Supporting Information

DNA Adsorption to and Elution from Silica Surfaces: Influence of Amino Acid Buffers

*Peter E. Vandeventer[1], Jorge Mejia[2], Ali Nadim[3], Malkiat S. Johal[2], Angelika Niemz[1]**

[1]Keck Graduate Institute of Applied Life Sciences, 535 Watson Drive, Claremont, CA 91711[1]
[2]Chemistry Department, Pomona College, 645 North College Avenue, Claremont, California 91711
[3]Claremont Graduate University, 150 E. Tenth St, Claremont, CA 91711

Table S1. ANOVA p-values for DNA adsorption to MagPrep silica particles

	ARG	HIS	ASP	GLU	SER	ASN	GLN	LEU	GLY	PRO
ARG		0.7478	<0.0001	<0.0001	0.0153	0.0573	<0.0001	0.0622	0.0033	0.3325
HIS	0.7478		<0.0001	<0.0001	0.0044	0.0208	<0.0001	0.0229	0.0007	0.1536
ASP	<0.0001	<0.0001		0.2657	<0.0001	<0.0001	0.0559	<0.0001	0.0005	<0.0001
GLU	<0.0001	<0.0001	0.2657		0.0095	0.0018	0.6060	0.0016	0.0410	<0.0001
SER	0.0153	0.0044	<0.0001	0.0095		0.563	0.0188	0.5373	0.5591	0.0447
ASN	0.0573	0.0208	<0.0001	0.0018	0.563		0.0033	0.9691	0.2467	0.1794
GLN	<0.0001	<0.0001	0.0559	0.6060	0.0188	0.0033		0.0029	0.0824	<0.0001
LEU	0.0622	0.0229	<0.0001	0.0016	0.5373	0.9691	0.0029		0.2315	0.1944
GLY	0.0033	0.0007	0.0005	0.0410	0.5591	0.2467	0.0824	0.2315		0.0078
PRO	0.3325	0.1536	<0.0001	<0.0001	0.0447	0.1794	<0.0001	0.1944	0.0078	

Table S2. ANOVA p-values for DNA adsorption to Sigma silica particles

	ARG	HIS	ASP	GLU	SER	ASN	GLN	LEU	GLY	PRO
ARG		0.0255	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
HIS	0.0255		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
ASP	<0.0001	<0.0001		0.0060	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
GLU	<0.0001	<0.0001	0.0060		0.1125	0.0179	0.0601	0.0217	0.0291	0.1950
SER	<0.0001	<0.0001	<0.0001	0.1125		0.4547	0.7967	0.4991	0.5745	0.7460
ASN	<0.0001	<0.0001	<0.0001	0.0179	0.4547		0.6159	0.9414	0.8486	0.2741
GLN	<0.0001	<0.0001	<0.0001	0.0601	0.7967	0.6159		0.6685	0.7558	0.5524
LEU	<0.0001	<0.0001	<0.0001	0.0217	0.4991	0.9414	0.6685		0.9065	0.3074
GLY	<0.0001	<0.0001	<0.0001	0.0291	0.5745	0.8486	0.7558	0.9065		0.3660
PRO	<0.0001	<0.0001	<0.0001	0.1950	0.7460	0.2741	0.5524	0.3074	0.3660	

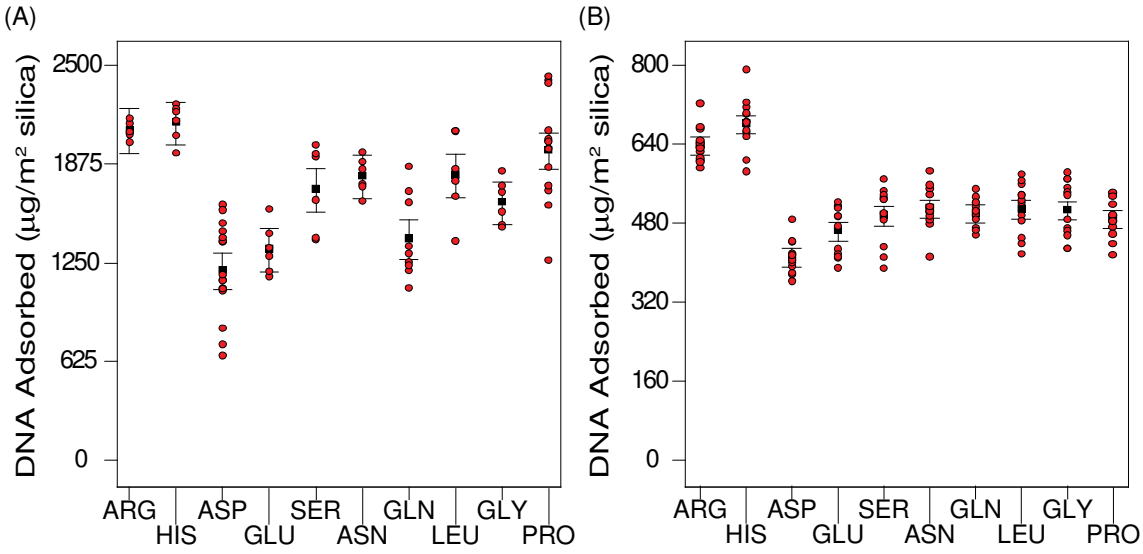

Figure S1. ANOVA results for DNA adsorption to (A) Magprep silica paritcles (Figure 1A, grey), and (B) Sigma silica particles (Figure 1A, white). (A) 1 ARG outlier was removed for the MagPrep silica particles data and (B)1 SER outlier was removed for the Sigma silica particles data.Outliers were defined as data points outside of three standard deviations from the mean.

Table S3. ANOVA p-values for DNA elution from MagPrep silica particles

	ARG	HIS	ASP	GLU	SER	ASN	GLN	LEU	GLY	PRO
ARG		0.6928	<0.0001	<0.0001	0.0713	0.0765	<0.0001	0.0043	0.0032	<0.0001
HIS	0.6928		<0.0001	<0.0001	0.0357	0.0384	<0.0001	0.0181	0.0015	<0.0001
ASP	<0.0001	<0.0001		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
GLU	<0.0001	<0.0001	<0.0001		0.0002	0.0001	<0.0001	<0.0001	0.0073	<0.0001
SER	0.0713	0.0357	<0.0001	0.0002		0.9732	<0.0001	<0.0001	0.2246	<0.0001
ASN	0.0765	0.0384	<0.0001	0.0001	0.9732		<0.0001	<0.0001	0.2122	<0.0001
GLN	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001		<0.0001	<0.0001	<0.0001
LEU	0.0043	0.0181	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001		<0.0001	0.0051
GLY	0.0032	0.0015	<0.0001	0.0073	0.2246	0.2122	<0.0001	<0.0001		<0.0001
PRO	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	0.0051	<0.0001	

Table S4. ANOVA p-values for DNA elution from Sigma silica particles

	ARG	HIS	ASP	GLU	SER	ASN	GLN	LEU	GLY	PRO
ARG		0.3724	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
HIS	0.3724		<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
ASP	<0.0001	<0.0001		0.2248	<0.0001	0.0003	0.0002	<0.0001	0.0008	<0.0001
GLU	<0.0001	<0.0001	0.2248		<0.0001	0.0093	0.0089	<0.0001	0.0224	0.0002
SER	<0.0001	<0.0001	<0.0001	<0.0001		0.0976	0.1008	0.9454	0.0486	0.7020
ASN	<0.0001	<0.0001	0.0003	0.0093	0.0976		0.9860	0.0956	0.7284	0.1776
GLN	<0.0001	<0.0001	0.0002	0.0089	0.1008	0.9860		0.0990	0.7153	0.1831
LEU	<0.0001	<0.0001	<0.0001	<0.0001	0.9454	0.0956	0.0990		0.0459	0.7417
GLY	<0.0001	<0.0001	0.0008	0.0224	0.0486	0.7284	0.7153	0.0459		0.0923
PRO	<0.0001	<0.0001	<0.0001	0.0002	0.7020	0.1776	0.1831	0.7417	0.0923	

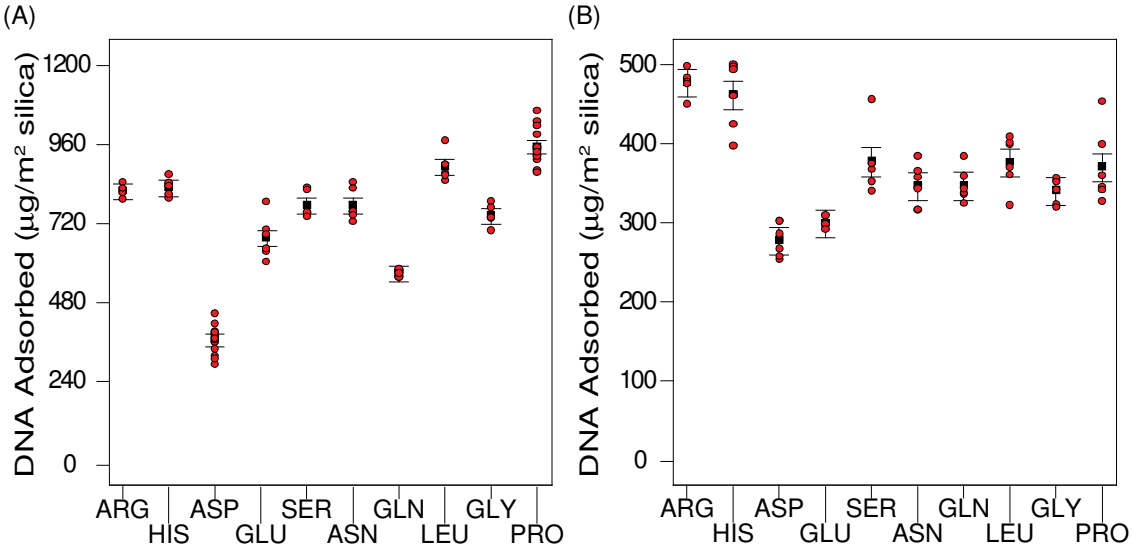

Figure S2. ANOVA results for DNA elution from (A) Magprep silica paritcles (Figure 1B, hashed), and (B) Sigma silica particles (Figure 1C, hashed), when originally adsorbed out of an amino acid buffers. For the (A) MagPrep silica paticles, 1 outlier was removed from HIS, 3 outliers were removed from GLN, and 1 outlier was removed from PRO, For the (B) Sigma silca particles, 1 outlier was removed from SER. Outliers were defined as data points outside of three standard deviations from the mean.

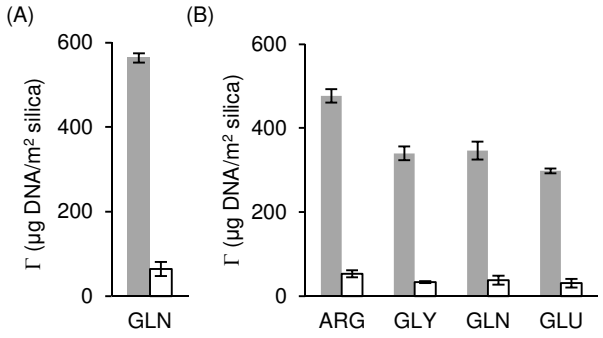

Figure S3. DNA eluted from (A) MagPrep and (B) Sigma silica particles during the first (grey) and second (white) elution step. Only a small amount of DNA was eluted during the second elution step.This suggests that a build up in concentration of DNA during the first elution step is not substantionally limiting additional elution of bound DNA.

Table S5. ANOVA p-values for DNA elution yield (DNA eluted/adsorbed) using MagPrep silica particles

	ARG	HIS	ASP	GLU	SER	ASN	GLN	LEU	GLY	PRO
ARG		0.6066	0.0036	0.0035	0.1053	0.4491	0.1204	0.0056	0.1311	0.0112
HIS	0.6066		0.0307	0.0011	0.0411	0.2181	0.0477	0.0018	0.0525	0.0034
ASP	0.0036	0.0307		<0.0001	<0.0001	0.0002	<0.0001	<0.0001	<0.0001	<0.0001
GLU	0.0035	0.0011	<0.0001		0.1699	0.0266	0.1499	0.8684	0.1380	0.3767
SER	0.1053	0.0411	<0.0001	0.1699		0.3815	0.9452	0.2262	0.9097	0.4786
ASN	0.4491	0.2181	0.0002	0.0266	0.3815		0.4197	0.0394	0.4456	0.0883
GLN	0.1204	0.0477	<0.0001	0.1499	0.9452	0.4197		0.2014	0.9644	0.4310
LEU	0.0056	0.0018	<0.0001	0.8684	0.2262	0.0394	0.2014		0.1864	0.4876
GLY	0.1311	0.0525	<0.0001	0.1380	0.9097	0.4456	0.9644	0.1864		0.4017
PRO	0.0112	0.0034	<0.0001	0.3767	0.4786	0.0883	0.4310	0.4876	0.4017	

Table S6. ANOVA p-values for DNA elution yield (DNA eluted/adsorbed) using Sigma silica particles

	ARG	HIS	ASP	GLU	SER	ASN	GLN	LEU	GLY	PRO
ARG		0.0941	0.1677	0.3514	0.5872	0.3469	0.6153	0.1806	0.8937	0.8254
HIS	0.0941		0.7603	0.4471	0.2849	0.4524	0.2354	0.7287	0.0716	0.1438
ASP	0.1677	0.7603		0.6478	0.4340	0.6542	0.3754	0.9666	0.1313	0.2442
GLU	0.3514	0.4471	0.6478		0.7274	0.9930	0.6655	0.6781	0.2876	0.4755
SER	0.5872	0.2849	0.4340	0.7274		0.7211	0.9491	0.4576	0.5032	0.7390
ASN	0.3469	0.4524	0.6542	0.9930	0.7211		0.6591	0.6845	0.2837	0.4701
GLN	0.6153	0.2354	0.3754	0.6655	0.9491	0.6591		0.3980	0.5251	0.7776
LEU	0.1806	0.7287	0.9666	0.6781	0.4576	0.6845	0.3980		0.1419	0.2612
GLY	0.8937	0.0716	0.1313	0.2876	0.5032	0.2837	0.5251	0.1419		0.7233
PRO	0.8254	0.1438	0.2442	0.4755	0.7390	0.4701	0.7776	0.2612	0.7233	

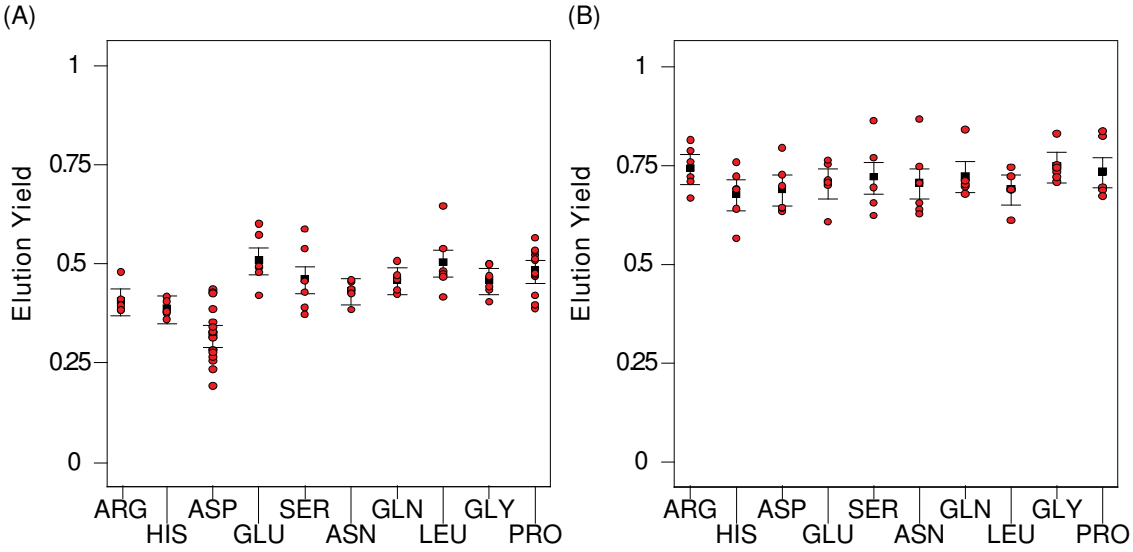

Figure S4. ANOVA results for DNA elution yield from (A) Magprep silica paritcles (Figure 2B, grey), and (B) Sigma silica particles (Figure 2B, white), when originally adsorbed out of an amino acid buffers. For the (A) MagPrep silica paticles, 1 outlier was removed from HIS, 3 outliers were removed from GLN, and 2 outlier was removed from PRO, For the (B) Sigma silca particles, 1 outlier was removed from SER. Outliers were defined as data points outside of three standard deviations from the mean.

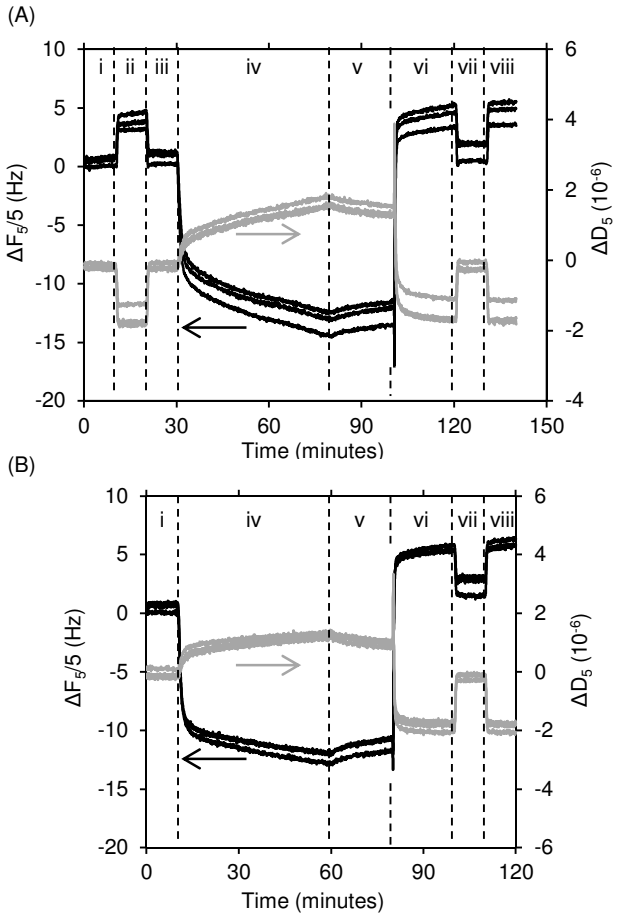

Figure S5. Comparison of QCM-D data (A) with and (B) without an initial TE baseline. (A) In the case where an initial TE baseline was performed, we established (i) an initial glycine baseline followed by (ii) a TE baseline and then a (iii) glycine baseline. (B) In the case when we did not establish an initial TE baseline we only (i) established an initial glycine baseline. The othersteps are the same for both experiments (A and B). These steps are (iv) DNA adsorption to a quartz crystal out of GLY buffer, (v)followed by a wash with GLY buffer, and (vi) elution using TE buffer (vi). Final baselines with (vii) GLY buffer and (viii) TE buffer were then established. Exposure of the quartz crystals to TE buffer prior to DNA adsorption does not substantially alter DNA adsorption and elution behavior. This suggests that both the silica surface is not irreveribly changed by establishing an initial TE baseline and that the higher elution yield of the quartz crystals compared to the bulk depletion experiments is not due to initial exposure of the crystals to TE buffer. Data is averaged over 5 second intervals.

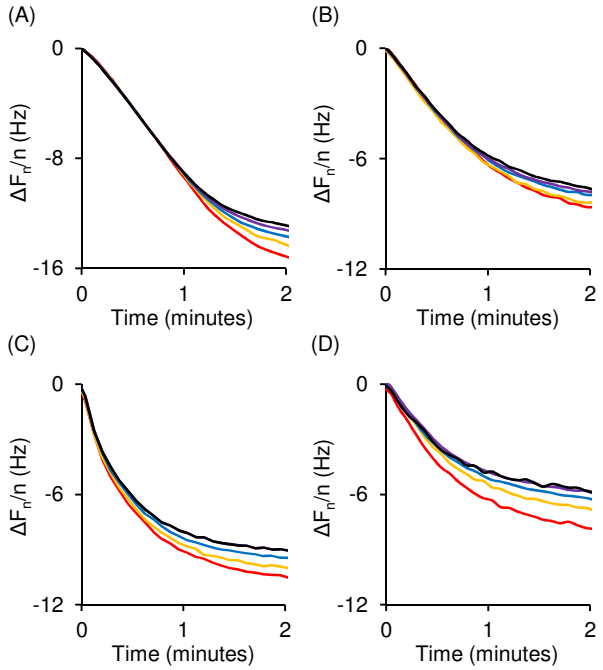

Figure S6. Initial DNA adsorption out of (A) ARG, (B) GLY, (C) GLN, and (D) GLU as monitored using the 3rd (red), 5th (orange), 7th (blue), 9th (purple), and 11th (black) overtones. Data is averaged over 5 second intervals.

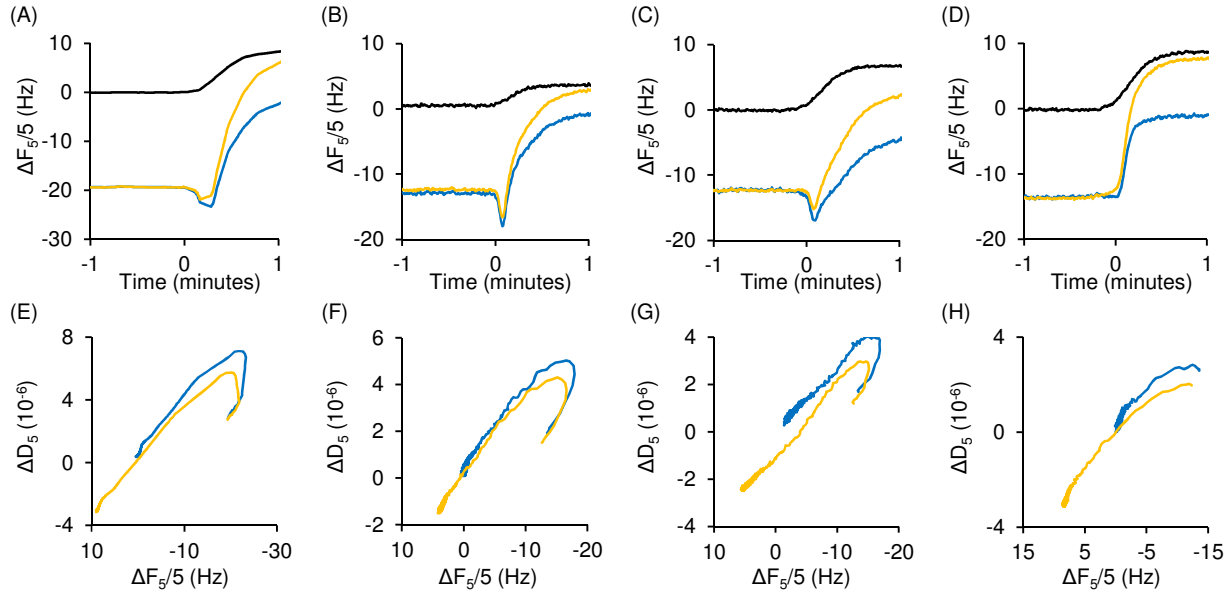

Figure S7. To determine the signal from the adsorbed DNA film alone (blue), we first align and then baseline subtract the raw elution signal (orange, Figure 3 phase v to vi) from the initial amino acid to TE buffer baselines (black, Figure 3 phase i to ii). Zero time denotes the onset of switching from the amino acid buffers (A) ARG, (B) GLY, (C) GLN, and (D) GLU to TE buffer. Plots of *ΔD* versus *ΔF* for the baseline subtracted signal (blue) and raw elution signal (orange) are shown for the amino acids (E) ARG, (F) GLY, (G) GLN, and (D) GLU. Data is averaged over 0.5 second intervals.

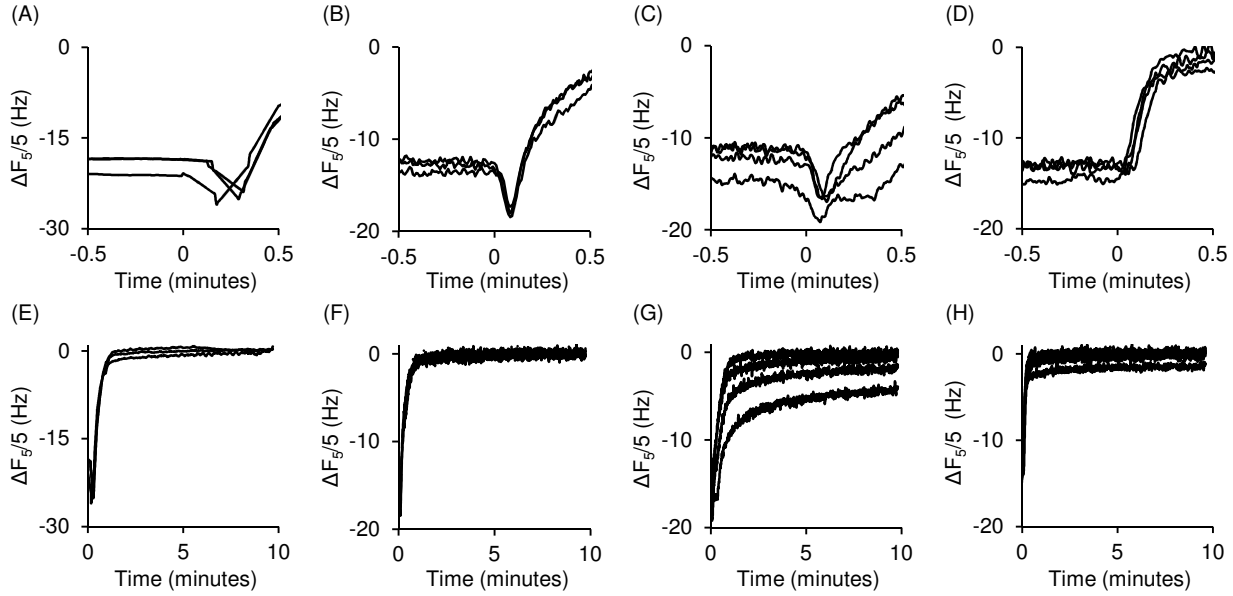

Figure S8. Baseline subtracted elution replicates when DNA was originally adsorbed out of ARG (A,E), GLY (B,F), GLN (C,G), and GLU (D,H). The initial switch from the respective amino acid buffer to TE buffer occurs at 0 minutes.