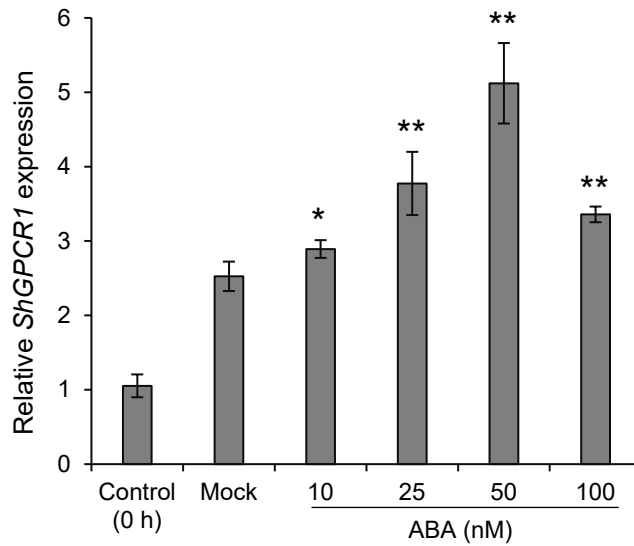
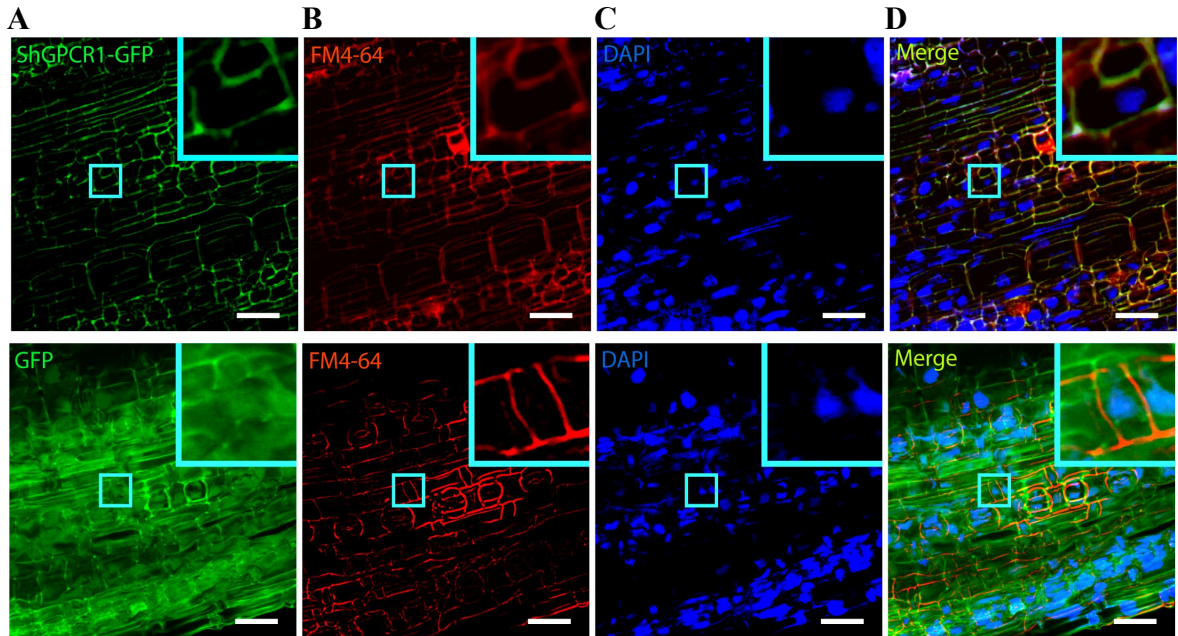


ShGPCR1	1	MGWGTVVYEGAVVGSSVVLGLWAGLWFLNRRLYKEEERRVVLQVILFGLVFAFSCNLFELVLVFEILPVLSKHARFLNWHL
Sorghum GPCR-like	1	MGWGTVVYEGAVVGSSVLGLWAGLWFLNRRLYKEYEERRVVLQVILFGLVFAFSCNLFELVLVFEILPVLSKHARFLNWHL
Maize GPCR-like	1	MGWGTVVYEGAVVGSSVLGLWAGLWFLNRRLYKEYEERRVVLQVILFGLVFAFSCNLFELVLVFEILPVLSKHARFLNWHL
Rice Cold1-like	1	MGWAVVYEGAVVGCASVLGLWAGLWFLNRRLYKEYEERRALVQILFGLVFAFSCNLFQVLVFEILPVLSKHARFLNWHL
Brachypodium GPCR-like	1	MGWGTVVYEGAVVGSSVLGLWAGLWFLNRRLYKEYEERRVVLQVILFGLVFAFSCNLFQVLVFEILPVLSKHARFLNWHL
Foxtail millet GPCR-like	1	MGWGTVVYEGAVVGSSVLGLWAGLWFLNRRLYKEYEERRVVLQVILFGLVFAFSCNLFQVLVFEILPVLSKHARFLNWHL
Arabidopsis AtGTG	1	MSVWALYEGTVVITASLILGLWAGLWFLNRRLYKEYEERRALVQILFSLVFAFSCNLLQLVLFELIPVLSSEARMINNKKV
Cabbage GPCR-like	1	MGWALTEGILVMGSLCLILGSAGLWFLNRRLYKEYEERRALVQILFSLVFAFSCNLLQLVLFELIPVLSSEARMINNKKV
Cotton GPCR-like	1	MGWGTVYEGAVVIGSLVLLWAGLWFLNRRLYKEYEERRALVQILFSLVFAFSCNLLQLVLFELIPVLSSEARMINNKKV
Citrus GPCR-like	1	MGWGIALYEGTVVTGSLILGLWAGLWFLNRRLYKEYEERRALVQILFSLVFAFSCNLLQLVLFELIPVLSSEARMINNKKV
Potato GPCR-like	1	MGWGRATYEGVIVVGSLLCLLGLWFLNRRLYKEYEERRALVQILFSLVFAFSCNLLQLVLFELIPVLSSEARMINNKKV
Consensus		*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*
ShGPCR1	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Sorghum GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Maize GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Rice Cold1-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Brachypodium GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Foxtail millet GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Arabidopsis AtGTG	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Cabbage GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Cotton GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Citrus GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Potato GPCR-like	81	DLFCLILLLVFVLPYYHCYLLLRNSGVRRRERASLVAALFLLVFLYGFWRMGHFFMPSPPEKGFFTMPQLVSRIGVIGSV
Consensus		*****.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*
ShGPCR1	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Sorghum GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Maize GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Rice Cold1-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Brachypodium GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Foxtail millet GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Arabidopsis AtGTG	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Cabbage GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Cotton GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Citrus GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Potato GPCR-like	161	MAVLSGFGAVNLPYSYLSLFIREIDEDIKTLERQLMQSIECTIAKKKKIILSQMEMERIQGSSEKILKARSFLKRIVGTV
Consensus		*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*
ShGPCR1	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Sorghum GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Maize GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Rice Cold1-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Brachypodium GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Foxtail millet GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Arabidopsis AtGTG	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Cabbage GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Cotton GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Citrus GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Potato GPCR-like	241	VRSVQEDQTEQDIKINLEAEVQALEELSQQFLFLEIYELRQAKIAAAYSRTWRGHLQNLGLYALSVCYVKMKLSQSVVFK
Consensus		*****.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*
ShGPCR1	321	ESGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Sorghum GPCR-like	321	ESGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Maize GPCR-like	321	ESGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Rice Cold1-like	321	EAGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Brachypodium GPCR-like	321	SAGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Foxtail millet GPCR-like	321	ESGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Arabidopsis AtGTG	321	EAGKDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Cabbage GPCR-like	321	EAGKDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Cotton GPCR-like	321	EAGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Citrus GPCR-like	321	EAGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Potato GPCR-like	321	EAGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIGMLVVISVRGFLANVMKFFFAVSRVSGSGSTTNVVLFLSEIMGM
Consensus		*****.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*
ShGPCR1	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Sorghum GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Maize GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Rice Cold1-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Brachypodium GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Foxtail millet GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Arabidopsis AtGTG	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Cabbage GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Cotton GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Citrus GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Potato GPCR-like	401	YFISSILLIRKSLANEYRVIIITDVLGGDIQDFYHRWFDAIFVASAFLSLLLSAQYTRQTDKHPID*
Consensus		*****.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*

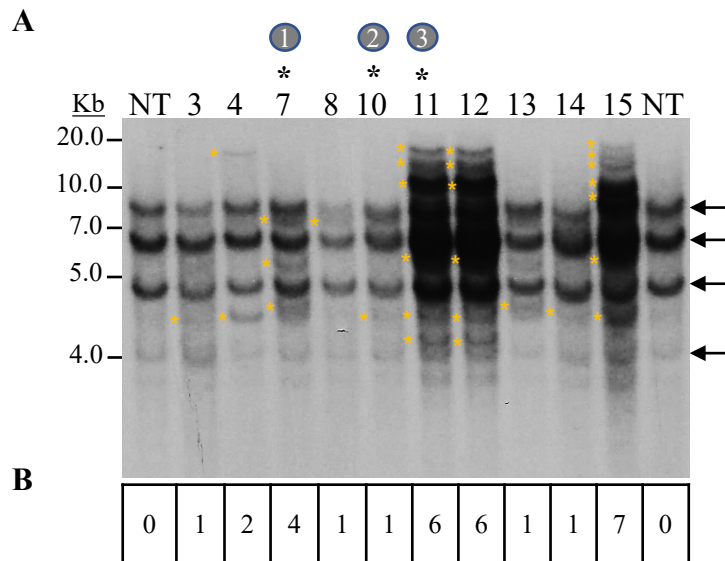
Supplemental Figure S1. Sequence homology of the sugarcane *ShGPCR1* protein with its orthologs in plants. Amino acid sequences were aligned using the BOXSHADE multiple sequence alignment program (version 3.21). Gene abbreviations and GenBank accession numbers are as follows: *Sorghum bicolor* (sorghum) (GPCR-like protein, XP_021317902.1), *Oryza sativa* (COLD1, LOC_Os04g51180.1), *Brachypodium distachyon* (GPCR-like protein, XP_003580421.1), *Zea mays* (maize) (GPCR-like protein, PWZ44530.1), *Setaria italica* (foxtail millet) (GPCR-like protein, XP_012702662.1), *Arabidopsis thaliana* (GTG1, AT1G64990.1), *Brassica oleracea* (cabbage) (GPCR-like protein, XP_013600854.1), *Gossypium raimondii* (cotton) (GPCR-like protein, Gorai.003G057600.2), *Citrus sinensis* (citrus) (GPCR-like protein, XP_006494940.1) and *Solanum tuberosum* (potato) (GPCR-like protein, XP_006357657.1). The consensus (cons.) symbols are indicated below the alignments with 100% identical residues indicated by black shading and an asterisk (*). Amino acids with $\geq 50\%$ identity is shaded in gray and marked with a period.



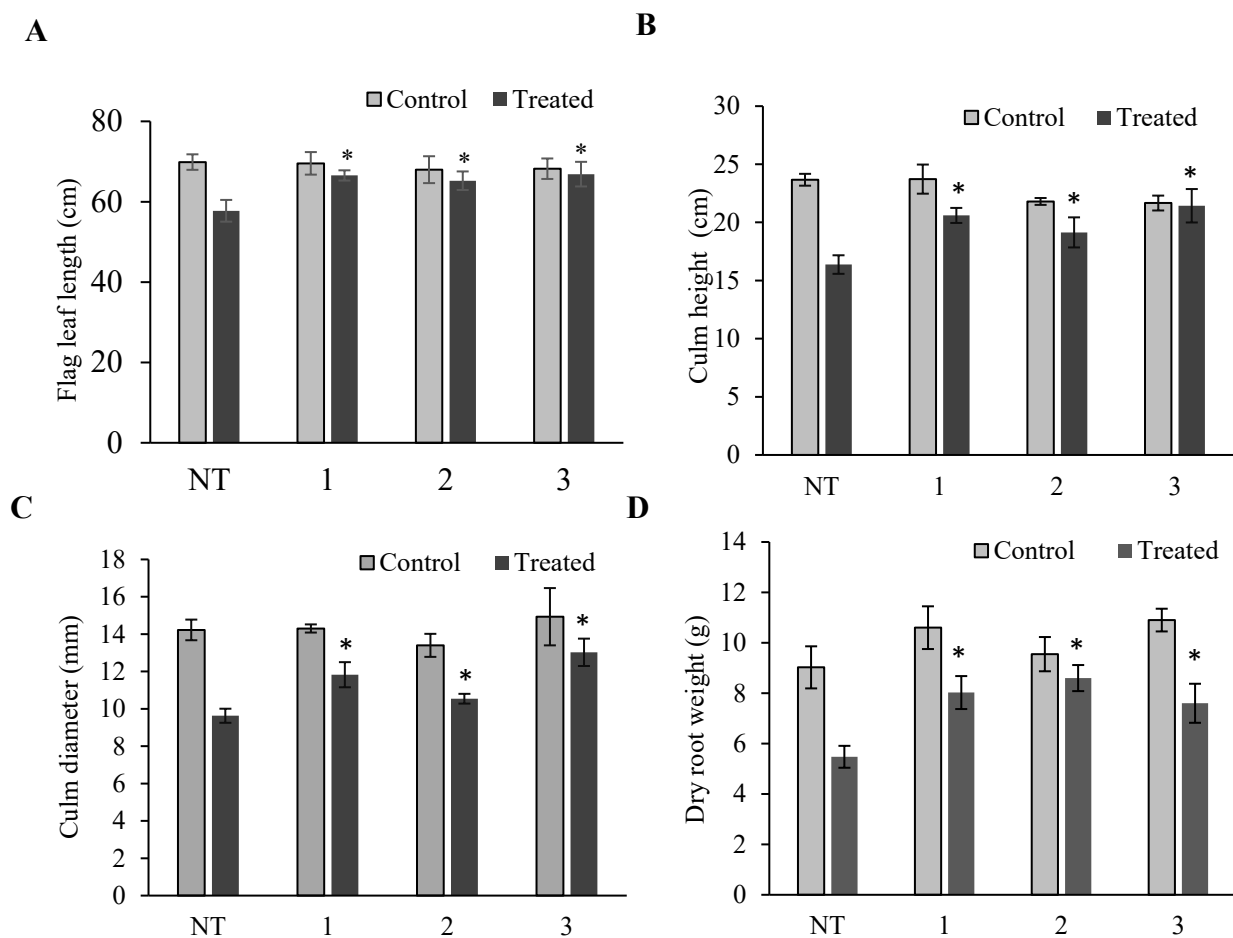
Supplemental Figure S2. Expression levels of *ShGPCR1* in detached sugarcane leaves after ABA treatment (10 h), as monitored by quantitative RT-PCR. Error bars represent the SE from three biological samples. Asterisks indicate statistically significant differences between control and treatment by Student's t-test (*, 95% confidence interval; $p < 0.05$; and **, 99% confidence interval; $p < 0.01$).



Supplemental Figure S3. Subcellular localization of *ShGPCR1* in sugarcane. Sugarcane embryogenic leaf rolls were bombarded either with *ShGPCR1::GFP* or *GFP* containing plasmids. **(A-D)** Visualization of *ShGPCR1::GFP* (top panels) or *GFP* (bottom panel) localization. *ShGPCR1::GFP* was predominantly localized to the plasma membrane (top inset in **A**), whereas *GFP* alone was detected predominantly in the cytosol (bottom inset in **A**). **(B-C)** The cells were stained with DAPI and FM4-64 to mark membrane and nuclear structures, respectively. **(D)** A merged image of all channels: *GFP*, FM4-64 and DAPI. Scale bar = 50 μm .



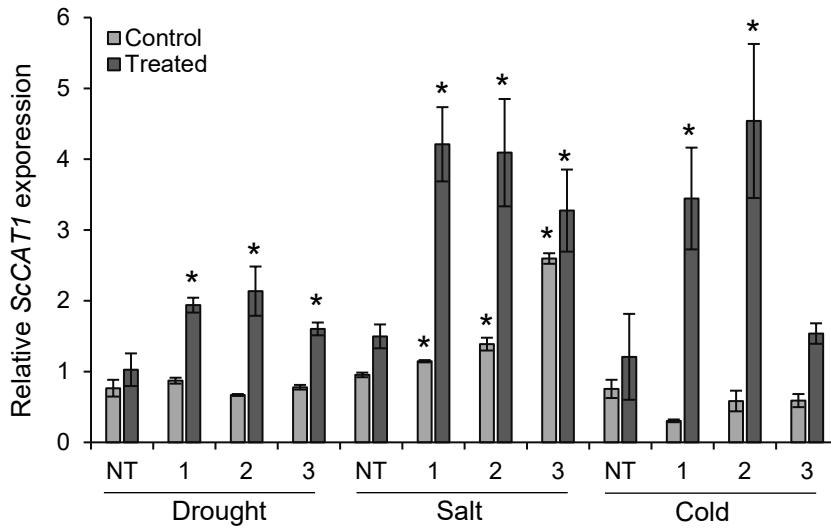
Supplemental Figure S4. Stable integration of *ShGPCR1* in the *ShGPCR1*-overexpressing (OE) lines as determined by Southern blot analysis. **(A)** *ShGPCR1* integration pattern of 10 lines. **(B)** Number of possible integrations (as indicated by yellow asterisks) of *ShGPCR1* in the sugarcane genome. The full-length *ShGPCR1* was used as a probe for hybridization. The signals observed in both non-transgenic (NT) plants and transgenic lines in the Southern blot are a result of the sugarcane endogenous *ShGPCR* hybridizing to the *ShGPCR1* probe. The hybridization bands found in NT are indicated by a black arrow. Black asterisks (*) and the number (7, 10, 11) indicate the selected *ShGPCR1*-OE lines used for characterization in abiotic stress tolerance assays.



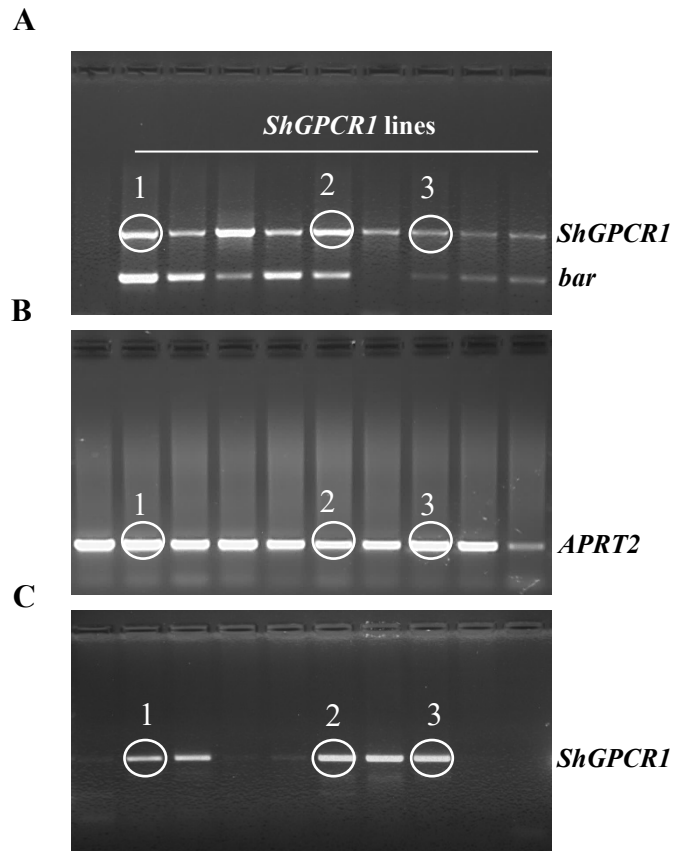
Supplemental Figure S5. Assessment of agronomic characters of three independent sugarcane *ShGPCR1*-overexpressing lines (1, 2 and 3) and non-transgenic (NT) plants (4-month-old) after 40 d of drought. **(A)** Flag leaf length, **(B)** culm height, **(C)** culm diameter, and **(D)** dry root weight. Asterisks indicate statistically significant differences between NT plants and *ShGPCR1*-OE lines by Student's t-test (*, 95% confidence interval; $p < 0.05$).



Supplemental Figure S6. Tolerance of the sugarcane *ShGPCR1*-overexpressing (OE) lines to cold stress. **(A, B)** Phenotype and severity index of independent *ShGPCR1*-*OE* lines (1, 2 and 3) in response to cold stress, compared to non-transgenic (NT) plants. For chilling stress tolerance assays, two-month-old greenhouse-grown *ShGPCR1:OE* and NT plants were treated at 4° C for three weeks followed by –5° C for 4 h in a temperature-controlled growth chamber. Scale bar = 2.5 cm.



Supplemental Figure S7. Expression levels of *Saccharum catalase1* (*ScCAT1*) gene in *ShGPCR1*-overexpression lines and NT plants after exposure to drought, salt, and cold treatment, as monitored by quantitative RT-PCR. Error bars represent the SE from three biological samples. Asterisks indicate statistically significant differences between control and treatment by Student's t-test (*, 95% confidence interval; $p < 0.05$).



Supplemental Figure S8. Uncropped raw agarose gel images used to prepare **Figures 2C, D** and **E**. Numbers correspond to the numbers of *ShGPCR1*-overexpressing lines (1, 2 and 3) selected for characterization in abiotic stress tolerance assays.

Supplementary Tables

A *Saccharum* spp. G-protein-coupled receptor, ShGPCR1, confers tolerance to multiple abiotic stresses.

Short Title: ShGPCR1 confers tolerance to multiple abiotic stresses in sugarcane.

Manikandan Ramasamy¹, Mona B. Damaj¹, Carol Vargas-Bautista^{1#}, Victoria Mora¹, Jiaxing Liu¹, Carmen S. Padilla¹, Sonia Irigoyen¹, Tripti Sani², Nirakar Sahoo², Jorge A. DaSilva^{1,3}, and Kranthi K. Mandadi^{1,4*}

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Supplementary Table S1. Primers used for quantifying expression levels of *ShGPCR1* and sugarcane stress-responsive marker genes. *LEA*: *LATE EMBRYOGENESIS ABUNDANT PROTEIN*; *DHY*: *DEHYDRIN*; *SCDR4*: *Saccharum DROUGHT RESPONSIVE 4*; *GOLS*: *GALACTINOL SYNTHASE*; *ERF3*: *ETHYLENE RESPONSIVE FACTOR 3*; *SOS1*: *SALT OVERLY SENSITIVE 1*; *ShNHX1*: *Saccharum VACUOLAR NA⁺/H⁺ ANTIporter 1*, *SsNAC23*: *NAM/ATAF1/2/CUC2*; *CBF2*: *COLD BINDING FACTOR 2*; *ScADH3*: *Saccharum ALCOHOL DEHYDROGENASE 3*; and *ScCAT1*: *Saccharum CATALASE 1*.

Primer	Sequence (5' to 3')	Reference
ShGPCR1-CF	CGGGATCCATGGGGTGGGGCACAGTGGTT	Present study
ShGPCR1-CR	GCCACGTGTCAATCAATCGGATGCTTGTCT	Present study
LEA-F	TGTTTCTCCATCTCCCGAGTG	(Reis et al., 2014)
LEA-R	CATGGCAGGGTCTCTCAAGC	(Reis et al., 2014)
DHY-F	ACCAGTACGGCAATCCAGTTG	(Reis et al., 2014)
DHY-R	CGGAGCGATGCAGGATG	(Reis et al., 2014)
SCDR4-F	ACGAGGAGCAGAGCTATGGT	(Reis et al., 2014)
SCDR4-R	CGGTTTTGGCTTCGGGTAA	(Reis et al., 2014)
GOLS-F	AGTACAGGCCGATCCCGAAC	(Iskandar et al., 2011)
GOLS-R	GCAGTAGTGCACGGCCTTC	(Iskandar et al., 2011)
ERF3-F	GATGGTCATGTGATTGCCGC	(Devi et al., 2019)
ERF3-R	CAAAGGCGCAAATCTGGCAG	(Devi et al., 2019)
SOS1-F	GAGGGTTCTCATAGCTGAAAGG	(Brindha et al., 2021)
SOS1-R	GCGTGATTAGAGTCAGGTTCTC	(Brindha et al., 2021)
ShNHX1-F	TGGTGGGCTGGACTGATGAGAGGCG	(Theerawitaya et al., 2020)
ShNHX1-R	TGCCGTGCAGCTGAGTGTGTCCAGA	(Theerawitaya et al., 2020)
SsNAC23-F	CGAGAAGACCAACTGGATCA	(Nogueira et al., 2005)
SsNAC23-R	GCCCTCCCTTCTTGTGTAG	(Nogueira et al., 2005)
CBF2-F	AGCGATGTATGGAGACTTGGC	(Mirkov et al., 2013)
CBF2-R	CTTGTGTGAGGTGGATGCGAT	(Mirkov et al., 2013)
ScADH3-F	AACCTTCTTCGGCAACTA	(Su et al., 2020)
ScADH3-R	CTCCAGCTCCTTCTTCAT	(Su et al., 2020)
ScCAT1-F	CTCTGCTCCTCCAATCCC	(Su et al., 2014)
ScCAT1-R	GAGTGACCTCAAAGAAACCCT	(Su et al., 2014)

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Supplementary Dataset

Short Title: ShGPCR1 confers tolerance to multiple abiotic stresses in sugarcane.

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>SC1-Coding Sequences (CDS)

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>SC1-Amino Acid Sequences

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LLISAQYTTRQTDKHPID*

>SC2- CDS

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>SC2-Amino Acid Sequences

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LLISAQYTTRQTDKHPID*

>SC3-CDS

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>SC3-Amino Acid Sequences

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LLISAQYTTRQTDKHPID*

>SC4-CDS

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>SC4-Amino Acid Sequences

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QLFLEIYELRQAKIAAAYSRTWRGHLQNLGYALSVYCVYKMLKSLQSVVFKESGSVDPVTMTITIFLRHFDIGIDAALLSQYISLMFIG
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LLISAQYTTRQTDKHPID*

>SC5-CDS

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>SC5-Amino Acid Sequences

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>EC1-CDS

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>EC1-Amino Acid Sequences

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>EC2-CDS

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>EC2- Amino Acid Sequences

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LLISAQYTTRQTDKHPID*

>EC3-CDS

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>EC3- Amino Acid Sequences

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LLISAQYTTRQTDKHPID*

>EC4-CDS

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>EC4- Amino Acid Sequences

MGWGTVVYEGAVVGSSLVGLGWAGLWFLNRRLYKEYEERRVLVQILFGLVFAFSCNLFELVLFEILPVLSKHARFLNWHLDLFLCLILL
LVFVLPPYHCYLLLRNSGVRRERSCLVAALFLLVFLYGFWRMGIHFPMPSPKEGFFTMPQLVSRIGVIGVSMAVLSGFGAVNLPYSYL
SLFIREIDETDIKTLERQLMQSMETCTAKKKKIILSQMEMERIQQSEEKLKARSFLKRIVGTVVRSVQEDQTEQDIKNLEAEVQALEELSK
QLFLEIYELRQAKIAAAAYSRTWRGHLQNLGYALSVYCVYKMLKSLQSVVFKESGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIG
MLVVISVRGFLANVMKFFFAVSRVSGSSTTNVVLFLSEIMGMYFISSILLIRKSLANEYRVIITDVLGGDIQDFYHRWFDAIFVASAFLSL
LLISAQYTTRQTDKHPID*

>EC5-CDS

ATGGGGTGGGGCACAGTGGTTTACGAGGGCGCGGCTCGTCGGCTCGTCGGTGGGGCTGGGCTGGGCGGGGCTGTGGTTCTCTGA
ACCGGCGGCTGTACAAGGAGTACGAGGAGCGGCGGGTGCTGGTGCAGATCCTCTTCGGCCTCGTCTTCGCCTTCTCCTGCAACCTC
TTCGAGCTCGTTCTCTTCGAGATCCTCCCCGCTCTCTCCAAGCATGCGCGCTTCTCAACTGGCACGTCGACCTCTTCTGCCTCATC
CTCCTCCTCGTCTTCGTGCTCCCCTACTACCACTGCTATCTTCTGCTCCGTAACCTCAGGAGTGAGGAGGGAGCGGTCTGCCTCGTC
GCGGCGCTCTTTCTGCTGGTCTTCTATACGGGTTCTGGCGCATGGGGATTCACTTCCCCATGCCTTCACCAGAGAAGGGTTTTTTT
ACGATGCCGCAGTTGGTCAGTAGGATTGGGGTGATTGGAGTGAGTGTATGCTGCTGTTCTTCTGGTTTTGGTGCTGTCAA TCTGCC
ATACAGTTATCTGTCACTCTTCATCAGGGAATTGATGAAACAGACATCAAAACCTTGGAACGGCAGCTGATGCAATCCATGGAG
ACATGTACTGCTAAGAAGAAGAAAATTATTTGTCCCAGATGGAGATGGAGAGGATTCAAGGATCAGAGGAGAAGCTAAAGGCC
AGATCGTTTCTGAAGCGTATAGTGGGAACTGTTGTCAGATCTGTGCAGGAAGATCAAACCTGAGCAGGATATAAAAACTTAGAAG
CAGAAGTCCAGGCACTAGAAGAGCTTTCCAAACAGCTGTTCCCTTGAGATATATGAACTCCGTCAGGCTAAGATAGCTGCTGCGTA
TTCTCGAACGTGGAGAGGGCATCTTCAGAATCTACTTGATATGCTTTGTCGGTGTATTGTGTTTATAAGATGCTCAAGTCCTTGC
AGAGTGTAGTCTTTAAGGAGTCAGGCTCTGTTGATCCTGTAACAATGACAATAACGATTTTCTGAGACATTTTGACATTGGCATT
GATGTTGCACTGTTATCTCAGTATATATCTTTGATGTTTCATTGGGATGTTGGTTGTCATATCTGTTGAGGTTTCTTGGCTAATGTTA
TGAAGTTCTTCTCGCTGTTTCTAGAGTTGGGAGTGGGTCGACAACCAATGTTGTCCTTTCTCTATCAGAGATCATGGGCATGTACT
TCATATCTTCCATTCTTCTTATAAGAAAAAGCCTGGCAAATGAATATAGGGTGATCATTACTGATGTTTTGGGTGGTGATATCCAA
TTTGACTTCTACCAACCGCTGGTTTGATGCTATATTTGTGGCTAGTGCGTTCTGTCTTCTGATTCTGCCAATACACCACCA
GGCAAACAGACAAGCATCCGATTGATTGA

>EC5- Amino Acid Sequences

MGWGTVVYEGAVVGSSLVGLGWAGLWFLNRRLYKEYEERRVLVQILFGLVFAFSCNLFELVLFEILPVLSKHARFLNWHVDLFLCLILL
LVFVLPPYHCYLLLRNSGVRRERSCLVAALFLLVFLYGFWRMGIHFPMPSPKEGFFTMPQLVSRIGVIGVSMAVLSGFGAVNLPYSYL
SLFIREIDETDIKTLERQLMQSMETCTAKKKKIILSQMEMERIQQSEEKLKARSFLKRIVGTVVRSVQEDQTEQDIKNLEAEVQALEELSK
QLFLEIYELRQAKIAAAAYSRTWRGHLQNLGYALSVYCVYKMLKSLQSVVFKESGSVDPVTMTITIFLRHFDIGIDVALLSQYISLMFIG
MLVVISVRGFLANVMKFFFAVSRVSGSSTTNVVLFLSEIMGMYFISSILLIRKSLANEYRVIITDVLGGDIQDFYHRWFDAIFVASAFLSL
LLISAQYTTRQTDKHPID*

Supplementary Dataset. Nucleotide and amino acid sequences of ten GPCR homeoalleles cloned and sequenced from sugarcane (SC) and energy cane (EC) varieties.