

Supplemental Table S1: Statistical descriptions of yield related traits in two population derived from Guangxiang 24S and R900

	Trait	Parents		population			
		Guangxiang24S	R900				
		Mean±SD	Mean±SD	Mean±SD	Range	Kurtosis	Skewness
F ₂	PN	7.00±1.56	4.00±0.71	4.34±1.24	2.00-11.00	0.85	0.68
	PL	18.07±0.83 cm	22.04±0.76 cm	20.26±1.48 cm	16.60-24.45 cm	-0.13	0.02
	PBN	11.33±0.516	17.80±2.28	15.32±1.58	12.00-20.00	-0.26	0.18
	SBN	27.67±3.011	69.20±17.23	48.43±11.36	26.50-86.00	0.73	0.64
	GN	157.17±13.32	290.20±51.85	253.94±56.50	118.50-403.00	-0.01	0.43
	FGN	132.50±12.62	267.80±58.18	237.99±56.18	108.00-395.00	0.21	0.42
	EGN	24.67±5.495	22.40±20.69	27.49±11.18	14.5-56.00	1.05	1.26
	SSR	84.2%±3.2%	92%±8.1%	94.02%±4.32%	80%-99%	0.32	-1.16
	PSD	8.71±0.73 per cm	13.21±2.56 per cm	12.50±2.45 per cm	5.23-19.44 per cm	0.50	0.48
F ₃	PN	9.25±3.49	5.92±2.16	8.89±2.15	5.470-20.250	0.46	0.72
	PL	23.90±0.94 cm	26.13±0.48 cm	27.04±1.84 cm	22.05-29.80 cm	-0.12	0.19
	PBN	12.25±0.96	18.50±1.29	15.90±1.53	12.25-20.00	-0.28	0.43
	SBN	50.25±5.97	84.50±6.56	73.38±12.59	39.00-113.33	0.16	0.60
	GN	235.00±35.64	390.25±26.09	347.07±60.92	209.67-532.00	0.02	0.53
	FGN	15.4±4.98	258.50±25.96	245.72±58.38	42.67-398.75	0.60	0.28
	EGN	182.75±47.97	131.75±25.90	101.36±57.99	13.00-395.00	0.88	0.83
	SSR	6.78%±2.76%	66.28%±4.80%	72.42%±11.62%	31%-94%	-0.02	0.46
	PSD	9.82±1.10 per cm	14.93±0.68 per cm	12.86±2.22 per cm	8.25-19.81 per cm	0.32	-0.64

SD: standard deviation; Trait: PL: panicle length; PN: panicle number per plant; PBN: primary branch number; SBN: secondary branch number; GN: grain number per panicle; FGN: filled grain number per panicle; EGN: empty grain number per panicle; SSR: seed setting rate; PSD: panicle setting density;

Supplemental Table S2: The physical positions and primer information of marker pairs

Chr.	Marker Name	Physical Position (bp)	Primer Information	
			Forward Primer	Reverse Primer
1	RM3252	319100	GGTAACTTTGTTCCCAT GCC	GGTCAATCATGCATGCAA GC
	RM6786	7121400	TTGACGATGGCAAGCTC C	GATTTCCGCAGCAAGTAT CC
	RM583	8420150	AGATCCATCCCTGTGGA GAG	GCGAACTCGCGTTGTAAT C
	RM493	12557603	TAGCTCCAACAGGATCG ACC	GTACGTAAACGCGGAAGG TG
	STS	15282195	ATGCTCTGTTTGGCTTAT TTCACG	ATACAGTTCGTCCGCTAC AGGC
	CM1-6	20278362	GCCACTGCCAGGATCTG TAA	TCAAACATACTCGGTACT TCTCA
	CM1-9	26119472	ATCCTTTGTCCCTCGTCG TC	TGTCCGTCCACTGATCAT GT
	CM1-10	30289346	CTTGAGACGTGCTGGTG TG	TCACTGGATCCACATGCC AT
	RM8097	32464694	TACATACACGTTTCATGT GCC	CGAGCGTAGGAAGACTAC C
	CM1-19	34129535	CGGATGGTCAAACGTTG GAT	AAAGAGTCCCCAGTTCCC G
	CM1-31	40159465	AGCCTCTCCAAATCGAA CTCT	ACATGTGGGTTCCTGTGT CA
	STS	43348400	GGGTCATATTTCTATTA ATTC	AAGGAAAATCCACCACTA ATC
	RM6321	44042256	GGCTCTACCTCGCTGTT GTC	ACGAATATAACCTGCGGC AG
2	CM2-2	54737	TTTTGGCCATGCAAAC CCA	TGCTACACATAGATCCCT CGT
	CM2-3	2166682	TCCGAAAACCCCTTCTG ACA	TGGGAGAGAGTGATGGAG GA
	CM2-5	3964175	GGAAACCAGGGACAAC GAAC	GGGAACGTGTGTGTGAAC AA
	CM2-35	21342166	GCTAAGAATCGAACGGG TCAC	ATGTGTTGAATCGAGCCG TC
	CM2-12	25293066	TCTCGTCGGTAATCTCG TGA	ACAAGATACGACATCAAG CACA
	CM2-13	28641860	AGCTCTTCAAAAGGCAA GTCA	CCGATGCATGACTTCCTTC TG
	RM3763	29600800	TCTCTGAACACACCCAC ACC	TGTTTTGATCTCAGCTCCC C

3	STS	30538814	CCACAACACCAACGATG CTA	TAGGACTGACCCCTCTGC AT
	STS	30925200	GCATAGTTGAACCAGTA GCATG	GAAGTGGCAGAATTGAGT GTC
	RM3316	32365700	TTCGACGATTCTGTACA CGC	CATGATCCCAAATGCATG GG
	CM2-37	35703922	TCTACCACGTGCCAAAA TACA	GTCCATGATCCATCCAAG CAC
	CM2-15	37682703	TGAATCATGGTATGGAG GCAC	AGATCACTGATGGCACGT CA
	CM3-25	2151293	TCAGATCATCCAGCACA GCA	ATGAGGTAGAAGGGGCCA AC
	CM3-23	5666302	GCAAGAATTAGACAGG AGTAGGT	GTGAGTTTCTACGTTGTGC CA
	CM3-8	13108039	ACTCCTTGCACACATCA AACA	TTATTGTGCTTATAAGGG CTGCA
	STS	16589300	TGTTGTTTTGGAGATTTG AAGG	GAGGCGAAAAGTCACGTA AGC
	CM3-11	18592767	CAAGCTAGCTGGAGGAG GAG	AGATTTCTCCTCCCCAACC G
	CM3-13	25808801	TGCATTTCCCAATTCTG AACCT	CCTGTAGGTTGACTGTTG CA
	CM3-16	31250982	GCATTCATGTCTCTTTAG GGTGT	GGCTCACCTCGTTTTACAT ATCT
	CM3-18	34893973	GGCCTCTATATCCGCAA GCA	ATCTCGACTTCCTGCTCAC C
	STS	352800	AGAATAGAGTGCATCAT CGTC	AACCTGATAGGTGGAAGA TGTAC
4	CM4-7	3945262	GCCAATGAGATGAAGG ACCC	ACCAATGTGTGAAGAAGG AGAT
	CM4-32	9460741	CGGATTCAAACAGGGCC ATT	AATTAGCGCGGAATTGAC GG
	CM4-15	12469155	CAGTCACAGGCGATCAA CAT	TGCAGGACCGTGTAATCA AC
	CM4-34	16820391	TAAAACCCTCGTCCTTC CCC	TCAGCTGGCCACTAAAAT GA
	CM4-19	19938120	TGGTAGTTGTGTCTCAT GTGC	AACAGGTGTCATGAGCTC CA
	CM4-21	22025422	TCTGTTAGCATCCCTCC ACT	TCCCATGCATGCGACAAA TT
	CM4-22	23799267	GTCCCCGATATCTTGCA GCT	GCTGACGTGGCTTATTGA CT
	RM3839	24155150	AATGGGACCAGAAAGC ACAC	AAAAAGAGCATGGGGGCT AC

5	CM4-25	27307764	TTGGCGGCTTGGTGTAG T	AAATGCCGCCATCTATAC AGT
	CM4-27	30155206	TAGGTATGGATTGAGTG GGTCT	TTCGACTGAATGGGAATA TGCT
	RM349	32971050	TTGCCATTTCGCGTGGAG GCG	GTCCATCATCCCTATGGTC G
	RM1113	34535150	GGGCGCATGTGTATTTC TTC	TGGGGAAAAACCACAAGC C
	CM4-29	35372209	TGAAACATGAAACAAAT CCGAGT	TGAAACAGCGCCCGATTG
	CM5-1	1969011	GATGCCGGACAAGCTTG AAT	TGTTCCAAACTCCAAACA TGCA
	CM5-4	3518668	ACGAATGGTCAAACATG TGAGA	TGGAGTACTGTACGTTCT CT
	CM5-5	6165831	GTCTCTTTTGCACCGTG ACC	GCAAGGGCGTTAGTAGAA TTTT
	CM5-12	18983377	TGCCAATTGTAGGTGTT GTGT	CACTTGATGGGATTGCTT GCT
	CM5-14	21885780	AAATCCGTGGCCCTCCT C	ATAGGGGAGGGAGTGGTG AT
	CM5-16	25003997	ACATGGAGTAGCAATCG ACCA	TGCCTGTGGTTTTTCGTTAC G
	CM5-17	27701004	GTGCGGATTTCTCCTCTC TC	TGCCGGTCCATTTCTAGA AG
	CM5-19	28837876	TTGAAACCCCAGTAGCA GCT	AGCTGAGAGAGAAGAGG GGA
	CM5-20	30147722	CAAGCCAGAGTCGACGA TTC	TGCCACTCCAATCTCTCTC TC
	CM5-21	31069576	GGAGGGGTGGCCATGTA TTA	GCCGGCTTGCTGACTATT AG
6	CM6-18	50357	CGGCCATGGTAGCTAGT GTA	CCCAGCTCAGATCATTG GA
	CM6-19	2058467	ATGCAATGTCAGGCGAA ACT	TGGTGGTTGAAATTGTTG CAG
	RM217	4059800	ATCGCAGCAATGCCTCG TG	TGCGTTTGTGTTTGGCTCG
	RM1971 5	7947000	CCAATCTAAATTACGCC GCTAGG	GCCAGCTGTTGTTTGTAGT TTCG
	CM6-21	10486154	CATACGTGCCTGAGTTT CCG	TCTCTCTTTCCTGCCCTGT T
	CM6-11	14064647	ATCCTGATCCTTCCTTGC CG	TCGCTACTCAATCGACG G
	CM6-13	15772370	TGGCCCAGCAACTATCG AG	ATGTACCAAGAGCTTCGC CT

7	CM6-14	17528519	CTTTTATCTCCATGGCCG CC	CTACTGTCGCACCTCCTTC C
	CM6-26	20558014	CACGCTGTGTCTTCCGTT AA	ATTGCTGTAGAGGCCTGG TT
	CM6-28	22384871	TAATTCACCACTTCCAC CGC	AGTGTTGTGATTTCAGG GC
	STS	230388	TATGTCCTTAGCATGGA AGACC	CGTTGTTGATCATCTGGTA CG
	CM7-2	4570930	TGAGGCTTGACTTGGAT GGA	CAAACGAAACGAACGCCA AC
	STS	6071141	TTCTTCCATGTAGCAAG CATT	CCTACTGCCTGCCAAATC TAT
	CM7-10	8013115	CACATGGACAAAACAA AGGCA	TGAACGGTCATGTATGGT TTGA
	RM3755	14833204	TGTGGACAACCTCAACT GAAAGC	CATAATCACCAACATCGG AGAAGC
	CM7-6	16779869	AGCAAGCCGTCCTGTTC TT	CCGGTGATTTCGTCGTCAG
	RM11	19866268	TCTCCTCTTCCCCGATC	ATAGCGGGCGAGGCTTAG
8	RM1132	24658736	TCAAGGTCGACATGTTA GGTATGC	AACCCTATCACCTGAGAA ACATCC
	RM3555	28314588	TGGAAGTTTCCTGGCGA TAG	TGGTTGGACTGAAAAGTC CC
	RM5556	4531170	ATCTCCCTCCCTCTCCTC AC	TCCACACCTTCACAGTTG AC
	CM8-6	7674992	TTTAGACTTTGGTTGTGG CTAAC	TGGCTCATACTCTCAGAC CA
	CM8-19	9392969	TCCCGGCGTCATATCTC TTC	GACTTGTATCGCCCAACA CC
	CM8-11	12800306	GGCGAAGAAAACCCGG TG	GTCGAGTTTTGATCTCCG GC
	CM8-13	14440957	ACCACTACTGTTGAGGG CTC	GCAGCGACAGACTTGGTC
	CM8-21	18439042	CAAACGGGATCATCGGT CG	CGCCTTGTCCGATTCCAAT T
	CM8-15	22826955	GGCAACTGTTCTCCAAT TTGT	TCTGCCTGTTACTCCACCT T
	CM8-23	24081606	GTAACCGTGTTTACCGC CG	TAATCTCCTCGCGCACTA GG
9	CM8-17	28644785	GGGAAGTACAATGTGAG GGC	CCACGTTTTACCAAGTAA CCA
	CM9-1	132368	CCACTTTCACACTTGA GGC	CGGAGGTCTATGTTGGGT GA
	STS	1800000	CCTGGTTAGCACTACAG	TAGTTGGCTATGTCCACA

			CTC	CC
	CM9-6	5086933	TTTTGGTGTTCATCCCC GG	TTTCTCCGTTTGACACCTG C
	CM9-7	9141690	AGGTAGCCTCGACATTA ACGT	CAGCGTCAATCCATCGAT CG
	CM9-9	12219870	TCCTAGGTGATGTGGTG TTGT	AGGGGCGAGCATAAGGTA AA
	CM9-10	13261506	GAAGGCGTCATCCATTT CCG	AGATGCAGGAGAGGATG AGC
	CM9-13	17254623	TCACAACTCACAAGCCA TGC	TCGGTCTCTATCTCGGTCT TT
	CM9-15	19117217	ACACCATGAGTACACCA ACAA	AGCCTACTCACGGACTGT TT
	STS	22641750	TGACTCAAGGCATATGC AGC	TTGTCCATGCTGTTAGCCT G
10	STS	1100000	GCATAGCGTGACCACCG AGAA	ACCGCACAATGATTGGGA AATAC
	CM10-4	4321523	AATTCCTGAGCAGAAAG TTTGTT	CATTTCGAACACTAGGGT CTGT
	CM10-7	6023938	AGAGCTTCCATCTGTAC AGC	GGTTTGGAATATTCATGA GCCCT
	CM10-9	11676474	CATCACCTCACCTACC CG	CGGTGAACTCGGTCCACT
	CM10-10	13332668	ACCTCCAAACCAAACAC GTT	TGGAAGGGCTTGTTCACT TG
	RM5689	15482350	GCACATGGTGAGACGTC CTC	AAGTCCTGTAGTAGGTCA CACCG
	RM1375	18668850	CTACACGCGCAAACCTCT GTC	ATGAAGGTCTAGGCTGCA CC
	CM10-14	21113520	TGCTCCTTACCACCAAC CAT	TCTACCAGTACCGCACCA AG
	CM10-16	24181832	CTCTAGGAGGAGTGGAG CTG	CTACTCATTCCGTTTCACA ATGT
11	CM11-5	5211088	TTTCGTCTTCAAAAGGG TTTTCA	GGAAGAAGATGAAAATG ACCAGG
	STS	7903900	CGCTTGAAAGGACTCCA GAC	CCATCTACTACCAAACG TTCC
	CM11-7	9163957	GGTCTGCTTAGATCCAA AGGC	GGAAGTGAAGTATAGATGG ACAGC
	CM11-12	12265617	AAGCTTTAGGAGTTAGT CGGTT	CTGTCTGGCCCTGAACAA AC
	CM11-32	13710632	AAGATGGTGACGAACG GACA	AATGGGCCCAACTATCAT GC
	CM11-39	15054692	GTTCTTTCCTCTTGCCCG	ATCAACTGAGTTTGCTGG

		TG	GC
		ATCAGGACAGATGCCCT	AAGTCCAGCCTCATCACG
CM11-41	17212175	TCA	AT
		CCCAAATCACACACTCT	CCGCTGCTCTTATCTCTCC
CM11-21	22085028	TCGT	T
		CGTCTTGTTAGCTGCCG	GGCTTCTAAAACGGTGCT
CM11-29	24203520	AAT	CC
		GGGCAAATAAACTGTGT	CAAGGGGAAAACGGCCAT
CM11-23	25500867	CACC	C
		GCAGGCATGGACAAACT	CTGATGAGTTGGCATATG
CM11-37	2966139	TCA	TCCC
		ATGGACCATGGCTCAGC	GCACCGCAGCACCAGATG
12	CM12-4	AG	
		GCCCAGCTACAAATACC	TGGTTGTCTTTCCTTATCC
CM12-6	6061157	CCA	GGA
		GTGAATGGTCAAGTGAC	ACACAACATGTTCCCTCC
RM101	7782800	TTAGGTGGC	CATGC
		GTATCCTTTCTCGCAATC	GTGGCCCCGAACCTGTATA
RM1337	11058050	GC	AC
		ATTTCCGCCACAGATTT	GGGGAAGAGATTGAGCCA
CM12-11	14353137	GCC	GA
		AGTTGAGGTATAAGGCC	TGGCCATGTCACTGCTGA
CM12-15	18412824	CCG	TA
		GGAGTGGAAGACATCA	AGAAGGCTCGATTGTTGC
SSR	20654550	GGGA	AT
		CACTTTGTGTCTGTGCTTG	CTAGCCTAGACACGAGAC
CM12-27	23723600	GG	GG
		ATCACCGTTTGCATTCA	CGTTTGCCCTGTTTGTGTTG
CM12-28	25594702	GGC	T
