

Supplementary Figure S1

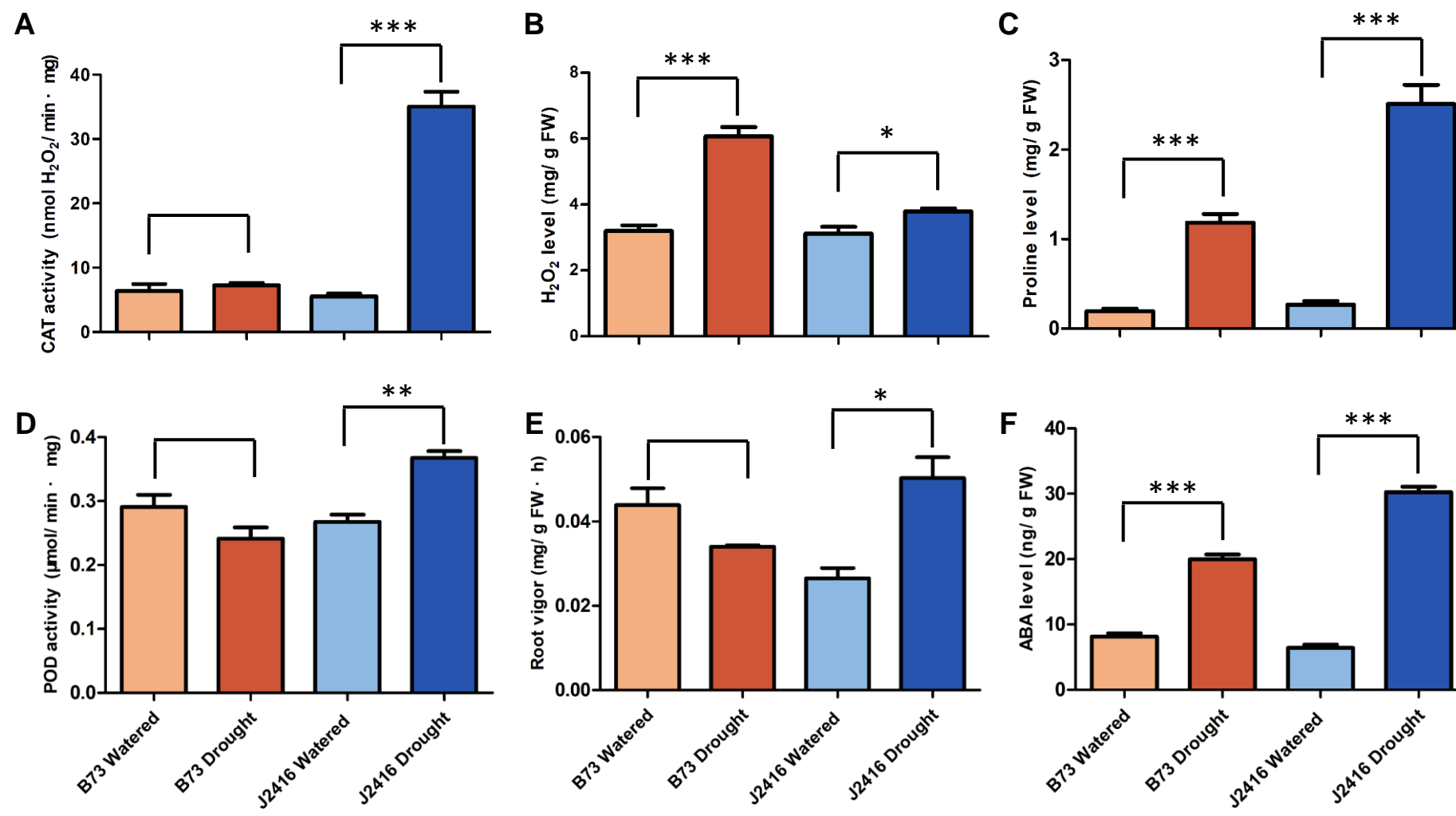


Figure S1. Physiological parameters determined before and after drought treatment in two maize lines.

Supplementary Figure S2

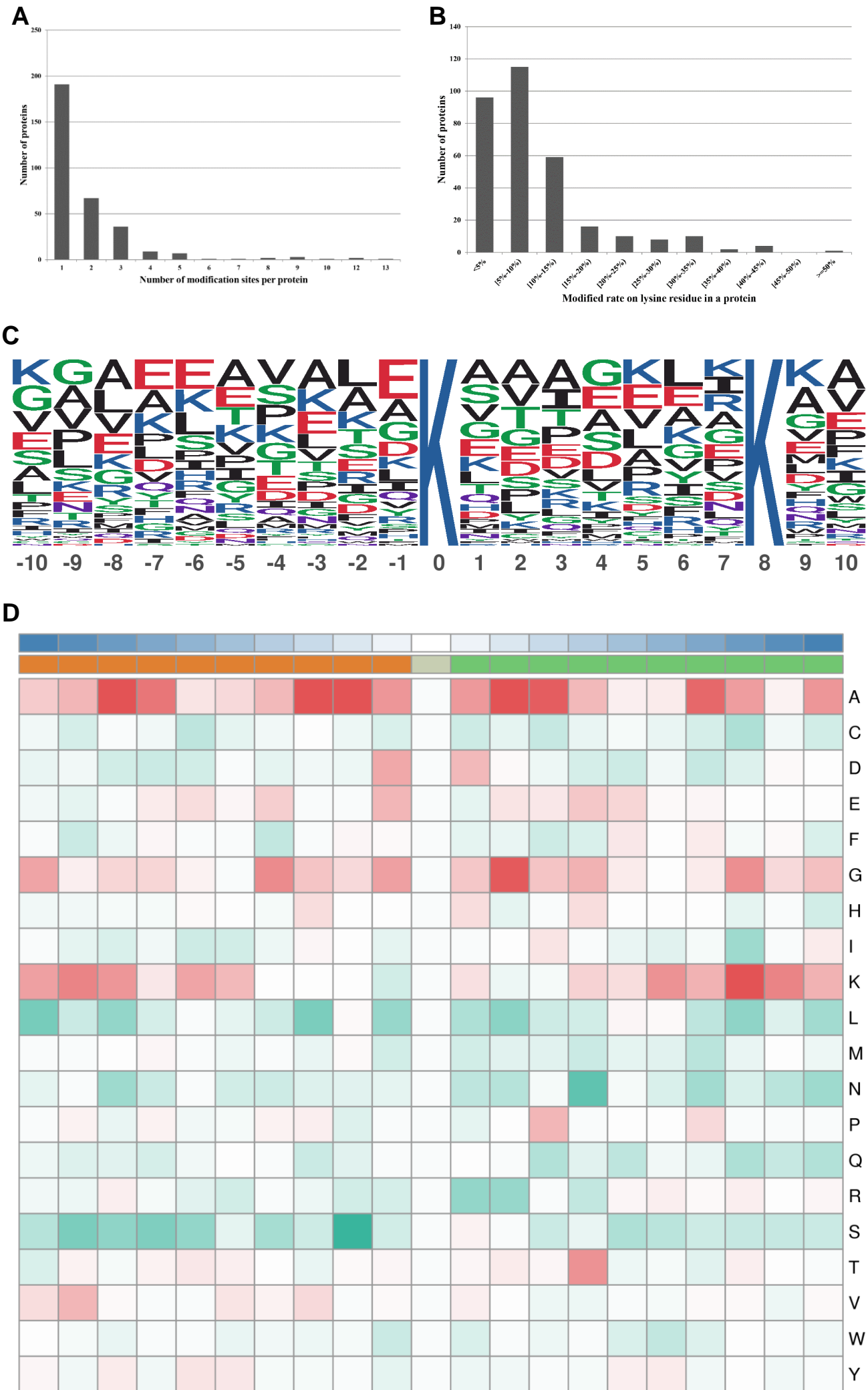


Figure S2. Characteristics of K_{la} modified proteins and sites in maize roots.

Supplementary Figure S3

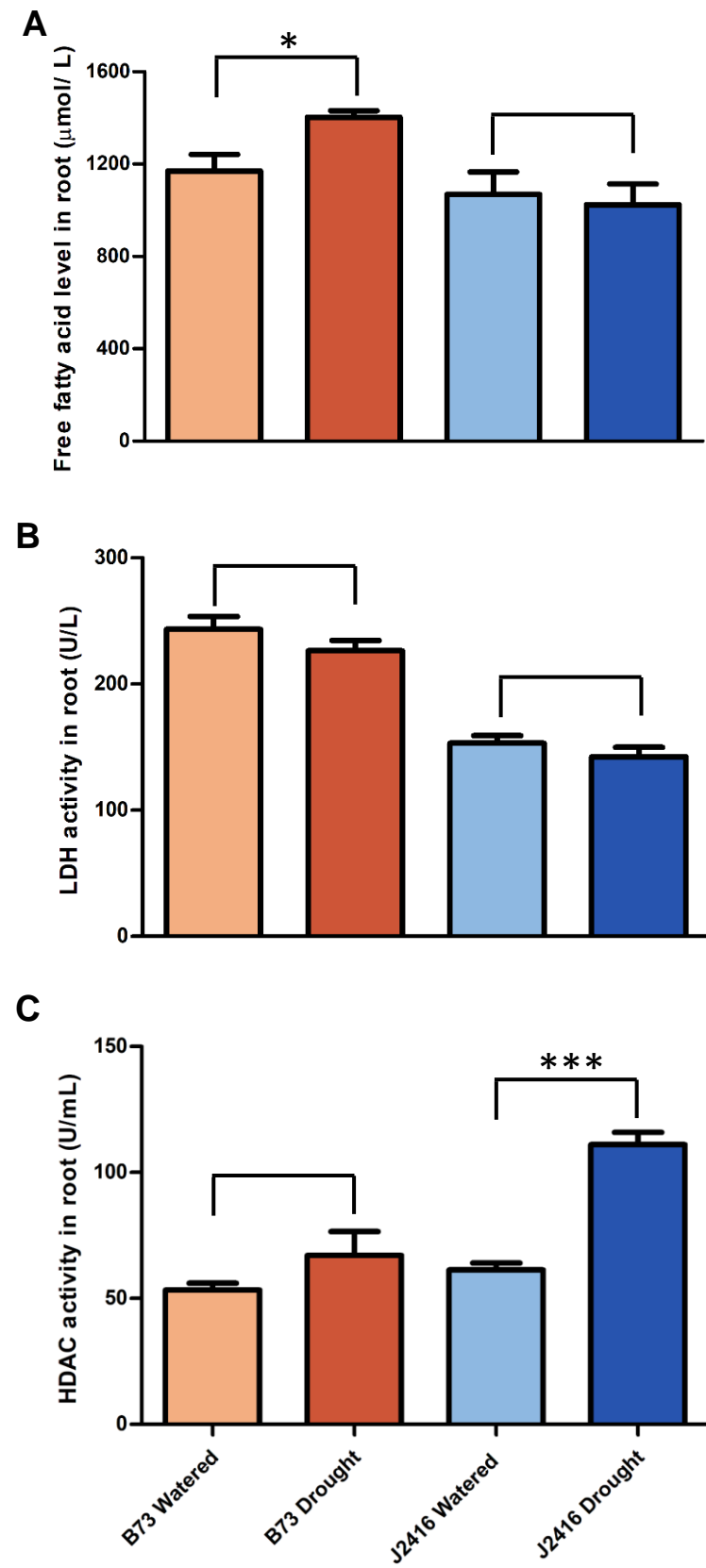


Figure S3. The level of fatty acids, LDH, and HDAC activity in maize roots during drought stress.

Supplementary Figure S4

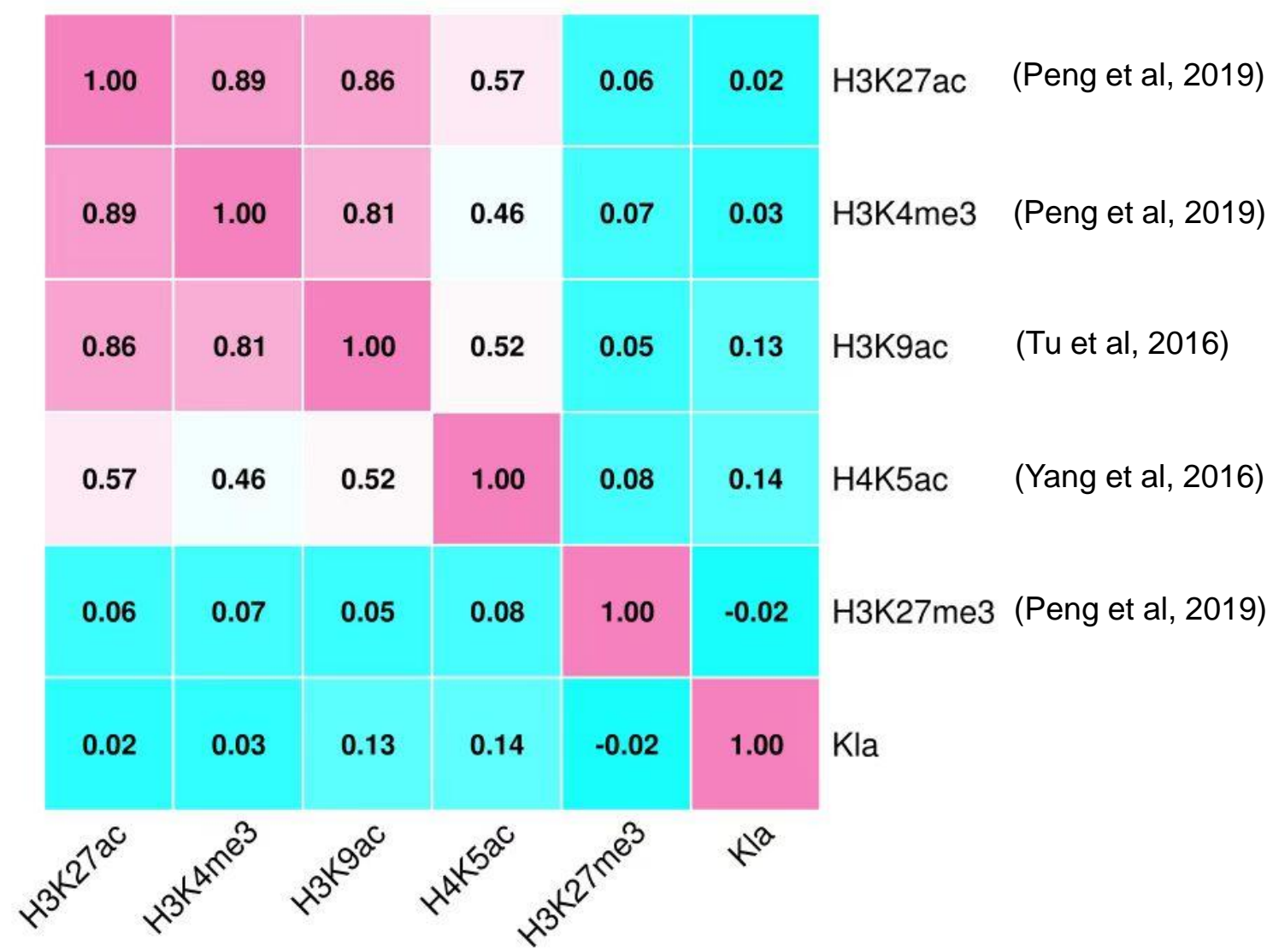


Figure S4. The correlogram of Kla and other histone modifications.

Supplementary Figure S5

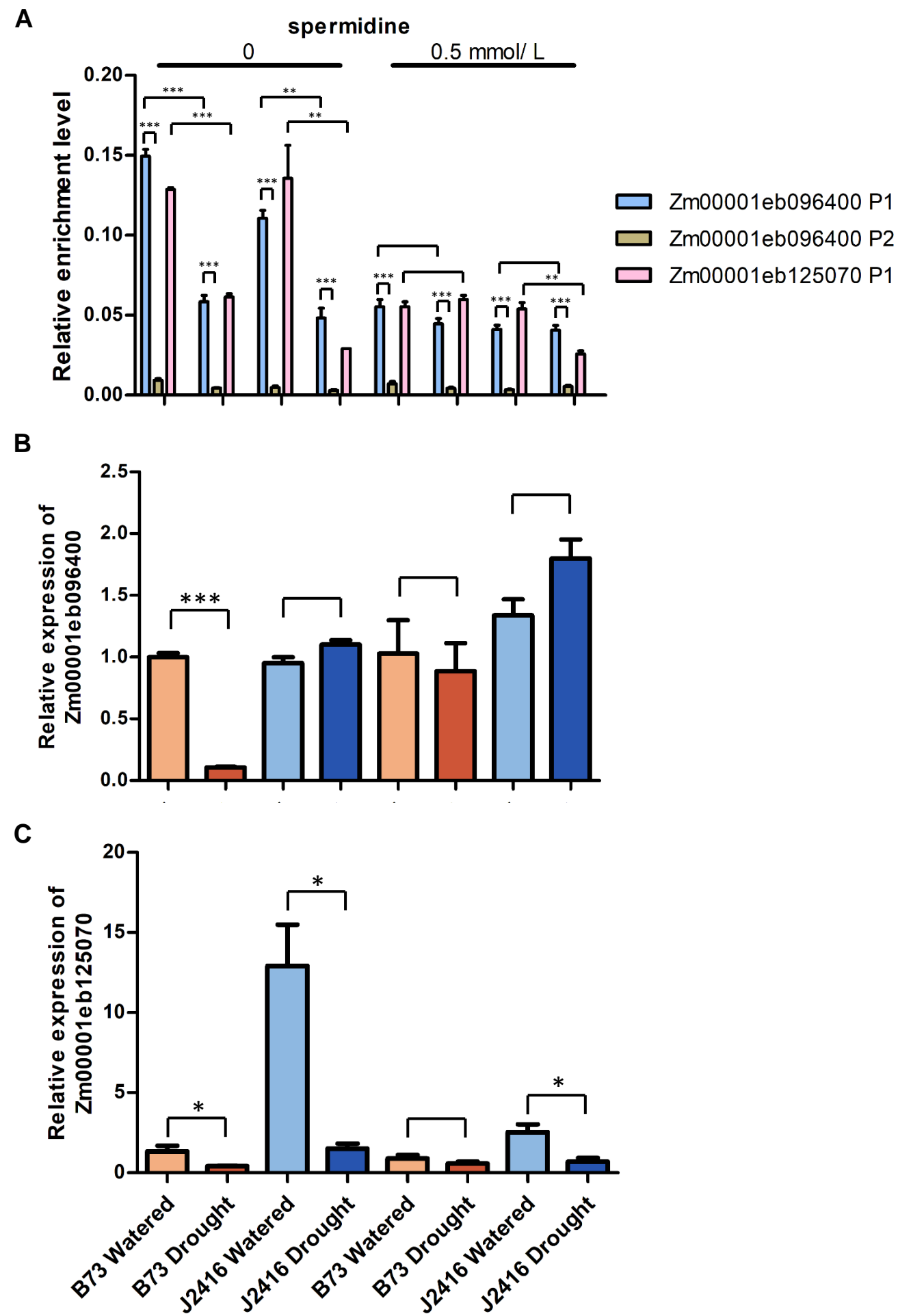


Figure S5. ChIP-qPCR and qPCR validation of Zm00001eb096400 and Zm00001eb125070 in spermidine treated B73 and J2416.

Supplement Figure 6

A

Name	La (K)										
Description	Lactylation										
Composition	H(4) O(2) C(3) Change 72.0211293726										
Position	Not C-term										
Type	Standard										
New terminus	None										
Specificities	<div style="display: flex; align-items: center;"> + - Neutral losses + - C ↑ ↓ N S E </div> <table border="1" style="margin-top: 5px;"> <thead> <tr> <th>AA</th> <th>Name</th> <th>Short name</th> <th>Composition</th> <th>Mass</th> </tr> </thead> <tbody> <tr> <td style="background-color: #0056b3; color: white;">K</td> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table>	AA	Name	Short name	Composition	Mass	K				
AA	Name	Short name	Composition	Mass							
K											

B

Analysis	Software/ Methods	Version and website
GO	eggNOG-mapper	v2.0 https://github.com/eggNOGdb/eggNOG-mapper
	eggNOG	v5.0 http://eggNOG5.embl.de/
Domain	PfamScan	v1.6 https://www.ebi.ac.uk/seqdb/confluence/display/THD/PfamScan
	Pfam	v33.1 https://pfam.xfam.org/
KEGG	DIAMOND	v0.9.24 https://github.com/bbuchfink/diamond/releases
	KEGG Mapper	v2.5 http://www.kegg.jp/kegg/mapper.html
Subcellular	Wolf Psort	v1.0 https://wolfsort.hgc.jp/
COG/KOG	eggNOG-mapper	v2.0 https://github.com/eggNOGdb/eggNOG-mapper
	eggNOG	v5.0 http://eggNOG5.embl.de/
Enrichment analysis	Python module	v1.4.1 https://pypi.org/project/scipy/1.4.1/
Motif	MoMo	v5.0.2 https://meme-suite.org/meme/tools/momo

Figure S6. Parameters and tools used for lactylation definition and protein annotation. **A.**

MaxQuant interface showing parameters for lactylation identification. **B.** Analytical tools used for annotation and enrichment analysis.

Table S1. Identified K-La sites and proteins in four samples.

	Identified K-La sites	Identified K-La proteins	Total identified proteins
B73 Control	253	166	6897
B73 Drought	272	171	6728
J2416 Control	290	174	6748
J2416 Drought	291	164	6387

Table S2. roteins identified in fatty acid degradation pathways by lactylome.

Protein accession	Position	Protein description	Gene name	Modified sequence	B73CK1	B73CK2	B73CK3	B73SD1	B73SD2	B73SD3	J2416CK1	J2416CK2	J2416CK3	J2416SD1	J2416SD2	J2416SD3	J2416SD/J 2416CK Ratio	J2416SD/J 2416CK P value	Subcellular localization	KEGG KO No.	KEGG Gene	KEGG pathway
A0A1D6N7A4	498	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d042884 PE=3 SV=1	ZEAMMB73_Zm00001d042884	ALYAEFLGAQK(1)K							0.756	1.052	0.928	0.289	0.854	0.354	0.547	0.1091353	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
A0A1D6N7A4	179	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d042884 PE=3 SV=1	ZEAMMB73_Zm00001d042884	HHDK(1)WLVATE NYDIK							0.654	0.645							chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	443	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	ILMK(1)T LSQLTSG K	1.198	1.354	1.28												chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	314	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	K(1)QFGS QDGGPE TK							1.087	1.177	1.151	0.386	0.256	0.268	0.266	0.0005321	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome

B4F8X3	659	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=1001914 69 PE=2 SV=1	100191469	PLLK(1)Q QLK							0.75	0.539	0.693					chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	663	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=1001914 69 PE=2 SV=1	100191469	QQLK(1)L SR	1.05	0.964								1.428				chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	309	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm0000 01d037521	K(1)QFGA PLAAFQL NQEK							0.72	0.863	0.85					chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	350	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm0000 01d037521	LYESGK(1) MTPGR									0.801					chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	430	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm0000 01d037521	PAVSAK(1) SR									0.801					chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome

A0A1D6F4B6	155	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	AIYLSTAK(1)TLAAIHK							0.747	0.896						cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism	
A0A1D6F4B6	826	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	IADGPDEVHLGTIAK(1)LELR							0.84							cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism	
A0A1D6F4B6	172	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	VDINAIGLQK(1)YGR							0.987	1.015	0.878	0.434			0.452	cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism	
A0A1D6K4Z6	218	Putative acetyl-CoA acetyltransferase cytosolic 2 OS=Zea mays OX=4577 GN=100282283 PE=3 SV=1	100282283	K(1)LRPSFK														cytoplasm	K00626	E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	map00071 Fatty acid degradation; map00072 Synthesis and degradation of ketone bodies; map00280 Valine, leucine and isoleucine degradation; map00310 Lysine degradation; map00380 Tryptophan metabolism; map00620 Pyruvate metabolism; map00630 Glyoxylate and dicarboxylate metabolism; map00640 Propanoate metabolism; map00650 Butanoate metabolism; map00900 Terpenoid backbone biosynthesis; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism	
A0A1D6N7A4	346.1923	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm0001d042884 PE=3 SV=1	ZEAMMB73_Zm0001d042884	ALYAEFLGAQK(2)K							0.9697801	0.8580984	0.8116136	0.4554742	1.146	0.182	0.4065464	-0.1080711	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome

A0A1D6N7A4	338.3297	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d042884 PE=3 SV=1	ZEAMMB73_Zm00001d042884	HHDK(2)WLVATE NYDIK							0.9881776	0.8578443	0.8010909	0.4671753	1.236		0.4044845		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	330.467	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	ILMK(2)T LSQLTSG K		0.902	1.354	0.648											chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	322.6044	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	K(2)QFGS QDGGPE TK															chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	314.7418	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	PLLK(2)Q QLK															chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	306.8791	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	QQLK(2)L SR		0.754		0.332											chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome

B4G0E0	299.0165	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d037521 PE=2 SV=1	ZEAMMB73_Zm00001d037521	K(2)QFGA PLAAFQL NQEK							1.0801649	0.8565738	0.7484773	0.5256804				0.3941753	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	291.1538	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d037521 PE=2 SV=1	ZEAMMB73_Zm00001d037521	LYESGK(2)MTPGR							1.0985624	0.8563197	0.7379545	0.5373814				0.3921134	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	283.2912	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d037521 PE=2 SV=1	ZEAMMB73_Zm00001d037521	PAVSAK(2)SR							1.1169598	0.8560656	0.7274318	0.5490825				0.3900515	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
A0A1D6F4B6	275.4286	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	AIYLSTAK(2)TLAAIHK							1.1353573	0.8558115	0.7169091	0.5607835				0.3879897	cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism
A0A1D6F4B6	267.5659	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	IADGPDEVHLGTIAK(2)LELR							1.1537548	0.8555574	0.7063864	0.5724845				0.3859278	cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism

A0A1D6F4B6	259.7033	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	VDINAIG LQK(2)YGR																	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism
A0A1D6K4Z7	251.8407	Putative acetyl-CoA acetyltransferase cytosolic 2 OS=Zea mays OX=4577 GN=100282283 PE=3 SV=2	100282283	K(2)LRPSFK																	E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.10]	map00071 Fatty acid degradation; map00072 Synthesis and degradation of ketone bodies; map00280 Valine, leucine and isoleucine degradation; map00310 Lysine degradation; map00380 Tryptophan metabolism; map00620 Pyruvate metabolism; map00630 Glyoxylate and dicarboxylate metabolism; map00640 Propanoate metabolism; map00650 Butanoate metabolism; map00900 Terpenoid backbone biosynthesis; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01213 Fatty acid metabolism
A0A1D6N7A4	243.978	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm0001d042884 PE=3 SV=1	ZEAMMB73_Zm0001d042884	ALYAEFLGAQK(3)K																	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
A0A1D6N7A4	236.1154	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm0001d042884 PE=3 SV=1	ZEAMMB73_Zm0001d042884	HHDK(3)WLVATENYDIK																	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	228.2527	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	ILMK(3)T LSQLTSGK	0.606	1.354	0.016														E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome

B4F8X3	220.3901	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=1001914 69 PE=2 SV=1	100191469	K(3)QFGS QDGGPE TK							1.2457421	0.8542869	0.6537727	0.6309897	1.956	-0.076	0.3756186	-0.4338807	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	212.5275	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=1001914 69 PE=2 SV=1	100191469	PLLK(3)Q QLK							1.2641395	0.8540328	0.64325	0.6426907	2.046		0.3735567		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	204.6648	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=1001914 69 PE=2 SV=1	100191469	QQLK(3)L SR	0.458						1.282537	0.8537787	0.6327273	0.6543918	2.136		0.3714948		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	196.8022	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm000 01d037521	K(3)QFGA PLAAFQL NQEK							1.3009345	0.8535246	0.6222045	0.6660928			0.369433		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	188.9396	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm000 01d037521	LYESGK(3)MTPGR							1.3193319	0.8532705	0.6116818	0.6777938			0.3673711		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome

B4G0E0	181.0769	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d037521 PE=2 SV=1	ZEAMMB73_Zm00001d037521	PAVSAK(3)SR							1.3377294	0.8530164	0.6011591	0.6894948				0.3653093	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6]	map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
A0A1D6F4B6	173.2143	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	AIYLSTAK(3)TLAAIHK							1.3561268	0.8527623	0.5906364	0.7011959				0.3632474	cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism
A0A1D6F4B6	165.3516	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	IADGPDEVHLGTIAK(3)LELR							1.3745243	0.8525082	0.5801136	0.7128969				0.3611856	cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism
A0A1D6F4B6	157.489	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	VDINAIGLQK(3)YGR							1.3929218	0.8522541	0.5695909	0.7245979				0.3591237	cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism
A0A1D6K4Z8	149.6264	Putative acetyl-CoA acetyltransferase cytosolic 2 OS=Zea mays OX=4577 GN=100282283 PE=3 SV=3	100282283	K(3)LRPSFK															cytoplasm	K00626	E2.3.1.9, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.11]	map00071 Fatty acid degradation; map00072 Synthesis and degradation of ketone bodies; map00280 Valine, leucine and isoleucine degradation; map00310 Lysine degradation; map00380 Tryptophan metabolism; map00620 Pyruvate metabolism; map00630 Glyoxylate and dicarboxylate metabolism; map00640 Propanoate metabolism; map00650 Butanoate metabolism; map00900 Terpenoid backbone biosynthesis; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01214 Fatty acid metabolism

A0A1D6N7A4	141.7637	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d042884 PE=3 SV=1	ZEAMMB73_Zm00001d042884	ALYAEFLGAQK(4)							1.4113192	0.852	0.5590682	0.736299	2.226	-0.162	0.3570619	-0.5424838	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
A0A1D6N7A4	133.9011	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=ZEAMMB73_Zm00001d042884 PE=3 SV=1	ZEAMMB73_Zm00001d042884	HHDK(4)WLVATENYDIK							1.4297167	0.8517459	0.5485455	0.748	2.316		0.355		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	126.0385	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	ILMK(4)TLSQLTSG	0.31	1.354	-0.616				1.4481142	0.8514918	0.5380227	0.759701	2.406		0.3529381		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	118.1758	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	K(4)QFGSQDGGPE							1.4665116	0.8512377	0.5275	0.7714021	2.496	-0.248	0.3508763	-0.651087	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4F8X3	110.3132	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=100191469 PE=2 SV=1	100191469	PLLK(4)QQLK							1.4849091	0.8509836	0.5169773	0.7831031	2.586		0.3488144		chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome

B4F8X3	102.4505	Acyl-coenzyme A oxidase OS=Zea mays OX=4577 GN=1001914 69 PE=2 SV=1	100191469	QQLK(4)LSR	0.162	-0.932				1.5033066	0.8507295	0.5064545	0.7948041	2.676		0.3467526	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome
B4G0E0	94.58791	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm0000 01d037521	K(4)QFGA PLAAFQL NQEK						1.521704	0.8504754	0.4959318	0.8065052		0.3446907	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome	
B4G0E0	86.72527	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm0000 01d037521	LYESGK(4)MTPGR						1.5401015	0.8502213	0.4854091	0.8182062		0.3426289	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome	
B4G0E0	78.86264	Acyl-coenzyme A oxidase 4 peroxisomal OS=Zea mays OX=4577 GN=ZEAMM B73_Zm0000 1d037521 PE=2 SV=1	ZEAMMB 73_Zm0000 01d037521	PAVSAK(4)SR						1.5584989	0.8499672	0.4748864	0.8299072		0.340567	chloroplast	K00232	E1.3.3.6, ACOX1, ACOX3; acyl-CoA oxidase [EC:1.3.3.6] map00071 Fatty acid degradation; map00410 beta-Alanine metabolism; map00592 alpha-Linolenic acid metabolism; map00640 Propanoate metabolism; map01040 Biosynthesis of unsaturated fatty acids; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01200 Carbon metabolism; map01212 Fatty acid metabolism; map04146 Peroxisome	
A0A1D6F4B6	71	Putative acyl-CoA dehydrogenase 1BR3 OS=Zea mays OX=4577 GN=1005023 33 PE=4 SV=1	100502333	AIYLSTAK(4)TLAAIHK						1.5768964	0.8497131	0.4643636	0.8416082		0.3385052	cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7] map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism	

A0A1D6F4B6	63.13736	Putative acyl-CoA dehydrogenase IBR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	IADGPDE VHLGTIA K(4)LELR							1.5952939	0.849459	0.4538409	0.8533093						cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism
A0A1D6F4B6	55.27473	Putative acyl-CoA dehydrogenase IBR3 OS=Zea mays OX=4577 GN=100502333 PE=4 SV=1	100502333	VDINAIG LQK(4)Y GR							1.6136913	0.8492049	0.4433182	0.8650103						cytoplasm	K00249	ACADM, acyl-CoA dehydrogenase [EC:1.3.8.7]	map00071 Fatty acid degradation; map00280 Valine, leucine and isoleucine degradation; map01100 Metabolic pathways; map01110 Biosynthesis of secondary metabolites; map01212 Fatty acid metabolism

Table S3. Primers used in the study.

Chip-qPCR

Zm00001eb096400-P1_F	GTACATGCCGTCGTGGCAG
Zm00001eb096400-P1_R	GACGGCCACGACATCTCAT
Zm00001eb096400-P2_F	TCGTCTGAAGGTCATTATATCCGAG
Zm00001eb096400-P2_R	AAAGGCCTACGTCCTTCGAAG
Zm00001eb125070-P1_F	TTTTTTTGTCCGGCTTTGTTGG
Zm00001eb125070-P1_R	AGTCAGCCACCTGCAGAACAC

qPCR

Zm00001eb096400_F	TGGTGCCCATGACGTACAT
Zm00001eb096400_R	GATCTTGATGGATTTGAACTGC
Zm00001eb125070_F	TGAGATGACCGAGATGGACA
Zm00001eb125070_R	TCCAGCTCCTTCATATTTGC