Restriction enzymes as a target for DNA based sensing and structural rearrangement: Supplemental Information

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Table SI. DNA Sequences

Name	Sequence	Modification	Tm (1X TAE 12.5 mM $MgCl_2$)	Source
Arm 1	GGTTCAGCCGCAATCCGGCACAGCTATAATAA*****GAGTT TGATGAAATGGAGCGGACGTGAGATGG	*Internal Cy3	79.0	IDT
Arm2	GCAAGACTCGTGCTCAGGTCCTAAGTTGGTTCT*ACCGC ATGGTATATGGGGCTTACGGTGGTGCG	*Internal Cy3.5	79.7	Operon
Arm 3	GGATCAGAGCTGGACGGGAGCCTATCGGGTAG*****TTATG TTGTTCGCTGGTGTTACTGCATCCAGG	*Internal Cy5	79.3	IDT
Cap 1	CCATCTCACGTCCGCTGGATTGCGGCTGAACC		76.7	IDT
Cap 2	CGCACCACCGTAAGCCTGAGCACGAGTCTTGC		76.5	IDT
Cap 3	CCTGGATGCAGTAACACGTCCAGCTCTGATCC		73.9	IDT
Link1 Xba I	GCCGGAGACCATATACCATGCGGTGCTCTAGACGTTAT TATAGCTGTGCC		77.2	IDT
Link2 Eco RI	CCTGTACGCCAGCGAACAACATAACGGAATTCGCGAAC CAACTTAGGACC		77.9	IDT
Link3 Bam HI	GATACGGACCATTTCATCAAACTCCGGGATCCGGCTAC CCGATAGGCTCC		78.2	IDT
Link1 Nco I	GCCGGAGACCATATACCATGCGGTGCCCATGGCGTTAT TATAGCTGTGCC		79.0	IDT
Link Xho I	GCCGGAGACCATATACCATGCGGTGGCTCGAGCCTTAT TATAGCTGTGCC		78.5	IDT
Link1 Sma I	GCCGGAGACCATATACCATGCGGTGGCCCGGGCCTTAT TATAGCTGTGCC		79.8	IDT
Link3 Sma I	GATACGGACCATTTCATCAAACTCGGCCCGGGCCCTAC CCGATAGGCTCC		79.5	IDT
Comp Xba I	CGTCTAGAGC		41.5	IDT
Comp Eco RI	GCGAATTCCG		45.4	IDT
Comp Bam HI	CCGGATCCCG		50.0	IDT

Comp Nco I	CGCCATGGGC	53.0	IDT
Comp Xho I	GGCTCGAGCC	49.3	IDT
Comp Sma I	GGCCCGGGCC	57.7	IDT

*in sequence indicates modifier placement

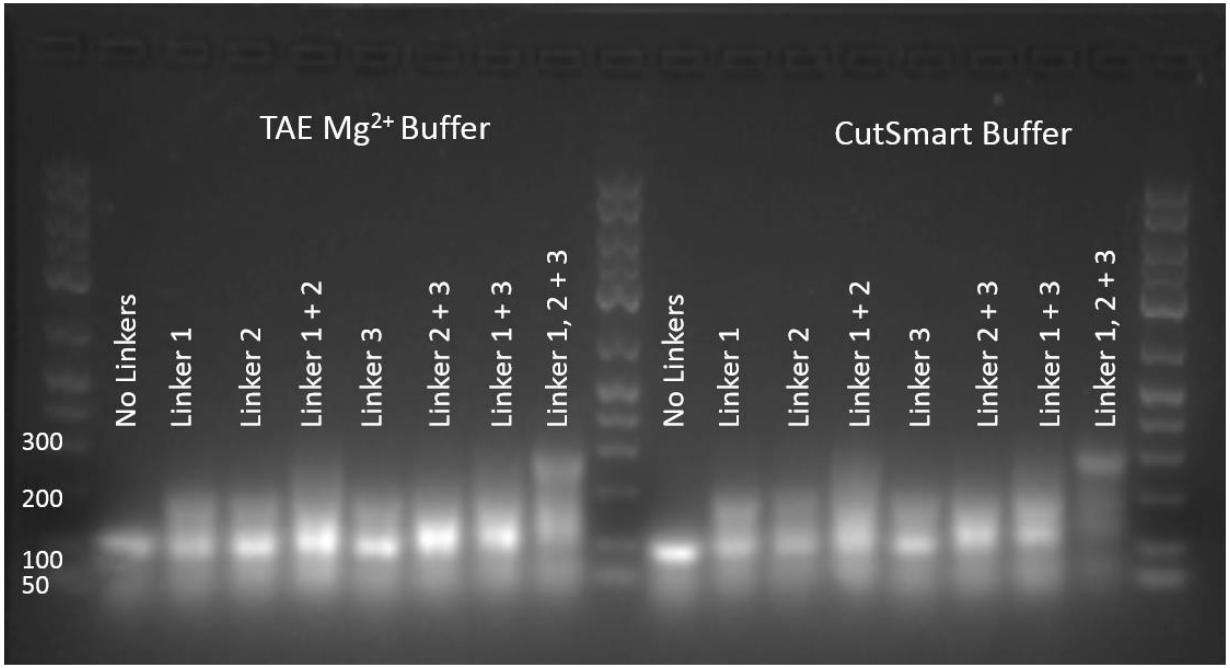
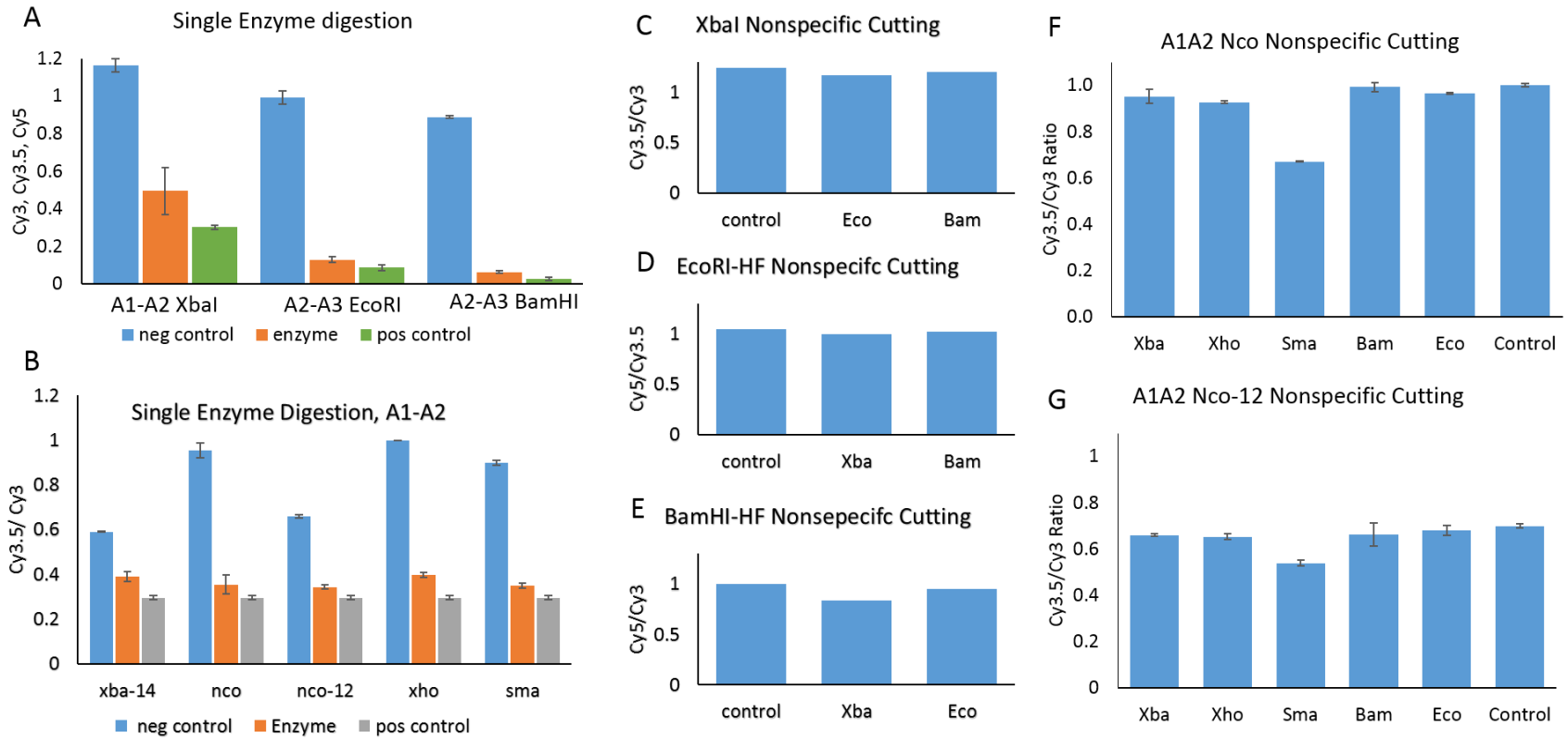


Figure S1: Gel electrophoresis of all eight permutations in TAE with Mg and CutSmart buffer



FigureS2: A-B) enzyme cutting data for all enzymes tested. The Arms used are indicated with a negative and positive control given for each set. C-E) ratio output for non-specific enzyme assay where all other enzymes are presented against the specified sequence. F-G) Non-specific cutting assay for the NCO enzyme. This shows non-specific behavior with the Sma I enzyme in both the NCO-10 and NCO-12 assemblies.

Table S2. Table of all possible enzyme combinations. Bold indicates compatible sets.

Link 1	Link 2	Link 3
NcoI-HF	BamHI-HF	EcoRI-HF
NcoI-HF	**BamHI-HF**	**XhoI**
NcoI-HF	BamHI-HF	SmaI
NcoI-HF	**EcoRI-HF**	**XhoI**
NcoI-HF	EcoRI-HF	SmaI
NcoI-HF	XhoI	SmaI
BamHI-HF	EcoRI-HF	XhoI
BamHI-HF	EcoRI-HF	SmaI
XhoI	**SmaI**	**BamHI-HF**
XhoI	**EcoRI-HF**	**SmaI**

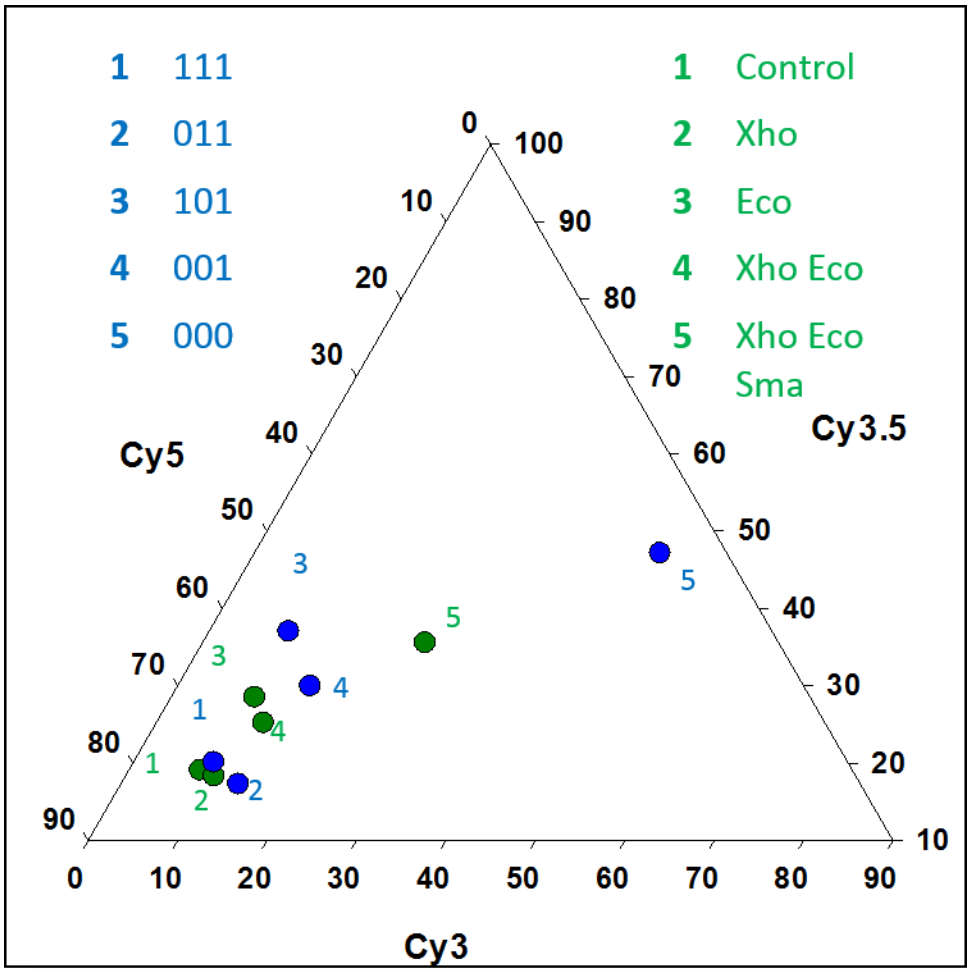


Figure S3: Ternary plot of dye contribution for the triple digestion experiment

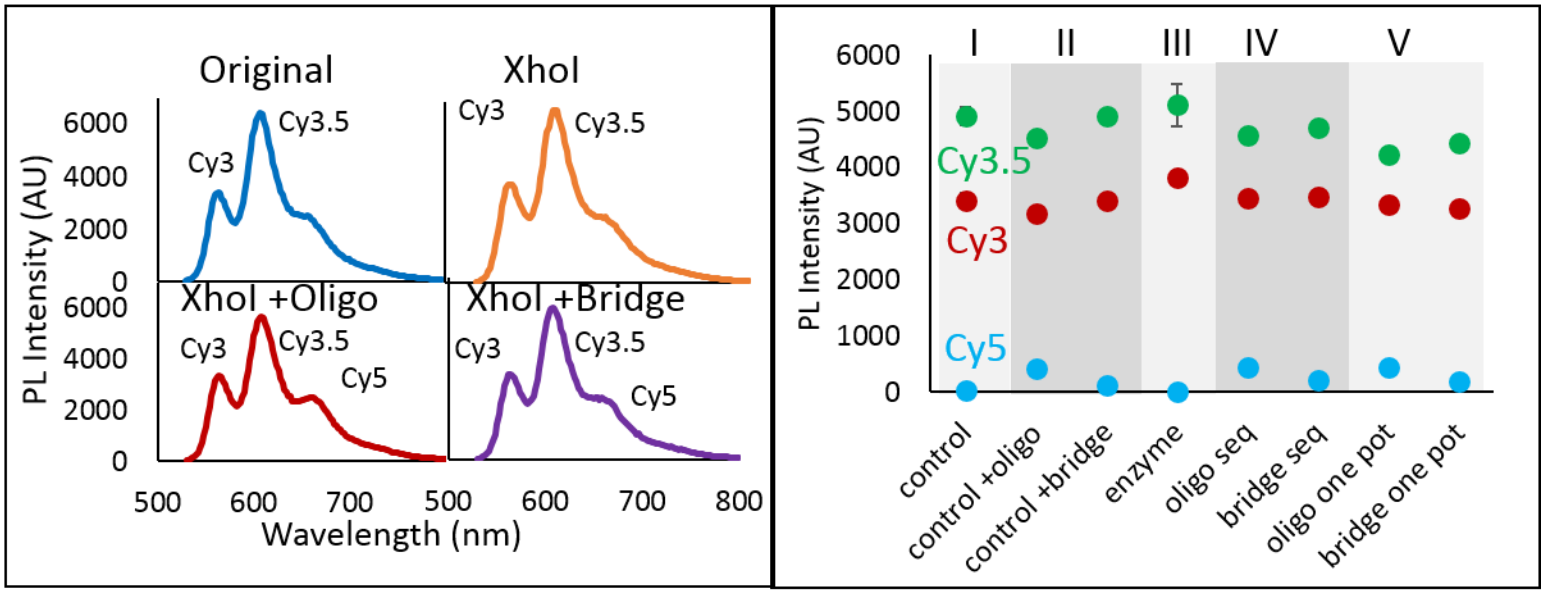


Figure S4: Data from the full structure enzyme cleavage and rearrangement via addition of an additional Cy5 containing DNA oligo. Left panel shows the PL Intensity of each of the structures depicted with XhoI +Oligo and XhoI + Bridge both being one pot reactions. The right panel shows PL peak height plots for each of the three dyes in the system. The addition was performed both as a one-pot reaction and a sequential reaction. The controls of the switch plus the oligo or bridge are done in the absence of enzyme and show little to no reaction without the presence of the enzyme.