

Figure S1: Protein sequences of the inteins used in this study. Sequence alignment of *Npu*DnaE, *Npu*DnaB^{Δ283}, *Pho*RadA, and *Tvo*VMA, inteins. The sequences were aligned using ClustalW (Thompson 1994) and manually adjusted based on pairwise structural alignments with DALI server (Hasegawa 2009). β-strands and α-helixes are presented above the sequences by filled arrows and squiggles, respectively. Functional split sites are indicated by filled triangles and non-functional split sites by open triangles. The native split site of *Npu*DnaE intein is marked with an asterisk and the endonuclease domain insertion site in *Npu*DnaB^{Δ283} intein is denoted with a diamond in grey. The boundaries between intein and exteins are indicated by slashes.







Figure S2: Sequences of the inteins used for structural studies. (a) Sequence alignment of *Npu*DnaB^{Δ 283} and *Npu*DnaB^{Δ 290} inteins. (b) Sequence alignment of *Tvo*VMA, *Tvo*VMA^{Δ 13}, and *Tvo*VMA^{Δ 21} inteins. Split sites in *Npu*DnaB^{Δ 290} and *Tvo*VMA inteins are indicated with triangles below the sequence alignment. Functional split sites are indicated by filled triangles and non-functional split sites by open triangles. Endonuclease domain insertion site in the minimized *Npu*DnaB inteins is shown by a diamond in grey. Secondary structures are indicated above the alightments by filled arrows (β -strands) and squiggles (α -helixes). Functional split sites are indicated by filled triangles and non-functional split sites by open triangles. The boundaries between intein and exteins are indicated by slashes.



Figure S3: (a) $[{}^{1}H, {}^{15}N]$ -TROSY-HSQC spectrum of 0.4 mM *Tvo*VMA intein, 10 mM sodium phosphate, pH 6 recorded at a ${}^{1}H$ frequency of 600 MHz at 307 K. (b) $[{}^{1}H, {}^{15}N]$ -HSQC spectrum of 0.5 mM *Tvo*VMA^{Δ 21} intein, 20 mM sodium phosphate, pH 7 recorded at a ${}^{1}H$ frequency of 800 MHz at 298 K.

(b) *Npu*DnaB^{∆283} intein

(C) PhoRadA intein

Figure S4: Analysis of *in vivo* PTS by new split inteins by SDS-PAGE. (a) PTS of new split inteins derived from NpuDnaE intein and of the previously described split NpuDnaE_{C35}, NpuDnaE_{C14} and NpuDnaE_{C6} inteins. (b) PTS of new split inteins derived from NpuDnaB^{Δ283} intein. (c) PTS of new split inteins derived from *Pho*RadA intein. (d) PTS of new split inteins derived from *Tvo*VMA intein. Image analysis of SDS-PAGE gels of the elution fractions from *in vivo* dual-expression of the two precursors. Intensities analysed by ImageJ (NIH) are plotted for each pair of split intein precursors. Split sites are indicated above the lanes.

Figure S5: Relative ligation yield multiplied by the normalized ligation yield. Inteins and split sites are indicated below the chart. Data presents mean values \pm s.d. (n=3).

Block A split inteins

Figure S6: SDS-PAGE analysis of in vivo cross-reactivity among split inteins with split sites near the N terminus. Combinations of the split inteins within the block A are tested. Different pairs are indicated above the lanes. The expected bands by PTS due to cross-activity between different split inteins are highlighted by rectangles. M stands for molecular weight markers.

Figure S7: SDS-PAGE analysis of *in vivo* cross-reactivities of different split inteins near the C-terminus. (a) Combinations of different split inteins at the loop within the block F (b) combinations of the split inteins split within the block G. different pairs are indicated above the lanes. The expected bands by PTS due to cross-activity between different split inteins are highlighted by rectangles. M stands for molecular weight markers.

Construct	Plasmid name	Addgene ID	Ref
H ₆ -Smt3-NpuDnaE _{AC35}	pSARSF53-1	_	#
H_6 -Smt3-NpuDnaE _{AC14}	pHYRSF53-36	-	(Aranko et al. 2009)
H_6 -Smt3-NpuDna E_{AC6}	pSARSF53-93	-	#
H_6 -Smt3-NpuDna E_{AC3}	pSARSF53-HY171	_	#
H_6 -Smt3-NpuDna E_{AC2}	pSARSF53-HY172	_	#
H_{6} -Smt3-NpuDna E_{N25}	pSARSF53-218	-	#
H_6 -Smt3- Npu Dna E_{N11}	pSARSF53-756	_	#
H ₆ -Smt3-NpuDnaB $^{\Delta 283}$	pSARSF53-259	-	#
H ₆ -Smt3-NpuDnaB $^{\Delta 283}$ AC13	pSARSF53-115	_	#
H_6 -Smt3-NpuDnaB ^{Δ283} N34	pSARSF53-254	_	#
H_6 -Smt3-NpuDnaB ^{Δ283} N24	pSARSF53-253	_	#
H_6 -Smt3- Npu Dna $B^{\Delta 283}$ _{N13}	pSARSF53-HY100	_	#
H_6 -Smt3- Tvo VMA $_{AC48}$	pSARSF53-343	_	#
H ₆ -Smt3-TvoVMA _{AC16}	pSARSF53-143	_	#
H_6 -Smt3- <i>Tvo</i> VMA _{AC7}	pSARSF53-HY176	_	#
H_6 -Smt3-TvoVMA _{N11}	pSARSF53-110	_	#
H ₆ -Smt3-PhoRadA _{AC46}	pSARSF53-344	_	#
H_6 -Smt3- <i>Pho</i> RadA _{AC14}	pSARSF53-166	-	#
H ₆ -Smt3-PhoRadA _{AC6}	pSARSF53-165	-	#
H ₆ -Smt3-PhoRadA _{N38}	pSARSF53-459	_	#
H_{c} -Smt3- <i>Pho</i> RadA _{N13}	pSARSF53-455	-	#
H ₆ -Smt3-PhoRadA _{N11}	pSARSF53-168	-	#
H ₆ -Smt3-PhoRadA _{N6}	pSARSF53-176	-	#
H ₆ -Smt3-PhoRadA _{N5}	pSARSF53-175	-	#
$NpuDnaE_{C25}$ -GB1-H ₆	pMHBAD14C	42304	(Buchinger et al 2010)
Npu Dna E_{C14} -GB1-H ₆	pMKBAD28	45595	(Aranko et al 2013)
$NpuDnaE_{C6}-GB1-H_6$	pHYBAD94	42305	(Oeemig et al 2009)
Npu Dna E_{C2} -GB1-H ₆	pSABAD148	-	#
NpuDnaE _{C2} -GB1-H ₆	pSABAD147	-	#
NpuDnaE _{AN25} -GB1-H ₆	pSABAD219	45596	(Aranko et al 2013)
NpuDnaE _{AN11} -GB1-H ₆	pSABAD14-HY43	-	#
Npu DnaB ^{<math>\Delta 283$\Delta 283$-GB1-H₆</math>}	pSABAD250	45612	(Aranko et al 2013)
$NpuDnaB^{\Delta 283}$ C13-GB1-H ₆	pSABAD14-116	_	#
$NpuDnaB^{\Delta 283}$ AN34-GB1-H ₆	pSABAD252	_	#
$NpuDnaB^{\Delta 283}$ AN24-GB1-H ₆	pSABAD251	_	#
$NpuDnaB^{\Delta 283}$ AN12-GB1-H ₆	pSABAD14-111	-	#
TvoVMA _{C48} -GB1-H ₆	pSABAD331	45609	(Aranko et al 2013)
TvoVMA _{C16} -GB1-H ₆	pSABAD14-142	-	#
TvoVMA _{C7} -GB1-H ₆	pHYBAD177	-	#
TvoVMA _{AN11} -GB1-H ₆	pSABAD14-98	-	#
PhoRadA _{C46} -GB1-H ₆	pSABAD332	45610	(Aranko et al 2013)
PhoRadA _{C14} -GB1-H ₆	pSABAD14-167	-	#
$PhoRadA_{C6}$ -GB1-H ₆	pSABAD14-172	-	#
PhoRadA _{AN38} -GB1-H ₆	pSABAD14-467	-	#
$PhoRadA_{\Lambda N13}$ -GB1-H ₆	pSABAD14-466	-	#
PhoRadA _{AN11} -GB1-H ₆	pSABAD14-371	-	#
$PhoRadA_{AN6}$ -GB1-H ₆	pSABAD14-738	-	#
PhoRadA _{AN38} -GB1-H ₆	pSABAD14-467	-	#
PhoRadA _{AN13} -GB1-H ₆	pSABAD14-466	-	#
PhoRadA _{AN11} -GB1-H ₆	pSABAD14-371	-	#
$PhoRadA_{AN6}$ -GB1-H ₆	pSABAD14-738	-	#
$PhoRadA_{AN5}$ -GB1-H ₆	pSABAD14-737	-	#
H_6 -Smt3-SspDnaB ^{$\Delta 275$} _{N11}	pSARSF53-HY41	-	#
$SspDnaB^{\Delta 275}$ AN10-GB1-H ₆	pSABAD14-HY42	-	#
H_6 -GB1- <i>Tvo</i> VMA _{N11}	pSADuet110	-	#
H_6 -GB1- <i>Pho</i> RadA _{AC6}	pSADuet165	-	#
H_6 -Smt3-A_NpuDnaB ^{Δ 290} _A	pCARSF02	-	#
H ₆ -Smt3-A_TvoVMA_A	pHYRSF175	-	#
H_6 -Smt3-A_TvoVMA^{\overline{\Delta}_{21}}A	pJORSF73	-	#
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Table S1: Summary of plasmids used in this study

[#]described here

Construct	Plasmid name	Addgene ID	Ref
H ₆ -Smt3-NpuDnaE _{AC35}	pSARSF53-1	_	#
H_6 -Smt3-NpuDnaE _{AC14}	pHYRSF53-36	-	(Aranko et al. 2009)
H_6 -Smt3-NpuDna E_{AC6}	pSARSF53-93	-	#
H_6 -Smt3-NpuDna E_{AC3}	pSARSF53-HY171	_	#
H_6 -Smt3-NpuDna E_{AC2}	pSARSF53-HY172	_	#
H_{6} -Smt3-NpuDna E_{N25}	pSARSF53-218	-	#
H_6 -Smt3- Npu Dna E_{N11}	pSARSF53-756	_	#
H ₆ -Smt3-NpuDnaB $^{\Delta 283}$	pSARSF53-259	-	#
H ₆ -Smt3-NpuDnaB $^{\Delta 283}$ AC13	pSARSF53-115	_	#
H_6 -Smt3-NpuDnaB ^{$\Delta 283$} N34	pSARSF53-254	_	#
H_6 -Smt3- Npu Dna $B^{\Delta 283}$ _{N24}	pSARSF53-253	_	#
H_6 -Smt3- Npu Dna $B^{\Delta 283}$ _{N13}	pSARSF53-HY100	_	#
H_6 -Smt3- Tvo VMA $_{AC48}$	pSARSF53-343	_	#
H_6 -Smt3-TvoVMA _{AC16}	pSARSF53-143	_	#
H_6 -Smt3- <i>Tvo</i> VMA _{AC7}	pSARSF53-HY176	_	#
H_6 -Smt3-TvoVMA _{N11}	pSARSF53-110	_	#
H ₆ -Smt3-PhoRadA _{AC46}	pSARSF53-344	_	#
H_6 -Smt3- <i>Pho</i> RadA _{AC14}	pSARSF53-166	-	#
H ₆ -Smt3-PhoRadA _{AC6}	pSARSF53-165	-	#
H ₆ -Smt3-PhoRadA _{N38}	pSARSF53-459	_	#
H_{c} -Smt3- <i>Pho</i> RadA _{N13}	pSARSF53-455	-	#
H ₆ -Smt3-PhoRadA _{N11}	pSARSF53-168	-	#
H ₆ -Smt3-PhoRadA _{N6}	pSARSF53-176	-	#
H ₆ -Smt3-PhoRadA _{N5}	pSARSF53-175	-	#
$NpuDnaE_{C25}$ -GB1-H ₆	pMHBAD14C	42304	(Buchinger et al 2010)
Npu Dna E_{C14} -GB1-H ₆	pMKBAD28	45595	(Aranko et al 2013)
$NpuDnaE_{C6}-GB1-H_6$	pHYBAD94	42305	(Oeemig et al 2009)
Npu Dna E_{C2} -GB1-H ₆	pSABAD148	-	#
NpuDnaE _{C2} -GB1-H ₆	pSABAD147	-	#
NpuDnaE _{AN25} -GB1-H ₆	pSABAD219	45596	(Aranko et al 2013)
NpuDnaE _{AN11} -GB1-H ₆	pSABAD14-HY43	-	#
Npu DnaB ^{<math>\Delta 283$\Delta 283$-GB1-H₆</math>}	pSABAD250	45612	(Aranko et al 2013)
$NpuDnaB^{\Delta 283}$ C13-GB1-H ₆	pSABAD14-116	_	#
$NpuDnaB^{\Delta 283}$ AN34-GB1-H ₆	pSABAD252	_	#
$NpuDnaB^{\Delta 283}$ AN24-GB1-H ₆	pSABAD251	_	#
$NpuDnaB^{\Delta 283}$ AN12-GB1-H ₆	pSABAD14-111	-	#
TvoVMA _{C48} -GB1-H ₆	pSABAD331	45609	(Aranko et al 2013)
TvoVMA _{C16} -GB1-H ₆	pSABAD14-142	-	#
TvoVMA _{C7} -GB1-H ₆	pHYBAD177	-	#
TvoVMA _{AN11} -GB1-H ₆	pSABAD14-98	-	#
PhoRadA _{C46} -GB1-H ₆	pSABAD332	45610	(Aranko et al 2013)
PhoRadA _{C14} -GB1-H ₆	pSABAD14-167	-	#
$PhoRadA_{C6}$ -GB1-H ₆	pSABAD14-172	-	#
PhoRadA _{AN38} -GB1-H ₆	pSABAD14-467	-	#
$PhoRadA_{\Lambda N13}$ -GB1-H ₆	pSABAD14-466	-	#
PhoRadA _{AN11} -GB1-H ₆	pSABAD14-371	-	#
$PhoRadA_{AN6}$ -GB1-H ₆	pSABAD14-738	-	#
PhoRadA _{AN38} -GB1-H ₆	pSABAD14-467	-	#
PhoRadA _{AN13} -GB1-H ₆	pSABAD14-466	-	#
PhoRadA _{AN11} -GB1-H ₆	pSABAD14-371	-	#
$PhoRadA_{AN6}$ -GB1-H ₆	pSABAD14-738	-	#
$PhoRadA_{AN5}$ -GB1-H ₆	pSABAD14-737	-	#
H_6 -Smt3-SspDnaB ^{$\Delta 275$} _{N11}	pSARSF53-HY41	-	#
$SspDnaB^{\Delta 275}$ AN10-GB1-H ₆	pSABAD14-HY42	-	#
H_6 -GB1- <i>Tvo</i> VMA _{N11}	pSADuet110	-	#
H_6 -GB1- <i>Pho</i> RadA _{AC6}	pSADuet165	-	#
H_6 -Smt3-A_NpuDnaB ^{Δ 290} _A	pCARSF02	-	#
H ₆ -Smt3-A_TvoVMA_A	pHYRSF175	-	#
H_6 -Smt3-A_TvoVMA^{\overline{\Delta}_{21}}A	pJORSF73	-	#
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Table S1: Summary of plasmids used in this study

[#]described here

Split	intein	Plasmid name	Oligonucleotides	Template	Ref
fragments			-	*	
NpuDnaE _{N35}		pSARSF53-218	SK092, HK476	pSKDuet16	(Ellilä et al. 2011)
NpuDnaE _{N11}		pSARSF53-756	SK012, SA035	pHYDuet36	(Aranko et al. 2009)
<i>Npu</i> DnaB ^{∆2}	83 ΔC39	pSARSF53-259	HK151, HK297	pMMDuet19	(Ellilä et al. 2011)
<i>Npu</i> DnaB ^{∆2}	83 ΔC13	pSARSF53-115	SK012, HK267	pMMDuet19	(Ellilä et al. 2011)
<i>Npu</i> DnaB ^{∆2}	83 N34	pSARSF53-254	HK151, HK519	pMMDuet19	(Ellilä et al. 2011)
<i>Npu</i> DnaB ^{∆2}	83 N24	pSARSF53-253	HK151, HK518	pMMDuet19	(Ellilä et al. 2011)
$TvoVMA_{\Delta C4}$	8	pSARSF53-343	SK181, HK594	pSKDuet26	(Ellilä et al. 2011)
$TvoVMA_{\Delta C1}$	6	pSARSF53-143	SK181, HK331	pSKDuet26	(Ellilä et al. 2011)
$TvoVMA_{\Delta C7}$		pSARSF53-HY176	SK181, HK346	pSKDuet26	(Ellilä et al. 2011)
TvoVMA _{N11}		pSARSF53-110	Duet-MCS1-fw,	pSKDuet26	(Ellilä et al. 2011)
			HK236		
$PhoRadA_{\Delta CA}$	16	pSARSF53-344	HK375, HK593	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{\Delta C}$	4	pSARSF53-166	HK375, HK387	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{\Delta C}$	5	pSARSF53-165	HK375, HK393	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{N38}$		pSARSF53-459	HK375, HK658	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{N13}$		pSARSF53-455	HK375, HK656	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{N11}$		pSARSF53-168	SK012, HK386	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{N6}$		pSARSF53-176	SK012, HK406	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{N5}$		pSARSF53-175	SK012, HK405	pHYDuet183	(Ellilä et al. 2011)
NpuDnaE _{C3}		pSABAD14	HK341, SZ015	pSKBAD2	(Iwai et al. 2006)
NpuDnaE _{C2}		pSABAD147	HK340, SZ015	pSKBAD2	(Iwai et al. 2006)
NpuDna $E_{\Delta N}$	11	pSABAD14-HY43	HK145, SK095	pSKDuet16	(Ellilä et al. 2011)
NpuDnaB ^{∆2}	83 C13	pSABAD14-116	HK268, SZ015	pMMDuet19	(Ellilä et al. 2011)
NpuDnaB ^{∆2}	83 ΔN34	pSABAD252	HK517, HK212	pMMDuet19	(Ellilä et al. 2011)
NpuDnaB ^{∆2}	83 ΔN24	pSABAD251	HK516, HK212	pMMDuet19	(Ellilä et al. 2011)
NpuDnaB ^{∆2}	83 ΔN12	pSABAD14-111	HK261, SZ015	pMMDuet19	(Ellilä et al. 2011)
TvoVMA _{C16}		pSABAD14-142	HK330, SK182	pSKDuet26	(Ellilä et al. 2011)
$TvoVMA_{C7}$		pHYBAD177	HK347, HK158	pSKDuet26	(Ellilä et al. 2011)
$TvoVMA_{\Delta N1}$	1	pSABAD14-98	HK225, SK182	pSKDuet26	(Ellilä et al. 2011)
$PhoRadA_{C14}$		pSABAD14-167	HK388, SZ015	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{C6}$		pSABAD14-172	HK398, SZ015	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{\Delta N}$	38	pSABAD14-467	HK657, SZ015	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{\Delta N}$	13	pSABAD14-466	HK655, SZ015	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{\Delta N}$	11	pSABAD14-371	HK617, SZ015	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{\Delta N}$	5	pSABAD14-738	SA033, SZ015	pHYDuet183	(Ellilä et al. 2011)
$PhoRadA_{\Delta N}$	5	pSABAD14-737	SA032, SZ015	pHYDuet183	(Ellilä et al. 2011)
SspDnaB ^{△27}	5 ΔN10	pSABAD14-HY42	HK144, HK042	pTWIN2	(Evans & Xu 1999)

Table S2: Construction of split inteins described in this article

Table S3: List of oligonucleotides used

HK0395'-CTGGATCCTGTATCTCTGGCGATAGTCHK0405'-GTCAAGCTTAGAATTCTAGTTTACGGGGTAGHK0425'-TCGGTACCAATAGAGTTGTGACAATGATGTCHK1295'-CGTAACGGAAGGATCCGGATGCATCTGGCGATAGTCTGHK1305'-CAGACTATCGCCAGAGATGCATCCGGATCCTTCCGTTACGHK1425'-CTGATCAGCCTGGCTTAAACAGGAAAAAGAGTTTCHK1435'-GAAACTCTTTTTCCTGTTTAAGCCAGGCTGATCAGHK1445'-AACATATGGCTAGCACAGGAAAAAGAGHK1455'-AACATATGGATAGTGATCATGGATAGTCHK1515'-AAGATTCCGTTACGGTGTAGGCAATGTCHK1585'-AAGATTCCGTTACGGTGTAGGAATATGGAATATGGATTATTACCGATTGHK2255'-AAGATTCCGTTACGGTGTAGGAACAATHK2265'-ATTCAAGCTTACGCAAGGAAAAAGAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGAATCCGAAGCTAAGTGCCAATTAAAGHK2635'-ATTGGAAGCTTAAGCTTAGGCTATCAATGAATAAAAGHK2645'-GTCAAGCTTAAGCCTTAGGTATCTACTAATGTCACHK2675'-AATAAGCTTAACCAGGAACGAGAAGTCHK2675'-ATAAGCTTAACCAGGAACGAGTAGGTC	
HK0405'-GTCAAGCTTAGAATTCTAGTTTACGGGGTAGHK0425'-TCGGTACCAATAGAGTTGTGTACAATGATGTCHK1295'-CGTAACGGAAGGATCCGGATGCATCTCGGCGATAGTCTGHK1305'-CAGACTATCGCCAGAGATGCATCCGGATCCTTCCGTTACGHK1425'-CTGATCAGCCTGGCTTAAACAGGAAAAAGAGTTTCHK1435'-GAAACTCTTTTTCCTGTTTAAGCCAGGCTGATCAGHK1445'-AACATATGGCTAGCACAGGAAAAAGAGHK1455'-AACATATGGCATAGGATTATTACCGATTGHK1515'-AGAATCCGTTGTTAAGCAGGCGATAGTCHK1585'-AGAATTCCGTTACGGTGTAGGATAGTCHK2255'-AACATATGGATGGCAAGGAACAATHK2255'-AACATATGGATGGCAAGGAACAATAAAAATAAAGHK2615'-AACATATGGATGCCAAGGACAATAAAAATAAAGHK2625'-ATTGAGATAGCTAAGCTTAAGCTAGCCAATTAAGGHK2635'-ATTGGACTAAGCTTAGCTATGTAACTAATGTCACHK2645'-GTCAAGCTTAACGCTAGGTATCTACTAATGTCACHK2675'-AATAGCTTAACGGAACGGTGAGGACC	
HK0425'-TCGGTACCAATAGAGTTGTGTACAATGATGTCHK1295'-CGTAACGGAAGGATCCGGATGCATCTCTGGCGATAGTCTGHK1305'-CAGACTATCGCCAGAGATGCATCCGGGATAGTCTGHK1425'-CTGATCAGCCTGGCTTAAACAGGAAAAAGAGTTTCHK1435'-GAAACTCTTTTTCCTGTTTAAGCCAGGCTGATCAGHK1445'-AACATATGGCTAGCACAGGAAAAAGAGHK1455'-AACATATGGATATGGATTATTACCGATGHK1455'-AACATATGGATATGGATTATTACCGATAGTCHK1515'-AGGATCCGGTTGTTTAGCAGGCGATAGTCHK1585'-AGAATTCCGTTACGGTGTAGGTTTTGHK2255'-AACATATGGATGGCAAGACAATAAAAATAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGGHK2635'-ATTGGCACTAAGCTTAAGCTAAGTGCCAATTAAGGHK2645'-GTCAAGCTTACGCATGGAAGTACGAGAAGTCHK2675'-AATAGCTTAACCAGGAACGGTGAGGTC	
HK1295'-CGTAACGGAAGGATCCGGATGCATCTCTGGCGATAGTCTGHK1305'-CAGACTATCGCCAGAGATGCATCCGGGATCCTTCCGTTACGHK1425'-CTGATCAGCCTGGCTTAAACAGGAAAAAGAGTTTCHK1435'-GAAACTCTTTTTCCTGTTTAAGCCAGGCTGATCAGHK1445'-AACATATGGCTAGCACAGGAAAAAGAGHK1455'-AACATATGGATAGGATATGGATTATTACCGATTGHK1515'-TAGGATCCGGTTGTTAAGCAGGCGATAGTCHK1585'-AGAATTCCGTTACGGTGTAGGTTTTGHK2125'-GAGGTACCAATGGAATGGAACAATHK2255'-AACATATGGATGGCAAGGACAATAAAAATAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAAGTGTCACAATTAAGGHK2645'-GTCAAGCTTACGCATGGAAGTACGAGAAGTCHK2675'-AATAGCTTAACCAGGAACGAGTACGAGAAGTC	
HK1305'-CAGACTATCGCCAGAGATGCATCCGGATCCTTCCGTTACGHK1425'-CTGATCAGCCTGGCTTAAACAGGAAAAAGAGTTTCHK1435'-GAAACTCTTTTTCCTGTTTAAGCCAGGCAGGACAGGHK1445'-AACATATGGCTAGCACAGGAAAAAGAGHK1455'-AACATATGGATAGGATAATGGATTATTACCGATTGHK1515'-TAGGATCCGGTTGTTAAGCAGGCGATAGTCHK1585'-AGAATCCGTTACGGTGTAGGTTTTGHK2125'-GAGGTACCAATGGAAGACAATHK255'-AACATATGGATGGCAAGACAATHK2615'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTCHK2615'-ATTCAAGCTTAAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGAATAGCTAAGCTTAAGTGCCAATTAAGGHK2645'-GTCAAGCTTAAGCTTAGGATAGCTAAGTACGAGAAGTCHK2675'-AATAAGCTTAACCAGGAACGAGACAATCAATGTCAC	
HK1425'-CTGATCAGCCTGGCTTAAACAGGAAAAAGAGTTTCHK1435'-GAAACTCTTTTTCCTGTTTAAGCCAGGCTGATCAGHK1435'-AACATATGGCTAGCACAGGAAAAAGAGHK1445'-AACATATGGATATGGATTATGCAGGCGATAGTGHK1455'-AAGATATGGATATGGATATTACCGATGGHK1515'-TAGGATCCGGTTGTTAGGAGGCGATAGTCHK1585'-AGAATTCCGTTACGGTGTAGGATATTGGAACAATHK2125'-GAGGTACCAATGGAAGACAATGGAACAATHK2255'-AACATATGGATGGCAAGACAATAAAAATAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGHK2625'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAGCTAAGTACCAATTCAATGTCACHK2645'-GTCAAGCTTAACGCTTGGAAGTACGAGAAGTCHK2675'-AATAAGCTTAACCAGGAACGGTGAGGTC	
HK1435'-GAAACTCTTTTCCTGTTTAAGCCAGGCTGATCAGHK1435'-AACATATGGCTAGCACAGGAAAAAGAGHK1445'-AACATATGGATAGGATTATTACCGATTGHK1555'-AACATATGGATATGGATTATTACCGATTGHK1515'-TAGGATCCGGTTGTTTAGCAGGCGATAGTCHK1585'-AGAATTCCGTTACGGTGTAGGTTTTGHK2125'-GAGGTACCAATGGAATGTGAACAATHK2255'-AACATATGGATGGCAAGACAATAAAAATAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGATCCGGACTGCAAGTGCCAATTAAGHK2625'-ATTGAGATAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCACHK2645'-GTCAAGCTTAACGCTTAGCAGTACGAGAAGTCHK2675'-AATAAGCTTAACCAGGAACGGTGAGGTC	
Inkias5'-AACATATGGCTAGCACAGGAAAAAGAGHK1445'-AACATATGGCTAGGAATATGGAATATGGAATATGCAATGGHK1455'-AACATATGGAATATGGATTATTACCGATTGHK1515'-AGGATCCGGTTGTTTAGCAGGCGATAGTCHK1585'-AGAATTCCGTTACGGTGTAGGTTTTGHK2125'-GAGGTACCAATGGAATGTGAACAATHK2255'-AACATATGGATGGCAAGACAATAAAAATAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGHK2625'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCACHK2645'-GTCAAGCTTAACGCTTAGCAGTACGAGAAGTCHK2675'-AATAAGCTTAACCAGGAACGGTGAGGTC	
IRCHTD-ARCHATGGE ATGGE	
HK14.5D-AACATATOGATATATOGATATATOGATATOHK1515'-AGGATCCGGTTGTTAGGCGATGCCHK1585'-AGAATTCCGTTACGGTGTAGGTTTTGHK2125'-GAGGTACCAATGGAATGGCAAGACAATHK2255'-AACATATGGATGGCAAGACAATAAAAATAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGHK2625'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCACHK2645'-GTCAAGCTTACGCATTGTGAAGTACGAGAAGTCHK2675'-AATAGCTTAACCAGGAACGGTGAGGTC	
HK151 5'-AGGATCCGUTTACGGTGTAGGCUATAGTC HK158 5'-AGGATCCGUTTACGGTGTAGGTTTTG HK212 5'-GAGGTACCAATGGAAGTGCAAGACAAT HK225 5'-AACATATGGATGGCAAGACAATAAAAATAAAG HK236 5'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTC HK261 5'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAG HK262 5'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGG HK263 5'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCAC HK264 5'-GTCAAGCTTAACGCATGCAAGTACGAGAAGTC HK267 5'-AATAGCTTAACCAGGAACGGTGAGGTC	
HK1585 -AGAATTCCGTTACGGTGTAGGTTTGGHK2125'-GAGGTACCAATGGAATGGCAAGGAACAATHK2255'-AACATATGGATGGCAAGGCAAGACAATAAAAAAAAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGHK2625'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCACHK2645'-GTCAAGCTTAACGCTTGCAAGTACGAGAAGTCHK2675'-AATAAGCTTAACCAGGAACGGTGAGGTC	
HK2125'-GAGGTACCAATGGAATGGAACAATHK2255'-AACATATGGATGGCAAGACAATAAAAATAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGHK2625'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCACHK2645'-GTCAAGCTTAACGTTGGAACTACGAGAAGTCHK2675'-AATAAGCTTAACCAGGAACGGTGAGGTC	
HK2255'-AACAIAIGGAIGGCAAGACAAIAAAAAIAAAGHK2365'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTCHK2615'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAGHK2625'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGGHK2635'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCACHK2645'-GTCAAGCTTAACGTGTGGAAGTACGAGAAGTCHK2675'-AATAGCTTAACCAGGAACGGTGAGGTC	
HK236 5'-ATTCAAGCTTACGCAAGGTAAACTGGTGTTTC HK261 5'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAG HK262 5'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGG HK263 5'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCAC HK264 5'-GTCAAGCTTAACGCTTGGGAAGTACGAGAAGTC HK267 5'-AATAGCTTAACCAGGAACGGTGAGGTC	
HK261 5'-AACATATGGGATCCGGACTGCAAGTGCCAATTAAG HK262 5'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGG HK263 5'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCAC HK264 5'-GTCAAGCTTACGCGTGTGGAAGTACGAGAAGTC HK267 5'-AATAGCTTAACCAGGAACGGTGAGGGCC	
HK262 5'-ATTAGTAGATAGCTAAGCTTAAGTGCCAATTAAGG HK263 5'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCAC HK264 5'-GTCAAGCTTACGCGTTGTGAAGTACGAGAAGTC HK267 5'-AATAAGCTTAACCAGGAACGGTGAGGTC	
HK263 5'-ATTGGCACTTAAGCTTAGCTATCTACTAATGTCAC HK264 5'-GTCAAGCTTACGCGTTGTGAAGTACGAGAAGTC HK267 5'-AATAAGCTTAACCAGGAACGGTGAGGTC	
HK264 5'-GTCAAGCTTACGCGTTGTGAAGTACGAGAAGTC HK267 5'-AATAAGCTTAACCAGGAACGGTGAGGTC	
HK267 5'-AATAAGCTTAACCAGGAACGGTGAGGTC	
HK268 5'-GGCATATGTTGCATAATTTTGTTGCAA	
HK297 5'-GTGAAGCTTAATTTCTTGGTAAACTGAGATGTTCT	
HK313 5'-GGTGGATCCGGTAAGGCCGTATCAGGTGAAAC	
HK330 5'-TTCATATGTACGGCAGGAACTTTATAG	
HK331 5'-GTCAAGCTTATTCTGGTACGGAAAGATCG	
HK336 5'-GCTTCATATAAGCTTATTGTTTCAATGGTACCCAG n	
HK337 5'-TTGAAACAATAAGCTTATATGAAGCCATTTTTGAG	
HK338 5'-GCTTCATAGCTTAAGCTTGTTTCAATGGTACCCAG	
HK339 5' ATTGA A ACA AGCTTA AGCTATGA AGCCATTTTTG	
HK340 5' TO ATAGETCTA ATGETTC A ATGETACC	
HK341 5-1CALATOGETTETAATOGETTECAATOGETACCCAG	
IIK340 5-0CTTCATATOCCACTTCTCCCACTACT	
III V270 S CACCATACOCCCCCCTA ACCCCCCTC	
HK3/5 5-AAGGAICCGGGAAGIGCTTIGGTAGGGAIACCGGA	
HK386 5-GIGIGGIACAGAAGCIIAIICAIAAAACIIC	
HK387 5'-GCTTCATATAAGCTTATTGTTTCAATGGTACCCAG	
HK388 5-CCCATATGACCCACAACTTCATAGC	
HK393 5'-TATTATGGAGAAAAGCTTAATTGGGAGCTATGAAG	
HK398 5'-ATCATATGGGACTTGTTCTCCATAA	
HK405 5'-CAGAAGCTTAATCCCTAGCAAAGCACTTC	
HK406 5'-CAGAAGCTTAGGTATCCCTAGCAAAGCAC	
HK476 5'-ATCAAGCTTAATTATCAACGCTATAAACAG	
HK504 5'-TTGTACTGGGTACCTCCCGAGTTGTGAACAATAATATT	
HK505 5'-GAACATCTCGCTTTACCCCGGAATTCTGGTAGTGATATTTATT	
HK506 5'-CCCAATAAATATCACTACCAGAATTCCGGGGTAAAGCGAGATGTTC	
HK516 5'-AACATATGAAATCTGGTTTTGCAG	
HK517 5'-AACATATGGAAGCTACAATGCAGC	
HK518 5'-TGAAGCTTAACCTACTAATTCCTTAATTG	
HK519 5'-GTCAAGCTTAGTTCAATGCCCAAACTG	
HK593 5'-ATCAAGCTTATCTTCTCAGTACCTCTTCCC	
HK594 5'-TTCAAGCTTATGCTTCCATCACGCATTCCTC	
HK617 5'-GACATATGAACGATACTGTACCACACATG	
HK655 5'-GCATATGACTGTACCACATGGAATC	
HK657 5'-ACATATGAATGGTTACGCAGTTCC	
HK763 5' TAGGATCGGTGGTGGTTTAGCAGGCGATAG	
W23 5' CTGTAGCAGA A ACCGCTAGTGA A GCGACATTCGATAGAG	
I_{A} 5' CTCTATCGA ATGTCCCTTCACCCCTTTCTCCTACAC	
SA02 5' ACCATATGACGA ACTIVATAGAAAAACCATA	
SA022 5 - AUCCATATUACCOARDI LA LA DAAAACOALAC SA022 5' ACCOATATUACA A A A COATACTO A A A COATACTO A A COATACTO A A	
SAUSS J-AUULAIAIUUAAUIIIAIUAAAAUUAIAUUAIAUUAIAU	
SAUSS S-CCAAUCITATACIGICAAIAIIICCGIIICAIAG	
SKU12 ST-LUCT IACAIATGUAGIAUAAAUTTATCCTG	
SK092 5-ACGGAICCIGITIAAGCIAIGAACGGAAAIATIG	
SKU95 5'-TAGGTACCATTGAAACAATTAGAAGCTATG	
SK181 5'-AAGGAICCAAGIGCGIATCAGGIGAAACAC	
SK182 5'-ATGGTACCTATAACCGTGTTGTGAAGTACGAG	
SZ015 5 ³ -TGCCAAGCTTATTCCGTTACGGTG	
Duet-MCS1-fw 5'-GGATCTCGACGCTCTCCCT	