

**Table S1.** Chromosome-specific primers used in the study.

Marker type	Name	Chr	Gene	Sequence (5' - 3')	Fragment size in parental lines (female/male), bp	Reference
SSR	Xtxp18	8	<i>Rf1</i>	F:actgtctagaacaacctgcg R:ttgctctagctaggcatttc	235/237	[5,6]
SSR	Xtxp50	2	<i>Rf2</i>	F:tgatgttggtacccttctgg R:agcctatgtatgtgttcgtcc	304/317	[7]
SSR	Xnhsbm1089	5	<i>Rf5</i>	F:catttcacattcaaggatcatgg R:acatttatgggtgcgtgctt	227/224	[8]
SSR	SB2386	4	<i>Rf6</i>	F:ggcggtaggtgtaaaaaggaagga R:gcatgccctacgactcttgtgtct	172/166	[9]
SSR	Sb5_236	3		F:gccaagagaaacacaaacaa R:agcaatgtatttaggcaacaca	175/177	[35]
SSR	<i>Sb6_342</i>	7		F:tgcttgtagagatgcctccct R:gtgaacctgctgcttagtcgatg	290/285	[35]
SSR	<i>Sb6_34</i>	8		F:aacagcagtaatgccacac R:tgacttggtagagaactgtcttc	204/194	[35]
STS	2459403	2		F:caggggccaaatgtgttac R: cacagttttatatttccgtgatagtg	935	[26]
CAPS/ MseI	CAPS-572	2		F:caggggccaaatgtgttac R:cacagttttatatttccgtgatagtg	+572/-572	This study
CAPS/ HpaI	CAPS-935	2		F:caggggccaaatgtgttac R:cacagttttatatttccgtgatagtg	935/935+753+182	This study

**Table S2.** CAPS and SSR polymorphic markers used for Principal component analysis.

№	Sample	Marker/chromosome																	
		CAPS-572		CAPS-935		SSR Xtxp18		SSR-Xtxp50		SSR-Xnhsbm1089		SSR-SB2387		SSR-Sb5_236		SSR-Sb6_342		SSR-Sb6_34	
		Chr2		Chr2		Chr8		Chr2		Chr5		Chr4		Chr3		Chr7		Chr8	
		allele		allele		allele		allele		allele		allele		allele		allele		allele	
		-572	+572	935+753+182	935	235	237	304	317	227	224	172	166	175	177	290	285	204	194
1	Nizkorosloe 81s	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0
2	929-3	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1
3	928-1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1
4	R-929-1	0	1	0	1	1	0	0	1	1	0	1	0	1	0	1	0	1	0
5	R-929-2	0	1	0	1	1	0	0	1	1	0	1	0	1	0	1	0	1	0
6	R-929-3	0	1	0	1	1	0	0	1	1	0	1	0	0	1	1	0	1	0
7	R-928-1	0	1	0	1	1	0	0	1	1	0	1	0	1	0	1	0	1	0
8	R-928-2	0	1	0	1	1	0	0	1	1	0	1	0	1	0	1	0	1	0
9	R-928-3	0	1	0	1	1	0	0	1	0	1	1	0	1	0	1	0	0	1
10	R-928-4	0	1	0	1	1	0	0	1	0	1	1	0	1	0	1	0	0	1
11	R-928-5	0	1	0	1	1	0	0	1	0	1	1	0	1	0	1	0	0	1

Table S3. Sequence polymorphisms within the *Rf2* candidate gene fragment

GenBank accession, genotype	Nucleotide position according to GenBank accession number Sobic.002G057050	Reference
	1087-1097*	
Sobic.002G057050	GTT <b><u>AA</u></b> CCTTAA	<a href="https://bioinformatics.psb.ugent.be/plaza/versions/">https://bioinformatics.psb.ugent.be/plaza/versions/</a>
XM_002459403	GTT <b><u>AA</u></b> CCTTAA	<a href="https://www.ncbi.nlm.nih.gov/">https://www.ncbi.nlm.nih.gov/</a>
FambeA, CMS line	GTT <b><u>A</u></b> TTTTTGC	[11]
Lata (R male inbred line)	GTT <b><u>T</u></b> TTTTTGC	[11]
Nizkorosloe 81s	GTT <b><u>AA</u></b> CCTTAA	[15]
928-2, R-line	GTT <b><u>T</u></b> TTTTTGC	[15]
929-3, R-line	GTT <b><u>T</u></b> TTTTTGC	[15]

\* positions 1090 and 1091 are highlighted in bold and underlined

**Table S4.** Sedimentation values for studied sorghum lines.

Flour	Sedimentation value/Acetic acid variant (AA), ml	Sedimentation value/SDS variant, ml	SDS/AA
Nizkorosloe 81s	43,0±1,0	29,5±0,5	0,7±0,0
929-3	47,0±1,0	46,0±1,0	1.0±0,0
928-1	46,5±1,5	46,5±2,5	1,0±0,0
R-929-1	38,0±0,0	51,0±1,0	1,3±0,0
R-929-2	38,5±2,5	49,0±1,0	1,3±0,1
R-929-3	40,5±0,5	55,5±2,5	1,4±0,1
R-928-1	38,5±0,5	44,5±0,5	1,2±0,0
R-928-2	39,0±1,0	39,0±1,0	1,0±0,0
R-928-3	38,0±2,0	46,5±0,5	1,2±0,1
R-928-4	38,0±0,0	48,0±2,0	1,3±0,1
R-928-5	38,0±0,0	46,0±0,0	1,2±0,0

**Table S5.** The rheological characteristics of sorghum-wheat flour composites (average value \* for studied lines).

Composite ratio (% Sorghum)	Development time (min).	Stability (min).	Liquefaction of the dough in 10 minutes from the start point of the experiment; BU***	Liquefaction of the dough in 12 minutes from the extreme point on the farinogram (from the moment the dough is ready); BU***	Flour quality indicator (mm is Quality Number)	Valorimeter value; BU***
10%	3,20±0,09	1,08±0,05	66,37±5,1	85,50±5,07	44,75±1,28	48,12±1,4
30%	5,34±1,13	3,926±1,31	17,63±6,16	39,12±6,73	143,87±24,56	64,00±3,7
0% **	3,02	0,87	113,00	143,00	39,00	41,00

\*sample average value

\*\*Test: wheat flour

\*\*\*BU – Brabender units