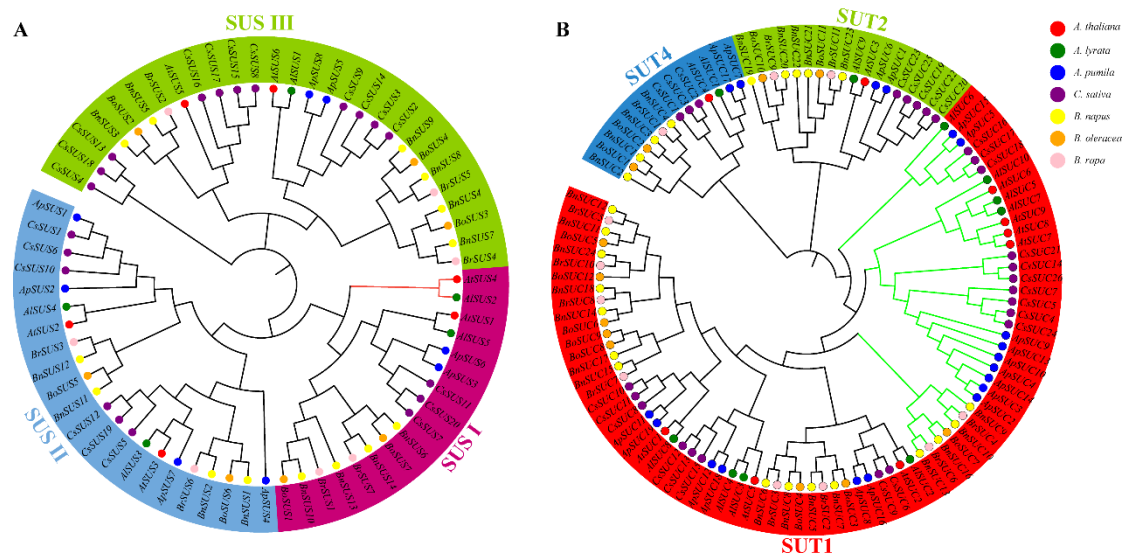


**Figure S1** The number of the identified sugar pathway gene members associated with flowering from seven Brassicaceae species



**Figure S2** Phylogenetic trees of SUS and SUC families from seven cruciferous plant. A: Phylogenetic trees of SUS gene family; B: Phylogenetic trees of SUC gene family. The red line indicates the genetic evolution branches of *atsus4* and six other plants, The green line indicates the genetic evolution branches of *AtSUC9* and six other plants, details of the original names corresponding to the names of members of SUS and SUC gene families in table S4 and table S5.

**Table S1** Genes related to flowering transition in the sugar pathway in *Arabidopsis thaliana*

Abbreviation of gene	Full name of gene	Gene ID	References
<i>TPS1</i>	<i>TREHALOSE-6-PHOSPHATE SYNTHASE 1</i>	AT1G78580	Wahl et al, 2013
<i>AKIN10, SNRK1.1</i>	<i>SNF1 KINASE HOMOLOG 10</i>	AT3G01090	Jeong et al, 2015
<i>SUS4</i>	<i>SUCROSE SYNTHASE 4</i>	AT3G43190	Baroja-Fernández et al, 2012
<i>PGI1</i>	<i>PHOSPHOGLUCOSE ISOMERASE 1</i>	AT4G24620	Yu et al, 2000
<i>HXK1, GIN2</i>	<i>HEXOKINASE 1</i>	AT4G29130	Yang et al, 2013
<i>SUC9</i>	<i>SUCROSE-PROTON SYMPORTER 9</i>	AT5G06170	Sivitz et al., 2007
<i>IDD8, NUC</i>	<i>INDETERMINATE DOMAIN 8</i>	AT5G44160	Seo et al., 2011
<i>ADG1, APS1</i>	<i>ADP GLUCOSE PYROPHOSPHORYLASE 1</i>	AT5G48300	Yu et al, 2000
<i>PGM1</i>	<i>PHOSPHOGLUCOMUTASE</i>	AT5G51820	Yu et al, 2000

**Table S2** Names of SUS gene family members in seven Brassicaceae species

Species	Gene	Gene ID
<i>Arabidopsis thaliana</i>	<i>AtSUS1</i>	AT5G20830.1
	<i>AtSUS2</i>	AT5G49190.1
	<i>AtSUS3</i>	AT4G02280.1
	<i>AtSUS4</i>	AT3G43190.1
	<i>AtSUS5</i>	AT5G37180.1
	<i>AtSUS6</i>	AT1G73370.1
<i>Arabidopsis lyrata</i>	<i>AlsUS1</i>	fgenes1_pm.C_scaffold_2001317
	<i>AlsUS2</i>	fgenes2_kg.5__780__AT3G43190.1
	<i>AlsUS3</i>	fgenes2_kg.6__3476__AT4G02280.1
	<i>AlsUS4</i>	fgenes2_kg.8__796__AT5G49190.1
	<i>AlsUS5</i>	scaffold_602179.1
<i>Arabidopsis pumila</i>	<i>ApSUS1</i>	evm.model.9__7__CONTIGS_16776222.209
	<i>ApSUS2</i>	evm.model.12__9__CONTIGS_14700693.1833
	<i>ApSUS3</i>	evm.model.4__12__CONTIGS_18100624.2820
	<i>ApSUS4</i>	evm.model.4__12__CONTIGS_18100624.738.1
	<i>ApSUS5</i>	evm.model.11__11__CONTIGS_16209776.1538
	<i>ApSUS6</i>	evm.model.6__5__CONTIGS_17268225.1633
	<i>ApSUS7</i>	evm.model.6__5__CONTIGS_17268225.236.1
	<i>ApSUS8</i>	evm.model.14__14__CONTIGS_14340626.772
<i>Camelina sativa</i>	<i>CsSUS1</i>	Csa11g078470.1
	<i>CsSUS2</i>	Csa16g036080.1
	<i>CsSUS3</i>	Csa16g036080.2
	<i>CsSUS4</i>	Csa03g006230.1
	<i>CsSUS5</i>	Csa08g052190.1
	<i>CsSUS6</i>	Csa18g018540.1
	<i>CsSUS7</i>	Csa08g014600.1
	<i>CsSUS8</i>	Csa10g040720.1
	<i>CsSUS9</i>	Csa09g077930.1
	<i>CsSUS10</i>	Csa02g035280.1
	<i>CsSUS11</i>	Csa20g032780.1
	<i>CsSUS12</i>	Csa02g005510.1
	<i>CsSUS13</i>	Csa20g016510.1
	<i>CsSUS14</i>	Csa07g040560.1
	<i>CsSUS15</i>	Csa11g050910.1
	<i>CsSUS16</i>	Csa12g074560.2
	<i>CsSUS17</i>	Csa12g074560.1
	<i>CsSUS18</i>	Csa20g016510.2
	<i>CsSUS19</i>	Csa13g054950.1
	<i>CsSUS20</i>	Csa13g024710.1
<i>BnSUS</i>	<i>BnSUS1</i>	GSBRNA2T00007838001
	<i>BnSUS2</i>	GSBRNA2T00018414001
	<i>BnSUS3</i>	GSBRNA2T00036780001

<i>Brassica napus</i>	<i>BnSUS4</i>	GSBRNA2T00049086001
	<i>BnSUS5</i>	GSBRNA2T00066235001
	<i>BnSUS6</i>	GSBRNA2T00094365001
	<i>BnSUS7</i>	GSBRNA2T00099500001
	<i>BnSUS8</i>	GSBRNA2T00102645001
	<i>BnSUS9</i>	GSBRNA2T00103416001
	<i>BnSUS10</i>	GSBRNA2T00140859001
	<i>BnSUS11</i>	GSBRNA2T00143079001
	<i>BnSUS12</i>	GSBRNA2T00144354001
	<i>BnSUS13</i>	GSBRNA2T00148916001
	<i>BnSUS14</i>	GSBRNA2T00154198001
<i>Brassica oleracea</i>	<i>BoSUS1</i>	BolC03g010920.2J
	<i>BoSUS2</i>	BolC06g017370.2J
	<i>BoSUS3</i>	BolC06g032260.2J
	<i>BoSUS4</i>	BolC06g044870.2J
	<i>BoSUS5</i>	BolC07g038200.2J
	<i>BoSUS6</i>	BolC09g001700.2J
	<i>BoSUS7</i>	BolC09g051640.2J
<i>Brassica rapa</i>	<i>BrSUS1</i>	BraA03g009830.3C
	<i>BrSUS2</i>	BraA05g015010.3C
	<i>BrSUS3</i>	BraA06g034940.3C
	<i>BrSUS4</i>	BraA07g028740.3C
	<i>BrSUS5</i>	BraA07g037520.3C
	<i>BrSUS6</i>	BraA09g001880.3C
	<i>BrSUS7</i>	BraA10g019840.3C

**Table S3** Names of members of the SUC gene family members in seven *Brassicaceae* species

Species	Gene	Gene ID
<i>Arabidopsis thaliana</i>	<i>AtSUC1</i>	AT1G71880
	<i>AtSUC2</i>	AT1G22710
	<i>AtSUC3</i>	AT2G02860
	<i>AtSUC4</i>	AT1G09960
	<i>AtSUC5</i>	AT1G71890
	<i>AtSUC6</i>	AT5G43610
	<i>AtSUC7</i>	AT1G66570
	<i>AtSUC8</i>	AT2G14670
	<i>AtSUC9</i>	AT5G06170
<i>Arabidopsis lyrata</i>	<i>ALSUC1</i>	fgenes2_kg.1_1061_AT1G09960.1
	<i>ALSUC2</i>	fgenes2_kg.1_2467_AT1G22710.1
	<i>ALSUC3</i>	fgenes2_kg.2_1445_AT1G71890.1
	<i>ALSUC4</i>	fgenes2_kg.106_1_AT1G71890.1
	<i>ALSUC5</i>	fgenes2_kg.6_554_AT1G66570.1
	<i>ALSUC6</i>	scaffold_603288.1
	<i>ALSUC7</i>	Al_scaffold_0002_1232
	<i>ALSUC8</i>	scaffold_202108.1
	<i>ALSUC9</i>	fgenes2_kg.5_187_AT2G02860.1
	<i>ALSUC10</i>	fgenes1_pm.C_scaffold_3002472
<i>Arabidopsis pumila</i>	<i>ApSUC1</i>	evm.model.13_8_CONTIGS_14517794.145
	<i>ApSUC2</i>	evm.model.4_12_CONTIGS_18100624.3403
	<i>ApSUC3</i>	evm.model.4_12_CONTIGS_18100624.1444
	<i>ApSUC4</i>	evm.model.4_12_CONTIGS_18100624.1470
	<i>ApSUC5</i>	evm.model.4_12_CONTIGS_18100624.219
	<i>ApSUC6</i>	evm.model.3_5_CONTIGS_18323972.2753
	<i>ApSUC7</i>	evm.model.2_6_CONTIGS_19393823.2691
	<i>ApSUC8</i>	evm.model.2_6_CONTIGS_19393823.1520
	<i>ApSUC9</i>	evm.model.7_7_CONTIGS_17117682.171
	<i>ApSUC10</i>	evm.model.7_7_CONTIGS_17117682.2745
	<i>ApSUC11</i>	evm.model.11_11_CONTIGS_16209776.1689
	<i>ApSUC12</i>	evm.model.11_11_CONTIGS_16209776.1688
	<i>ApSUC13</i>	evm.model.6_5_CONTIGS_17268225.2998
	<i>ApSUC14</i>	evm.model.6_5_CONTIGS_17268225.3022
	<i>ApSUC15</i>	evm.model.6_5_CONTIGS_17268225.747
	<i>ApSUC16</i>	evm.model.1_5_CONTIGS_22361435.2083
	<i>ApSUC17</i>	evm.model.1_5_CONTIGS_22361435.899
	<i>ApSUC18</i>	evm.model.14_14_CONTIGS_14340626.915
	<i>ApSUC19</i>	evm.model.14_14_CONTIGS_14340626.916
<i>CsSUC</i>	<i>CsSUC1</i>	Csa03g013400.1
	<i>CsSUC2</i>	Csa14g011470.1
	<i>CsSUC3</i>	Csa17g013590.1

<i>Camelina sativa</i>	<i>CsSUC4</i>	Csa04g024680.1
	<i>CsSUC5</i>	Csa04g024680.2
	<i>CsSUC6</i>	Csa17g029640.1
	<i>CsSUC7</i>	Csa09g035840.1
	<i>CsSUC8</i>	Csa09g075220.1
	<i>CsSUC9</i>	Csa14g027910.1
	<i>CsSUC10</i>	Csa07g038820.1
	<i>CsSUC11</i>	Csa16g034520.1
	<i>CsSUC12</i>	Csa07g038830.1
	<i>CsSUC13</i>	Csa16g034540.1
	<i>CsSUC14</i>	Csa20g008390.1
	<i>CsSUC15</i>	Csa09g075230.1
	<i>CsSUC16</i>	Csa02g028390.1
	<i>CsSUC17</i>	Csa13g043590.1
	<i>CsSUC18</i>	Csa08g037440.1
	<i>CsSUC19</i>	Csa09g005070.1
	<i>CsSUC20</i>	Csa04g008350.2
	<i>CsSUC21</i>	Csa08g058350.1
	<i>CsSUC22</i>	Csa04g008350.1
	<i>CsSUC23</i>	Csa06g002850.1
	<i>CsSUC24</i>	Csa06g018450.1
	<i>CsSUC25</i>	Csa09g005070.2
	<i>CsSUC26</i>	Csa20g008380.1
<i>Brassica napus</i>	<i>BnSUC1</i>	GSBRNA2T00037540001
	<i>BnSUC2</i>	GSBRNA2T00156127001
	<i>BnSUC3</i>	GSBRNA2T00019276001
	<i>BnSUC4</i>	GSBRNA2T00011511001
	<i>BnSUC5</i>	GSBRNA2T00033135001
	<i>BnSUC6</i>	GSBRNA2T00015756001
	<i>BnSUC7</i>	GSBRNA2T00061853001
	<i>BnSUC8</i>	GSBRNA2T00119488001
	<i>BnSUC9</i>	GSBRNA2T00134421001
	<i>BnSUC10</i>	GSBRNA2T00049405001
	<i>BnSUC11</i>	GSBRNA2T00103236001
	<i>BnSUC12</i>	GSBRNA2T00102508001
	<i>BnSUC13</i>	GSBRNA2T00029602001
	<i>BnSUC14</i>	GSBRNA2T00137296001
	<i>BnSUC15</i>	GSBRNA2T00099581001
	<i>BnSUC16</i>	GSBRNA2T00107013001
	<i>BnSUC17</i>	GSBRNA2T00062437001
	<i>BnSUC18</i>	GSBRNA2T00116464001
	<i>BnSUC19</i>	GSBRNA2T00073348001
	<i>BnSUC20</i>	GSBRNA2T00030810001
	<i>BnSUC21</i>	GSBRNA2T00115350001

	<i>BnSUC22</i>	GSBRNA2T00062975001
	<i>BnSUC23</i>	GSBRNA2T00081619001
	<i>BnSUC24</i>	GSBRNA2T00081760001
<i>Brassica oleracea</i>	<i>BoSUC1</i>	BolC05g007810.2J
	<i>BoSUC2</i>	BolC08g056300.2J
	<i>BoSUC3</i>	BolC07g020620.2J
	<i>BoSUC4</i>	BolC05g021040.2J
	<i>BoSUC5</i>	BolC06g043310.2J
	<i>BoSUC6</i>	BolC02g028540.2J
	<i>BoSUC7</i>	BolC09g065780.2J
	<i>BoSUC8</i>	BolC09g022600.2J
	<i>BoSUC9</i>	BolC06g033450.2J
	<i>BoSUC10</i>	BolC02g050720.2J
	<i>BoSUC11</i>	BolC07g032500.2J
	<i>BoSUC12</i>	BolC07g057680.2J
<i>Brassica rapa</i>	<i>BrSUC1</i>	BraA09g062110.3C
	<i>BrSUC2</i>	BraA07g014520.3C
	<i>BrSUC3</i>	BraA09g040330.3C
	<i>BrSUC4</i>	BraA03g002390.3C
	<i>BrSUC5</i>	BraA07g036350.3C
	<i>BrSUC6</i>	BraA10g028880.3C
	<i>BrSUC7</i>	BraA07g029350.3C
	<i>BrSUC8</i>	BraA02g020540.3C
	<i>BrSUC9</i>	BraA02g035840.3C
	<i>BrSUC10</i>	BraA03g058820.3C
	<i>BrSUC11</i>	BraA06g039570.3C



**Table S4** Accession numbers of RNA-Seq data of *Arabidopsis pumila* nine different tissues

Accession number	Library ID	Tissues
SRR14470720	EM	Embryo
SRR14470722	YR	Young root
SRR14470717	MR	Mature root
SRR14470714	RL	Rosette leaf
SRR14470712	CL	Cauline leaf
SRR14470713	BU	Bud
SRR14470719	FL	Flower
SRR14470724	SL	Silique
SRR14470710	SE	Seed

**Table S5** Primer sequences used in qPCR assay

Primer	Primer sequence (5'→3')
ApADG1-1-F	GACATCTTTCCCGTGCGTAT
ApADG1-1-R	AGTCTCCCTATGCGCTTGAA
ApADG1-2-F	AAGGCCATGAAGGTTGACAC
ApADG1-2-R	CTTCGCTTCCGAAGTCATTC
ApADG1-4-F	GCTGATGCTGTGAGGCAGTA
ApADG1-4-R	AGGAAGAGCAGCAACCGTAA
ApGADPH-F	CTCCCATGTTTGTTGTTGGTGTC
ApGADPH-R	CTCCACCTCTCCAGTCCTTCATT

**Table S6** Information on the identified sugar pathway gene members identified to be associated with flowering from seven Brassicaceae species

Species	Gene	Gene ID	Chromosome No.	Amino acid No.	Molecular weight (kDa)	PI	Subcellular localization
<i>Arabidopsis thaliana</i>	<i>AtTPS1</i>	AT1G78580	Chr1	942	105.98	6.70	Cell wall and Vacuole
	<i>AtSNRK1.1</i>	AT3G01090	Chr3	535	61.18	8.44	Nucleus
	<i>AtSUS4</i>	AT3G43190	Chr3	808	93.00	6.12	Chloroplast
	<i>AtPGI1</i>	AT4G24620	Chr4	613	67.05	5.47	Cytoplasm
	<i>AtH XK1</i>	AT4G29130	Chr4	496	53.71	5.76	Chloroplast and Mitochondrion
	<i>AtSUC9</i>	AT5G06170	Chr5	491	52.58	9.13	Cell membrane
	<i>AtIDD8</i>	AT5G44160	Chr5	466	51.19	8.36	Nucleus
	<i>AtADG1</i>	AT5G48300	Chr5	520	56.65	6.13	Chloroplast
	<i>AtPGM1</i>	AT5G51820	Chr5	623	67.99	5.48	Chloroplast
<i>Arabidopsis lyrata</i>	<i>AtTPS1</i>	fgenes2_kg.2_2152_AT1G78580.1	Chr2	955	107.40	6.92	Cell wall; Cytoplasm and Vacuole
	<i>AtSNRK1.1</i>	fgenes1_pm.C_scaffold_3000097	Chr3	509	58.05	8.01	Nucleus
	<i>AtSUS4</i>	fgenes2_kg.5_780_AT3G43190.1	Chr5	808	92.64	6.02	Chloroplast
	<i>AtPGI1</i>	fgenes2_kg.7_1814_AT4G24620.1	Chr7	613	67.13	5.42	Cytoplasm
	<i>AtH XK1</i>	scaffold_701340.1	Chr7	496	53.74	5.66	Chloroplast and Mitochondrion
	<i>AtIDD8</i>	scaffold_800604.1	Chr8	464	51.17	8.61	Nucleus
	<i>AtADG1</i>	fgenes2_kg.8_698_AT5G48300.1	Chr8	521	57.06	6.30	Chloroplast
	<i>AtPGM1</i>	fgenes2_kg.8_1063_AT5G51820.1	Chr8	618	67.31	5.32	Chloroplast
<i>Arabidopsis pumila</i>	<i>ApTPS1-1</i>	evm.model.14_14_CONTIGS_14340626.258	Chr14	944	106.24	6.80	Cell wall and Vacuole
	<i>ApTPS1-2</i>	evm.model.11_11_CONTIGS_16209776.830	Chr9	947	106.59	6.81	Cell wall; Cytoplasm and Vacuole
	<i>ApSNRK1.1-1</i>	evm.model.5_10_CONTIGS_17087769.3140	Chr7	397	45.83	6.29	Nucleus
	<i>ApSNRK1.1-2</i>	evm.model.8_3_CONTIGS_16920646.3113	Chr8	392	45.19	5.93	Nucleus
	<i>ApPGI1-1</i>	evm.model.0_8_CONTIGS_29314649.4500	Chr5	613	67.29	5.43	Cytoplasm
	<i>ApPGI1-2</i>	evm.model.0_8_CONTIGS_29314649.1181	Chr11	614	67.46	5.49	Cytoplasm
	<i>ApH XK1-1</i>	evm.model.0_8_CONTIGS_29314649.4954	Chr5	498	53.89	5.71	Chloroplast and Mitochondrion

<i>Camelina sativa</i>	<i>ApH XK1-2</i>	evm.model.0__8_CONTIGS_29314649.1623	Chr11	498	54.03	5.80	Chloroplast and Mitochondrion
	<i>ApIDD8-1</i>	evm.model.12__9_CONTIGS_14700693.2307	Chr15	465	50.76	8.46	Nucleus
	<i>ApIDD8-2</i>	evm.model.9__7_CONTIGS_16776222.2421	Chr10	460	50.27	8.44	Nucleus
	<i>ApADG1-1</i>	evm.model.12__9_CONTIGS_14700693.1936	Chr15	510	55.71	5.92	Chloroplast
	<i>ApADG1-2</i>	evm.model.9__7_CONTIGS_16776222.114	Chr10	511	55.97	5.80	Chloroplast
	<i>ApADG1-3</i>	evm.model.5__10_CONTIGS_17087769.582	Chr7	518	56.76	6.30	Chloroplast
	<i>ApADG1-4</i>	evm.model.8__3_CONTIGS_16920646.847	Chr8	518	56.79	6.11	Chloroplast
	<i>ApPGM1-1</i>	evm.model.9__7_CONTIGS_16776222.478	Chr10	626	68.17	5.40	Chloroplast
	<i>ApPGM1-2</i>	evm.model.12__9_CONTIGS_14700693.1587	Chr15	626	68.18	5.55	Chloroplast
	<i>CsTPS1-1</i>	Csa09g092680.1	Chr9	1038	117.18	6.95	Vacuole
	<i>CsTPS1-2</i>	Csa07g057580.1	Chr7	1010	113.44	6.51	Cell wall; Cytoplasm and Vacuole
	<i>CsTPS1-3</i>	Csa16g048140.1	Chr16	1095	122.76	8.07	Cell wall and Vacuole
	<i>CsSNRK1.1-1</i>	Csa19g002550.1	Chr19	509	57.98	8.01	Nucleus
	<i>CsSNRK1.1-2</i>	Csa15g001490.1	Chr15	509	57.97	8.01	Nucleus
	<i>CsSNRK1.1-3</i>	Csa01g001460.1	Chr1	509	58.01	8.01	Nucleus
	<i>CsPGI1-1</i>	Csa12g029700.1	Chr12	617	67.62	5.41	Cytoplasm
	<i>CsPGI1-2</i>	Csa10g018420.1	Chr10	615	67.32	5.30	Cytoplasm
	<i>CsPGI1-3</i>	Csa11g020110.1	Chr11	616	67.43	5.37	Cytoplasm
<i>Camelina sativa</i>	<i>CsH XK1-1</i>	Csa12g020330.1	Chr12	496	53.65	5.86	Chloroplast and Mitochondrion
	<i>CsH XK1-2</i>	Csa10g013440.1	Chr10	499	54.02	5.77	Chloroplast and Mitochondrion
	<i>CsH XK1-3</i>	Csa11g014380.1	Chr11	499	54.05	5.77	Chloroplast and Mitochondrion
	<i>CsIDD8-1</i>	Csa20g071190.1	Chr20	464	50.68	8.58	Nucleus
	<i>CsIDD8-2</i>	Csa18g009620.1	Chr18	468	51.27	8.45	Nucleus
	<i>CsIDD8-3</i>	Csa20g071190.2	Chr20	453	49.38	8.52	Nucleus
	<i>CsIDD8-4</i>	Csa11g070530.1	Chr11	391	42.20	6.38	Nucleus
	<i>CsADG1-1</i>	Csa18g014380.1	Chr18	518	56.65	5.87	Chloroplast

	<i>CsADG1-2</i>	Csa11g074430.1	Chr11	520	56.83	5.87	Chloroplast
	<i>CsADG1-3</i>	Csa20g041200.1	Chr20	523	57.22	5.87	Chloroplast
	<i>CsPGM1-1</i>	Csa18g022680.1	Chr18	619	67.24	5.38	Chloroplast
	<i>CsPGM1-2</i>	Csa02g044730.1	Chr2	617	66.90	5.09	Chloroplast
	<i>CsPGM1-3</i>	Csa11g083410.1	Chr11	617	66.87	5.13	Chloroplast
<i>Brassica napus</i>	<i>BnTPS1-1</i>	GSBRNA2T00148002001	ChrC06	951	107.08	6.63	Cell wall; Cytoplasm and Vacuole
	<i>BnTPS1-2</i>	GSBRNA2T00146430001	ChrA07	950	106.94	6.63	Cell wall; Cytoplasm and Vacuole
	<i>BnTPS1-3</i>	GSBRNA2T00084348001	ChrC02	932	104.80	6.74	Cell wall; Cytoplasm and Vacuole
	<i>BnTPS1-4</i>	GSBRNA2T00036543001	ChrA02	774	87.35	6.63	Cytoplasm and Vacuole
	<i>BnSNRK1.1-1</i>	GSBRNA2T00017357001	ChrCnn	511	58.04	8.01	Nucleus
	<i>BnSNRK1.1-2</i>	GSBRNA2T00057213001	ChrA01	511	58.08	8.01	Nucleus
	<i>BnSNRK1.1-3</i>	GSBRNA2T00064166001	ChrA05	506	57.63	8.03	Nucleus
	<i>BnSNRK1.1-4</i>	GSBRNA2T00076301001	ChrC05	506	57.67	8.03	Nucleus
	<i>BnPGI1-1</i>	GSBRNA2T00116085001	ChrC01	615	66.98	5.23	Cytoplasm
	<i>BnPGI1-2</i>	GSBRNA2T00048977001	ChrA03	613	66.84	5.38	Cytoplasm
	<i>BnPGI1-3</i>	GSBRNA2T00056331001	ChrA01	616	67.02	5.22	Cytoplasm
	<i>BnPGI1-4</i>	GSBRNA2T00154458001	ChrC07	614	66.88	5.23	Cytoplasm
	<i>BnH XK1-1</i>	GSBRNA2T00059441001	ChrA07	500	54.03	5.49	Chloroplast and Mitochondrion
	<i>BnH XK1-2</i>	GSBRNA2T00138056001	ChrC07	499	53.93	5.63	Chloroplast and Mitochondrion
	<i>BnH XK1-3</i>	GSBRNA2T00091626001	ChrA09	499	53.90	5.40	Chloroplast and Mitochondrion
	<i>BnH XK1-4</i>	GSBRNA2T00115923001	ChrC09	499	54.04	5.27	Chloroplast and Mitochondrion
	<i>BnIDD8-1</i>	GSBRNA2T00018774001	ChrA06	464	50.61	8.60	Nucleus
	<i>BnIDD8-2</i>	GSBRNA2T00158200001	ChrC07	464	50.63	8.69	Nucleus
	<i>BnADG1-1</i>	GSBRNA2T00076549001	ChrCnn	511	56.14	6.30	Chloroplast
	<i>BnADG1-2</i>	GSBRNA2T00144434001	ChrA06	513	56.12	6.73	Chloroplast
	<i>BnADG1-3</i>	GSBRNA2T00110776001	ChrCnn	520	57.07	5.99	Chloroplast

	<i>BnADG1-4</i>	GSBRNA2T00038740001	ChrA07	520	57.04	5.86	Chloroplast
	<i>BnPGM1-1</i>	GSBRNA2T00110218001	ChrA10	635	69.12	5.77	Chloroplast
	<i>BnPGM1-2</i>	GSBRNA2T00042494001	ChrCnn	629	68.52	5.48	Chloroplast
<i>Brassica oleracea</i>	<i>BoTPS1-1</i>	BolC06g049480.2J	Chr6	951	107.08	6.63	Cell wall; Cytoplasm and Vacuole
	<i>BoTPS1-2</i>	BolC02g034630.2J	Chr2	947	106.42	6.87	Cell wall; Cytoplasm and Vacuole
	<i>BoSNRK1.1-1</i>	BolC01g057210.2J	Chr1	511	58.04	8.01	Nucleus
	<i>BoSNRK1.1-2</i>	BolC05g062460.2J	Chr5	513	58.35	8.00	Nucleus
	<i>BoSNRK1.1-3</i>	BolC03g035940.2J	Chr3	528	59.97	8.79	Nucleus
	<i>BoPGII-1</i>	BolC01g019030.2J	Chr1	592	64.42	5.05	Cytoplasm
	<i>BoPGII-2</i>	BolC01g019040.2J	Chr1	518	56.52	5.43	Cytoplasm
	<i>BoH XK1-1</i>	BolC07g001520.2J	Chr7	499	53.92	5.63	Chloroplast and Mitochondrion
	<i>BoH XK1-2</i>	BolC09g014060.2J	Chr9	499	54.04	5.27	Chloroplast and Mitochondrion
	<i>BoIDD8</i>	BolC07g025980.2J	Chr7	464	50.60	8.69	Nucleus
	<i>BoADG1-1</i>	BolC07g037440.2J	Chr7	511	56.07	6.14	Chloroplast
	<i>BoADG1-2</i>	BolC07g010610.2J	Chr7	627	69.16	6.51	Chloroplast
	<i>BoPGM1</i>	BolC09g038330.2J	Chr9	629	68.52	5.48	Chloroplast
<i>Brassica rapa</i>	<i>BrTPS1-1</i>	BraA07g041670.3C	Chr9	975	109.93	6.65	Vacuole
	<i>BrTPS1-2</i>	BraA02g024760.3C	Chr2	921	103.67	6.75	Cell wall and Vacuole
	<i>BrSNRK1.1-1</i>	BraA01g044590.3C	Chr1	511	58.06	8.01	Nucleus
	<i>BrSNRK1.1-2</i>	BraA05g040920.3C	Chr5	506	57.63	8.03	Nucleus
	<i>BrSNRK1.1-3</i>	BraA03g030660.3C	Chr3	523	59.642	8.86	Nucleus
	<i>BrPGII-1</i>	BraA01g015390.3C	Chr1	616	67.08	5.32	Cytoplasm
	<i>BrPGII-2</i>	BraA03g052000.3C	Chr3	613	66.79	5.33	Cytoplasm
	<i>BrH XK1-1</i>	BraA07g000960.3C	Chr7	500	54.06	5.42	Chloroplast and Mitochondrion
	<i>BrH XK1-2</i>	BraA09g012100.3C	Chr9	499	53.93	5.40	Chloroplast and Mitochondrion
	<i>BrIDD8</i>	BraA06g043270.3C	Chr6	453	49.34	8.76	Nucleus

<i>BrADG1-1</i>	BraA07g007620.3C	Chr7	520	57.04	5.86	Chloroplast
<i>BrADG1-2</i>	BraA06g035670.3C	Chr6	513	56.32	7.09	Chloroplast
<i>BrPGM1</i>	BraA10g010420.3C	Chr10	670	73.34	5.80	Chloroplast

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**Table S7** The non-synonymous (*Ka*) and synonymous (*Ks*) of orthologous gene pairs of the sugar pathway members in seven Brassicaceae spp.

Collinear gene pair	Protein sequence similarity (%)	<i>Ka</i>	<i>Ks</i>	<i>Ka/Ks</i>	Evolutionary selection
<i>AtTPS1</i> / <i>AITPS1</i>	96.957	0.008360514	0.163302835	0.051196379	Purification selection
<i>AtSNRK1.1</i> / <i>AlSNRK1.1</i>	98.242	0.005539404	0.089613416	0.061814456	Purification selection
<i>AtSUS4</i> / <i>AlSUS4</i>	96.287	0.017094757	0.214461180	0.079710263	Purification selection
<i>AtPGI1</i> / <i>AlPGI1</i>	98.695	0.005781072	0.104807563	0.055158917	Purification selection
<i>AtH XK1</i> / <i>AlH XK1</i>	98.185	0.008011946	0.091830529	0.087247081	Purification selection
<i>AtIDD8</i> / <i>AlIDD8</i>	94.433	0.019881252	0.164226135	0.121060223	Purification selection
<i>AtADG1</i> / <i>AlADG1</i>	95.202	0.023799080	0.19262735	0.123549851	Purification selection
<i>AtPGM1</i> / <i>AlPGM1</i>	94.409	0.016342081	0.160534265	0.101798085	Purification selection
<i>AtTPS1</i> / <i>ApTPS1-1</i>	98.095	0.008949432	0.221002578	0.040494696	Purification selection
<i>AtTPS1</i> / <i>ApTPS1-2</i>	97.996	0.007428389	0.201750621	0.036819659	Purification selection
<i>AtSNRK1.1</i> / <i>ApSNRK1.1-1</i>	97.906	0.045932229	0.190464354	0.241159190	Purification selection
<i>AtSNRK1.1</i> / <i>ApSNRK1.1-2</i>	96.859	0.023642620	0.139939467	0.168948905	Purification selection
<i>AtPGI1</i> / <i>ApPGI1-1</i>	96.580	0.017070955	0.206122272	0.082819555	Purification selection
<i>AtPGI1</i> / <i>ApPGI1-2</i>	96.585	0.016351402	0.185184129	0.088298072	Purification selection
<i>AtH XK1</i> / <i>ApH XK1-1</i>	96.192	0.016110405	0.241283866	0.066769506	Purification selection
<i>AtH XK1</i> / <i>ApH XK1-2</i>	95.795	0.017912636	0.204157582	0.087739264	Purification selection
<i>AtIDD8</i> / <i>ApIDD8-1</i>	89.496	0.031409280	0.311738291	0.100755284	Purification selection
<i>AtIDD8</i> / <i>ApIDD8-2</i>	89.006	0.035545868	0.343426052	0.103503702	Purification selection
<i>AtADG1</i> / <i>ApADG1-1</i>	91.939	0.035091555	0.343030784	0.102298560	Purification selection
<i>AtADG1</i> / <i>ApADG1-2</i>	91.747	0.038032815	0.344430181	0.110422424	Purification selection
<i>AtPGM1</i> / <i>ApPGM1-1</i>	95.056	0.022179474	0.255276137	0.086884243	Purification selection
<i>AtPGM1</i> / <i>ApPGM1-2</i>	95.056	0.021471555	0.261003181	0.082265490	Purification selection
<i>AtTPS1</i> / <i>CsTPS1-1</i>	91.584	0.008492083	0.256483393	0.033109681	Purification selection
<i>AtTPS1</i> / <i>CsTPS1-2</i>	90.981	0.010174782	0.252744167	0.040257236	Purification selection



<i>AtTPS1 / CsTPS1-3</i>	90.616	0.010209674	0.249271378	0.040958066	Purification selection
<i>AtSNRK1.1 / CsSNRK1.1-1</i>	98.441	0.005407608	0.211016385	0.025626485	Purification selection
<i>AtSNRK1.1 / CsSNRK1.1-2</i>	98.441	0.006264125	0.214912300	0.029147353	Purification selection
<i>AtSNRK1.1 / CsSNRK1.1-3</i>	98.428	0.007122392	0.234105159	0.030423898	Purification selection
<i>AtPGII / CsPGII-1</i>	95.146	0.020770138	0.266728913	0.077869840	Purification selection
<i>AtPGII / CsPGII-2</i>	94.805	0.023009900	0.281944598	0.081611424	Purification selection
<i>AtPGII / CsPGII-3</i>	95.138	0.020778972	0.272702072	0.076196604	Purification selection
<i>AtH XK1 / CsH XK1-1</i>	95.372	0.024771448	0.298468499	0.082995183	Purification selection
<i>AtH XK1 / CsH XK1-2</i>	95.200	0.021124992	0.277648587	0.076085358	Purification selection
<i>AtH XK1 / CsH XK1-3</i>	95.000	0.022017456	0.278585585	0.079033007	Purification selection
<i>AtIDD8 / CsIDD8-1</i>	89.316	0.045943437	0.312769448	0.146892342	Purification selection
<i>AtIDD8 / CsIDD8-2</i>	89.362	0.045261267	0.356748483	0.126871645	Purification selection
<i>AtADG1 / CsADG1-1</i>	92.352	0.034242133	0.270302224	0.126680916	Purification selection
<i>AtADG1 / CsADG1-2</i>	91.238	0.038266396	0.287413777	0.133140439	Purification selection
<i>AtADG1 / CsADG1-3</i>	91.082	0.041795361	0.309945327	0.134847529	Purification selection
<i>AtPGM1 / CsPGM1-1</i>	93.770	0.026675886	0.261633355	0.101959043	Purification selection
<i>AtPGM1 / CsPGM1-2</i>	94.089	0.023837326	0.258881933	0.092077982	Purification selection
<i>AtPGM1 / CsPGM1-3</i>	93.610	0.026051823	0.271503172	0.095954029	Purification selection
<i>AtTPS1 / BnTPS1-1</i>	94.087	0.029508645	0.511502962	0.057690076	Purification selection
<i>AtTPS1 / BnTPS1-2</i>	93.559	0.025706022	0.475556168	0.054054649	Purification selection
<i>AtTPS1 / BnTPS1-3</i>	92.986	0.022313588	0.402708913	0.055408726	Purification selection
<i>AtTPS1 / BnTPS1-4</i>	90.262	0.020975365	0.413475221	0.050729437	Purification selection
<i>AtSNRK1.1 / BnSNRK1.1-1</i>	96.296	0.021060047	0.465442982	0.045247319	Purification selection
<i>AtSNRK1.1 / BnSNRK1.1-2</i>	96.296	0.020990410	0.465577393	0.045084685	Purification selection
<i>AtSNRK1.1 / BnSNRK1.1-3</i>	94.553	0.022495881	0.429194243	0.052414220	Purification selection
<i>AtSNRK1.1 / BnSNRK1.1-4</i>	94.163	0.023380402	0.419115704	0.055785079	Purification selection

<i>AtPGII / BnPGII-1</i>	88.835	0.054501272	0.409567118	0.133070429	Purification selection
<i>AtPGII / BnPGII-2</i>	90.610	0.037963946	0.47951917	0.079170862	Purification selection
<i>AtPGII / BnPGII-3</i>	88.817	0.055939718	0.437028046	0.128000294	Purification selection
<i>AtPGII / BnPGII-4</i>	89.786	0.045152666	0.464090537	0.097292796	Purification selection
<i>AtH XK1 / BnH XK1-1</i>	88.889	0.063668035	0.775598690	0.082088889	Purification selection
<i>AtH XK1 / BnH XK1-2</i>	89.113	0.063170901	0.734716061	0.085980019	Purification selection
<i>AtH XK1 / BnH XK1-3</i>	89.006	0.059354730	0.789800307	0.075151566	Purification selection
<i>AtH XK1 / BnH XK1-4</i>	89.006	0.061272677	0.806339797	0.075988656	Purification selection
<i>AtIDD8 / BnIDD8-1</i>	83.898	0.069187549	0.535738564	0.129144239	Purification selection
<i>AtIDD8 / BnIDD8-2</i>	83.263	0.068909307	0.516395270	0.133442947	Purification selection
<i>AtADG1 / BnADG1-2</i>	90.286	0.040269220	0.565200964	0.071247614	Purification selection
<i>AtPGM1 / BnPGM1-1</i>	91.209	0.032680215	0.270049062	0.121015842	Purification selection
<i>AtTPS1 / BoTPS1-1</i>	94.087	0.029508645	0.511502962	0.057690076	Purification selection
<i>AtTPS1 / BoTPS1-2</i>	94.474	0.022429819	0.389099133	0.057645513	Purification selection
<i>AtSNRK1.1 / BoSNRK1.1-1</i>	96.296	0.021060047	0.465442982	0.045247319	Purification selection
<i>AtSNRK1.1 / BoSNRK1.1-2</i>	92.898	0.023387196	0.418580664	0.055872613	Purification selection
<i>AtSNRK1.1 / BoSNRK1.1-3</i>	87.354	0.062715840	0.342335817	0.183199760	Purification selection
<i>AtPGII / BoPGII-1</i>	84.653	0.060747164	0.396151692	0.153343190	Purification selection
<i>AtH XK1 / BoH XK1-1</i>	89.113	0.062197437	0.757847384	0.082071191	Purification selection
<i>AtH XK1 / BoH XK1-2</i>	89.006	0.061253807	0.815954500	0.075070125	Purification selection
<i>AtIDD8 / BoIDD8</i>	83.475	0.066819183	0.510542686	0.130878738	Purification selection
<i>AtADG1 / BoADG1-1</i>	91.188	0.043036288	0.593963011	0.072456176	Purification selection
<i>AtPGM1 / BoPGM</i>	92.540	0.030784565	0.258696710	0.118998671	Purification selection
<i>AtTPS1 / BrTPS1-1</i>	90.862	0.026189111	0.458301878	0.057143801	Purification selection
<i>AtTPS1 / BrTPS1-2</i>	90.967	0.025208384	0.395376097	0.063757986	Purification selection
<i>AtSNRK1.1 / BrSNRK1.1-1</i>	96.491	0.020409423	0.448233073	0.045533058	Purification selection

<i>AtSNRK1.1 / BrSNRK1.1-2</i>	94.553	0.022054012	0.426661883	0.051689670	Purification selection
<i>AtSNRK1.1 / BrSNRK1.1-3</i>	83.178	0.054675538	0.350843509	0.155840244	Purification selection
<i>AtPGII / BrPGII-1</i>	88.817	0.055393667	0.428558370	0.129255829	Purification selection
<i>AtPGII / BrPGII-2</i>	90.280	0.039502423	0.479011438	0.082466555	Purification selection
<i>AtH XK1 / BrH XK1-1</i>	89.091	0.062834942	0.791996084	0.079337441	Purification selection
<i>AtH XK1 / BrH XK1-2</i>	89.006	0.058404221	0.773309913	0.075524987	Purification selection
<i>AtIDD8 / BrIDD8</i>	81.568	0.070950392	0.536154259	0.132332050	Purification selection
<i>AtADG1 / BrADG1-1</i>	87.739	0.082251649	2.062148102	0.039886393	Purification selection
<i>AtPGM1 / BrPGM</i>	91.843	0.053214663	0.304380839	0.174829216	Purification selection

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