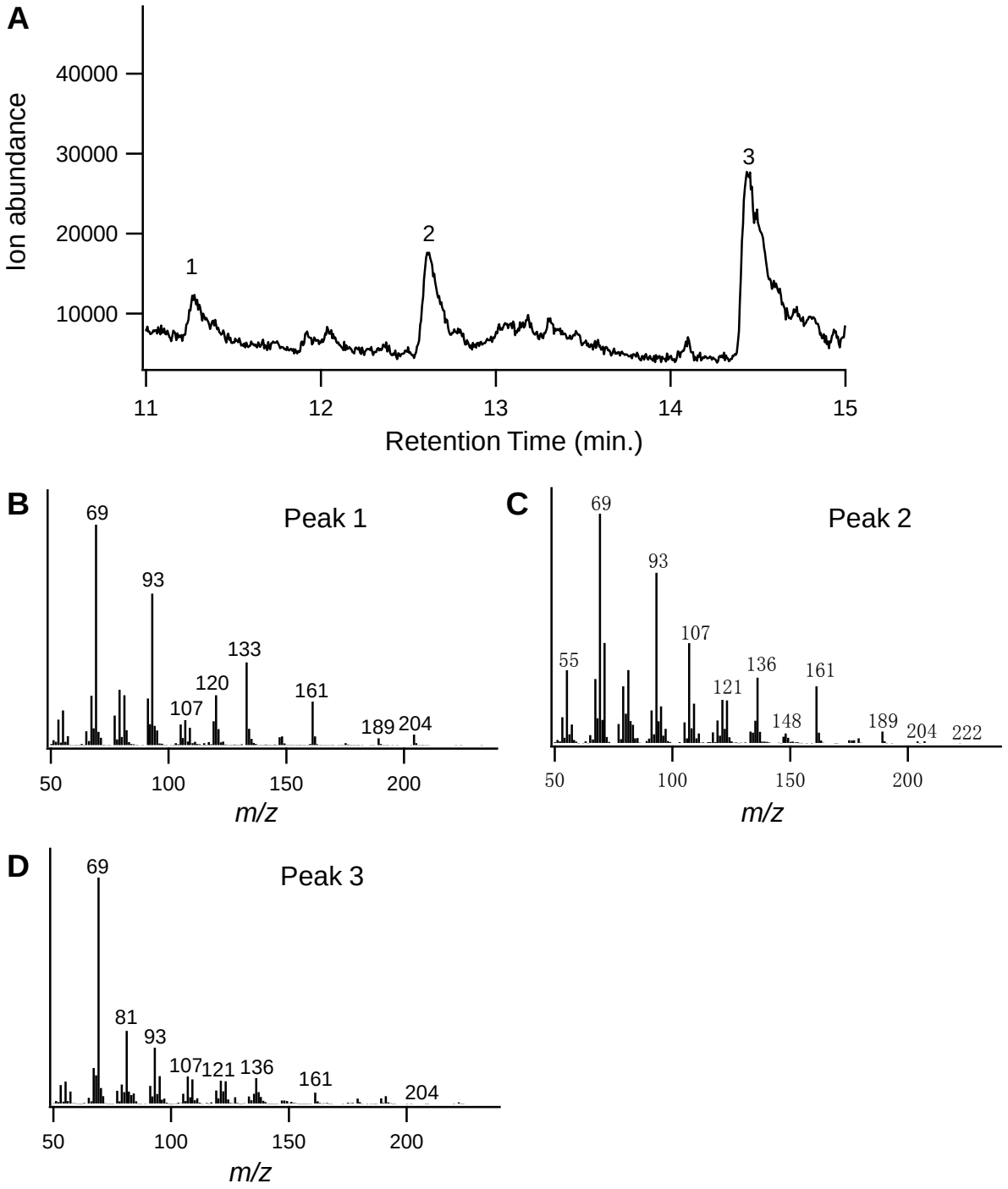
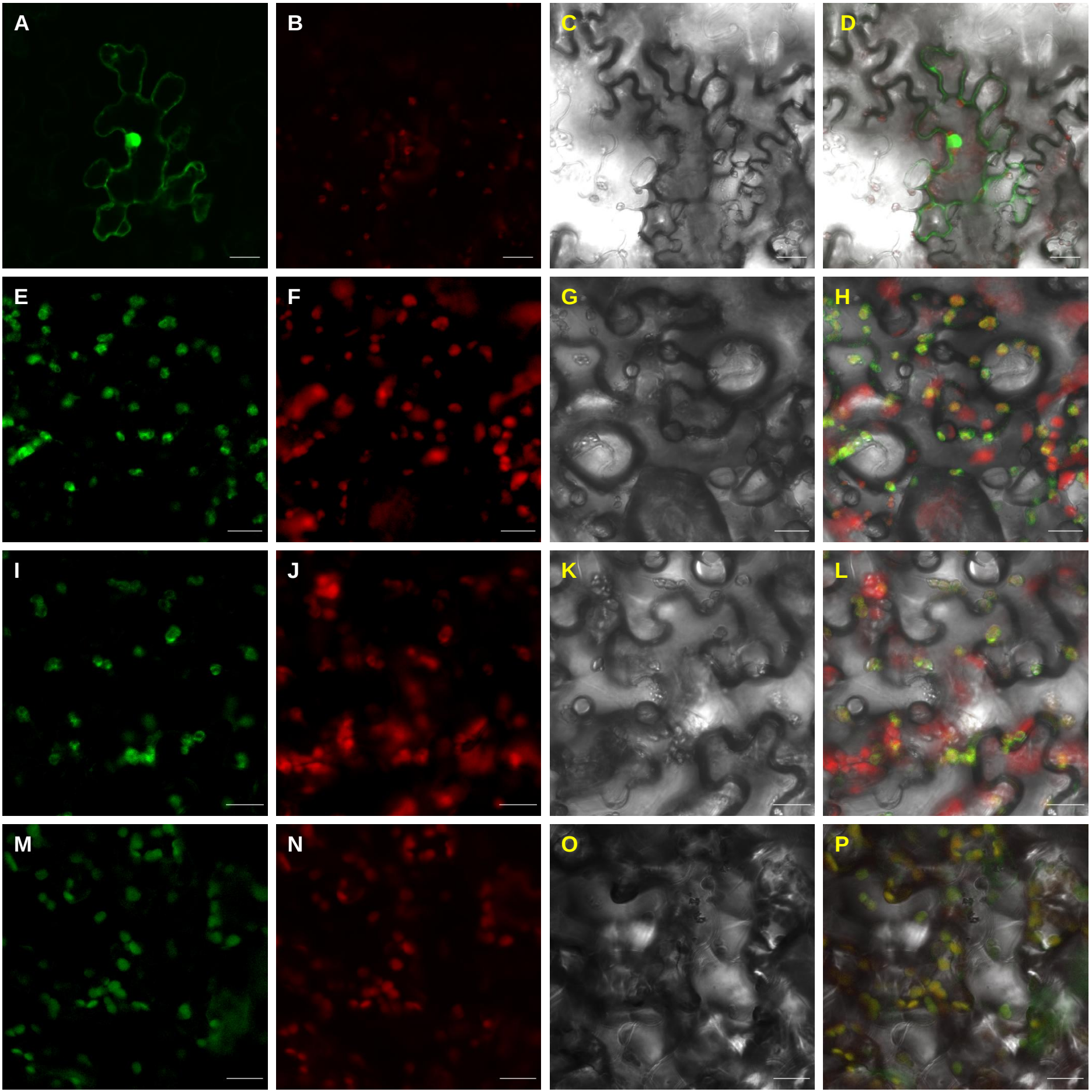
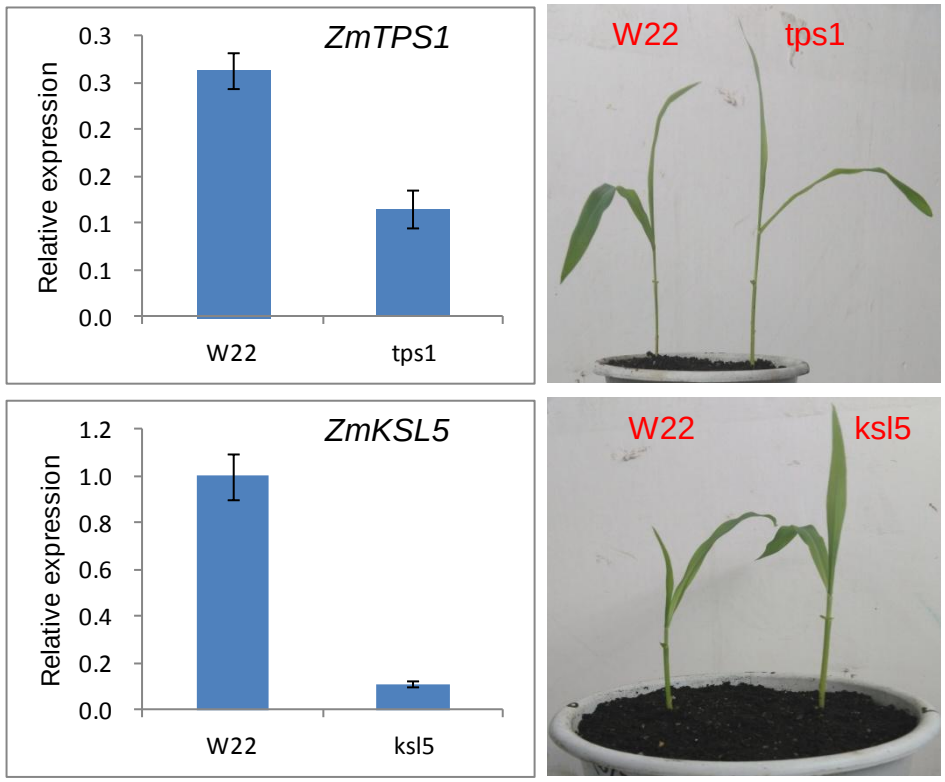


Supplemental Figure S1. GC-MS analysis of ZmTPS1 sesquiterpene products.
A, Total ion chromatogram of GC-MS analysis for coexpression products of ZmTPS1 and IspA (FPP synthase from *E. coli*).
B to D, Mass spectra of ZmTPS1 sesquiterpene products, which are identified through mass spectra comparison with that of NIST MS library as *β*-farnesene (Peak 1, B), nerolidol (Peak 2, C) and farnesol (Peak 3, D).

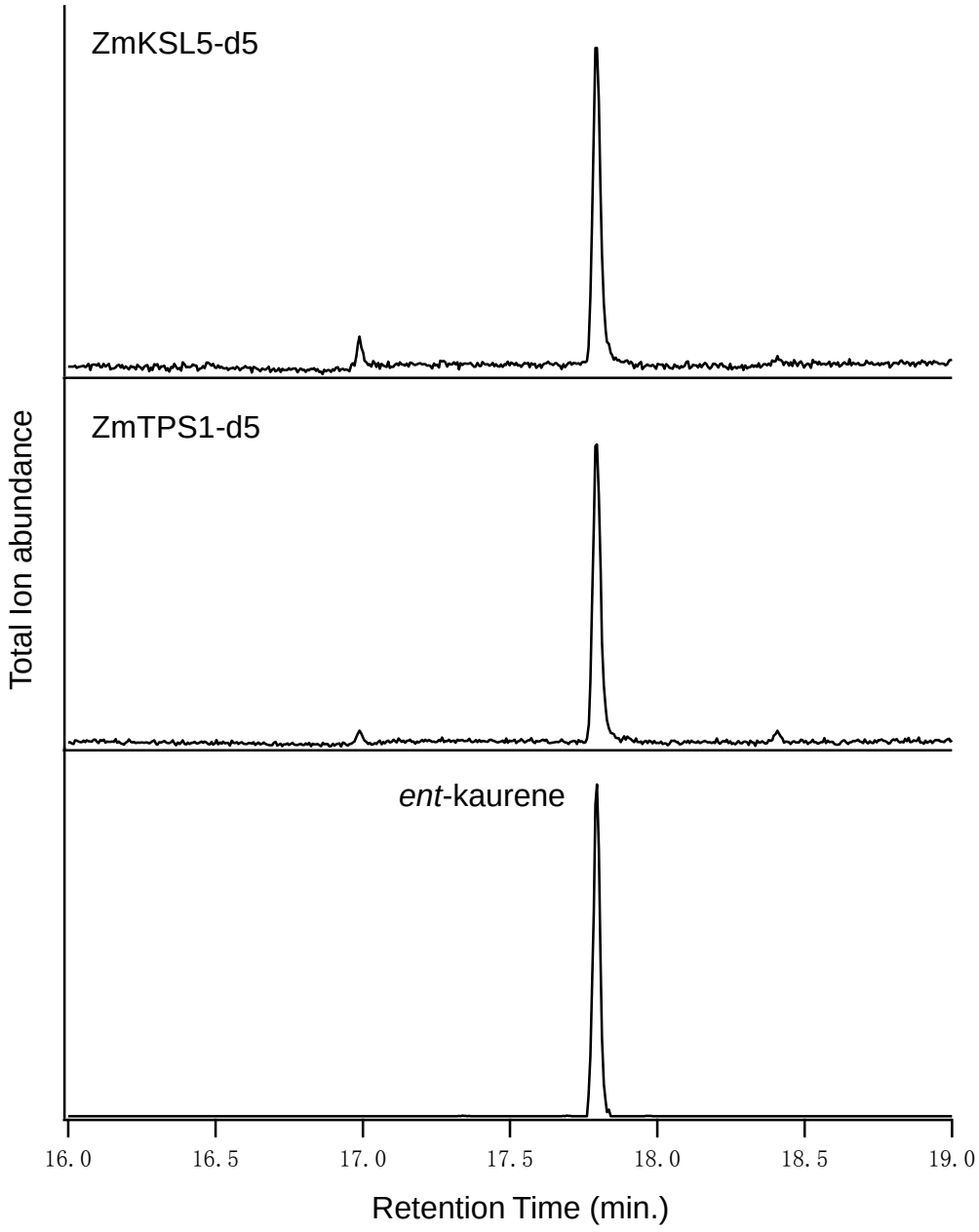

A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P

Supplemental Figure S2. Plastidic localization of ZmTPS1, ZmKSL5 and ZmKSL3. Images of the leaf epidermis of *N. benthamiana* expressing different eGFP fusion protein are shown, eGFP (A to D), eGFP fused to ZmTPS1 (E to H), eGFP fused to ZmKSL5 (I to L) and eGFP fused to ZmKSL3 (M to P). All expression was controlled with CaMV 35S promoter.
A, E, I and M, eGFP fluorescence.
B, F, J and N, Chlorophyll autofluorescence.
C, G, K and O, Bright-field image.
D, H, L and P, Overlay images.
Scale bar indicates 20 μm.

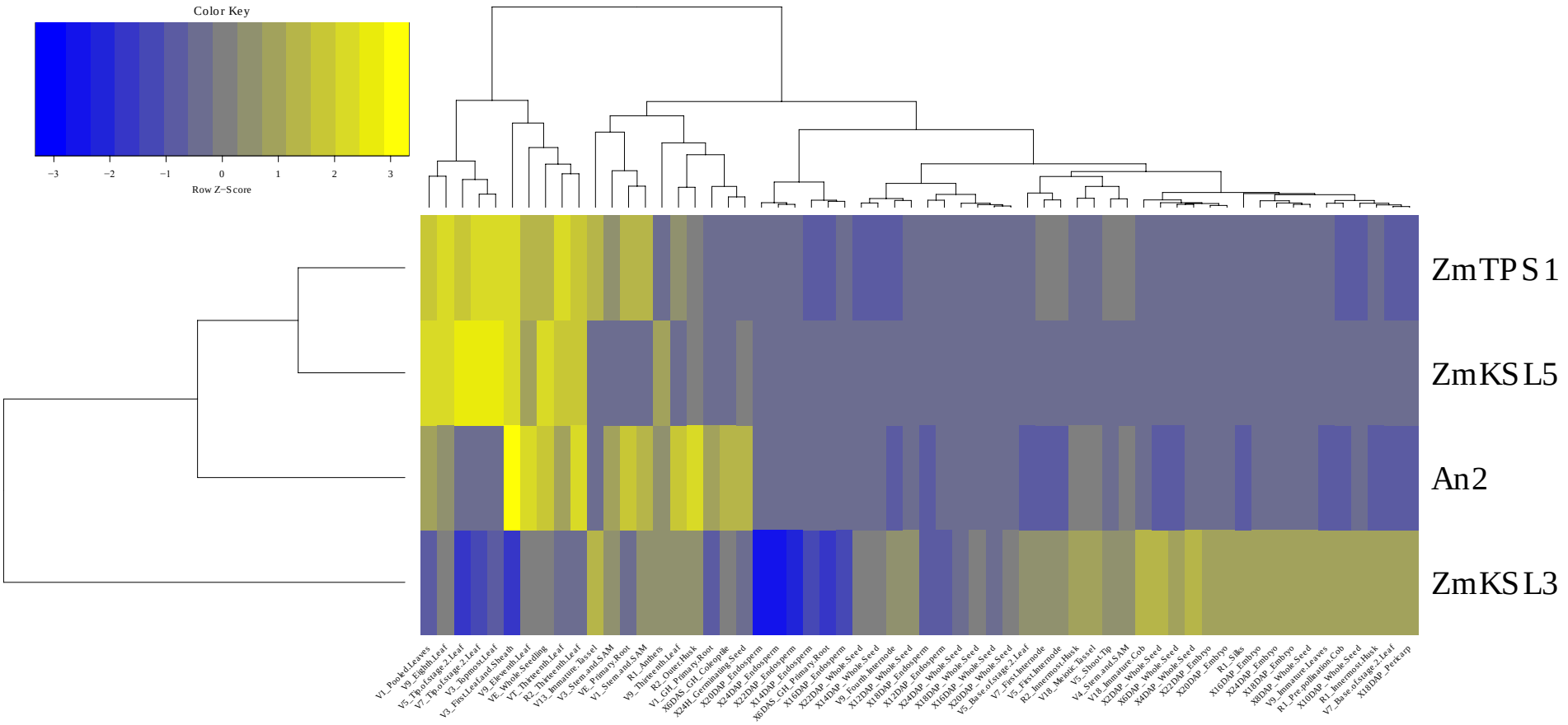
Supplemental Figure S3. Maize *d5* mutant seedlings and height restoration by GA treatment.
A, The *d5* mutants showed dwarfism (marked with red arrow).
B, The 10 days *d5* mutant (marked with red arrow) and WT seedling.
C, The height restoration of *d5* (marked with red arrow) with GA treatment.



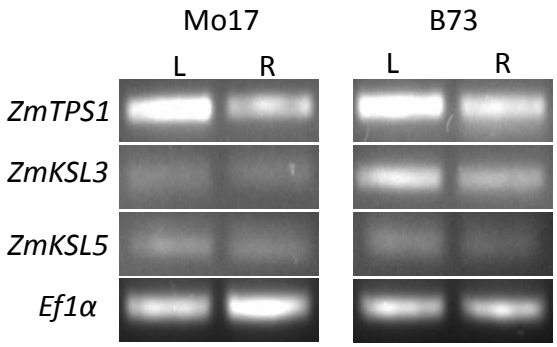
Supplemental Figure S4. *ZmTPS1* and *ZmKSL5* mutants did not show dwarf phenotype. Gene expression of ZmTPS1 and *ZmKSL5* was analyzed with qRT-PCR to identify their mutants, in comparison to that of wild type line W22.



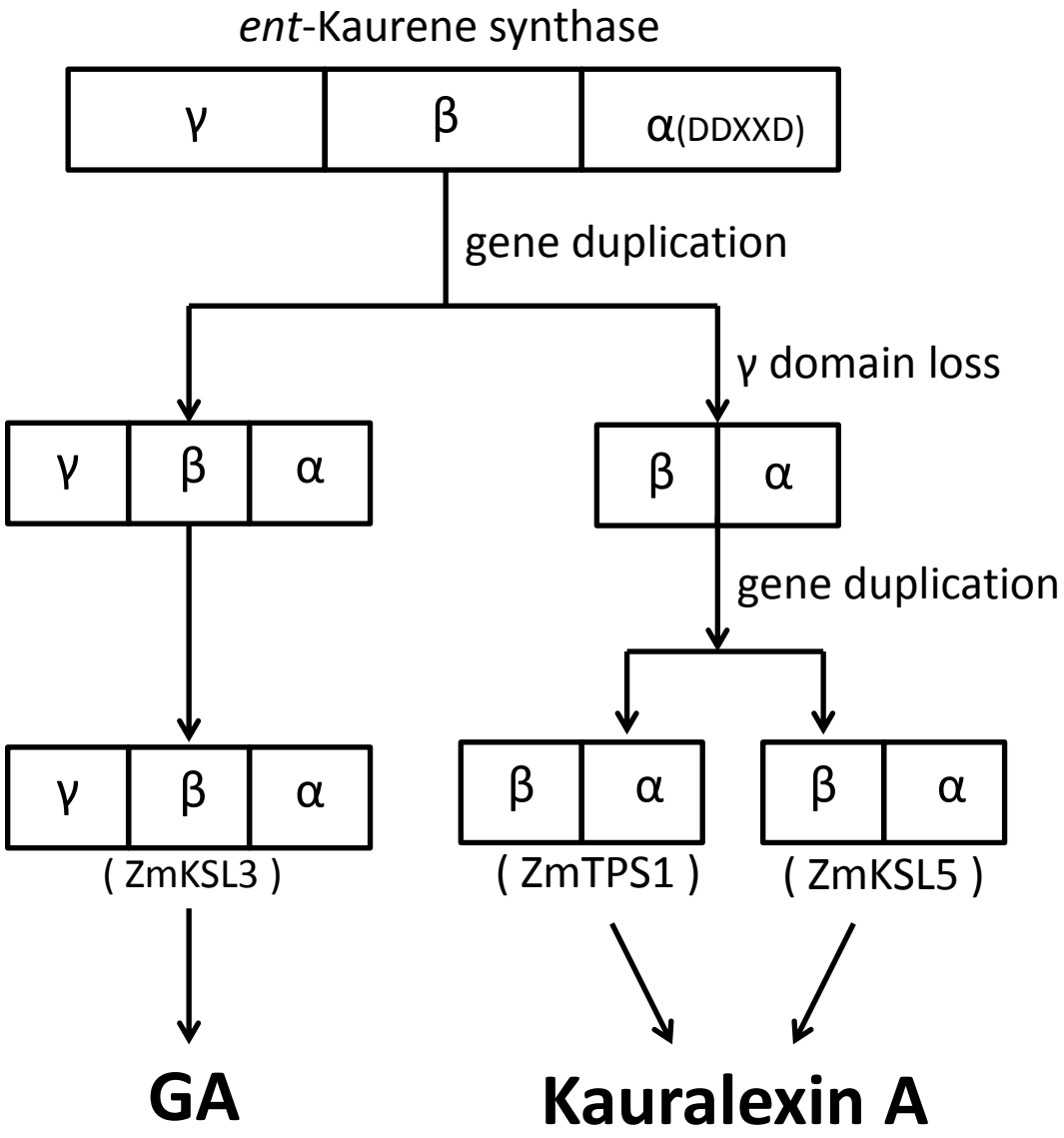
Supplemental Figure S5. GC-MS analysis of KS activity for ZmTPS1 and ZmKSL5 in *d5*.



Supplemental Figure S6. Heat map of KSL gene expression in B73 with *An2*. Expression data was obtained from PLEXdb and MaizeGDB for heat map plotting. *ZmTPS1* and *ZmKSL5* have correlated expression patterns with *An2* in B73 tissues, in contrast to *ZmKSL3*.



Supplemental Figure S7. Constitutive gene expression pattern of *ZmTPS1*, *ZmKSL3* and *ZmKSL5*. RT-PCR analysis for constitutive expression of three KS genes in root (R) and above ground tissues (L) of Mo17 and B73 young seedling. *Ef1α* was used as control.



Supplemental Figure S8. Proposed evolution of maize tandem KS gene array.

Supplemental Table S1. Plastid localization prediction results

	ChloroP	Predator	PCLA	iPSORT
ZmKSL1	—	—	—	—
ZmKSL2	Y	—	Y	Y
ZmKSL3	Y	Y	—	Y
ZmKSL4	Y	Y	Y	Y
ZmKSL5	Y	Y	Y	Y
ZmTPS1	Y	Y	Y	Y
TaKSL5	Y	—	Y	—

Supplemental Table S2. Predicted cis-regulatory elements in 1.5 kb promoter region of three KS genes.

	W-Box	ABRE (ABA response)	TCA (SA response)	CGTCA (MeJA response)
ZmKSL5	-457	-873, -1137, -298, -135	none	-756
ZmTPS1	-1416, -928	-33	-570	-928, -813, -570
ZmKSL3	none	none	none	-487, -1046, -1043, -902, -763

Supplemental Table S3. Primers used for semiquantitative (S) and quantitative RT-PCR

Primer	Sequence (5'-3')	Amplicon size (bp)
ZmKSL3-F1 (S)	GATTCCGAGCAGAGGCAGAG	341
ZmKSL3-R1 (S)	ACGCAAGAACACATGCCAAC	
ZmTPS1-F	CGGTGATCAATGAGCCACTA	173
ZmTPS1-R	TGACAACATGTGCCAACTCC	
ZmKSL5-F	TTCTGGAAAATGTGCAAGGTC	103
ZmKSL5-R	GCTCGTTGATCACTGCATTC	
ZmKSL3-F	TGGGTTTCTATGGTGCCAGT	140
ZmKSL3-R	AGAACATCCTTGCTGACCGA	
An2-f	GATGATGAGCCATGTCGATG	113
An2-r	GAAAGGTCTGCCTTGTCTCG	
Ef1α-F	TGGTGTCATCAAGCCTGGTA	118
Ef1α-R	AACATTGTCACCCGGAAGAG	

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ZmKSL5-d5  GGCGGGCATGCGCACCGCTTCGCCTCGTCGCTACCGTGCGGGAGGACGACGCCGACGCCACGGACCACG 138
   ZmKSL5  GGCGGGCATGCGCACCGCTTCGCCTCGTCGCTACCGTGCGGGAGGACGACGCCGACGCCACGGACCACG 138

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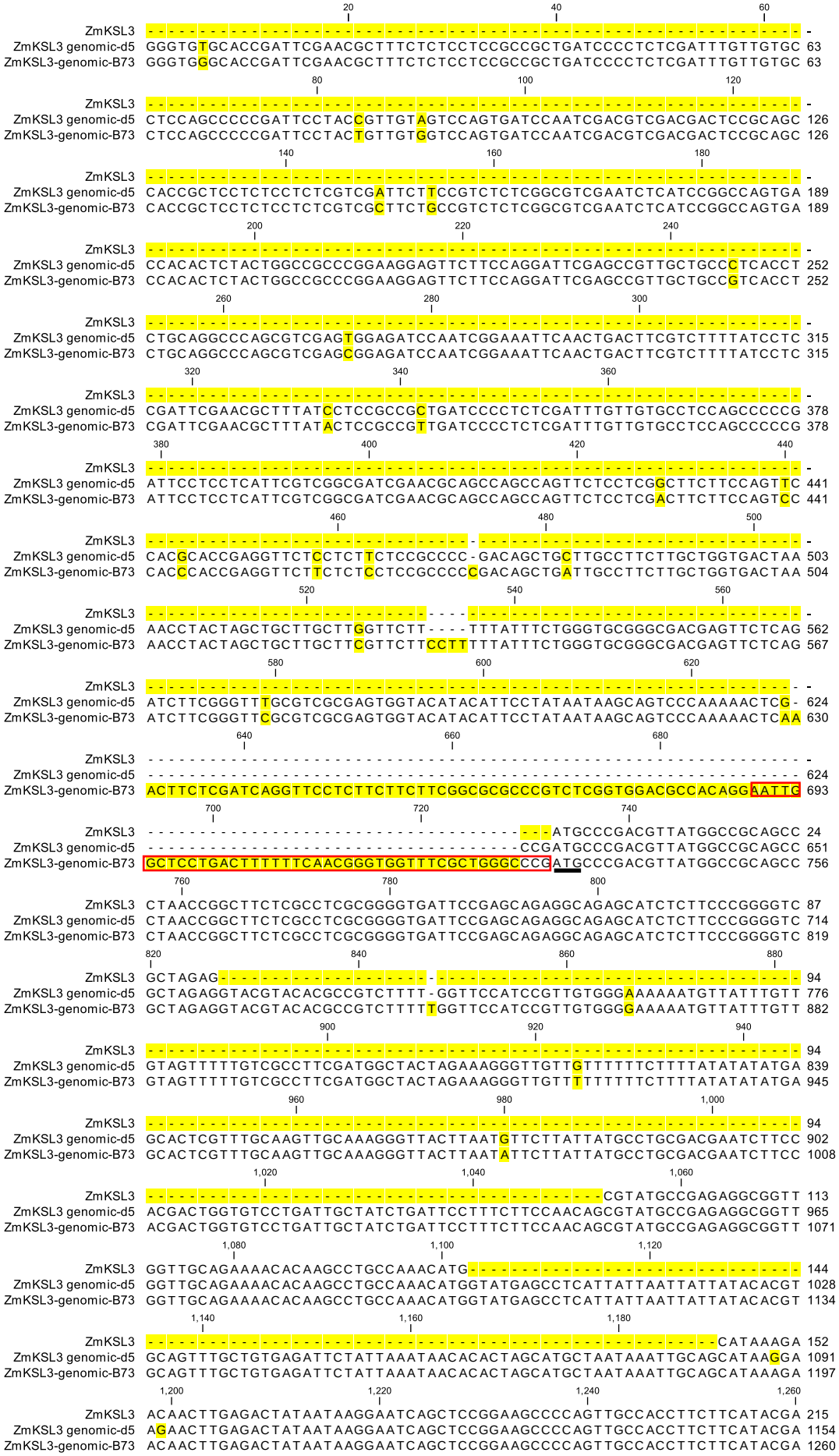
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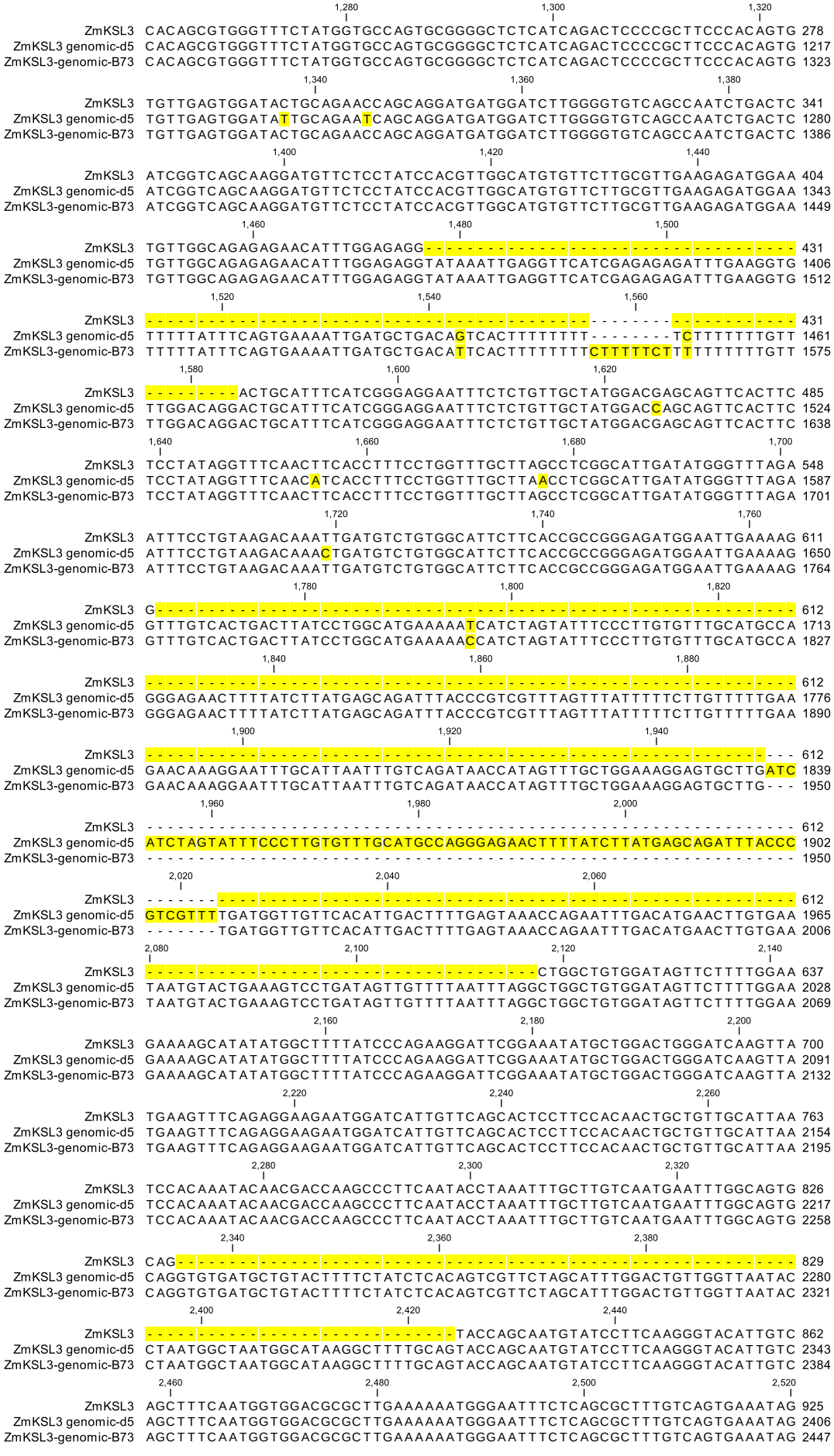
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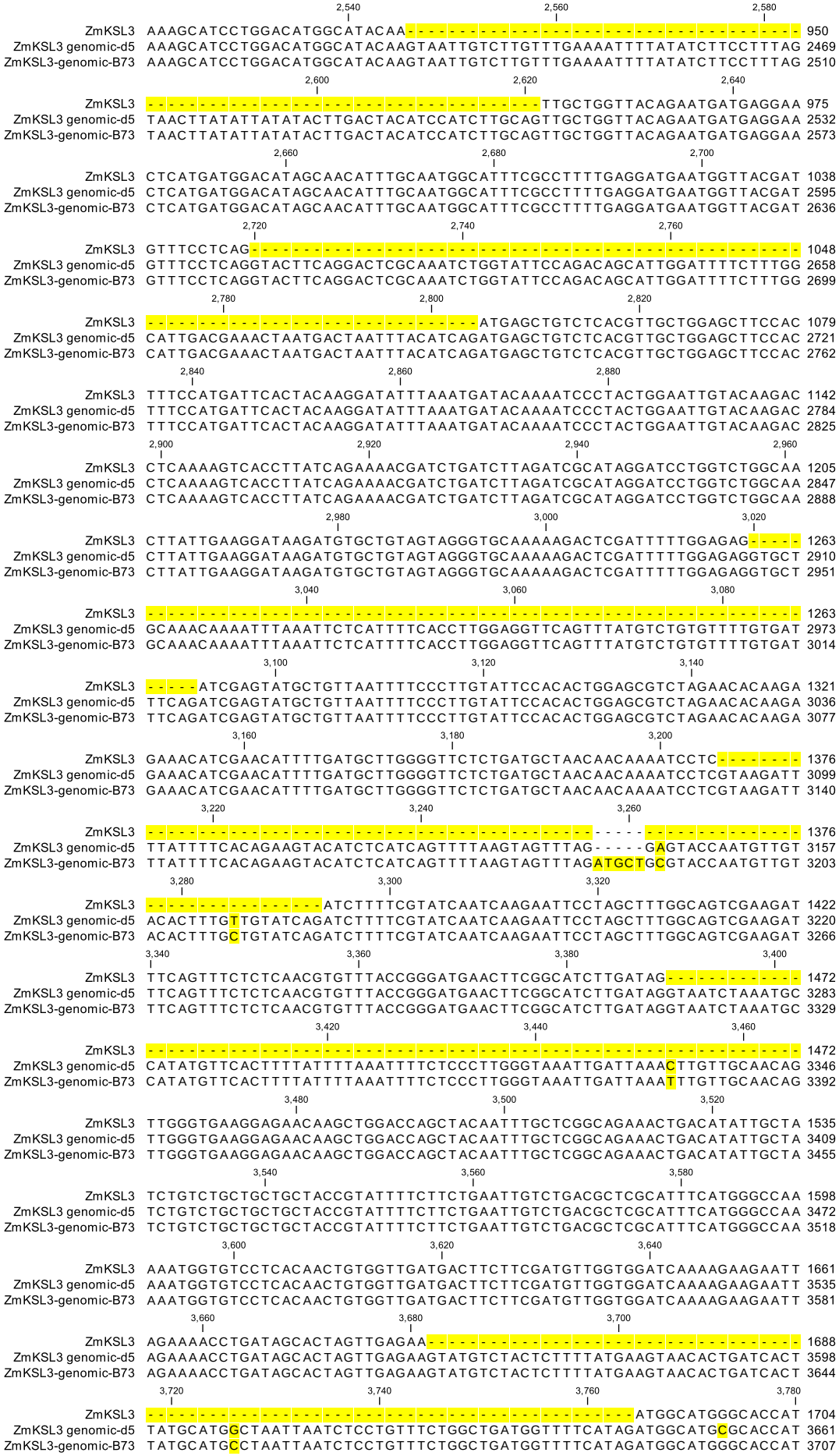
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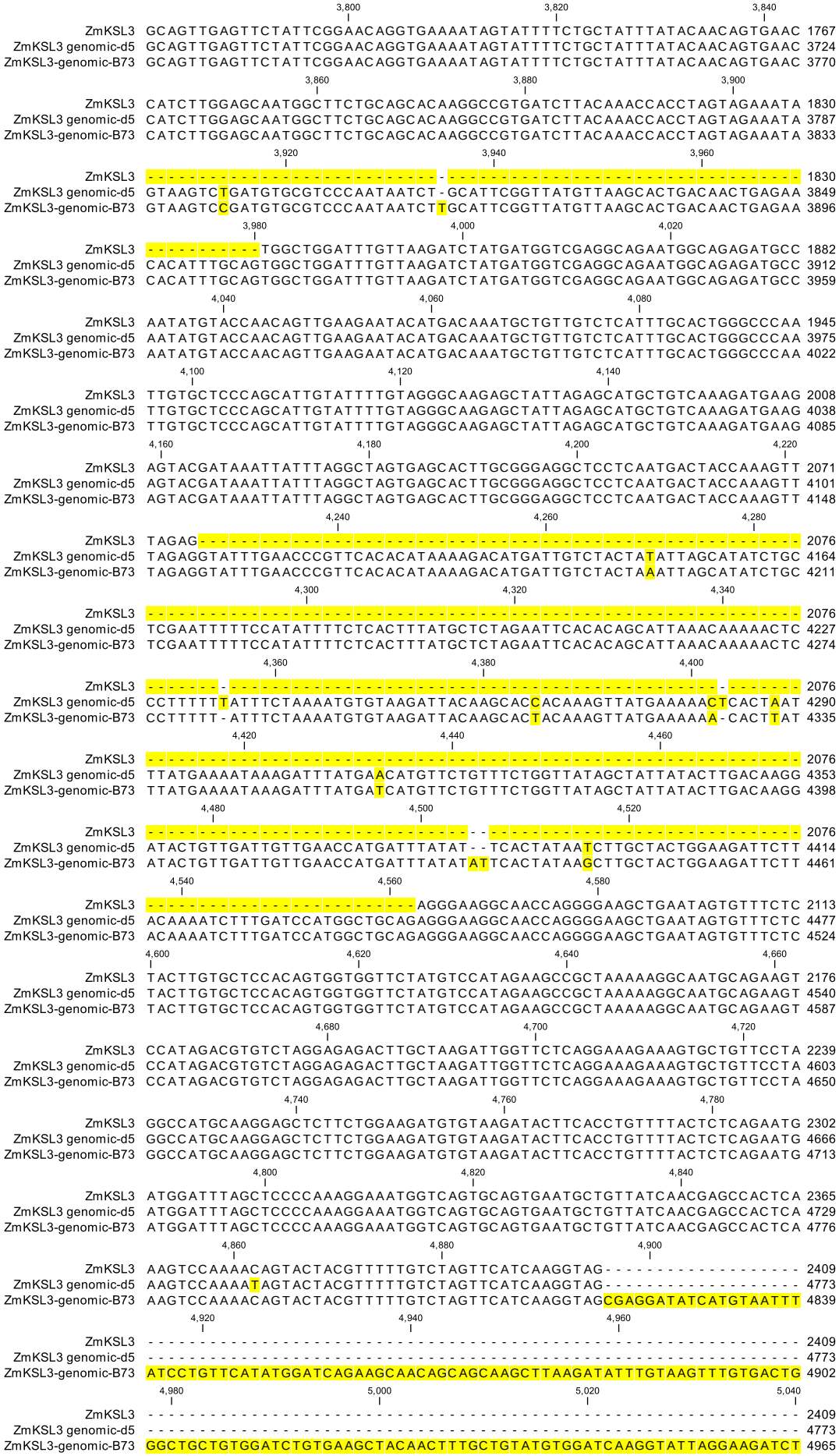
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