

## Supplementary file

Table S1: Identified common candidate motifs in PHT genes promoter regions of *Saccharum* spp. hybrid

Discovered motifs	Number of motifs (%)	E-value	Motif width	Total no. of binding sites
Motif 1	69.6	1.50E-20	41	16
Motif 2	100	7.10E-19	29	23
Motif 3	39	1.10E-26	50	9
Motif 4	30.4	2.5E-13	50	7
Motif 5	65.2	7.70E-24	41	15

Table S2: Identified common candidate motifs in PHT genes promoter regions of *Sorghum bicolor*

Discovered motif	Number of motifs (%)	E-value	Motif width	Total no. of binding sites
Motif 1	37	3.60E-107	50	10
Motif 2	33.3	1.60E-59	50	9
Motif 3	37	6.30E-48	41	10
Motif 4	85	1.00E-30	29	23
Motif 5	51.9	3.20E-14	14	14

Table S3: List of matches to the query motif from the database JASPAR2018\_CORE\_vertbrates\_non redundant for *Sorghum bicolor*

Matrix ID	Gene name	E-value	Overlap	Offset	Orientation	TF Family/Class
MA1723.1	PRDM9	2.47E-03	24	-5	Reverse Complement	C2H2 zinc finger factors
MA0528.2	ZNF263	5.85E-03	12	-5	Reverse Complement	C2H2 zinc finger factors
MA1965.1	SP5	8.78E-02	10	-6	Normal	C2H2 zinc finger factors
MA0149.1	EWSR1-FLI1	9.32E-02	18	-11	Reverse Complement	Ets-related
MA1961.1	PATZ1	9.66E-02	12	-5	Reverse Complement	C2H2 zinc finger factors
MA1713.1	ZNF610	1.11E-01	14	-1	Normal	C2H2 zinc finger factors
MA1653.1	ZNF148	1.78E-01	12	-4	Normal	C2H2 zinc finger factors
MA1522.1	MAZ	1.83E-01	11	-4	Normal	C2H2 zinc finger factors

MA1981.1	ZNF530	1.84E-01	18	-3	Reverse Complement	C2H2 zinc finger factors
MA1627.1	Wt1	2.84E-01	14	-6	Normal	C2H2 zinc finger factors

Table S4: MspI cutting sites and fragment sizes for PHT genes in the promoter regions in *Sorghum bicolor*

Promoter ID	No. of cut sites	Nucleotide positions of MspI sites
SbPHT1-1	3	1417, 1442, 1757
SbPHT1-2	0	-
SbPHT1-3	3	1207, 1570, 1834
SbPHT1-4	5	270, 1266, 1364, 1814, 1878
SbPHT1-5	10	1087, 1103, 1307, 1379, 1511, 1540, 1544, 1631, 1946, 1975
SbPHT1-6	3	1632, 1723, 1822
SbPHT1-7	3	1020, 1877, 1889
SbPHT1-8	4	62, 1478, 1759, 1906
SbPHT1-9	13	41, 54, 74, 127, 136, 147, 201, 222, 288, 309, 342, 961, 1208
SbPHT1-10	0	
SbPHT1-11	4	683, 1888, 1964, 1989
SbPHT1-12	5	218, 508, 1886, 1979, 1984
SbPHT2-1	3	28, 642, 1682
SbPHT3-1	5	228, 1530, 1557, 1577, 1790
SbPHT3-2	8	751, 1017, 1065, 1255, 1302, 1307, 1855, 1974
SbPHT3-3	2	1664, 1929
SbPHT3-4	7	24, 213, 337, 691, 1115, 1142, 1785
SbPHT3-5	8	231, 293, 299, 1654, 1807, 1818, 1834, 1993
SbPHT3-6	5	566, 661, 890, 897, 1618
SbPHT4-1	8	427, 481, 534, 588, 673, 703, 773, 1287
SbPHT4-2	3	778, 1571, 1709
SbPHT4-3	7	47, 933, 1537, 1595, 1609, 1714, 1927
SbPHT4-4	4	344, 456, 1663, 1834
SbPHT4-5	4	5, 147, 437, 1867
SbPHT4-6	15	34, 81, 794, 1133, 1234, 1291, 1301, 1358, 1403, 1456, 1464, 1479, 1486, 1585, 1637
SbPH01-1	3	230, 568, 1326
SbPH01-2	1	426

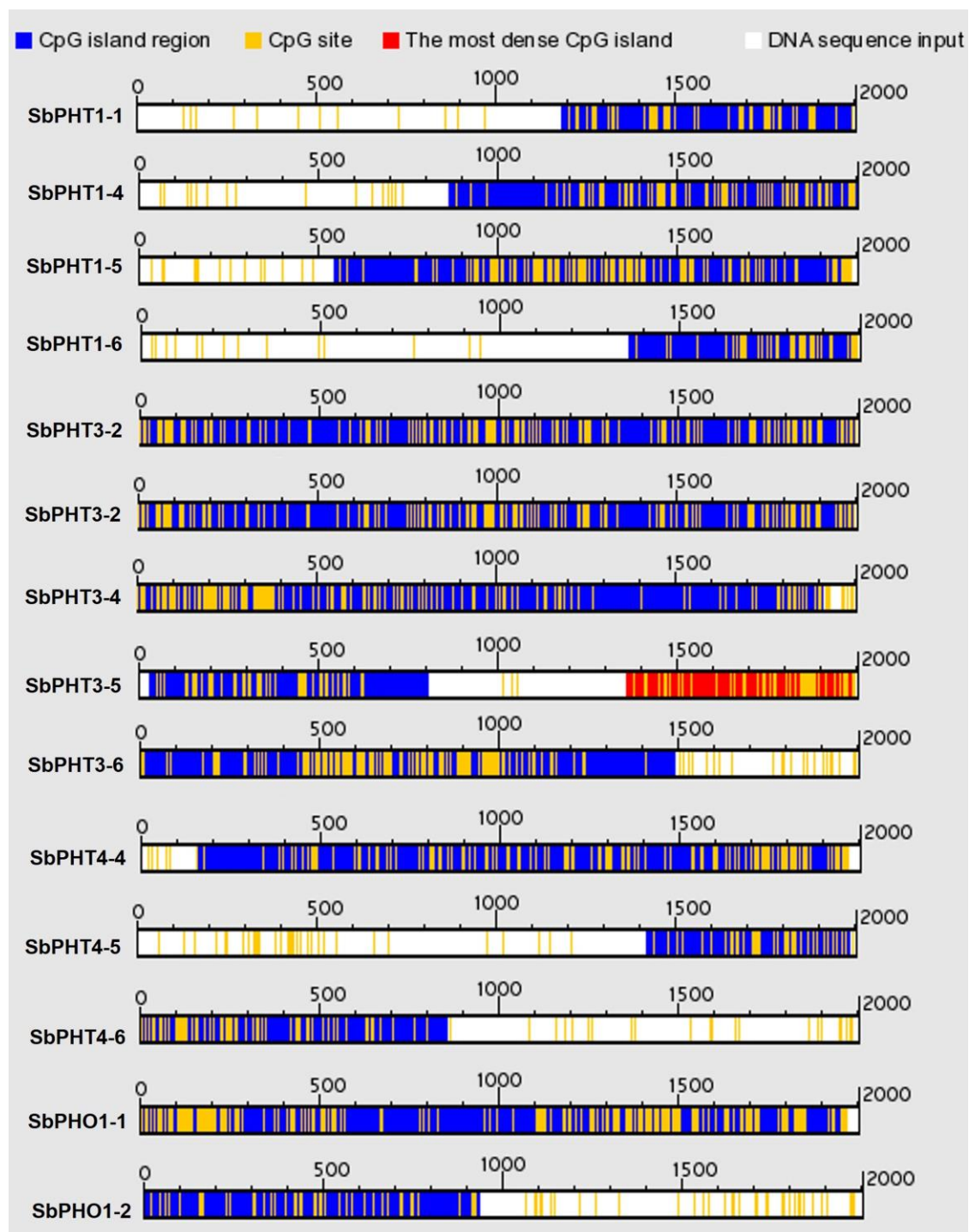


Figure S1: Visualization of promoter-associated CpG islands in the *SbPHT* genes promoter region using CpGi130.

## Promoter sequences used in this study.

**Promoter sequences of *Sorghum bicolor* (v3.1.12) PHT gene (SbPHT). The green highlights are the UTR regions.**

### >SbPHT1-1

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### >SbPHT1-2

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### >SbPHT1-3

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#### >SbPHT1-4

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#### >SbPHT1-5

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#### >SbPHT1-6

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#### >SbPHT1-7

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#### >SbPHT1-8

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#### >SbPHT1-9

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### >SbPHT1-10

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### >SbPHT1-11

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### >SbPHT1-12

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#### >SbPHT2-1

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### >SbPHT3-1

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### >SbPHT3-2

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### >SbPHT3-3

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#### >SbPHT3-4

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#### >SbPHT3-5

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### >SbPHT3-6

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### >SbPHT4-1

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#### >SbPHT4-2

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#### >SbPHT4-3

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#### >SbPHT4-4

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**TTGAGAATGTGCTAACCTAACCTGTCACAATAGATTCTAGTCCCAATTGTCCAACGAACCTGAAC**  
**TCTGCAGCACACTCCATCATGCACATGATATAAGTCCACACACCCAAAGC**

**Promoter sequences of *Saccharum* spp. hybrid (Sh) cultivar R570 PHT gene (ShPHT).**

>ShPHT1-1

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