

Supplementary Information:

Supplementary Table S1 Genome-wide association study results of hemicellulose content in different tissues of 139 rapeseed samples in different environments.

Tissue site	Correlation interval	Peak SNPs	P value
Stalk	qHCs.C05	Bn-scaff_16045_1-p235411	9.86E-05
	qHCs.C02	Bn-scaff_22144_1-p207843	1.46E-04
	qHCs.C08	Bn-scaff_16197_1-p2621761	1.89E-04
	qHCs.C05	Bn-scaff_16414_1-p1114696	2.78E-04
	qHCs.C02	Bn-scaff_17831_1-p193351	2.86E-04
	qHCs.C02	Bn-scaff_17831_1-p205619	4.11E-04
	qHCs.A06	Bn-A06-p24220121	4.41E-04
	qHCs.C02	Bn-scaff_17109_4-p159217	5.45E-04
	qHCs.C02	Bn-scaff_22144_1-p223560	6.67E-04
	qHCs.C02	Bn-scaff_22144_1-p224402	6.67E-04
	qHCs.A01	Bn-A01-p25561204	6.83E-04
	qHCs.A05	Bn-A08-p1404439	7.32E-04
	qHCs.C05	Bn-scaff_16414_1-p1115223	7.46E-04
	qHCs.C08	Bn-scaff_16197_1-p2853374	8.08E-04
	qHCs.C08	Bn-scaff_16197_1-p2852488	8.08E-04
	qHCs.C02	Bn-scaff_17831_1-p161012	8.09E-04
	qHCs.C02	Bn-scaff_17831_1-p173520	8.09E-04
	qHCs.C02	Bn-scaff_17831_1-p215612	8.09E-04
	qHCs.C02	Bn-scaff_17831_1-p198992	8.09E-04
	qHCs.C05	Bn-scaff_18181_1-p176182	8.87E-04
	qHCs.C02	Bn-scaff_17831_1-p211127	9.98E-04
Taproot	qHCt.A09	Bn-A09-p5255753	3.67E-04
	qHCt.A09	Bn-A09-p4683160	4.29E-04
	qHCt.A09	Bn-A09-p4683384	4.29E-04
	qHCt.C05	Bn-scaff_16414_1-p1114696	4.46E-04
	qHCt.C08	Bn-scaff_16545_1-p80303	8.46E-04
	qHCt.C05	Bn-scaff_16414_1-p1115223	9.18E-04
	qHCt.C08	Bn-scaff_16545_1-p238397	9.61E-04

Supplementary Table S2 Significant differentially expressed genes associated with hemicellulose in rapeseed stalk and taproot.

Candidate genes	Physical position	Homologs in Arabidopsis	Gene annotation
<i>BnaC09G0154700ZS</i>	chrC09_1212404 5-12126631	<i>AT1G64440</i>	Involved in growth and cell wall carbohydrate biosynthesis.
<i>BnaA09G0143100ZS</i>	chrA09_7954088 -7957666	<i>AT1G64440</i>	Involved in growth and cell wall carbohydrate biosynthesis.
<i>BnaA07G0274700ZS</i>	chrA07_2335402 9-23358595	<i>AT1G68560</i>	Maintain cell wall integrity and regulate seed germination.
<i>BnaC06G0311300ZS</i>	chrC06_3918844 5-39192967	<i>AT1G68560</i>	Maintain cell wall integrity and regulate seed germination.
<i>BnaA07G0302500ZS</i>	chrA07_2503336 7-25037553	<i>AT1G68560</i>	Maintain cell wall integrity and regulate seed germination.
<i>BnaA03G0389200ZS</i>	chrA03_2084519 1-20849607	<i>AT2G06850</i>	endoxyloglucan transferase (EXGT-A1) gene.
<i>BnaC03G0481900ZS</i>	chrC03_3483819 2-34840257	<i>AT2G06850</i>	endoxyloglucan transferase (EXGT-A1) gene.
<i>BnaA07G0164200ZS</i>	chrA07_1681301 6-16815286	<i>AT2G28760</i>	Encodes a cytosolic isoform of UDP-glucuronic acid.
<i>BnaA03G0176300ZS</i>	chrA03_9010734 -9025747	<i>AT2G36870</i>	Encodes a xyloglucan endotransglycosylase/hydrolase.
<i>BnaC04G0096900ZS</i>	chrC04_8674178- 8676284	<i>AT2G36870</i>	Encodes a xyloglucan endotransglycosylase/hydrolase.
<i>BnaA04G0236500ZS</i>	chrA04_1929114 2-19293359	<i>AT2G36870</i>	Encodes a xyloglucan endotransglycosylase/hydrolase.
<i>BnaC04G0551800ZS</i>	HiCscfoid2136 _2695-4910	<i>AT2G36870</i>	Encodes a xyloglucan endotransglycosylase/hydrolase.
<i>BnaC01G0472900ZS</i>	chrC01_5137137 8-51376055	<i>AT3G10740</i>	It may be involved in cell wall modification.
<i>BnaC01G0284100ZS</i>	chrC01_2447897 0-24480096	<i>AT3G48580</i>	Encodes a cell-wall localized xyloglucan endotransglucosylase/hydrolase.
<i>BnaC09G0010900ZS</i>	chrC09_1333387- 1335694	<i>AT4G02500</i>	Encodes a protein with xylosyltransferase activity.
<i>BnaC09G0019300ZS</i>	chrC09_1842588- 1844340	<i>AT4G03210</i>	Encodes a member of xyloglucan endotransglucosylase/hydrolases (XTHs).
<i>BnaC09G0316000ZS</i>	chrC09_3387978 8-33883916	<i>AT4G08160</i>	Encodes a putative glycosyl hydrolase family 10 protein (xylanase).
<i>BnaA09G0268200ZS</i>	chrA09_2067678 1-20702031	<i>AT4G08160</i>	Encodes a putative glycosyl hydrolase family 10 protein (xylanase).
<i>BnaA03G0482400ZS</i>	chrA03_2680380	<i>AT4G24910</i>	glucuronoxylan 4-O-methyltransferase-like protein (DUF579)

	1-26807421		
<i>BnaC02G0002600ZS</i>	chrC02_379722-381857	<i>AT5G01360</i>	Involved in the synthesis and deposition of secondary wall cellulose.
<i>BnaC03G0005500ZS</i>	chrC03_270684-276603	<i>AT5G01360</i>	Involved in the synthesis and deposition of secondary wall cellulose.
<i>BnaA03G0517200ZS</i>	chrA03_2907845-5-29089840	<i>AT5G48070</i>	putative xyloglucan endotransglycosylase/hydrolase.
<i>BnaC01G0083600ZS</i>	chrC01_4911787-4913194	<i>AT5G01360</i>	Involved in the synthesis and deposition of secondary wall cellulose.
<i>BnaC07G0495800ZS</i>	chrC07_5597120-9-55990650	<i>AT5G01360</i>	Involved in the synthesis and deposition of secondary wall cellulose.
<i>BnaC02G0539800ZS</i>	chrC02_6448455-4-64496214	<i>AT5G64020</i>	Involved in the synthesis and deposition of secondary wall cellulose.
<i>BnaC02G0544000ZS</i>	chrC02_6419131-2-64201889	<i>AT5G64570</i>	Encodes a secreted beta-d-xylosidase that belongs to family 3 of glycoside hydrolases.
<i>BnaA07G0142000ZS</i>	chrA07_1527917-8-15280808	<i>AT5G67230</i>	Encodes a member of the GT43 family glycosyltransferases involved in glucuronoxylan biosynthesis.

Supplementary Table S3 Differentially expressed genes in rape stems in related regions.

Candidate genes	Homologs in <i>Arabidopsis</i>	Functional annotation	log2FC
<i>BnaC02G0460900ZS</i>		unknown	-5.52
<i>BnaC02G0467000ZS</i>	<i>AT3G27970</i>	Exonuclease family protein	-4.18
<i>BnaC02G0467600ZS</i>	<i>AT3G28007</i>	Intercellular exchange of sugar efflux transporter	-2.86
<i>BnaC02G0050400ZS</i>	<i>AT5G12120</i>	Ubiquitin-associated/translation elongation factor EF1B protein	-5.85
<i>BnaC02G0468300ZS</i>	<i>AT3G28180</i>	encodes a gene similar to cellulose synthase	-4.71
<i>BnaC02G0469400ZS</i>	<i>AT3G28420</i>	Putative membrane lipoprotein	-3.32
<i>BnaC02G0050600ZS</i>	<i>AT5G12140</i>	Encodes a cystatin	-4.70
<i>BnaC02G0470400ZS</i>	<i>AT3G28740</i>	Encodes a member of the cytochrome p450 family	7.48
<i>BnaC02G0050700ZS</i>	<i>AT5G12170</i>	Encodes one of the CRT-Like transporters	-3.21
<i>BnaC02G0470600ZS</i>	<i>AT2G43800</i>	Participate in intercellular plasmodesmata	-4.94
<i>BnaC02G0471200ZS</i>	<i>Atlg56140</i>	Leucine-rich repeat transmembrane protein kinase	-2.45
<i>BnaC02G0471700ZS</i>	<i>Atlg56140</i>	Leucine-rich repeat transmembrane protein kinase	-5.00
<i>BnaC02G0050900ZS</i>	<i>AT5G12270</i>	2-oxoglutarate (2OG) and Fe (II)-dependent oxygenase superfamily protein	-6.54
<i>BnaC02G0051000ZS</i>	<i>AT5G12290</i>	Encodes a mitochondrial outer membrane protein	-5.29
<i>BnaC05G0022700ZS</i>	<i>AT1G03780</i>	Involved in mitotic spindle assembly during late prophase and early prometaphase	-2.95
<i>BnaC05G0025600ZS</i>	<i>AT1G04220</i>	Encodes KCS2, a member of the 3-ketoacyl-CoA synthase family	-3.70
<i>BnaC05G0025700ZS</i>	<i>AT1G04240</i>	SHY2/IAA3 regulates multiple auxin responses in roots	-3.51
<i>BnaC05G0028200ZS</i>	<i>AT1G04520</i>	Encodes a plasmodesmal protein that may be involved in the intercellular movement of molecules through the plasmodesmata	-2.87
<i>BnaC05G0030000ZS</i>	<i>AT1G04680</i>	Pectin lyase-like superfamily protein	-3.39
<i>BnaC05G0031100ZS</i>	<i>AT1G80960</i>	F-box and Leucine Rich Repeat domains containing protein	4.87
<i>BnaC05G0034700ZS</i>	<i>AT1G14400</i>	ubiquitin carrier protein	-6.00
<i>BnaC05G0036500ZS</i>	<i>AT1G05291</i>	GPI inositol-deacylase C, putative (DUF1218)	3.48
<i>BnaC05G0037000ZS</i>	<i>AT2G32210</i>	cysteine-rich/transmembrane domain A-like protein	2.55
<i>BnaC05G0040300ZS</i>	<i>AT1G44130</i>	Eukaryotic aspartyl protease family protein	-3.32
<i>BnaC05G0040700ZS</i>	<i>AT3G12630</i>	Encodes a protein with E3 ligase activity	4.86
<i>BnaC05G0042000ZS</i>	<i>AT3G24610</i>	Galactose oxidase/kelch repeat superfamily protein	-5.44
<i>BnaC05G0043700ZS</i>	<i>AT1G06090</i>	Membrane bound acyl-lipid desaturases which can perform $\Delta 9$ desaturation	-2.96
<i>BnaC05G0044400ZS</i>	<i>AT1G06180</i>	member of MYB3R- and R2R3- type MYB- encoding genes	-3.40
<i>BnaC05G0047700ZS</i>	<i>AT1G06570</i>	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE	3.55
<i>BnaC05G0048000ZS</i>	<i>AT1G06645</i>	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	3.00
<i>BnaC05G0049800ZS</i>	<i>AT1G06930</i>	TPRXL	-3.61
<i>BnaC05G0061300ZS</i>	<i>AT1G08310</i>	alpha/beta-Hydrolases superfamily protein	3.24
<i>BnaC05G0063900ZS</i>	<i>AT1G08560</i>	member of SYP11 syntaxin Gene Family localized in the trans-Golgi network	-3.01
<i>BnaC05G0068200ZS</i>	<i>AT1G09155</i>	phloem protein 2-B15	-2.49
<i>BnaC05G0070100ZS</i>	<i>AT1G09310</i>	ABA responsive trichome formation regulator	-7.73
<i>BnaC05G0073600ZS</i>	<i>AT1G09600</i>	Protein kinase superfamily protein	-2.23
<i>BnaC05G0076800ZS</i>	<i>AT1G09890</i>	Rhamnogalacturonate lyase family protein	-4.14

<i>BnaC05G0077900ZS</i>	<i>AT4G10320</i>	tRNA synthetase class I (I, L, M and V) family protein	-5.36
<i>BnaC05G0078800ZS</i>	<i>AT1G10060</i>	encodes a mitochondrial branched-chain amino acid aminotransferase	-4.22
<i>BnaC05G0081300ZS</i>	<i>AT1G10370</i>	Encodes GSTU17 (Glutathione S-Transferase U17). Functions as a negative component of stress-mediated signal transduction pathways	-2.64
<i>BnaC05G0081400ZS</i>	<i>AT1G10370</i>	Encodes GSTU17 (Glutathione S-Transferase U17). Functions as a negative component of stress-mediated signal transduction pathways	-2.40
<i>BnaC05G0085100ZS</i>	<i>AT1G10640</i>	Pectin lyase-like superfamily protein	-5.81
<i>BnaC05G0086000ZS</i>	<i>AT1G25480</i>	Encodes a phosphorylation-dependent anion channel	4.09
<i>BnaC05G0087700ZS</i>		unknown	-5.72
<i>BnaC05G0088300ZS</i>	<i>AT1G60950</i>	encodes a major leaf	-3.06
<i>BnaC05G0088700ZS</i>	<i>AT1G14800</i>	Nucleic acid-binding, OB-fold-like protein	-5.99
<i>BnaC05G0089100ZS</i>	<i>AT1G11080</i>	serine carboxypeptidase-like 31	7.77
<i>BnaC05G0089400ZS</i>	<i>AT1G11120</i>	CTTNBP 2 amino-terminal-like protein	-2.97
<i>BnaC05G0090000ZS</i>	<i>AT1G11170</i>	lysine ketoglutarate reductase trans-splicing-like protein (DUF707)	3.71
<i>BnaC05G0091400ZS</i>	<i>AT1G80740</i>	ecotype KI-0 chromomethylase (CMT1). Reduce the tumor formation mediated by Agrobacterium	-3.46
<i>BnaC05G0092200ZS</i>	<i>AT1G11545</i>	xyloglucan endotransglucosylase/hydrolase 8	-2.99
<i>BnaC05G0094000ZS</i>	<i>AT1G11790</i>	Encodes a plastid-localized arogenate dehydratase involved in phenylalanine biosynthesis	-2.93
<i>BnaC05G0094900ZS</i>	<i>AT1G13340</i>	Regulator of Vps4 activity in the MVB pathway protein	3.46
<i>BnaC05G0098800ZS</i>	<i>AT1G12845</i>	transmembrane protein	-3.29
<i>BnaC05G0103000ZS</i>	<i>AT1G15880</i>	Golgi SNARE 11 protein (GOS11)	4.20
<i>BnaC05G0104300ZS</i>		unknown	-3.59
<i>BnaC05G0106400ZS</i>	<i>AT1G11900</i>	Tetratricopeptide repeat (TPR)-like superfamily protein	5.16
<i>BnaC05G0110200ZS</i>	<i>AT1G13830</i>	Carbohydrate-binding X8 domain superfamily protein	4.49
<i>BnaC05G0111300ZS</i>	<i>AT1G14020</i>	O-fucosyltransferase family protein	5.08
<i>BnaC05G0111400ZS</i>	<i>AT1G14020</i>	O-fucosyltransferase family protein	6.22
<i>BnaC05G0112400ZS</i>	<i>AT1G14100</i>	member of Glycosyltransferase Family- 37	-3.68
<i>BnaC05G0112800ZS</i>	<i>AT1G14170</i>	RNA-binding KH domain-containing protein	-4.68
<i>BnaC05G0113000ZS</i>	<i>AT1G14180</i>	RING/U-box superfamily protein	3.37
<i>BnaC05G0115700ZS</i>	<i>AT1G14450</i>	NADH dehydrogenase (ubiquinone)s	-5.61
<i>BnaC05G0115900ZS</i>	<i>AT5G07300</i>	Encodes a copine-like protein, a member of a newly identified class of calcium-dependent	6.33
<i>BnaC05G0116300ZS</i>		unknown	4.63
<i>BnaC05G0118100ZS</i>	<i>AT1G14600</i>	Homeodomain-like superfamily protein	-3.00
<i>BnaC05G0118400ZS</i>	<i>AT1G14630</i>	XRI1-like protein	-4.21
<i>BnaC05G0118600ZS</i>	<i>AT1G14660</i>	member of putative Na ⁺ /H ⁺ antiporter (AtNHX) family. Functions as a plasma membrane Li ⁺ /H ⁺ antiporter. Involved in Li ⁺ efflux and detoxification	-4.61
<i>BnaC05G0121900ZS</i>	<i>AT3G30739</i>	hypothetical protein	7.30
<i>BnaC05G0124600ZS</i>	<i>AT1G15050</i>	Belongs to auxin inducible gene family	-4.57
<i>BnaC05G0125800ZS</i>	<i>AT1G15210</i>	pleiotropic drug resistance 7	-4.89
<i>BnaC05G0127100ZS</i>	<i>AT1G48900</i>	Signal recognition particle, SRP54 subunit protein	-3.44
<i>BnaC05G0127900ZS</i>	<i>AT1G15380</i>	Member of the GLY1 family	2.67

<i>BnaC05G0130700ZS</i>	<i>AT1G15670</i>	Encodes a member of a family of F-box proteins (KMD)	-2.71
<i>BnaC05G0133500ZS</i>	<i>AT1G15980</i>	encodes the chloroplast NAD(P)H dehydrogenase complex	2.69
<i>BnaC05G0133700ZS</i>		unknown	4.30
<i>BnaC05G0134100ZS</i>	<i>AT1G16070</i>	Member of TLP family	-4.53
<i>BnaC05G0136700ZS</i>	<i>AT1G16410</i>	member of CYP79F, Encodes cytochrome P450	-10.74
<i>BnaC05G0137500ZS</i>	<i>AT1G16490</i>	Member of the R2R3 factor gene family	-3.53
<i>BnaC05G0138800ZS</i>	<i>AT1G16630</i>	transmembrane protein	-4.66
<i>BnaC08G0417900ZS</i>	<i>AT3G63010</i>	Encodes a gibberellin (GA) receptor ortholog of the rice GA receptor gene (OsGID1)	3.29
<i>BnaC08G0418800ZS</i>	<i>AT3G63110</i>	Encodes cytokinin synthase involved in cytokinin biosynthesis	4.97
<i>BnaC08G0419600ZS</i>	<i>AT3G63200</i>	PATATIN-like protein 9	-2.59

Supplementary Table S4 The 139 rapeseed core germplasm resources with hemicellulose content measured.

ID	Accession name	Origin
1	28	Hubei (China)
2	R6	Hubei (China)
3	1019B	Hubei (China)
4	R9	Hubei (China)
5	1055B	Hubei (China)
6	Chuan2121	Hubei (China)
7	6098B	Hubei (China)
8	HPR1	Hubei (China)
9	Zayou66	Hubei (China)
10	K219	Hubei (China)
11	8089	Hubei (China)
12	Shan2C	Shanxi (China)
13	8908B	Hubei (China)
14	Zhongshuang2	Hubei (China)
15	Shan2B	Shanxi (China)
16	Zhongshuang6	Hubei (China)
17	R1	Hubei (China)
18	R11	Hubei (China)
19	R2	Hubei (China)
20	Zhongshuang11	Hubei (China)
21	Nilla	European
22	OG3186	Hubei (China)
23	Cibrabra	European
24	OG3237	Hubei (China)
25	Apomix	European
26	OG3151	Hubei (China)
27	OG2097	Hubei (China)
28	OG3156	Hubei (China)
29	OG2086	Hubei (China)
30	OG3174	Hubei (China)
31	OG2118	Hubei (China)
32	OG3183	Hubei (China)
33	OG3229	Hubei (China)
34	OG3187	Hubei (China)
35	Oscar	Hubei (China)

36	OG3190	Hubei (China)
37	OG3191	Hubei (China)
38	Zheyoun50	Zhejiang (China)
39	HM42	Zhejiang (China)
40	Huashuang5	Hubei (China)
41	Huyou17	Shanghai (China)
42	L233	Chongqing (China)
43	Rivette	Australia
44	RR001	Australia
45	0331-1	Hubei (China)
46	Zheyoun21	Zhejiang (China)
47	Zhongshuang4	Hubei (China)
48	Zheshuang6	Zhejiang (China)
49	Zhongshuang10	Hubei (China)
50	Zheyoun28	Zhejiang (China)
51	Zheshuang72	Zhejiang (China)
52	Westar	Canada
53	Zheshuang8	Zhejiang (China)
54	BLN3344	Australia
55	BLN3346	Australia
56	BLN3350	Australia
57	BLN3352	Australia
58	RT006	Australia
59	RT108	Australia
60	RT123	Australia
61	FC03	Australia
62	Huyoun21	Shanghai (China)
63	YangJ6711	Jiangsu (China)
64	Zheng2736	Jiangsu (China)
65	HX0352	Hubei (China)
66	BLN3342	Australia
67	Zhen2609	Jiangsu (China)
68	Zhen3736	Hubei (China)
69	Ningyoun16	Jiangsu (China)
70	Zhongyoun821	Hubei (China)
71	Ningyoun18	Jiangsu (China)
72	Fan168	Hubei (China)
73	Zhenyoun5	Jiangsu (China)
74	Fan189	Hubei (China)
75	Yangyoun4	Jiangsu (China)
76	J110	Hubei (China)
77	Yangyoun6	Jiangsu (China)
78	J474	Hubei (China)
79	Huyoun15	Shanghai (China)
80	Zhongshuang7	Hubei (China)
81	Huyoun16	Shanghai (China)
82	Zhongshuang9	Hubei (China)
83	Huyoun19	Shanghai (China)
84	Zheyoun18	Zhejiang (China)
85	P10	Chongqing (China)
86	901	Hubei (China)
87	P96	Chongqing (China)
88	Huashuang3	Hubei (China)

89	P130	Chongqing (China)
90	Huashuang4	Hubei (China)
91	F403	Chongqing (China)
92	F406	Chongqing (China)
93	RR013	Australia
94	F421	Chongqing (China)
95	Trigold	Australia
96	F426	Chongqing (China)
97	RR005	Australia
98	F428	Chongqing (China)
99	AV-SAPPHIRE	Australia
100	F437	Chongqing (China)
101	AG-outback	Australia
102	F459	Chongqing (China)
103	Purler	Australia
104	L239	Chongqing (China)
105	RR002	Australia
106	L238	Chongqing (China)
107	GSL2	India
108	L230	Chongqing (China)
109	Monty	Australia
110	L229	Chongqing (China)
111	TQ055-02W2	Australia
112	L228	Chongqing (China)
113	Skipton	Australia
114	BST7-02M2	Australia
115	0594-1	Hubei (China)
116	0789-3	Hubei (China)
117	2772193	Hubei (China)
118	0802-1	Hubei (China)
119	2776848	Hubei (China)
120	0832-1	Hubei (China)
121	2797029	Hubei (China)
122	303577	Hubei (China)
123	9559-30	Hubei (China)
124	2445726	Hubei (China)
125	2923858	Hubei (China)
126	2446821	Hubei (China)
127	2924133	Hubei (China)
128	2599067	Hubei (China)
129	Wanyou12	Anhui (China)
130	2601379	Hubei (China)
131	Wanyou20	Anhui (China)
132	2675828	Hubei (China)
133	Zheshuang3	Zhejiang (China)
134	2677350	Hubei (China)
135	Zheshuang758	Zhejiang (China)
136	2734208	Hubei (China)
137	NY 7	Jiangsu (China)
138	2734969	Hubei (China)
139	Matador	European

Supplementary Figure S1 Temperature changes of rapeseed planted in three environments.

