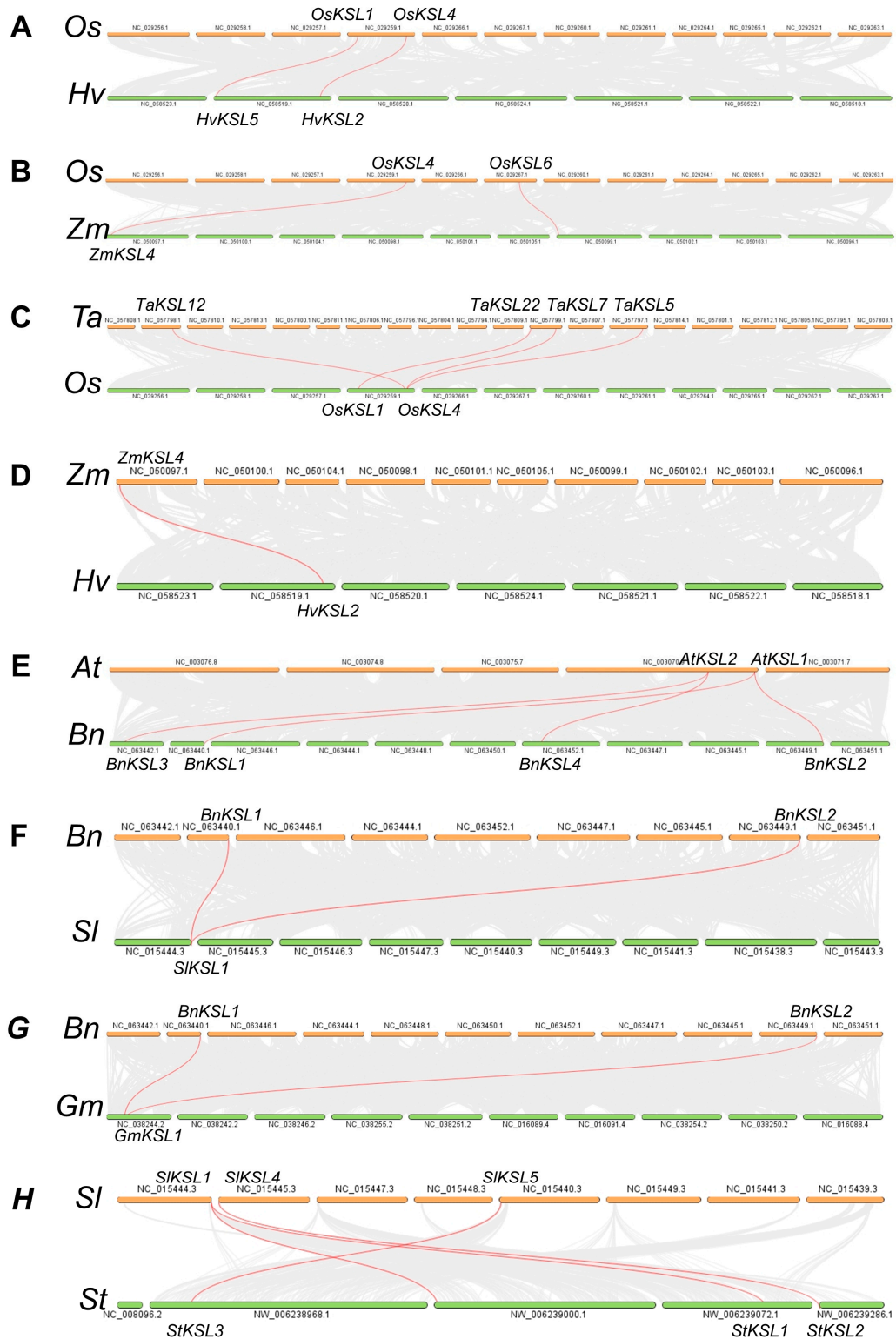


**Figure S1 Representation of the Amino Acid Residue Sequences for the Identified 15 Motifs.**

Detailed sequences of the identified motifs are depicted as they appear in Figure 2A. Analysis of motif sequences was conducted utilizing the MEME Suite (<https://meme-suite.org/meme/>).



**Figure S2 Collinearity analysis of KSLs gene across monocotyledonous and dicotyledonous species.**

(A-D) the conservation of synteny for KSL genes within selected monocotyledonous species. *Hv*, *Hordeum vulgare*; *Os*, *Oryza sativa*; *Ta*, *Triticum aestivum*; *Zm*, *Zea may*.

(E-H) the conservation of synteny for KSL genes within selected dicotyledonous species. *Sl*, *Solanum lycopersicum*; *St*, *Solanum tuberosum*; *Bn*, *Brassica napus*; *At*, *Arabidopsis thaliana*.

HvKSL5 1 M S T A K V L L P V P K S V S H H Q R N P L R L A F A H G S T E A F F P P S I R . . . . . R R F S L H S I R T R S R  
 OsKSL1 1 M A S P M E A V A R S S L V L A P R R R R A L G L L P A A A A A P F V L D C R R H N G G M R R P H V S F A C S A E L  
 TaKSL22 1 M A T P T Q A G A S F R L L Q S G P H Q S I L L A T A L S L V P K C G L Q V R . . H G T R T P R V S F V S A E Q

HvKSL5 55 K I S A . . . . . C T A Y V E S R P L G E R N V N R Q N M D R E A R I R Q L Q N P K F S P S P Y D T  
 OsKSL1 61 D T G R R Q L P S T G T R A V M S S C P G Y V E G R M V G . E N T S Q I N M G W E A R I L R H L E N P E F L P S S Y D I  
 TaKSL22 59 A F R R . . . P S T . . . . . E P P C V E A I L A G . E N I G L R N V E R D A R I R H L K K P E L S P S A Y D T

HvKSL5 101 A W V A M V P L F . . G S L Q D P C F E Q C V E W I L Q N Q H G N G Y W G S G E F D S P A S R D V L L S T L A S V I A L  
 OsKSL1 120 A W V A M V P L F G T D H L Q A P C F E Q C V E W I L Q N Q H S N G S W G V N E F D S S A S K D L L S T L A C I I A L  
 TaKSL22 107 A W V A M V P L F . D S A P Q A P C F E Q C V E W I L Q N Q H C S G Y W G I N E F G L L P N K D L L S T L A C I I A L

HvKSL5 159 K K W N V G P F E I M R G L O F T E R N F S I T M D E C T T A P I G V N L T F S S L L I L A I E M G L E L P V S H A D I  
 OsKSL1 180 E K W N V G S E O I R R G L H F T A K N F S I V I D D C I A A P I G N L F P P A M V N L A I K M G L E P P A S E I S I  
 TaKSL22 166 K K W N V G S D H I R R G L E F I G K N I S T V M D E C I V P P I G F S L I E P G M L N H A I G M G L E P P V K E N D I

HvKSL5 219 N V I V R H R E M E L E R L D A F K S S T K E V Y S S Y V A E G . L V N V I D L G E V M T F Q K N G S L F N S P S A T  
 OsKSL1 240 D Q I L H I R D M E L K R L A G D E S L G K E A Y F A Y I A R G L E E S M V D W S E V M K F Q G K N G S L F N S P A A T  
 TaKSL22 226 S C I L H I R E M E L T R L A G E K S C G K E A Y L A Y V A Q E G L V S L I D C N E V M N E Q R K N G S L F N S P A A T

HvKSL5 278 A A A L I R N Y D L G A F E Y T N L I V S E F G S A V P A M Y P L T V H Y Q L S M V D T L Q K V G I S R F S S B I N H  
 OsKSL1 300 A A A L V H R Y D D K A L G Y L S V V N K F G G E V P T V Y P L N I F S Q L S M V D T L V N I G I S R F S S B I K R  
 TaKSL22 286 A A A L V H R Y D D K A L Q Y L D S I V N I G S A V P T V Y P Q N I Y Y Q L S M V D A L K K I G I S R F S S B I N S

HvKSL5 338 I L D K K Y S L L L K R D D E I M S N V E T C A V A F R I L R M N R Y D V S S D V L S H V A E A S T L L D P P Q E Y V T  
 OsKSL1 360 I L D K K Y I L W S Q R D E E V M L D L P T C A M A F R L L R M N G Y G V S S D D L S H V A E A S T F H N S V E G Y L D  
 TaKSL22 346 I L D K K A Y I S W L Q R D D E I M L D V E T C A M A F R L L R M N G Y D V S S D E L S H V A E A S T F H S S L E G Y L N

HvKSL5 398 D T K S L L E L Y K A S K V I L S O N E L V L E K I E K W S R S L L E I M C S D M A Q R I P A V I E E V E Y A L K I P  
 OsKSL1 420 D T K S L L E L Y K A S K V S L S E N E P I L E K M G C W S G S L L E K I C S D D I R G T P . I L R E V E Y A L K F P  
 TaKSL22 406 D T K S L L E L Y K A S K V C L S E N E L I L E N I S N W S G R L L E K I C D G T D R M P . I F G E V E Y T L K F P

HvKSL5 458 F Y A T V D P L D H K W S I E H F D A M D S H M K K T K Y I I R S C C V N K D I L A L A V E D F C V S Q S I Y Q R E V E  
 OsKSL1 479 F Y A T L E P L D H K W N I E N F D A R A Y Q K I K T K N M P . . C H V N D L L A L A E D F S F C Q S T Y Q N E I Q  
 TaKSL22 465 F Y A T V E P L D H K T N I E H F D S R V F T Q L K T K N V P . . S H V N D L L D F A V E D F S F S Q S I Y Q D E L G

HvKSL5 518 H L D S W E K E C R L G E L Q F A R Q . K M K Y C Y I C A A A S I T P H E L S E A R V A C A K A T I T L T I V I D D F F D  
 OsKSL1 537 H L E S W E K E N K L D O L E P T R K . N L I N S Y I S A A A T I S P Y E L S D A R T A C A K S I A L T I V A D D F F D  
 TaKSL22 523 H I E S W E K E N R L D Q L K F L R K G T L I N C Y I S A A A T I S T H E L S D A R T T C A K T I A L V I V A D D F F D

HvKSL5 577 S C A G S P E A L A N L I S L A E K W D P H E D D H S E D V K I I F Y A L Y K T M N Q I A A A S P T Q N R D V T K  
 OsKSL1 596 V G S . S K E E Q E N L I S L V E K W D Q Y H K V E F Y S E N V K A V F F A L Y S T V N Q L G A M A S A V Q N R D V T K  
 TaKSL22 583 V G A . S K E E Q E N L I A L E K W D Q H Q V E F Y S E Q V E V V F S A F Y T V N Q I G E M A S A V Q K C D I T K

HvKSL5 637 E L V E H W L A L M R T E M T E V E W R N S K H L P S F E E Y M K V A Y V S F A L G P I V H T P M Y F L G V N F P E H V  
 OsKSL1 655 Y N V E S W L D Y L R S L A T D A E W Q R S K Y V P T M E E Y M K N S I V T F A L G P T I L I A I Y F M G Q N L W E D I  
 TaKSL22 642 H I V E H W L H Y L R S V A T E A E W Q R N Q Y V P T V E E Y M T E G A T S Y A M G P I M L T S L Y F V Q Q S L K E Y I

HvKSL5 697 L R D E E Y D E L F T I M S C C R L L N D I R G F E R E L S H G K L N S T L L V R H S G G S L S I E A K Q E I Q R  
 OsKSL1 715 V H N A E Y D E L F R L M N T C G R L N D I Q S F E R E C K D G K L N S V S L L V L D S K D V M S V E A K E A I N E  
 TaKSL22 702 I K S P E Y N E L V R L R G I C G R L N D I T R S F E R E S S D G K L N I I S L L V L H S G G S L S I E A A Q E V I Q E

HvKSL5 757 S T A S L T T D L L R L L L R E D K V V P M P C K E F F W R F N Q C H F Y T R I D C G F S P E M V G A V N A V V Y  
 OsKSL1 775 S T S C R R E L L R L V V R E D G V I P K S C K E M F W N L Y K T S H V F Y S Q A D G F S P E M M G A M G V I F  
 TaKSL22 762 S T A I C R K D L L R V V V R E D R V I P R P C K E M F W R F C R T S H L F Y S Q T D G F S P E M L H T M N A I F R

HvKSL5 817 D P L K L Q G G T V P S L S A Q L E N  
 OsKSL1 835 D P L K T R G . N . . . . .  
 TaKSL22 822 D P L K L Q T . S G S F V V Q P D K

**Figure S3 Protein sequences alignment of KSLs related to OsKSL1 in collinearity analysis.**

Residues in white characters on a red background denote fully conserved amino acids across the sequences. Red characters encased in blue boxes exhibit a high level of sequence similarity. The alignment underscores the conserved regions and similar motifs within the KSL family in relation to OsKSL1.

```

HvKSL2      .....
ZmKSL4      .....
OsKSL4      .....
TaKSL12     1  VVTFPQLVGVDPDTALLILAAFAASTFRRCPNPFCKPCKT
TaKSL5      .....
TaKSL7      1  .....MAISEQCEWQLYEVGLWLGIG.....

HvKSL2      .....
ZmKSL4      1  ....MPDVMAAALTGFSPRGVIPSRCFASLPGVARAYAERRLVAENTSIP.....
OsKSL4      1  .....MFQLELVNVVMHQKKA.....
TaKSL12     61 RDVVVERGLAVPLKDGAVDGAIALVDKIDQPLERAPALRCEAFPGSSRASVTGWGLAA
TaKSL5      1  .....MTDDVT..HAAGSGAPPTSGG...LMVSAFAKAAAS.....D
TaKSL7      22  ....WVAFILFRLGGRDVG..SUDAPQRHRSDFTSGRRRPRMCDVRGLRAVA.....P

HvKSL2      1  .....MERKARIRKQLEPELPSYDT
ZmKSL4      17  .....IEDTMKKKKQKHKFMIPSYDT
OsKSL4      121 AGSGRGVRGDSPTLTCGRVQLANVEEASAEENACLQNMEQKARIRKQLEPELPSYDT
TaKSL12     36 SSP.....VVIVLLPLGL.....QLPLSERKARIRKQLEPELPSYDT
TaKSL5      68 SSVGCGQLGCAALLLEGSETENPERGSAENTSQNMEKARIRKQLEPELPSYDT

HvKSL2      24  AAVMVPLPSSP..RVPFFPQCVRNQLNQCCNGSGWGLVCDSSVNDVHSLACVLALK
ZmKSL4      74  AAVSMVPLPSSP..OTRFFPQCVRNQLNQCCNGSGWGLVCDSSVSDVLSTLACVLALK
OsKSL4      42  AAVMVPLPSSP..RVPFFPQCVRNQLNQCCNGSGWGLVCDSSVSDVLSTLACVLALK
TaKSL12     181 AAVMVPLPSSP..QVPFFPQCVRNQLNQCCNGSGWGLVCDSSVNDVHSLACVLALK
TaKSL5      77  AAVMVPLPSSP..QVPFFPQCVRNQLNQCCNGSGWGLVCDSSVNDVHSLACVLALK
TaKSL7      128 AAVMVPLPSSP..QVPFFPQCVRNQLNQCCNGSGWGLVCDSSVNDVHSLACVLALK

HvKSL2      83  RNVVGGELIRGLRFIGRNLSTIATDEQSVADIGFNITTSQMLSGIEMGLEPFVGTIDVD
ZmKSL4      133 RNVVGGELIRGLRFIGRNLSTIATDEQSVADIGFNITTSQMLSGIEMGLEPFVGTIDVD
OsKSL4      101  ....RGLRFIGRNLSTIATDEQSVADIGFNITTSQMLSGIEMGLEPFVGTIDVD
TaKSL12     240 RNVVGGELIRGLRFIGRNLSTIATDEQSVADIGFNITTSQMLSGIEMGLEPFVGTIDVD
TaKSL5      136 RNVVGGELIRGLRFIGRNLSTIATDEQSVADIGFNITTSQMLSGIEMGLEPFVGTIDVD
TaKSL7      187 RNVVGGELIRGLRFIGRNLSTIATDEQSVADIGFNITTSQMLSGIEMGLEPFVGTIDVD

HvKSL2      143  RILHLRSELKRLVGLKSDGRAYMAFAECGNLIDWNVMSQRRKNGSLNPSSTAA
ZmKSL4      193  GILHLRSELKRLVGLKSDGRAYMAFAECGNLIDWNVMSQRRKNGSLNPSSTAA
OsKSL4      151  RVLHLRSELKREYENYRGNITMAVYSEGNGAQDWNVMSQRRKNGSLNPSSTAA
TaKSL12     300  RILHLRSELKRLVGLKSDGRAYMAFAECGNLIDWNVMSQRRKNGSLNPSSTAA
TaKSL5      196  RILHLRSELKRLVGLKSDGRAYMAFAECGNLIDWNVMSQRRKNGSLNPSSTAA
TaKSL7      247  RILHLRSELKRLVGLKSDGRAYMAFAECGNLIDWNVMSQRRKNGSLNPSSTAA

HvKSL2      203  ALIHNFDDKALQVNLIVSKFGNSVPTVPTNTYSQSLVDSLENTIGSHHSSEISLIL
ZmKSL4      253  ALIHRYNDQALQVNLIVNPEGSVAFAMPSRHHQSLNVADLRKQISQRRVSEISLIL
OsKSL4      211  ALIHRYNDQALQVNLIVNPEGSVAFAMPSRHHQSLNVADLRKQISQRRVSEISLIL
TaKSL12     360  ALIHNFDDKALQVNLIVSKFGNSVPTVPTNTYSQSLVDSLENTIGSHHSSEISLIL
TaKSL5      256  ALIHNFDDKALQVNLIVSKFGNSVPTVPTNTYSQSLVDSLENTIGSHHSSEISLIL
TaKSL7      307  ALIHNFDDKALQVNLIVSKFGNSVPTVPTNTYSQSLVDSLENTIGSHHSSEISLIL

HvKSL2      263  DVAVSFWLQDEEEMLDVAACAMAFRLRMNGYDVSSDGLVVD..ETTFNHSRQGYLNDT
ZmKSL4      313  DVAVSFWLQDEEEMLDVAACAMAFRLRMNGYDVSSDGLVVD..ETTFNHSRQGYLNDT
OsKSL4      268  DVAVSFWLQDEEEMLDVAACAMAFRLRMNGYDVSSDGLVVD..ETTFNHSRQGYLNDT
TaKSL12     420  DVAVSFWLQDEEEMLDVAACAMAFRLRMNGYDVSSDGLVVD..ETTFNHSRQGYLNDT
TaKSL5      316  DVAVSFWLQDEEEMLDVAACAMAFRLRMNGYDVSSDGLVVD..ETTFNHSRQGYLNDT
TaKSL7      367  DVAVSFWLQDEEEMLDVAACAMAFRLRMNGYDVSSDGLVVD..ETTFNHSRQGYLNDT

HvKSL2      322  KSLIELYRSELVSVSNELCHDNLGDTSGKLLTEKLFSQDWQ..LTFHDCQVHAKEBFLY
ZmKSL4      373  KSLIELYRSELVSVSNELCHDNLGDTSGKLLTEKLFSQDWQ..LTFHDCQVHAKEBFLY
OsKSL4      328  RILIELYRSELVSVSNELCHDNLGDTSGKLLTEKLFSQDWQ..LTFHDCQVHAKEBFLY
TaKSL12     479  KSLIELYRSELVSVSNELCHDNLGDTSGKLLTEKLFSQDWQ..LTFHDCQVHAKEBFLY
TaKSL5      376  KSLIELYRSELVSVSNELCHDNLGDTSGKLLTEKLFSQDWQ..LTFHDCQVHAKEBFLY
TaKSL7      426  KSLIELYRSELVSVSNELCHDNLGDTSGKLLTEKLFSQDWQ..LTFHDCQVHAKEBFLY

HvKSL2      381  AEMEREGSKRNIEHFQVCGSQ..MKKTEHLPCHVNDQFLALAVEEMFSOSIQDSILHLE
ZmKSL4      432  AEMEREGSKRNIEHFQVCGSQ..MKKTEHLPCHVNDQFLALAVEEMFSOSIQDSILHLE
OsKSL4      388  AEMEREGSKRNIEHFQVCGSQ..MKKTEHLPCHVNDQFLALAVEEMFSOSIQDSILHLE
TaKSL12     538  AEMEREGSKRNIEHFQVCGSQ..MKKTEHLPCHVNDQFLALAVEEMFSOSIQDSILHLE
TaKSL5      434  AEMEREGSKRNIEHFQVCGSQ..MKKTEHLPCHVNDQFLALAVEEMFSOSIQDSILHLE
TaKSL7      485  AEMEREGSKRNIEHFQVCGSQ..MKKTEHLPCHVNDQFLALAVEEMFSOSIQDSILHLE

HvKSL2      440  SWANRNRQDLRFARQKLTVGYIAAATTFPEHSDARMSKNGVLTIVVDDFFDVGGSS
ZmKSL4      491  SWANRNRQDLRFARQKLTVGYIAAATTFPEHSDARMSKNGVLTIVVDDFFDVGGSS
OsKSL4      448  SWANRNRQDLRFARQKLSGYIAAATTFPEHSDARMSKNGVLTIVVDDFFDVGGSS
TaKSL12     596  SWANRNRQDLRFARQKLSGYIAAATTFPEHSDARMSKNGVLTIVVDDFFDVGGSS
TaKSL5      493  SWANRNRQDLRFARQKLSGYIAAATTFPEHSDARMSKNGVLTIVVDDFFDVGGSS
TaKSL7      544  SWANRNRQDLRFARQKLSGYIAAATTFPEHSDARMSKNGVLTIVVDDFFDVGGSS

HvKSL2      500  KSEHENDLALVERNDDBSKDEFYSEQVRLHCAIYITVNNLAAVASAQSRDQKHLEL
ZmKSL4      551  KSEHENDLALVERNDDBSKDEFYSEQVRLHCAIYITVNNLAAVASAQSRDQKHLEL
OsKSL4      508  KSEHENDLALVERNDDBSKDEFYSEQVRLHCAIYITVNNLAAVASAQSRDQKHLEL
TaKSL12     656  KSEHENDLALVERNDDBSKDEFYSEQVRLHCAIYITVNNLAAVASAQSRDQKHLEL
TaKSL5      553  KSEHENDLALVERNDDBSKDEFYSEQVRLHCAIYITVNNLAAVASAQSRDQKHLEL
TaKSL7      604  KSEHENDLALVERNDDBSKDEFYSEQVRLHCAIYITVNNLAAVASAQSRDQKHLEL

HvKSL2      560  WIDLRSMMSEBEMRQVPTTBOYMSNAVVSFLGPFVLTSLYFIPKISDCVNNDSB
ZmKSL4      611  WIDLRSMMSEBEMRQVPTTBOYMSNAVVSFLGPFVLTSLYFIPKISDCVNNDSB
OsKSL4      568  WIDLRSMMSEBEMRQVPTTBOYMSNAVVSFLGPFVLTSLYFIPKISDCVNNDSB
TaKSL12     716  WIDLRSMMSEBEMRQVPTTBOYMSNAVVSFLGPFVLTSLYFIPKISDCVNNDSB
TaKSL5      613  WIDLRSMMSEBEMRQVPTTBOYMSNAVVSFLGPFVLTSLYFIPKISDCVNNDSB
TaKSL7      664  WIDLRSMMSEBEMRQVPTTBOYMSNAVVSFLGPFVLTSLYFIPKISDCVNNDSB

HvKSL2      620  VNELFRLSTIGRLNDIRGLERESRFGNDIYSLLVHSGGSGSEBARETIKRAASFC
ZmKSL4      671  VNELFRLSTIGRLNDIRGLERESRFGNDIYSLLVHSGGSGSEBARETIKRAASFC
OsKSL4      628  VNELFRLSTIGRLNDIRGLERESRFGNDIYSLLVHSGGSGSEBARETIKRAASFC
TaKSL12     776  VNELFRLSTIGRLNDIRGLERESRFGNDIYSLLVHSGGSGSEBARETIKRAASFC
TaKSL5      673  VNELFRLSTIGRLNDIRGLERESRFGNDIYSLLVHSGGSGSEBARETIKRAASFC
TaKSL7      724  VNELFRLSTIGRLNDIRGLERESRFGNDIYSLLVHSGGSGSEBARETIKRAASFC

HvKSL2      680  RGLLRLVLENTVVPFPCKELFWKMKKTVHLFYSCDGGSPSPMEMVSAVAVISEPLIL
ZmKSL4      731  RGLLRLVLENTVVPFPCKELFWKMKKTVHLFYSCDGGSPSPMEMVSAVAVISEPLIL
OsKSL4      688  RGLLRLVLENTVVPFPCKELFWKMKKTVHLFYSCDGGSPSPMEMVSAVAVISEPLIL
TaKSL12     836  RGLLRLVLENTVVPFPCKELFWKMKKTVHLFYSCDGGSPSPMEMVSAVAVISEPLIL
TaKSL5      733  RGLLRLVLENTVVPFPCKELFWKMKKTVHLFYSCDGGSPSPMEMVSAVAVISEPLIL
TaKSL7      784  RGLLRLVLENTVVPFPCKELFWKMKKTVHLFYSCDGGSPSPMEMVSAVAVISEPLIL

HvKSL2      740  QTSQPSVPVQSEK.....
ZmKSL4      791  QNSTFLSSSSR.....
OsKSL4      748  AAVVASQEPYIIIPAS.....
TaKSL12     896  GINNPLPLVQSEN.....
TaKSL5      793  QIRNFPSPAMQSEKLRYSNQVLS
TaKSL7      844  QIRNFPSPAMQSEKLRYSNQVLS

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**Figure S4 Protein sequences alignment of KSLs related to OsKSL4 in collinearity analysis.**

Residues depicted in white text on a red background denote identical amino acids across the aligned sequences. Those highlighted by red text within a blue box signify conserved residues exhibiting high similarity.







|        |     |  |
|--------|-----|--|
| AtKSL2 | 1   | MSSSYGSSNDLHAFVNEIKGEIQLSNINLDPYSFVSPSAYDTAWLSMIEEDINVDDN..    |
| BnKSL3 | 1   | MKFPYGSNDLHALVNIKSIIQLSTINFDPYSFVSPSAYDMAWLAHVEEDHNVDHDD       |
| BnKSL4 | 1   | MKFPYGSNDLHALVNIKSIIQLSTINFDPYSFVSPSAYDMAWLAHVEEDHNVDHDD..     |
|        |     |  |
| AtKSL2 | 59  | ELKPMFQGGCLDWIMCNQNAREGFWMNSTSYTVAAGRDEGEKDMCLTSTLACVVAIQ      |
| BnKSL3 | 61  | DELKPMFQDCLDWILCNQNAREGYWNGSGCPTFVSSEAGED..RDDMYTLTSTLACVLVH   |
| BnKSL4 | 59  | DELKPMFQDCLDWILCNQNAREGYWNGSGCPTFVSSEAGED..RDDMYTLTSTLACVLAH   |
|        |     |  |
| AtKSL2 | 118 | KWNICGFHLHKCTRYIERNTETIIKTYINEEGSYPRWFAIKFTGILELAQKGLHVFVSS    |
| BnKSL3 | 119 | KWNICGFHLHKCKRYIERRTETIIEKYNNEEGSYPRWFIKFTGILELAQQLDHLVFVSS    |
| BnKSL4 | 117 | KWNICGFHLHKCKRYVERRTETIIEKYNNEEGSYPRWFIKFTGILELAQQLDHLVFVSS    |
|        |     |  |
| AtKSL2 | 178 | RCTEMIKGMFYQROEITQREKLVHDCNHYKPLLAYLEVLPSELYVTNQEDTIIVKSLDSMDG |
| BnKSL3 | 179 | RCTQMIKEVIFYQROEITLREKLLDDCNHIFPLLAYLEVLPSELYVENHEDMIVKSLDNIDG |
| BnKSL4 | 177 | RCTQMIKEVIFYQROEITLREKLLDDCNHIFPLLAYLEVLPSELYVENHEDMIVKSLDNIDG |
|        |     |  |
| AtKSL2 | 238 | SLFQSPSATASAFMTTRNTKCLAYLRNLYVQKCPNGVPQKYPLNEELIKLSMVNLTIESGL  |
| BnKSL3 | 239 | SLFQSPSATASAFMTTRNAKCLAYLRNATQRCPNGVPQKYPLNEELIKLSMVNVNLTENIGL |
| BnKSL4 | 237 | SLFQSPSATASAFMTTRNAKCLAYLRNVVQRCPNGVPQKYPLNEELIKLSMVNVNLTENIGL |
|        |     |  |
| AtKSL2 | 298 | GEFFGDIIEHVLEQVYSRYEENKDFERMPMSYLADQLHKDSLAFRMLRMHGRDVSPRSFCW  |
| BnKSL3 | 299 | GEFFGSDIEHVLEQVYSRYEENIERMPMSYLADKLHKDSLAFRMLRMHGRHTVSPRSFCW   |
| BnKSL4 | 297 | GEFFGSDIEHVLEQVYSRYEENIERMPMSYLADKLHKDSLAFRMLRMHGRHTVSPRSFCW   |
|        |     |  |
| AtKSL2 | 358 | FLNDQETRNHLERNIDSLFLVILSVYRATDLMFPGBEHLQEAAREYTRNLLSKRSTKEKX   |
| BnKSL3 | 359 | FLNDQETRNHLERNIDSLFLVILSVNRATDLMFPGBEHLQEAAREYTRNLLSQSRSIDERM  |
| BnKSL4 | 357 | FLNDQETRNHLERNIDSLFLVILSVNRATDLMFPGBEHLQEAAREYTRNLLSQSRSIDERM  |
|        |     |  |
| AtKSL2 | 418 | IMHELSTPWIARLKHLDHRMWIEDKNSNVLSMKASFLRLHSSYSYDKLTHLAARNEFFQO   |
| BnKSL3 | 419 | IKHELSTPWIARLKHLDHRMWIEDKNSNVLSAKASFLRLHNRNRYINKLTYLATRNFLFRQ  |
| BnKSL4 | 417 | IKHELSTPWIARLKHLDHRMWIEDKNSNVLSVKASFLRLHNRNINIKLTYLATRNFLFRQ   |
|        |     |  |
| AtKSL2 | 478 | AKYCRELEELTMWVKKWGLSDIFGFGREKTTYCYFATVTSLPYEYAIRKGLAKTAILIT    |
| BnKSL3 | 479 | AMMRSLEELTIWVRKWGLNDIFGFGREKTTYCYFATATSLPFESAIRKVGKLTAKTAILIT  |
| BnKSL4 | 477 | AMMRRLEELTIWVRKWGLNDIFGFGREKTTYCYFATATSLPEESAIRKVGKLTAKTAILIT  |
|        |     |  |
| AtKSL2 | 538 | IADDFDEKGSFNDLEGLTKAVLRWEGEELKSYGNIFRALDDIVRETANTCRTHHKTQDI    |
| BnKSL3 | 539 | VADDFDEEGSLDDLEALTKAVLRWEGEELGYGKIFRALDEIVRETTEACRKQHGTDI      |
| BnKSL4 | 537 | VADDFDEEGSLDDLEALTKAVLRWEGEELGYGKIFRALDEIVRETTEACRKQHGTDI      |
|        |     |  |
| AtKSL2 | 598 | IVHLRNIWGETFESWLREAEWSKKGHTSMDEYIRNGMISIAAHTIALSISCLMEPCFFH    |
| BnKSL3 | 599 | TVQLRNIWGETFESWLREAEVWSKKGHIPSMEEYLHSGMISIAAHTMALSVSCLMEPCFFQ  |
| BnKSL4 | 597 | TVQLRNIWGETFESWLREAEVWSKKGHIPSMEEYLHSGMISIAAHTMALSVSCLMEPCFFQ  |
|        |     |  |
| AtKSL2 | 658 | NKIKPCNYDSITTLIMIIIPRLNLDLSYQREOEQGGKMNSVLLHMKNNHPGLEIEDSIAHIE |
| BnKSL3 | 659 | QKINPCNYDTLTISLMIIIPRLNLDLSYQREOEQGGKINSVLLHMRNTSGLDIENSIAHIE  |
| BnKSL4 | 657 | QKINPCNYDTLTISLMIIIPRLNLDLSYQREOEQGGKINSVLLHMRNTSGLDIENSIAHIE  |
|        |     |  |
| AtKSL2 | 718 | KIIDSKRKEFLEHVLVDGLSDLPKPCKEIHMSCCKVFEFFFNKKNRYDSNTEMLHDIKKA   |
| BnKSL3 | 719 | KIIDSNRKEFLKHVLMGGLSDLPKPCKEIHMSCCKVFEFFFNKKNRYDSNTEMLQDIKKA   |
| BnKSL4 | 717 | KIIDSNRKEFLEHVLMDGLSDLPKPCKEIHMSCCQVFEFFFNKKNRYDSNTEMLQDIKKA   |
|        |     |  |
| AtKSL2 | 778 | LYDPINVYETSEMEMPFLMAHGDEYMTLPPLLNSLPNILEFKRKDDGYGAMKTSMCFGRSY  |
| BnKSL3 | 779 | FYDPVNVNSETIEPEKPLMVHGDEFMLPLLLNLSLPKILEFKRKDEHCAVKTSMCLRRSF   |
| BnKSL4 | 777 | FYDPVNVNSETIEPEKPCMVHGDEFMLPLLLNLSLPKILEFKRKDEYRAIKTFMCLGRIS   |
|        |     |  |
| AtKSL2 | 838 | RVNKRVMASQLDDQHKPLKIVASORKPVPMMQSIIFAPCFY                      |
| BnKSL3 | 839 | HAQKRAIS.....LQPLKIVASOSIVVPMMPTKIFAPCFY                       |
| BnKSL4 | 837 | HAQKRGIA.....LQPLKIVASOSIVVPMMPTKIFAPCFY                       |

Figure S7 Protein sequences alignment of KSLs related to AtKSL2 pair in collinearity analysis.



AtKSL1 1 .....MSINLRSS..GCSPI~~SAT~~LERRLD  
 BnKSL1 1 .....MSISSSTN..LRRSPI~~SAT~~LERRLD  
 BnKSL2 1 .....MSISSSTN..LRRSPI~~SAT~~LERRLD  
 GmKSL1 1 MHFTLLHTYTCFHFVGNCSNTIFFHSLD...DAMSLSHLTTPLCCTST~~SS~~SLITASC  
 SlKSL1 1 MSATTIFPAASSSSSYLSVVKHQITRDINTLTANT~~TP~~ERRLDGGLSFTQ~~SH~~STACVVD  
 StKSL1 1 MSATFIFPAASSSSSYLSVVKHQITRDINTLTANT~~TP~~ERRLDGGLSFTQ~~SH~~STACVVD

AtKSL1 24 SEVQTRANNVSP~~Q~~TK~~IR~~KMLEKVE~~LS~~VSA~~YD~~TS~~WV~~AM~~W~~PS~~SS~~QNA~~P~~FP~~QC~~LN~~W~~LD  
 BnKSL1 24 AVEHTRANNVSP~~Q~~TK~~IR~~KMLEKVE~~LS~~VSA~~YD~~TS~~WV~~AM~~W~~PS~~SS~~QNA~~P~~FP~~QC~~LN~~W~~LD  
 BnKSL2 24 AVEHTRANNVSP~~Q~~TK~~IR~~KMLEKVE~~LS~~VSA~~YD~~TS~~WV~~AM~~W~~PS~~SS~~QNA~~P~~FP~~QC~~LN~~W~~LD  
 GmKSL1 57 VKKMNSTALCH~~EA~~K~~IR~~KLFNKVE~~LS~~VSA~~YD~~TS~~WV~~AM~~W~~PS~~SS~~PH~~TP~~FP~~QC~~LN~~W~~LD  
 SlKSL1 55 ATRGPDFALQCN~~EA~~K~~IR~~KLFNKVE~~LS~~VSA~~YD~~TS~~WV~~AM~~W~~PS~~SS~~PH~~TP~~FP~~QC~~LN~~W~~LD  
 StKSL1 61 ATRVDFALQCN~~EA~~K~~IR~~KLFNKVE~~LS~~VSA~~YD~~TS~~WV~~AM~~W~~PS~~SS~~PH~~TP~~FP~~QC~~LN~~W~~LD

AtKSL1 84 DNQ~~ED~~GSWGLDNH~~DH~~Q~~SL~~KK~~DL~~SL~~AS~~TL~~AL~~KK~~RG~~IG~~ER~~Q~~IN~~RG~~IF~~EL~~NS~~AL~~VT~~LD  
 BnKSL1 84 DNQ~~ED~~GSWGLD...H~~PS~~KK~~DL~~SL~~AS~~TL~~AL~~KK~~RG~~IG~~ER~~Q~~IN~~RG~~IF~~EL~~NS~~AL~~VT~~LD  
 BnKSL2 84 DNQ~~ED~~GSWGLD...H~~PS~~KK~~DL~~SL~~AS~~TL~~AL~~KK~~RG~~IG~~ER~~Q~~IN~~RG~~IF~~EL~~NS~~AL~~VT~~LD  
 GmKSL1 117 YNQL~~ED~~GSWGLPDR~~HF~~LL~~MD~~DL~~SL~~AS~~TL~~AL~~KK~~RG~~IG~~ER~~Q~~IN~~RG~~IF~~EL~~NS~~AL~~VT~~LD~~  
 SlKSL1 115 HNQL~~ED~~GSWGLPHH~~Q~~PL~~LL~~KK~~DL~~SL~~AS~~TL~~AL~~KK~~RG~~IG~~ER~~Q~~IN~~RG~~IF~~EL~~NS~~AL~~VT~~LD  
 StKSL1 121 HNQL~~ED~~GSWGLPHH~~Q~~PL~~LL~~KK~~DL~~SL~~AS~~TL~~AL~~KK~~RG~~IG~~ER~~Q~~IN~~RG~~IF~~EL~~NS~~AL~~VT~~LD

AtKSL1 144 ETIQ~~ED~~GS~~GL~~DI~~FP~~PM~~IE~~YARD~~NL~~VE~~LG~~SE~~V~~DD~~MI~~TK~~RR~~DD~~DC~~KDSEK~~FG~~RE~~AY~~LD  
 BnKSL1 141 ETIEK~~PA~~G~~FI~~FP~~PM~~IEYARD~~NL~~VE~~LG~~SE~~V~~DD~~MI~~TK~~RR~~DD~~DC~~KDSEK~~FG~~RE~~AY~~LD  
 BnKSL2 141 ETIEK~~PA~~G~~FI~~FP~~PM~~IEYARD~~NL~~VE~~LG~~SE~~V~~DD~~MI~~TK~~RR~~DD~~DC~~KDSEK~~FG~~RE~~AY~~LD  
 GmKSL1 176 ENQHP~~ED~~GS~~GL~~DI~~FP~~PM~~IE~~YARD~~NL~~VE~~LG~~SE~~V~~DD~~MI~~TK~~RR~~DD~~DC~~KDSEK~~FG~~RE~~AY~~LD  
 SlKSL1 174 EDOYSP~~GF~~DI~~FP~~PM~~IE~~YARD~~NL~~VE~~LG~~SE~~V~~DD~~MI~~TK~~RR~~DD~~DC~~KDSEK~~FG~~RE~~AY~~LD  
 StKSL1 180 KDOYSP~~GF~~DI~~FP~~PM~~IE~~YARD~~NL~~VE~~LG~~SE~~V~~DD~~MI~~TK~~RR~~DD~~DC~~KDSEK~~FG~~RE~~AY~~LD

AtKSL1 204 AYV~~LE~~GR~~NR~~LK~~DW~~DL~~IV~~Y~~OR~~KNGSL~~FD~~SP~~AT~~TAA~~AF~~TQ~~FN~~DC~~CH~~RY~~LS~~QL~~OR~~EA~~AV~~  
 BnKSL1 197 AYV~~LE~~GR~~NR~~LK~~DW~~DL~~IV~~Y~~OR~~KNGSL~~FD~~SP~~AT~~TAA~~AF~~TQ~~FN~~DC~~CH~~RY~~LS~~QL~~OR~~EA~~AV~~  
 BnKSL2 199 VYV~~LE~~GR~~NR~~LK~~DW~~DL~~IV~~Y~~OR~~KNGSL~~FD~~SP~~AT~~TAA~~AF~~TQ~~FN~~DC~~CH~~RY~~LS~~QL~~OR~~EA~~AV~~  
 GmKSL1 236 AYV~~LE~~GR~~NR~~LK~~DW~~DL~~IV~~Y~~OR~~KNGSL~~FD~~SP~~AT~~TAA~~AF~~TQ~~FN~~DC~~CH~~RY~~LS~~QL~~OR~~EA~~AV~~  
 SlKSL1 234 AYV~~LE~~GR~~NR~~LK~~DW~~DL~~IV~~Y~~OR~~KNGSL~~FD~~SP~~AT~~TAA~~AF~~TQ~~FN~~DC~~CH~~RY~~LS~~QL~~OR~~EA~~AV~~  
 StKSL1 240 AYV~~LE~~GR~~NR~~LK~~DW~~DL~~IV~~Y~~OR~~KNGSL~~FD~~SP~~AT~~TAA~~AF~~TQ~~FN~~DC~~CH~~RY~~LS~~QL~~OR~~EA~~AV~~

AtKSL1 264 SVV~~YF~~DOY~~AR~~SV~~ID~~HL~~ES~~LG~~DR~~DR~~KE~~IR~~TV~~DE~~YR~~GW~~LR~~GE~~BE~~IR~~LD~~LA~~TC~~AL~~AF~~  
 BnKSL1 257 PTVV~~YF~~DOY~~AR~~SV~~ID~~HL~~ES~~LG~~DR~~DR~~KE~~IR~~TV~~DE~~YR~~GW~~LR~~GE~~BE~~IR~~LD~~LA~~TC~~AL~~AF~~  
 BnKSL2 259 PTVV~~YF~~DOY~~AR~~SV~~ID~~HL~~ES~~LG~~DR~~DR~~KE~~IR~~TV~~DE~~YR~~GW~~LR~~GE~~BE~~IR~~LD~~LA~~TC~~AL~~AF~~  
 GmKSL1 296 PTIV~~YF~~DOY~~AR~~SV~~ID~~HL~~ES~~LG~~DR~~DR~~KE~~IR~~TV~~DE~~YR~~GW~~LR~~GE~~BE~~IR~~LD~~LA~~TC~~AL~~AF~~  
 SlKSL1 294 PTIV~~YF~~DOY~~AR~~SV~~ID~~HL~~ES~~LG~~DR~~DR~~KE~~IR~~TV~~DE~~YR~~GW~~LR~~GE~~BE~~IR~~LD~~LA~~TC~~AL~~AF~~  
 StKSL1 300 PTIV~~YF~~DOY~~AR~~SV~~ID~~HL~~ES~~LG~~DR~~DR~~KE~~IR~~TV~~DE~~YR~~GW~~LR~~GE~~BE~~IR~~LD~~LA~~TC~~AL~~AF~~

AtKSL1 324 RL~~LL~~LAH~~GY~~D~~VS~~Y~~DP~~K~~PF~~AE~~SG~~FS~~DT~~LE~~GY~~KN~~TF~~SV~~LR~~EL~~FK~~AA~~QS~~..YP~~HE~~SA~~LR~~K~~QC~~  
 BnKSL1 317 RL~~LL~~LAH~~GY~~D~~VS~~Y~~DP~~K~~PF~~AE~~SG~~FS~~DT~~LE~~GY~~KN~~TF~~SV~~LR~~EL~~FK~~AA~~QS~~..YP~~HE~~SA~~LR~~K~~QC~~  
 BnKSL2 319 RL~~LL~~LAH~~GY~~D~~VS~~Y~~DP~~K~~PF~~AE~~SG~~FS~~DT~~LE~~GY~~KN~~TF~~SV~~LR~~EL~~FK~~AA~~QS~~..YP~~HE~~SA~~LR~~K~~QC~~  
 GmKSL1 356 RML~~RL~~NG~~YD~~V~~SS~~DP~~YQ~~YS~~DK~~FA~~ES~~SL~~KY~~UK~~DV~~GA~~VL~~LY~~RA~~SA~~QI~~IH~~DE~~SL~~VR~~OS  
 SlKSL1 354 RL~~RL~~NG~~YD~~V~~SS~~DP~~YQ~~YS~~DK~~FA~~ES~~SL~~KY~~UK~~DV~~GA~~VL~~LY~~RA~~SA~~QI~~IH~~DE~~SL~~VR~~OS  
 StKSL1 360 RL~~RL~~NG~~YD~~V~~SS~~DP~~YQ~~YS~~DK~~FA~~ES~~SL~~KY~~UK~~DV~~GA~~VL~~LY~~RA~~SA~~QI~~IH~~DE~~SL~~VR~~OS

AtKSL1 382 CW~~TK~~QY~~EM~~RL~~SW~~VKTSVR~~DK~~Y~~L~~KK~~EV~~DA~~AF~~PP~~SY~~AS~~LE~~RD~~HR~~KL~~NG~~SA~~VE~~NT  
 BnKSL1 375 LW~~TK~~QY~~EM~~RL~~SW~~VKTSVR~~DK~~Y~~L~~KK~~EV~~DA~~AF~~PP~~SY~~AS~~LE~~RD~~HR~~KL~~NG~~SA~~VE~~NT  
 BnKSL2 377 LW~~TK~~QY~~EM~~RL~~SW~~VKTSVR~~DK~~Y~~L~~KK~~EV~~DA~~AF~~PP~~SY~~AS~~LE~~RD~~HR~~KL~~NG~~SA~~VE~~NT  
 GmKSL1 410 LKH~~HL~~Q~~ES~~Y~~RL~~AD~~KL~~SY~~DL~~EL~~VE~~Y~~AN~~LE~~DR~~OS~~ME~~NT~~VE~~LD  
 SlKSL1 410 SSS~~LOS~~IQ~~RL~~SG~~EF~~Y~~PP~~NGLT~~KQ~~I~~HE~~Q~~VD~~DL~~VF~~PS~~AN~~IK~~RV~~AN~~RR~~NI~~KH~~YD~~VN~~TD  
 StKSL1 416 SSS~~LOS~~IQ~~RL~~SG~~EF~~Y~~PP~~NGLT~~KQ~~I~~HE~~Q~~VD~~DL~~VF~~PS~~AN~~IK~~RV~~AN~~RR~~NI~~KH~~YD~~VN~~TD

AtKSL1 440 RV~~TK~~RS~~YR~~HL~~NI~~CT~~SD~~IL~~KL~~AV~~DF~~NF~~CS~~IH~~RE~~EM~~ER~~LR~~WV~~EN~~NR~~OE~~LK~~FA~~RK~~AY  
 BnKSL1 434 RV~~TK~~RS~~YR~~HL~~NI~~CT~~SD~~IL~~KL~~AV~~DF~~NF~~CS~~IH~~RE~~EM~~ER~~LR~~WV~~EN~~NR~~OE~~LK~~FA~~RK~~AY  
 BnKSL2 436 RV~~TK~~RS~~YR~~HL~~NI~~CT~~SD~~IL~~KL~~AV~~DF~~NF~~CS~~IH~~RE~~EM~~ER~~LR~~WV~~EN~~NR~~OE~~LK~~FA~~RK~~AY  
 GmKSL1 473 RIL~~KAS~~Y~~RS~~ON~~LAN~~OE~~IL~~KL~~AV~~DF~~NF~~CS~~IH~~RE~~EM~~ER~~LR~~W~~V~~EN~~NR~~OE~~LK~~FA~~RK~~AY  
 SlKSL1 468 RVL~~KAS~~Y~~RS~~ON~~LAN~~OE~~IL~~KL~~AV~~DF~~NF~~CS~~IH~~RE~~EM~~ER~~LR~~W~~V~~EN~~NR~~OE~~LK~~FA~~RK~~AY  
 StKSL1 474 RVL~~KAS~~Y~~RS~~ON~~LAN~~OE~~IL~~KL~~AV~~DF~~NF~~CS~~IH~~RE~~EM~~ER~~LR~~W~~V~~EN~~NR~~OE~~LK~~FA~~RK~~AY

AtKSL1 500 CY~~FS~~CA~~AT~~TS~~PE~~LS~~DA~~RI~~SW~~AR~~GG~~VL~~TV~~VD~~DF~~DV~~GG~~SE~~BE~~HN~~LL~~FK~~KW~~DV~~ST~~  
 BnKSL1 494 CY~~FS~~CA~~AT~~TS~~PE~~LS~~DA~~RI~~SW~~AR~~GG~~VL~~TV~~VD~~DF~~DV~~GG~~SE~~BE~~HN~~LL~~FK~~KW~~DV~~ST~~  
 BnKSL2 496 CY~~FS~~CA~~AT~~TS~~PE~~LS~~DA~~RI~~SW~~AR~~GG~~VL~~TV~~VD~~DF~~DV~~GG~~SE~~BE~~HN~~LL~~FK~~KW~~DV~~ST~~  
 GmKSL1 533 CY~~FS~~CA~~AT~~TS~~PE~~LS~~DA~~RI~~SW~~AR~~GG~~VL~~TV~~VD~~DF~~DV~~GG~~SE~~BE~~HN~~LL~~FK~~KW~~DV~~ST~~  
 SlKSL1 528 CY~~FS~~CA~~AT~~TS~~PE~~LS~~DA~~RI~~SW~~AR~~GG~~VL~~TV~~VD~~DF~~DV~~GG~~SE~~BE~~HN~~LL~~FK~~KW~~DV~~ST~~  
 StKSL1 534 CY~~FS~~CA~~AT~~TS~~PE~~LS~~DA~~RI~~SW~~AR~~GG~~VL~~TV~~VD~~DF~~DV~~GG~~SE~~BE~~HN~~LL~~FK~~KW~~DV~~ST~~

AtKSL1 560 EY~~CS~~SH~~VE~~II~~FS~~V~~LR~~D~~TL~~EG~~KA~~FT~~OG~~RS~~VN~~TH~~IV~~K~~IWL~~DL~~LK~~SM~~LR~~EA~~WS~~SK~~ST~~  
 BnKSL1 554 EY~~CS~~SH~~VE~~II~~FS~~V~~LR~~D~~TL~~EG~~KA~~FT~~OG~~RS~~VN~~TH~~IV~~K~~IWL~~DL~~LK~~SM~~LR~~EA~~WS~~SK~~ST~~  
 BnKSL2 556 EY~~CS~~SH~~VE~~II~~FS~~V~~LR~~D~~TL~~EG~~KA~~FT~~OG~~RS~~VN~~TH~~IV~~K~~IWL~~DL~~LK~~SM~~LR~~EA~~WS~~SK~~ST~~  
 GmKSL1 593 EY~~CS~~SH~~VE~~II~~FS~~V~~LR~~D~~TL~~EG~~KA~~FT~~OG~~RS~~VN~~TH~~IV~~K~~IWL~~DL~~LK~~SM~~LR~~EA~~WS~~SK~~ST~~  
 SlKSL1 588 EY~~CS~~SH~~VE~~II~~FS~~V~~LR~~D~~TL~~EG~~KA~~FT~~OG~~RS~~VN~~TH~~IV~~K~~IWL~~DL~~LK~~SM~~LR~~EA~~WS~~SK~~ST~~  
 StKSL1 594 EY~~CS~~SH~~VE~~II~~FS~~V~~LR~~D~~TL~~EG~~KA~~FT~~OG~~RS~~VN~~TH~~IV~~K~~IWL~~DL~~LK~~SM~~LR~~EA~~WS~~SK~~ST~~

AtKSL1 620 PSL~~ED~~Y~~ME~~NAV~~YS~~FAL~~GP~~IN~~LP~~AT~~Y~~L~~IG~~PP~~LS~~ET~~VS~~PE~~YN~~OL~~YR~~VM~~ST~~GR~~LL~~ND~~IG~~  
 BnKSL1 614 PSL~~ED~~Y~~ME~~NAV~~YS~~FAL~~GP~~IN~~LP~~AT~~Y~~L~~IG~~PP~~LS~~ET~~VS~~PE~~YN~~OL~~YR~~VM~~ST~~GR~~LL~~ND~~IG~~  
 BnKSL2 616 PSL~~ED~~Y~~ME~~NAV~~YS~~FAL~~GP~~IN~~LP~~AT~~Y~~L~~IG~~PP~~LS~~ET~~VS~~PE~~YN~~OL~~YR~~VM~~ST~~GR~~LL~~ND~~IG~~  
 GmKSL1 653 PSL~~ED~~Y~~ME~~NAV~~YS~~FAL~~GP~~IN~~LP~~AT~~Y~~L~~IG~~PP~~LS~~ET~~VS~~PE~~YN~~OL~~YR~~VM~~ST~~GR~~LL~~ND~~IG~~  
 SlKSL1 648 PSL~~ED~~Y~~ME~~NAV~~YS~~FAL~~GP~~IN~~LP~~AT~~Y~~L~~IG~~PP~~LS~~ET~~VS~~PE~~YN~~OL~~YR~~VM~~ST~~GR~~LL~~ND~~IG~~  
 StKSL1 654 PSL~~ED~~Y~~ME~~NAV~~YS~~FAL~~GP~~IN~~LP~~AT~~Y~~L~~IG~~PP~~LS~~ET~~VS~~PE~~YN~~OL~~YR~~VM~~ST~~GR~~LL~~ND~~IG~~

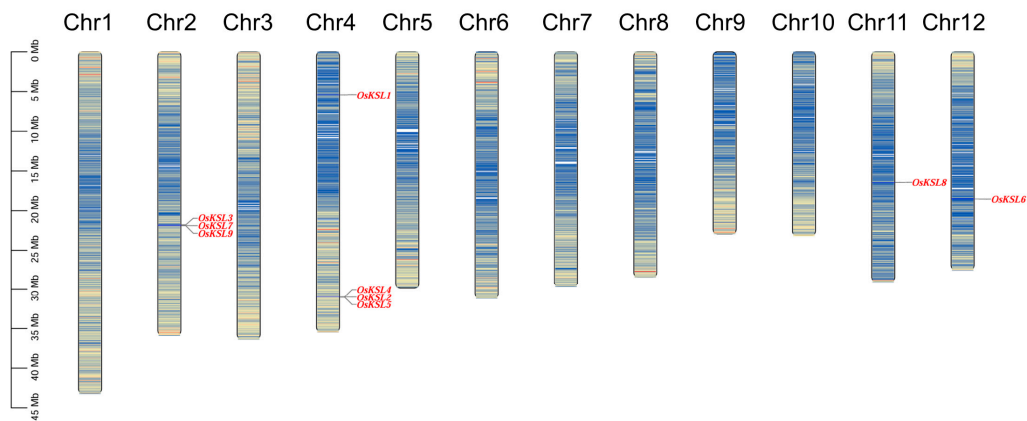
AtKSL1 680 FK~~RES~~A~~Q~~GL~~NA~~VS~~YH~~MR~~DR~~NR~~SK~~VE~~II~~SK~~GL~~A~~ER~~KK~~VE~~OK~~LV~~EEK~~GS~~VV~~PR~~EC  
 BnKSL1 674 FK~~RES~~A~~Q~~GL~~NA~~VS~~YH~~MR~~DR~~NR~~SK~~VE~~II~~SK~~GL~~A~~ER~~KK~~VE~~OK~~LV~~EEK~~GS~~VV~~PR~~EC  
 BnKSL2 676 FK~~RES~~A~~Q~~GL~~NA~~VS~~YH~~MR~~DR~~NR~~SK~~VE~~II~~SK~~GL~~A~~ER~~KK~~VE~~OK~~LV~~EEK~~GS~~VV~~PR~~EC  
 GmKSL1 713 FK~~RES~~A~~Q~~GL~~NA~~VS~~YH~~MR~~DR~~NR~~SK~~VE~~II~~SK~~GL~~A~~ER~~KK~~VE~~OK~~LV~~EEK~~GS~~VV~~PR~~EC  
 SlKSL1 708 FK~~RES~~A~~Q~~GL~~NA~~VS~~YH~~MR~~DR~~NR~~SK~~VE~~II~~SK~~GL~~A~~ER~~KK~~VE~~OK~~LV~~EEK~~GS~~VV~~PR~~EC  
 StKSL1 714 FK~~RES~~A~~Q~~GL~~NA~~VS~~YH~~MR~~DR~~NR~~SK~~VE~~II~~SK~~GL~~A~~ER~~KK~~VE~~OK~~LV~~EEK~~GS~~VV~~PR~~EC

AtKSL1 740 KEA~~PL~~K~~MS~~KV~~LN~~LFY~~RK~~DD~~GF~~TS~~ND~~L~~MS~~V~~VK~~SV~~MY~~EV~~SL~~ED...ES~~LT~~.....  
 BnKSL1 734 KEA~~PL~~K~~MS~~KV~~LN~~LFY~~RK~~DD~~GF~~TS~~ND~~L~~MS~~V~~VK~~SV~~MY~~EV~~SL~~ED...ES~~LT~~.....  
 BnKSL2 736 KEA~~PL~~K~~MS~~KV~~LN~~LFY~~RK~~DD~~GF~~TS~~ND~~L~~MS~~V~~VK~~SV~~MY~~EV~~SL~~ED...ES~~LT~~.....  
 GmKSL1 773 KDL~~FW~~K~~MS~~KV~~LN~~LFY~~RK~~DD~~GF~~TS~~ND~~L~~MS~~V~~VK~~SV~~MY~~EV~~SL~~ED...ES~~LT~~.....  
 SlKSL1 768 KDL~~FW~~K~~MS~~KV~~LN~~LFY~~RK~~DD~~GF~~TS~~ND~~L~~MS~~V~~VK~~SV~~MY~~EV~~SL~~ED...ES~~LT~~.....  
 StKSL1 774 KDL~~FW~~K~~MS~~KV~~LN~~LFY~~RK~~DD~~GF~~TS~~ND~~L~~MS~~V~~VK~~SV~~MY~~EV~~SL~~ED...ES~~LT~~.....

AtKSL1 ..  
 BnKSL1 ..  
 BnKSL2 ..  
 GmKSL1 833 ML  
 SlKSL1 ..  
 StKSL1 ..

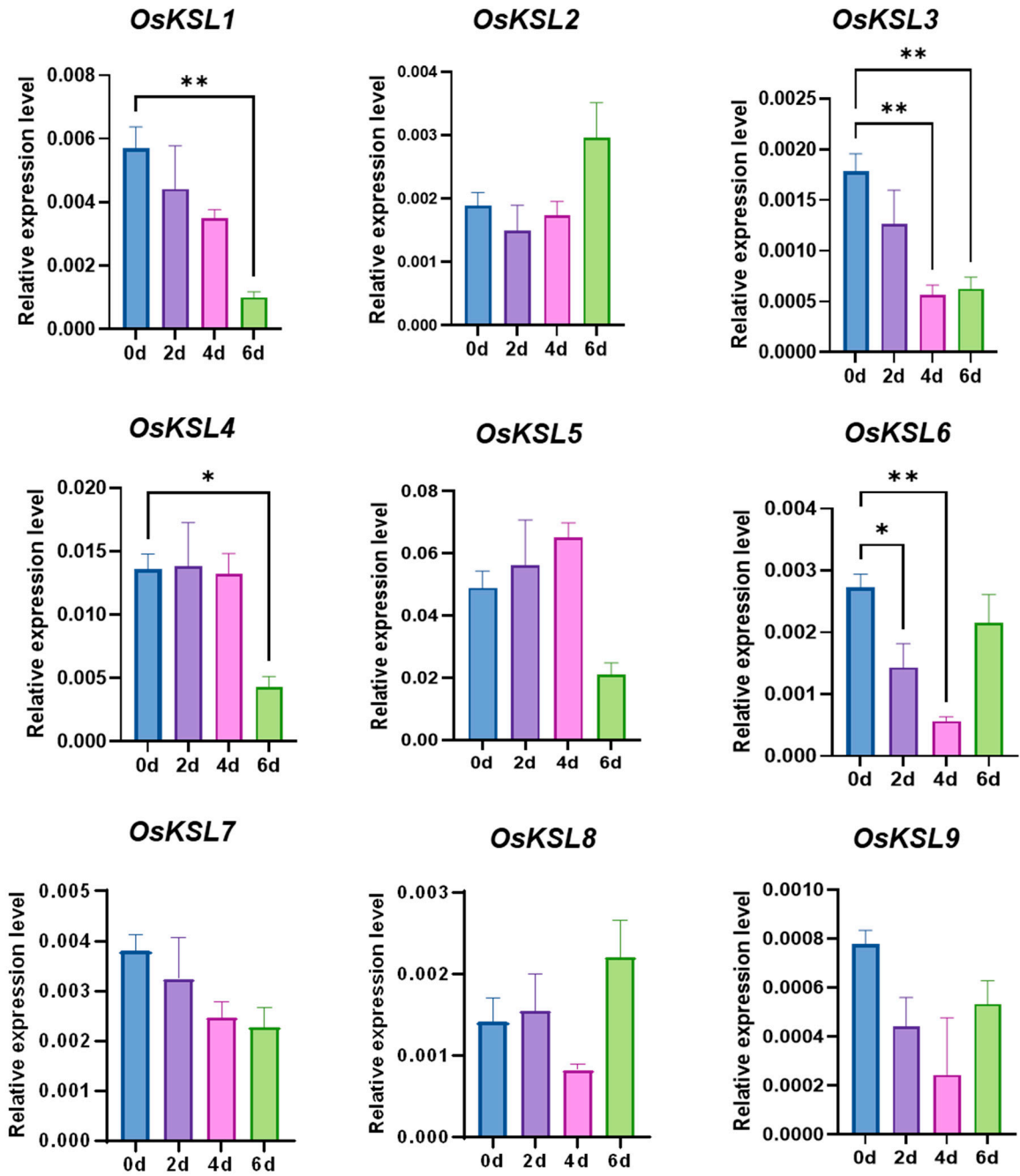
Figure S8 Protein sequences alignment of KSLs related to AtKSL1 pair in collinearity analysis.





**Figure S9 Chromosomal Localization of *OsKSL* Gene Members in *Oryza sativa*.**

The diagram illustrates the positioning and relative distribution of *OsKSL* genes across the twelve rice chromosomes. Chromosome numbers are indicated at the top of each chromosome representation. A scale bar is provided on the left to denote the chromosomal length in megabase pairs (Mbp).



**Figure S10 qRT-PCR analysis of *OsKSL* gene family in darkness**

6 d-old seedlings grew without light for 6 days. Aerial tissues were sampled in description time points (0d, 2d, 4d, and 6d) (n = 4) for RNA extraction and qRT-PCR. \*  $P < 0.05$  and \*\* $P < 0.01$  (Student's *t*-test).

Three biological replications were performed. Bar graphs show means. Error bars represent  $\pm$  SE (n = 3).

*OsUBQ6* was used as internal control.

**Table S1 Plant genomes used in this study**

| Species                           | GenBank             | RefSeq              | Size (Mb) | WGS accession | Assembly                                 |
|-----------------------------------|---------------------|---------------------|-----------|---------------|--|
| <i>Selaginella moellendorffii</i> | GCA_0001<br>43415.2 | GCF_0001<br>43415.4 | 212.3     | ADFJ01        | V1.0                                     |
| <i>Arabidopsis thaliana</i>       | GCA_0000<br>01735.2 | GCF_0000<br>01735.4 | 119.1     | N/A           | TAIR10.1                                 |
| <i>Brassica napus</i>             | GCA_0203<br>79485.1 | GCF_0203<br>79485.1 | 1,001     | JAGKQM01      | Da-Ae                                    |
| <i>Phalaenopsis equestris</i>     | GCA_0012<br>63595.1 | GCF_0012<br>63595.1 | 1,064     | APLD01        | ASM126359v1                              |
| <i>Nicotiana tabacum</i>          | GCA_0007<br>15135.1 | GCF_0007<br>15135.1 | 3,643     | AYMY01        | Ntab-TN90                                |
| <i>Solanum lycopersicum</i>       | GCA_0001<br>88115.4 | GCF_0001<br>88115.5 | 827.4     | AEKE03        | SL3.1                                    |
| <i>Solanum tuberosum</i>          | GCA_0002<br>26075.1 | GCF_0002<br>26075.1 | 705.8     | AEWC01        | SolTub_3.0                               |
| <i>Lactuca sativa</i>             | GCA_0028<br>70075.4 | GCF_0028<br>70075.4 | 2,590     | NBSK02        | Lsat_Salinas_v11                         |
| <i>Helianthus annuus</i>          | GCA_0021<br>27325.2 | GCF_0021<br>27325.2 | 3,010     | MNCJ02        | HanXRQr2.0-<br>SUNRISE                   |
| <i>Glycine max</i>                | GCA_0000<br>04515.5 | GCF_0000<br>04515.6 | 978.4     | ACUP04        | Glycine_max_v4.<br>0                     |
| <i>Pisum sativum</i>              | GCA_0243<br>23335.2 | GCF_0243<br>23335.1 | 3,796     | JAMSHJ01      | CAAS_Psat_ZW<br>6_1.0                    |
| <i>Vigna radiata</i>              | GCA_0007<br>41045.2 | GCF_0007<br>41045.1 | 463.1     | JJMO01        | Vradiata_ver6                            |
| <i>Arachis hypogaea</i>           | GCA_0030<br>86295.2 | GCF_0030<br>86295.2 | 2,557     | PIVG01        | arahy.Tifrunner.g<br>nm1.KYV3            |
| <i>Gossypium hirsutum</i>         | GCA_0079<br>90345.1 | GCF_0079<br>90345.1 | 2,305     | VKGJ01        | Gossypium_hirsu<br>tum_v2.1              |
| <i>Oryza sativa</i>               | GCA_0014<br>33935.1 | GCF_0014<br>33935.1 | 373.8     | N/A           | IRGSP-1.0                                |
| <i>Zea mays</i>                   | GCA_9021<br>67145.1 | GCF_9021<br>67145.1 | 2,182     | CABHLF01      | Zm-B73-<br>REFERENCE-<br>NAM-5.0         |
| <i>Triticum aestivum</i>          | GCA_0182<br>94505.1 | GCF_0182<br>94505.1 | 14,567    | JAGHKL01      | IWGSC CS<br>RefSeq v2.1                  |
| <i>Hordeum vulgare</i>            | GCA_9048<br>49725.1 | GCF_9048<br>49725.1 | 4,226     | CAJHDD01      | MorexV3_pseudo<br>molecules_asse<br>mbly |
| <i>Sorghum bicolor</i>            | GCA_0000<br>03195.3 | GCF_0000<br>03195.3 | 708.7     | ABXC03        | Sorghum_bicolor<br>_NCBIv3               |

N/A: data was not available.

**Table S2 The primers list**

| <b>Primer</b> | <b>Sequence</b>       |
|---------------|-----------------------|
| OsKSL1-qpcr-F | CTCTCTGCTGCTGCCACCAT  |
| OsKSL1-qpcr-R | GGCAACAAGTGTGAGCGCAA  |
| OsKSL2-qpcr-F | GCGTGGCGGTCACAAGAGAT  |
| OsKSL2-qpcr-R | CCTGATGTGCTCCTGCCCAA  |
| OsKSL3-qpcr-F | CGCAAAGGCTTCCGCGTTAC  |
| OsKSL3-qpcr-R | GGCAGATGCTGGCTCCTCTG  |
| OsKSL4-qpcr-F | TCCATGCTTCCCACAATGCGT |
| OsKSL4-qpcr-R | GCCAGTGTGGACAAGAGAGCA |
| OsKSL5-qpcr-F | CCGGATGGCGATGGAGATGG  |
| OsKSL5-qpcr-R | TTCCACCGTGGCAGATCACC  |
| OsKSL6-qpcr-F | TTGGTGAGCTCAGCGAAGGC  |
| OsKSL6-qpcr-R | GGCAAACGCTCCAGACACCT  |
| OsKSL7-qpcr-F | CGAACACTATCGGCCGCCTT  |
| OsKSL7-qpcr-R | CCATCGATGCCTCCGGTGAG  |
| OsKSL8-qpcr-F | CAAGCGTATCGGCGCAAAGG  |
| OsKSL8-qpcr-R | CTCTGCCTCGGTCAGCATGG  |
| OsKSL9-qpcr-F | TGTTGACCGAGGCCGAATGG  |
| OsKSL9-qpcr-R | ATGCCGCCGAGGTGATGATG  |
| OsUBQ6-qpcr-F | TGCTATGTACGTCGCCATCCA |
| OsUBQ6-qpcr-R | AATGAGTAACCACGCTCCGTC |