

**Supplemental Table 1.** Synthetic oligonucleotides used to generate of constructs used in this study.

Name	Sequence (5'-3')
pVOTE.POLYA441G	GAAGATTGCAGGAGGATTCGGCTTC
pVOTE.POLYA441G c	GAAGCCGAATCCTCCTGCAATCTTC
pVOTE.POLYF442G	GAAGATTGCAGGAGCAGGCGGCTTCAAAGAC
pVOTE.POLYF442G c	GTCTTTGAAGCCGCCTGCTCCTGCAATCTTC
pVOTE.POLYA441G/F442G	CCTGAAGATTGCAGGAGGAGGCGGCTTCAAAGACATAATCC
pVOTE.POLYA441G/F442G c	GGATTATGTCTTTGAAGCCGCCTCCTCCTGCAATCTTCAGG
pVOTE.POLYD391N	GTTACAGAATACGGCCGATTTAATCCAGGAGCCATGAACTACAC
pVOTE.POLYD391N c	GTGTAGTTCATGGCTCCTGGATTAAATCGGCCGTATTCTGTAAC
pVOTE.POLYD431N	GTGAATACTTCATGGAGGTGGCCAATCTCAACTCTCCCCTGAAGATTG
pVOTE.POLYD431N c	CAATCTTCAGGGGAGAGTTGAGATTGGCCACCTCCATGAAGTATTCAC

**Supplemental Table 2.** Data collection and refinement statistics.

<b>Data collection</b>	D431N
Space group	P2 <sub>1</sub> 3
Cell dimensions	
<i>a</i> = <i>b</i> = <i>c</i> (Å)	326.72
Wavelength	0.933
Resolution (Å)	50-3.1
<i>R</i> <sub>sym</sub>	0.12
<i>I</i> /σ <i>I</i>	9.3
Completeness (%)	99.0
Redundancy	5.3
<b>Refinement</b>	
Resolution (Å)	20.0-3.1
No. reflections	187110
Cutoff	3σ <sub>F</sub>
<i>R</i> <sub>work</sub> / <i>R</i> <sub>free</sub>	0.28/0.28
No. residues	
Protein	428
Ligand/ion	1
Water	-
Averaged B-factors	26.7
R.m.s deviations	
Bond lengths (Å)	0.006
Bond angles (°)	0.803