Supplementary Information

Two distinct domains contribute to the substrate acyl chain length selectivity of plant acyl-ACP thioesterase

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Supplementary Figure 1. Free FA titer and profile, and western blot analysis upon the expression of wild-type and seven representative CvFatB2 mutant enzymes in *E. coli* strains. Fatty acid titer is an average of 4 replicates, with error bars representing the standard error of the mean. The western blot analyses were conducted on $35 \,\mu g$ of soluble protein extracted from each *E. coli* strain, and CvFatB2 antibody was used to immunologically detect CvFatB2 variants. The multiple bands are probably the result of post-extraction proteolytic clipping of the expressed TEs. Because all the bands are immunologically recognized by our CvFatB2 antibody, we have integrated the signal from the entire collection of bands to compare the relative expression of the TE variants.

Supplementary Figure 2

									– Section 1
	(1) 1	.1	0	20		30	4	0	52
AEM72523 CvFatB2	(1)	– – T <mark>AA<mark>S</mark>SA</mark>	FFP <mark>V</mark> P		- <mark>S</mark> ADT <mark>S</mark>	S <mark>RP</mark> G-	-KL <mark>G</mark> NG	PSSSFS	PLK-PK <mark>S</mark>
AEM72524 CvFatB3	(1) - <mark>M</mark>	VA <mark>A</mark> AA <mark>S</mark> SA	FFSF <mark>P</mark>		- <mark>TP</mark> GT <mark>S</mark>	P <mark>KP</mark> G-	- K F <mark>G</mark> N W	PSSLS	IPFNPK <mark>s</mark>
AAC49180 CpFatB2	(1) - M	VA <mark>A</mark> AA <mark>SA</mark> A	FFS <mark>V</mark> A		- <mark>TP</mark> RTN	IS <mark>P</mark>		-S <mark>SL</mark> S	VPFKPK <mark>s</mark>
AAB51525 GmFatB1	(1) - M	VATAATS <mark>S</mark>	FFP <mark>L</mark> T		- <mark>sp</mark> s <mark>g</mark> d	A <mark>K</mark> SG-	– N P <mark>G</mark> K G	SV <mark>S</mark> FG	SMKSKS <mark>A</mark>
EER87824 SbFatB1	(1) -M	A <mark>gs<mark>laas</mark>a</mark>	FFPGP	G A	A <mark>sp</mark> a <mark>as</mark>	A <mark>K</mark> TSF	NLA <mark>G</mark> EL	PDNLS	VRGIVAK
EER88593 SbFatB2	(1) - M	A <mark>as</mark> i <mark>aas</mark> s	FVPG		- <mark>sp</mark> ap <mark>a</mark>	PAAPF	SGL <mark>g</mark> er	PESLD	VRGVAAK
AEM72519 CnFatB1	(1) - M	VA <mark>s</mark> va <mark>a</mark> sa	FFPTP	si	F <mark>S</mark> ST <mark>AS</mark>	A <mark>K</mark> AS-	KTI <mark>G</mark> EG	SE <mark>SL</mark> D	VRGIVAK
AAD42220 EqFatB	(1) - M	VA <mark>s</mark> iv <mark>awa</mark>	FFPTP	si	FSPTAS	A <mark>K</mark> AS-	KTI <mark>G</mark> EG	SENLN	VRGIIAK
AEM72520 CnFatB2	(1) - M	VA <mark>s</mark> ia <mark>a</mark> sa	FFPTPS-	s	S <mark>S</mark> SA <mark>AS</mark>	A <mark>K</mark> AS-	KTI <mark>G</mark> EG	PGSLD	VRGIVAK
AAG43857 IqFatB1	(1)	MA <mark>svaa</mark> sa	FFP <mark>V</mark> PSS	SASTTSS	s <mark>s</mark> st <mark>as</mark>	A <mark>kp</mark> ss	ISL <mark>G</mark> KG	PDSLD	SRGLIAK
AAG43858 IgFatB2	(1) -M	A <mark>asvsasa</mark>	FFP <mark>V</mark> PSS	SSSSSSS	S <mark>S</mark> LT <mark>G</mark> S	A <mark>kp</mark> ss	ISL <mark>G</mark> KG	PDSLY	VRGLMAK
EDO65090 PpFatB	(1)								
EER96252 SbFatB3	(1)	– – – – – – M <mark>A</mark>	TTPAP		QT <mark>AS</mark>	RVAS-	<mark>G</mark> RL	IFGEP	RLRGVR <mark>S</mark>
AAC48990 ChFatB1	(1) -M	VATAA <mark>s</mark> sa	FFP <mark>L</mark> P		SADTS	S <mark>RP</mark> G-	-KL <mark>G</mark> NK	PSSLS	PLK-PK <mark>S</mark>
AEM72521 CnFatB3	(1) M <mark>V</mark>	A <mark>svaass</mark> s	FFP <mark>V</mark> P	s	s <mark>s</mark> ss <mark>a</mark> s	A <mark>K</mark> AS-	RGI	PDGLD	VRGIVAK
AAB71731 UaFatB1	(1)								
AAC49269 ChFatB2	(1) - M	VA <mark>A</mark> AA <mark>S</mark> SA	FFP <mark>V</mark> P		- <mark>AP</mark> G <mark>AS</mark>	P <mark>KP</mark> G-	- K F <mark>G</mark> NW	PSSLS	PSFKPK <mark>S</mark>
CAB60830 CIFAtB3	(1) -M	VA <mark>A</mark> AA <mark>T</mark> SA	FFP <mark>V</mark> P		- <mark>AP</mark> GT <mark>S</mark>	P <mark>KP</mark> G-	- KS <mark>G</mark> NW	PSSLS	PTFKPK <mark>S</mark>
AAC49784 CwFatB2	(1) MV	va <mark>a</mark> aa <mark>s</mark> sa	FFP <mark>V</mark> P		- <mark>ap</mark> rp <mark>t</mark>	P <mark>KP</mark> G-	- K F <mark>G</mark> N W	PSSLS	QPFKPK <mark>s</mark>
AAC49179 CpFatB1	(1) - M	VA <mark>A</mark> AA <mark>s</mark> sa	CFP <mark>V</mark> P		- <mark>SPGAS</mark>	P <mark>KP</mark> G-	-KL <mark>G</mark> NW	SS <mark>SL</mark> S	PSLKPK <mark>S</mark>
AEM72522 CvFatB1	(1) - M	VA <mark>A</mark> AA <mark>T</mark> SA	FFP <mark>V</mark> P		- <mark>AP</mark> GT <mark>S</mark>	P <mark>KP</mark> G-	-KS <mark>G</mark> NW	PSSLS	PTFKPK <mark>S</mark>
						_			– Section 2
	(53) <u>53</u>	60		70	80		90		104
AEM72523 CvFatB2	(37) I P	N <mark>GG</mark> I	QVKASAS	S A P P K <mark>I</mark> N (<mark>gs</mark> svgl	K <mark>S</mark> GGI	KTH <mark>DD</mark> A	. P <mark>S</mark> AP –	PPR
AEM72524 CvFatB3	(41) NH	N <mark>GG</mark> I	QVKA <mark>n</mark> as	5 <mark>AHPK</mark> AN(SSA <mark>V</mark> SL	KAG <mark>S</mark> I	ETQ <mark>ED</mark> T	S <mark>S</mark> PS-	PP <mark>PR</mark>
AAC49180 CpFatB2	(34) NH	N <mark>GG</mark> – – – – F	'QVKA <mark>N</mark> AS	S <mark>AHPK</mark> ANO	<mark>ss</mark> a <mark>v</mark> sl	K <mark>S</mark> G <mark>S</mark> I	ETQ <mark>ED</mark> K	T <mark>S</mark> SS.	PP <mark>PR</mark>
AAB51525 GmFatB1	(41) AS	SR <mark>G</mark> I	QVKA <mark>n</mark> a(2 <mark>a</mark> pt <mark>ki</mark> n(38		T	DD <mark>A</mark> QL	PA <mark>PR</mark>
EER87824 SbFatB1	(45) PN	APSGNM	iqvka <mark>q</mark> aq	2 <mark>ALPK<mark>V</mark>N(</mark>	G <mark>T</mark> K <mark>V</mark> NL	K <mark>S</mark> A <mark>S</mark> I	'DKE <mark>E</mark> AI	PYTAP	<mark>K</mark>
EER88593 SbFatB2	(42) PG	ASSNAVRA	GKTRAHA	A <mark>avpk<mark>v</mark>n(</mark>	GGK	SAV <mark>a</mark> i	GEH <mark>D</mark> TV	P <mark>SS</mark> VP	<mark>K</mark>
AEM72519 CnFatB1	(44) PT	SSSAAM	I <mark>q</mark> g <mark>k</mark> vk <mark>a</mark> q	2 <mark>avpk<mark>i</mark>no</mark>	G <mark>T</mark> K <mark>V</mark> GL	KTESC	KA <mark>E</mark> E	D <mark>AA</mark> PS	SA <mark>PR</mark>
AAD42220 EgFatB	(44) PT	SSSAAK	QG <mark>K</mark> VM <mark>A</mark> Q	2 <mark>avpk<mark>i</mark>no</mark>	G <mark>a</mark> kvgl	KAESQ	KA <mark>E</mark> E	D <mark>aa</mark> ps	SA <mark>PR</mark>
AEM72520 CnFatB2	(45) PT	SSSAAM	I <mark>qek</mark> vkvq	2 P V <mark>P K I N</mark> O	G <mark>a</mark> kvgl	K VE T C	KA <mark>D</mark> E	E <mark>SS</mark> PS	SA <mark>PR</mark>
AAG43857 IgFatB1	(51) SV	WLWLRR	LASE- <mark>G</mark> Q	2CPESHE	QR <mark>V</mark> QG	RVENF	QAKV <mark>e</mark> d	GR <mark>S</mark> VL	PSSSA <mark>PR</mark>
AAG43858 IgFatB2	(52) PA	SSSGSI	QVKV <mark>N</mark> AQ	2 <mark>A</mark> AT <mark>RVN(</mark>	<mark>SS</mark> K <mark>V</mark> GL	KTDTN	IKL <mark>E</mark> D	APFIP	SSAFA
AAG43858 IgFatB2 EDQ65090 PpFatB	(52) PA (1)	SSSGSI -MS	<mark>QVK</mark> V <mark>N</mark> A(-RVVPP]	2 <mark>A</mark> AT <mark>RVN(</mark> ILLE <mark>K</mark> DS <mark>2</mark>	<mark>GS</mark> K <mark>V</mark> G <mark>L</mark> AAFR	KTDTN 	KL <mark>E</mark> D	APFIP	
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3	(52) PA (1) (31) FG	SSSGSI -MS N <mark>GG</mark>	QVKVNA(- RVVPP] - AS <mark>G</mark> RRV	2 <mark>A</mark> AT <mark>RVN(</mark> ILLE <mark>K</mark> DS <mark>)</mark> V <mark>S</mark> VEA <mark>VN(</mark>	<mark>SSKV</mark> GL AAFR S <mark>A</mark> VRP-	KTDTN 	KL <mark>E</mark> C	APFIP	
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1	(52) PA (1) (31) FG (40) TP	SSSGSI -MS N <mark>GG</mark> I N <mark>GG</mark> I	QVKVNAC -RVVPPJ -AS <mark>G</mark> RRV QVKANAS	Q <mark>A</mark> AT <mark>RV</mark> N(ILLE <mark>K</mark> DS <mark>2</mark> V <mark>S</mark> VEA <mark>VN(</mark> S <mark>APPKIN(</mark>	GSK <mark>V</mark> GL AAFR G <mark>A</mark> VRP- GSP <mark>V</mark> GL	KTDTN K <mark>S</mark> GGI	KL <mark>E</mark> D KTQ <mark>ED</mark> A	APFIP .H <mark>SA</mark> P-	PPR
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1 AEM72521 CnFatB3	<pre>(52) PA (1) (31) FG (40) TP (42) PA</pre>	SSSGSI -MS N <mark>GG</mark> N <mark>GG</mark> I SSSGWM	QVKVNAC - RVVPPI - AS <mark>G</mark> RRV QVKA <mark>N</mark> AS IQAKASA	2AAT <mark>RV</mark> N(ILLEKDS V <mark>S</mark> VEA <mark>VN(</mark> SAP <mark>PKIN(</mark> R <mark>AIPKI</mark> DI	GSK <mark>V</mark> GL AAFR GAVRP- GSPVGL O <mark>T</mark> K <mark>V</mark> GL	KTDTN KSGGI RTDVE	KL <mark>E</mark> C KTQ <mark>ED</mark> A : E D	APFIP .H <mark>SA</mark> P- .A <mark>AS</mark> TA	PPR RR
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1 AEM72521 CnFatB3 AAB71731 UaFatB1	(52) PA (1) (31) FG (40) TP (42) PA (1) -G	SSSGSI -MS N <mark>GG</mark> N <mark>GG</mark> I SSSGWM S <mark>GA</mark> I	QVKVNAC - RVVPPJ - AS <mark>G</mark> RRV QVKA <mark>N</mark> AS IQAKASAF QVKAS <mark>S</mark> (2AAT <mark>RVN(</mark> ILLEKDS VSVEAVN(SAPPKIN(RAIPKID) 2APPKLN(GSKVGL AAFR GAVRP- GSPVGL O <mark>T</mark> KVGL GSNVGL	KTDTN KSGGI RTDVE VKS <mark>S</mark> -		APFIP H <mark>SA</mark> P- A <mark>AS</mark> TA DDTTS	PPR RR PPAR
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1 AEM72521 CnFatB3 AAB71731 UaFatB1 AAC49269 ChFatB2	(52) PA (1) (31) FG (40) TP (42) PA (1) -G (41) IP	SSSGSI -MS N <mark>GG</mark> SSSGWM S <mark>GA</mark> I N <mark>GG</mark> F	- RVVPPI - AS <mark>G</mark> RRV QVKA <mark>N</mark> AS QAKASAF QVKAS <mark>S</mark> Q QVKASS	QAAT <mark>RVNO</mark> ILLEKDS V <mark>S</mark> VEAVNO RAIPKINO QAPPKINO SAHPKANO	SKVGL AAFR AVRP- SPVGL SSVVGL SSNVGL SSVSL	KTDTN KSGGI RTDVE VKS <mark>S</mark> - KSG <mark>S</mark> I	KLED KTQEDA ED QIVKKG	APFIP H <mark>SA</mark> P- A <mark>AS</mark> TA DDTTS S <mark>SS</mark>	
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1 AEM72521 CnFatB3 AAB71731 UaFatB1 AAC49269 ChFatB2 CAB60830 ClFAtB3	(52) PA (1) (31) FG (40) TP (42) PA (1) -G (41) IP (41) IP	SSSGSI -MS N <mark>GG</mark> I SSSGWM S <mark>GA</mark> I NGGF NAGF	QVKVPP - RVVPP - AS <mark>G</mark> RRV QVKA <mark>N</mark> AS QVKASS QVKASS QVKANAS	QAAT <mark>RVN(</mark> ILLEKDS SAPPKIN(RAIPKIN(CAPPKIN(SAPPKIN(SAHPKAN(SAHPKAN(GSKVGL AAFR GAVRP- GSPVGL GSNVGL GSAVSL GSAVSL GSAVNL	KTDT KSGGI RTDVE VKS <mark>S</mark> - KSGSI KSGSI	E KTQEDA E QIVKKG NTQEDT NTQEDT	APFIP HSAP- AASTA DDTTS SSS SSS	PPPR PPPR PPPR
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1 AEM72521 CnFatB3 AAB71731 UaFatB1 AAC49269 ChFatB2 CAB60830 ClFAtB3 AAC49784 CwFatB2	(52) PA (1) (31) FG (40) TP (42) PA (1) -G (41) IP (41) IP (42) NP	SSS GSI - MS N <mark>GG</mark> I SSS GWM S <mark>GA</mark> I N GG F N AG F N <mark>G</mark> R F	- RVVPPI - ASCRRV QVKANAS QVKANAS QVKAS QVKANAS QVKANAS QVKANAS	QAAT <mark>RVN</mark> ILLEKDS SAPPKIN RAIPKID QAPPKIN SAHPKAN SAHPKAN SPHPKAN	GSKVGL AAFR GAVRP- GSPVGL OTKVGL GSNVGL GSAVSL GSAVSL GSAVSL	KTDT KSGGI RTDVE VKSS- KSGSI KSGSI KSGSI		APFIP H <mark>SA</mark> P- A <mark>AS</mark> TA DDTTS S <mark>SS</mark> S <mark>SS</mark> PS <mark>S</mark>	
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1 AEM72521 CnFatB3 AAB71731 UaFatB1 AAC49269 ChFatB2 CAB60830 ClFAtB3 AAC49784 CwFatB2 AAC49179 CpFatB1	(52) PA (1) (31) FG (40) TP (42) PA (1) -G (41) IP (41) IP (42) NP (41) IP (41) IP	SSS GSI - MS N <mark>GG</mark> I SSS GWM S GA I N GG F N AG F N <mark>G</mark> G F	OVKVNAC - RVVPPI - ASGRRV OVKANAS OVKANS OVKANS OVKANS OVKANS OVKANS OVKANS	QAAT <mark>RVN</mark> ILLEKDS SAPPKIN RAIPKID QAPPKIN SAHPKAN SAHPKAN SPHPKAN SAHPKAN	GSKVGL AAFR GAVRP- GSPVGL GSPVGL GSAVGL GSAVSL GSAVSL GSAVSL GSAVTL	KTDT KSGGI RTDVE VKSS- KSGSI KSGSI KSGSI KSGSI		APFIP H <mark>SA</mark> P A <mark>AS</mark> TA DDTTS S <mark>SS SSS PSS LSSS</mark>	
AAG43858 IgFatB2 EDQ65090 PpFatB EER96252 SbFatB3 AAC48990 ChFatB1 AEM72521 CnFatB3 AAB71731 UaFatB1 AAC49269 ChFatB2 CAB60830 ClFAtB3 AAC49784 CwFatB2 AAC49179 CpFatB1 AEM72522 CvFatB1	(52) PA (1) (31) FG (40) TP (42) PA (1) -G (41) IP (41) IP (41) IP (41) IP (41) IP	SSS GSI - MS N GG SSS GWM SGA I N GG F N AG F N GG F N GG F	QVKVNAC - RVVPPI - ASCRRV QVKANAS QKASAF QVKASS QVKANS QVKANS QVKANS QVKANAS QVKANAS	QAAT <mark>RVN</mark> ILLEKDS SAPPKIN RAIPKID QAPPKIN SAHPKAN SAHPKAN SPHPKAN SAHPKAN SAHPKAN	SSKVGL AAFR SPVGL SPVGL SSVVGL SSAVSL SSAVSL SSAVSL SSAVSL SSAVSL SSAVSL	KTDT KSGGI RTDVE KSGSI KSGSI KSGSI KSGSI KSGSI KSGSI		APFIP H <mark>SA</mark> P AASTA DDTTS SSS SSS LSSS S <mark>S</mark> SSS	

	Section 3
(105) 105 ,110 ,120 ,130 ,140	156
AEM72523 CvFatB2 (80) TFINQLPDWSMLLAAITTAFLAAEKQWMMLDRKPKRLDMLED	PFGLG <mark>RV</mark> VQD
AEM72524 CvFatB3 (85) TFISQLPDWSMLVSAITTVFVAAEKQWTMLDRKSKRPDVLVE	P <mark>FVQD</mark>
AAC49180 CpFatB2 (79) TFINQLPVWSMLLSAWTTVFGVAEKQWPMLDRKSKRPDMLVE	PL <mark>GV</mark> D <mark>RIVYD</mark>
AAB51525 GmFatB1 (72) TFINQLPDWSMLLAAITTVFLAAEKQWMMLDWKPRPDMLID	FGLG <mark>r</mark> ivqd
EER87824 SbFatB1 (89) TF YNQLPDWSMLLA <mark>AW</mark> TT <mark>I</mark> FLAAEKQWT <mark>L</mark> LDWKPK <mark>K</mark> PDML <mark>W</mark> DI	FGFG <mark>RII</mark> QD
EER88593 SbFatB2 (86) TFYNQLPDWSMLLA <mark>AITTI</mark> FLAAEKQWTMLDWKP <mark>R</mark> RPDMLTDT	FGFG <mark>RII</mark> HD
AEM72519 CnFatB1 (89) TFYNQLPDWS <mark>VLLAAVTTIFLAAEKQWTILDW</mark> KP <mark>RRPDML</mark> TD	FSLG <mark>K</mark> IVQD
AAD42220 EgFatB (89) TFYNQLPDWS<mark>V</mark>LLA<mark>AWTT<mark>I</mark>FLAAEKQWT<mark>L</mark>LDWKP<mark>R</mark>RPDMLTG<mark>A</mark></mark>	FSLG <mark>K</mark> IVQD
AEM72520 CnFatB2 (90) TFYNQLPDWS <mark>V</mark> LLA <mark>AWTTI</mark> FLAAEKQWTLLDWKPRRPDMLAD	FGLG <mark>k</mark> ivqd
AAG43857 IgFatB1 (100) TFYNQLPDWS <mark>V</mark> LLA <mark>AITTIFLAAEKQWTLI</mark> DWKRGGPDMLTD	FGLG <mark>KII</mark> EN
AAG43858 IgFatB2 (98) TFYNQLPDWS <mark>VLLAAITTIFLAAEKQWTLI</mark> DWKRGGPDMLSDA	FGLP <mark>KII</mark> EN
EDQ65090 PpFatB (19)AILAAIAGVALAAENQRRHDKTEVPVDV	/FRQ <mark>GRLV</mark> ES
EER96252 SbFatB3 (53)DGAAAVADVRLVPAPPPAS <mark>VE</mark> GDDGGD	FRLGKFVEG
AAC48990 ChFatB1 (83) TFINQLPDWSMLLAAITTVFLAAEKQWMMLDWKPKRPDMLVD	PFGLGSIVQD
AEM72521 CnFatB3 (83) TSYNQLPDWSMLLA <mark>A</mark> IRTIFSAAEKQWTLLDSKKRGADAVADF	S <mark>GVGKMV</mark> KN
AAB71731 UaFatB1 (44) TFINQLPDWSMLLA <mark>AITTL</mark> FLAAEKQWMMLDWKPKRPDML <mark>V</mark> D	PFGLG <mark>R</mark> FVQD
AAC49269 ChFatB2 (84) TFLHQLPDWSRLLTAITTVFWK-SKRPDMHDRKSKRPDMLVDS	FGLESTVQD
CAB60830 CIFAtB3 (84) AFLNQLPDWSMLLTAITTVFVAAEKQWTMLDRKSKRPDMLVDS	VGLKSIVRD
AAC49784 CwFatB2 (85) TFLNQLPDWSRLRTAITTVFVAAEKQFTRLDRKSKRPDMLVDW	V <mark>FG</mark> SET <mark>IVQ</mark> D
	- ar
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMD2	SF.GTEKAAÖD
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMD AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLWD	VGLERVVQD VGLKSIVRD
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMD AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLWD	VGLERVVQD VGLKS <mark>IV</mark> RD —— Section 4
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLVDS (157) 157 ,170 ,180 ,190	SEGLERVOOD VGLKSIVRD —— Section 4 208
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLWDS (157) 157 ,170 ,180 ,190 AEM72523 CvFatB2 (132) GLVFRQNFSIRSYEIGADRTASIETWMNHLQETALNHVKTAGI	SPELE KV VOD VGLKSIVRD Section 4 208 SNDGFGRTP
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLWDS (157) 157 ,170 ,180 ,190 AEM72523 CvFatB2 (132) GLVFRQNFS IRSYEIGADRTASIETWMNHLQETALNHVKTAGI AEM72524 CvFatB3 (132) GWSFRQSFS IRSYEIGVDRTASIETLMNIFQETSLNHCKSLGI	SPELE KY VOD VGLKSIVRD Section 4 208 SNDGFGRTP
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLWDS (157) 157170180190 AEM72523 CvFatB2 (132) GLVFRQNFS IRSYEIGADRTASIETWMNHLQETALNHVKTAGI AEM72524 CvFatB3 (132) GWSFRQSFS IRSYEIGVDRTASIETLMNIFQETSLNHCKSLGI AAC49180 CpFatB2 (131) GWSFRQSFS IRSYEIGADRTASIETLMNMFQETSLNHCKIIGI	SUBLE SURVED SUGLKSIVRD Section 4 208 SNDGFGRTP LINDGFGRTP
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLWDS (157) 157	SUBLE SURVED VGLKSIVRD Section 4 208 SNDGFGRTP LNDGFGRTP LNDGFGRTP LNDGFGRTP
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLWDS (157) 157 [170]180]190 AEM72523 CvFatB2 (132) GLVFRQNFS IRSYEIGADRTASIETWMNHLQETALNHVKTAGI AEM72524 CvFatB3 (132) GWSFRQSFS IRSYEIGVDRTASIETLMNIFQETSLNHCKSLGI AAC49180 CpFatB2 (131) GWSFRQSFS IRSYEIGADRTASIETLMNMFQETSLNHCKIIGI AAB51525 GmFatB1 (124) GLVFRQNFS IRSYEIGADRTASIETWMNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFLIRSYEIGADRTASIETUMNHLQETALNHVKTAGI	SNDGFGRTP Section 4 208 SNDGFGRTP LNDGFGRTP LNDGFGRTP LGDGFGSTP
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS (157) 157 [170]180]190 AEM72523 CvFatB2 (132) GLVFRQNFS IRSYEIGADRTASIETWMNHLQETALNHVKTAGI AEM72524 CvFatB3 (132) GWSFRQSFS IRSYEIGVDRTASIETLMNIFQETSLNHCKSLGI AAC49180 CpFatB2 (131) GWSFRQSFS IRSYEIGADRTASIETLMNMFQETSLNHCKIGI AAC49180 CpFatB1 (124) GLVFRQNFS IRSYEIGADRTASIETWMNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETWMNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI EER88593 SbFatB2 (138) GLMFRQNFS IRSYEIGADRTASIETLMNHLQETALNHVKTAGI	SUBLE KV VQD VGLKSIVRD Section 4 208 SNDGFGRTP LNDGFGRTP LGDGFGSTP LGDGFGSTP
AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS (157) 157 [170]180]190 AEM72523 CvFatB2 (132) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI AEM72524 CvFatB3 (132) GWSFRQSFS IRSYEIGVDRTASIETUMNIFQETSLNHCKIGI AAC49180 CpFatB2 (131) GWSFRQSFS IRSYEIGADRTASIETUMNFQETSLNHCKIGI AAC49180 CpFatB1 (124) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI AEM72519 CnFatB1 (141) GLTFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI	SUBCERVED VGLKSIVRD Section 4 208 SNDGFGRTP LNDGFGRTP LGDGFGSTP LGDGFGSTP LGDGFGSTP
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AAC491/9 CpFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPNMLMDS (157) 157 170 180 190 AEM72523 CvFatB2 (132) GVFRQNFS IRSYEIGADRTASIETWNHLQETALNHVKTAGI AEM72524 CvFatB3 (132) GVSFRQSFS IRSYEIGADRTASIETUMNIFQETSLNHCKSLGI AAC49180 CpFatB2 (131) GVSFRQSFS IRSYEIGADRTASIETUMNIFQETSLNHCKSLGI AAC49180 CpFatB1 (124) GLVFRQNFS IRSYEIGADRTASIETUMNHQETSLNHCKIGI EER87824 SbFatB1 (124) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AAD42200 EgFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AAD42200 EgFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AAD42200 EgFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AAD42200 EgFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AAAA3857 IgFatB1 (152) GLVFKQNFS IRSYEIGADRTASIETUMNHLQETALNHVKSAGI AAG43857 IgFatB1 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKGAGI	SIDERMYOUD SUGLKSIVRD Section 4 208 SNDGFGRTP LDGFGGRTP LGDGFGGTP LGDGFGGTP LGDGFGATP LGDGFGATP LGDGFGATP LGDGFGATP LGNGFGSTP LGNGFGSTP
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AAC491/9 CPFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CVFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLVDS (157) 157 170 180 190 AEM72523 CVFatB2 (132) GVFRQNFS IRSYEIGADRTASIETVMNHLQETALNHVKTAGI AEM72524 CVFatB3 (132) GVSFRQSFS IRSYEIGADRTASIETUMNIFQETSLNHCKIGG AAC49180 CPFatB2 (131) GVSFRQSFS IRSYEIGADRTASIETUMNIFQETSLNHCKIGG AAC49180 CPFatB1 (124) GVFRQNFS IRSYEIGADRTASIETUMNHQETSLNHCKIGG AAC49180 CPFatB1 (124) GVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI EER87824 SbFatB1 (124) GVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AAD42220 EgFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AEM72519 CNFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKTAGI AAD42220 EgFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKAGI AAG43857 IgFatB1 (152) GLVFRQNFS IRSYEIGADRTASIETUMNHQETALNHVKSAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHQETALNHVKSAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHQETALNHVKCAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHQETALNHVKCAGI AAC48990 CNFatB1 (135) GLVYRQNFS IRSYEIGADRTASIETUMNHQETALNHVKCAGI AAC48990 CNFatB1 (152) GLVYRQNFS IRSYEIGADRTASIETUMNHQETALNHVKCAGI AAC48990 CNFatB1 (155) GLVYRQNFS IRSYEIGADRTASIETUMNHQETALNHVKCAGI AAC48900 CNFatB1 (155) GLVYRQNFS IRSYEIGADRTASIETUMNHQETALNHVKCGI AAC48900 CNFatB1 (156) GLVYRQ	SIND GEGERTP Section 4 208 SND GEGERTP LND GEGERTP LND GEGERTP LGD GEGERTP
AAC491/9 CPFatB1 (85) AFFNQLPDWSMLLTAITTVFWAPEKRWTMFDRKSKRPNMLMDS AEM72522 CVFatB1 (84) AFLNQLPDWSMLLTAITTVFWAAEKQWTMLDRKSKRPDMLVDS (157) 157 170 180 190 AEM72523 CVFatB2 (132) GVFRQNFS IRSYEIGADRTASIETVMNHLQETALNHVKTAGI AEM72524 CVFatB3 (132) GVSFRQSFS IRSYEIGADRTASIETVMNHLQETSLNHCKIG AAC49180 CPFatB2 (131) GVSFRQSFS IRSYEIGADRTASIETVMNHLQETSLNHCKIG AAC49180 CPFatB2 (131) GVSFRQSFS IRSYEIGADRTASIETVMNHLQETALNHVKTAGI EER87824 SbFatB1 (124) GLVFRQNFS IRSYEIGADRTASIETVMNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFS IRSYEIGADRTASIETVMNHLQETALNHVKTAGI EER88593 SbFatB2 (138) GLMFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI AAD42220 EGFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKTAGI AAD42220 EGFatB (141) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKAGI AAAA3857 IGFatB1 (152) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKAGI AAG43857 IGFatB1 (152) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKAGI AAG43858 IGFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKAGI AAG43858 IGFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKCAGI AAG43858 IGFatB2 (150) GLLYRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKCAGI AAG43859 OCFatB1 (135) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKCAGI AAC48990 ChFatB1 (135) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKCAGI AAC48900 ChFatB1 (151) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKCAGI AAC48900 ChFatB1 (155) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKCAGI AAC48900 ChFatB1 (155) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKCAGI AAC48900 ChFatB1 (155) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKSVGI AAC4900 ChFatB1 (155) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKSVGI AAC4900 ChFatB1 (155) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKSVGI AAC490269 ChFatB2 (155) GLVFRQNFS IRSYEIGADRTASIETUMNHLQETALNHVKSVGI	SIND GF GR TP Section 4 208 SND GF GR TP LND GF GR TP LND GF GR TP LGD GF GR TP
AAC49179 CpFatB1 (85) AF FNOL PDWSMLLTAITTVFWA PEKRWTMFDRKSKRPNMLMDS AEM72522 CvFatB1 (84) AF LNOL PDWSMLLTAITTVFWA PEKRWTMFDRKSKRPNMLMDS (157) 157 170 180 190 (157) 157 170 180 190 AEM72523 CvFatB2 (132) GLVFRQNFS IRSYEI GADRTAS I ETWMNHLQETALNHVKTAGI AAC49180 CpFatB2 (131) GWSFRQSFS IRSYEI GADRTAS I ETLMN IF QE TSLNHCKI G AAC49180 CpFatB2 (131) GWSFRQSFS IRSYEI GADRTAS I ETLMN MFQE TSLNHCKI G AAC49180 CpFatB2 (131) GWSFRQSFS IRSYEI GADRTAS I ETLMN MFQE TSLNHCKI G AAE91525 GmFatB1 (124) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKTAGI EER88593 SbFatB2 (138) GLWFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKTAGI AEM72519 CnFatB1 (144) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKTAGI AEM72519 CnFatB1 (144) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKTAGI AAD42220 EgFatB (144) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKAGI AAD42200 EgFatB (144) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKAGI AAD42200 EgFatB (144) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKAGI AAG43857 IgFatB1 (152) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKSAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKSAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKSAGI AAG43858 IgFatB2 (150) GLLYRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKSGI AAC48990 ChFatB1 (135) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKCGI AAC48990 ChFatB1 (135) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKCGI AAC48990 ChFatB1 (152) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKCGI AAC48990 ChFatB1 (155) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKCGI AAC48990 ChFatB1 (155) GLVFRQNFS IRSYEI GADRTAS I ETMNHLQE TALNHVKCGI AAC48990 ChFatB1 (155) GLVFRQNFS IRSYEI GADRTAS I ETMNHLQE TALNHVKSVGI AAC4990 ChFatB1 (156) GLVFRQNFS IRSYEI GADRTAS I ETMNHLQE TALNHVKSVGI AAC4990 ChFatB1 (156) GLVFRQNFS IRSYEI GADRTAS I ETMNHLQE TALNHVKSVGI AAC4990 ChFatB1 (96) GLVFRQNFS IRSYEI GADRTAS I ETMNHLQE TALNHVKSVGI AAC4990 ChFatB1 (156) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKSVGI AAC4990 ChFatB1 (156) GLVFRQNFS IRSYEI GADRTAS I ETLMNHLQE TALNHVKSVGI AAC4990 ChFatB1	SIND GF GR TP Section 4 208 SND GF GR TP LND GF GR TP LND GF GR TP LGD GF GR TP
AAC491/9 CpFatB1 (85) AF FNOLPDWSMLLTALTTVFVA PEKRWTMFDRKSKRPNMLMPS AEM72522 CvFatB1 (84) AF LNOLPDWSMLLTALTTVFVA AEKOWTMLDRKSKRPDMLVDS (157) 157 170 180 190 AEM72523 CvFatB2 (132) GLVFRONFSIRSYEI GADRTASIET WNNHLOETALNHVKTAGI AEM72524 CvFatB3 (132) GVSFRQSFSIRSYEI GADRTASIET WNNHLOETALNHVKTAGI AAC49180 CpFatB2 (131) GVSFRQSFSIRSYEI GADRTASIET LMNNFQETSLNHCKSLGI AAC49180 CpFatB1 (124) GLVFRQNFSIRSYEI GADRTASIET LMNNFQETSLNHCKIG AB51525 GmFatB1 (124) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKTAGI AEM72519 CnFatB1 (144) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKTAGI AAD42200 EgFatB (141) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKTAGI AAD42200 EgFatB (142) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKTAGI AAC43857 IgFatB1 (152) GLIYRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKSAGI AAG43858 IgFatB2 (150) GLLYRQKFSIRSYEI GADRTASIET LMNHLQETALNHVKSAGI AAG43858 IgFatB2 (150) GLLYRQKFSIRSYEI GADRTASIET LMNHLQETALNHVKSGI AAC48990 ChFatB1 (152) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKSGI AAC48990 ChFatB1 (153) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKSGI AAC48990 ChFatB1 (155) GLVFRQNFSIRSYEI GADRTASIET LMNHLQETALNHVKSGI AAC48990 ChFatB1 (155) GLVFRQNFSIRSYEI GADRTASIET MNHLQETALNHVKSGI AAC48990 ChFatB1 (155) GLVFRQNFSIRSYEI GADRTASIET MNHLQETALNHVKSGI AAC48990 ChFatB1 (155) GLVFRQNFSIRSYEI GADRTASIET MNHLQETALNHVKSGI AAC49909 ChFatB1 (155) GLVFRQNFSIRSYEI GADRTASIET MNHLQETALNHVKSGI AAC49909 ChFatB1 (156) GLVFRQNFSIRSYEI GADRTASIET MNHLQETSLNHCKSVGI AAC49269 ChFatB2 (157) GLVFRQNFSIRSYEI GADRTASIET MNHLQETSLNHCKSVGI AAC49269 ChFatB2 (156) GLVFRQNFSIRSYEI GADRTASIET MNHLQETSLNHCKSVGI AAC49784 CWFatB2 (157) GLVFRRNFSIRSYEI GADRTASIET MNHLQETSLNHCKSVGI	SIND GFGRTP Section 4 208 SND GFGRTP LND GFGRTP LND GFGRTP LGD GFGATP LGD GFGATP
AAC491/9 CpFatB1 (85) AF FNOLPDWSMLLTALTTVFWAPEKRWTMFDRKSKRPNMLMPE AEM72522 CvFatB1 (84) AF LNOLPDWSMLLTALTTVFWAPEKRWTMFDRKSKRPDMLVDS (157) 157 170 180 190 (157) 157 170 180 190 AEM72524 CvFatB2 (132) GV FRQ SFSIRSYEI GADRTASIET MNHLQETALNHVKTAGI AEM72524 CvFatB3 (132) GV SFRQ SFSIRSYEI GADRTASIET MNHLQETALNHVKTAGI AAC49180 CpFatB2 (131) GV SFRQ SFSIRSYEI GADRTASIET MNHLQETALNHVKTAGI EER87824 SbFatB1 (124) GV FRQ FSIRSYEI GADRTASIET MNHLQETALNHVKTAGI EER87824 SbFatB1 (124) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKTAGI EER87824 SbFatB1 (141) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKTAGI AAD42220 CgFatB (141) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKTAGI AAD42220 CgFatB (141) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKTAGI AAD42220 CgFatB (141) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKAGI AAC43857 IgFatB1 (152) GL I YRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI EEQ6500 PpFatB (150) GL I YRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI EEQ6500 PpFatB (150) GL I YRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI EEQ6500 PpFatB (150) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI AAC43858 IgFatB2 (150) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI EEQ6500 PpFatB (56) RLVYGQ FVIRSYEI GADRTASIET MNHLQETALNHVKCAGI AAC48990 ChFatB1 (155) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI AAC48990 ChFatB1 (155) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI AAC4990 ChFatB1 (156) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETALNHVKCAGI AAC49269 ChFatB2 (157) GL VFRQ NFSIRSYEI GADRTASIET MNHLQETSINCKSIGI AAC49784 CWFatB2 (157) GL VFRQ SFSIRSYEI GADRTASIET MNHLQETSINCKSIGI AAC49784 CWFatB2 (157) GL VFRQ SFSIRSYEI GADRTASIET MNHLQETSINCKSIGI	SIND GF GR TP Section 4 208 SND GF GR TP LND GF GR TP LND GF GR TP LGD GF GR TP LLD GF GR TP LLD GF GR TP LLD GF GR TP

												– Sectio	on 5
(209)	209		220		230		2	240		25	50		260
AEM72523 CvFatB2 (184)	E M Y K F	D <mark>LIWV</mark>	VAKMQ'	V <mark>M</mark> VNR	YPTWG	DTV	EVN	rwv <mark>z</mark>	K <mark>S</mark> G	K <mark>N</mark> GM	RRD	WLIS	DCN
AEM72524 CvFatB3 (184)	EMCK	D <mark>LIWV</mark>	VTKMQ	IEVNR	Y P <mark>T</mark> W G	DTI	EVT	rwv <mark>s</mark>	E <mark>S</mark> G	K <mark>N</mark> GM	SRD	WLIS	DСН
AAC49180 CpFatB2 (183)	EMCK	D <mark>LIWV</mark>	VTKMQ	IEVNR	Y P <mark>T</mark> W G	DTI	EVN	rwv <mark>s</mark>	ASG	кн <mark>см</mark>	GRD	WLIS	DСН
AAB51525 GmFatB1 (176)	E <mark>m</mark> ske	RN <mark>LIWV</mark>	VTKMQ	VEV <mark>D</mark> R	Y P <mark>T</mark> W G		2 V D	rwv <mark>s</mark>	ASG	K <mark>N</mark> GM	RRD	WLLR	DG <mark>N</mark>
EER87824 SbFatB1 (193)	E <mark>m</mark> ski	RN <mark>LIWV</mark>	VSKIQ	LLVEQ	Y P <mark>S W G</mark>		2 V D	rwv <mark>a</mark>	AAG	K <mark>N</mark> GM	RRD	WHVR	DYN
EER88593 SbFatB2 (190)	e <mark>m</mark> ske	NLFWV	v <mark>somo</mark> i	AIVER	Y P C W G	DTV	EVD	rwv <mark>s</mark>	ANG	K <mark>N</mark> GM	RRD	WHIR	DSI
AEM72519 CnFatB1 (193)	e <mark>m</mark> ske	RN <mark>LIWV</mark>	VTKMO	VLVEH	Y P <mark>S</mark> WG		evd	rwvG	ASG	K <mark>N</mark> GM	RRD	WHVR	DYR
AAD42220 EgFatB (193)	e <mark>m</mark> ski	RNLIWV	VTKMO	VLIEH	Y P S W G		evd	rwve	ASG	K <mark>N</mark> GM	RRD	WHVR	DYR
AEM72520 CnFatB2 (194)	EMSKE	RN <mark>LIWV</mark>	VTKMR	VLIER	Y P S W G		evd	rwve	PTG	K <mark>N</mark> GM	RRD	WHVR	DHR
AAG43857 IgEatB1 (204)	e <mark>m</mark> ske	RN <mark>LIWV</mark>	VTKMO	V <mark>LV</mark> EH	Y P <mark>S</mark> W G	DVI	evd	rwag	G <mark>S</mark> G	K <mark>N</mark> GM	RRD	WHVR	DS <mark>O</mark>
AAG43858 IgEatB2 (202)	EMSKN	4 <mark>NLIWV</mark>	VTKMQ	V <mark>LV</mark> EH	Y P <mark>S</mark> W G	DVI	evd	rwa <mark>z</mark>	ASG	K <mark>N</mark> GM	RRD	WHVR	DWQ
EDO65090 PpEatB (108)	AMSCI	JNLIWV	VT <mark>R</mark> MO	VHVEO	YPAWO			rwvz	ASG	K N G M	RRD		DYK
FER96252 SbEatB3 (142)	OMSL	KLIWV	VTRIN	IOVDK	YSRWO			rwvz	ssg	KNGM	RRD	WITR	DRN
AAC48990 ChFatB1 (187)	EMYK	DLIWV	VAKMO'		YPTWG	DTV		rwv <mark>a</mark>	KSG	KNGM	RRD	WLIS	DCN
AFM72521 CnFatB3 (187)	EMTR	RNLIWV	VAKML	VHVER	Y P W W G		O I N	rwıs	SSG	K <mark>N</mark> GM	GRD	<mark>ин</mark> ин	DCO
AAB71731 UaFatB1 (148)	EMSL	RN <mark>LIWV</mark>	VTKMO	VAVDR	Y P T W G		ovs	T A W Z	AIG	K <mark>N</mark> GM	rr <mark>e</mark>	TVIW	DFR
AAC49269 ChFatB2 (187)	EMCK	DLIWV	VIKMO		YPAWO		TN	RF	RLG	KIGM	GRD	WLIS	DCN
CAB60830 CIFAtB3 (188)	GMCK	JDLIWV	LTKMO	IMVNR	YPTWG	DTV	TN	TWFS	OSG	KIGM	ASD	WLIS	DCN
AAC49784 CwFatB2 (189)	EMCT	DLIWV	LTKMO	IVVNR	YPTWG	DTV	TN	WFS	osg	KIGM	GRE	WLIS	DCN
(105) (105)					V D II W C		R V S	ΓWT.S	osg	K T G M	GRD	WLTS	DCN
AAC49179 CpFatB1 (189)	EMCK	DLIWV	VTRMK	LHVNK	IPIWO		$ \sim \sim $						
AAC49179 CpFatB1 (189) AFM72522 CvFatB1 (188)	EMCKI GMCKI	ND <mark>LIWV</mark> ND LIWV	VT <mark>R</mark> MK LTKMQ	IMVNR	YPTWG YPTWG	DTV	IN	TWFS	QSG	KIGM	ASD	WLIS	DCN
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188)	EMC <mark>KI</mark> G <mark>M</mark> C <mark>K</mark> I	ND <mark>li</mark> mv ND <mark>li</mark> wv	VT <mark>R</mark> MK LTKMQ	IMVNR IM <mark>V</mark> N <mark>R</mark>	YPTWG Y <mark>PTW</mark> G		E I N	rw F S	Q <mark>S</mark> G	K I GM	ASD	WLIS – Sectio	DCN on 6
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261)	EMCKI GMCKI 261	DLIWV 1DLIWV 27	VT <mark>R</mark> MK LTKMQ 70	IMVNR IMVNR 28	YPTWG YPTWG 30		290	rw F s	Q <mark>S</mark> G	кі <mark>см</mark> 300	ASD	WLIS – Sectio	DCN on 6 312
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236)	EMCKI GMCKI 261 TGEII	DLIWV NDLIWV 27	VT <mark>R</mark> MK LTKMQ 70 VWV <mark>MM</mark>	IMVNR IMVNR 20 NQKTR	YPTWC 30 Klsk <mark>i</mark>	DTV	290		Q <mark>S</mark> G	KIGM 300 D <mark>S</mark> AP	ASD	WLIS – Section	DCN on 6 <u>312</u> D-R
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236)	EMCKI GMCKI 261 TGEII SGEII	DLIWV NDLIWV 27 TRA <mark>SS</mark> TRATS	VT <mark>R</mark> MK LTKMQ 70 VWVMM VWAMM	IMVNR IMVNR 28 NQKTR NOKTR	YPTWG 80 <mark>K</mark> lski rlski	PDE	290	TWFS	QS <mark>G</mark> HFV YFV	300 300 DSAP	A S D V V	WLIS - Section	$D \subset N$ on 6 <u>312</u> D - R D - R
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236) AAC49180 CpFatB2 (235)	261 GMCKI 261 TGEII SGEII TGEII	DLIWV DLIWV 27 TRA <mark>S</mark> S IRATS LIRATS	VT <mark>R</mark> MK LTKMQ 70 VWVMM VWAMM VWAMM	INVNR INVNR 20 NQKTR NQKTR NQKTR	YP TWO 30 Rlski rlski	PDE PDE PDE	290 VRRI VRQI	TWF CIEF CIVF	QSG HFV YFV QFV	300 DSAP DSAP DSAP	A S D V V V	WLIS - Section IEDD IED- IVD-	DCN on 6 <u>312</u> D-R D-R D-R
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236) AAC49180 CpFatB2 (235) AAB51525 GmFatB1 (228)	EMCKI GMCKI 261 TGEII TGEII TGEII TGEII	DLIWV 1DLIWV 27 TRA <mark>S</mark> S IRATS IRATS LTRA <mark>S</mark> S	VTRMK LTKMQ 70 VWVMM VWAMM VWAMM VWVMM	INVNR INVNR 2/ NQKTR NQKTR NQKTR NQKTR	YPTWO 30 Klski rlski rlski	PDE PDE PDE PZE	290 VRR VRQI VRQI VRQI	FWF EIEF EIVF EIEF EIGS	QS <mark>G</mark> HFV YFV QFV YFV	300 DSAP DSAP DSAP DSAP NSDP	ASD V V V	VLIS - Section IED IED - IVD - VEED	$D \subset \mathbf{N}$ on 6 312 $D - \mathbf{R}$ $D - \mathbf{R}$ $D - \mathbf{R}$ $G - \mathbf{R}$
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236) AAC49180 CpFatB2 (235) AAB51525 GmFatB1 (228) EER87824 SbFatB1 (245)	261 GMCKI TGEII TGEII TGEII TGETI SGRT	RDLIWV NDLIWV 27 TRASS LTRASS LRATS TRASS LRATS	VTRMK TKMQ 70 VWVMM VWAMM VWAMM VWVMM	2 1 M V N V K T R K N K N K N K N K N K N K N K N K N K N K K K K K K K K K K K K K	YPTWO 30 RLSKI RLSKI RLSKI RLSKI RLSKI	PDTVI PDE PDE PYE PEE	290 Z R R Z R R Z R Q Z R R Z R Q Z R R Z R R Z R R Z R R R Z R R R R R R	TWFS TEF TEF TEF TEF TEF TEF	QSG HFV YFV QFV YFV YFN	300 DSAP DSAP DSAP NSDP GRS-	V V V V V	VLIS - Section IED- IED- VEED TDEQ	DCN 000 6 <u>312</u> D-R D-R G-R G-R S-E
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AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236) AAC49180 CpFatB2 (235) AAB51525 GmFatB1 (228) EER87824 SbFatB1 (245) EER88593 SbFatB2 (242) AEM72519 CnFatB1 (245) AAD42220 EgFatB (245) AAD42220 EgFatB (245) AAD42220 EgFatB (246) AAG43857 IgFatB1 (256) AAG43857 IgFatB1 (256) AAG43858 IgFatB2 (254) EDQ65090 PpFatB (160) EER96252 SbFatB3 (194) AAC48990 ChFatB1 (239) AEM72521 CnFatB3 (239) AAB71731 UaFatB1 (200) AAC49269 ChFatB2 (239)	261 TGEI TGEI TGEI TGEI TGET TGET TGET TGOT TGOT TGOT TGOT TGOT	LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS		INVNK 21 NQKTR NQKTR NQKTR NKLTR NKLTR NKLTR NKLTR NKLTR NKTR STR NKTR NN N N N N N N N N N N N N N N N N N	30 SC SC SC SC SC SC SC SC SC SC	PDE PDE PDE PDE PDE PDE PDE PEE PDE PDE	2900 2900		QS <mark>G</mark> HFV YFV YFV YFV YFV YFV YFV YFV YFV YFV F YFV F F SFF F F F F F F	K I GM 300 DSAP DSAP DSAP DSAP CRS- ERS-	A S D 	VEED VDED VDED VDED VDED VDED VDED VDED	
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236) AAC49180 CpFatB2 (235) AAB51525 GmFatB1 (228) EER87824 SbFatB1 (245) EER88593 SbFatB2 (242) AEM72519 CnFatB1 (245) AAD42220 EgFatB (245) AAD42220 EgFatB (245) AAD42220 EgFatB (246) AAG43857 IgFatB1 (256) AAG43857 IgFatB1 (256) AAG43858 IgFatB2 (254) EDQ65090 PpFatB (160) EER96252 SbFatB3 (194) AAC48990 ChFatB1 (239) AEM72521 CnFatB3 (239) AAB71731 UaFatB1 (200) AAC49269 ChFatB2 (239) CAB60830 CIFAtB3 (240) AAC49784 CwFatB2 (241)	261 TGEI TGEI TGEI TGEI TGEI TGEI TGEI TGEI	LINU TRASS TRASS TRASS TRASS TRASS TRASS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS		INVNK 22 NQKTRR NQKTRR NQKTR NKLTR NKITR NKITR NKHTRR NKHTRR NKTRR NKKTRR NQKTR NQKTR NQKTR NQKTR NQKTR	30 SC SC SC SC SC SC SC SC SC SC	PDE PDE PDE PDE PDE PDE PEE PEE PDE PDE	2900 2900 VRC VRC VRC VRC VRC VRC VRC VRC VRC VRC		QS <mark>G</mark> HFVVYFVYYYYYYYYYYYYYYYYYYYYYYYYYYY HFSI HFSI HFSI HFVV	K I GM 300 DSAPP DSAP DSAP DSAP DSAP CRS- ERS-	ASD V V V AI -AI -AI -AI PI KD IAA V V V 	VEED VEED VEED VDED VDED VDED VDED VDED	
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236) AAC49180 CpFatB2 (235) AAB51525 GmFatB1 (228) EER87824 SbFatB1 (245) EER88593 SbFatB2 (242) AEM72519 CnFatB1 (245) AAD42220 EgFatB (245) AAD42220 EgFatB (245) AAD42220 EgFatB (246) AAG43857 IgFatB1 (256) AAG43858 IgFatB2 (254) EDQ65090 PpFatB (160) EER96252 SbFatB3 (194) AAC48990 ChFatB1 (239) AEM72521 CnFatB3 (239) AAB71731 UaFatB1 (200) AAC49269 ChFatB2 (239) CAB60830 CIFAtB3 (240) AAC49784 CwFatB2 (241) AAC49179 CpFatB1 (241)	261 TGEI TGEI TGEI TGEI TGET TGET TGET TGET	LINU TRASS TRASS TRATS TRATS TRATS TRATS TRATS TRATS LRATS LRATS LRATS LRATS ARATS ARATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS LRATS			30 KLSKI RLSKI RRLSKI RRLSKI KLSKI KLSKI KLSKI KLSKI RLSKI RLSKI RLSKI RRLSKI RRLSKI RFSKI RFSKI	PDE PDE PDE PDE PDE PDE PEE PEE PDE PDE	2900 2900 2900 2900 2900 2900 2900 2900		QS <mark>G</mark> HFVVVFVVFVV YFVVFVV YFVVFVV YFFV YFFV Y	K I GM 300 D SAPP D SAPP D SAPP D SAPP C RS E RA E RA E RA E RA E RA E RA E RA E RA D SPP D SPP D SPP D SPP	ASD 	VEED VDED VDED VDED VDED VDED VDED VDED	
AAC49179 CpFatB1 (189) AEM72522 CvFatB1 (188) (261) AEM72523 CvFatB2 (236) AEM72524 CvFatB3 (236) AAC49180 CpFatB2 (235) AAB51525 GmFatB1 (228) EER87824 SbFatB1 (245) EER87824 SbFatB1 (245) AEM72519 CnFatB1 (245) AEM72519 CnFatB1 (245) AEM72520 CnFatB2 (244) AAG43857 IgFatB1 (256) AAG43858 IgFatB2 (254) EDQ65090 PpFatB (160) EER96252 SbFatB3 (194) AAC48990 ChFatB1 (239) AAB71731 UaFatB1 (200) AAC49269 ChFatB2 (239) CAB60830 CIFAtB3 (240) AAC49784 CwFatB2 (241) AAC49179 CpFatB1 (241)	261 TGEI SGEI TGEI TGEI TGEI TGEI TGEI TGQT TGQT TGQT TGQT TGQT TGQT TGQT TGQ	LINN TRASS TRASS TRATS TRASS TRASS TRASS TRASS TRASS TRASS ARATS ARATS ARATS ARATS ARATS ARATS ARATS ARATS ARATS ARATS ARATS ARATS			30 KLSKI RLSKI RLSKI RLSKI RLSKI KLSKK KLSKK KLSKK KLSKK RLSKI RLSKI RRLSKI RFSKI RFSKI RFSKI RFSKI	PDE PDE PDE PDE PDE PDE PDE PEE PEE PDE PEE PE	2900 2900 2900 2900 2900 2900 2900 2900		QS <mark>G</mark> HFVVYFVYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY HFSSLFVVVYYYYY	K I GM 300 D S APP D S APP D S APP D S APP C RS		VEED VDED VDED VDED VDED VDED VDED VDED	

						Section 7
(313)	313	320	,330	,340	,350	364
AEM72523 CvFatB2 (285)	<mark>K I</mark> P	KLDEK	- <mark>s</mark> ads <mark>ir<mark>kgl</mark>t</mark>	PRWNDLDVN(2HV <mark>N</mark> NA <mark>KYIG</mark>	WILESTPPEV
AEM72524 CvFatB3 (284)	K L H	KLDVK	- <mark>TG</mark> DS <mark>IR</mark> N <mark>GL</mark> T	PRWNDFDVN(2HV <mark>NN</mark> VKYI <mark>A</mark> I	W <mark>ll</mark> ksvpt <mark>ev</mark>
AAC49180 CpFatB2 (283)	K F H	KLDLK	- <mark>TGD</mark> S <mark>I</mark> CN <mark>GLT</mark>	PRWTDLDVN(2HV <mark>NN</mark> VKYIG	WILQSVPT <mark>EV</mark>
AAB51525 GmFatB1 (277)	K <mark>V</mark> T	KLDDN	- TADF <mark>V</mark> R <mark>KGL</mark> T	PKWNDLDIN(2HV <mark>NN</mark> VKYIG	W <mark>ILES</mark> A <mark>P</mark> QP <mark>I</mark>
EER87824 SbFatB1 (294)	K L A	K PGSTSDGD	TMKQF <mark>IR<mark>K</mark>GLT</mark>	PRWGDLDVN(2HV <mark>NN</mark> VKYIG	WILESAPISI
EER88593 SbFatB2 (291)	K I P	KLP-DGQST	SA <mark>A</mark> KY <mark>VR</mark> T <mark>GLT</mark>	PRWADLDIN(2HV <mark>NN</mark> VKYI <mark>A</mark> I	WILESA <mark>PI</mark> SI
AEM72519 CnFatB1 (294)	K I P	KLDD	D <mark>TAD</mark> Y <mark>IK</mark> W <mark>GL</mark> T	PRWSDLDVN(2HV <mark>NN</mark> VKYIG	WILESA <mark>PI</mark> SI
AAD42220 EgFatB (294)	K I P	KLDD	D <mark>TAD</mark> Y <mark>IK</mark> W <mark>GL</mark> T	PRWSDLDVN(2HV <mark>NN</mark> VKYIG	WILESA <mark>PI</mark> SI
AEM72520 CnFatB2 (295)	K L P	KLDE	D <mark>T</mark> TDY <mark>IKKGL</mark> T	PRWGDLDVN(2HV <mark>NN</mark> VKYIG	WILESAPISI
AAG43857 IgFatB1 (305)	K I P	KLDD	D <mark>TAD<mark>HV</mark>RS<mark>GL</mark>T</mark>	PKWSDLDVN(2HV <mark>NN</mark> VKY <mark>L</mark> G	WILESAPISM
AAG43858 IgFatB2 (303)	<mark>K I</mark> P	KLDD	D <mark>TAD<mark>HV</mark>RN<mark>GL</mark>T</mark>	PRWSDLDVN(2HVK <mark>NV</mark> KY <mark>IG</mark> I	WILESAPISI
EDQ65090 PpFatB (211)	KIC	RLNG	- <mark>sae</mark> y <mark>vr</mark> s <mark>gl</mark> t	PRRSDLDMN(2HV <mark>NN</mark> VKYIG	W <mark>MLET</mark> VPPA <mark>V</mark>
EER96252 SbFatB3 (246)	K I E	KLTDS	- <mark>TAE</mark> H <mark>IR</mark> S <mark>GL</mark> A	PRWSDMDVN(2HV <mark>NN</mark> VKYIG	WILESV <mark>PLD</mark> V
AAC48990 ChFatB1 (288)	K L P	KLDEK	- <mark>TAD</mark> SIR <mark>KGL</mark> T	PRWNDLDVN(2HV <mark>NN</mark> VKYIG	WILESTPPEV
AEM72521 CnFatB3 (288)	K L P	KFDD	D <mark>SA</mark> AH <mark>VRRGL</mark> T	PRWHDFDVN(QHV <mark>NN</mark> VKY <mark>V</mark> G	WILESVPVWM
AAB71731 UaFatB1 (251)	K L T	RFDES	- <mark>SADFIR</mark> X <mark>GL</mark> T	PRWSDLDIN(2HV <mark>NN</mark> VKYIG	WLLESAPPEI
AAC49269 ChFatB2 (287)	K V H	KFKVK	- <mark>TGDSIQKGL</mark> T	PGWNDLDVN(2HVS <mark>NV</mark> KYIG	WILESMPTEV
CAB60830 CIFAtB3 (289)	K I H	KFDVK	- <mark>TG</mark> DS <mark>IR</mark> KGLT	PRWNDLDVN(2HVS <mark>NVKYIG</mark>	WILESM <mark>PIE</mark> V
AAC49784 CwFatB2 (290)	K I H	KFDVK	- <mark>TGDSICKGLT</mark>	PGWNDFDVN(2HVS <mark>NVKYIG</mark>	WILESMPTEV
AAC49179 CpFatB1 (290)	KLQ	KF <mark>D</mark> VK	- <mark>TG</mark> DS <mark>IR</mark> KGLT	PGWYDLDVN(2HVS <mark>NVKYIG</mark>	WILESMPTEV
AEM72522 CvFatB1 (289)	<mark>k l</mark> r	KFDVK	- <mark>TG</mark> DS <mark>IR<mark>K</mark>GL</mark> T	PRWNDLDVN(2HVS <mark>NV</mark> KY <mark>IG</mark>	WILESMPIEV
						—— Section 8
(365)	365	370	380	390	400	416
AEM72523 CvFatB2 (332)	LET	QELC <mark>S</mark> LTLE	<mark>Y</mark> RR <mark>EC</mark> GR <mark>E</mark> SVL	E <mark>SLTAV</mark> DP <mark>S</mark> (GE <mark>G</mark> YG	S
AEM72524 CvFatB3 (331)	FET	Q <mark>el</mark> cg <mark>ltle</mark>	Y <mark>rr<mark>ec</mark>rdsvl</mark>	E <mark>SVTAM</mark> DP <mark>S</mark> I	KE <mark>G</mark> DR	S
AAC49180 CpFatB2 (330)	F <mark>E</mark> T	Q <mark>el</mark> cg <mark>l</mark> tle	<mark>Y</mark> RR <mark>EC</mark> GRDSVL	E <mark>SVTAM</mark> DP <mark>S</mark> I	KE <mark>G</mark> DR	s
AAB51525 GmFatB1 (324)	LET	R <mark>elsavtle</mark>	<mark>Y</mark> RR <mark>EC</mark> GRDSVL	R <mark>SLTAV</mark> SGG(GV <mark>G</mark> DLGHA·	GN <mark>V</mark>
EER87824 SbFatB1 (346)	LEK	HELAS <mark>MTL</mark> D	YR <mark>KEC</mark> GRDSVL	Q <mark>SLTT</mark> VAGE(CVDGHAD	ST <mark>I</mark>
EER88593 SbFatB2 (342)	LEN	HELAS <mark>IVL</mark> D	Y <mark>k</mark> r <mark>ec</mark> grdsvl	Q <mark>SHTSV</mark> QTD(CNSESGE	TT <mark>L</mark>
AEM72519 CnFatB1 (341)	LE N	HELAS <mark>M</mark> TLE	Y <mark>rr<mark>ec</mark>grdsvl</mark>	Q <mark>SLTAI</mark> SND(CT <mark>G</mark> GLPE	AS <mark>I</mark>
AAD42220 EgFatB (341)	LE N	HELAS <mark>MT</mark> LE	Y <mark>rr<mark>ec</mark>grdsvl</mark>	Q <mark>SLTAV</mark> AND(CT <mark>G</mark> GLPE	AS <mark>I</mark>
AEM72520 CnFatB2 (342)	LE N	HELAS <mark>MS</mark> LE	Y <mark>rr<mark>ec</mark>grdsvl</mark>	Q <mark>SLTAV</mark> SNDI	LTDGLVE	SG <mark>I</mark>
AAG43857 IgFatB1 (352)	LES	HELASFTLE	Y <mark>rr<mark>ec</mark>grdgvl</mark>	Q <mark>SLTAV</mark> SAD(CS <mark>A</mark> GPAE	LP <mark>I</mark>
AAG43858 IgFatB2 (350)	LES	HELAS <mark>M</mark> TLE	YRR <mark>EC</mark> GRDSVL	Q <mark>SLTSV</mark> SNN(CTDGSEE	LP <mark>I</mark>
EDQ65090 PpFatB (257)	LDG	YELVS <mark>MNLE</mark>	Y <mark>rrec</mark> gosd <mark>v</mark> v	Q <mark>SMT</mark>		TADGGN <mark>L</mark>
EEBOCOED OLE (DO (OOO)	TED		VPPPCPAGAT			TACCTCCCD
EER96252 SDFatB3 (293)	LED	TUTIOTIT	I KKRCK626 H H	E S L T S MAMAI	MTSSPPAEPP:	пкаатсеар <mark>т</mark>
AAC48990 ChFatB1 (335)	LED	QELCSLTLE	YRR <mark>EC</mark> GR <mark>E</mark> SVL	ESLISMAMAI E <mark>SLIAM</mark> DP <mark>S</mark> (MTSSPPAEPP: GG <mark>G</mark> YG	S
AAC48990 ChFatB1 (335) AEM72521 CnFatB3 (335)	LED LET L <mark>D</mark> G	QELCSLTLE Y <mark>evatmsle</mark>	YRRECGRESVL YRRECGRESVL YRRECRMDSV <mark>V</mark>	ESLIBMAMAI E <mark>sliam</mark> dp <mark>s</mark> Q <mark>sliav</mark> ssdi	MTSSPPAEPP: GG <mark>G</mark> YG HADG	SP <mark>I</mark>
EER96252 SDFatB3 (293) AAC48990 ChFatB1 (335) AEM72521 CnFatB3 (335) AAB71731 UaFatB1 (298)	LED LET LDG HES	QELCSLTLE YEVATMSLE HEIASLTLE	YRRECGR <mark>E</mark> SVL YRRECRMDSV <mark>V</mark> YRRECGRDSVL	ESLISMAMA ESLIAMDPS Q <mark>SLIAV</mark> SSDI N <mark>SAIKV</mark> SD <mark>S</mark>	MTSSPPAEPP. GG <mark>G</mark> YG HADG SQLGKS	SPI SPI AV
AAC48990 ChFatB3 (293) AAC48990 ChFatB1 (335) AEM72521 CnFatB3 (335) AAB71731 UaFatB1 (298) AAC49269 ChFatB2 (334)	LED LDG HES LET	QELCSLTLE YEVATMSLE HEIASLTLE QELCSLALE	YRRECGRESVL YRRECRMDSV <mark>V</mark> YRRECGRDSVL YRRECGRDSVL	ESLTAMDPS OSLTAVSSD NSATKVSDS E <mark>SVTAM</mark> DPS	MTSSPPAEPP. GG <mark>G</mark> YG HADG SQLGKS KV <mark>G</mark> VR	SP <mark>I</mark> SP <mark>I</mark> A <mark>V</mark> S
EER96252 SDFatB3 (293) AAC48990 ChFatB1 (335) AEM72521 CnFatB3 (335) AAB71731 UaFatB1 (298) AAC49269 ChFatB2 (334) CAB60830 ClFAtB3 (336)	LED LET LDG HES LET LET	QELCSLTLE YEVATMSLE HEIASLTLE QELCSLALE QELCSLT <mark>Y</mark> E	YRRECGRESVL YRRECRMDSV <mark>V</mark> YRRECGRDSVL YRRECGRDSVL YRRECGMDSVL	ESLTAMDPS OSLTAVSSD NSATKVSDS ESVTAMDPS ESVTAVDPS	MTSSPPAEPP. 3G <mark>G</mark> YG HADG SQLGKS KV <mark>G</mark> VR EN <mark>G</mark> GR	sp <mark>1</mark> sp <mark>1</mark> A <mark>V</mark> s
EER96252 SDFatB3 (293) AAC48990 ChFatB1 (335) AEM72521 CnFatB3 (335) AAB71731 UaFatB1 (298) AAC49269 ChFatB2 (334) CAB60830 ClFAtB3 (336) AAC49784 CwFatB2 (337)	LED LET HES LET LET	QELCSLTLE YEVATMSLE HEIASLTLE QELCSLALE QELCSLT <mark>V</mark> E QELCSLTLE	YRRECGRESVL YRRECRMDSV <mark>V</mark> YRRECGRDSVL YRRECGRDSVL YRRECGMDSVL YRRECGRESV <mark>V</mark>	ESLISMAMA ESLIAMDPS QSLIAVSSD NSAIKVSDS ESVIAMDPS ESVIAVDPS ESVISMNPS	MTSSPPAEPP GG <mark>G</mark> YG HADG SQLGKS KV <mark>G</mark> VR ENGGR KV <mark>G</mark> DR	SPI AV SPI
EER96252 SbFatB3 (293) AAC48990 ChFatB1 (335) AEM72521 CnFatB3 (335) AAB71731 UaFatB1 (298) AAC49269 ChFatB2 (334) CAB60830 ClFAtB3 (336) AAC49784 CwFatB2 (337) AAC49179 CpFatB1 (337)	LED LET HES LET LET LET	QELCSLTLE YEVATMSLE HELASLTLE QELCSLALE QELCSLTV QELCSLTLE QELCSLTLE	YRRECGRESVL YRRECGRDSVV YRRECGRDSVL YRRECGRDSVL YRRECGMDSVL YRRECGRESVV YRRECGRESVV	ESLISMANA ESLIAMDPS QSLIAVSSDI NSAIKVSDS ESVIAMDPS ESVISMNPS ESVISMDPS ESVISMDPS	MTSSPPAEPP GG <mark>G</mark> YG HADG SQLGKS KV <mark>G</mark> VR ENGGR KVGDR KV <mark>G</mark> DR	SPI AV
AAC48990 ChFatB3 (293) AAC48990 ChFatB1 (335) AEM72521 CnFatB3 (335) AAB71731 UaFatB1 (298) AAC49269 ChFatB2 (334) CAB60830 ClFAtB3 (336) AAC49784 CwFatB2 (337) AAC49179 CpFatB1 (337) AEM72522 CvFatB1 (336)	LED LET LET LET LET LET LET	QELCSLTLE YEVATMSLE HEIASLTLE QELCSLALE QELCSLTV QELCSLTLE QELCSLTLE QELCSLTV	YRRECGRESVL YRRECRMDSV <mark>V</mark> YRRECGRDSVL YRRECGMDSVL YRRECGRESV <mark>V</mark> YRRECGRESV <mark>V</mark> YRRECGRDSVL YRRECGMDSVL	ESLTAMDPS QSLTAVSSDI NSATKVSDS ESVTAMDPS ESVTAVDPS ESVTSMNPS ESVTSMDPS ESVTSMDPS ESVTAVDPS	MTSSPPAEPP GG <mark>9</mark> YG HADG SQLGKS KVGVR KVGDR KVGDR ENGGR	SP AV AV



Supplementary Figure 2. Multiple sequence alignment of 21 functionally characterized plant acyl-ACP TEs. The alignment was constructed with Vector NTI - Alignment X, and the default settings identify identical residues (yellow highlighted), highly conserved residues (blue highlighted), weakly similar residues (green highlighted), and non-similar residues are not highlighted. Sequences are identified by their GenBank Accession Numbers, and source organism: Cv, *Cuphea viscosissima*; Cp, *Cuphea palustris*; Gm, *Garcinia mangostana*; Sb, *Sorghum bicolor*; Cn, *Cocos nucifera*; Eg, *Elaeis guineensis*; Ig, *Iris germanica*; Pp, *Physcomitrella patens*; Ch, *Cuphea hookeriana*; Ua, *Ulmus americana*; Cl, *Cuphea lanceolata*; Cw, *Cuphea wrightii*.

Supplementary Table 1. DNA primers used for the amplification of six overlapping fragments of CvFatB1 and CvFatB2 used in domain-swapping experiments

Domain-	Forward primers	Reverse primers
swapping		
fragment		
I	pUC57F (5'-	Cv-R2 (5'-
	CGGCTCGTATGTTGTGTGG	GGTACGATCCGCGCCGATTTC-
	AAT-3')	3')
II	Cv-F2 (5'-	Cv-R3 (5'-
	GAAATCGGCGCGGATCGTA	CCAGGTCGGATAACGATTGAC-
	CC-3')	3')
III	Cv-F3 (5'-	Cv-R4 (5'-
	GTCAATCGTTATCCGACCTG	CGGGTTTTCTGGTTCATCAT-3')
	G-3')	
IV	Cv-F4 (5'-	Cv-R5 (5'-
	ATGATGAACCAGAAAACCC	TCGTTCCAACGCGGCGTCAGAC
	G-3')	C-3')
V	Cv-F5 (5'-	Cv-R6 (5'-
	GGTCTGACGCCGCGTTGGA	ATCTTCCAGACGCAGCAG-3')
	ACGA-3')	
VI	Cv-F6 (5'-	pUC57R (5'-
	CTGCTGCGTCTGGAAGAT-	CTGCAAGGCGATTAAGTTGGGT
	3')	AAC-3')

	Fragments	II				Ι	II						Г	V		
	Residue Number	194 ^a	213	217	218	219	223	226	227	248	257	260	268	276	282	289
	AEM72523 CvFatB2	V	V	V	А	Κ	Ν	R	R	V	L	Ι	Ι	А	D	L
	AEM72524 CvFatB3	V	V	V	S	E	Ν	S	R	А	L	Ι	Ι	А	D	L
	AAC49180 CpFatB2	V	V	V	S	А	Η	G	R	А	L	Ι	Ι	А	D	L
	AAB51525 GmFatB1	V	V	V	S	А	Ν	R	R	V	L	Ι	Ι	D	D	L
	EER87824 SbFatB1	V	V	V	А	А	Ν	R	R	V	L	Μ	Ι	S	Q	Р
p	EER88593 SbFatB2	V	V	V	S	А	Ν	R	R	V	L	Ι	Ι	S	D	L
Is	AEM72519 CnFatB1	V	V	V	G	А	Ν	R	R	V	L	Μ	Ι	А	D	L
Jas	AAD42220 EgFatB	V	V	V	G	А	Ν	R	R	V	L	Μ	Ι	А	D	L
\cup	AEM72520 CnFatB2	V	V	V	G	Р	Ν	R	R	V	L	V	Ι	А	D	L
	AAG43857 IgFatB1	V	V	А	G	G	Ν	R	R	V	L	F	Ι	V	D	L
	AAG43858 IgFatB2	V	V	А	А	А	Ν	R	R	V	L	F	Ι	А	D	L
	EDQ65090 PpFatB	V	Μ	V	А	А	Ν	R	R	V	L	Μ	Ι	F	Μ	L
	EER96252 SbFatB3	V	Ι	V	А	S	Ν	R	R	V	L	Ι	V	S	S	L
	AAC48990 ChFatB1	V	V	V	Α	Κ	Ν	R	R	V	L	Ι	Ι	Р	D	L
	AEM72521 CnFatB3	V	Ι	Ι	S	S	Ν	G	R	V	L	L	Ι	D	Ν	F
III	AAB71731 UaFatB1	V	V	А	Т	А	Ν	R	R	V	Ι	Ι	Ι	Р	D	F
nd	AAC49269 ChFatB2	V	Ι	F	S	R	Ι	G	R	А	L	L	Ι	Р	S	F
II a	CAB60830 ClFatB3	L	Ι	F	S	Q	Ι	А	S	А	F	L	L	Р	Ν	F
SS	AAC49784 CwFatB2	L	Ι	F	S	Q	Ι	G	R	А	F	L	Ι	Р	Ν	F
Cla	AAC49179 CpFatB1	V	V	L	S	Q	Ι	G	R	А	F	L	F	Р	Ν	F
	AEM72522 CvFatB1	L	Ι	F	S	Q	Ι	А	S	А	F	L	L	Р	Ν	F

Supplementary Table 2. Comparison of the 15 residues that are predicted to affect substrate specificity of acyl-ACP TEs

a. Numbering of the residues are according to the sequence of CvFatB2 (GenBank Accession AEM72523.1), and their positions among the domain-swapping fragments are indicated; b. Each acyl-ACP TE is identified as either belonging to the FatB subclass I or II and III¹, and they are each identified by their GenBank Accession Numbers, and source organism: Cv, *Cuphea viscosissima*; Cp, *Cuphea palustris*; Gm, *Garcinia mangostana*; Sb, *Sorghum bicolor*; Cn, *Cocos nucifera*; Eg, *Elaeis guineensis*; Ig, *Iris germanica*; Pp, *Physcomitrella patens*; Ch, *Cuphea hookeriana*; Ua, *Ulmus americana*; Cl, *Cuphea lanceolata*; Cw, *Cuphea wrightii*.

Sample					mol pe	ercenta	ge (%)					Total free
name	4:0	6:0	8:0	10:0	10:1	12:0	12:1	14:0	14:1	16:0	16:1	FAs (µM)
CvB2MT17	2.0	1.7	26.2	6.5	1.5	17.6	13.5	8.6	15.8	5.0	1.6	114±2
CvB2MT6	4.6	3.1	38.2	5.8	0.2	21.7	9.1	3.4	13.9	0.0	0.0	31±1
CvB2MT34	6.1	3.9	31.8	9.6	6.3	9.2	18.4	2.8	11.2	0.3	0.4	464±6
CvB2MT33	5.8	2.5	27.2	7.9	5.3	9.6	20.4	5.1	12.5	0.0	3.6	570±4
CvB2MT25	4.5	3.6	28.8	9.3	3.4	13.0	15.9	5.2	13.7	2.0	0.6	285±6
CvB2MT47	0.6	0.9	18.5	12.0	4.2	17.9	17.5	1.4	4.5	22.6	0.0	192±14
CvB2MT45	1.9	2.0	22.5	15.8	6.2	13.1	24.4	2.6	11.4	0.0	0.0	574±37
CvB2MT44	0.7	3.5	22.7	23.6	11.3	7.9	24.2	1.8	4.0	0.0	0.2	713±34
CvB2MT42	1.8	7.1	27.0	15.0	12.1	6.9	18.9	2.6	6.1	1.5	1.1	823±11
CvB2MT20	1.5	5.6	26.2	16.9	13.6	6.6	19.1	2.4	6.2	0.3	1.4	691±14
CvB2MT30	3.5	9.5	29.2	17.2	11.7	6.1	15.7	1.5	4.7	0.4	0.6	1031±22
CvB2MT48	0.1	1.2	13.7	38.6	18.1	6.7	17.5	0.0	3.9	0.2	0.0	137±4
CvB2MT40	1.8	4.8	61.4	12.5	8.5	3.3	6.2	0.6	0.9	0.0	0.0	1068±57
CvFatB1	0.0	3.5	45.3	26.1	8.9	3.9	9.6	1.1	0.9	0.0	0.6	542±32
CvB2MT29	2.4	1.5	11.4	7.2	2.5	15.0	18.1	12.1	20.5	0.4	8.9	287±12
CvB2MT12	2.2	1.6	12.5	7.2	1.6	16.4	15.4	15.3	20.0	0.0	7.8	149±4
CvB2MT2	1.0	0.7	8.9	4.6	1.1	10.0	9.7	24.5	19.9	0.1	19.5	82±8
CvB2MT32	3.1	1.3	21.5	7.3	3.9	4.8	14.4	9.5	30.6	0.0	3.4	331±11
CvB2MT16	2.2	0.9	15.4	5.6	1.6	3.9	9.6	22.8	30.9	0.0	7.0	308±19
CvB2MT31	3.4	2.2	17.9	5.9	3.7	9.0	19.6	12.1	17.3	0.7	8.1	393±7
CvB2MT19	4.4	2.1	18.2	6.3	2.8	10.3	22.0	8.5	18.4	0.6	6.3	168±6
CvB2MT15	4.0	2.1	16.1	7.5	1.2	15.6	19.8	9.2	19.8	0.7	4.0	150±6
CvB2MT27	3.3	2.0	20.8	9.9	5.8	10.3	21.5	5.3	17.6	0.3	3.2	230±5
CvB2MT18	4.2	1.9	21.9	8.4	3.1	13.6	19.9	6.1	15.3	2.3	3.2	300±8
CvB2MT22	2.9	1.6	20.7	9.2	1.5	13.0	15.6	8.9	16.7	0.0	10.0	85±6
CvB2MT10	3.0	2.2	21.6	9.6	4.6	8.8	14.1	9.8	16.4	0.0	9.9	171±13
CvB2MT38	8.5	31.1	37.2	3.1	0.6	5.7	4.2	1.6	8.1	0.0	0.0	1009±36
CvB2MT35	10.5	23.6	43.1	2.5	0.6	3.6	4.1	3.0	8.8	0.0	0.1	124±4
CvB2MT41	15.1	23.9	36.2	3.8	18.9	1.4	0.7	0.0	0.0	0.0	0.0	93±7
CvB2MT26	6.3	17.2	31.7	1.2	0.0	4.8	0.0	17.9	3.9	11.3	5.7	41±3
CvB2MT36	22.1	35.2	40.3	0.0	0.0	0.0	0.0	2.4	0.0	0.0	0.0	46±2
CvB2MT1	19.4	46.0	34.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.4±0.8
CvB2MT37	8.9	40.1	40.2	3.4	0.3	2.8	1.0	1.1	2.0	0.0	0.2	333±12

Supplementary Table 3. FA composition and total free FA accumulation of *E. coli* strains expressing acyl-ACP TE mutants

CvB2MT43	0.4	0.7	4.1	1.2	0.5	1.5	1.4	47.0	0.7	11.5	31.0	174±11
CvB2MT9	0.1	0.1	1.5	0.3	0.1	0.3	0.4	52.6	0.6	10.4	33.7	411±51
CvB2MT14	0.0	0.4	3.4	0.8	0.0	1.6	0.8	52.2	0.7	14.1	26.0	108±1
CvB2MT11	0.1	0.4	4.3	1.5	0.2	3.8	4.0	45.5	4.9	11.9	23.5	120±8
CvB2MT13	1.0	0.8	12.7	2.1	0.7	0.9	1.5	50.7	0.5	3.1	26.0	183±6
CvFatB2	0.0	0.3	5.4	5.4	1.4	1.3	3.2	45.2	0.6	5.5	31.7	175±19
CvB2MT23	0.6	0.4	5.6	1.0	0.3	0.8	0.8	54.2	0.9	6.6	28.7	385±16
CvB2MT8	0.2	0.4	3.9	0.3	0.0	0.0	0.0	58.0	0.0	4.4	32.8	74±6
CvB2MT7	0.7	0.7	6.1	0.6	0.0	0.0	0.0	62.2	0.0	0.9	28.8	47±13
CvB2MT4	0.2	0.3	3.7	0.6	0.1	0.0	0.2	60.9	0.0	9.3	24.5	199±18
CvB2MT24	0.2	0.1	3.6	0.4	0.1	0.0	0.3	73.6	0.2	1.4	20.0	401±49
CvB2MT5	0.0	0.1	1.5	0.2	0.0	0.0	0.0	81.5	0.0	2.9	13.9	457±33
CvB2MT28	1.7	1.4	17.6	5.0	1.2	7.5	3.7	40.1	4.1	3.4	14.3	328±21
CvB2MT21	1.9	1.1	17.8	3.4	0.6	4.6	2.7	43.8	4.5	2.0	17.5	201±7
CvB2MT3	2.6	1.9	17.2	4.1	1.5	2.1	4.6	40.1	4.3	0.0	21.6	90±6

Green-shading identifies the major fatty acids produced by each strain expressing the mutant acyl-ACP TE enzyme.

Supplementary Reference

 Jing, F. et al. Phylogenetic and experimental characterization of an acyl-ACP thioesterase family reveals significant diversity in enzymatic specificity and activity. *Bmc Biochem* 12, 44 (2011).