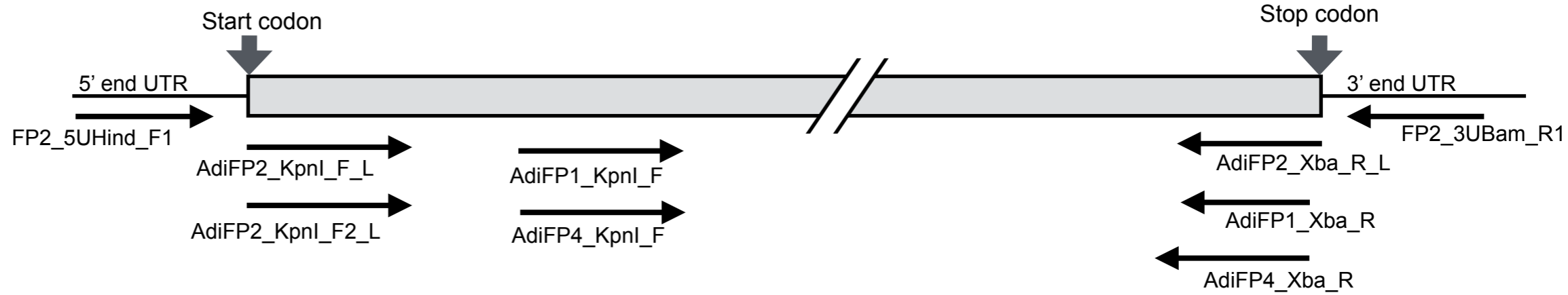


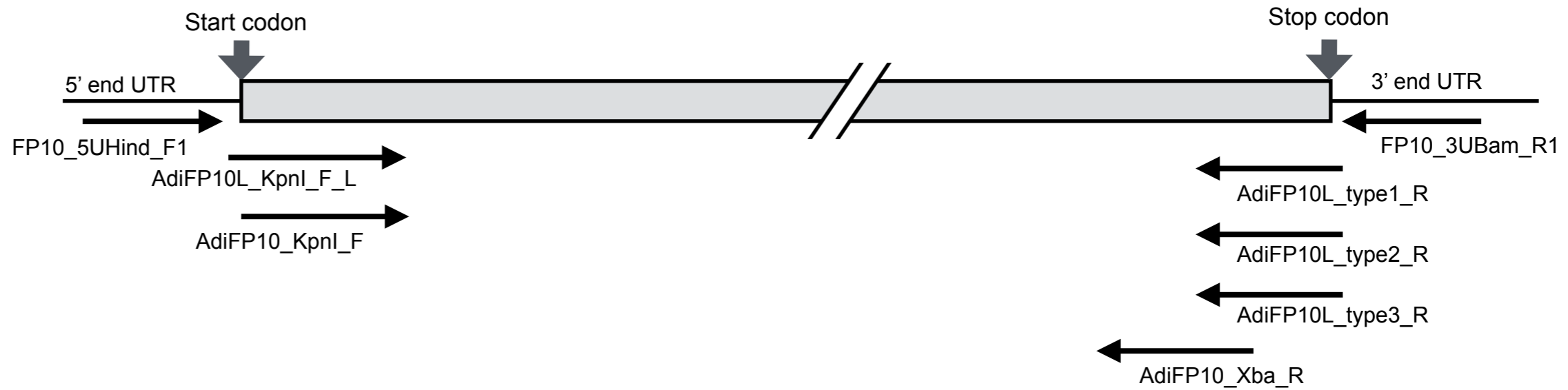
Supporting Figure S1.

(A)

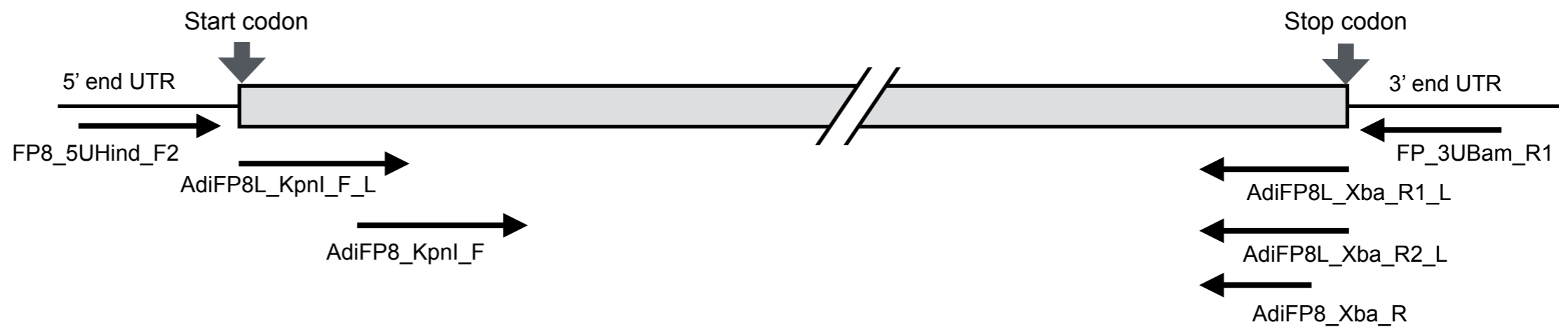
AdiFP2



AdiFP10L



AdiFP8L

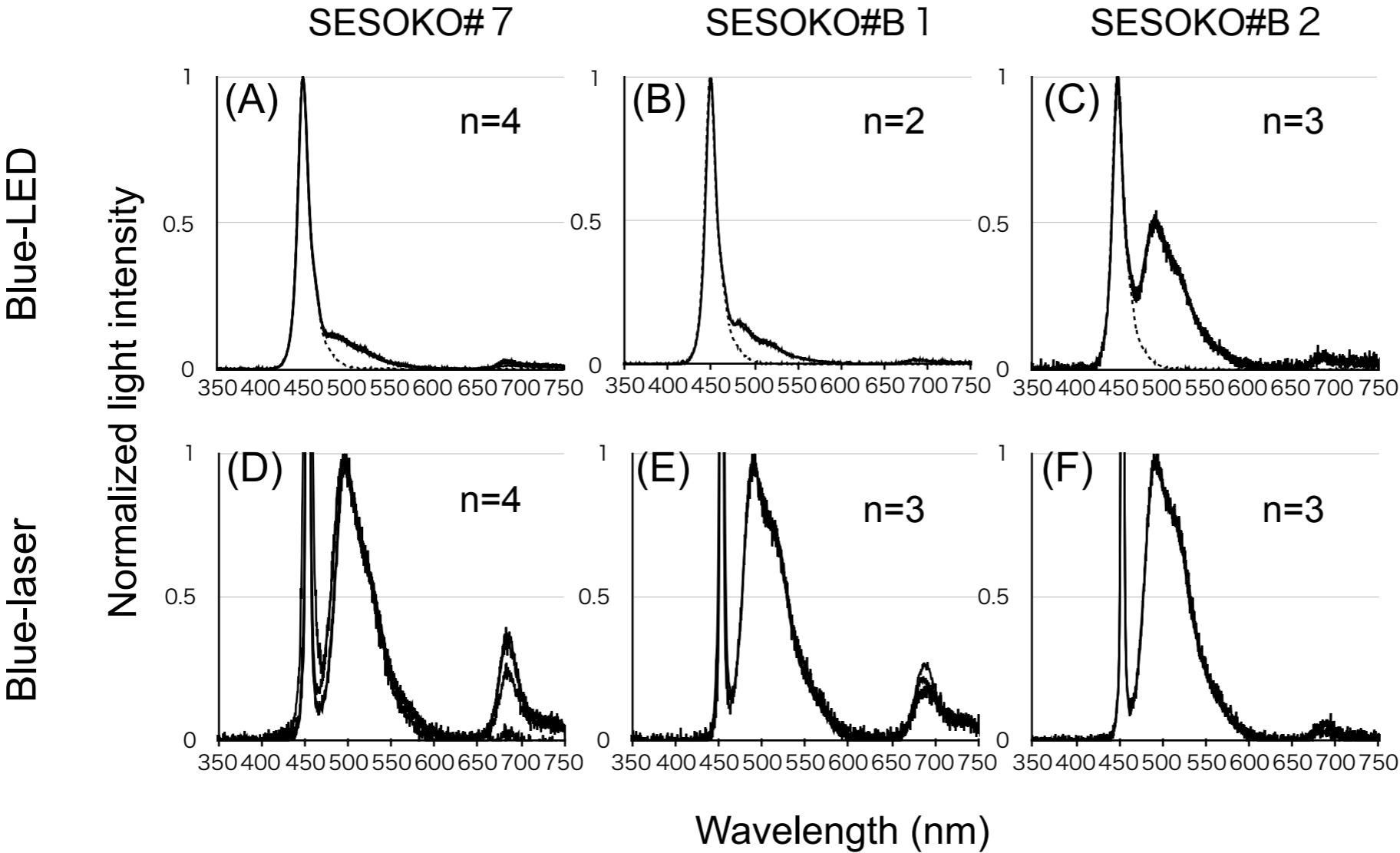


Supporting Fig. S1 continued

(B)

Name of primers	Sequence of primers
FP2_5UHind_F1	5'-CACACAAAGCTTGACRGAGTGAACTRCCGTRAACAG-3'
FP2_3UBam_R1	5'-CACACAGGATCCGTAAGTATTGAAAGTGCTTCCATC-3'
FP10_5UHind_F1	5'-CACACAAAGCTTGCARGAGAGTTACTHGASTTTTGTATCAC-3'
FP10_3UBam_R1	5'-CACACAGGATCCCAGAGWAATAAGCATGCGCATGTAAC-3'
FP8_5U_F2	5'-TCTCTTTCACGGAAGGAGCTACTTAA-3'
FP8_5U_R1	5'-GTYTACACTTCTTCGTTCTACTTC-3'
AdiFP1KpnI_F	5'-CAGGTACCATGAAGACAAAATACCATATGG-3'
AdiFP1XbaI_R	5'-TGTCTAGATTATTGAACCATCAAAGGGTTA-3'
AdiFP2KpnI_F	5'-AGGTACCATGTCTTATTCAAAGCAAGGCAT-3'
AdiFP2XbaI_R	5'-TGTCTAGATTATTTAACCTTCAAAGGGTTA-3'
AdiFP4KpnI_F	5'-CAGGTACCATGCGGACGAAAATACCATATG-3'
AdiFP4XbaI_R	5'-TGTCTAGATTAACTTCAAAGGATTAACATGAG-3'
AdiFP10KpnI_F	5'-CAGGTACCATGGAAGGGTCTGTGCGATGG-3'
AdiFP10XbaI_R	5'-TGTCTAGAGGAAGCAACAGCATGTTCTAC-3'
AdiFP8KpnI_F	5'-AGGTACCATGACCTACAAGGTTTATATGTC-3'
AdiFP8XbaI_R	5'-TGTCTAGATCAGGCGACCCACAGGTTTGC-3'
AdiFP2KpnI_F_L	5'-CACACAGGTACCATGTCTTATTCAAAGCAAGGCAT-3'
AdiFP2KpnI_F2_L	5'-CACACAGGTACCATGTCTCATTCAAAGCAAGGCAT-3'
AdiFP2XbaI_R_L	5'-TGTGTGTCTAGATTATTTAACCTTCAAAGGGTTA-3'
AdiFP10L_KpnIF_L	5'-CACACAGGTACCATGGCTCTGTCAAAGCACGGTCTA-3'
AdiFP10L_type1_R	5'-TGTGTGTCTAGATTATCCGGGCAATGCGGATC-3'
AdiFP10L_type2_R	5'-TGTGTGTCTAGATTATCAGGCCAATGCGGATC-3'
AdiFP10L_type3_R	5'-TGTGTGTCTAGATTATCAGGGCAATGCGGATC-3'
AdiFP8L_KpnIF_L	5'-CACACAGGTACCATGAGTGTGATCGCTAA-3'
AdiFP8XbaI_R1_L	5'-TGTGTGTCTAGATCAGGCGACCCACAGGTTTGC-3'
AdiFP8XbaI_R2_L	5'-TGTGTGTCTAGATCAGGCGACCACAAGTTTGC-3'
MWE_qPCR_F3	5'-TGACTATTCAAGCAAGCATTCCCAGATG-3'
MWE_qPCR_R1	5'-CGAATGTTCCAGCTGGCTGTAGC-3'
MLWE_qPCR_F3	5'-TTTCCTGCTGATGGACCTGTGATGA-3'
MLWE_qPCR_R1	5'-CCACCATCCTTCAGAAGGAGGTAC-3'
CP_qPCR_F1	5'-CAGTACGGAAGCATACCATTACCAAGTA-3'
MiA_CP_e3_R1	5'-TGGATGCTGGAATCATTGCTGACAGTACAC-3'
EF1a-qPCR_F1	5'-CTGTCTTGATTGTGGCTGCTGGAA-3'
EF1a-qPCR_R1	5'-GCTTTACTCCTAGGGTGTAAAGCCAACA-3'

Supporting Fig. S2

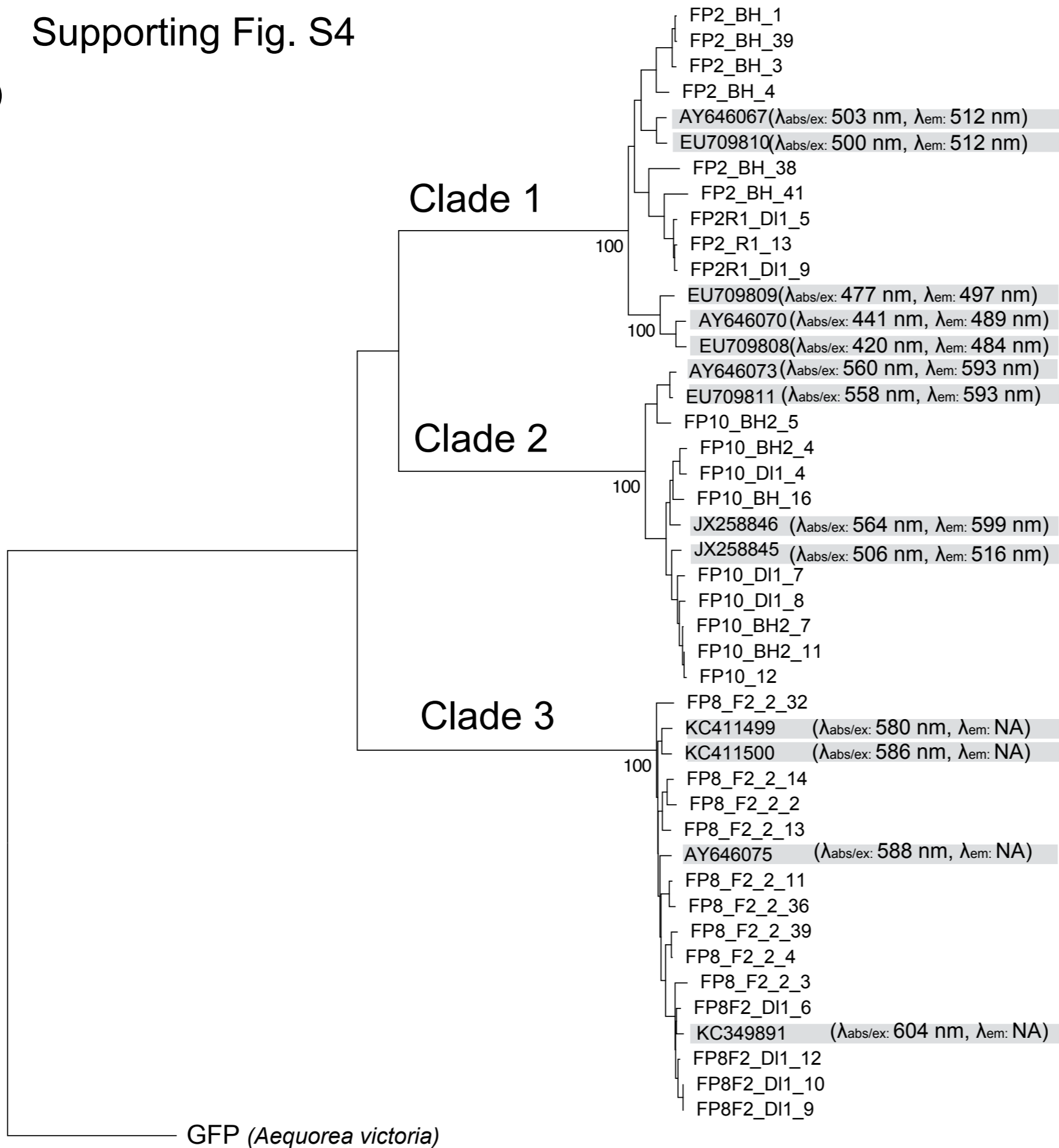


Supporting Fig. S3

amiLGFP(AY646067)	ATG TCTTATTCAAAGCAAGGCATCGTACAAGAAATGAAGACGAAATACCATATGGAAGGC
AdiFP2 (BR000963)	ATG TCTTATTCAAAGCAAGGCATCGTACAAGAAATGAAGACGAAATACCATATGGAAGGC
amiLRFP(AY646073)	ATG GCTCTGTCAAAGCACGGTTTAAACAAAGGACATGACGATGAAATACCACATGGAAGGG
AdiFP10(BR000970)	-----ATGGAAGGG
AdiFP10L	ATG GCTCTGTCAAAGCACGGTCTAACAAAGGACATGACGATGAAATACCGGATGGAAGGG
amiLCP (AY646075)	----- ATG AGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGC
AdiFP8 (AB698751)	-----ATGACCTACAAGGTTTATATGTCAGGC
AdiFP8L	----- ATG AGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGC

Supporting Fig. S4

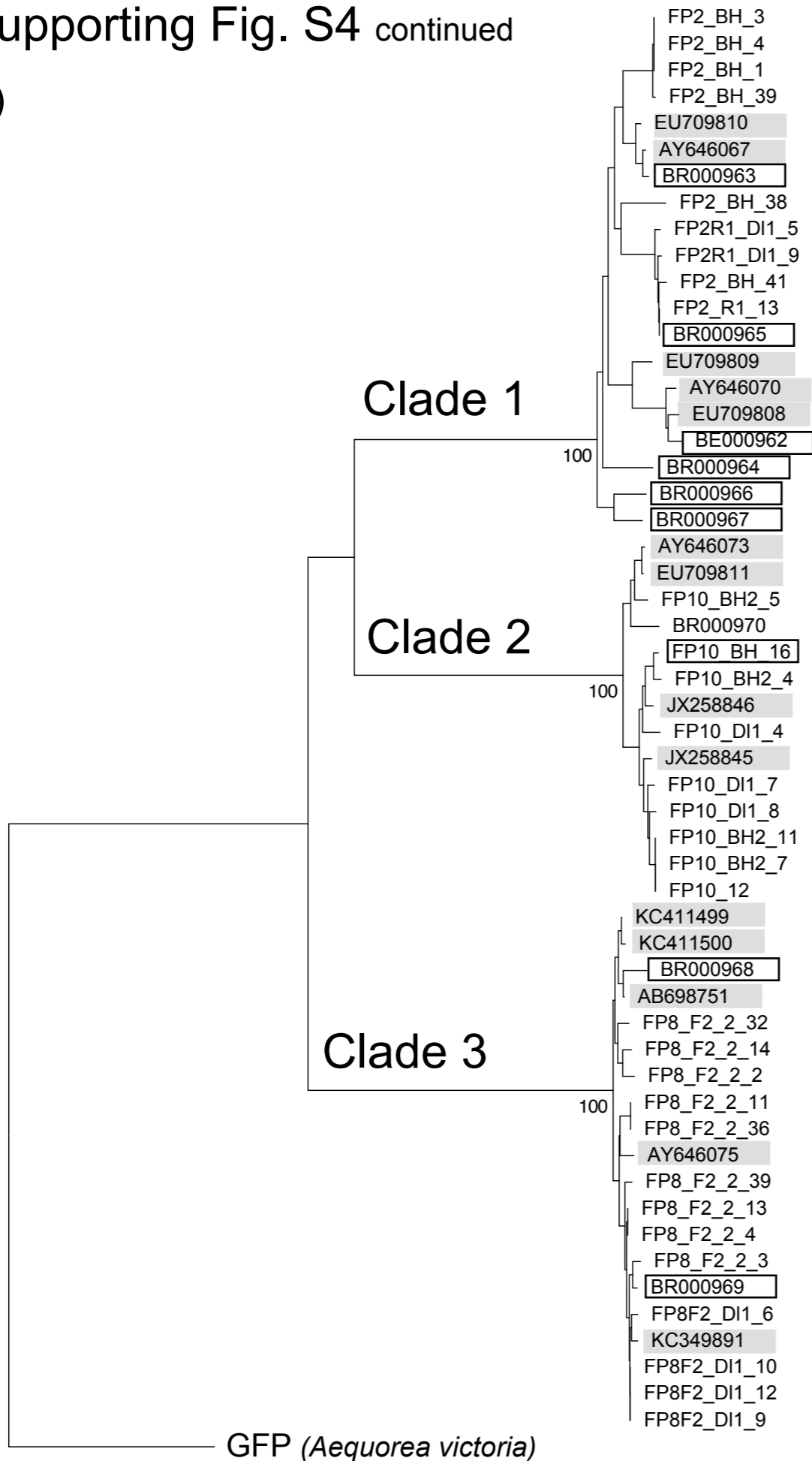
(A)



0.05

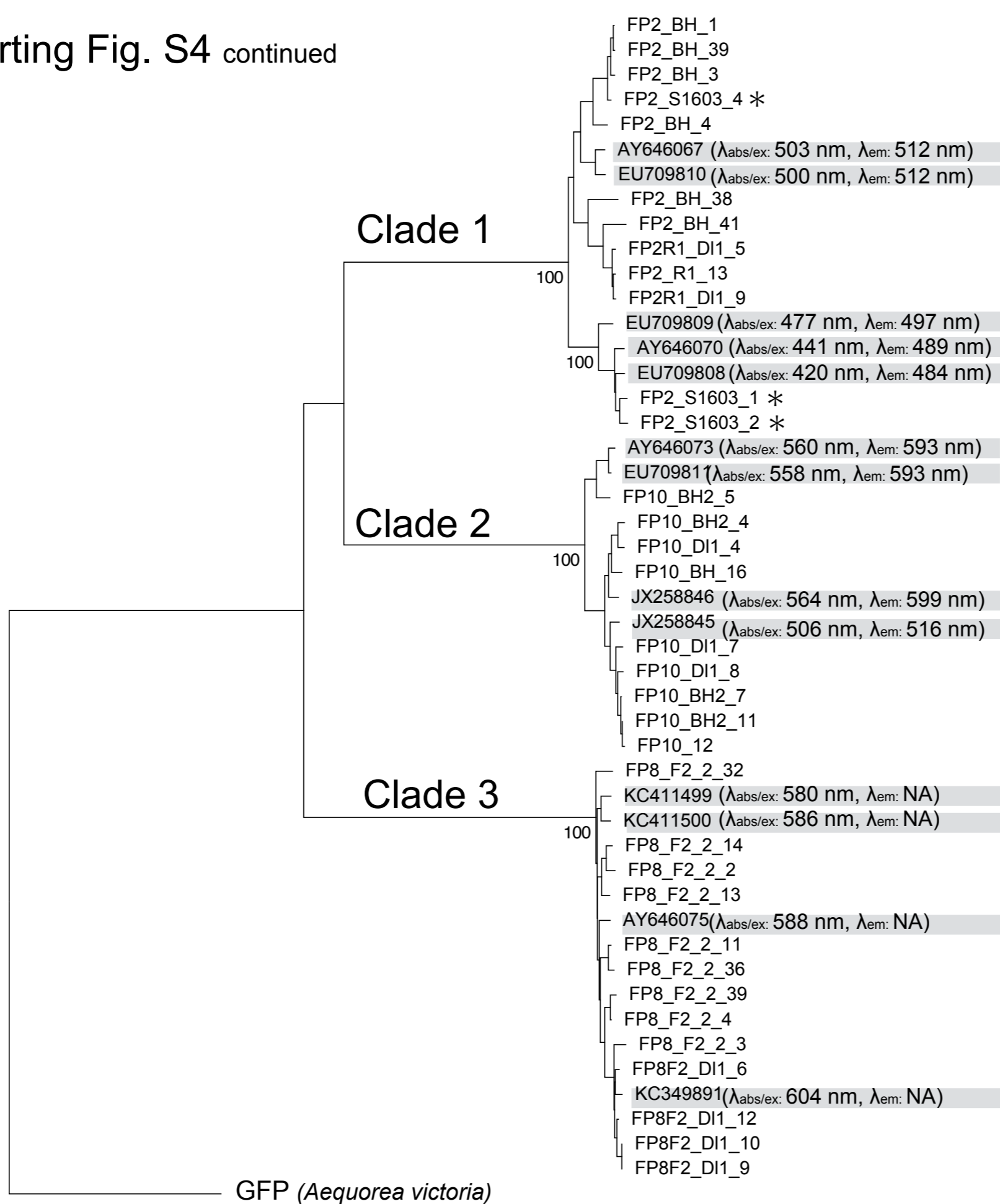
Supporting Fig. S4 continued

(B)

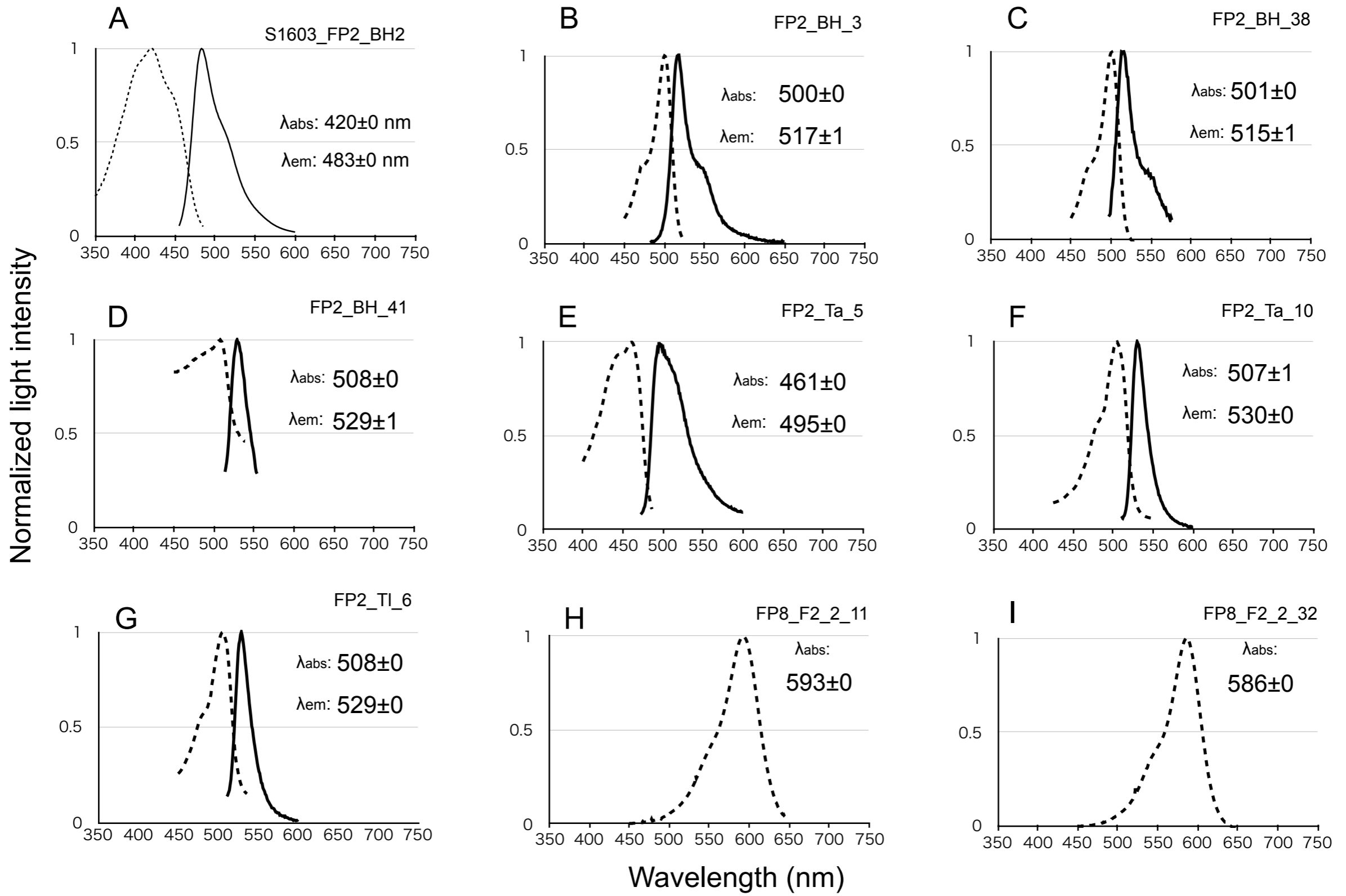


Supporting Fig. S4 continued

(C)



Supporting Fig. S5



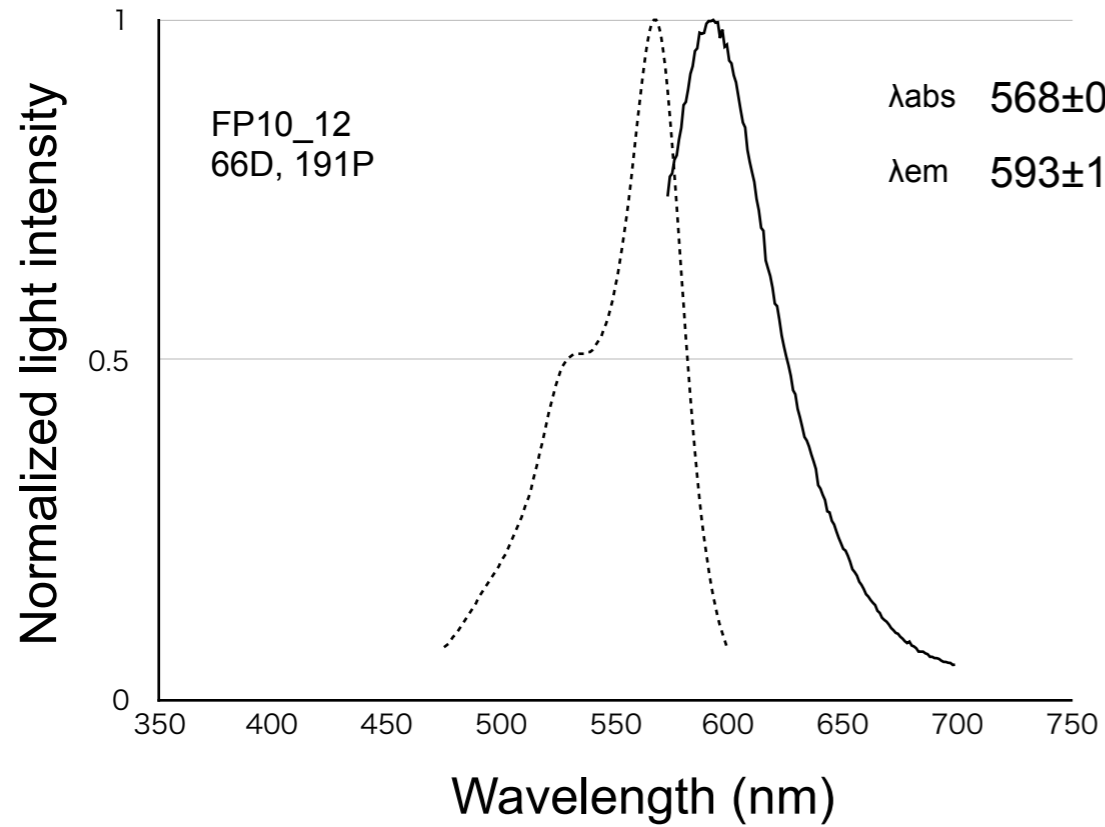
Supporting Fig. S6 continued

(B)

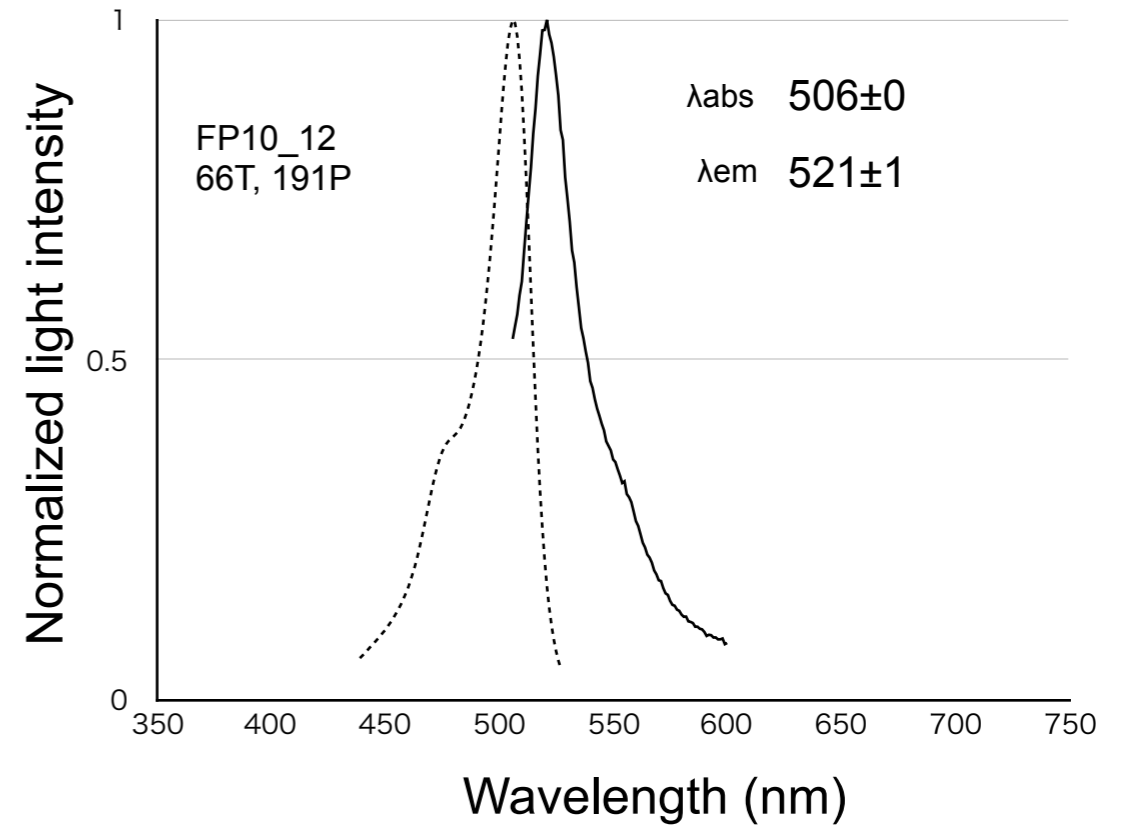
Nucleotide	1	1111111112	2222222223	3333333334	4444444445	5555555556	6666666667	7777777778	8888888889	9999999990	0000000001	1111111111	1111111111
site	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
amilRFP	MALSKHGLTK	DMTMKYHMEG	SVDGHKQVIT	GHGNGNPFEG	KQTMNLCVVE	GGPLPFSEDI	LSAAFDYGNR	VFTEYPQGMV	DFKNSCPAG	YTWHRSLLE	DGAVCTTSAD	ITVSVEENCF	
FP10_BH2_4R...	C.....S....	...I.....V.....	...D.....Q.....A...
FP10_12R...	C.....S....	...I.....V.T....Q.....A...

Nucleotide	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111112	2222222222	2222222222	2222222222	2222222222	222
Site	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	123
amilRFP	YHNSKFHGVN	FPADGPVMKK	MTTNWEPSCE	KIIPVPRQGI	LKGDIAMYLL	LKDGGRYRCQ	FDTIYKAKSD	PKEMPEWHFI	QHKLTREDRS	DAKNQKWQLV	EHAVASRSAL	PG*	
FP10_BH2_4	..E.....C..V.....V....T.	..K.....A	..S.....	..*	
FP10_12	..E.....C..V.....SV....T.	S.K.....A	..S.....	A*	

(C)



(D)

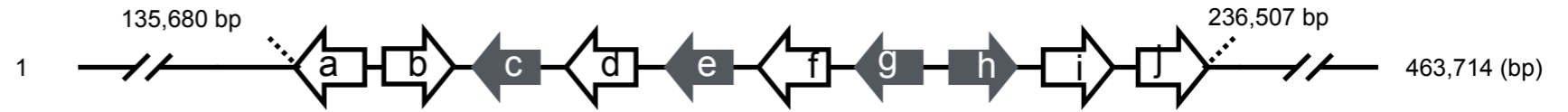


Supporting Fig. S7

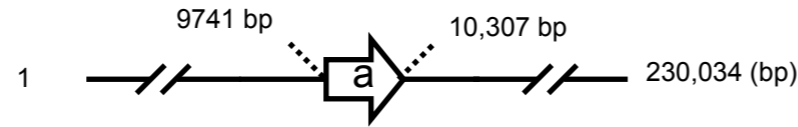
(A)

S/MWE

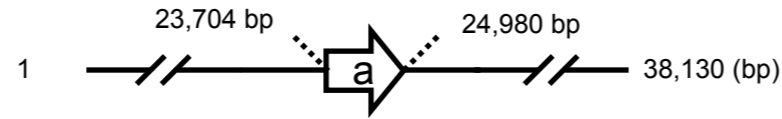
scaffold 84



scaffold 466



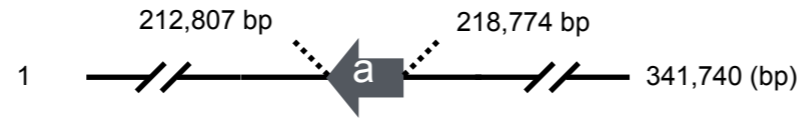
scaffold 2562



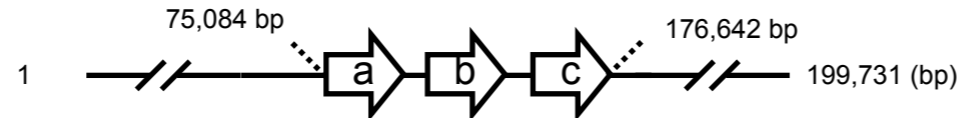
(B)

M/LWE

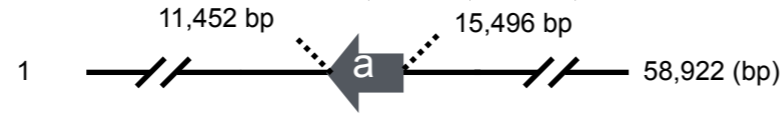
scaffold 205



scaffold 605



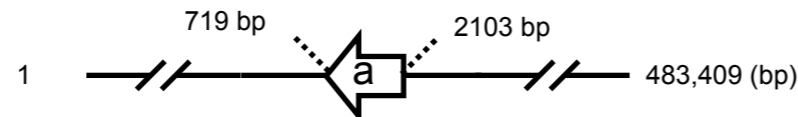
scaffold 2023



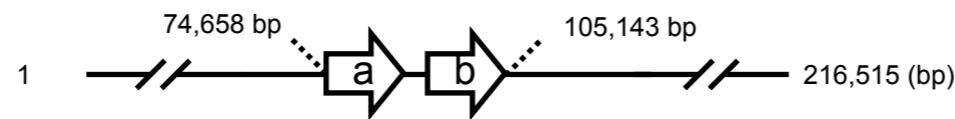
(C)

CP

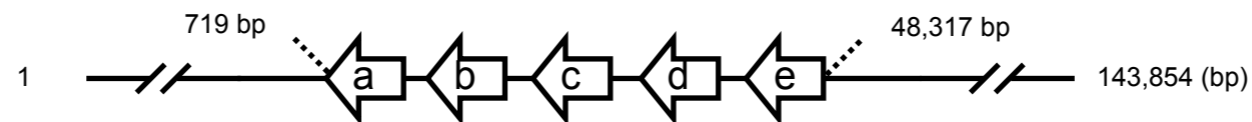
scaffold 75



scaffold 528

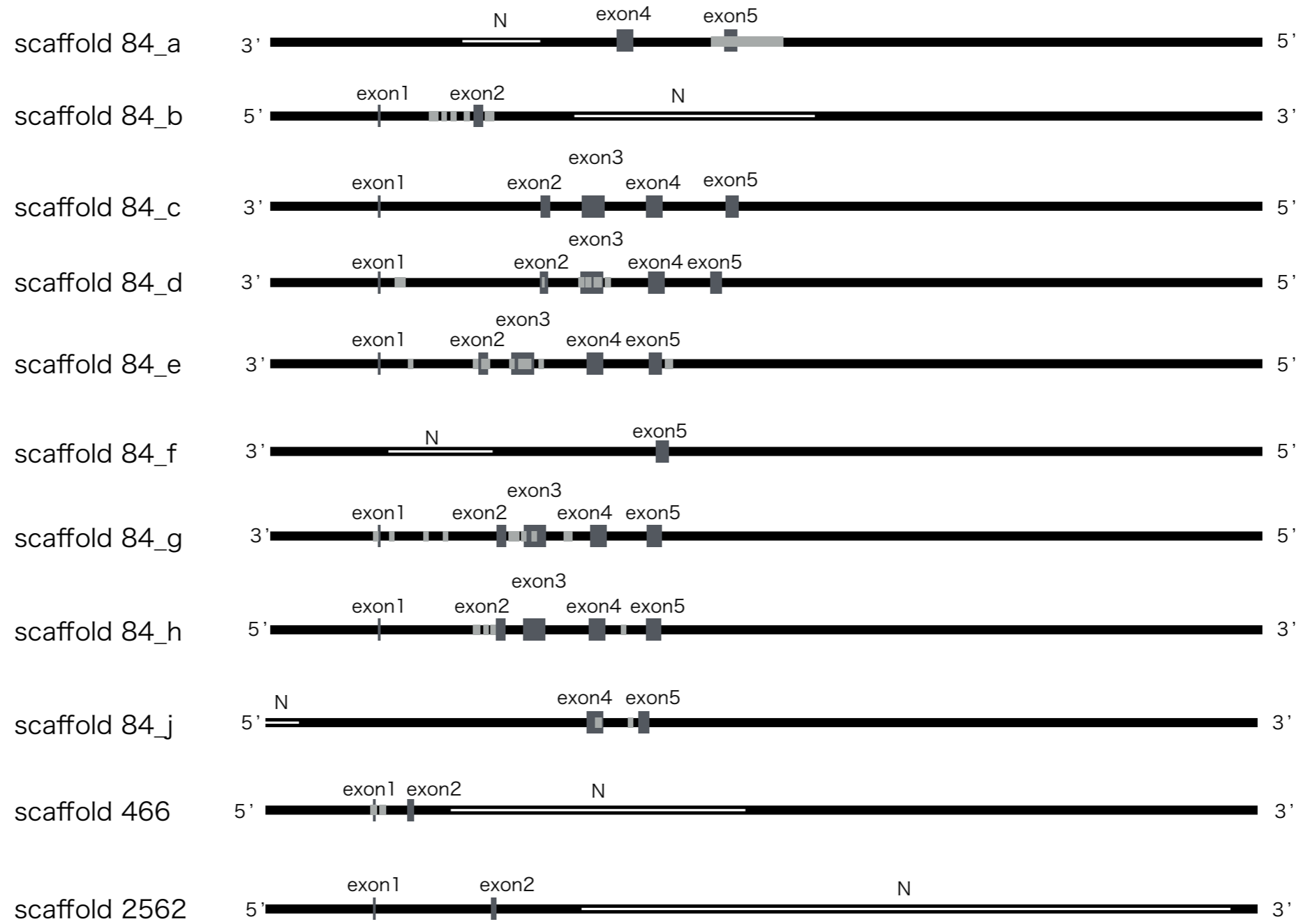


scaffold 947



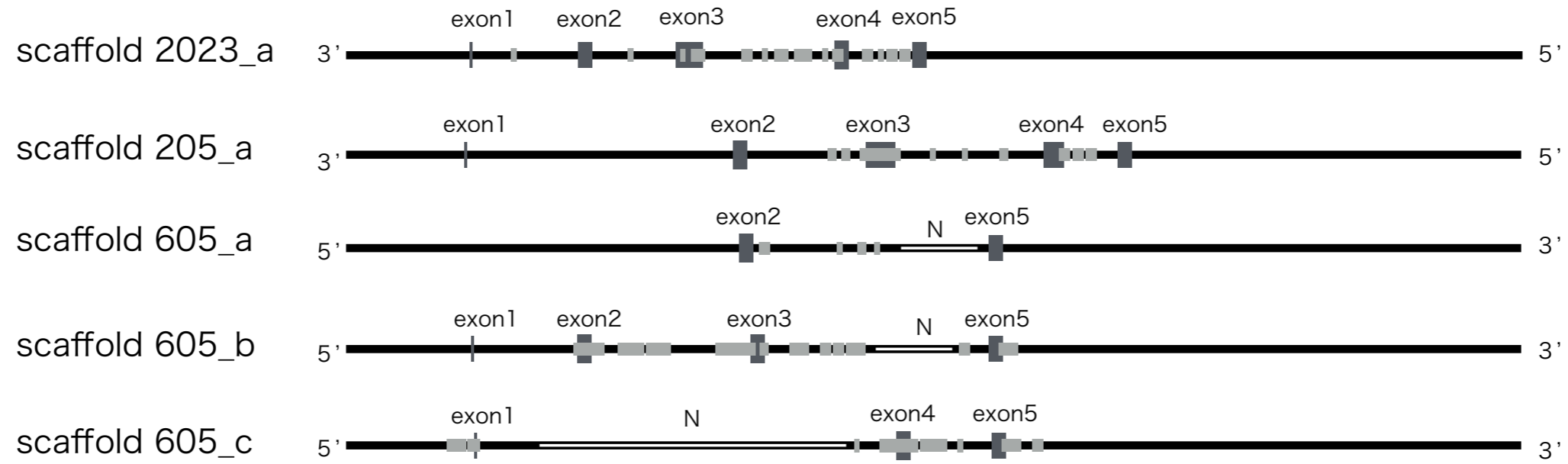
Supporting Fig. S7

(D) S/MWE



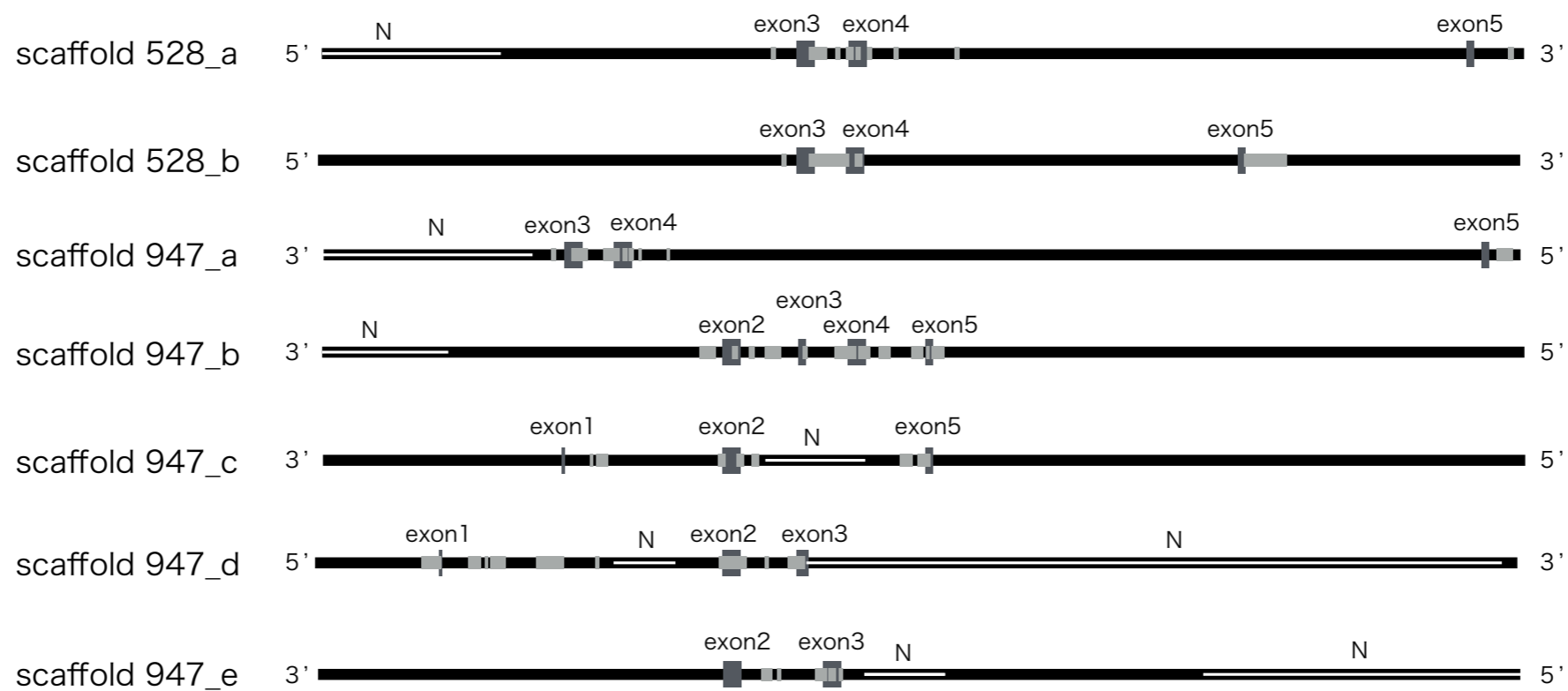
Supporting Fig. S7 continued

(E) M/LWE



Supporting Fig. S7 continued

(F) CP



Supporting Fig. S8 continued

(B)

M/LWE

1 1 1 1 1 1 1 1 1 2 3 4 5 5 5 6 6 6 6 6
 8 9 1 1 2 2 2 4 4 5 6 6 5 7 2 3 9 1 1 2 4 5
 4 0 1 4 0 3 9 1 7 3 5 7 1 7 5 4 1 2 8 1 2 1

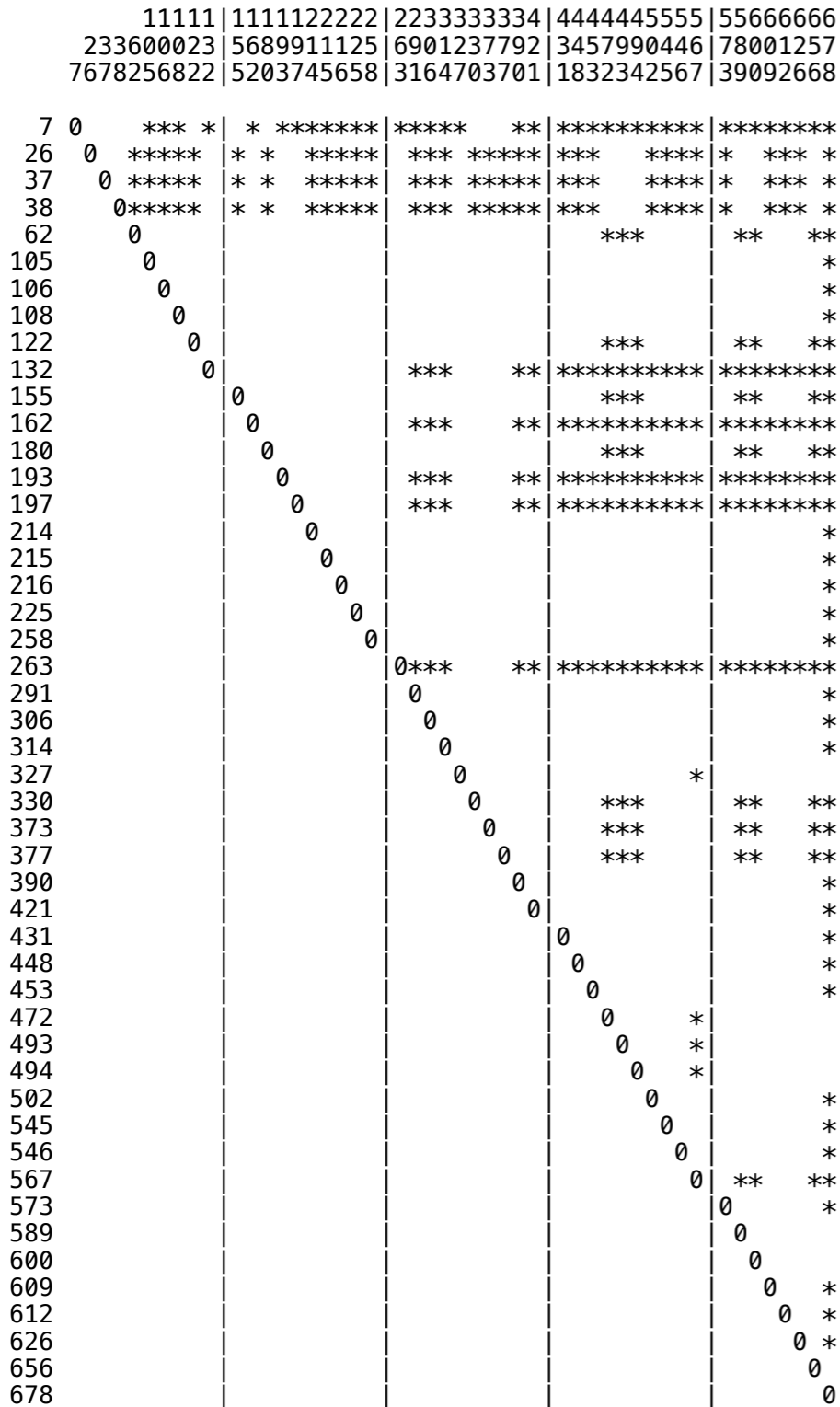
A. digitifera
 M/LWE_Consensus
 FP10_12
 FP10_BH_16
 FP10_BH2_11
 FP10_BH2_4
 FP10_BH2_5
 FP10_BH2_7
 FP10_Dl1_4
 FP10_Dl1_7
 FP10_Dl1_8

A. tenuis
 AdiFP10KX_Tl_1
 AdiFP10KX_Tl_2
 AdiFP10KX_Tl_3
 AdiFP10KX_Tl_6
 AdiFP10KX_Tl_8
 AdiFP10KX_Tl_9
 AdiFP10KX_Tl_12
 AdiFP10KX_Tl_13
 AdiFP10KX_Tl_15
 AdiFP10KX_Tl_16

G	G	T	C	G	A	T	T	T	G	A	T	G	G	T	C	G	G	C	G	G	A
.	T
.	A	A
.
.	A	.	T	C	G	.	A	.	.	.	A	.
.	A	T
.	.	.	T	C	G	G
T	C	.	.	A	.	.	.	A	.	.	A	G
.	A	G
C	.	C	.	A	.	.	C	.	.	.	A	A	G	T	.	.	.
C	.	.	.	G	.	C	.	.	.	C	A	.	T	.	.	.
.	.	.	A	.	.	C	.	.	.	C	A	.	T
.	.	T	.	G	.	C	.	.	.	C	A	G	T
C	C	.	.	G	.	C	.	.	.	A	A	G	T
C	C	.	.	.	C	A	G	T
T	C
.	.	T	.	G	.	C	.	.	.	C	G	T
.	.	T	.	G	.	C	.	.	.	C	A	G	T
C	C	.	.	G	.	C	.	.	.	A	A	G	T

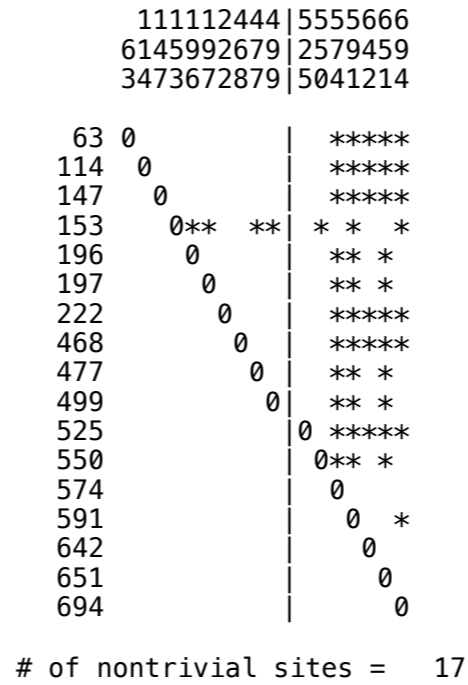
Supporting Fig. S9

(A) *A. digitifera*: MWE1

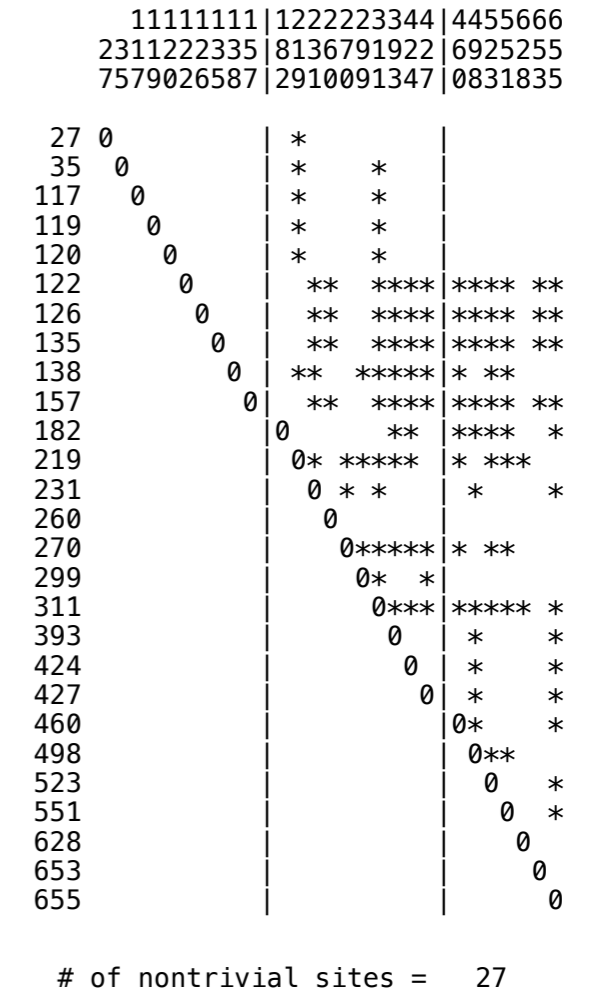


of nontrivial sites = 48

(B) *A. digitifera*: M/LWE

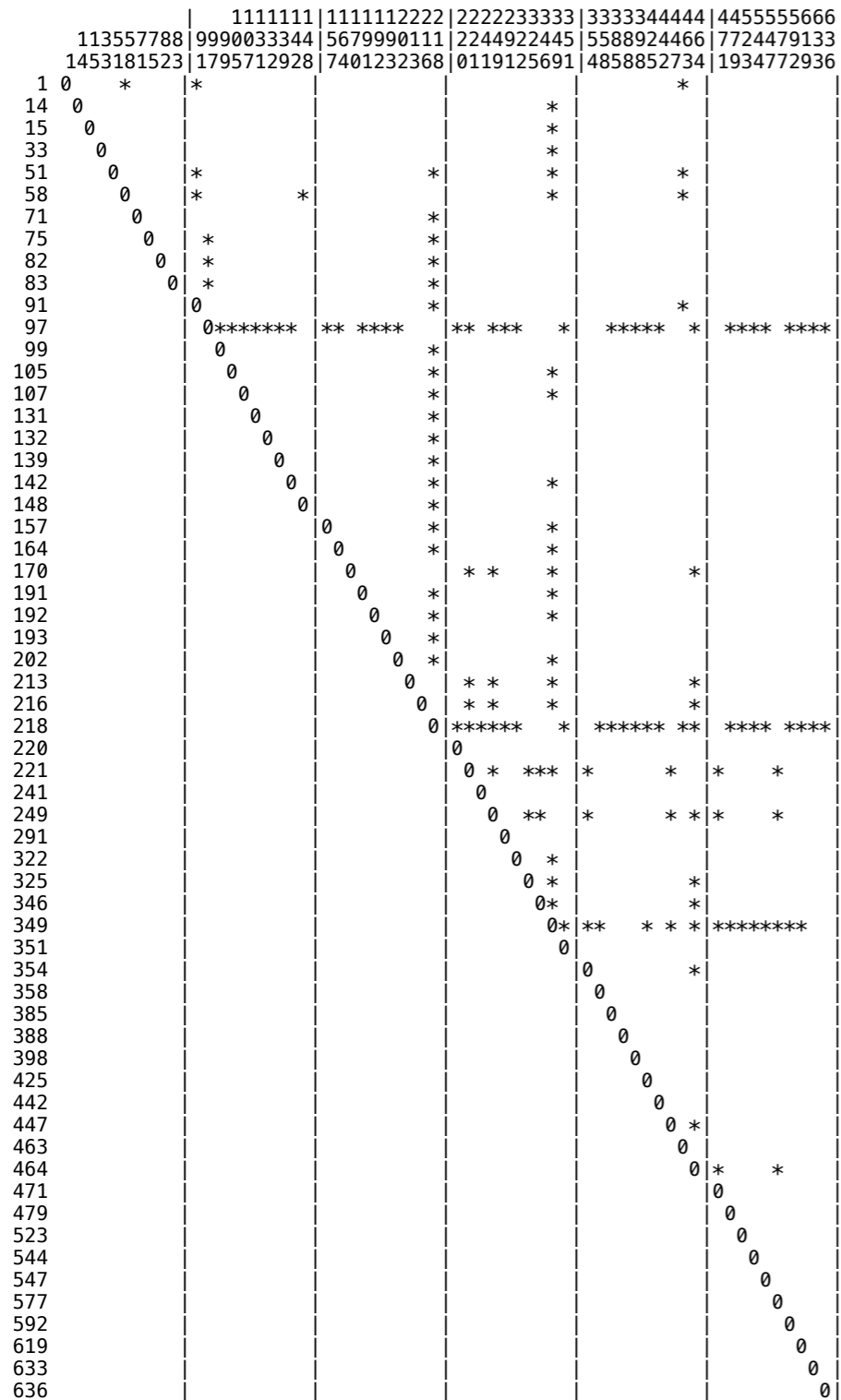


(C) *A. digitifera*: CP



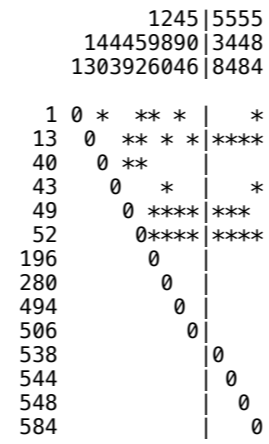
Supporting Fig. S9 continued

(D) *A.tenuis*: MWE1



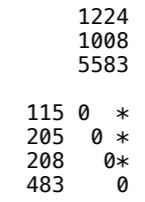
of nontrivial sites = 60

(E) *A.tenuis*: M/LWE



of nontrivial sites = 14

(F) *A.tenuis*: CP



of nontrivial sites = 4

Supporting Table S1.

Table S1

Sample name	Species	Life stage	Experiment
SESOKO#B1	<i>A. digitifera</i>	adult	fluorescence measurements
SESOKO#B2	<i>A. digitifera</i>	adult	fluorescence measurements
SESOKO#3	<i>A. digitifera</i>	adult	fluorescence measurements
SESOKO#4	<i>A. digitifera</i>	adult	fluorescence measurements
SESOKO#7	<i>A. digitifera</i>	adult	fluorescence measurements
Adigi1	<i>A. digitifera</i>	adult	RNA-seq analysis and FP sequence isolation from cDNA
Adigi2	<i>A. digitifera</i>	adult	FP gene copy number estimation from genomic DNA
Adigi3	<i>A. digitifera</i>	adult	FP gene copy number estimation from genomic DNA
Adigi4	<i>A. digitifera</i>	adult	FP gene copy number estimation from genomic DNA
Adigi5	<i>A. digitifera</i>	adult	FP gene copy number estimation from genomic DNA
S1603	<i>A. digitifera</i>	adult	FP sequence isolation from cDNA
D11	<i>A. digitifera</i>	larva	FP sequence isolation from cDNA
DI	<i>A. digitifera</i>	larvae	RNA-seq analysis
Ta	<i>A. tenuis</i>	adult	RNA-seq analysis and FP sequence isolation from cDNA
TI	<i>A. tenuis</i>	larvae	RNA-seq analysis and FP sequence isolation from cDNA

Table S2

Total number of reads	Mapped sequence	Length	Average coverage
<i>A. digitifera</i> larvae	<i>AdiFP10L</i>	699	93973
80,164,640	<i>AdiFP8L</i>	666	397662
	<i>AdiFP2</i>	696	18032
<i>A. digitifera</i> adult	<i>AdiFP10L</i>	699	37
94,059,356	<i>AdiFP8L</i>	666	194
	<i>AdiFP2</i>	696	37
<i>A. tenuis</i> larvae	<i>AdiFP10L</i>	699	50167
84,018,960	<i>AdiFP8L</i>	666	313
	<i>AdiFP2</i>	696	50805
<i>A. tenuis</i> adult	<i>AdiFP10L</i>	699	113
88,821,670	<i>AdiFP8L</i>	666	1071
	<i>AdiFP2</i>	696	203