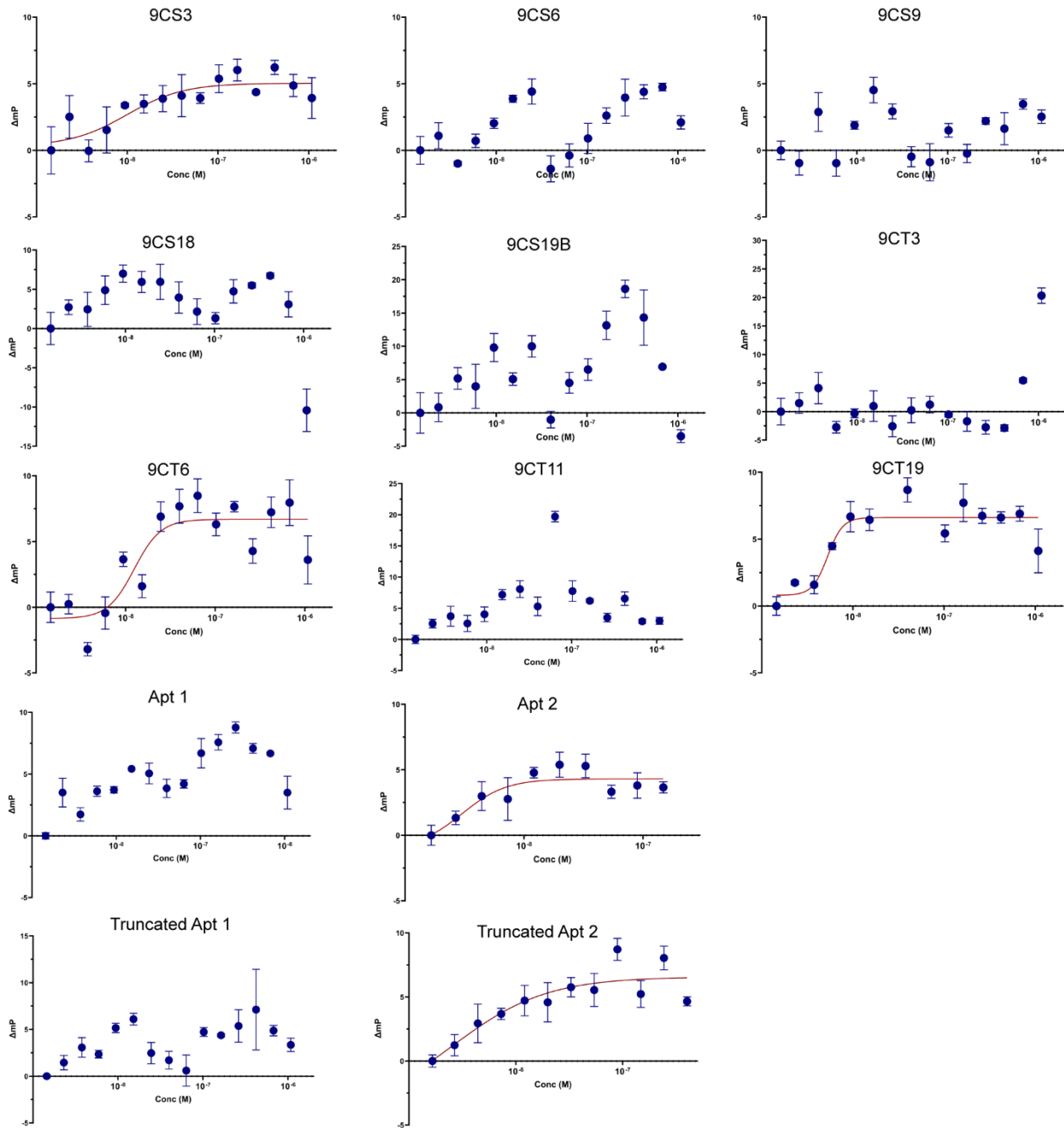


Figure S3. Fluorescence polarization of IL-17 binding aptamers. Binding constants were determined from non-linear fits using GraphPad Prism as described. Aptamers lacking curve fits appeared to have unusual binding behavior, potentially due to binding of two monomers of IL-17. Error bars represent the standard deviation for N=3 trials.

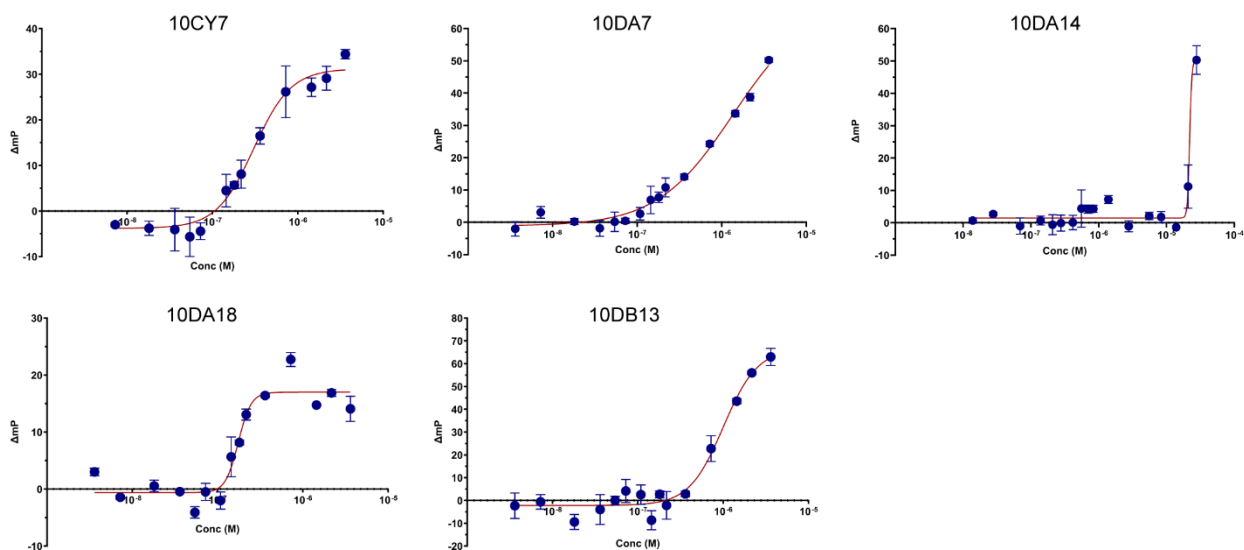


Figure S4. Fluorescence polarization of IL-20 binding aptamers. Binding constants were determined from non-linear fits using GraphPad Prism as described. Error bars represent the standard deviation for N=3 trials.

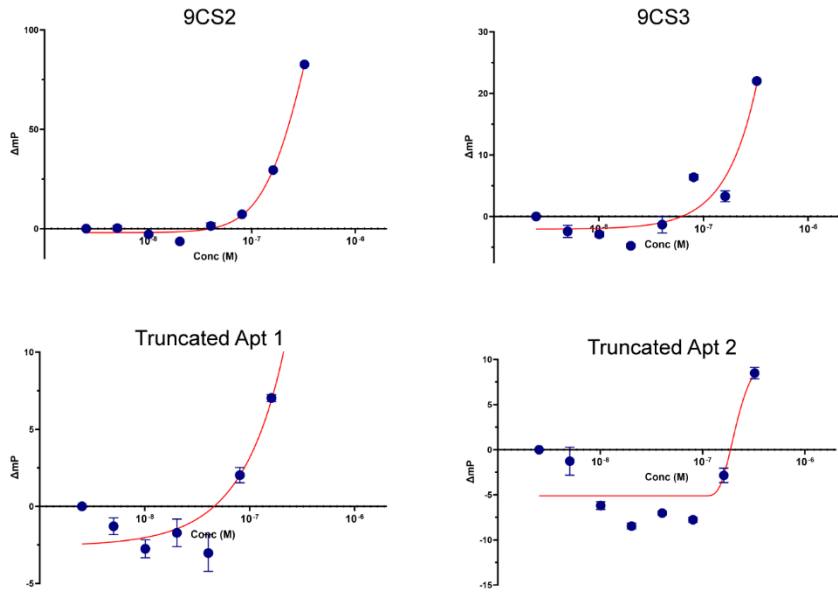


Figure S5. Fluorescence polarization of IL-17 binding aptamers with mouse IL-17 Binding curves were plotted with non-linear fits using GraphPad Prism as described. Error bars represent the standard deviation for N=3 trials.

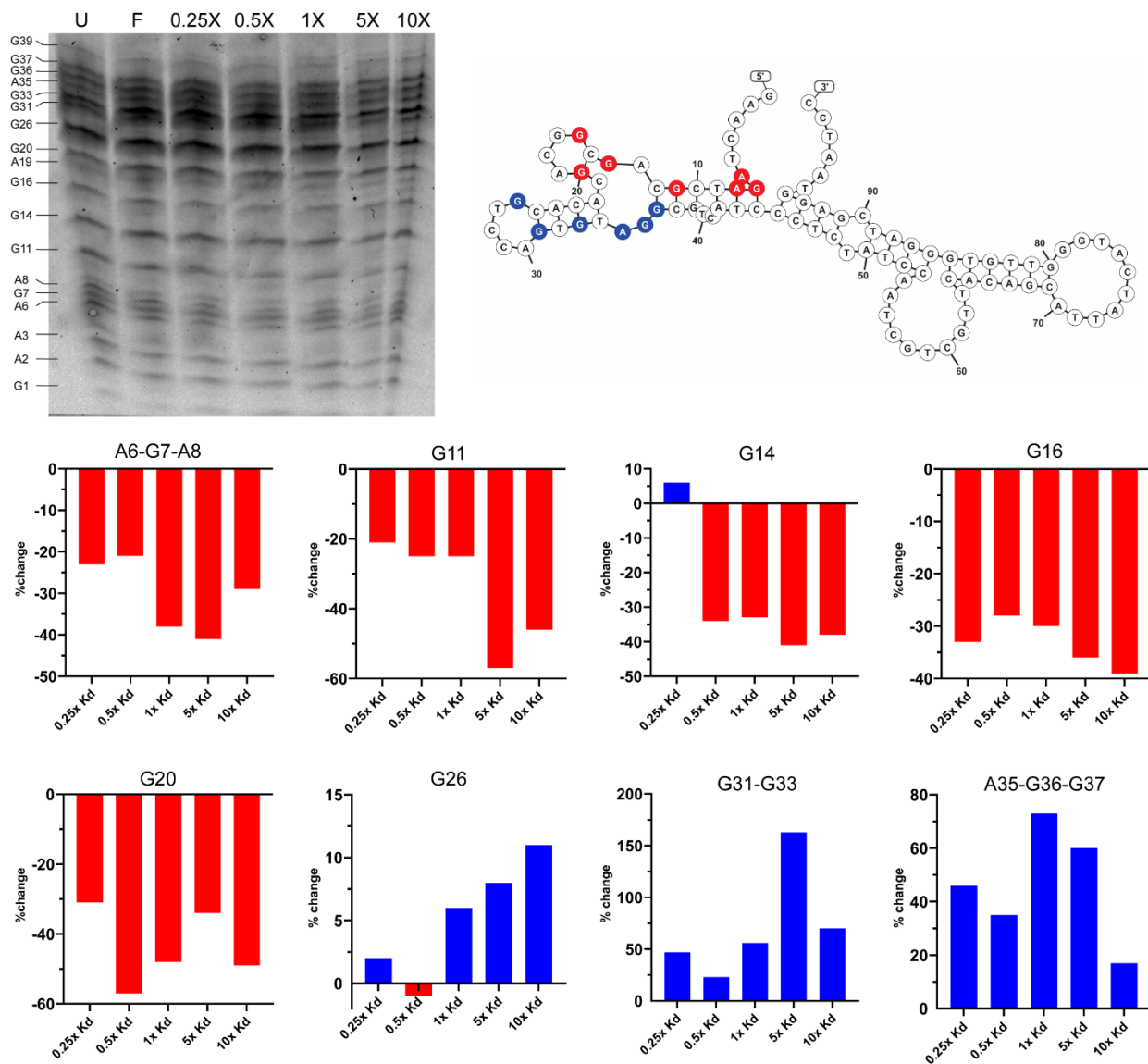


Figure S6. DMS probing of aptamer 10CZ1. 5' TAMRA-labeled 10CZ1 was incubated with increasing concentrations of IL-20 and DMS cleavage patterns were compared to unfolded (U) and folded (F) aptamer without IL-20. K_d for aptamer 10CZ1 was determined to be 120 nM via fluorescence polarization. The percent change refers to the change in band intensity relative to the folded aptamer lane. Increased cleavage, resulting in a stronger band intensity, is shown in blue, while decreased cleavage is represented in red. In some cases, groups of bands were quantified as a single unit. Gel image was analyzed using Image Lab. Secondary structure prediction was generated with SnapGene® software (from Dotmatics; available at snapgene.com).

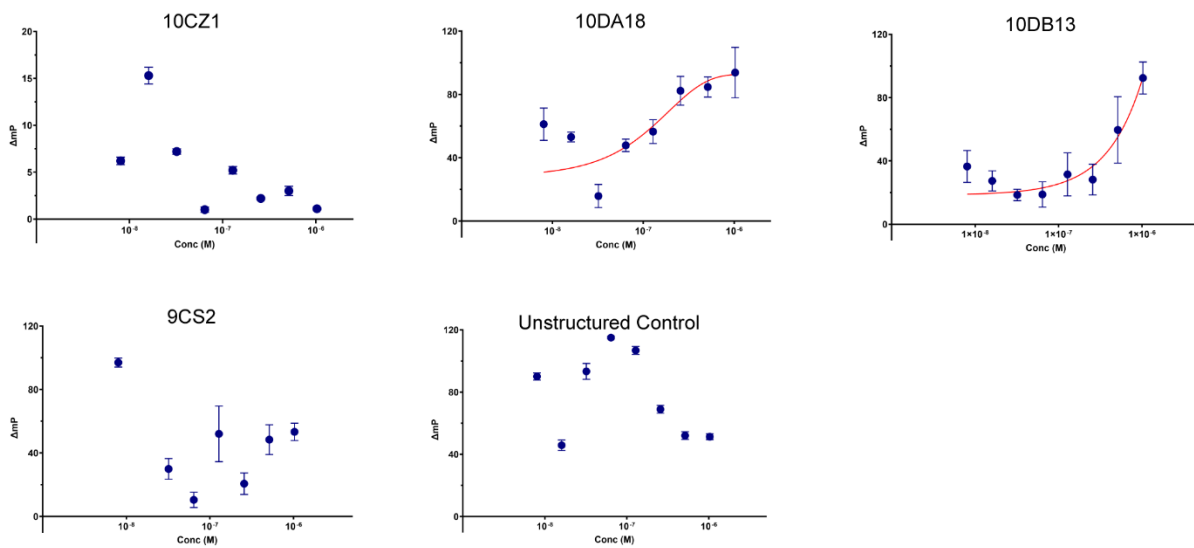


Figure S7. Fluorescence polarization of aptamers with IL-24 Binding curves were plotted with non-linear fits using GraphPad Prism as described. Error bars represent the standard deviation for N=3 trials.