

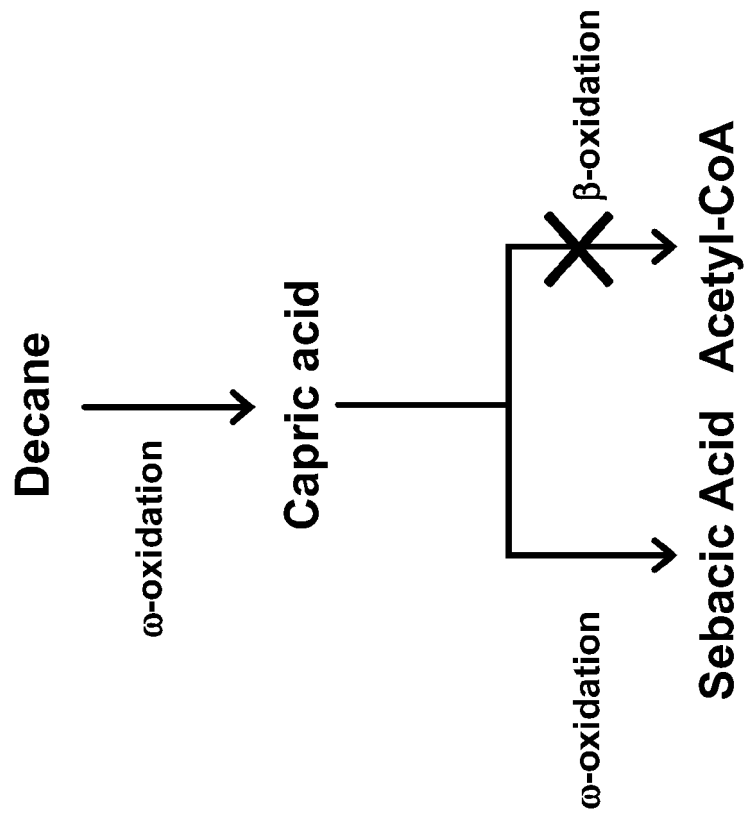


FIG. 1

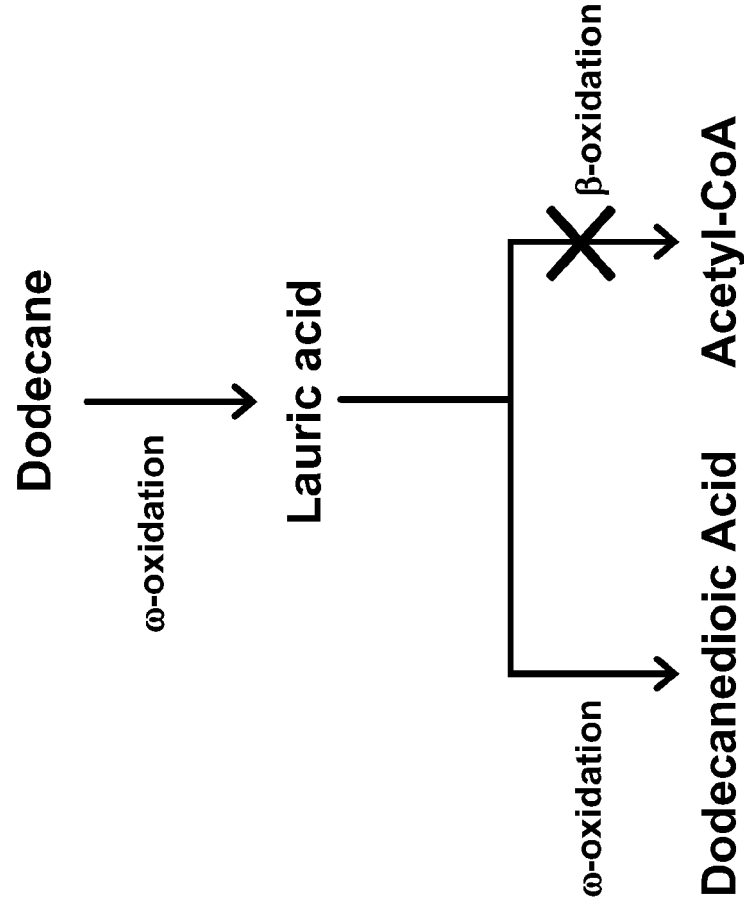


FIG. 2

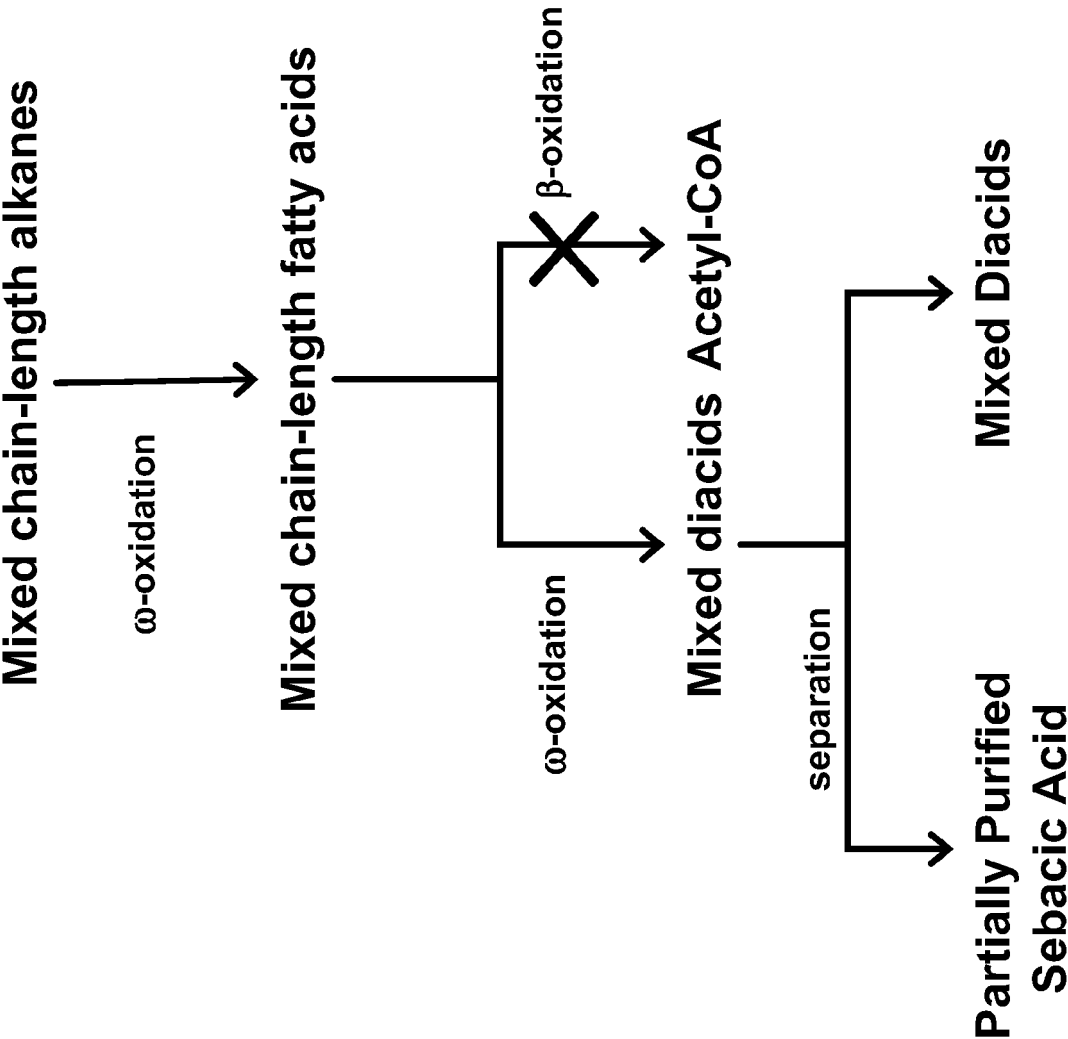


FIG. 3

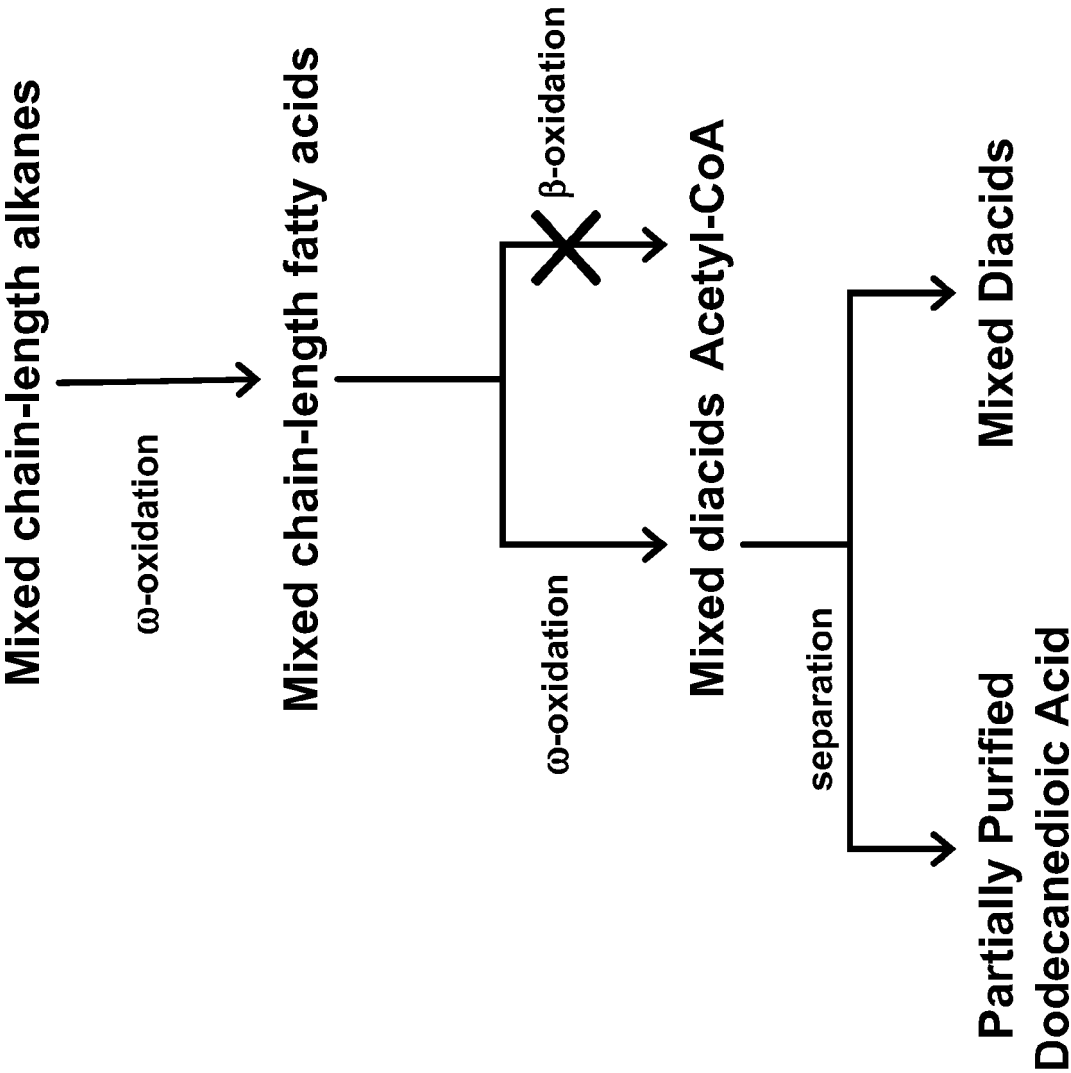


FIG. 4

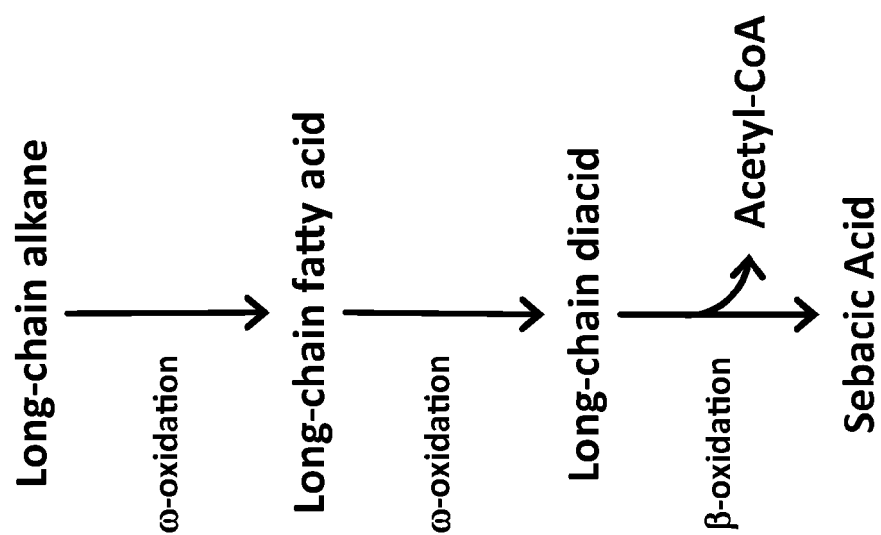


FIG. 5

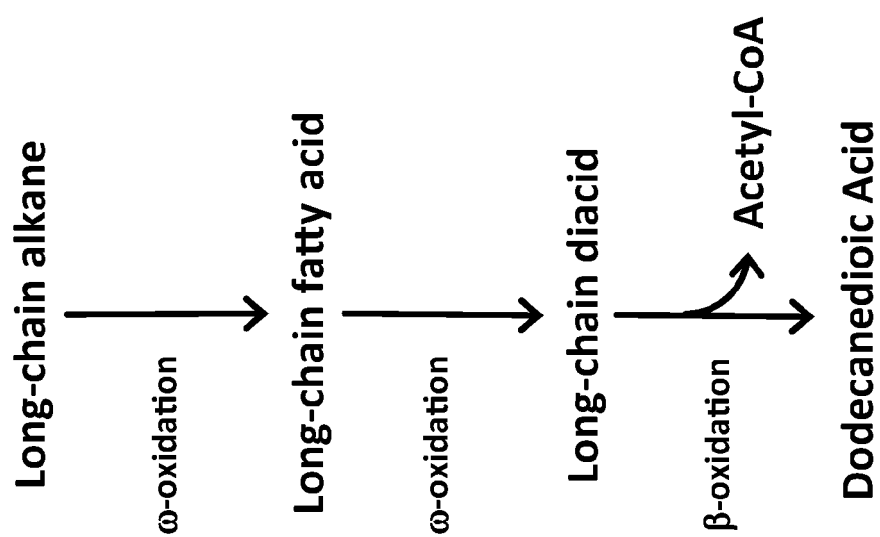


FIG. 6

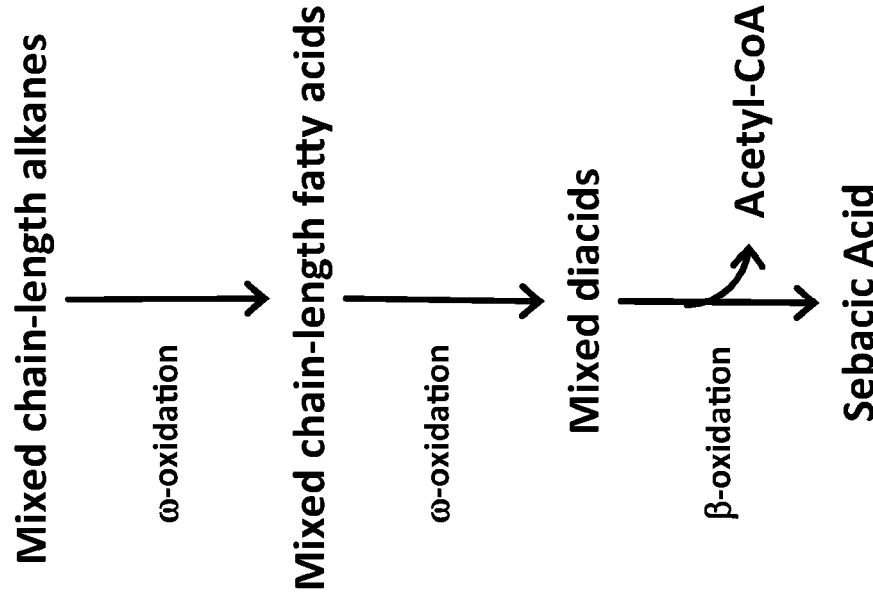


FIG. 7

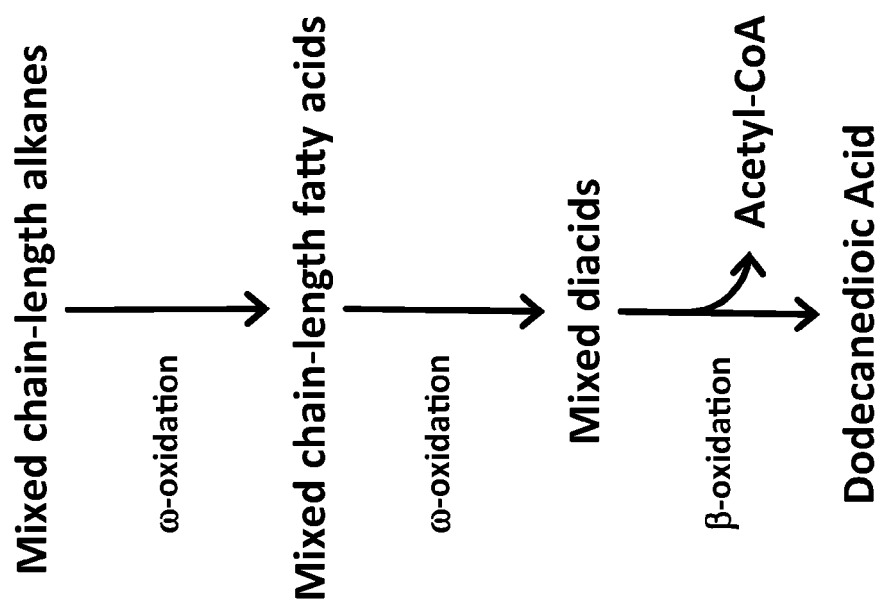


FIG. 8

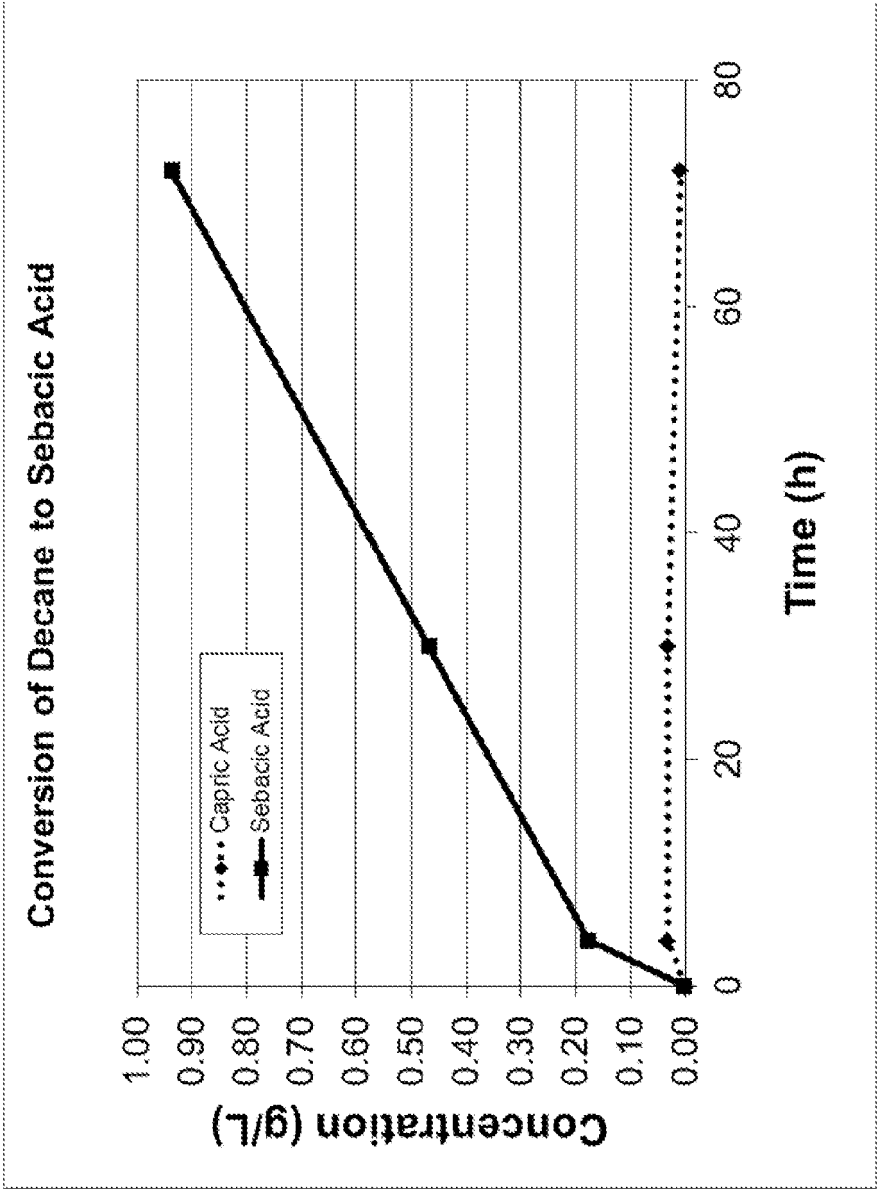


FIG. 9

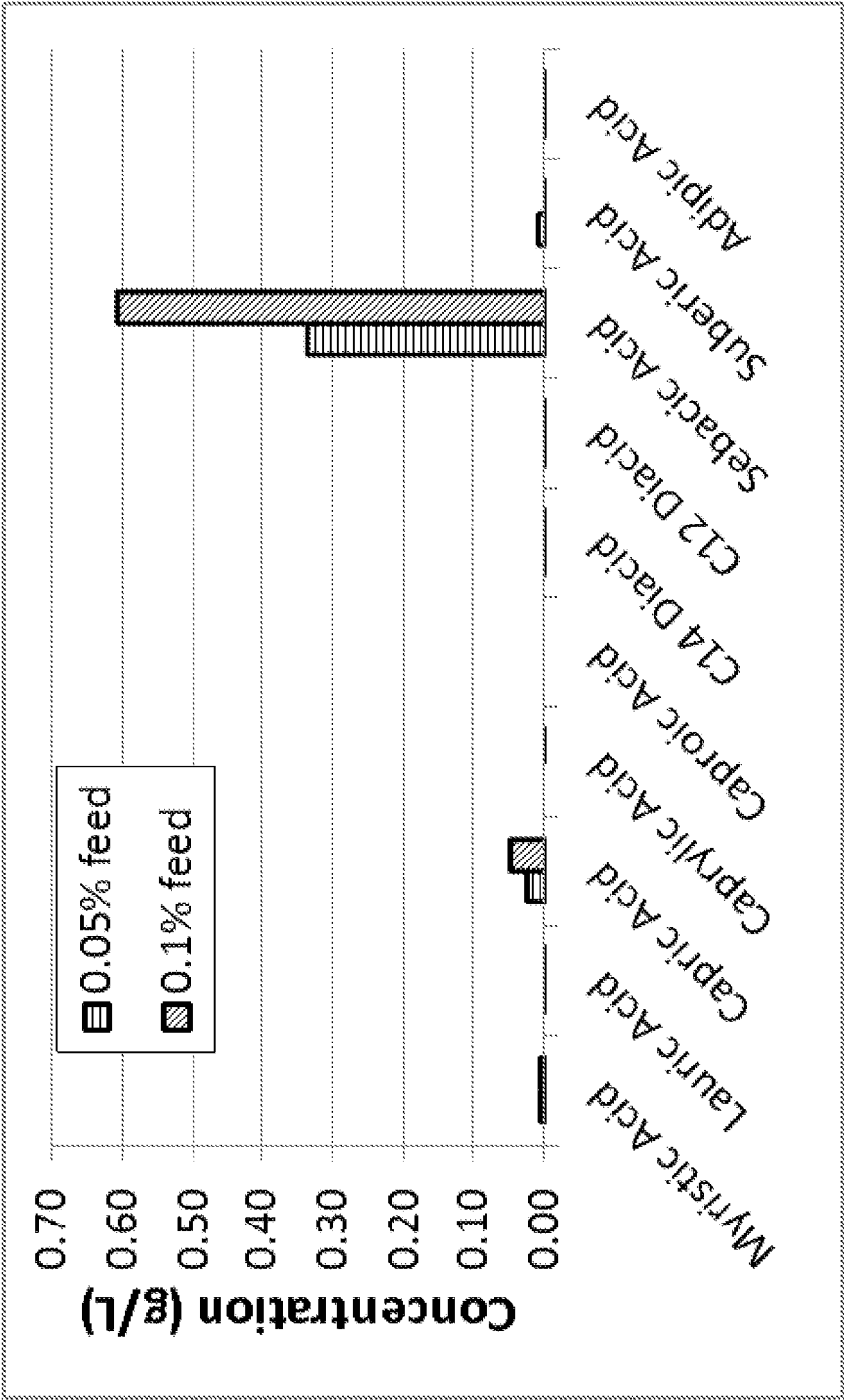


FIG. 10

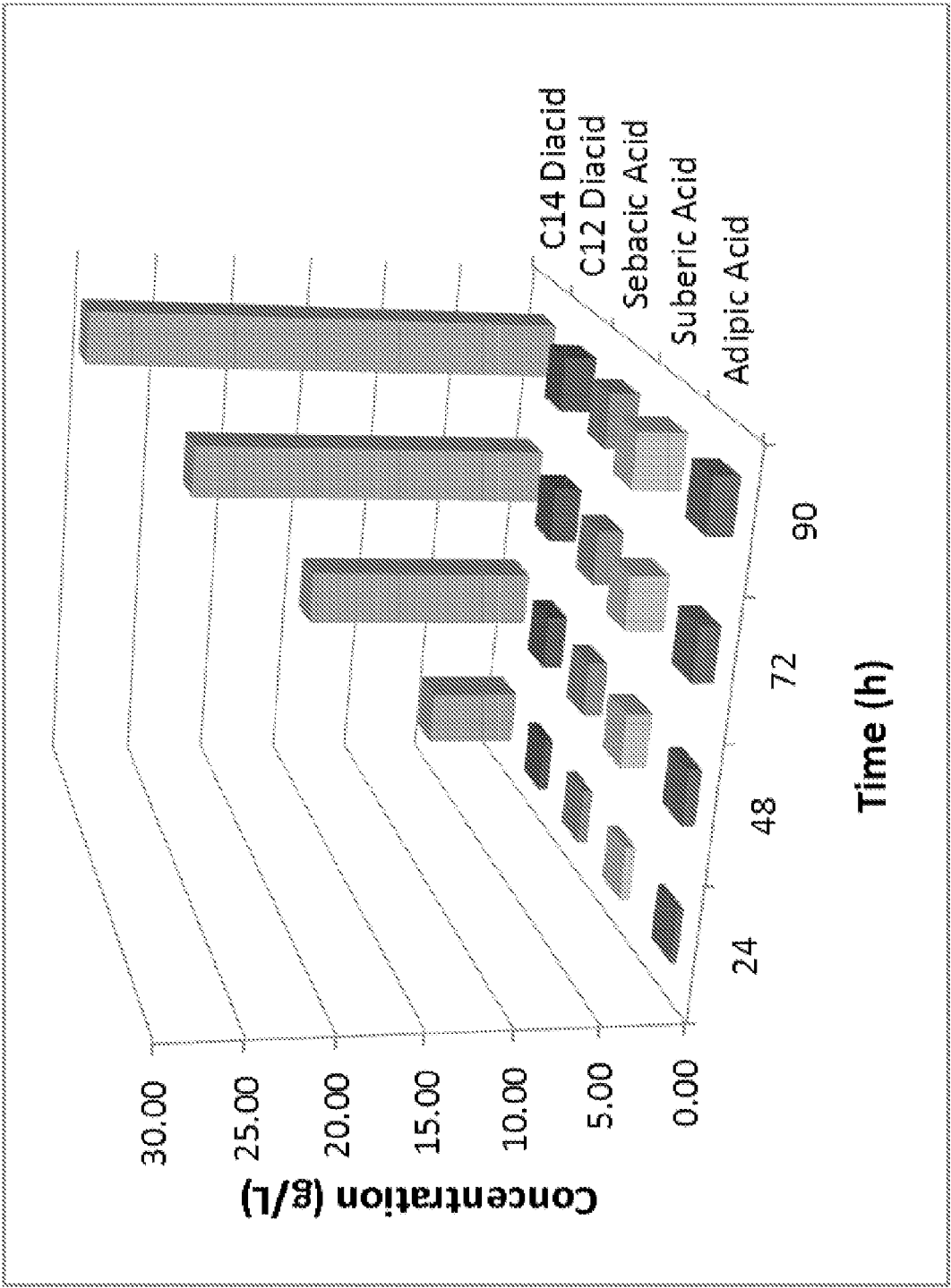


FIG. 11

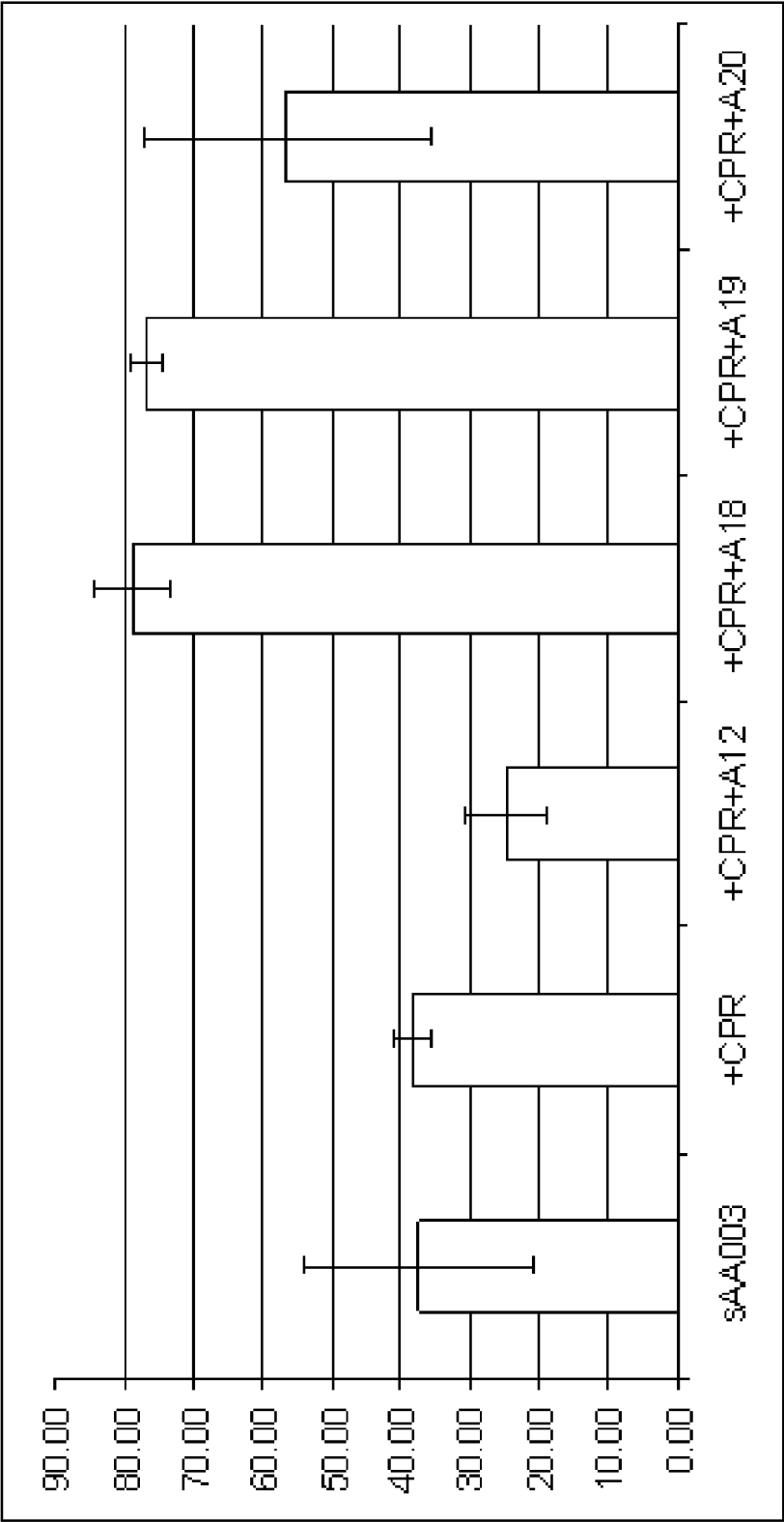


FIG. 12

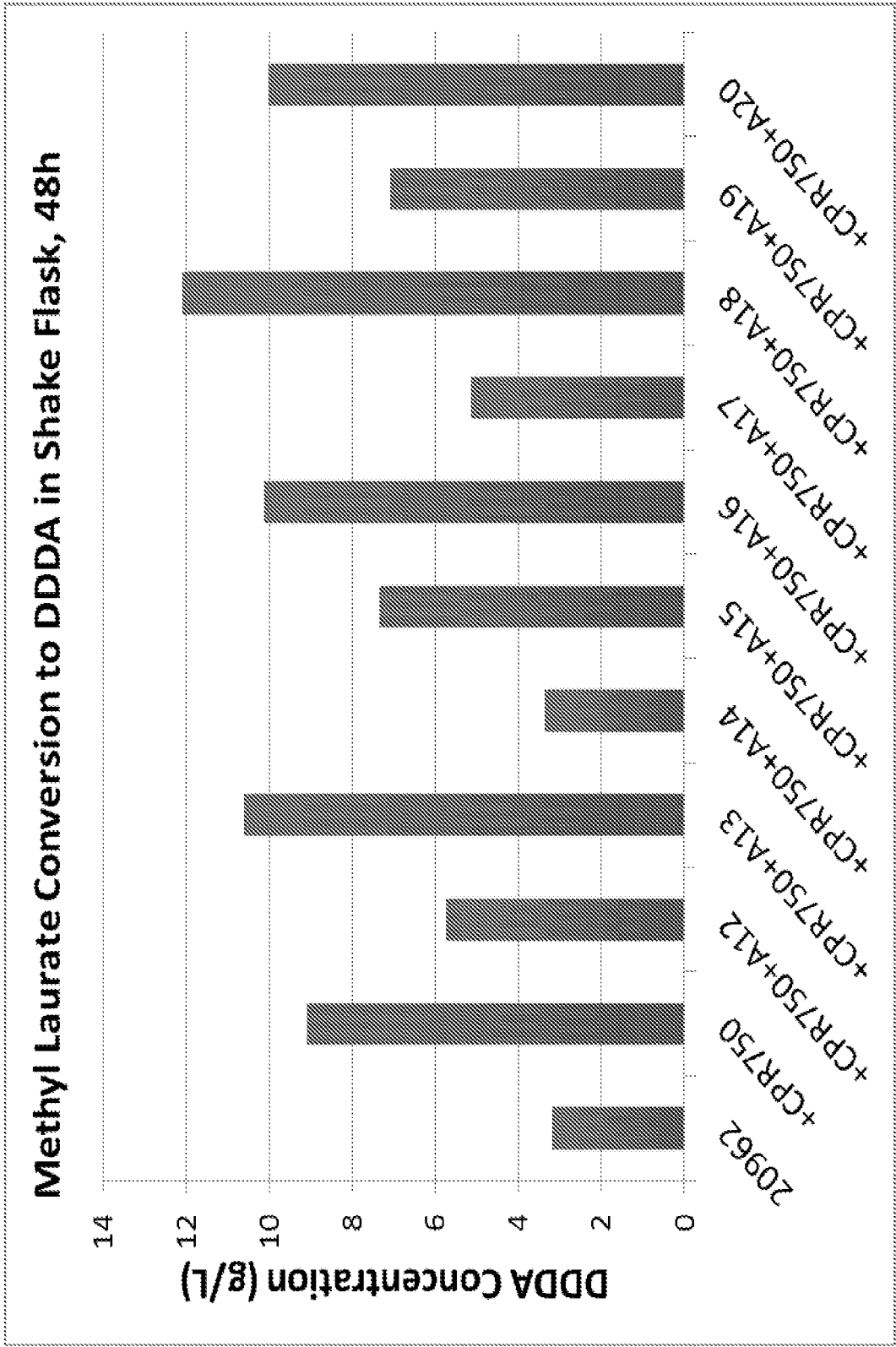


FIG. 13

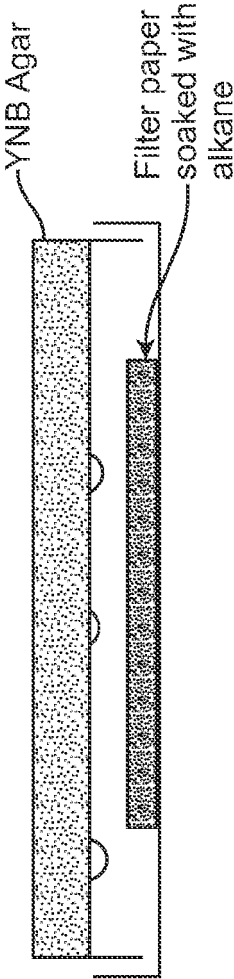


FIG. 14

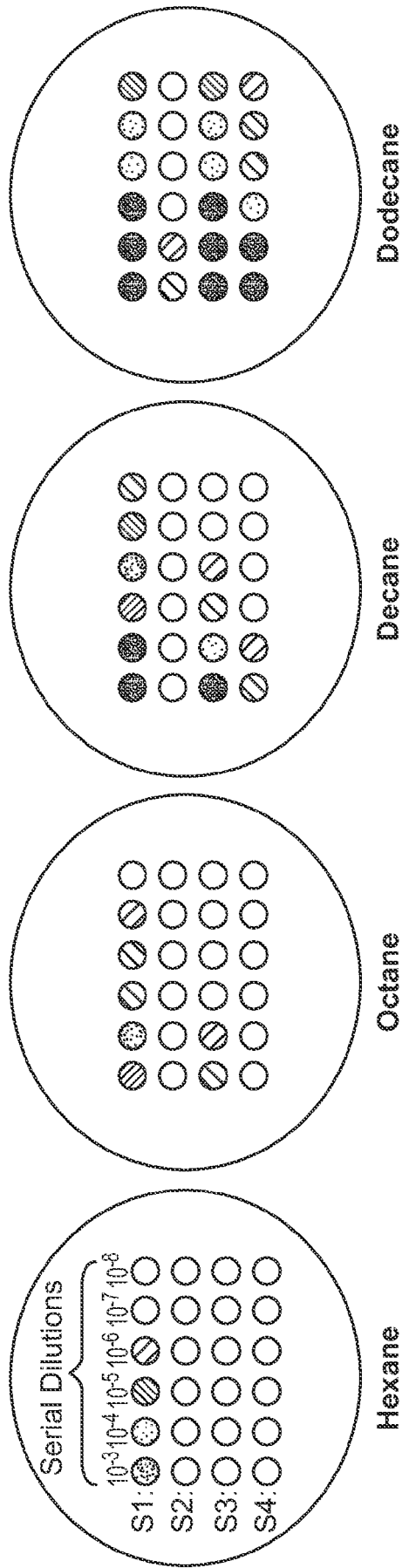


FIG. 15

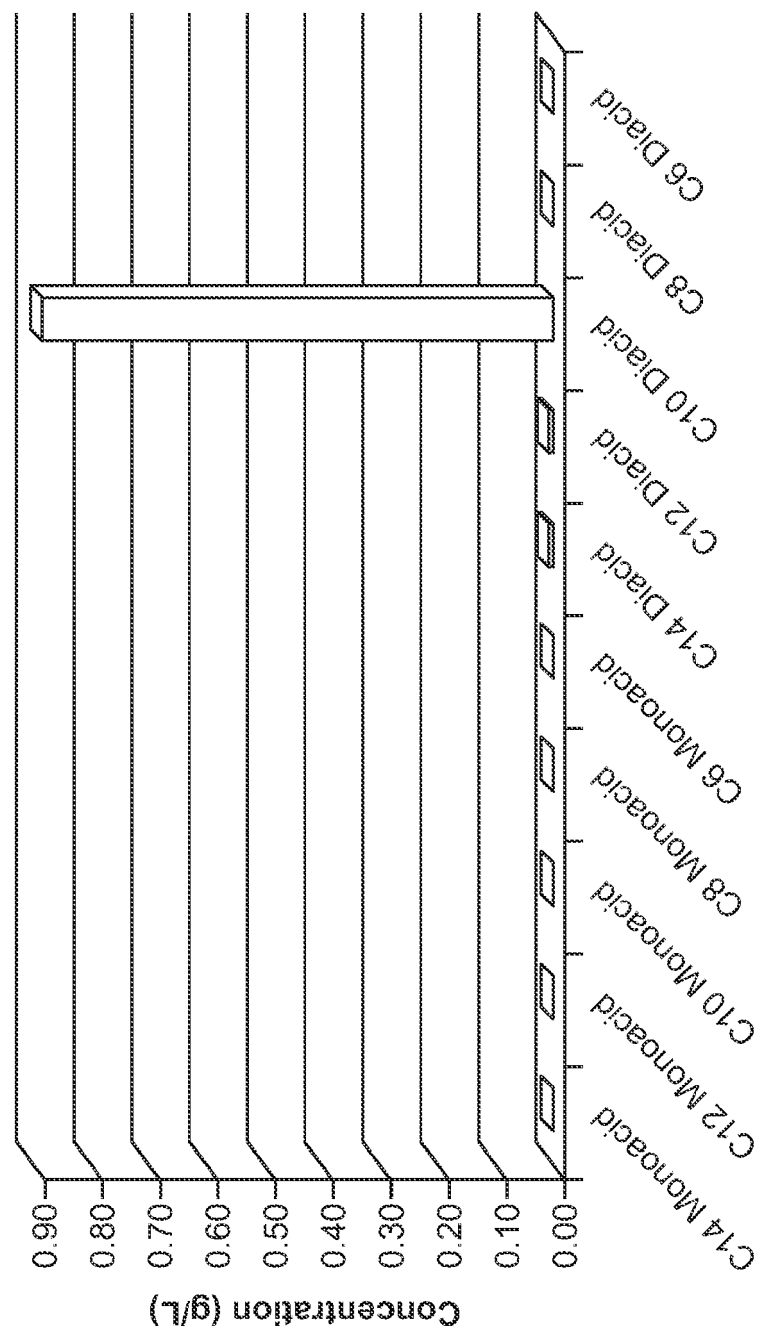


FIG. 16

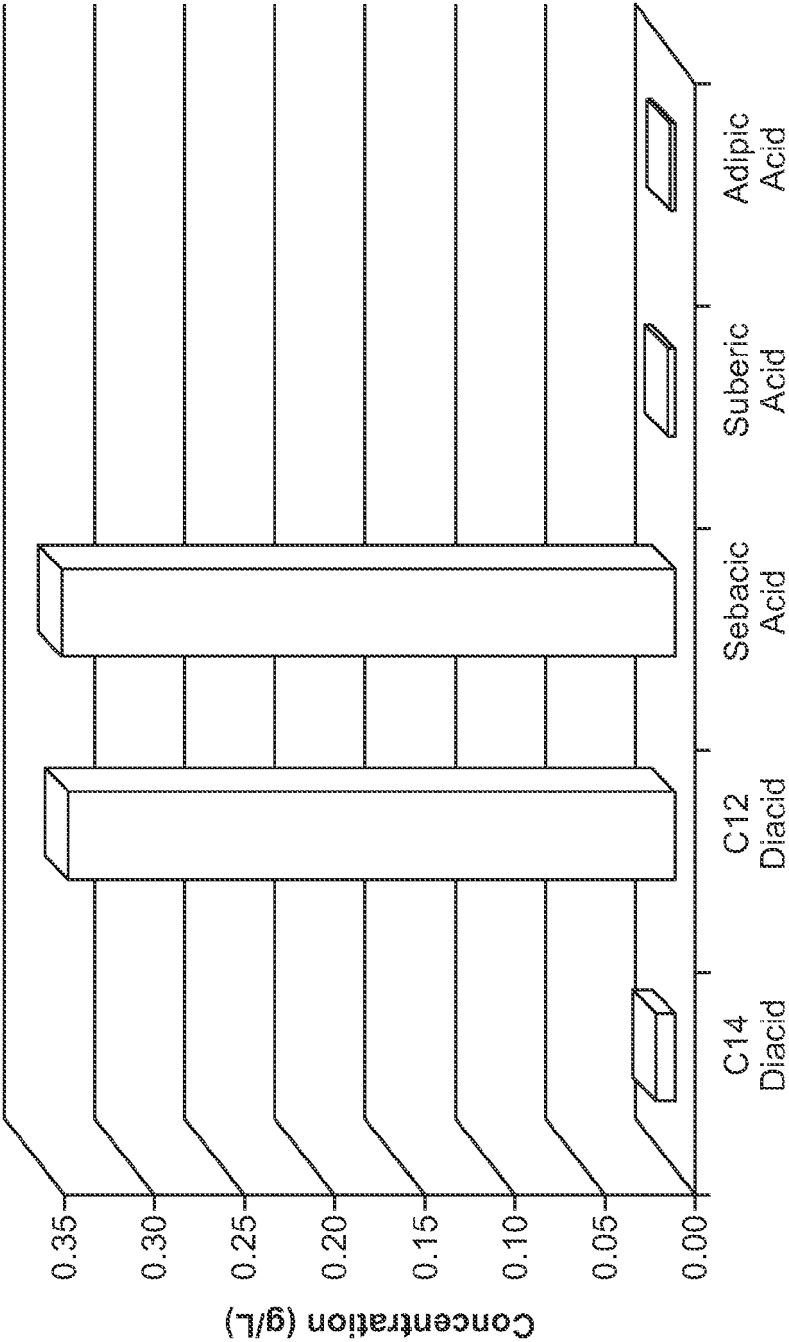


FIG. 17

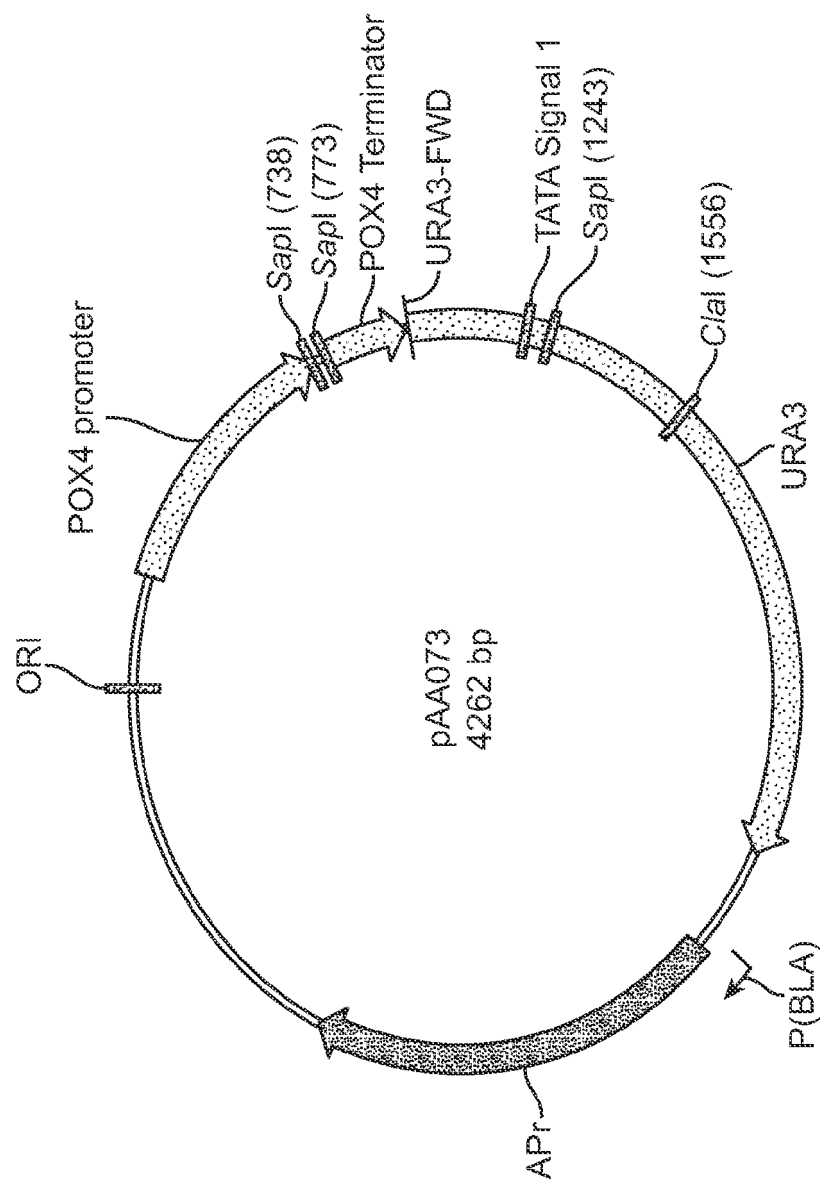


FIG. 18

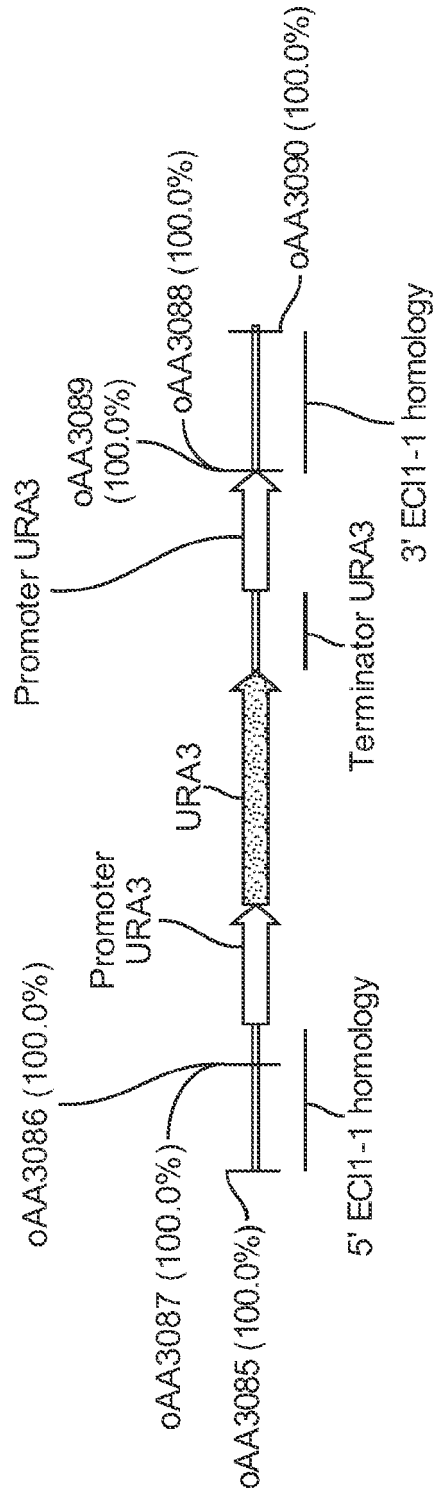


FIG. 19

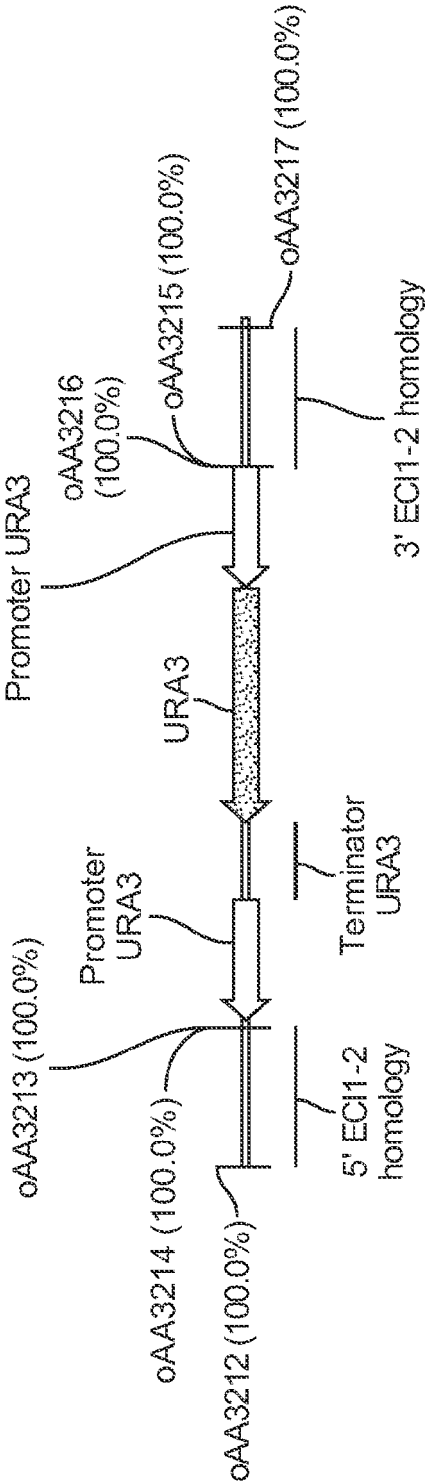


FIG. 20

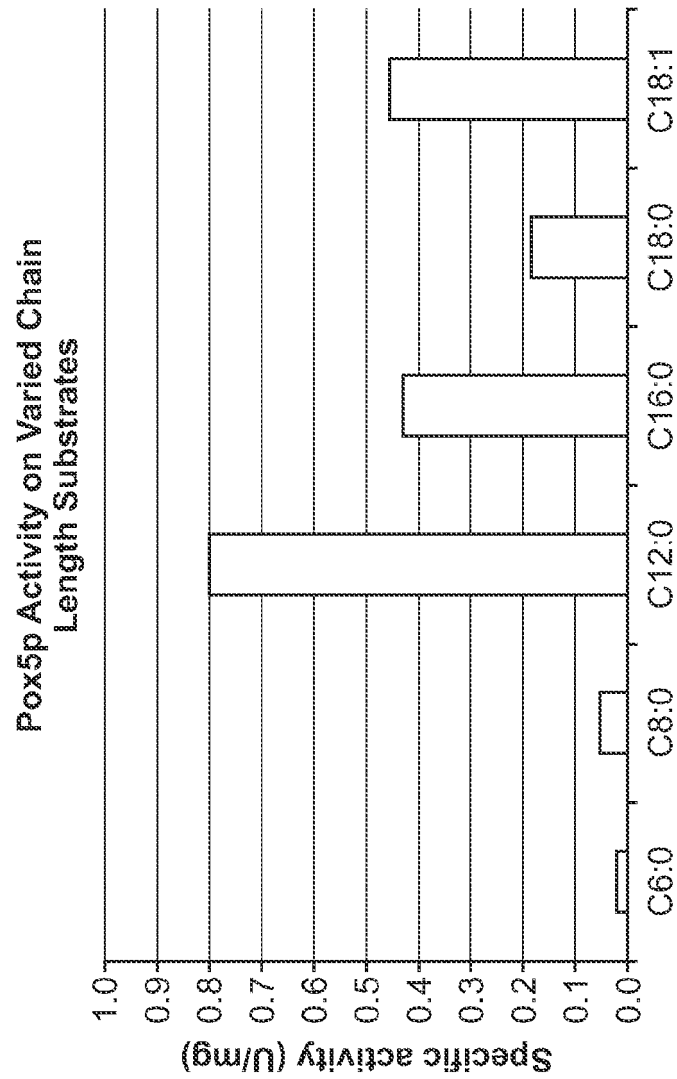


FIG. 21

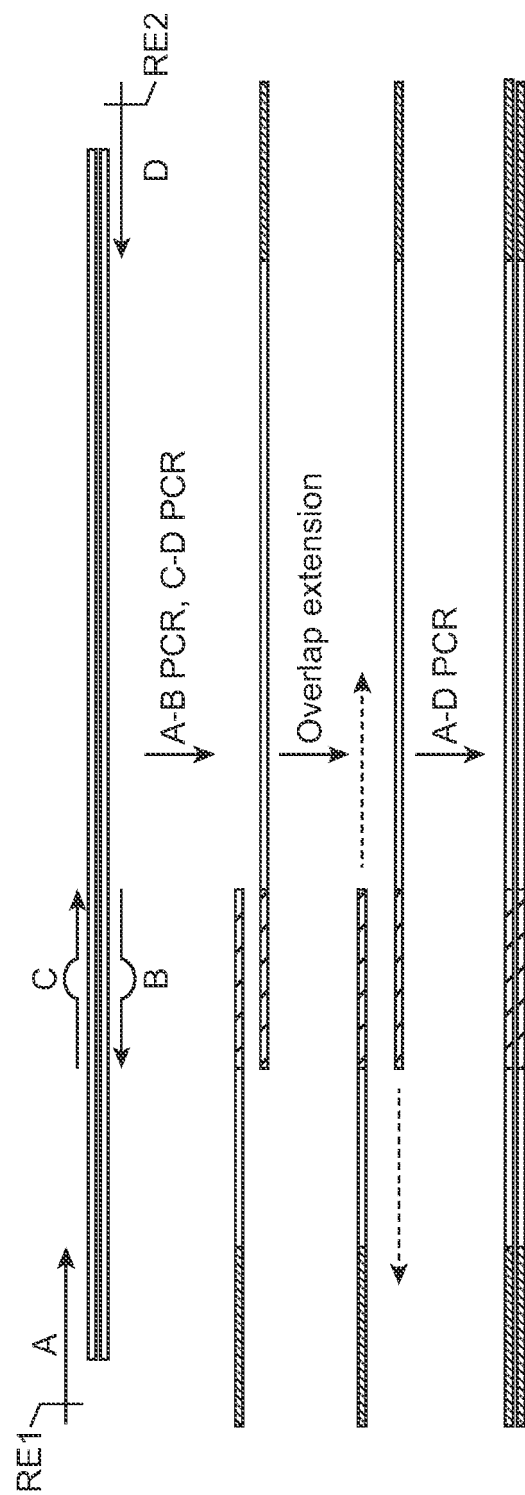


FIG. 22

AcoII	1	MNPDLRKERASATNP	PELITHILDGSPEN	TRRRREIENLI	NDPDEQHEDYNFL	TRSQRY	60
		MNPDLRKERASATNP	PELITHILDGSPEN	TRRRREIENLI	NDPDEQHEDYNFL	TRSQRY	
AcoI	1	MNPDLRKERASATNP	PELITHILDGSPEN	TRRRREIENLI	NDPDEQHEDYNFL	TRSQRY	60
AcoII	61	EVAVKKSATMVKKMREY	GISDPEEIMMEKNSVH	RGHPEPI	DLHLGMFLPTLLHQ	ATAEQQ	120
		EVAVKKSATMVKKMREY	GISDPEEIMMEK	EP+ L+ MF+PTLL+Q	T	QQ	
AcoI	61	EVAVKKSATMVKKMREY	GISDPEEIMMEK	LYIANFVEPVGLNYS	MFIP	TLNQGT	120
		EVAVKKSATMVKKMREY	GISDPEEIMMEK	LYIANFVEPVGLNYS	MFIP	TLNQGT	
AcoII	121	PREMPAWNLEIT	GTVAQTEM	GHGTHLRGLETT	TATYD	PKTQEF	180
		E++ P+ L+I	GTVAQTEM	GHGTHLRGLETT	ATYD	PKTQEF	
AcoI	121	EKMWRPSQEL	QIIIGTVAQTEM	GHGTHLRGLETT	ATYD	PKTQEF	180
		EKMWRPSQEL	QIIIGTVAQTEM	GHGTHLRGLETT	ATYD	PKTQEF	

FIG. 23

Pox5p (Candida strain ATCC20336)

MPTQLQKEREELTKFNPKELNYFLEGSQERSEIISNNMVEQMQLKQKDDPILKKVVDASYYNLT KDQ
 QREVTAKKIAARLLSR^YFE^{HE}Y^PD^QQ^AQ^RL^SI^LGV^FD^PQ^VFF^TR^IGV^NL^IGLFVSCVRGNGT N
 SQFFYWTINKGIDK^LLRGIYGCFCGMTELAHGSNVQGIE^TTAT^FDE^DT^TDE^FV^INT^PHI^GAT
 K^NWIGGA^AHSAT^HC^SV^AR^LK^VK^GK^DT^IE^TKK^LI^DY^PPL^RDS^NHD^LE^PGV^TVG^DIG^AK^MGR^D
 GIDNGW^IQ^FSN^VR^IPR^FFM^LQ^KY^CK^VSR^LGE^VTM^PPP^SE^QL^SY^SA^LI^GGR^VT^MM^MD^SY^RM^E
 TS^RFI^TI^AL^RY^AI^HRR^QFK^KD^TI^ETK^LI^DY^PPL^RDS^NHD^LE^PGV^TVG^DIG^AK^MGR^D
 TM^NA^TND^KL^DE^AV^SAG^EKE^AI^DA^IV^ESK^KL^FV^ASG^CKL^ST^CT^WL^TA^EA^IDE^AR^QAC^GG
 HGYSSYNG^FG^KA^YSD^WV^QCT^WE^GDN^IL^AM^NV^AK^PM^VRD^LL^KEP^EQ^KGL^LVS^SVA^DL^D
 D^PA^KL^VK^AF^DH^AL^SGL^AR^DIG^AV^AE^DGG^FDI^TGP^SL^VVS^KL^NA^HR^RFL^ID^GFF^EKK^RIT^PE
 W^SEV^LR^IPL^GF^LY^AD^WI^LT^NFG^AT^FL^QY^GI^ITP^DV^SR^KIS^SEH^FPA^LCA^KV^RPN^VGL^TD
 GFNLTD^MM^TNA^AI^GRY^DGN^VY^EHY^FEE^TV^KA^NPP^ENT^KAP^YSK^AL^EDM^LN^RPP^DLE^VRR^E
 GEKSEEA^EE^ILS

FIG. 24A

Pox4p (Candida strain ATCC20336)

MTF^TKK^NV^SVS^QGP^DPR^SSI^QK^ERD^SSK^WNP^QQ^MNY^LEG^SVE^RSE^TM^KA^LA^QQ^MER^DP
 IL^EDD^GSY^YY^DLL^TKK^DQ^QREL^TAV^KIN^RIA^RY^RE^QES^ID^TFN^KR^LS^LIG^IFD^PQ^VGT^RIG^V
 NL^GLF^FSS^CIR^GNG^TTS^QL^NY^WAN^EKE^EAD^VK^GI^YGC^FGM^TEL^AH^GSN^VAG^LET^TAT^FDK
 ES^DEE^VIN^TPH^IGA^TKK^WIG^GAA^HSA^THC^SV^YAR^LI^VD^GQ^DY^GV^KTF^VVP^LRD^SN^HDL^M
 PG^VTV^GDI^GAK^MGR^DGI^DNG^WI^QFS^NVR^IPR^FFM^LQ^KFC^KV^SAE^GEV^TLP^PLE^QLS^YSA
 LL^GGR^VMM^VLD^SY^RM^LARM^STI^AL^RY^AI^GRR^QFK^GDN^VDP^KDP^NA^LE^TQL^ID^YPL^HQ^KR
 LFP^YLA^AY^VIS^AGA^LKK^VED^TI^HNT^LAE^LDA^VE^KND^TKA^IFK^SIDD^MKS^LLF^VDS^GSL^K
 ST^AT^WLG^AE^AI^DQC^RQ^ACG^GH^GY^SSS^YNG^FGG^KAY^ND^WV^VQ^CT^WEG^DNN^VL^AMS^VG^KPI^VK
 QV^ISI^EDA^GKT^VRG^STA^FLN^QL^KD^YT^GSN^SSK^VV^LNT^VAD^LDD^IKT^VIK^AIE^VAI^IRL^S
 QEA^ASI^VKK^ES^FFD^YV^GAE^LV^QLS^KL^AHH^YLL^TE^YIR^RID^TDD^QK^DL^VPY^LIT^LG^KLY^A
 AT^IVL^DRF^AGV^FLT^TFN^VAST^EA^IT^ALA^SV^QI^PKL^CAE^VRP^NV^VAY^TDS^FQ^QSS^DMT^VNS^A
 IGR^YD^GDI^YEN^YFD^LV^KL^NPP^SKT^KAP^YSD^ALE^AML^NRP^TLD^ERR^EFE^KSD^ETA^AIL^S

FIG. 24B

RnAcoli

MNPDLRKKSATFNP~~EE~~LLITHTL~~LD~~GGSP~~EE~~~~TT~~RRRREIENLLI~~LN~~DDPPD~~EE~~Q~~HH~~ED~~Y~~FFLT~~TR~~SQR
 YEVAVKKSATM~~V~~KK~~EE~~LAQ~~IT~~GT~~Y~~AQ~~TE~~MG~~HH~~GF~~IM~~W~~FF~~K~~NS~~V~~HR~~G~~HP~~E~~PL~~D~~LD~~HL~~LG~~MF~~LL~~P~~TT~~LE~~HH~~QA~~TA~~E
 QQERFFMPA~~W~~NI~~V~~PR~~EN~~ML~~LM~~K~~YA~~Q~~TE~~MG~~Y~~GV~~K~~PD~~GT~~Y~~V~~K~~PP~~~~SS~~N~~KL~~TY~~GT~~MP~~V~~VR~~S~~FL~~V~~GN~~AA~~Q~~SS~~LS~~SK~~
 GGLGKTSN~~HA~~I~~V~~PR~~EN~~ML~~LM~~K~~YA~~Q~~TE~~MG~~Y~~GV~~K~~PD~~GT~~Y~~V~~K~~PP~~~~SS~~N~~KL~~TY~~GT~~MP~~V~~VR~~S~~FL~~V~~GN~~AA~~Q~~SS~~LS~~SK~~
 NGY~~LA~~Q~~IT~~GT~~Y~~AQ~~TE~~MG~~Y~~GV~~K~~PD~~GT~~Y~~V~~K~~PP~~~~SS~~N~~KL~~TY~~GT~~MP~~V~~VR~~S~~FL~~V~~GN~~AA~~Q~~SS~~LS~~SK~~
 ACTIAIRYS~~AV~~RL~~SE~~LP~~MM~~L~~Q~~T~~AR~~FL~~VE~~IA~~AK~~N~~LC~~LL~~YS~~LV~~SH~~R~~KS~~KE~~V~~AV~~WN~~LL~~TS~~V~~DL~~V~~RA~~SE~~AH~~C
 INESIGQ~~GD~~LE~~GL~~TE~~AA~~Y~~KL~~R~~AA~~V~~Q~~AV~~LN~~LC~~LL~~YS~~LV~~SH~~R~~KS~~KE~~V~~AV~~WN~~LL~~TS~~V~~DL~~V~~RA~~SE~~A~~H~~C
 T~~MP~~AC~~TI~~NS~~LE~~GL~~TE~~AA~~Y~~KL~~R~~AA~~V~~Q~~AV~~LN~~LC~~LL~~YS~~LV~~SH~~R~~KS~~KE~~V~~AV~~WN~~LL~~TS~~V~~DL~~V~~RA~~SE~~AH~~C
 TMV~~V~~V~~V~~K~~V~~FS~~DK~~LP~~KK~~I~~Q~~D~~KA~~V~~Q~~AV~~LN~~LC~~LL~~YS~~LV~~SH~~R~~KS~~KE~~V~~AV~~WN~~LL~~TS~~V~~DL~~V~~RA~~SE~~A~~H~~C
 HYV~~V~~V~~V~~K~~V~~FS~~DK~~LP~~KK~~I~~Q~~D~~KA~~V~~Q~~AV~~LN~~LC~~LL~~YS~~LV~~SH~~R~~KS~~KE~~V~~AV~~WN~~LL~~TS~~V~~DL~~V~~RA~~SE~~A~~H~~C
 RILELL~~TL~~IR~~PN~~AV~~AL~~V~~DA~~FD~~FK~~D~~MT~~LL~~GS~~V~~LG~~R~~Y~~D~~GN~~V~~Y~~EN~~LF~~FE~~MA~~KK~~SP~~LN~~KT~~EV~~HE~~S
 YHKKHL~~PL~~Q~~SK~~L

FIG. 25

[illegible]

2025

376		TYLRINETSIGQGDLS	-----ELPEHALTAGKATTTTANAGNEECRMAGCGHGSSSSGIPNIVTF	450
RnAcoII	(351)	TYLRINETSIGQGDLS	-----ELPEHALTAGKATTTTANAGNEECRMAGCGHGSSSSGIPNIVTF	
CvPox5p	(355)	TMNATNDKLDKADVSA	-----ELPEHALTAGKATTTTANAGNEECRMAGCGHGSSSSGIPNIVTF	
CvPox4p	(375)	THNTELAELDAEVEKNDITKAEFKSTDDMKSTDEYDSCSLKSTATWLLGAEALDQCRCACCGHGYSSNGFGKAYNDW		
Consensus	(376)	TI TND LD AV A D AI AI ELK LFV SG LKST TWLAAEAIDECRQACCGHGYSSNGFGKAY DW		
		451		525
RnAcoII	(415)	TPACITTEGENTVMNLTQARFLMKIYDQVRSG-KLVGCMVSVLNDELPSQRIQPQQVANWPTMVDINSLECGLTEAYK		
CvPox5p	(430)	VVQCTWEGDNNILLAMNVAKPMVRDLKEPEQ-----KGLVLSNADLDDPAKLVKAFD		
CvPox4p	(450)	VVQCTWEGDNNVLAHSVCKPDIKQVLSIEDAGKTVRGSTAFELNQLKDYTCSSNSKVVINTVADLDDIKTVIKAE		
Consensus	(451)	VVQCTWEGDNNVLAHVAKPIVK LI I DA K V G AFLN L LVL TVADLDDI LIKAFD		
		526		600
RnAcoII	(489)	LRAARIVEIAAKNLTQTHVSHRKSKEVAVNLTSSVDVRASEAHCYIVVMKVFSDKLPKIQDKAVQAVALRNCLLIS		
CvPox5p	(483)	HAEISGPARDIGAAE-----DKGPDITGPSNVLVSKLNARRELIDCFEKKHTPPENSEVLRP-----DGFLLA		
CvPox4p	(525)	VATIRSQEAAASVUK-----KESPDYVGAENQLSKLKAARHHELTETREXDTFDQKDLVPEYHITSGKLMA		
Consensus	(526)	LAIARLA DAAAIL D AFDITG DLV LSKL ARHFLI F KRI K L P L LG LYA		
		601		675
RnAcoII	(564)	LYGTSQ-KGGDEL EGSITTCGAQLSQVN-ARILELTLTIRPNNAVAVDADFPAKDMTLCGVLGRNDGNVYKENLREWA		
CvPox5p	(545)	DMLLTNI-EGATPQYGLITPPDVSRKTSSEHFPALCAKVPPNVVGLTDDGNLLTDMMTNAAIGRYDGNVYSEHYFETV		
CvPox4p	(591)	ATLVLDRTAGVETENVAISTEALTAASVQLPKNCAEVPPNVVAVYTDSEQQSDMLVANSATGRYDGNVYEDLV		
Consensus	(601)	WIISN FGG FL F IIT D IS IAS IP LCA VRPNVVALTDAFM SDMLNSAIGRYDGNVYENYFE V		
		676		720
RnAcoII	(637)	KK-SRLNATREVEHESYHKKHLKPLOSKL-----		
CvPox5p	(619)	KALNRPENKAPYSMALEDMLNRPDDDEVBERGEKSEEAELLS-		
CvPox4p	(666)	RLQNPSPSKTKAPYSDALEAMLNRPDTDEBERFEKSPDTAAJLSK-		
Consensus	(676)	K NPP KTKAPYS ALE MLNRP LD RER EKSD E A ILS		

FIG. 26 (Cont.)

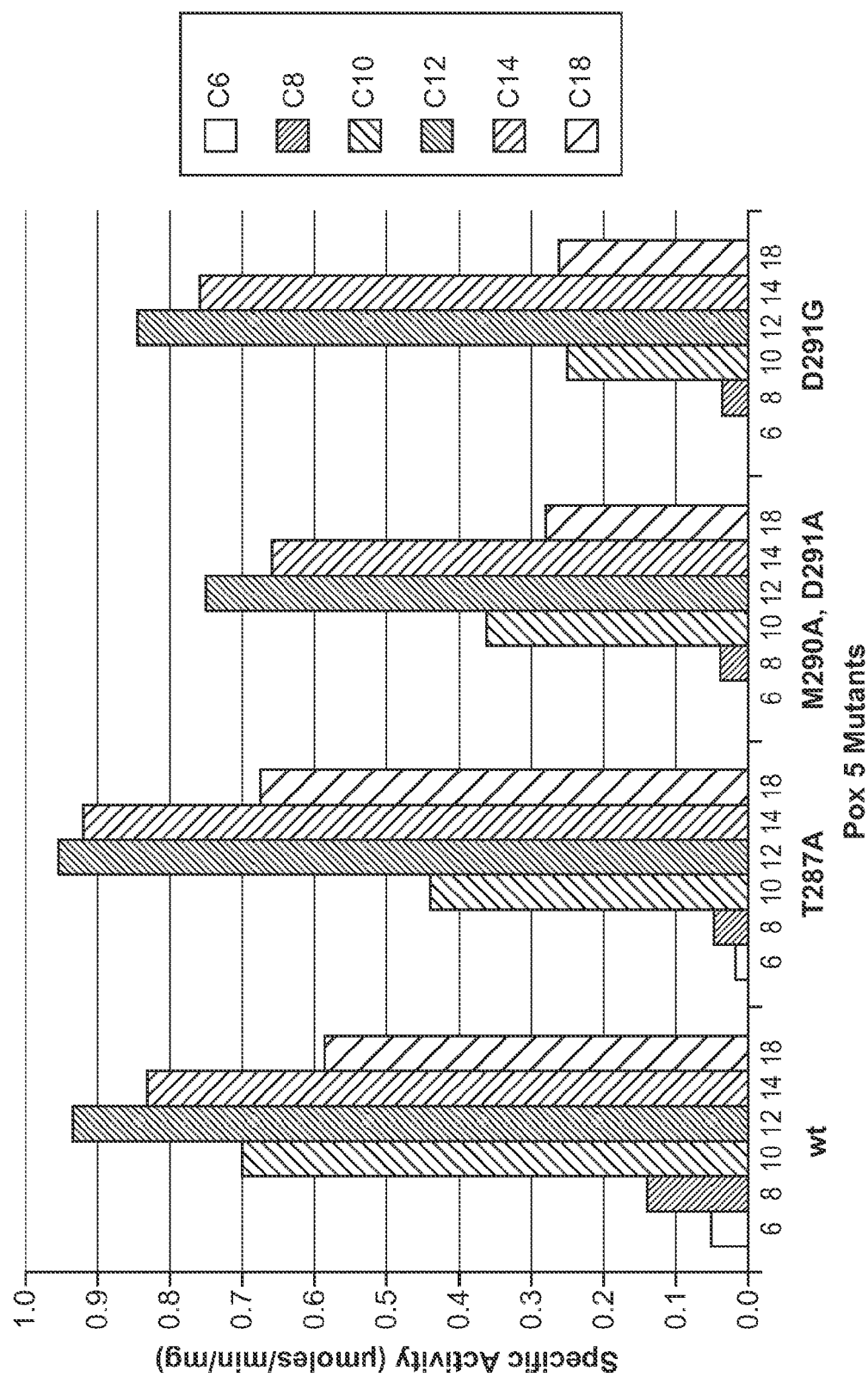


FIG. 27



FIG. 28

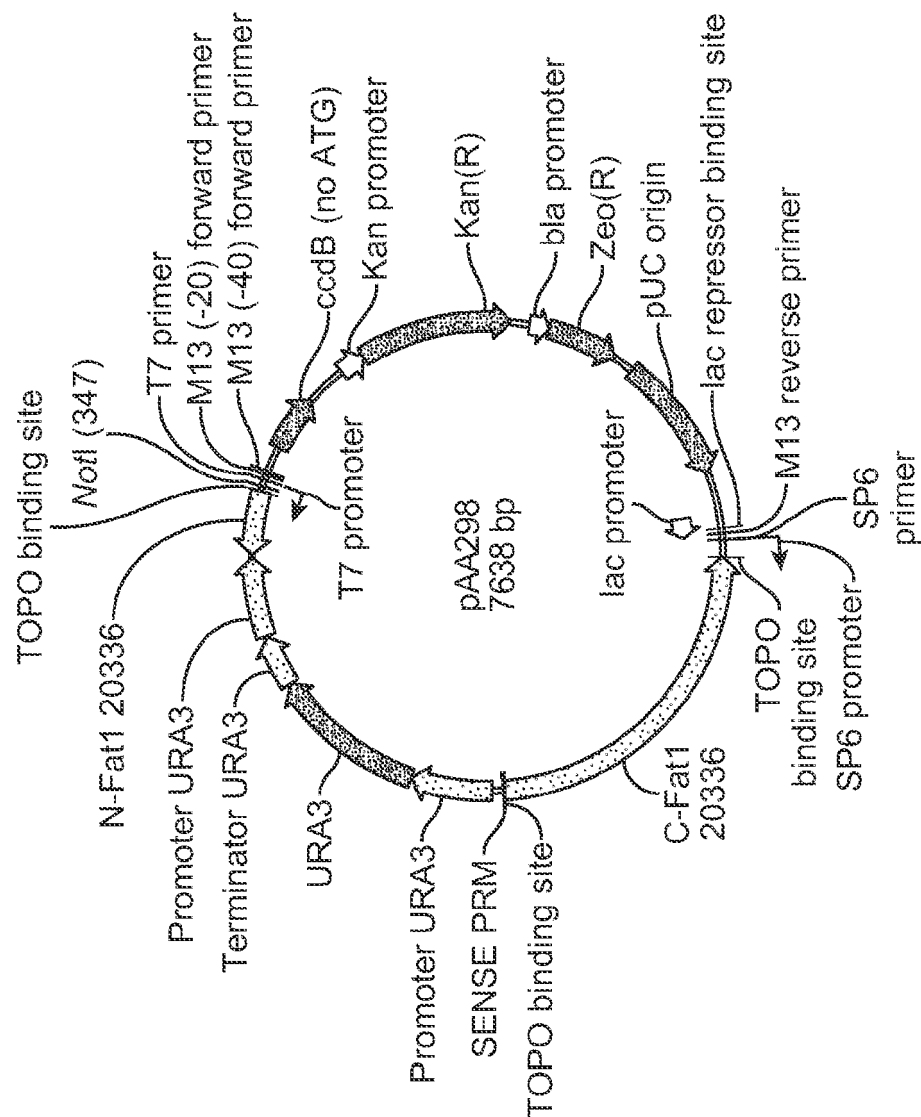


FIG. 29

FIG. 30A

		1		50
POX5	(1)	-----MPTELQKERELTKFNPKELNYPLEGSQE		
YlPox2	(1)	-MNPNTGTIEINGKEYNTFTTEPPVAMAQERAKTSFPVREMTYFLDGGEK		
YlPox3	(1)	MISPNLTANVEIDGKQYNTFTTEPPKALAGERAKVKFPIKDMTEFLHGGE		
YlPox5	(1)	--MNNNPTNVILGGKEYDTFTTEPPAQMELERAKTQFKVRDVTNFLTGSEQ		
POX4	(1)	-----MTFTKKNVSVSQGPDPRSSIQKERDSSKWNPPQQMNYFLEGSVE		
Consensus	(1)	N V I GK Y TFTEPP AL ERAKTKF VKDMTYFLEGSEE		
		51		100
POX5	(29)	RSEIISNMVEQMOKDPILKVDASYYNLTQDQOREVTAKKIARLSRYFEHE		
YlPox2	(50)	NTLKNEQIMEEIERDPLFNNDN-YYDLNKEQIRELTMERVAKLSLFVRDQ		
YlPox3	(51)	NVTMIERLMTELERDPVLNVSG-DYDMPKEQLRETAVARIAALS GHWKD		
YlPox5	(49)	ETLLTERIMREIERDPVLNVAG-DYDADLPTKRRQAVRIGALARYLPKD		
POX4	(44)	RSELMKALAQQMERDPILFTDGSYYDLTKDQORELTAVKINRIARYREQE		
Consensus	(51)	S LIE IM EIERDPILNV DG YYDL KDQ RELTV RIARLSRY D		
		101		150
POX5	(79)	YPDQQAQRLSILGVFDPQVFTRIGVNLGLFVSCVRGNGTNSQFFYWTINK		
YlPox2	(99)	PEDDIKKRFALIGIADMGTYTRLGVHYGLFFGAVRGTGTAEQFGHWIS-K		
YlPox3	(100)	TEKEALLRSQLHGIVDMGTRIRLGVHTGLFMGAIRSGTGKEQYDYWVR-K		
YlPox5	(98)	SEKEAILRQQLHGIVDMGTRIRI AVHYGLFMGAIRSGTGKEQYDYWA-K		
POX4	(94)	SIDTFNKRLSLIGIFDPQVGTRIGVNLGLFLSCIRGNGTTSQLNYWANEK		
Consensus	(101)	SEDE R SLIGI DMGT TRIGVH GLFMGAIRSGGT EQF YWV K		
		151		200
POX5	(129)	GIDKL RGIYGC FGMTELAHG S NVQGIETTATFDEDTDEFVINTPHIGATK		
YlPox2	(148)	GAGDLRK FYGCF SMTELGHGSNLAGLETTAIYDEETDEFIINTPHIAATK		
YlPox3	(149)	GAADVKG FYGCF AMTELGHGSNVAGLETTATYIQDTDEFIINTPNTGATK		
YlPox5	(147)	GAATLHK FYGCF AMTELGHGSNVAGLETTATLDKDTDEFIINTPNSGATK		
POX4	(144)	ETADVKG IYGC FGMTELAHG S NVAGLETTATFDKESDEFVINTPHIGATK		
Consensus	(151)	GAADLKG FYGCF AMTELGHGSNVAGLETTATFD DTDEFIINTPHIGATK		
		201		250
POX5	(179)	WWIGGAAHSATHCSVYARLKVKGKDYGVKTFV VPLRDSN-HDLEPGVTVG		
YlPox2	(198)	WWIGGAAHTATHTVVFARLIVKGKDYGVKTFV VQLRNINDHSLKVGISIG		
YlPox3	(199)	WWIGGAAHSATHTACFARLLVDGKDYGVKIFV VQLRDVSSHSLMPGIALG		
YlPox5	(197)	WWIGGAAHSATHTACLARLIVDGKDYGVKIFIVQLRDLN SHSLNLGIAIG		
POX4	(194)	WWIGGAAHSATHCSVYARLIVDGQDYGVKTFV VPLRDSN-HDLMPGVTVG		
Consensus	(201)	WWIGGAAHSATHTAVFARLIVDGKDYGVKTFV VQLRDIN HSLMPGITIG		
		251		300
POX5	(228)	DIGAKMGRDGIDNGW IQFSNVRI PRFFMLQKYCKVSRLGEVTMPPEQLS		
YlPox2	(248)	DIGKKMGRDGIDNGW IQFTNVRI PRQNLLMKYTKVOREGNVTQPPLAQLT		
YlPox3	(249)	DIGKKMGRDAIDNGW IQFTNVRI PRQNMLMKYAKVSSTGKVSQPPLAQLT		
YlPox5	(247)	DIGKKMGRDAIDNGW IQFTDVRIPRQNMLMRYDRVSRDGEVTTSELAQLT		
POX4	(243)	DIGAKMGRDGIDNGW IQFSNVRI PRFFMLQKFKVSAEGEVTLPPEQLS		
Consensus	(251)	DIGKKMGRDGIDNGW IQFTNVRI PRQNMLMKY KVSREGEVT PPLAQLT		
		301		350
POX5	(278)	YSALIGGRVTMMMDSYRMTSRFITIALRYA IHRRQFK-----KKD TD TIE		
YlPox2	(298)	YGSLITGRVSMASDSHQVGKRFITIALRYACIR RQFS-----TTPGQPE		
YlPox3	(299)	YGALIGGRVTMIADSFVVSQRFITIALRYACVRRQFG-----TTPGQPE		
YlPox5	(297)	YGALLSGRVTMIAESHLLSARFLTIALRYACIR RQFG-----AVPDKPE		
POX4	(293)	YSALLGGRVMMVLD SYRMLARMSTIALRYAIGRRQFKGDNVDPKDPNALE		
Consensus	(301)	YGALIGGRVTMIADSH MSARFITIALRYACIR RQF P PE		

FIG. 30B

		351	400
POX5	(323)	TKLIDYPLHQKRLFPFLAAAYLFSQGALYLEQTMNATNDKLDEAVSAGEK	
Y1Pox2	(342)	TKIIDYPYHQRRLLPLLAYVYALKMTADEVGALFSRTMLKMDDLKP-DDK	
Y1Pox3	(343)	TKIIDYPYHQRRLLPLLAFTYAMKMAADQSQIQYDQTTDLLQTIDP-KDK	
Y1Pox5	(341)	TKLIDYPYHQRRLLPLLAYTYAMKMGADQAQQYNSSFGALLKLNPKVDA	
POX4	(343)	TQLIDYPLHQKRLFPYLAAYVISAGALKVEDTIHNTLAELDAAVEKNDT	
Consensus	(351)	TKLIDYPYHQRRLLPLLAY YAMKMGAD V Y T LD L P DK	
		401	450
POX5	(373)	EAIDAAIVESKKLFVASGCLKSTCTWLTAEAIDEARQACGGHGYSSYNGF	
Y1Pox2	(391)	AGLNEVVSDVKELFSVSAGLKAFSTWACADVIDKTRQACGGHGYSGYNGF	
Y1Pox3	(392)	GALGKAIVDLKELFASSAGLKAFSTWTCANIIDQCRQACGGHGYSGYNGF	
Y1Pox5	(391)	EKFAVATADLKALFASSAGMKAFSTWAAAKIIDECRQACGGHGYSGYNGF	
POX4	(393)	KAIFKSIDDMKSLFVDSGSLKSTATWLGAEAIIDQCRQACGGHGYSSYNGF	
Consensus	(401)	AI AI DLK LFASSAGLKAFSTW AEIID CRQACGGHGYSGYNGF	
		451	500
POX5	(423)	GKAYSDWVVQCTWEGDNNILAMNVAKPMVRDLLKEPEQ-----	
Y1Pox2	(441)	GQAYADWVVQCTWEGDNNILTLISAGRALIQSAVALRKGE-PVGNVSYLK	
Y1Pox3	(442)	GQAYADWVVQCTWEGDNNVLC LSMGRGLIQSCLGHRKKG-PLGSSVGYLA	
Y1Pox5	(441)	GQAYADWVVQCTWEGDNNVLC LSMGRSLIQSCIAMRKKKGCHVKGSTAYLQ	
POX4	(443)	GKAYNDWVVQCTWEGDNNVLAMSVGKPIVKQVISIEDAGKTVRGSTAFLN	
Consensus	(451)	GQAYADWVVQCTWEGDNNVL LSMGR LIQS IAIRKG VG SV YL	
		501	550
POX5	(461)	-----KGLVLSSVADLD DPAKLVKAFDHALSGLARDIGAVAE---	
Y1Pox2	(490)	RY-----KDLANAKLNGRSLTDPKVLVEAWEVAAGNINRATDQYEKLI	
Y1Pox3	(491)	N-----KGLEQATLSGRDLKDPKVLIEAWEKVANGAIQRATDKFVELT	
Y1Pox5	(491)	RR-----DELQNAVRVDNKPLTDPAVLITAEWKVACEAINRATDSFIKLT	
POX4	(493)	QLKDYTGSSNSSKVVLNTVADLD DIKTVIKAIEVAIIRLSQEAAASIVK---	
Consensus	(501)	L NA LS RDL DPKVLI AWE AA LINRATD F L	
		551	600
POX5	(498)	---D---KGFDTITGPSLVLSKLNNAHRFLIDGFFKRITPEWSEVLRP---	
Y1Pox2	(534)	GEGLNADQAFEVLSSQQRFOAKVHTRRHLLIAAFFSRIDTEAGEAIKQPLL	
Y1Pox3	(534)	KGGLSPDQAFEELSQQRFQCAKIHTRKHLVTAFYERINASAKADV KPYLI	
Y1Pox5	(535)	QEGLSPDQAFEELSQQRFECARIHTRKHLITSFYARISK-AKARVKPHLT	
POX4	(540)	---K---ESFDYVGAELVQLSKLKAHHYLLTEYIRRIDTFDQKDLVPYLI	
Consensus	(551)	GL DQAFE LSQQRFO AKIHTRKHLITAFF RI A LKPYLI	
		601	650
POX5	(539)	-LGFLYADWILTN-FGATFLQYGIITPDVSRKISSEHFPALCAKVRPNVV	
Y1Pox2	(584)	NLALLFALWSIEE-DSGLFLREGFLEPKDIDTVT-ELVNKYCTTVREEVI	
Y1Pox3	(584)	NLANLFTLWSIEE-DSGLFLREGFLQPKDIDQVT-ELVNHYCKEVRDQVA	
Y1Pox5	(584)	VLANLFAVWSIEE-DSGLFLREGCFEPAEMDEIT-ALVDELCCCEAREQVI	
POX4	(584)	TLGKLYAATIVLDRFAGVFLTFNVASTEAITALASVQIPKLCAEVRPNVV	
Consensus	(601)	LA LFALWSIEE DSGLFLREG L P DID IT ELV LC EVRENV	
		651	700
POX5	(587)	GLTDGFNLDTMMTNAAIGRYDGNVYEHYFETVKALNPPENTKAPYSKALE	
Y1Pox2	(632)	GYTDAFNLSDFYFINAPIGCDYDAYRHYFQKVNEQNPARDPRPPYYASTL	
Y1Pox3	(632)	GYTDAFGLSDWFINAPIGNYDGDVYKHYFAKVNQQNPAQNPRPPYYESTL	
Y1Pox5	(632)	GFTDAFNLSDFFINAPIGRFDGDAYKHYMDEVKAANNPRNTHAPYYETKL	
POX4	(634)	AYTDSFQQSDMIVNSAIGRYDGDYENYFDLVKLQNPPSKTKAPYSDALE	
Consensus	(651)	GYTDAFNLSDFFINAPIGRYDGDVYKHYFD VK QNPP NTKAPYYEA L	
		701	727
POX5	(637)	DMLNRPDLEVRERCEKSEEAAEILSS-	
Y1Pox2	(682)	KPFLFREEEDDDICELDEE-----	
Y1Pox3	(682)	RPFLFREDEDDDDICELDEE-----	
Y1Pox5	(682)	RPFLFRPDEDEEICDLDE-----	
POX4	(684)	AMLNRPTLDERERFEKSDETAAILSK-	
Consensus	(701)	RPFLFREDEDDDEICELDEE	

FIG. 31

Sebacic (C10:2) from Linoleic acid

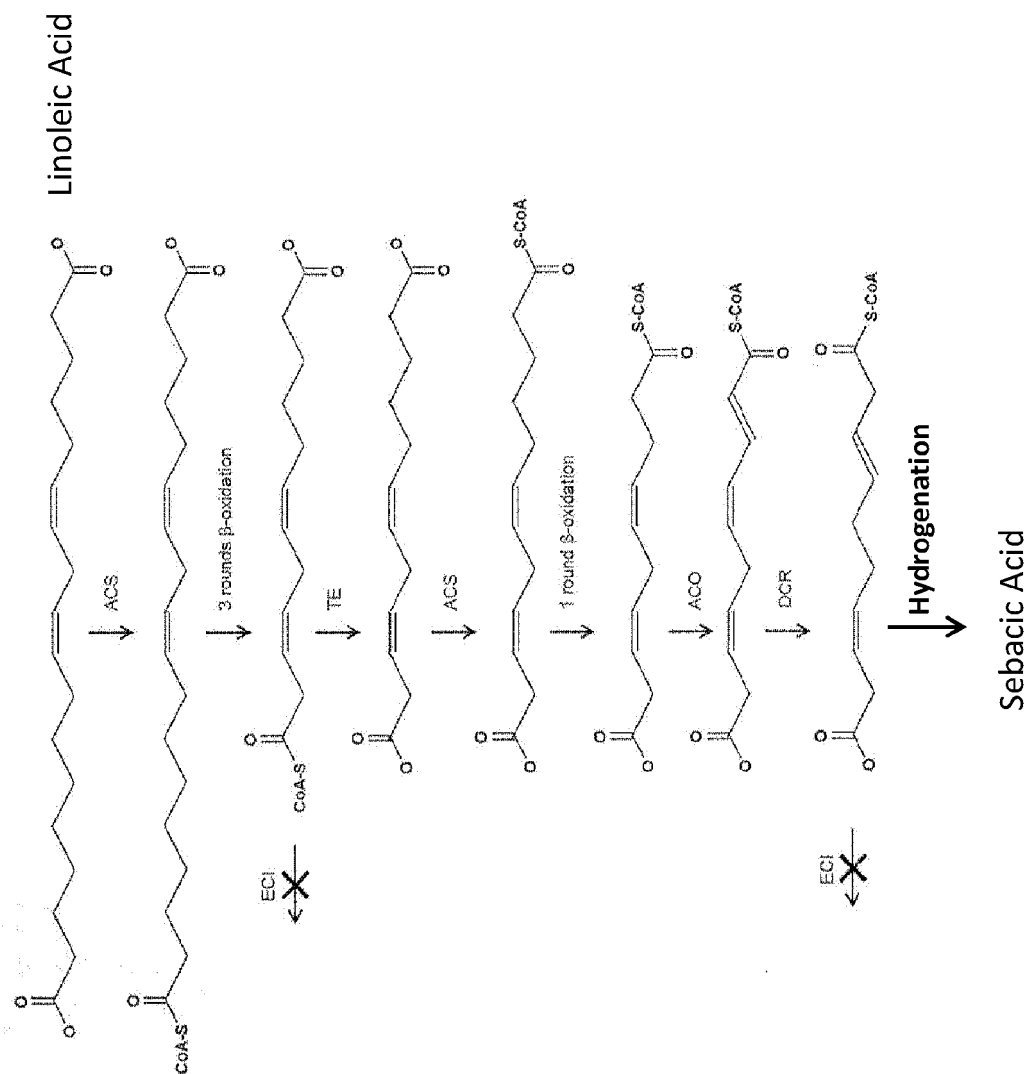


FIG. 32

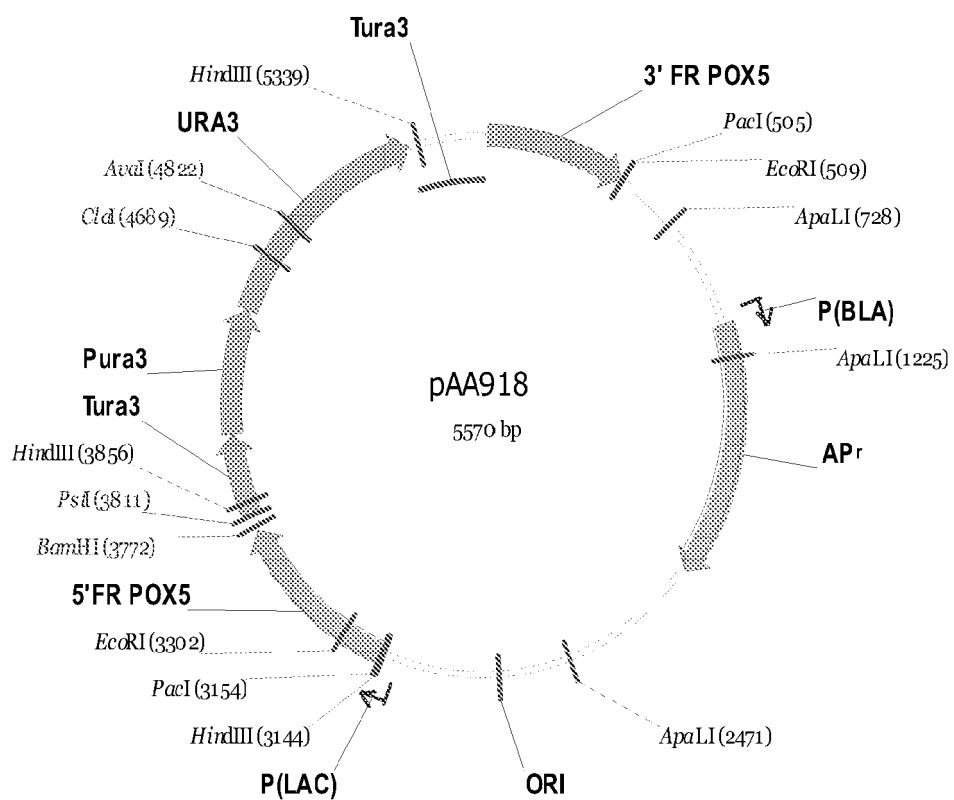


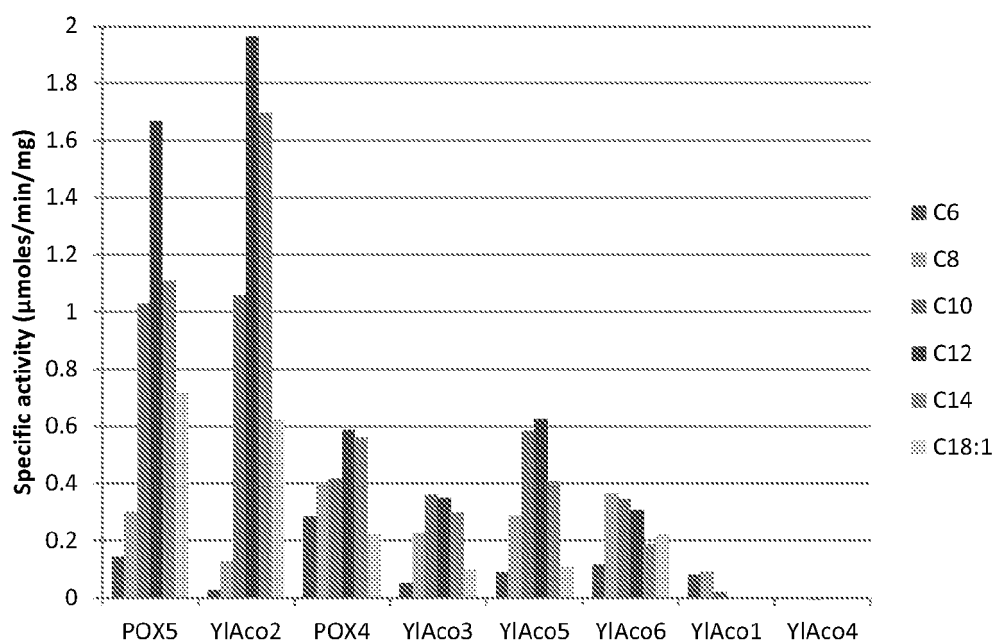
Fig. 33

FIG. 34

