Table S1. Metabolic pathways enriched in upregulated genes by *OsSRT1* RNAi

KEGG ID	Pathway name	P-value
osa00051	Fructose and mannose metabolism	0.00515
osa00010	Glycolysis/Gluconeogenesis	0.00528
osa00480	Glutatione metabolism	0.013078
osa04145	Phagosome	0.014308
osa00305	Tyrosine metabolism	0.01998
osa00940	Phenylpropanoid biosynthesis	0.020105
osa00030	Pentose phosphate pathway	0.02298
osa00710	Carbon fixation photosynthetic organism	0.024823

Table S2. OsGAPDH1 peptides Lys modification identified by mass spectrometry.

peptide	q-value
AVGKVLPDLNGKLTGMSFR	0.0016
IKSKTLLLGEKPVTVFGIR	0.0000
IKIGINGFGR	0.0000
KVVISAPSK	0.0000
LKGIIGYVEEDLVSTDFVGDSR	0.0000
SAIKSASEGKLK	0.0000
TLLLGEKPVTVFGIR	0.0000
TVDGPSSKDWR	0.0000
VIHDNFGIIEGLMTTVHAITATQKTVDGPSSK	0.0086
VLPDLNGKLTGMSFR	0.0030
VVISAPSKDAPMFVCGVNEDKYTSDIDIVSNASCT	0.0000
YDTVHGQWKHSDIK	0.0000
AASFNIIPSSTGAAKAVGK	0.0000
IEKAASYDAIK	0.0000
NPDEIPWAEAGAEYVVESTGVFTDKEK	0.0000
AASYDAIKSAIK	0.0000

Table S3. Summary of glycolytic genes used in the study

Locus	Annotation	Gene name
LOC_Os01g09570	ATP-dependent 6-phosphofructokinase 6	6-PFK 6
LOC_Os02g32490	Acetyl-coa synthetase	AcCoA Syn
LOC_Os04g38530	aldose 1-epimerase, putative, expressed	Ald-ep
LOC_Os04g38540	aldose 1-epimerase, putative, expressed	Ald-ep
LOC_Os05g36270	fructose-1,6-bisphosphatase, putative, expressed	F-1,6-BP
LOC_Os06g45590	glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic	GAPCP1
LOC_Os09g30240	ATP-dependent 6-phosphofructokinase 2	6-PFK 2
LOC_Os07g26540	hexokinase, putative, expressed	HXK1
LOC_Os08g03290	glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	GAPDH1

Table S4 Primers for qPCR, genotyping and amino acid mutagenesis

Pimer name	Sequence (5'-3')
LOC_Os01g09570F	TACTGCACCCTGCTAGCTC
LOC_Os01g09570R	CTCCGTGATTCTGTAGAACG
LOC_Os02g32490F	GTTGAGCATGAAGTGAAAGG
LOC_Os02g32490R	ATGAGGCTTTTCCGTAGTTC
LOC_Os04g38530F	GTGAACCACCCCAACTTC
LOC_Os04g38530R	AGAACGAGAACTTGTACACCAT
LOC_Os04g38540F	CAAGGTGTACCAGCAGTACG
LOC_Os04g38540R	GAGAACTTGAAGGCCATGT
LOC_Os05g36270F	CTGGGGAGCTATGATGACG
LOC_Os05g36270R	TGGTGAAGCCGTACCGTGT
LOC_Os06g45590F	CGAATGATTTCATTGGTGAC
LOC_Os06g45590R	TTGTCGTACCAAGAGACGAG
LOC_Os09g30240F	ATCAGCCCGACTTTATCCG
LOC_Os09g30240R	CTGGTTCAACCCAAACCAA
LOC_Os07g26540F	AGCAGACCTACGAGAAGCTCAT
LOC_Os07g26540R	CCTCCCGATCTTCTTCAGGAT
LOC_Os08g03290F	GATAACTTTGTCAAGCTTGTCGC
LOC_Os08g03290R	CAGCATAGACAAAGCATACCGG
GAPDHmutantF	TCAAATGCTAGCTGCACCAC
GAPDHmutantR	GCTTTCCCTCTGATGCAGAC
N	AATCCAGATCCCCCGAATTA
qRTActin1-F	TGTATGCCAGTGGTCGTACCA
qRTActin1-R	CCAGCAAGGTCGAGACGAA
R(57/74)-F	CAATGGAGGCACAGCGACATCAAGATCAAGGACTCCAAGACTCTGCTCTTGGGCGAGAGGCCGGTC
R(57/74)-R	GACCGGCCTCTCGCCCAAGAGCAGAGTCTTGGAGTCCTTGATCTTGATGTCGCTGTGCCTCCATTG
R(120)-F	GGTGCCAAGAGGGTTGTCATC
R(120)-R	GATGACAACCCTCTTGGCACC
R(217)-F	GGTGCTGCCAGAGCTGTTGGC
R(217)-R	GCCAACAGCTCTGGCAGCACC
R(261/265)-F	CTATCAGGAGTGCTATCAGGTCTGC
R(261/265)-R	GCAGACCTGATAGCACTCCTGATAG

Table S5 Primers for ChIP-PCR

Pimer name	Sequence (5'-3')
LOC_Os01g09570ChIP-F	GCACACACATCTTCTCTAG
LOC_Os01g09570ChIP-R	GTGCTTCTGGTTTGCGG
LOC_Os02g32490ChIP-F	CCGAATAAAAATTAACTAAAC
LOC_Os02g32490ChIP-R	CGCTGAATTGTAAAAAAG
LOC_Os04g38530ChIP-F	GCGAGCGAATATTCGCCG
LOC_Os04g38530ChIP-R	GATCCGTGCCCACGCGGCC
LOC_Os04g38540ChIP-F	CGTTTCAGTTTCTTTTTTTCC
LOC_Os04g38540ChIP-R	GATGACAATTTGTCATTGG
LOC_Os05g36270ChIP-F	GGAAGAAGGGGAGGTGATC
LOC_Os05g36270ChIP-R	CGTTGGCAAGCCGCGTCCGG
LOC_Os06g45590ChIP-F	GTAAAGAGAGAACAAAC
LOC_Os06g45590ChIP-R	TTAGATTGTTAATAACATG
LOC_Os09g30240ChIP-F	GTGGGACCAAGAGAGTCG
LOC_Os09g30240ChIP-R	GGGCTCGCGTTTATGGC
LOC_Os07g26540ChIP-F	CGAGAGGTGAAACATGTGA
LOC_Os07g26540ChIP-R	CAACAGGAGACTGCTACAGG
LOC_Os08g03290CHIP-F	CGTCCTCGCATCTCCACT
LOC_Os08g03290CHIP-R	GCGAAGCACCAGCAGTAA
LOC_Os01g09570CHIP-2F	TCGAAGTGAAGGAGTCCCG
LOC_Os01g09570CHIP-2R	CTTCTTCTTCATCGCCCAC
LOC_Os02g32490CHIP-2F	AGCCATCGCACTCTGCA
LOC_Os02g32490CHIP-2R	TGGCGGTCGTCTTCCTC
LOC_Os04g38530CHIP-2F	GAGACGCCTTGGGAGCA
LOC_Os04g38530CHIP-2R	GCCGGATGGACGGATAT
LOC_Os04g38540CHIP-2F	CGCTGCGACTTGAGGACA
LOC_Os04g38540CHIP-2R	CCAGCCTGGTTACGGACA
LOC_Os05g36270CHIP-2F	CGCCGCTACCTCCTCAT
LOC_Os05g36270CHIP-2R	TGCTCCTTGCGAAAACG
LOC_Os06g45590CHIP-2F	TGTTGTTCGTATGGCGATGT
LOC_Os06g45590CHIP-2R	GCGAACGAATCTCAACTGAA
LOC_Os09g30240CHIP-2F	GCCGCACATGACCACCA
LOC_Os09g30240CHIP-2R	GATCGGGTTCGGGATGG
LOC_Os07g26540ChIP-2F	GATCGCCAAGAAACCTTC
LOC_Os07g26540ChIP-2R	CGTCACCACCTTCTGATCT
LOC_Os08g03290CHIP-2F	GTTTGTGCTGTGCTGGGTG
LOC_Os08g03290CHIP-2R	CGATCCTTCCGAAACCTGA
ChIPActin1F	TGCGTGTCCTCTTCCTCATCT
ChIPActin1R	AAGGCGAATGAAGCGAAAAG

Table S5 Primers for ChIP-PCR (continue)

Pimer name	Sequence (5'-3')
LOC_Os01g09570CHIP-3F	CCGACAGCCCGCGTCGACC
LOC_Os01g09570CHIP-3R	AGGAGGGAGGGCCGCAAC
LOC_Os01g09570CHIP-4F	ATGTTTTTTTGGCCTGTG
LOC_Os01g09570CHIP-4R	ACATTTGCTTAAAACATTATC
LOC_Os02g32490CHIP-3F	CAGCGAGCAATCGGGTG
LOC_Os02g32490CHIP-3R	CATTACTCGTCATAAATTTG
LOC_Os02g32490CHIP-4F	GGGACATGAATATCAATC
LOC_Os02g32490CHIP-4R	AACCTTTAGCACATCAC
LOC_Os04g38530CHIP-3F	GACACAAAAGCCATCCAGATG
LOC_Os04g38530CHIP-3R	GATCGATGGTACATGGACGG
LOC_Os04g38530CHIP-4F	GCTCATATTTTCACTGTTTA
LOC_Os04g38530CHIP-4R	TGCTGTTCTACAATCCATA
LOC_Os04g38540CHIP-3F	GTGCGAGGAAGACGGTCG
LOC_Os04g38540CHIP-3R	GACGGTACCTTTGGAATC
LOC_Os04g38540CHIP-4F	GTACTTGTCTGATCAAGA
LOC_Os04g38540CHIP-4R	AAAATTCCACCATCTTTTTG
LOC_Os05g36270CHIP-3F	CGTCAACAAGGCCGGCCT
LOC_Os05g36270CHIP-3R	CATGGATTTGTGTGGAGGAAC
LOC_Os05g36270CHIP-4F	CAGCCACGAGTTCGACAAG
LOC_Os05g36270CHIP-4R	ATCGATATTTGAGGAGCC
LOC_Os06g45590CHIP-3F	ACGTGACTTCTCTTTTTGG
LOC_Os06g45590CHIP-3R	TTATTGAGGATTGACTCCG
LOC_Os06g45590CHIP-4F	AGATTATTCGAATTCCTTG
LOC_Os06g45590CHIP-4R	CACAGAGCAAAAACCACA
LOC_Os09g30240CHIP-3F	GAGAGCTCGTCGTCGGGCT
LOC_Os09g30240CHIP-3R	CGAGCGGGACGACCTCGT
LOC_Os09g30240CHIP-4F	ACTGCTGCCTCATCCCGGA
LOC_Os09g30240CHIP-4R	CTTGGGATGAGACGTTGGC
LOC_Os07g26540CHIP-3F	CTGTGCATCTTTGCTACGTTG
LOC_Os07g26540CHIP-3R	GCAACGGAAAAATAATAGGG
LOC_Os07g26540CHIP-4F	TCTCCTTCCCCGTGCACCAAA
LOC_Os07g26540CHIP-4R	TGCAGCGCCGCCACGACGTCCT
LOC_Os08g03290CHIP-3F	GTATGTGTCCAAAGATTCG
LOC_Os08g03290CHIP-3R	TGTATGACAGGTGGGATCA
LOC_Os08g03290CHIP-4F	CTACTGCATATGGCTTTGA
LOC_Os08g03290CHIP-4R	TTCCATTGGCCGTGCACGGTAT

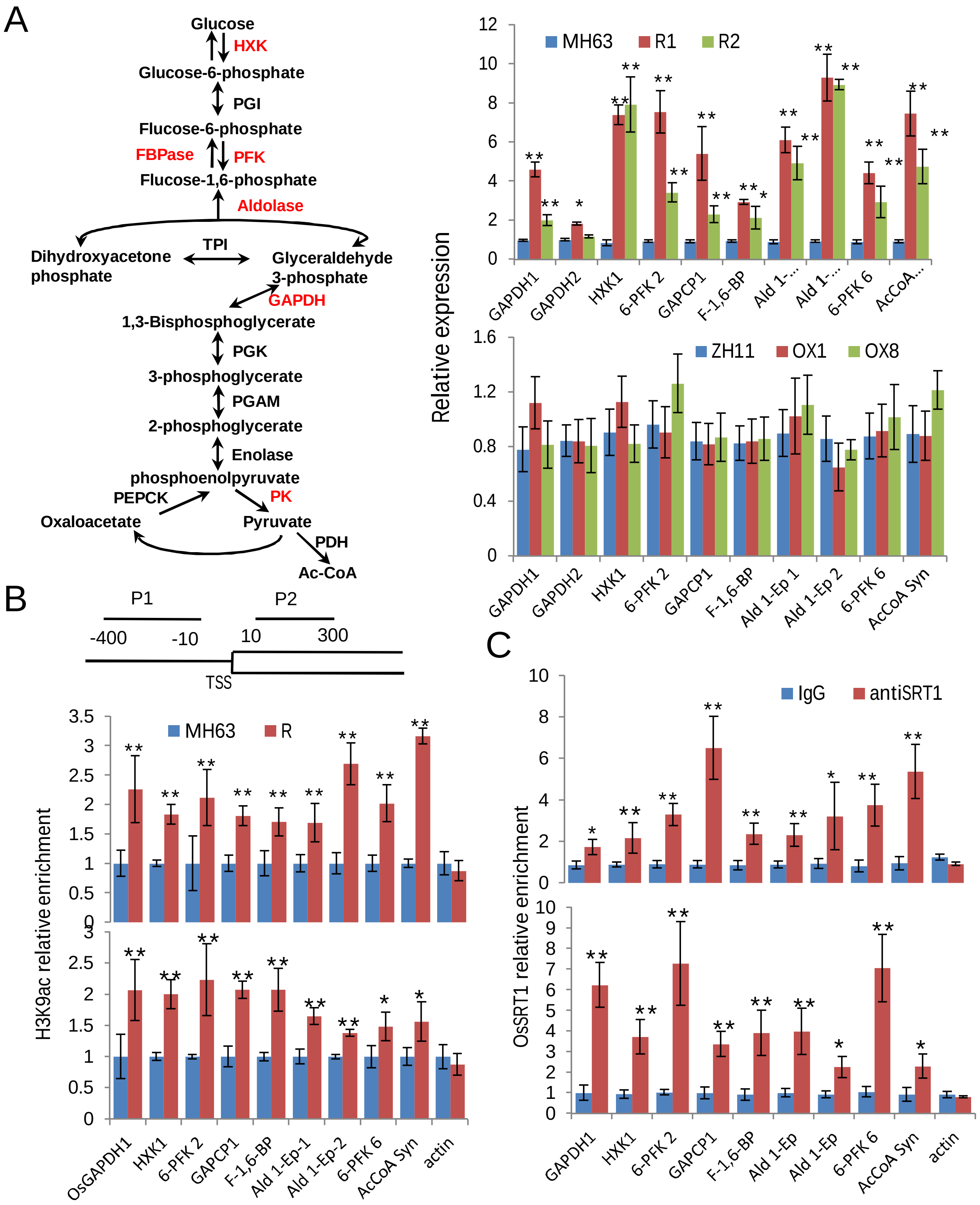


Figure S1. OsSRT1 represses glycolytic gene expression. (A) Left, analyzed genes in glycolysis pathway are indicated in red. Right, transcript levels of the genes in two O*sSRT1*RNAi lines (R1, R2) compared to wild type seedlings. (B) H3K9ac levels of glycolytic genes in wild type (MH63) and combined RNAi lines R1 and R2 (R) detected by ChIP-PCR. P1 is located between -400 to -10 relative to TSS. P2 is located between +10 to +300 relative to TSS. The exact positions of the primers are indicated in Table S2. (C) Enrichment of OsSRT1protein on glycolytic gene loci in wild type plants by ChIP-PCR using anti-OsSRT1 and IgG as controls. The used primer sets are the same as in (B). Bars represent means+/-SD of three biological replicates of the RT-PCR and ChIP-PCR experiments. Significance of differences are indicated (** $p<0.01$; *$p<0.05$).

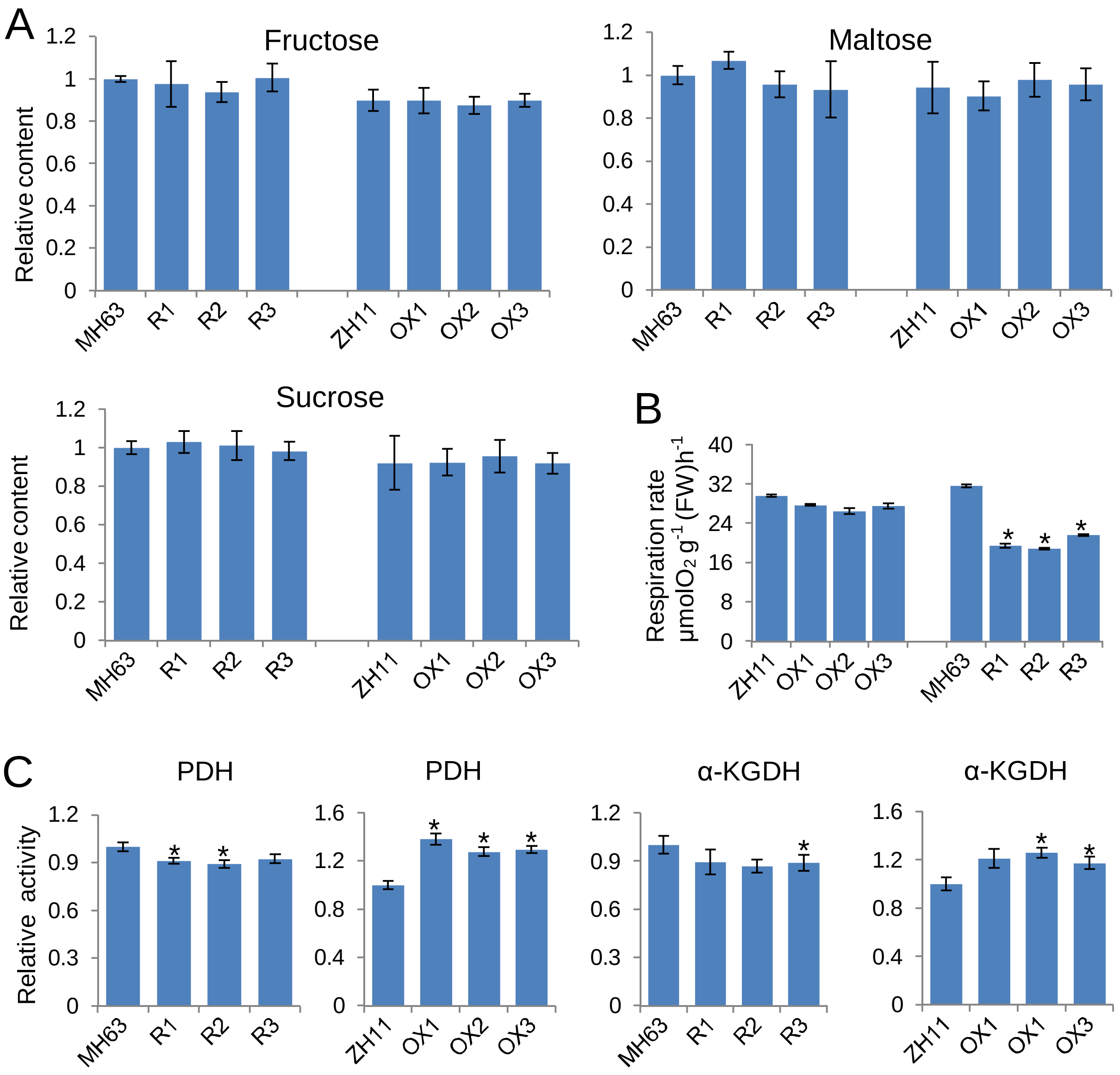


Figure S2. OsSRT1 RNAi and over-expression effects on sugar accumulation and mitochondrial respiration. (A) Sugar contents in *OsSRT1* transgenic (RNAi, over-expression) plants compared to the respective wild type (MH63 and ZH11). (B) Mitochondrial respiration rates in *OsSRT1* RNAi and over-expression leaves compared to the respective wild type, measured 30 min after light to dark transition. (C) Activities of pyruvate dehydrogenase and α-ketoglutarate dehydrogenase in OsSRT1 transgenic plants compared to wild type. Bars= means +/- SD of 3 biological replicates (each replicates with 3 technical repetitions). Significances of differences between wild type and transgenic lines are indicated (* P value < 0.05, Chi-2 tests).

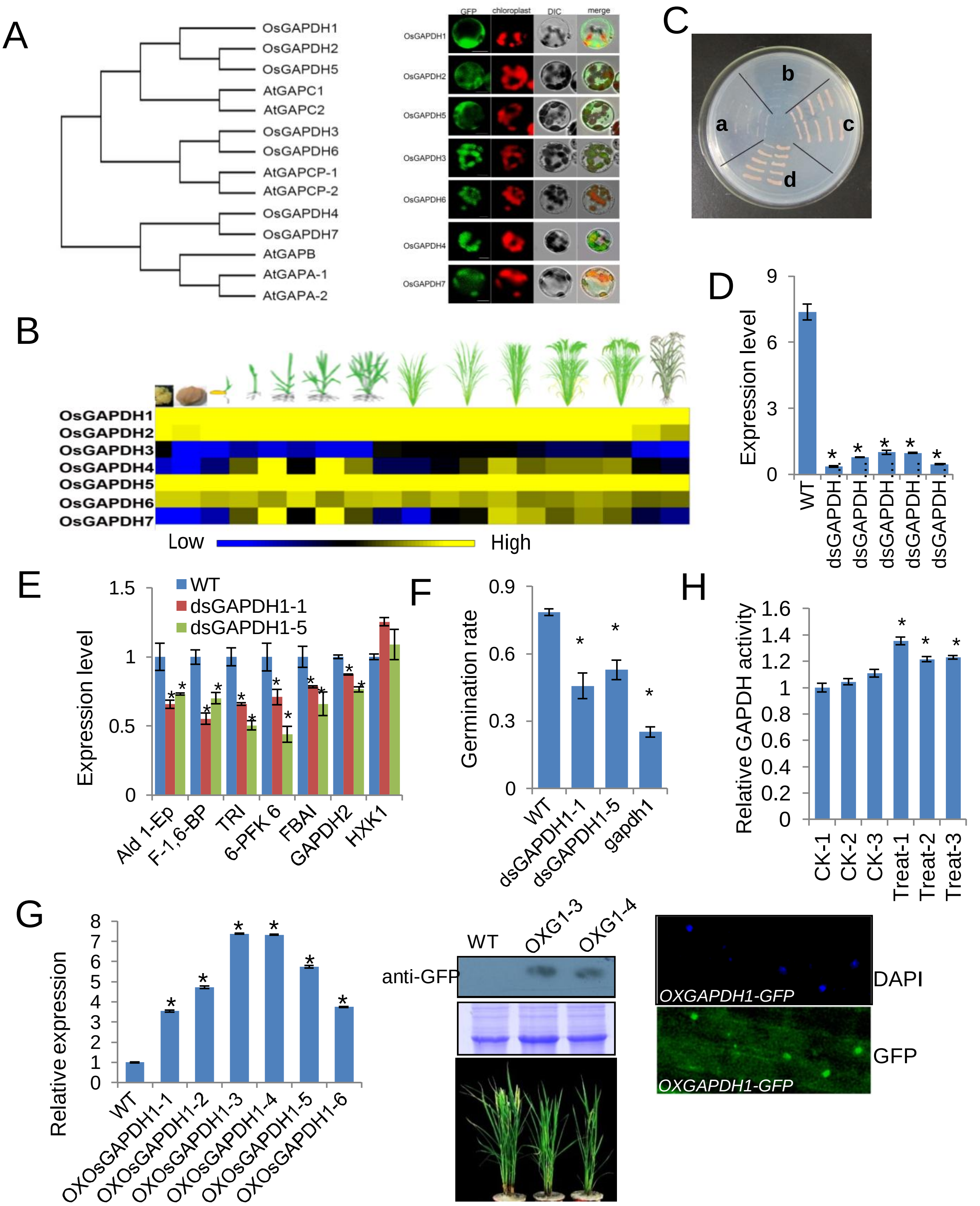


Figure S3. Rice GAPDH genes and OsGAPDH1 RNAi and over-expression lines. (A) Phylogenetic relationship of rice and Arabidopsis GAPDH gene families and the Subcellular localization of rice GAPDH-GFP proteins. (B) Expression profiles of rice GAPDH genes at different developmental stages. (C) Protein interaction between OsGAPDH1 and OsGAPDH2 in yeast two hybrid assays. (D) Transcript levels (relative to Actin1) of *OsGAPDH1* in wild type and 5 RNAi (ds) lines. (E) Transcript levels of glycolytic genes in two RNAi lines compared to wild type. (F) Seed germination rates of two RNAi lines and the T-DNA mutant compared to wild type. (G) Production of *OsSRT1* over-expression plants. Left, *OsGAPDH1* transcript levels in *35S::OsGAPDH1-GFP* transgenic lines. Middle, protein level of OsGAPDH1-GFP in two line and phenotype at mature stage. Right, detection of OsGAPDH1-GFP in root cells (upper part, DAPI; lower part, GFP fluorescence). (H) Relative GAPDH activity in 12 d seedlings treated with or without 0.1% H_2O_2. Bars are means +/- SD of three biological replicates. Significances of difference are indicated by * (p<0.01).

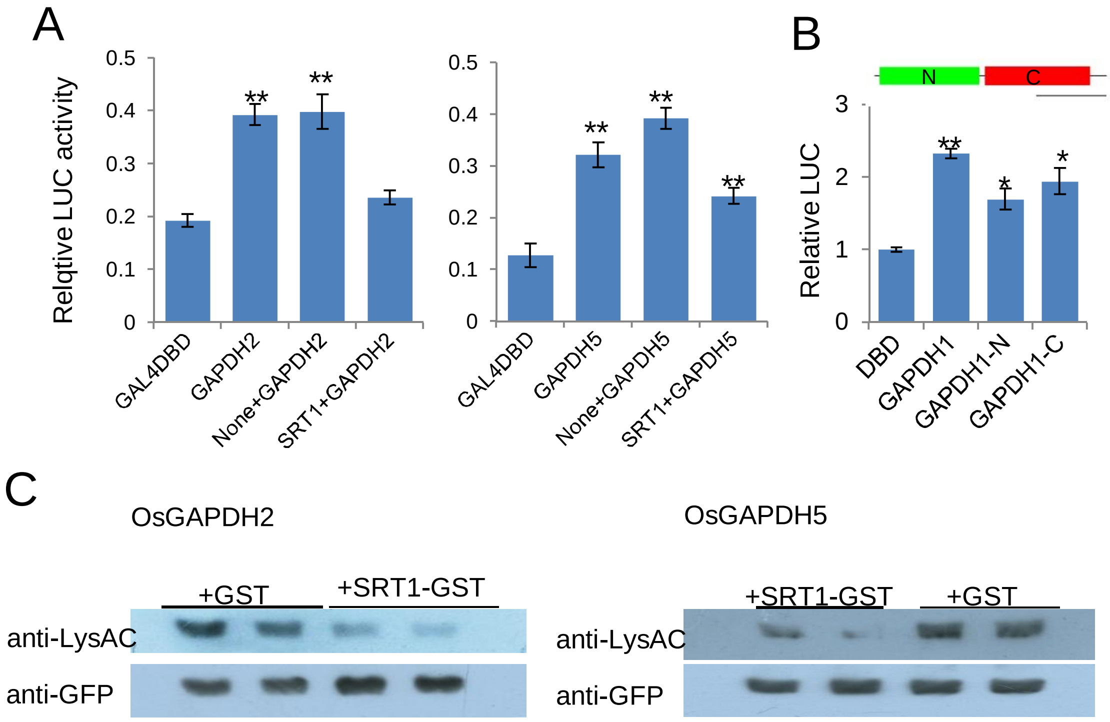


Figure S4. OsSRT1-regulated transcriptional function and lysine deacetylation of rice GAPDH proteins. (A) Transactivation of UAS reporter promoters (described in Figure 4A) by OsGAPDH2, and OsGAPDH5 fused with DBD in the presence or absence of OsSRT1 assayed in transfected tobacco protoplasts. (B) Deletion analysis of OsGAPDH1 transcription activity. Grey bar=100 amino acids. (C) E coli-produced OsSRT1-GST protein deacetylates tobacco cell –produced OsGAPDH2-GFP and OsGADH5-GFP in vitro. Anti-GFP was used for loading controls and anti-Lys detected lysine acetylation levels of OsGAPDH1-GFP in the absence or presence of OsSRT1-GST. Significances of differences between wild type and transgenic lines are indicated (* P value < 0.05; (** P value < 0.01).

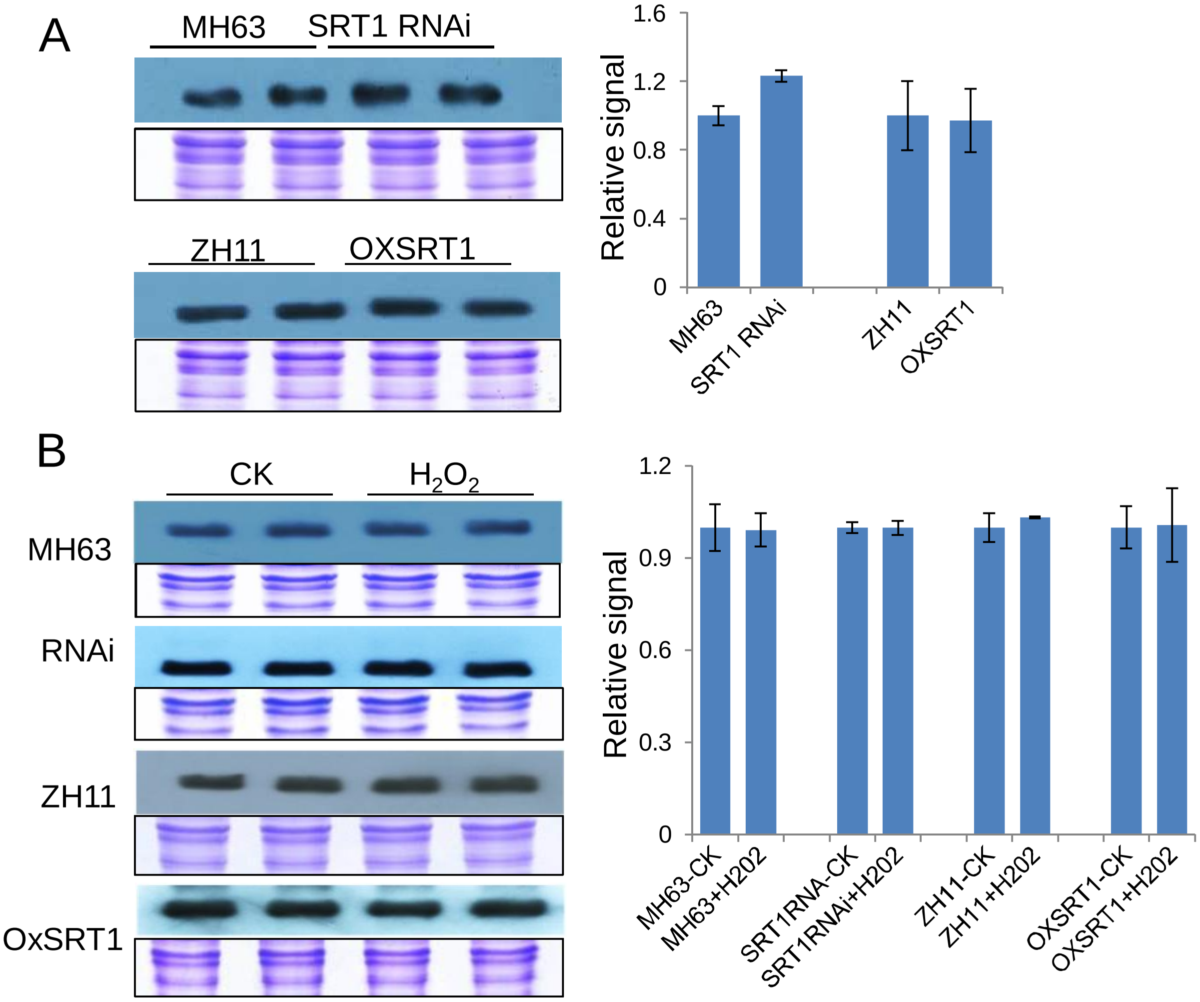
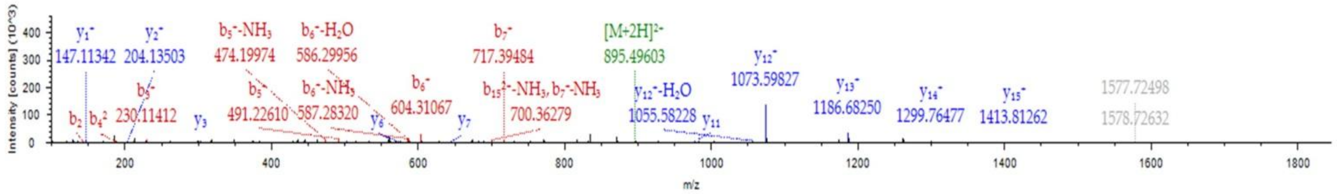


Figure S5. Relative endogenous GAPDH protein levels. GAPDH protein levels in Wild type (ZH11, MH63), SRT1 RNAi and overexpression (Ox) seedling leaves under normal growth conditions (A) and treated with or without H_2O_2 (0.1 %) during 30 min (B) were detected by immunoblots using anti-GAPDH antibody. The bands were quantified by the ImageJ program. Bars are means+/-SD from three measures of each of the two repeats.

Supplemental Data Set 1. MS spectra of 16 GAPDH1 peptides


AASFNIIPSSTGAAKAVGK

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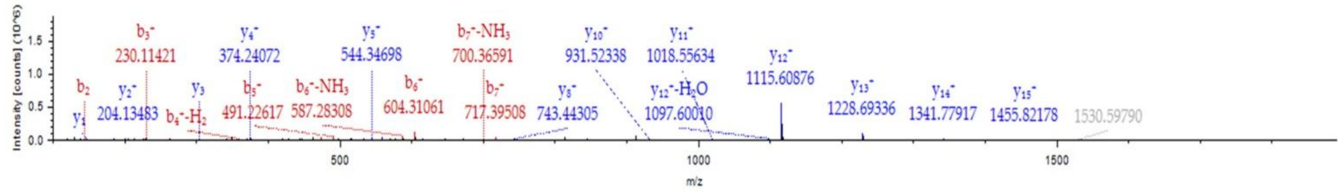
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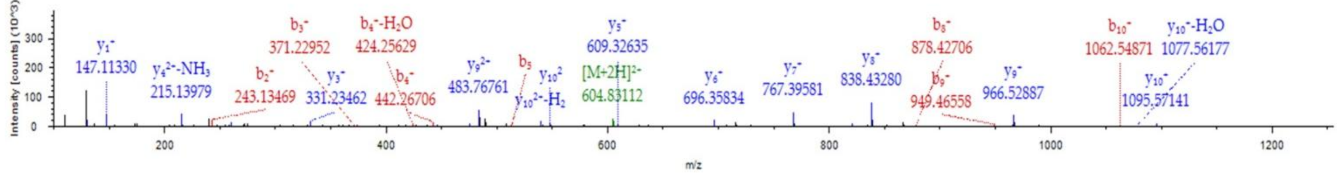
IEKAASYDAIK

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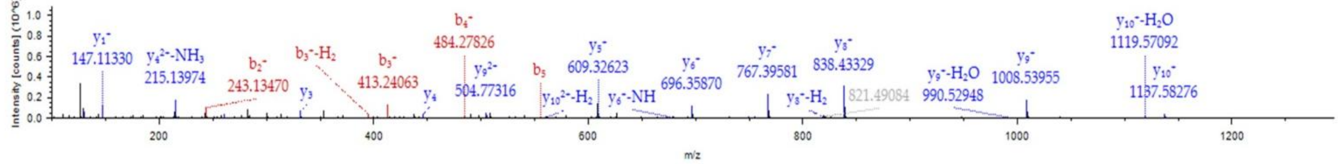
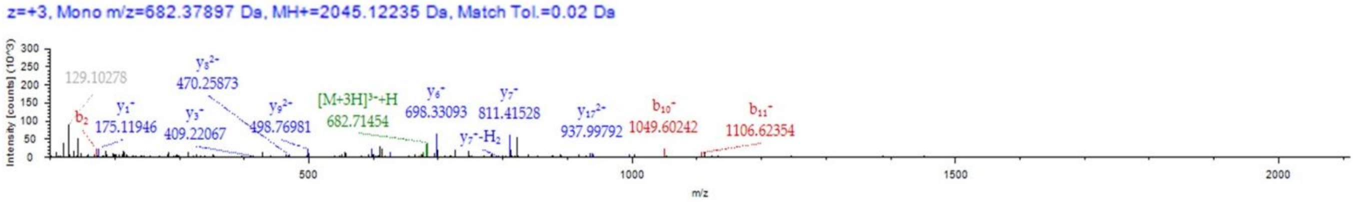

IEK(ac)AASYDAIK

z=+2, Mono m/z=625.83655 Da, MH+=1250.66582 Da, Match Tol.=0.02 Da

AVGKVLPDLNGKLTGMSFR


z=+3, Mono m/z=668.37726 Da, MH+=2003.11722 Da, Match Tol.=0.02 Da

AVGK(ac)VLPDLNGKLTGMSFR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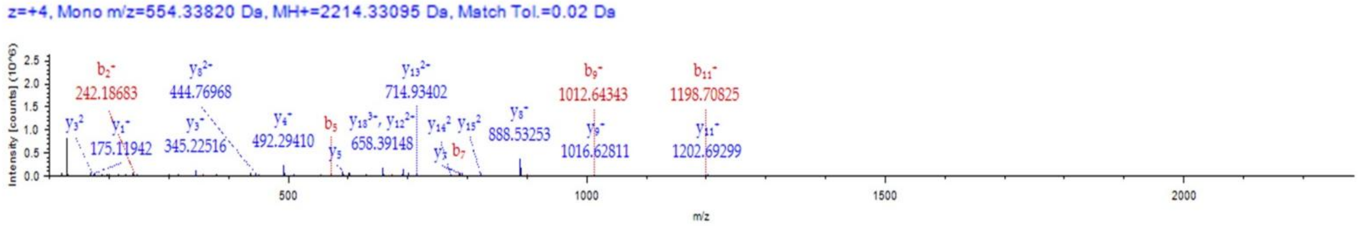
IKDSKTLLLGEKPVTVFGIR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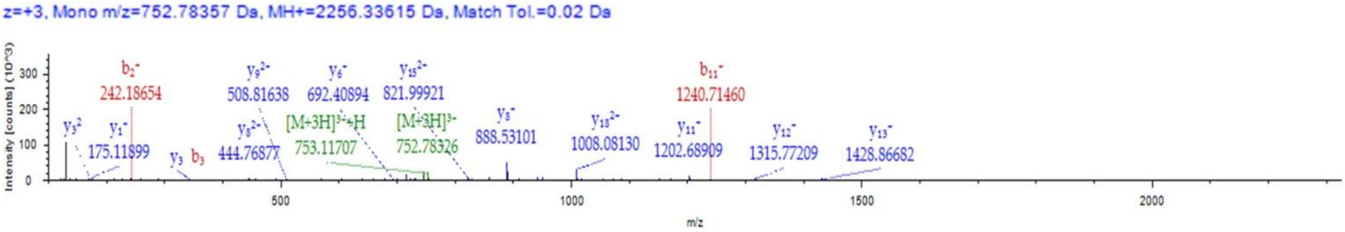
IKDSK（ac）TLLLGEKPVTVFGIR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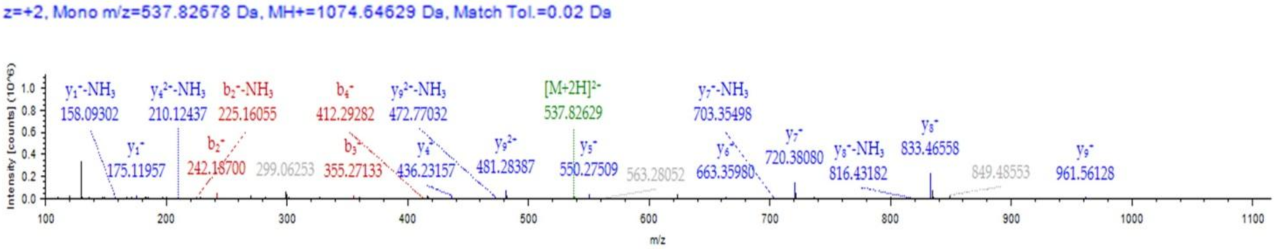
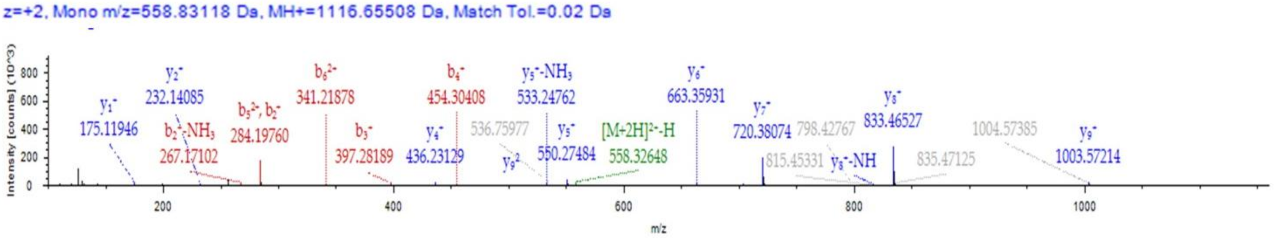
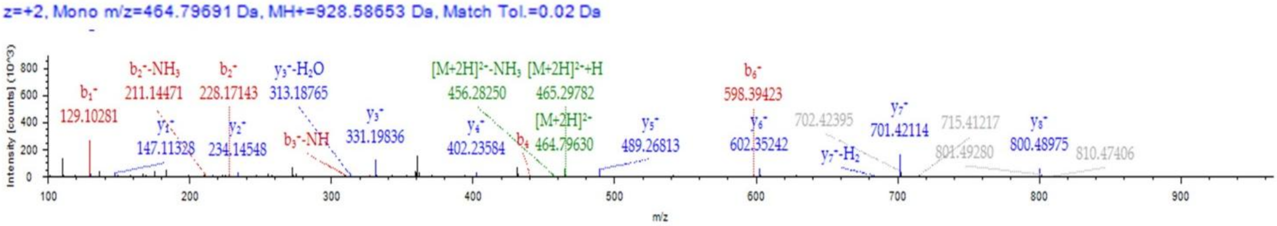
IKIGINGFGR



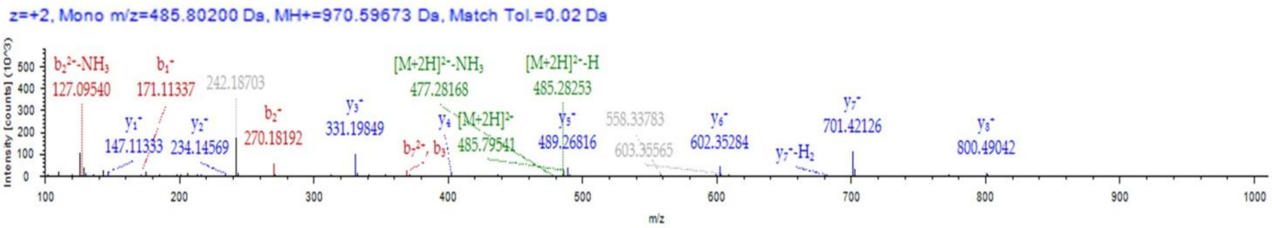
IK(ac)IGINGFGR



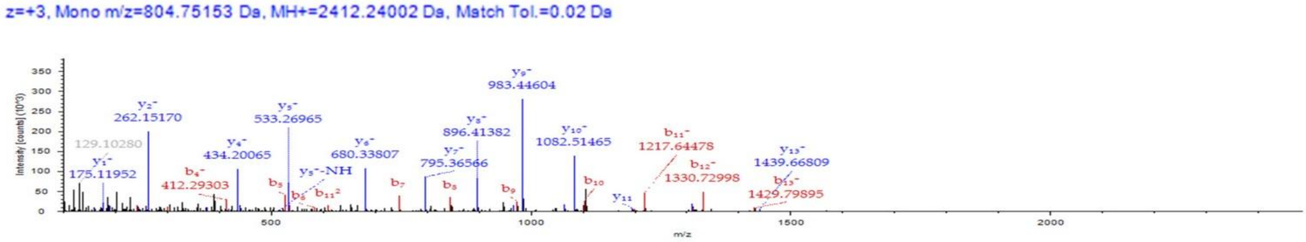
KVVISAPSK



K(ac)VVISAPSK



LKGIIGYVEEDLVSTDFVGDSR



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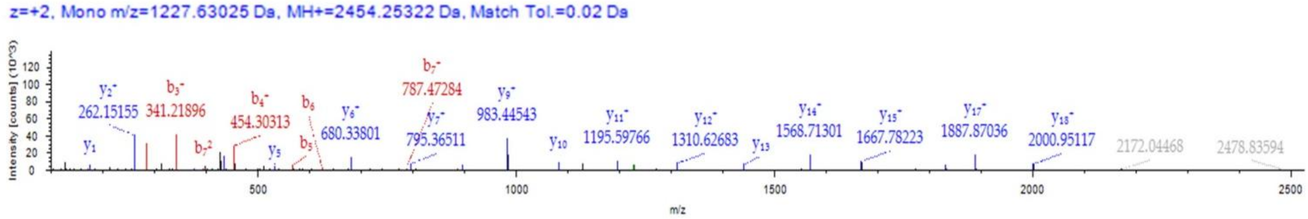
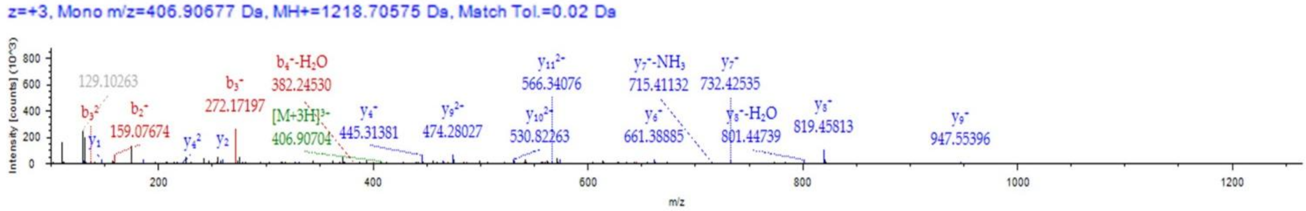


SAIKSASEGKLK



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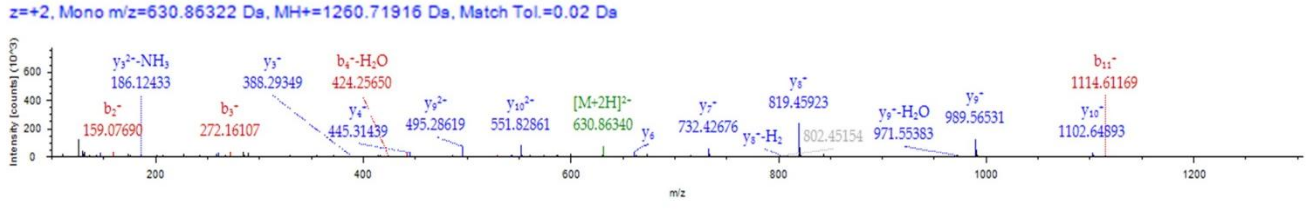

NPDEIPWAEAGAEYVVESTGVFTDKEK

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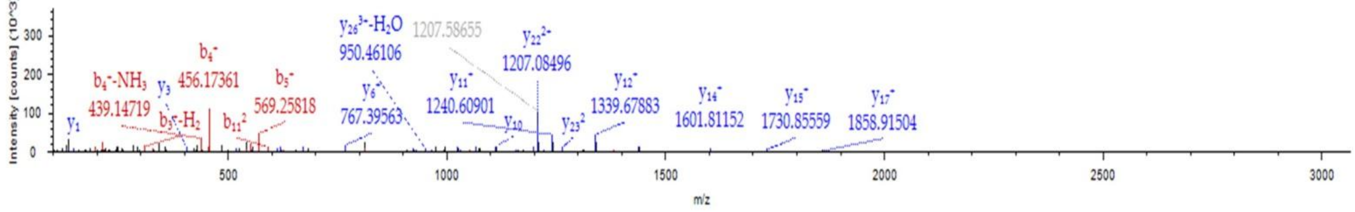

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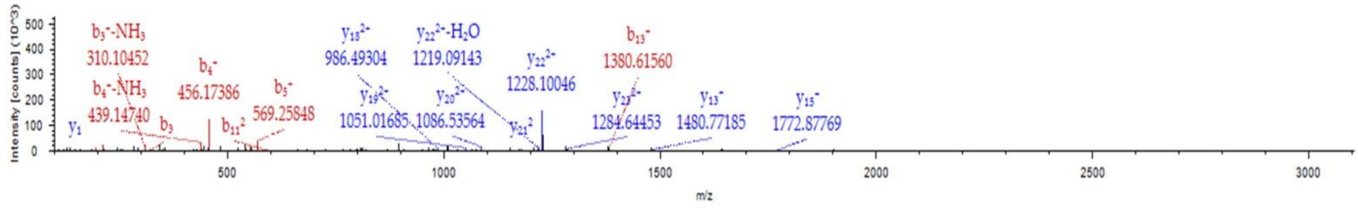

AASYDAIKSAIK

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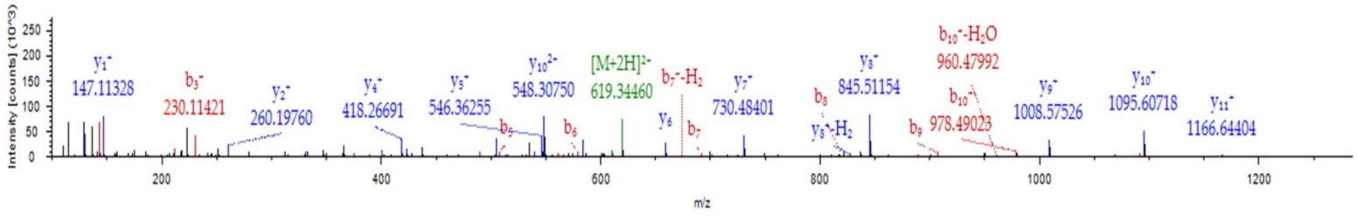

AASYDAIK（ac）SAIK

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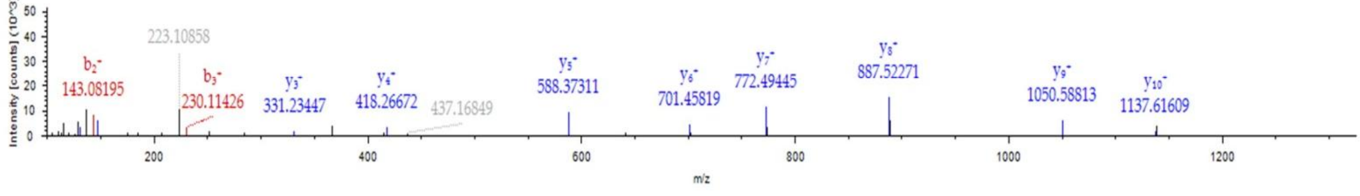

TLLLGEKPVTVFGIR

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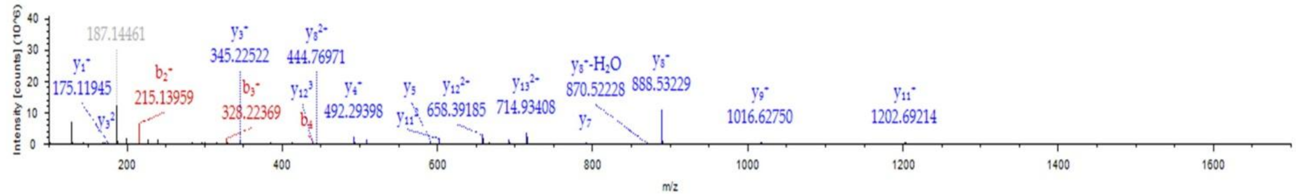

TLLLGEK(ac)PVTVFGIR

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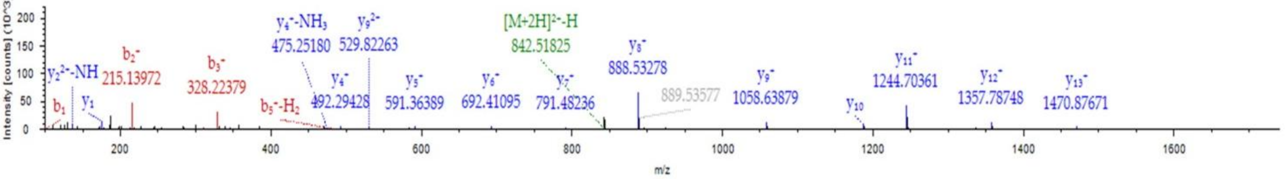

TVDGPSSKDWR

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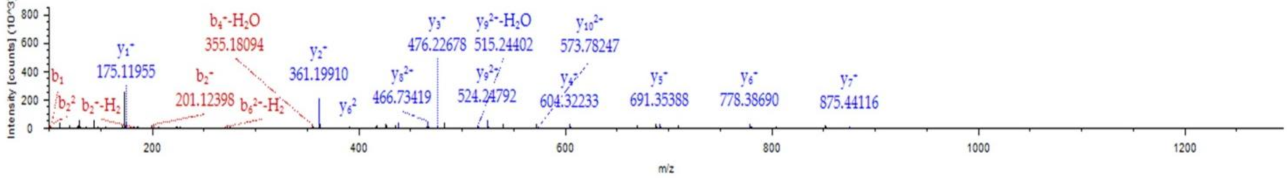

TVDGPSSK（ac）DWR

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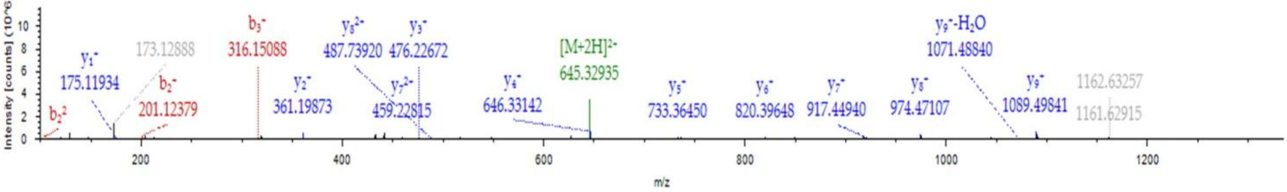

VIHDNFGIIEGLMTTVHAITATQKTVDGPSSK

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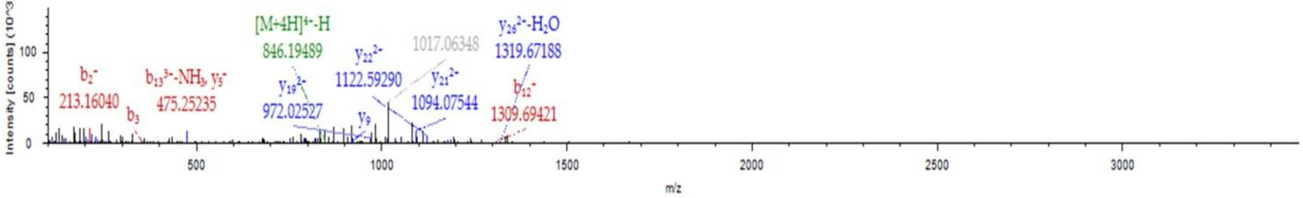
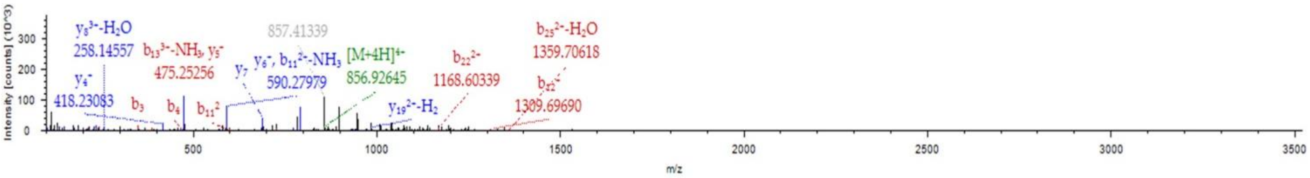


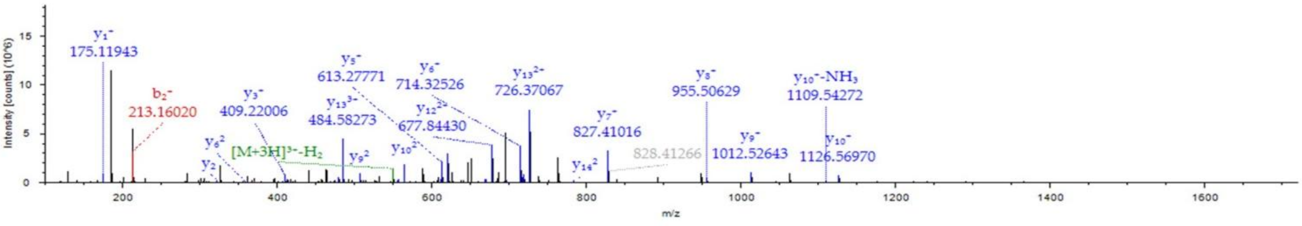
VIHDNFGIIEGLMTTVHAITATQK(ac)TVDGPSSK

z=+4, Mono m/z=856.94379 Da, MH+=3424.75332 Da, Match Tol.=0.02 Da



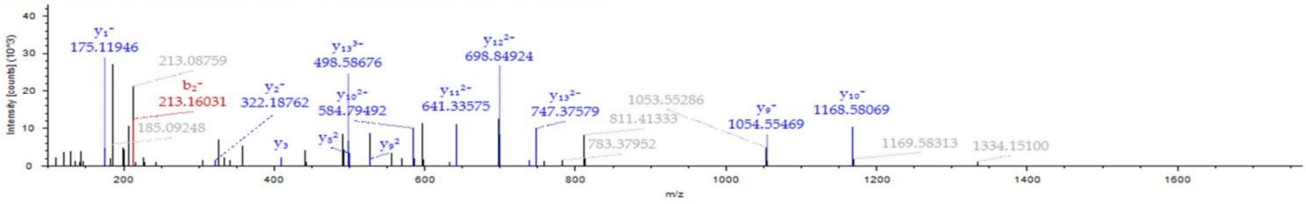
VLPDLNGKLTGMSFR

z=+3, Mono m/z=555.30176 Da, MH+=1663.89072 Da, Match Tol.=0.02 Da



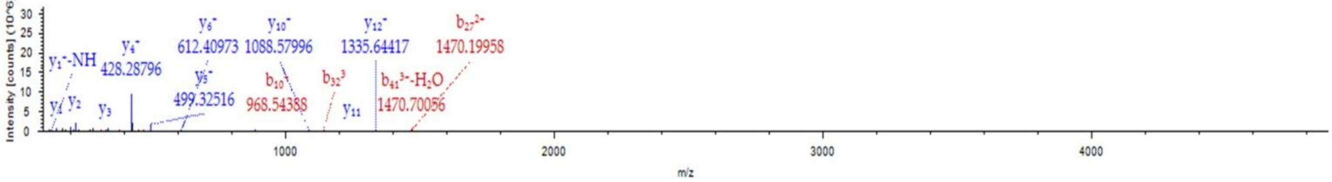
VLPDLNGK(ac)LTGMSFR

z=+3, Mono m/z=569.30463 Da, MH+=1705.89933 Da, Match Tol.=0.02 Da



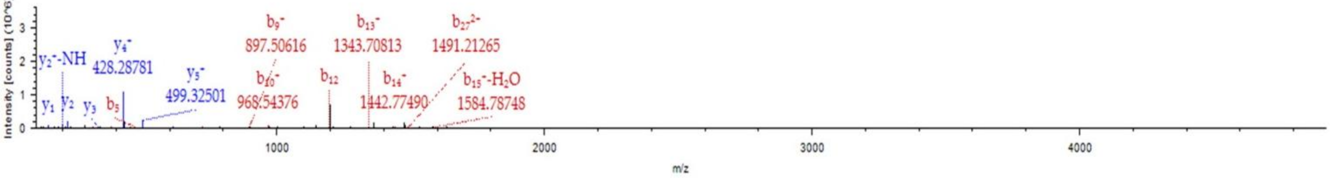
VVISAPSKDAPMFVCGVNEDKYTSDIDIVSNASCTTNCLAPLAK

z=+4, Mono m/z=1190.33044 Da, MH+=4758.29995 Da, Match Tol.=0.02 Da



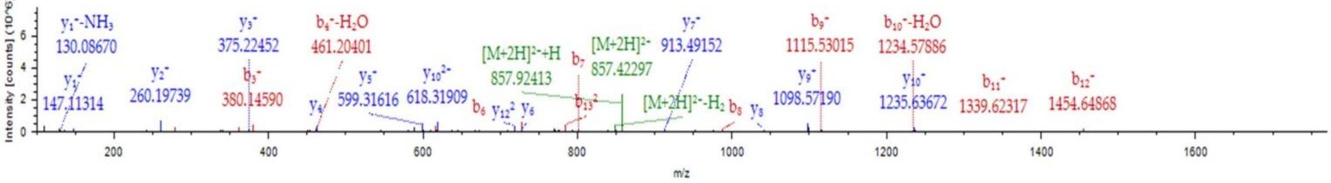
VVISAPSKDAPMFVCGVNEDK(ac)YTSDIDIVSNASCTTNCLAPLAK

z=+4, Mono m/z=1200.83789 Da, MH+=4800.32973 Da, Match Tol.=0.02 Da



YDTVHGQWKHSDIK

z=+2, Mono m/z=857.42371 Da, MH+=1713.84014 Da, Match Tol.=0.02 Da



YDTVHGQWK（ac）HSDIK

z=+3, Mono m/z=585.95520 Da, MH+=1755.85105 Da, Match Tol.=0.02 Da