

Supplemental Table 1 Statistics of sequencing data used for the Dungu genome assembly

Platform	Reads count	Total base (bp)	Depth	Reads N50 (bp)
Pacbio HiFi	1,782,239	31,804,067,296	70.6	19,313
Nanopore ultra-long	2,167,251	74,465,836,833	165.5	66,391
MGI	378,113,816	56,717,072,400	126	2 × 150
Hi-C	1,270,730,156	190,609,523,400	-	2 × 150

Supplemental Table 2 Repetitive annotation in Dungu genome

Type	Repeat size (%)	Percent (%)
Trf	26,839,556	6.32
Repeatmasker	150,482,219	35.45
Proteinmask	54,377,071	12.81
De novo	127,195,270	29.96
Total	217,289,039	51.19

Supplemental Table 3 Statistics of functional annotation in Dungu genome

		Gene	
		Number	Percent (%)
Annotated		40,166	93.43
	NR	39,321	91.47
	SwissProt	21,204	49.32
	TrEMBL	39,963	92.96
	KOG	24,248	56.41
	TF	2,219	5.16
	InterPro	29,423	68.44
	GO	20,980	48.8
	KEGG_ALL	34,717	80.76
	KEGG_KO	12,338	28.7
	Pfam	26,715	62.14
Unannotated		2,823	6.57
Total		42,989	100

Supplemental Table 4 Non-coding RNA in Dungu genome

Type	Number	Average length (bp)
miRNA	196	135
tRNA	619	75
rRNA	774	231
snRNA	694	122

Supplemental Table 5 Statistics of telomere and centromere features in Dungu genome

	Telomere		Centromere		
	Left	Right	Start	End	Length (bp)
Chr1	1,707	12	17,376,372	19,662,986	2,286,615
Chr2	487	195	21,373,450	22,977,714	1,604,265
Chr3	245	628	31,793,910	34,742,131	2,948,222
Chr4	86	2035	21,293,375	22,828,589	1,535,215
Chr5	182	157	20,497,825	21,963,768	1,465,944
Chr6	220	171	16,664,611	18045263	1,380,653
Chr7	0	1127	7,857,307	9,237,298	1,379,992
Chr8	2588	1417	19,334,095	23,184,898	3,850,804
Chr9	215	290	31,271,884	33,517,406	2,245,523
Total (bp)					18,697,233

Supplemental Table 6 Count of different types SVs between Dungu and 76-accession foxtail millet genomes

Statistic	Deletions	Insertions	Duplications	Inversions	Translocations	total
L18	810	296	30	11	45	1192
C34	1919	1609	63	18	56	3665
C28	2250	2090	96	27	66	4529
C36	2161	2069	93	22	69	4414
C33	1269	295	20	13	70	1667
C08	2159	1626	72	17	70	3944
C10	3345	2996	79	32	73	6525
C13	1364	958	46	22	77	2467
C12	1919	1557	76	15	81	3648
C07	2249	1483	93	30	81	3936
L17	3271	2909	79	20	88	6367
L06	3221	3159	144	24	90	6638
L19	3261	2716	96	27	90	6190
L04	3540	3085	119	23	94	6861
L05	3307	3309	149	23	97	6885
L16	3010	2951	86	20	104	6171
L34	2319	1542	34	24	104	4023
C18	3398	3334	126	23	106	6987
C14	2342	1682	57	30	111	4222
C01	3518	3663	129	30	112	7452
C26	2216	1645	86	20	113	4080
C35	2612	1946	78	22	115	4773
C09	3295	2793	97	30	119	6334
L38	2620	1957	70	19	122	4788
L26	3828	3693	84	30	128	7763
L40	4444	4408	132	31	128	9143
L15	3303	3044	130	26	133	6636
L08	3458	3562	87	29	134	7270
L21	4009	3762	143	32	135	8081
C30	2338	1895	67	26	138	4464
C20	3377	2692	131	29	145	6374
L10	3976	3950	85	28	146	8185
L39	3375	3269	135	25	147	6951
L22	3661	3365	106	31	147	7310
L37	3301	3162	136	28	151	6778
L12	4355	3848	136	28	156	8523
L32	3494	2788	97	32	156	6567
C19	3685	3865	48	23	157	7778
C24	3442	3170	79	21	161	6873
C16	3437	3345	114	26	161	7083
C32	3192	3032	117	26	168	6535
L28	3553	3029	158	35	168	6943
C27	3213	2908	90	23	175	6409
L02	4004	3571	128	27	178	7908
C21	3796	3423	168	29	178	7594
L09	4184	4081	73	26	179	8543
L36	3382	2546	135	25	182	6270
L29	3542	3075	69	35	188	6909
L33	3864	3726	126	44	188	7948
C03	3771	3836	111	27	189	7934

L27	3529	3241	150	24	190	7134
C17	3591	3168	146	28	194	7127
L07	3575	3346	105	29	196	7251
C31	3600	3327	84	27	200	7238
C02	3490	3491	147	22	202	7352
C22	3528	3127	118	25	202	7000
L25	4238	4182	106	34	202	8762
L13	3833	3734	155	25	203	7950
C04	3492	3366	94	22	216	7190
L24	4088	4090	142	23	216	8559
L30	3531	3406	100	28	216	7281
L11	3651	3402	102	29	216	7400
L14	3236	3080	107	21	217	6661
L03	4092	4065	116	23	219	8515
L01	4206	4195	196	26	224	8847
L35	3627	3681	128	37	225	7698
C29	3324	3063	169	23	231	6810
L23	4388	4221	156	36	238	9039
L31	4377	4763	136	35	248	9559
C05	3124	3073	156	18	276	6647
L20	4144	4012	195	30	293	8674
C11	1809	1387	115	12	326	3649
C15	2291	2110	117	22	363	4903
C23	3343	2929	174	27	455	6928
C25	3336	2909	161	36	513	6955
C06	2261	2084	142	25	605	5117

Supplemental Table 7 Count of SNPs and InDels between Dungu and 76-accession foxtail millet genomes

Statistic	SNP	Deletions (<50 bp)	Insertions (<50 bp)
C01	1673794	126004	123289
C02	1578506	123623	119794
C03	1729137	135558	130327
C04	1715828	132821	129254
C05	1457000	118453	112901
C06	1098407	106786	93561
C07	813725	72431	65703
C08	835947	74535	67158
C09	1462751	119151	111842
C10	1446867	116908	110019
C11	872104	88834	71499
C12	767439	63623	58431
C13	364606	40701	34844
C14	879126	78330	71992
C15	1092610	103122	89815
C16	1772193	130689	127070
C17	1600642	127214	125436
C18	1558666	121536	118171
C19	1630358	127764	124944
C20	1447203	137117	116542
C21	1692692	135304	128288
C22	1556752	127024	121259
C23	1609842	136493	126226
C24	1553835	125988	121193
C25	1541433	135483	122839
C26	761155	71976	65546
C27	1449244	115814	112176
C28	1098068	87927	81309
C29	1536798	122771	118068
C30	984221	87869	73505
C31	1714367	131814	129323
C32	1399327	114711	111690
C33	120987	22196	19847
C34	741556	64162	62903
C35	976322	85868	84114
C36	860931	70963	70436
L01	2115813	156734	150212
L02	1926750	153140	143349
L03	1943258	148182	141867
L04	1494849	122856	121977
L05	1564784	119942	118612
L06	1564515	118197	118277
L07	1696223	135052	128027
L08	1615862	126747	124271
L09	1953900	152092	150369
L10	1863908	146276	143634
L11	1694257	140504	126602

L12	1935115	155859	138641
L13	1797034	142818	135099
L14	1549148	128176	118095
L15	1526448	119607	114872
L16	1396059	112097	108588
L17	1443590	116593	111513
L18	121590	23923	17251
L19	1354764	114187	106981
L20	2186302	160788	155826
L21	1762407	142804	135590
L22	1701397	131366	128088
L23	2073752	159976	154238
L24	1952644	152837	146021
L25	2054541	158213	153098
L26	1779575	144930	139486
L27	1591558	132945	122084
L28	1625672	137496	125897
L29	1580248	134965	117586
L30	1628918	126660	124082
L31	2316079	178539	163125
L32	1391957	136596	108488
L33	1635335	144579	129488
L34	782565	81862	63601
L35	1688481	133021	127087
L36	1417046	135955	113630
L37	1488276	121798	116938
L38	1123157	93699	81186
L39	1551346	120154	118282
L40	2106238	167384	156000

Supplemental Table 9 Putative *SiSD1* interactors identified in a yeast one-hybrid library screen

Gene ID	Annotation
LOC101755201	ethylene-responsive transcription factor RAP2-13
LOC101766738	lachrymatory-factor synthase
LOC101768585	thylakoid membrane protein slr0575
LOC101777598	carbonic anhydrase, chloroplastic
LOC101760333	blue copper protein
LOC101764410	pEARL11-like lipid transfer protein 3
LOC101772959	ethylene-responsive transcription factor ERF073
LOC101775694	isoflavone reductase homolog IRL
LOC101773046	stem-specific protein TSJT1
LOC101757761	myb-like protein X
LOC101785584	thylakoid lumenal 15.0 kDa protein 2, chloroplastic
LOC101754192	protein CURVATURE THYLAKOID 1A, chloroplastic
LOC101758157	protein LSD1
LOC101783126	amidase 1
LOC101754843	ran-binding protein 1 homolog a
LOC101766967	photosystem II 10 kDa polypeptide, chloroplastic
LOC101754815	fructose-bisphosphate aldolase, chloroplastic
LOC101756150	protein DETOXIFICATION 27
LOC101768863	probable polyamine oxidase 2
LOC101783492	photosystem I reaction center subunit III, chloroplastic
LOC101760766	50S ribosomal protein L9, chloroplastic
LOC101761609	pyrophosphate-energized vacuolar membrane proton pump
LOC101768493	cysteine-rich repeat secretory protein 55
LOC101759067	aspartyl protease 25
LOC101776649	14-3-3-like protein GF14-E
LOC117855863	carbonic anhydrase, chloroplastic-like
LOC101782406	chlorophyll a-b binding protein, chloroplastic
LOC101777875	NADP-dependent malic enzyme, chloroplastic
LOC101754408	sphingosine kinase 1
LOC101760785	nitrogen regulatory protein P-II homolog
LOC101774788	xylanase inhibitor protein 1
LOC101758778	alpha-ketoglutarate-dependent dioxygenase alkB homolog 6
LOC101768406	dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase
LOC101761485	MADS-box transcription factor 47
LOC101779834	probable histone H2A.4
LOC101769331	probable protein phosphatase 2C 71
LOC101782134	transcription factor GHD7
LOC101774809	nicotianamine synthase 3
LOC101775953	serine/threonine-protein kinase BLUS1
LOC101786300	photosystem I reaction center subunit XI, chloroplastic
LOC101769572	protein TIFY 3
LOC101758402	protein YIPF6 homolog
LOC101784434	alanine aminotransferase 2
LOC101752744	chaperone protein dnaJ 6
LOC101772449	IQ domain-containing protein IQM1
LOC101760171	katanin p60 ATPase-containing subunit A-like 2
LOC101777700	ferrochelatase-1, chloroplastic
LOC101768770	ribulose biphosphate carboxylase small chain A, chloroplastic
LOC101783740	glucan endo-1,3-beta-glucosidase 14

LOC101757803	auxin-responsive protein IAA17
LOC101783411	9-cis-epoxycarotenoid dioxygenase NCED1, chloroplastic
LOC101760474	(+)-neomenthol dehydrogenase
LOC101763019	protein CURVATURE THYLAKOID 1A, chloroplastic
LOC101764229	ACT domain-containing protein DS12, chloroplastic
LOC101781774	glutathione S-transferase 1
LOC101762776	remorin
LOC101763211	2-alkenal reductase (NADP(+)-dependent)
LOC101777327	spermatogenesis-associated protein 20
LOC101779276	probable potassium transporter 11
LOC101780217	chlorophyll a-b binding protein 1, chloroplastic
LOC101775865	probable uridine nucleosidase 1
LOC101781974	DNA replication complex GINS protein SLD5
LOC101778594	20 kDa chaperonin, chloroplastic
LOC101777440	oxygen-evolving enhancer protein 2, chloroplastic
LOC101782250	RGG repeats nuclear RNA binding protein A
LOC101766513	tubulin beta-5 chain
LOC101765586	transmembrane 9 superfamily member 12
LOC101768099	UPF0603 protein Os05g0401100, chloroplastic
LOC101768485	fructose-bisphosphate aldolase, chloroplastic
LOC101778821	cytochrome b6-f complex iron-sulfur subunit, chloroplastic
LOC101779776	protein plastid transcriptionally active 16, chloroplastic
LOC101761222	aquaporin NIP2-2
LOC101759577	probable prolyl 4-hydroxylase 9
LOC101759686	ethylene-responsive transcription factor 7
LOC101766625	proline-rich protein 4
LOC101781007	ycf20-like protein
LOC101778441	photosynthetic NDH subunit of lumenal location 4, chloroplastic
LOC101785151	glyceraldehyde-3-phosphate dehydrogenase 3, cytosolic
LOC101771911	apoptosis-inducing factor 2
LOC101777297	VQ motif-containing protein 22
LOC101779804	ribonuclease 1-like
LOC101774077	ADP-ribosylation factor 2
LOC101780110	thioredoxin-like protein HCF164, chloroplastic
LOC101761607	uridylate kinase
LOC101769522	transcription factor ILR3
LOC101785701	thioredoxin H1
LOC101777579	thiol-disulfide oxidoreductase LTO1

Supplemental Table 10 Primers used in the entire article

Primer name	Sequence
SiSD1-deleteG-F	GTGTGTATGTGTGTGTGTGCGTG
SiSD1-deleteG-R	GAAAGGGACGGCGTCGTCAATG
SiSD1-QC-F	CAGTGGTCTCATGCAGAAGTCCTGCCCGAGGGTG
SiSD1-QC-R	CAGTGGTCTCAAACCGAAGTCCTGCCCGAGGG
	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGGACGCCCCGCCCG
SiSD1-F	GCCCAGC
	GGGGACCACTTTGTACAAGAAAGCTGGGTTCGGTGAAGCCGCCGCC
SiSD1-R-D	GCCACTGG
	GGGGACCACTTTGTACAAGAAAGCTGGGTCCCACCGCCGGTGCAGG
SiSD1-1020-R-D	CA
	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGGTGGCCGAGCAC
OsSD1-F	CCC
	GGGGACCACTTTGTACAAGAAAGCTGGGTTCGCTGGCCGCCTCGACC
OsSD1-R-D	TG
qRT-SiSD1-F	CAGGACTTCGAGGCAGTGG
qRT-SiSD1-R	GGGTAGTAGTTGCACCGCAT
qRT-SiGA20x3-F	GCTCGCCTTCTTCCTCAACC
qRT-SiGA20x3-R	GAAGGCGTCCATGGTGCTG
qRT-SiCYP714B1-F	GAACATCTACTTCGCCGGGT
qRT-SiCYP714B1-R	CGTCTCCTGGATCACCATCG
qRT-SiGA20x1-F	CCGAGCAAACGACGTCAATG
qRT-SiGA20x1-R	CTTGCAATTACCCTGTGCCG
qRT-SiGid1-F	AGAGCCTCATCATCGTGTCTG
qRT-SiGid1-R	TTAGCCCTGAGGAAGTCCGA
qRT-SiGid2-F	AGGATGCAGCTGAGAACACC
qRT-SiGid2-R	CCAGCTCTGAGATTGCCTCA
qRT-SiSLR1-F	GGTGATCGCCGTCAATTCAG
qRT-SiSLR1-R	GCCCTCGAGAGAATCGAACA
qRT-SiERF7-F	GCAGCAGGCGGTTGGTAAAG
qRT-SiERF7-R	AGTTGGAGGCCGTGGTCTTC
qRT-SiERF073-F	CAGGGCGTGTGCGGTGTAC
qRT-SiERF073-R	GAACTGGTCGCCGAAGATGA
SiSD1promoter-F	CGGGGTACCCTTGAGATTGACGAAGTCACACA
SiSD1promoter-R	ACGCGTCGACGCGAACTGCATTCTTTCCCC
	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGATGTGCGACACGG
SiERF7-F	CGG
	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCAGAGCCGCAGCTCC
SiERF7-R-D	GT
	GGGGACAAGTTTGTACAAAAAAGCAGGCTCCATGTGTGGTGGTGCGA
SiERF073-F	TCCT
	GGGGACCACTTTGTACAAGAAAGCTGGGTCTTAAACGACAGGTTGT
SiERF073-R-D	CCTCGACG
B-SiERF7-F	ATAGGTTGAGTAGGTTGCGCAGCAATGAAATCAAATCTTG
B-SiERF7-R	CAAGATTTGATTTTATTGCTGCGCAACCTACTCAACCTAT
C-SiERF7-F	ATAGGTTGAGTAGGTTGCGCAGCAATGAAATCAAATCTTG
C-SiERF7-R	CAAGATTTGATTTTATTGCTGCGCAACCTACTCAACCTAT
Si-ERF7-LUC-F	GGATCCCCCGGGCTGCAGGAATTCATGATGTGCGACACGGCGG
Si-ERF7-LUC-R	ATTTTTCGGGAGTACCCGGGTACCGAGCCGCAGCTCCGTGCA

T-ERF7-100-1-F	AAGCAAGTGGATTGATGTGATATCATGTTGTTTCGTTTCGTGAGT
T-ERF7-100-1-R	GAAGGGTCTTGCAGATCCTCTAGATTTTGATAATATGTGTGACTTCGT
B-SiERF073-1-F	GATCTAGGGTCATGTTTCATAGCCATTATGTGGGGGAAAGA
B-SiERF073-1-R	TCTTTCCCCCACATAATGGCTATGAACATGACCCTAGATC
C-SiERF073-1-F	GATCTAGGGTCATGTTTCATAGCCATTATGTGGGGGAAAGA
C-SiERF073-1-R	TCTTTCCCCCACATAATGGCTATGAACATGACCCTAGATC
Si-SiERF073-LUC-F	GGATCCCCCGGGCTGCAGGAATTCATGTGTGGTGGTGCGATCCT
Si-SiERF073-LUC-R	ATTTTTGCGGAGTACCCGGGTACCAAACGACAGGTTGTCCTCGACG
T-SiERF073-100-1-F	AAGCAAGTGGATTGATGTGATATCTGTTGTGCGTGATGAGAAATCG
T-SiERF073-100-1-R	GAAGGGTCTTGCAGATCCTCTAGAGCGAACTGCATTCTTTCCCC
qPCR-OsGA20ox1-F	CTTCTTCCTCTGCCCCGAGAT
qPCR-OsGA20ox1-R	TATTGTTGGTTGCAGGTGACG
qRT-OsGA20ox3-F	AGTTCACGCAGAGGCACTAC
qRT-OsGA20ox3-R	CTTTGCTTGATCCAGGCGAC
qRT-OsGA3ox1-F	CATGTTCTTCAAGGCGCTCG
gRT-OsGA3ox1-R	AAGAAGCCTGAGTCCGTGTG
qRT-OsGA3ox2-F	TGTTCTTGAGGGCGCTGG
qRT-OsGA3ox2-R	CGTCGCCGTCATCCTCTC
qRT-OsGA2ox3-F	ATGGGAGGTTCAAGAGCGTG
qRT-OsGA2ox3-R	AGCCTTGATTTGTAGGCAGC
qRT-OsGA2ox5-F	GATGCCCATTAACGGAGCTT
qRT-OsGA2ox5-R	AAGCGGTGCAGTCCAATCTT
qRT-OsGA2ox10-F	AATGAGTACGTTGTGGCGGT
qRT-OsGA2ox10-R	TGGGTAGTGGTTCACCCTCA
qRT-OsCYP714B1-F	CGATCTGATGGTGGACTCGG
qRT-OsCYP714B1-R	TCCCGCCACTTCTGTCAATC
qRT-OsGid1-F	CGTCAAGGTTGTCCAATGCG
qRT-OsGid1-R	GCGTTGAGGAAGTCGGAGAT
qRT-OsGid2-F	CAACTCTCCTGACCGTGCTT
qRT-OsGid2-R	CTTGGGGGCCTCCTTGATT
qRT-OsSLR1-F	CTTCTGCACGCCCACTTCTA
qRT-OsSLR1-R	CGAGGATGGCTTGATTTGCG
qRT-OsSD1-F	GTGCAACTACTACCCGCCAT
qRT-OsSD1-R	AAGGTGTCGCCGATGTTGAT
P950-F	TAGCCTAGTATGACTTGGTACATG
P950-R	AGATATTTACGGTTTGACCCC
P1500-F	AAGCTGCTCCCTTTGCCT
P1500-R	GGGCCCTTGTGAGTAACTTTGA
P1255-F	TACCGCTTTCAGGCTTCAAC
P1255-R	GCCAAGCTTTGTCAGCAATAAA
P350-F	CTATCTCCTTTGGCCATTCTTTTC
P350-R	GATGATTTGAGGAGATCCACTGG
P650-F	AGGATGGGACGAGACGAAA
P650-R	ATACAAACGAAACGCTACAGTG
P250-F	CCAAATTGGACCTAACTCACGA
P250-R	GTGCCGAGATAGATTCTGTTGTC
P1130-F	CACTAGTCCCTCGCTACTCC

P1130-R	TCGCAAAGTACAACAAAACCTGTG
PL170-F	TGTTGGGCTCTGAATCAGTTTG
PL170-R	TTCAGTCTCCTCAACATCCTAGC
PL100-F	ATCCAAGTGGAACATTCAACAC
PL100-R	TATGGTCAGACGCACATCATG
PL20-F	TCCGTGTCACATCGAATATTCG
PL20-R	TGAAAAGAAGAAGGAGCTCGAAC
PR20-F	CTGATTGCGGCCAAGAGTAAG
PR20-R	TAGCCAACAAGACCCTCATCAG
PR100-F	CAATTTGGCACACGAACTGAC
PR100-R	CGTGCAAGAGAGAAGGTACTG
