A Rapid Screen of Potential i-Motif Forming Sequences in DNA Repair Gene Promoters

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Supporting Information

Table S1: Tabulated results for all oligodeoxynucleotides studied; Low pH CD maxima; IDS λ_{max} pH_T values (± std. error); T_M values (± std. error); calculated UV molar absorptivity values at 260 nm (ε_{260}).

Sequence Name	CD λ_{max} (nm)	IDS λ_{max} (nm)	IDS λ_{min} (nm)	pH_T (± std. error)	T_M at pH 5 (± std. error) in ºC	T_M at pH 6 (± std. error) in ºC	ε_{260} (L µmol^{-1} cm^{-1})
***APE1* – 4 track**	286.6	243.7	292.4	6.07 (0.01)	55.6 (0.1)	24.0 (1.2)	0.1827
***APE1* – 5 track**	285.9	241.1	291.5	6.15 (0.02)	56.1 (0.1)	37.1 (2.4)	0.2935
FEN1	284.8	240.8	292.2	6.36 (0.03)	58.0 (0.1)	37.1 (0.1)	0.4249
MGMT	286.0	243.2	293.9	6.67 (0.03)	72.6 (0.1)	47.7 (0.3)	0.3611
NEIL1	286.9	241.6	293.4	6.48 (0.01)	63.3 (0.1)	37.5 (0.3)	0.2232
***NEIL2* – 4 track**	286.5	242.2	292.8	5.68 (0.02)	57.6 (0.7)	ND	0.1802
***NEIL2* – 5 track**	286.7	243.6	293.1	6.09 (0.02)	39.8 (1.8)	ND	0.2659
***NEIL2* – 6 track**	286.7	243.5	294.0	6.30 (0.03)	55.8 (0.9)	32.2 (1.2)	0.3046
***NEIL3* – 4 track**	287.5	240.3	291.1	5.14 (0.02)	ND	ND	0.2086
***NEIL3* – 5 track**	286.0	240.9	291.1	5.79 (0.01)	55.7 (1.2)	ND	0.3023
***NTHL1* – 4 track**	285.3	240.6	291.5	5.34 (0.01)	59.5 (1.4)	ND	0.2099
***NTHL1* – 5 track**	286.1	249.5	294.3	5.65 (0.02)	57.7 (0.2)	ND	0.3044
***PCNA* – Sequence 1**	285.9	242.2	292.8	5.91 (0.02)	59.7 (0.1)	45.1 (1.9)	0.3017
***PCNA* – Sequence 2**	287.3	240.1	292.5	6.63 (0.02)	68.0 (0.1)	45.4 (0.4)	0.2647
Polβ	286.5	240.8	293.5	6.46 (0.01)	61.2 (0.4)	37.4 (0.2)	0.2519
Polη	287.1	239.9	291.2	6.19 (0.01)	56.4 (0.1)	31.3 (0.7)	0.2255
***RAD17* – Sequence 1**	287.4	240.3	293.5	6.24 (0.01)	56.3 (0.1)	33.3 (0.1)	0.2835
***RAD17* – Sequence 2**	288.5	239.9	293.9	6.90 (0.02)	74.5 (0.1)	63.2 (0.3)	0.2005
RAD21	286.0	240.2	293.5	6.53 (0.04)	64.7 (0.1)	40.7 (0.1)	0.3017
RAD54L	287.6	239.7	295.0	6.51 (0.04)	71.3 (0.1)	45.0 (0.2)	0.3649
***UDG* – 4 track**	286.9	241.4	292.8	6.69 (0.02)	60.1 (0.1)	35.0 (0.4)	0.2196
***UDG* – 5 track**	285.6	244.2	293.0	6.26 (0.03)	58.6 (0.1)	38.7 (0.3)	0.4926
XRCC2	285.1	241.1	292.7	5.99 (0.08)	48.6 (0.1)	31.4 (0.6)	0.4162
XRCC3	287.0	241.3	293.4	5.78 (0.05)	61.3 (0.3)	45.0 (1.0)	0.2522
XRCC5	284.6	240.6	293.2	6.44 (0.02)	56.1 (0.2)	34.3 (0.1)	0.2475

Figures S1 – S25; Example pH-dependent CD spectra from a single replicate experiment (left); pH_T regression curves using data extracted from pH-dependent CD spectra at the CD maximum wavelength *circa* 285 nm; representative normalized T_M curves at pH 5 and 6.

Figure S1: *APE1* – 4 track

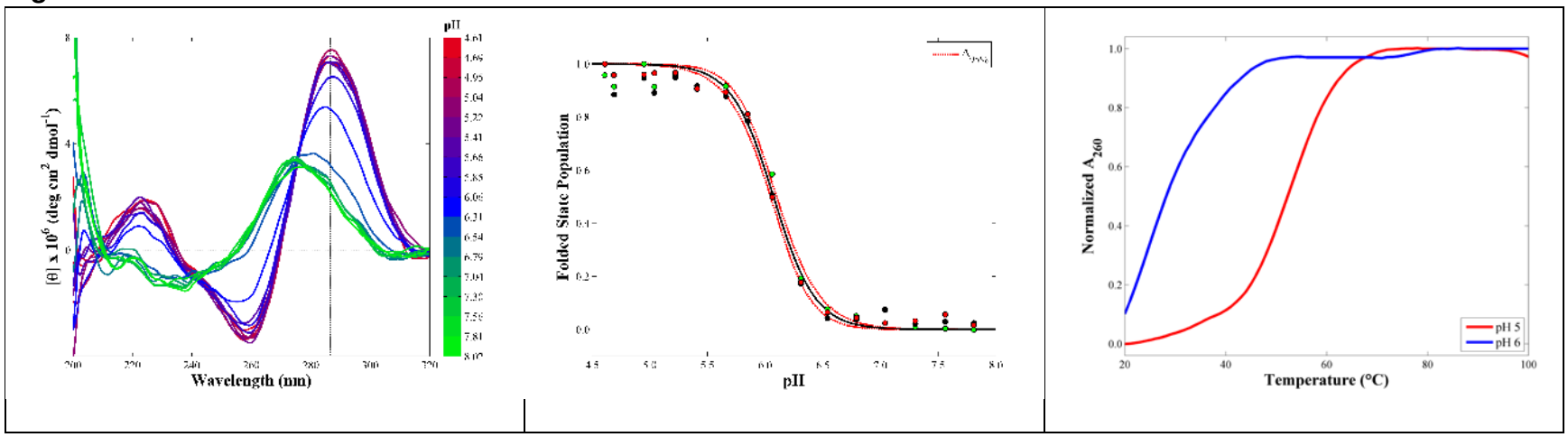

Figure S2: *APE1* – 5 track

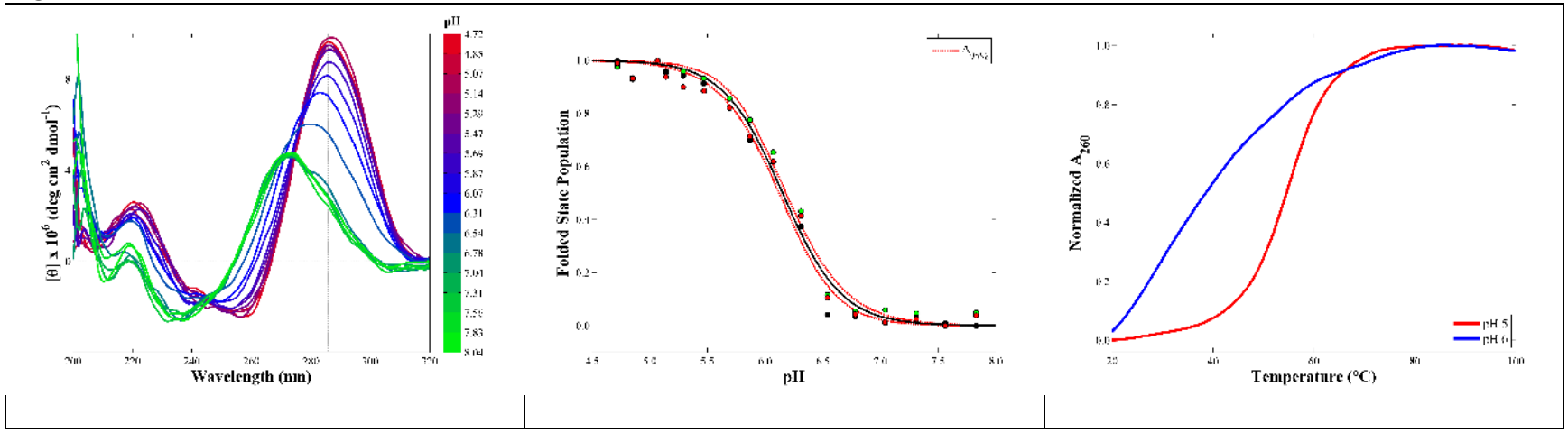

Figure S3: *FEN1*

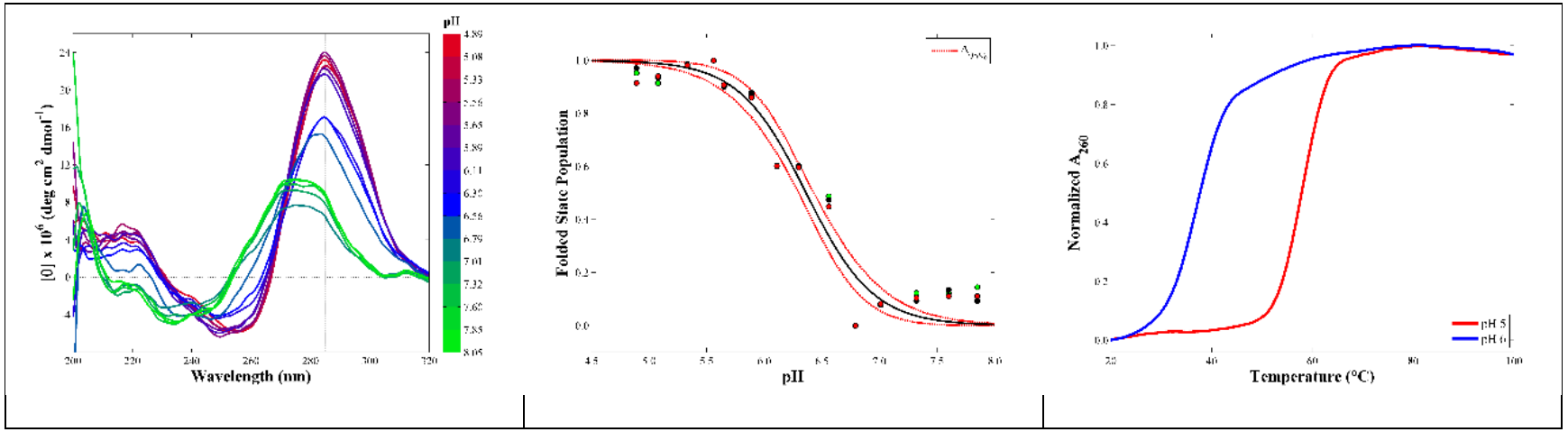

Figure S4: *MGMT*

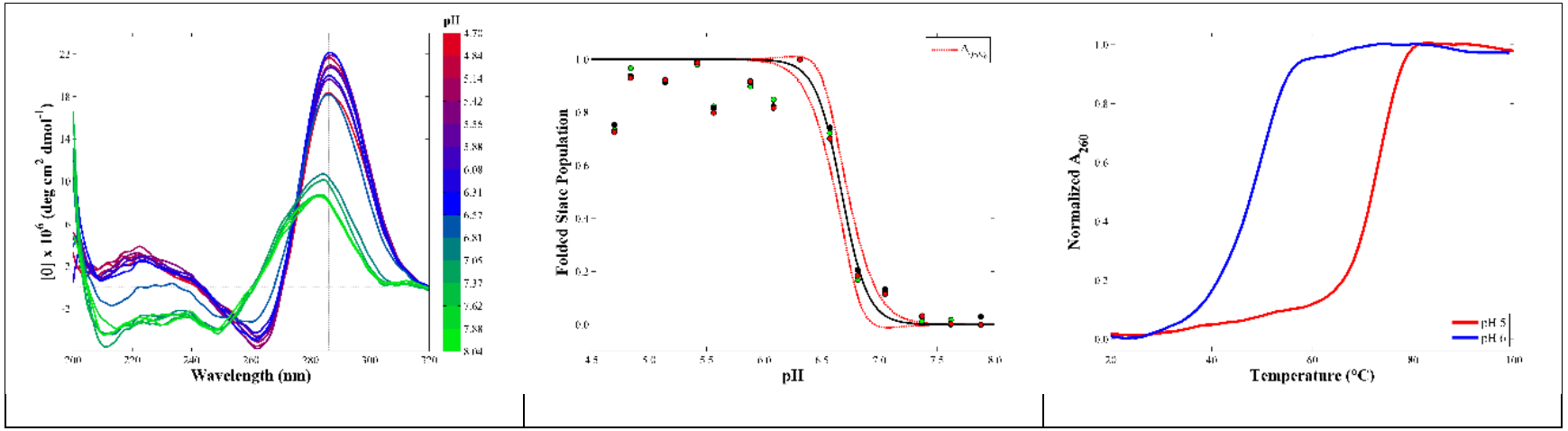

Figure S5: *NEIL1*

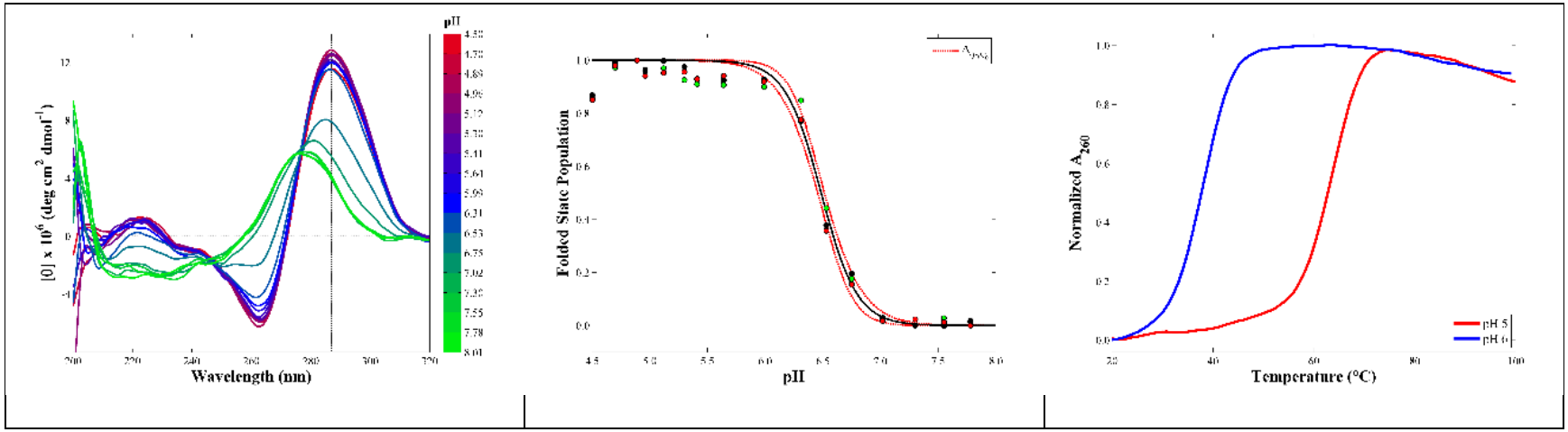

Figure S6: *NEIL2* – 4 track

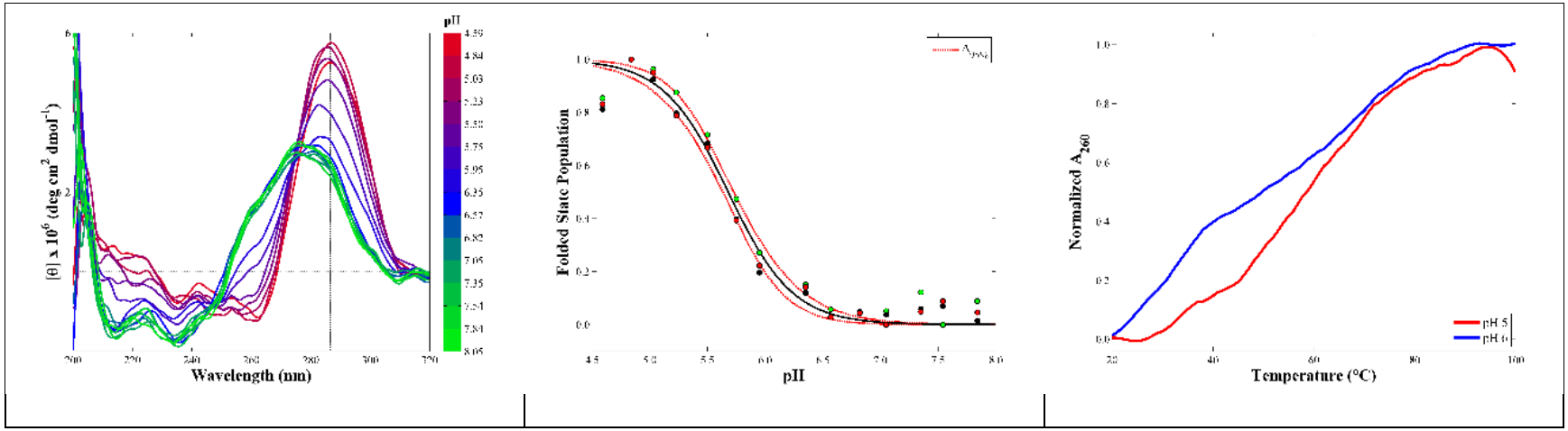

Figure S7: *NEIL2* – 5 track

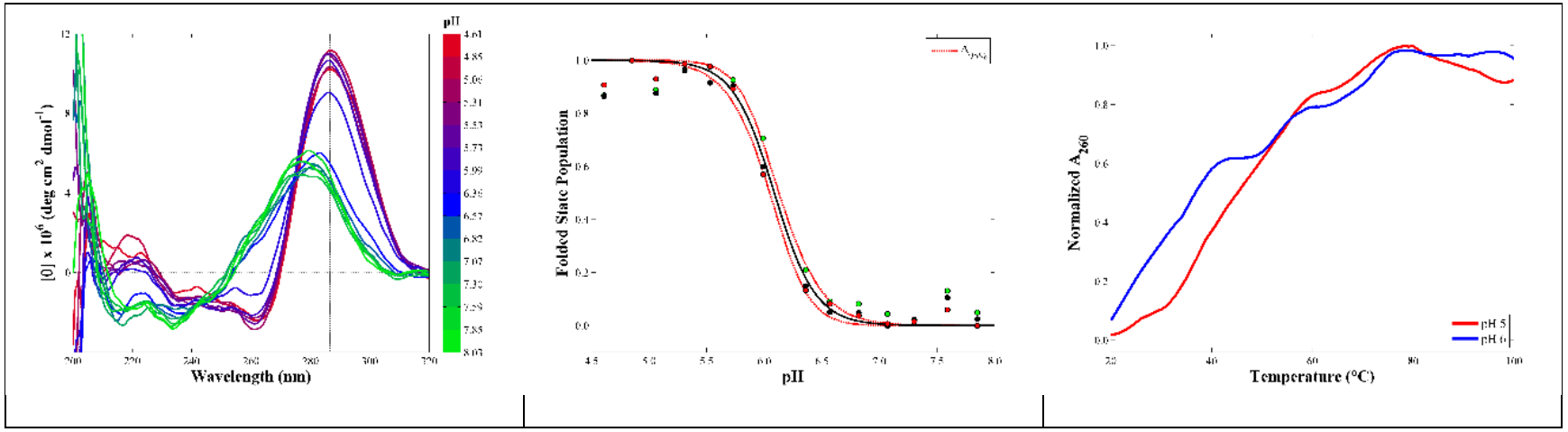

Figure S8: *NEIL2* – 6 track

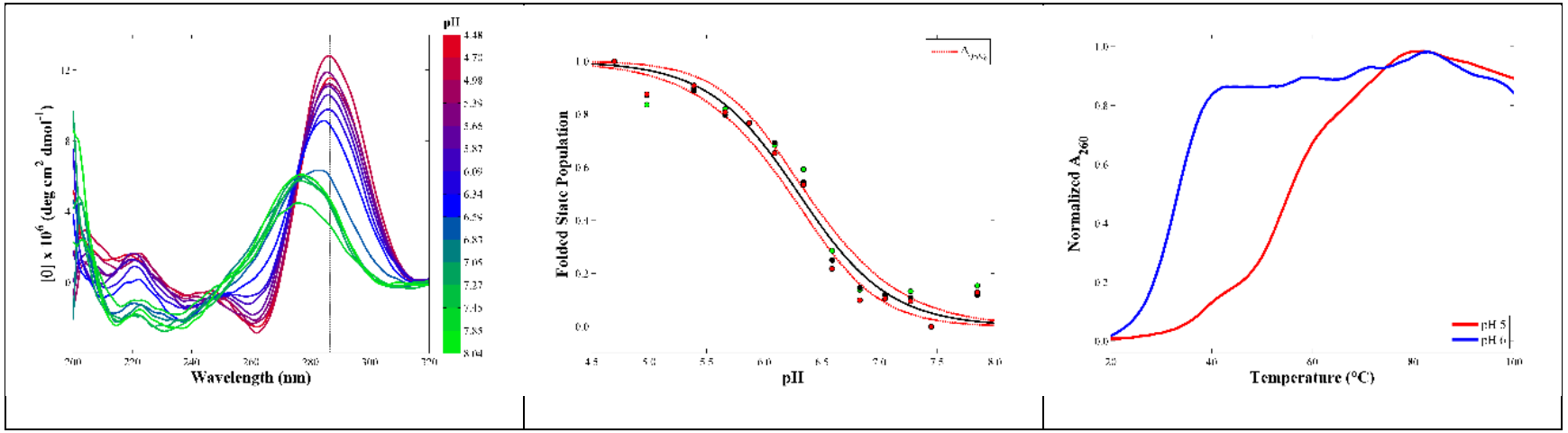

Figure S9: *NEIL3* – 4 track

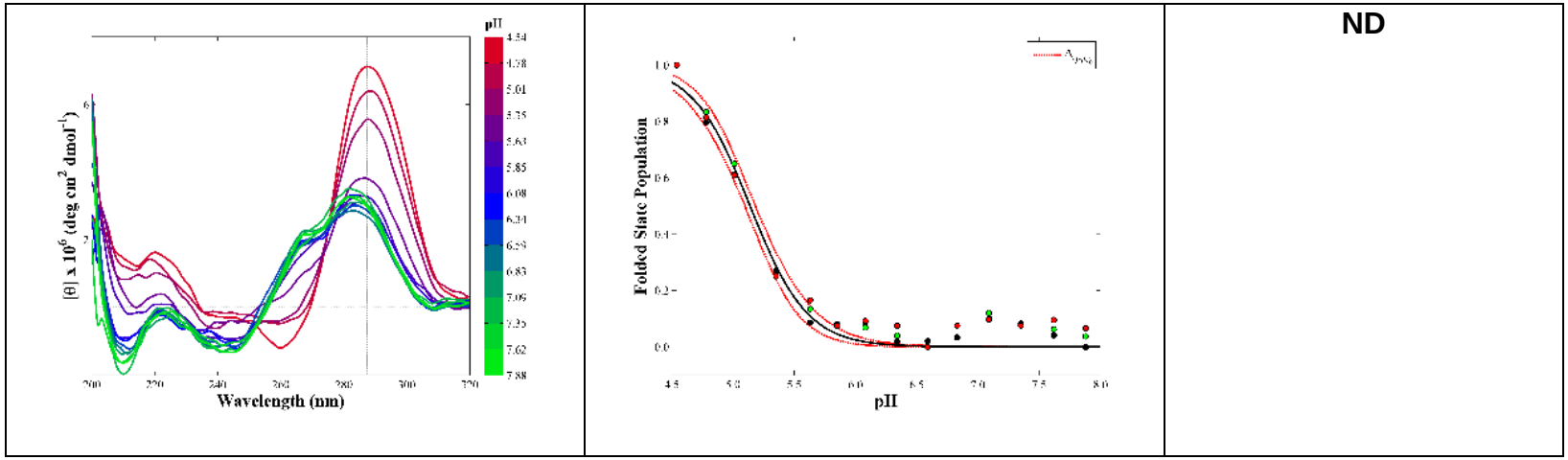

Figure S10: *NEIL3* – 5 track

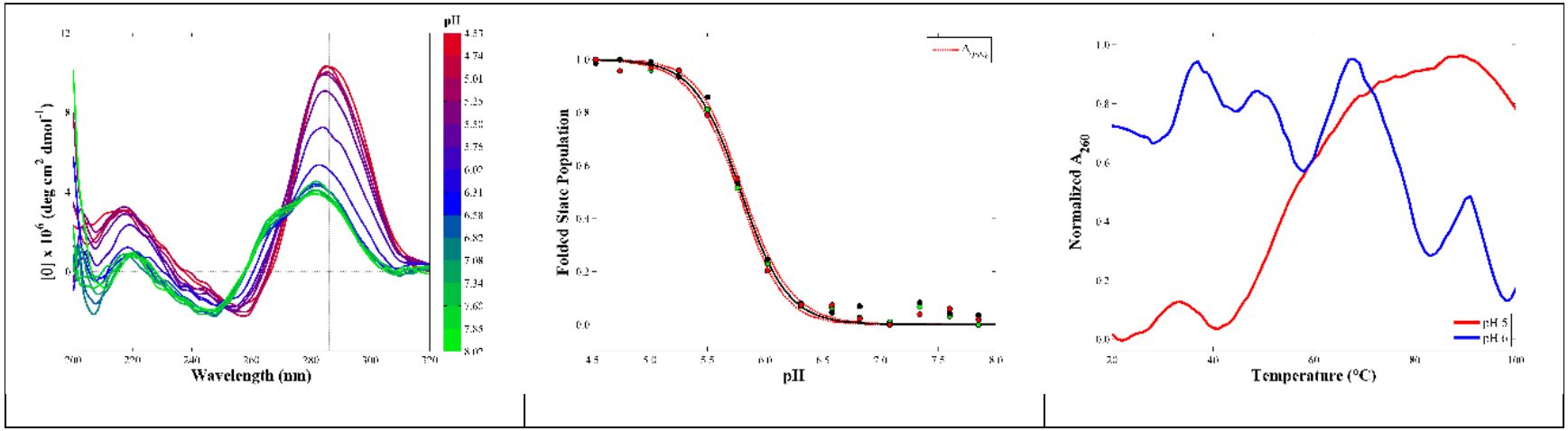

Figure S11: *NTHL1* – 4 track

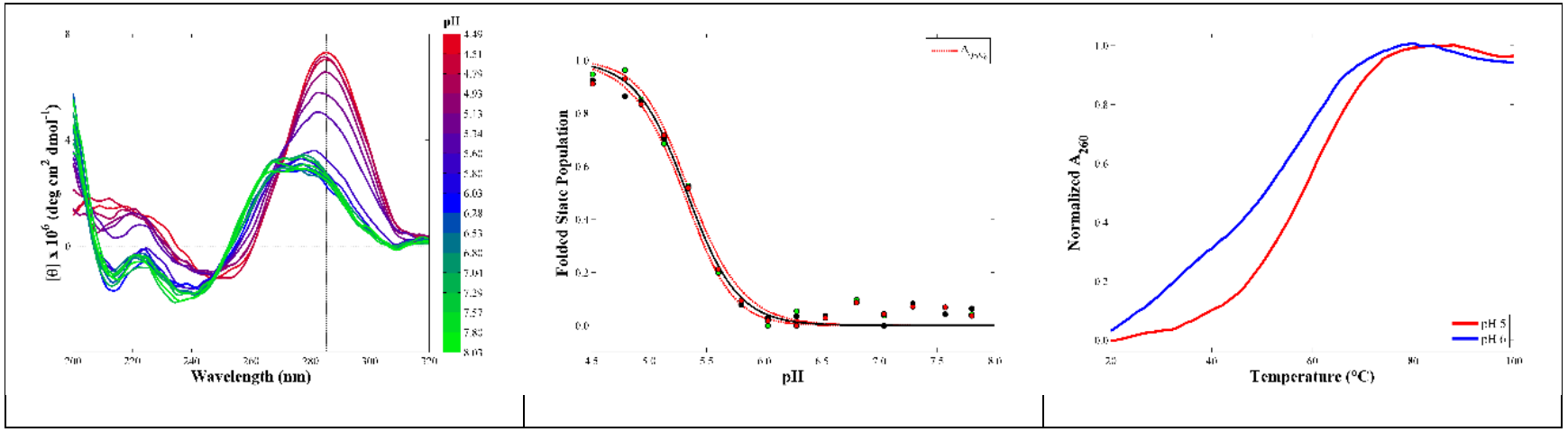

Figure S12: *NTHL1* – 5 track

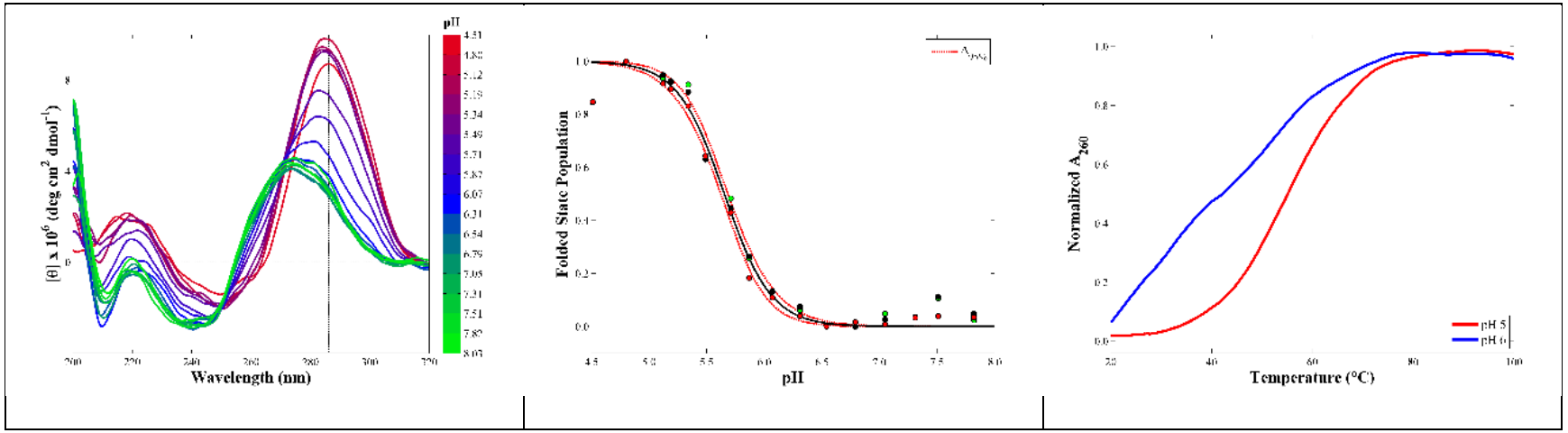

Figure S13: *PCNA* – Sequence 1

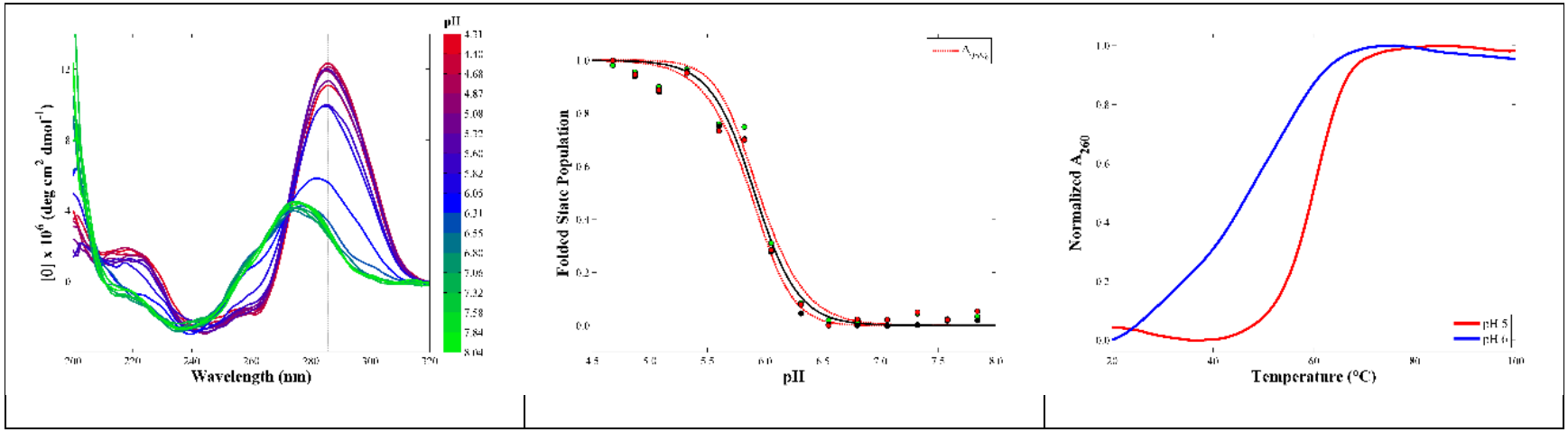

Figure S14: *PCNA* – Sequence 2

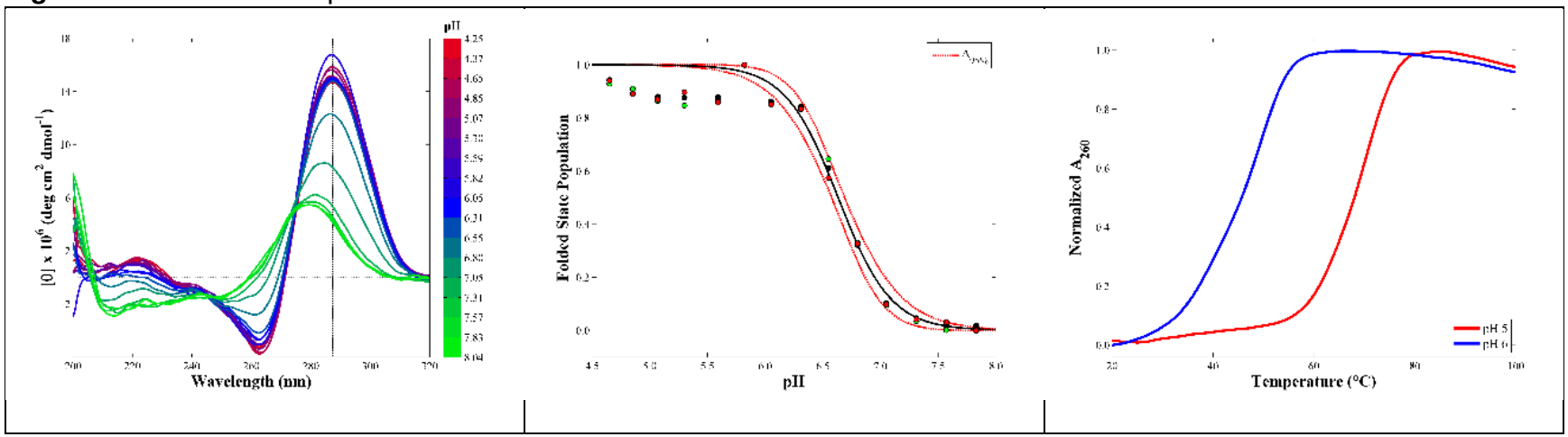

Figure S15: *Polβ*

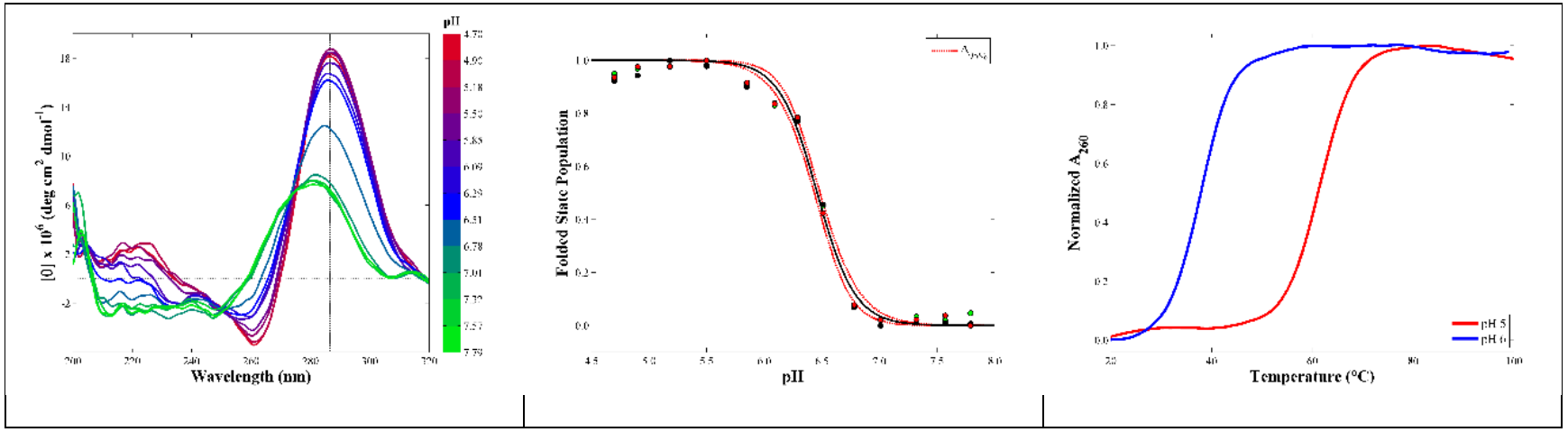

Figure S16: *Polη*

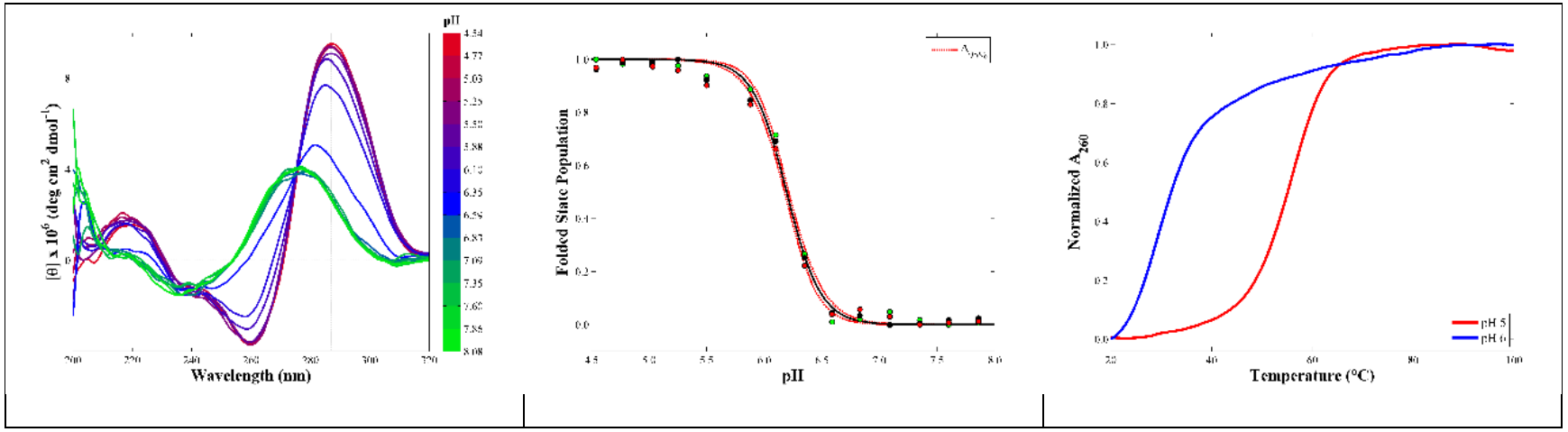

Figure S17: *RAD17* – Sequence 1

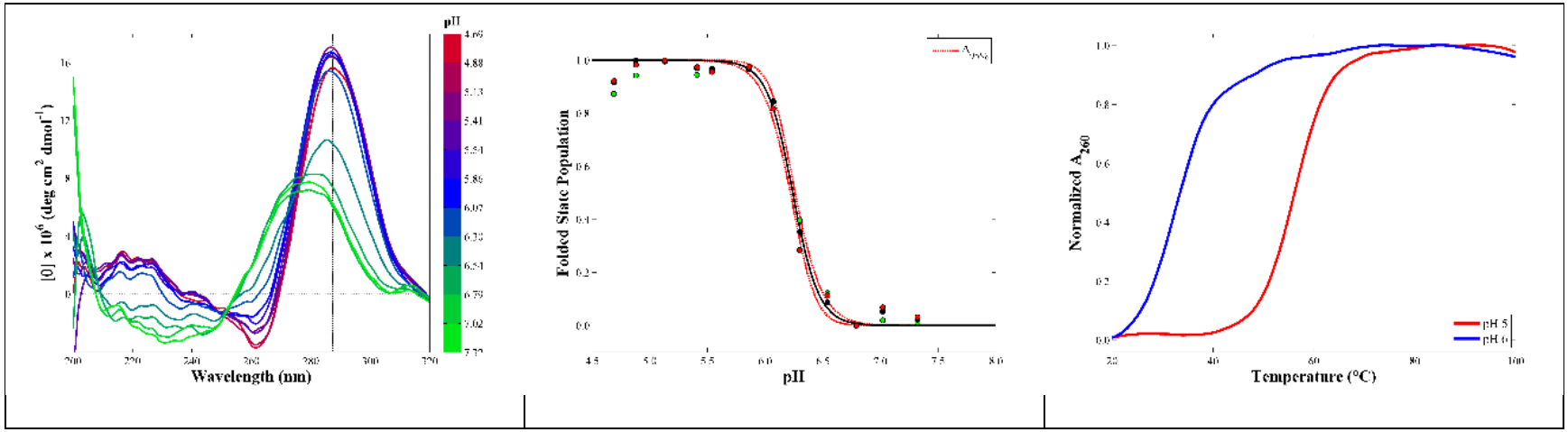

Figure S18: *RAD17* – Sequence 2

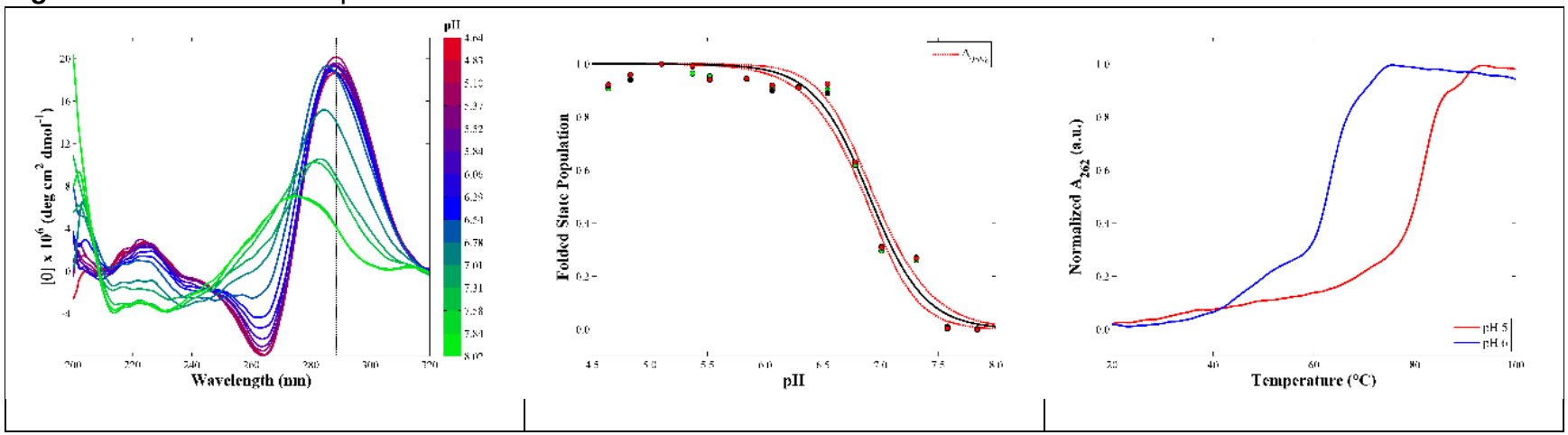

Figure S19: *RAD21*

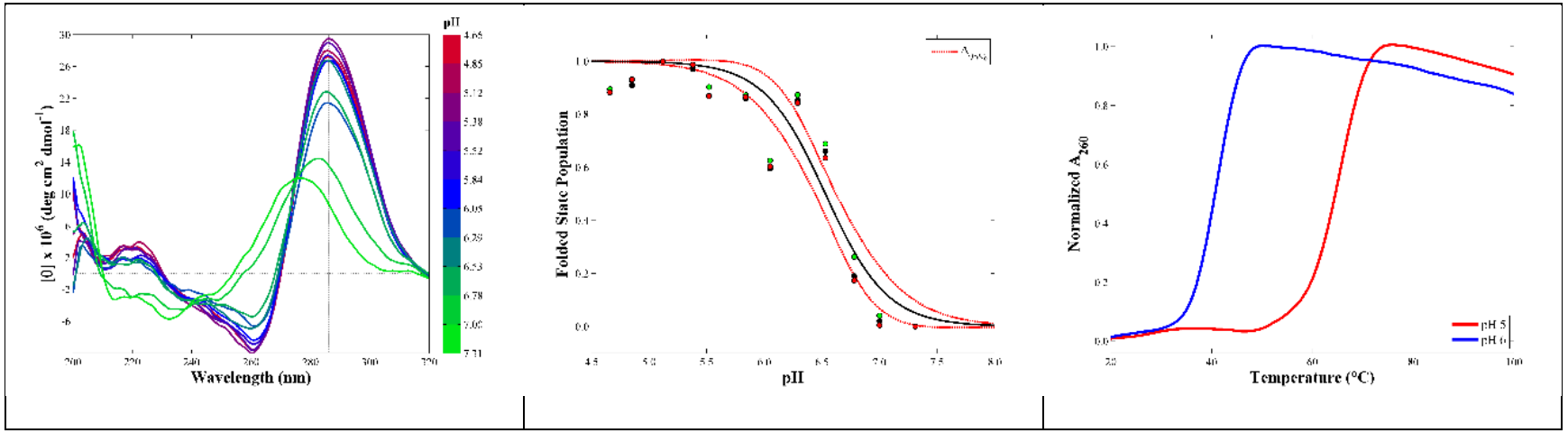

Figure S20: *RAD54L*

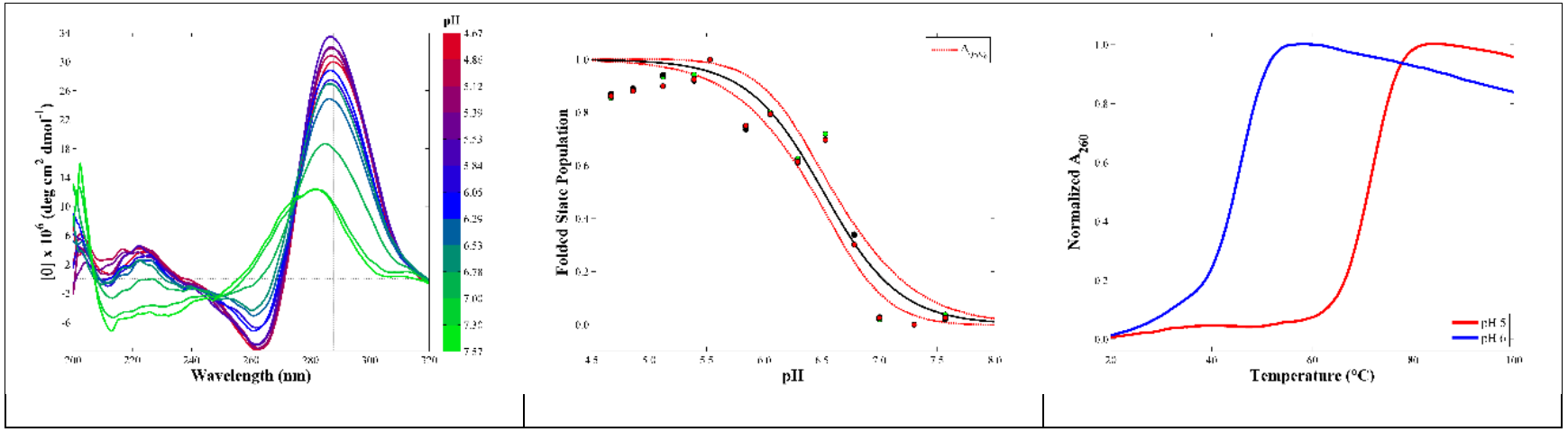

Figure S21: *UDG* – 4 track

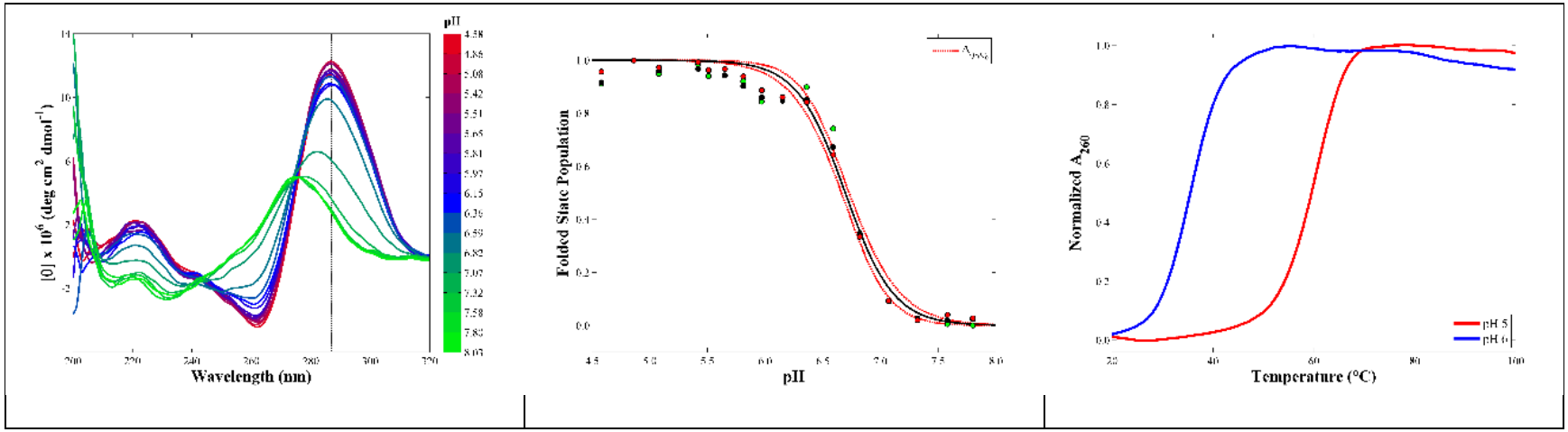

Figure S22: *UDG* – 5 track

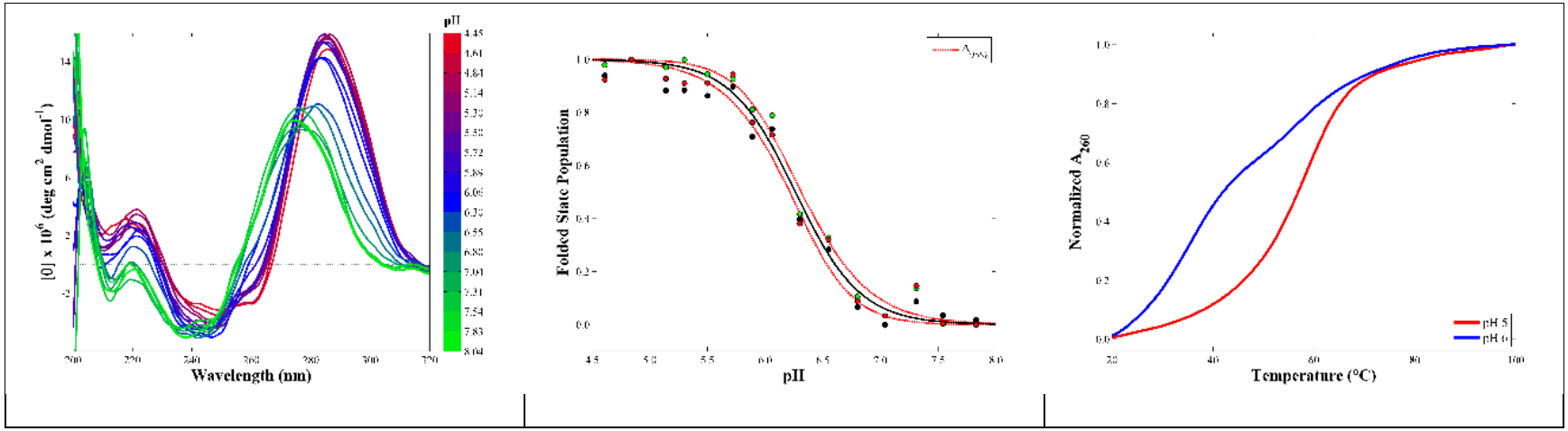

Figure S23: *XRCC2*

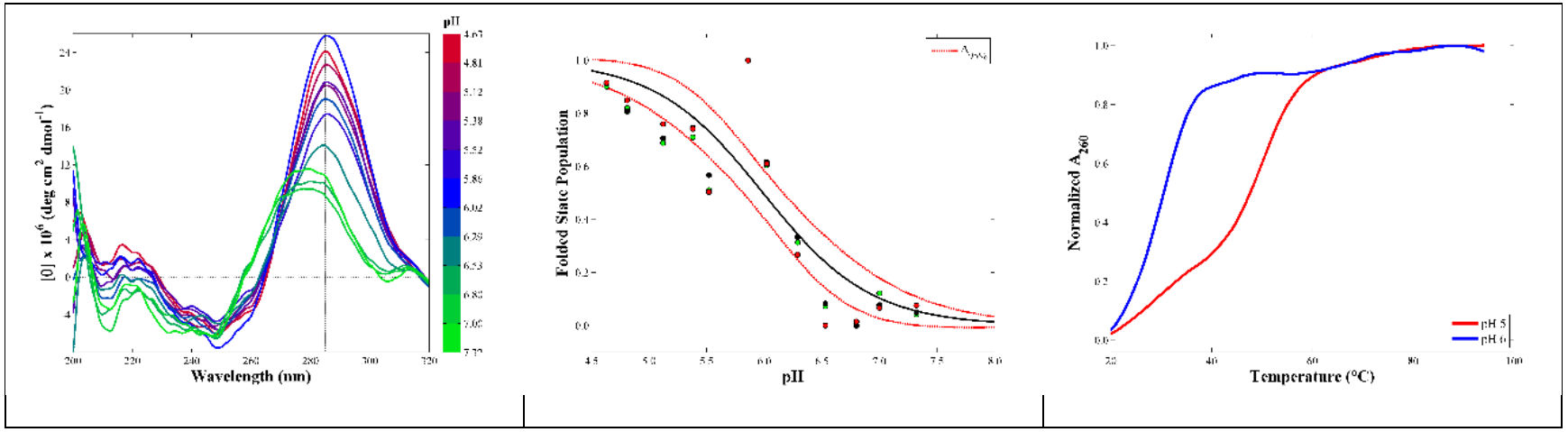

Figure S24: *XRCC3*

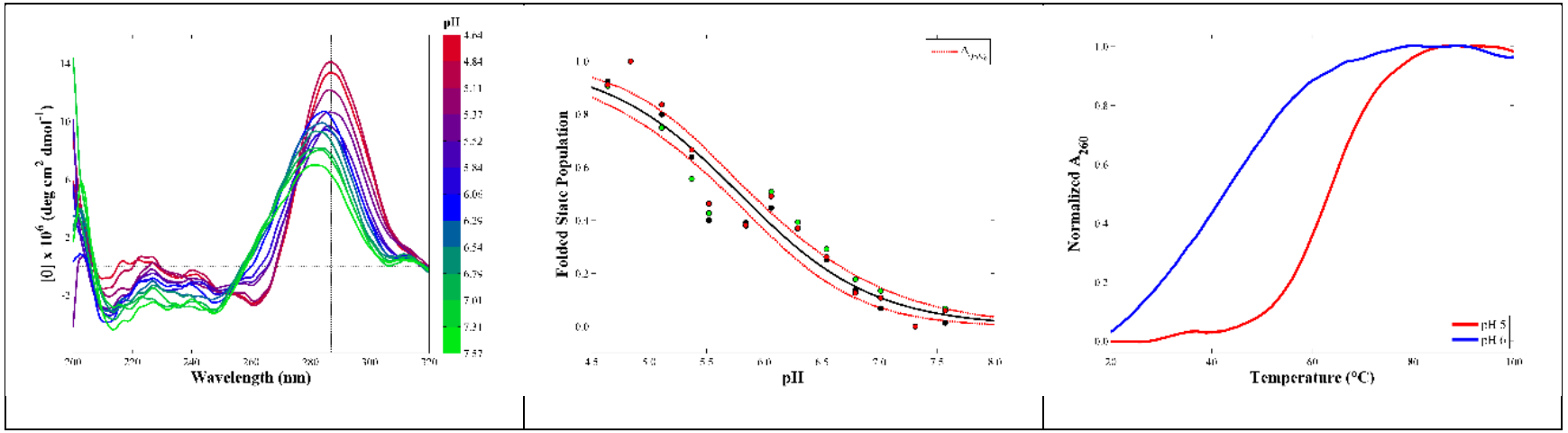

Figure S25: *XRCC5*

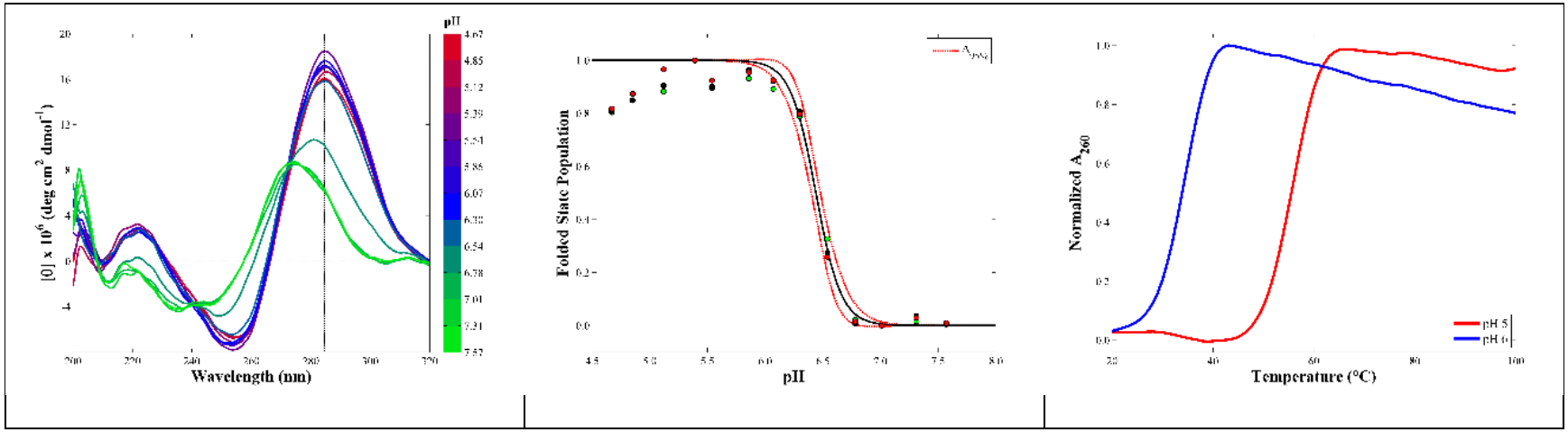

Figure S26: Top-to-bottom direct comparison of Figures 1 and 2 in the manuscript for ease of visual comparison of pH_T values.