

SUPPLEMENTARY INFORMATION

Spectral Tuning Mechanism of Primate Blue-Sensitive Visual Pigment Elucidated by FTIR Spectroscopy

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Table 1

Table1: Frequency of HOOP bands (Table.1)					
	(-) C ₁₁ =C ₁₂ HOOP	(+) C ₁₁ HOOP	(+) C ₁₂ HOOP	Δ (C ₁₁ -C ₁₂ HOOP)	S ^a
MB	961	928	865	63	0.00252
MB Y265W	963	924	865	59	0.00190
MRh W265Y	970	923	857	66	0.00299
MRh	966	917	857	60	0.00238
MG	973	907 ^b	848	59	0.00540
MR	973	906 ^c	847	59	0.00516

^a Sum of the intensity of negative bands from C₁₁=C₁₂ HOOP

^b Average of two positive bands (911cm⁻¹ and 903cm⁻¹)

^c Average of two positive bands (909cm⁻¹ and 903cm⁻¹)

Supplementary Figure legends

Figure S1. Amino acid sequences of monkey blue, rhodopsin (bovine and monkey), monkey green, and monkey red. (a) 26 amino acids within 5 Å from the retinal chromophore in the X-ray structure of bovine rhodopsin are shown. The amino acids are identical between bovine and monkey rhodopsins. The two key residues for monkey blue, Glu113 and Tyr265 are highlighted by red. The residue numbers are based on the bovine rhodopsin sequence. (b) Schematic representation of the 26 amino acid differences around 11-*cis*-retinal among each pigments.

Figure S2. Light-induced difference FTIR and UV-visible absorption spectra of mutant proteins, and correlation between the retinal C=C stretching frequency and λ_{\max} . (a) Light-induced difference FTIR spectra of MB, MB-Y265W, MRh-W265Y, MRh, MG and MR in the 1800-800 cm^{-1} region at 77 K. One division of the y-axis corresponds to 0.0013 absorbance units. (b) Expanded spectra from (a) in the 1630-1450 cm^{-1} region. One division of the y-axis corresponds to 0.0013 absorbance units. (c) UV-visible absorption spectra of MB ($\lambda_{\max} = 417$ nm), MB-Y265W ($\lambda_{\max} = 434$ nm), MRh-W265Y ($\lambda_{\max} = 481$ nm), MRh ($\lambda_{\max} = 499$ nm), MG ($\lambda_{\max} = 530$ nm) and MR ($\lambda_{\max} = 563$ nm). (d) Correlation of the unphotolyzed retinal C=C stretching frequencies of MB (1576 cm^{-1}), MB-Y265W (1566 cm^{-1}), MRh-W265Y (1564 cm^{-1}), MRh (1561 cm^{-1}), MG (1534 cm^{-1}) and MR (1526 cm^{-1}) from (b) with their absorption maxima from (c).

Figure S3. Structural changes from rhodopsin (green) to bathorhodopsin (red), and representation around retinal binding pocket. (a) Structural changes from rhodopsin (green) to batho-intermediate state, bathorhodopsin (red) are viewed from extracellular side. The double bond at the position C₁₁ and C₁₂ (C₁₁=C₁₂) is highlighted about highly distortion. (b) Part of the retinal binding pocket are viewed from helix VI, where the curvature along the polyene chain of retinal is emphasised, and side chain of W265 is facing towards atoms of C₁₁ and C₁₂.

Figure S4. HOOP band correlation diagrams for dark and batho-intermediate state among each pigments with their absorption maxima, and summary of the HOOP band frequencies of the batho-intermediate state. (a) Correlation of the C₁₁=C₁₂ HOOP band frequencies of different pigments in the dark state with their absorption maxima. (b) Correlation of the C₁₁ or C₁₂ HOOP band frequencies of different pigments in the batho-intermediate state with their absorption maxima. (c) Calculated area of C₁₁=C₁₂ HOOP band of different pigments in the dark state with their absorption maxima. (d) Summary of the HOOP band frequencies of different pigments in the batho-intermediate state.

Figure S5. Light-induced difference FTIR of MB, MB-Y265W, MRh-W265Y and MRh in the 3400-3200 cm^{-1} region at 77 K. One division of the y-axis corresponds to 0.0005 absorbance units.

Figure S6. Light-induced difference FTIR of MB (blue solid and dotted lines), MB-Y265W (light blue) and MB-E113D (magenta) in the 2730-2460 cm^{-1} region at 77 K. One division of the y-axis corresponds to 0.00016 absorbance units.

Figure S7. Light-induced difference FTIR of MB, MB-Y265W, MRh-W265Y, MRh, MG and MR in the 3600-3380 cm^{-1} region at 77 K. One division of the y-axis corresponds to 0.0005 absorbance units.

Figure S8. Light-induced difference FTIR of MB, MRh, MG and MR in the 2150-1930 cm^{-1} region at 77 K. One division of the y-axis corresponds to 0.00004 absorbance units.

Figure S1

(a)

		113		125	164	181		191												
monkey blue (417nm)	:	E	G	..	G	T	..	G	L	..	G	G	E	...	S	C	G	P	..	W
rhodopsin (499nm)	:	E	G	..	A	T	..	G	E	..	L	A	E	...	S	C	G	I	..	Y
monkey green (530nm)	:	E	G	..	V	S	..	G	I	..	L	A	H	...	S	C	G	P	..	V
monkey red (563nm)	:	<u>E</u>	<u>G</u>	..	<u>V</u>	<u>S</u>	..	<u>G</u>	<u>I</u>	..	<u>L</u>	<u>S</u>	<u>H</u>	...	<u>S</u>	<u>C</u>	<u>G</u>	<u>P</u>	..	<u>V</u>
		Helix III					Helix IV			E-II loop										
		207		212	261	265		269	292		296									
monkey blue (417nm)	:	L	F	..	C	F	F	...	Y	..	Y	A	A	F	..	S	K			
rhodopsin (499nm)	:	M	F	..	H	F	F	...	W	..	Y	A	A	F	..	A	K			
monkey green (530nm)	:	L	M	..	C	C	F	...	W	..	Y	A	A	Y	..	A	K			
monkey red (563nm)	:	<u>L</u>	<u>M</u>	..	<u>C</u>	<u>C</u>	<u>Y</u>	...	<u>W</u>	..	<u>Y</u>	<u>T</u>	<u>A</u>	<u>Y</u>	..	<u>A</u>	<u>K</u>			
		Helix V				Helix VI				Helix VII										

(b)

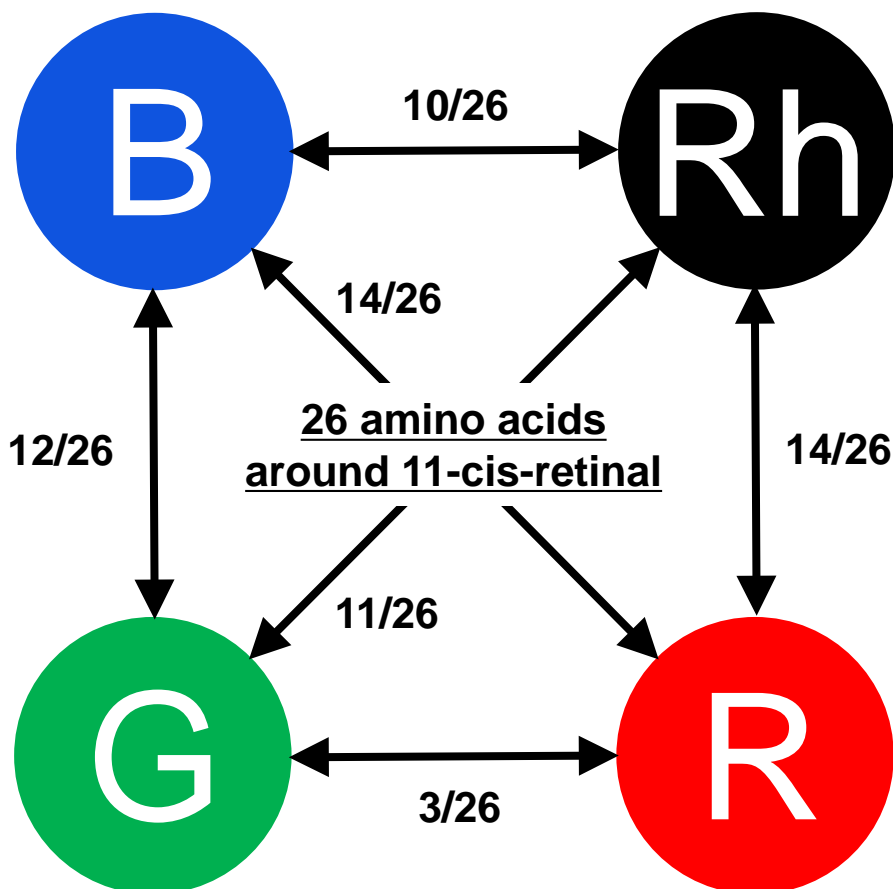


Figure S2

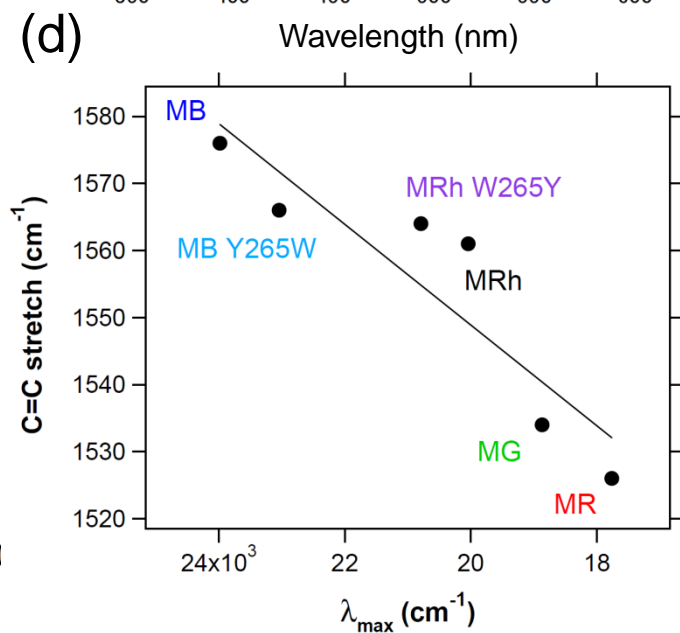
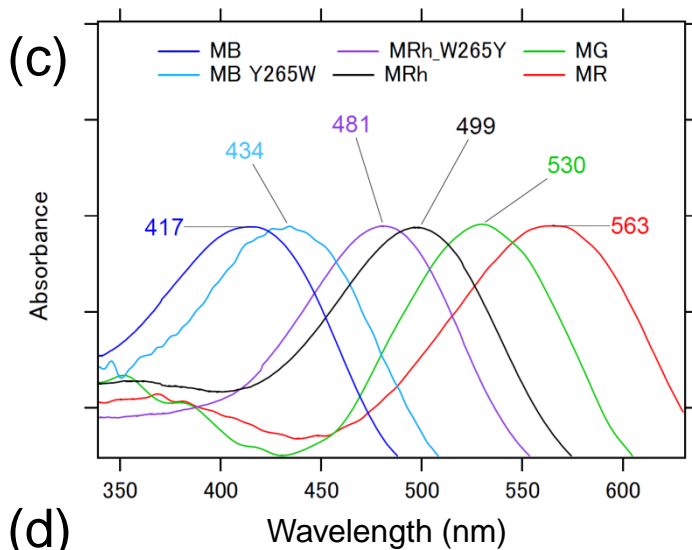
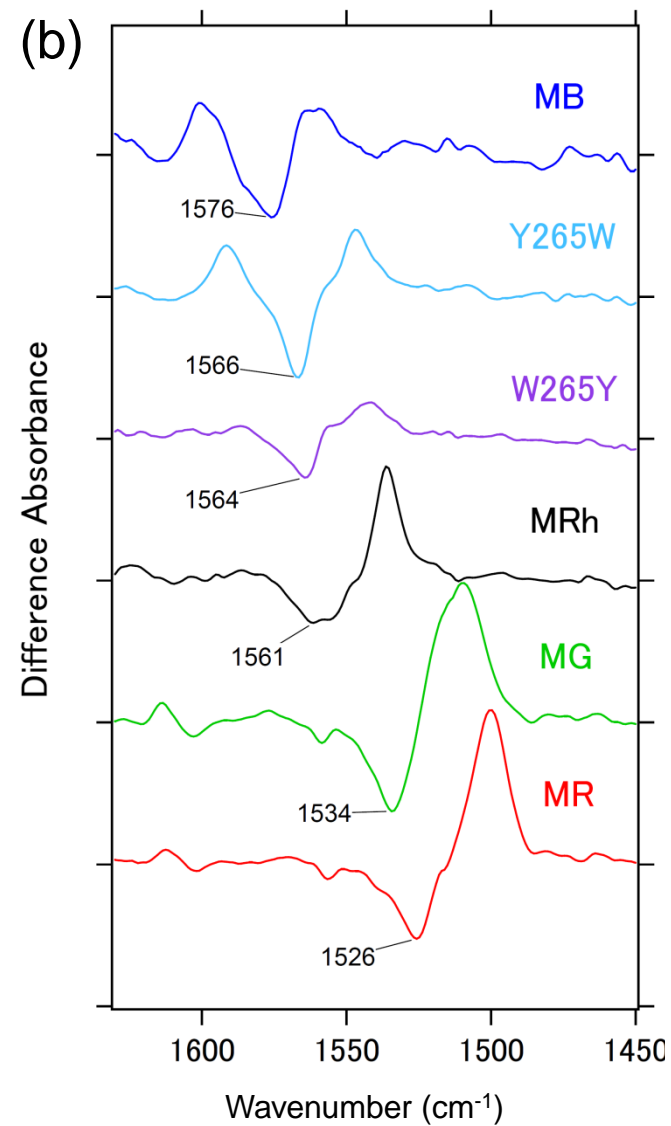
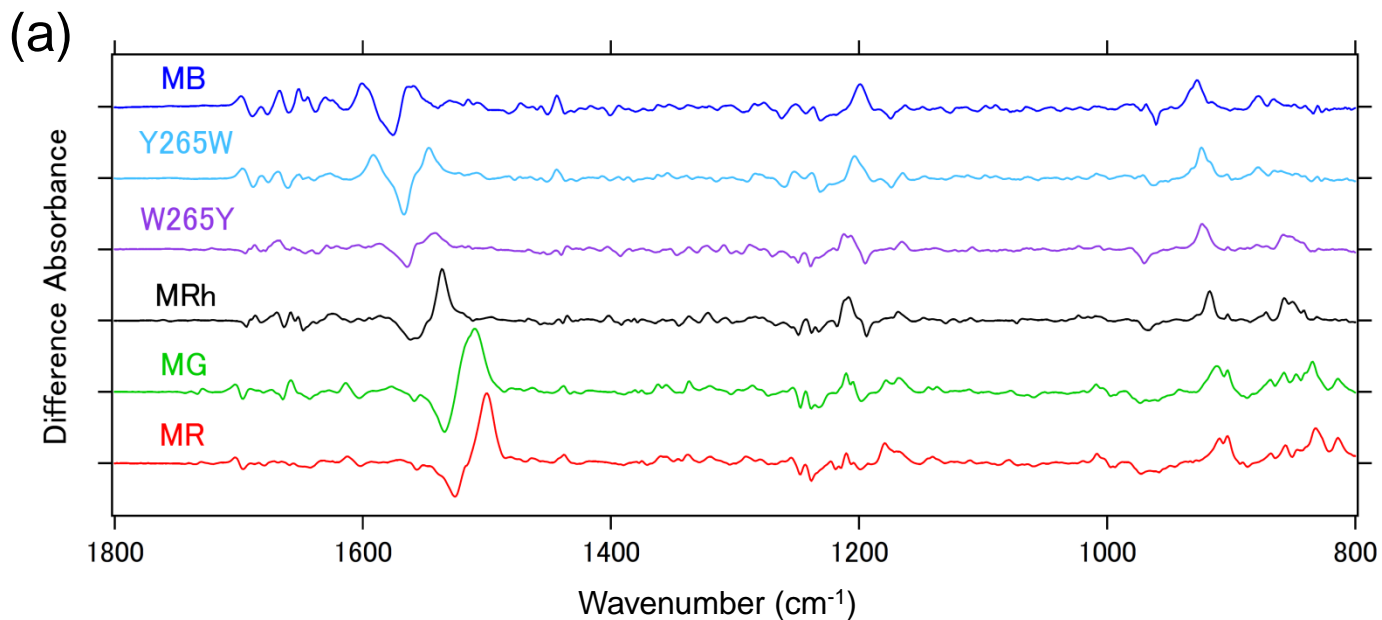
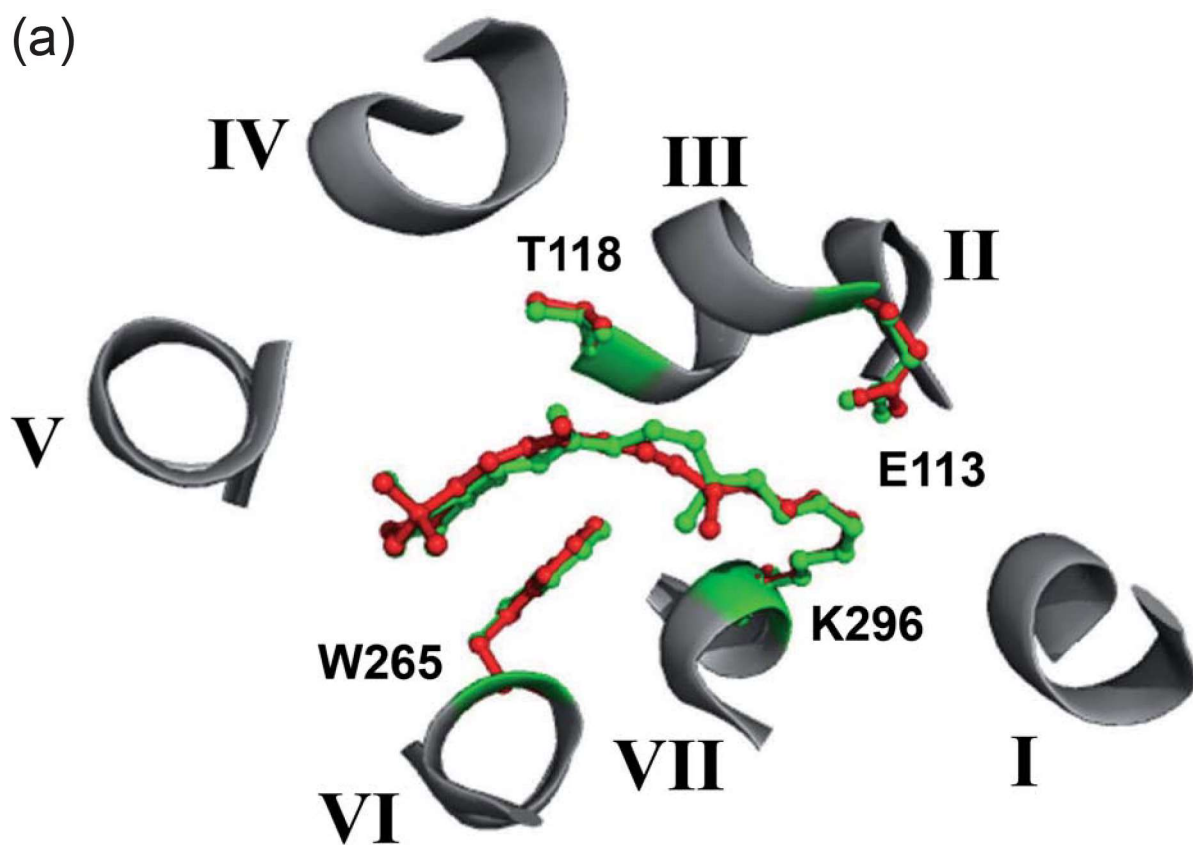


Figure S3

(a)



(b)

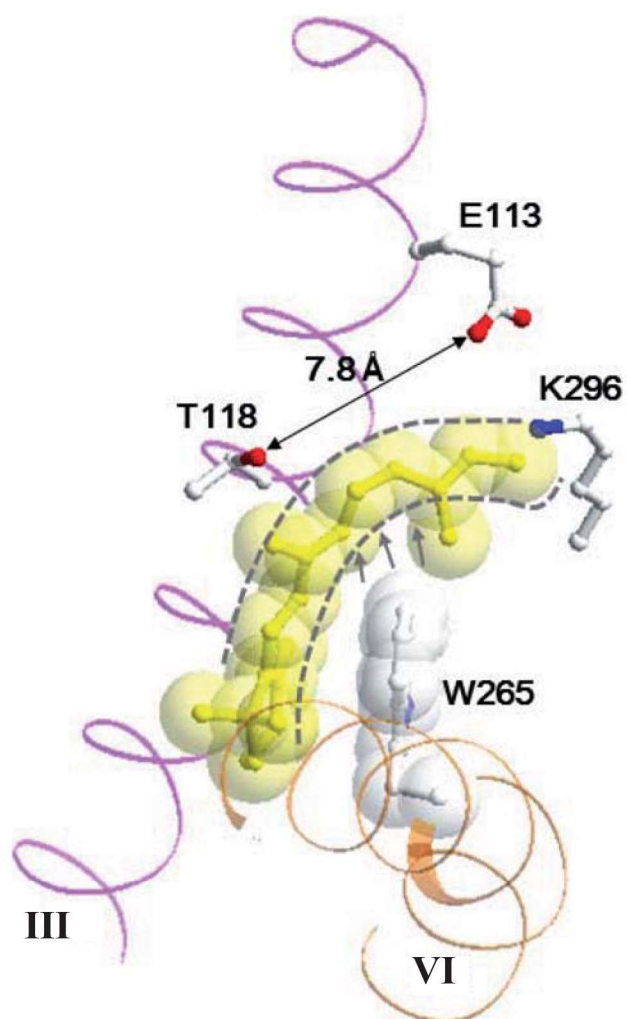


Figure S4

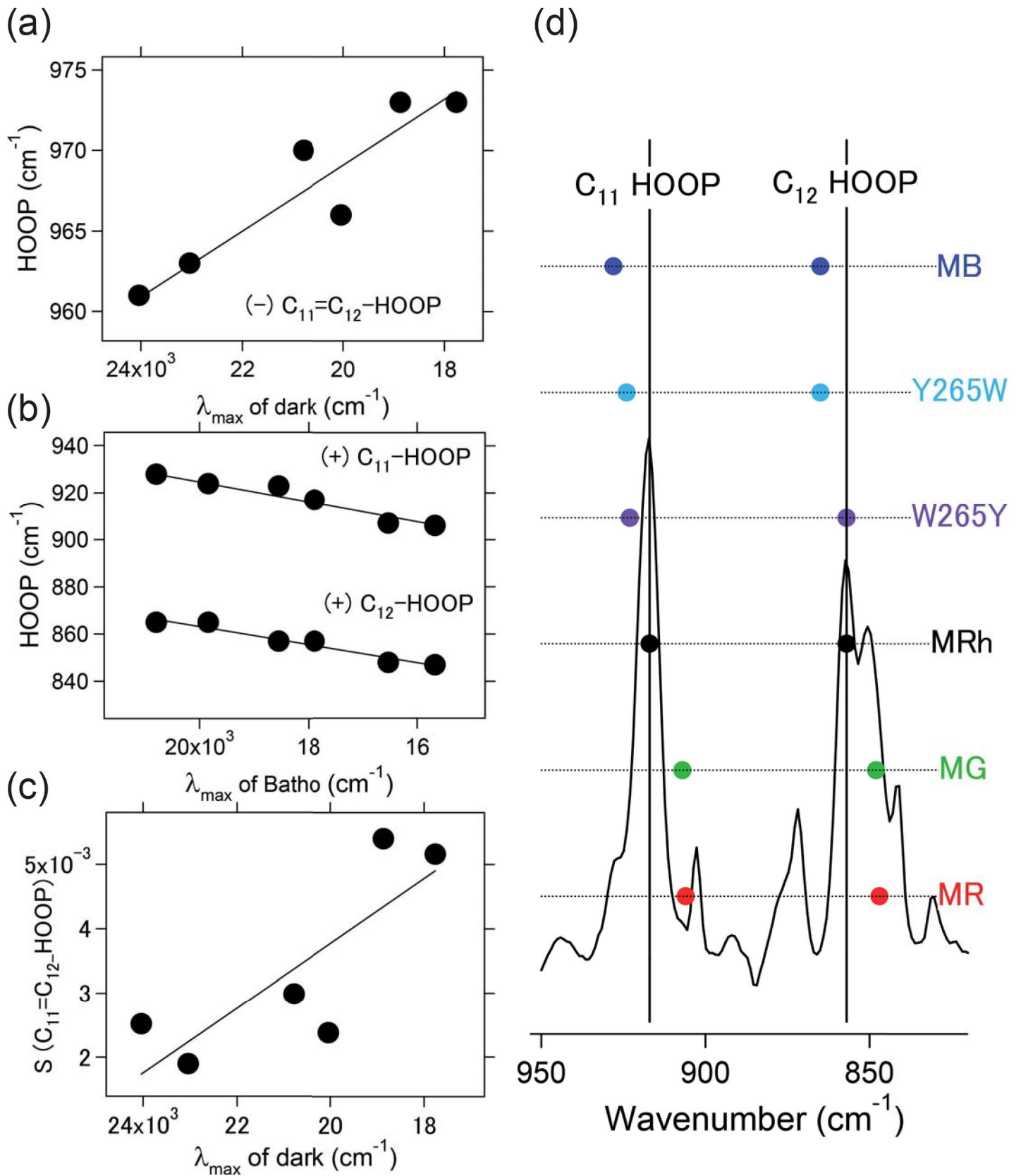


Figure S5

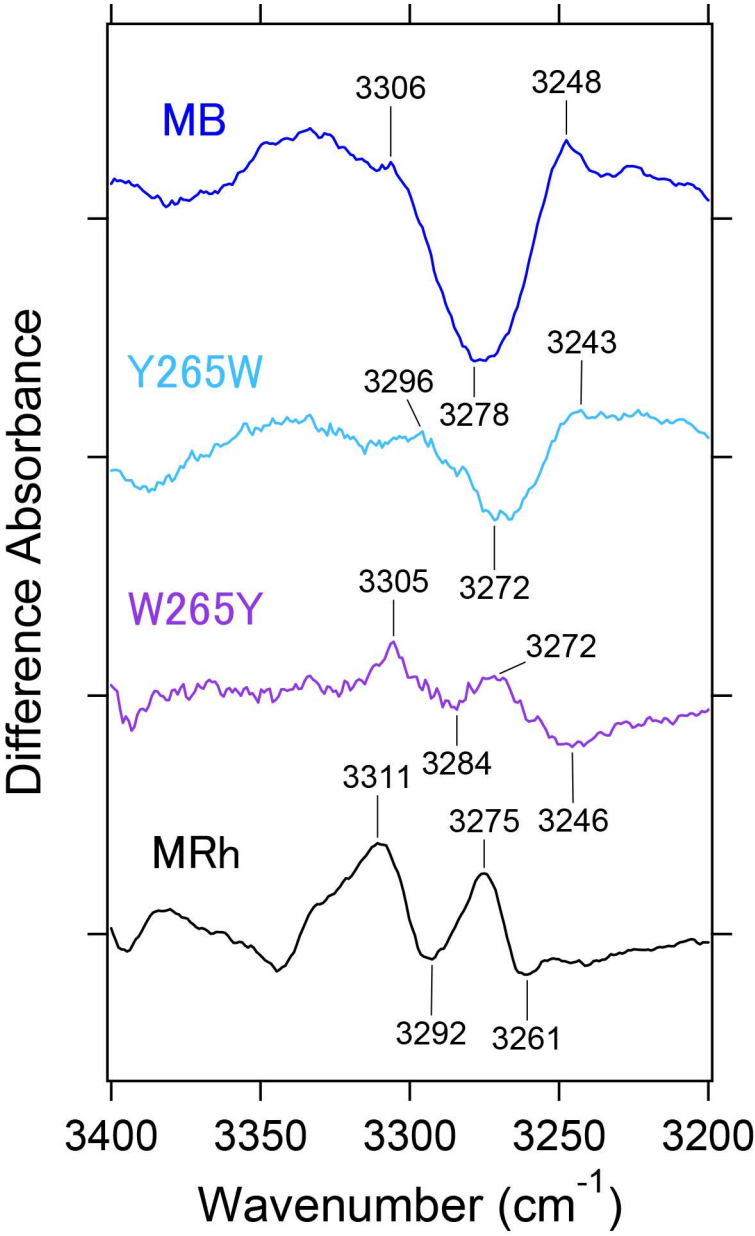


Figure S6

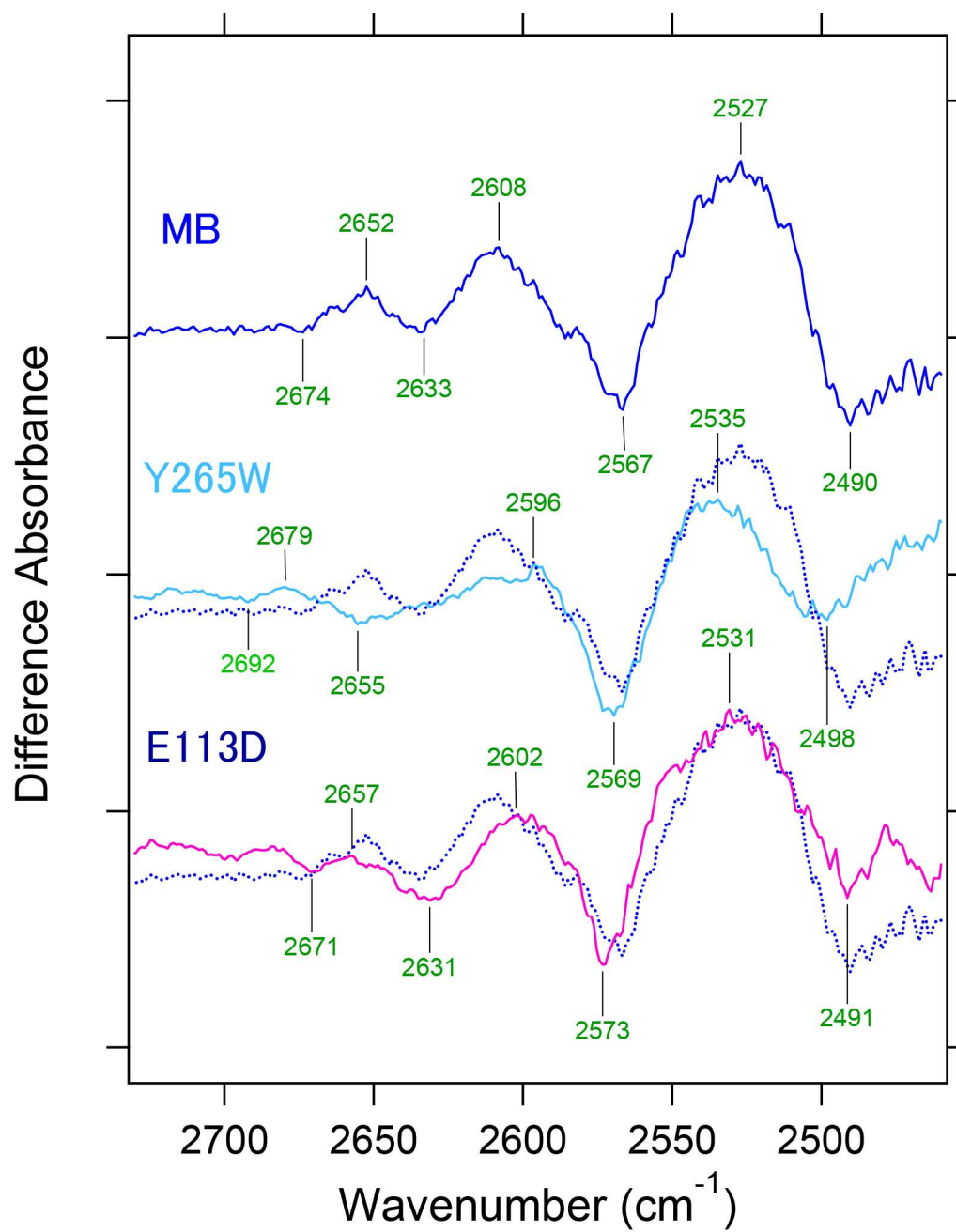


Figure S7

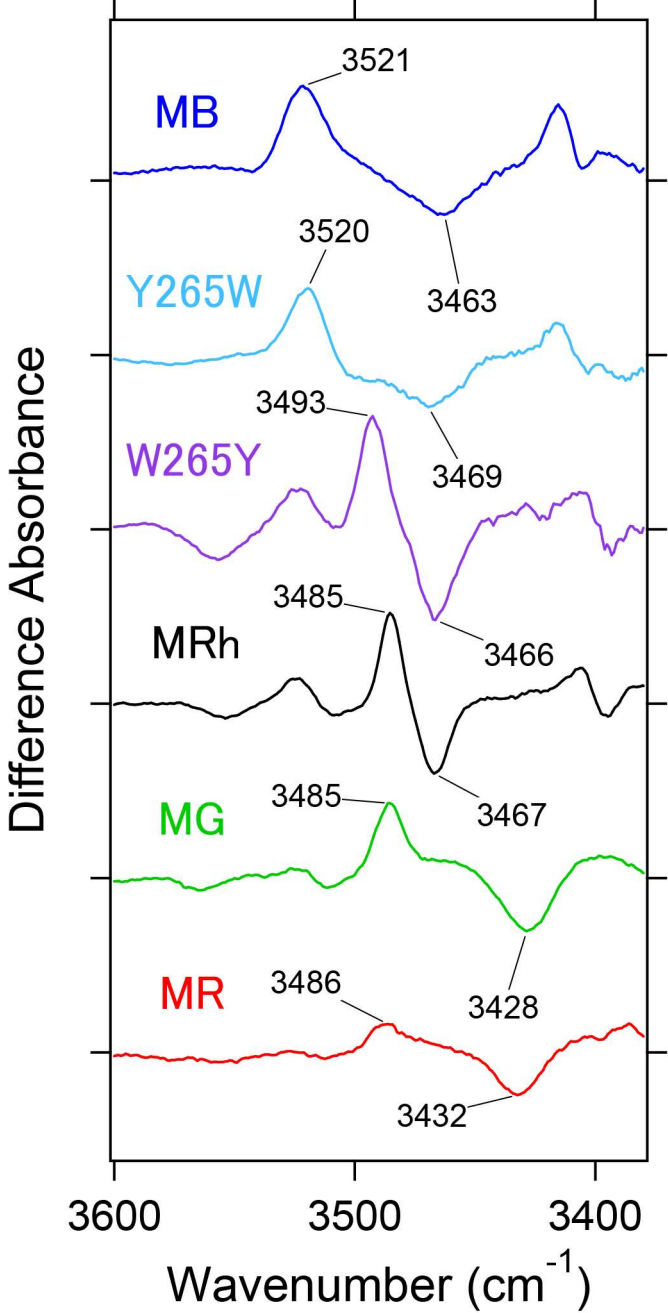


Figure S8

