Supplementary Tables

Supplementary Table 1. WRKY genes of *indica* and *japonica* rice

Chromosome No.	**Number of WRKY genes in rice chromosomes**	
	indica	***japonica***
1	23	26
2	6	9
3	10	12
4	8	6
5	17	20
6	4	4
7	7	5
8	1	12
9	5	8
10	2	2
11	12	9
12	6	13
Total	**101**	**126**

Supplementary Table 2. WRKY TF gene models in *indica* rice

Gene symbol	**Gene ID**	**Chromosome no.**	**Gene names**	**Group**	**Conserved motif**	**Domain number**	**Zinc finger**
WRKY 01	BGIOSGA013535	3	OsI_13453	II	WRKYGQK	1	C2H2
WRKY 01	BGIOSGA035895	12	OsI_38986	II	WRKYGQK	1	C2H2
WRKY 02	BGIOSGA033505	10	OsI_34795	II	WRKYGQK	1	C2H2
WRKY 03	BGIOSGA000583	1	OsI_04237	III	WRKYGQK	1	C2HC
WRKY 03	BGIOSGA009781	3	OsI_13604	II	WRKYGQK	1	C2H2
WRKY 04	BGIOSGA010657	3	OsI_11758	Ia	2XWRKYGQK	2	C2H2
WRKY 04	BGIOSGA013598	3	-	Ia	2XWRKYGQK	2	C2H2
WRKY 05	BGIOSGA003851	1	OsI_02595	II	WRKYGQK	1	C2H2
WRKY 06	BGIOSGA013733	3	OsI_13911	II	WRKYGQK	1	C2H2
WRKY 06	BGIOSGA023966	7	OsI_26732	Ia	2XWRKYGQK	2	C2H2
WRKY 07	BGIOSGA020266	5	OsI_20783	II	WRKYGQK	1	C2H2
WRKY 08	BGIOSGA017481	4	OsI_21151	II	WRKYGQK	1	C2H2
WRKY 09	BGIOSGA003306	1	OsI_01473	IV	WRKYGQK	1	NA
WRKY 10	BGIOSGA002237	1	OsI_00691	II	WRKYGQK	1	C2H2
WRKY 11	BGIOSGA004027	1	OsI_02930	II	WRKYGQK	1	C2H2
WRKY 12	BGIOSGA001178	1	OsI_02922	II	WRKYGQK	1	C2H2
WRKY 13	BGIOSGA000826	1	OsI_03741	II	WRKYGQK	1	C2H2
WRKY 14	BGIOSGA000873	1	OsI_03623	II	WRKYGQK	1	C2H2
WRKY 15	BGIOSGA001093	1	OsI_03124	III	WRKYGQK	1	C2HC
WRKY 16	BGIOSGA001069	1	OsI_03172	II	WRKYGQK	1	C2H2
WRKY 17	BGIOSGA005267	1	OsI_05398	II	WRKYGQK	1	C2H2
WRKY 18	BGIOSGA004703	1	OsI_04233	III	WRKYGQK	1	C2HC
WRKY 18	BGIOSGA032700	10	OsI_33087	III	WRKYGQK	1	C2HC
WRKY 20	BGIOSGA004704	1	OsI_04235	III	WRKYGQK	1	C2HC
WRKY 21	BGIOSGA004705	1	OsI_04239	III	WRKYGQK	1	C2HC
WRKY 22	BGIOSGA004701	1	OsI_04231	III	WRKYGQK	1	C2HC
WRKY 22	BGIOSGA020451	5	OsI_21160	II	WRKYGQK	1	C2H2
WRKY 23	BGIOSGA004404	1	OsI_03639	II	WRKYGQK	1	C2H2
WRKY 24	BGIOSGA004722	1	OsI_04274	Ia	2XWRKYGQK	2	C2H2
WRKY 25	BGIOSGA027404	7	OsI_28346	II	WRKYGQK	1	C2H2
WRKY 27	BGIOSGA001327	1	OsI_02614	II	WRKYGQK	1	C2H2
WRKY 28	BGIOSGA020778	6	OsI_23911	II	WRKYGQK	1	C2H2
WRKY 29	BGIOSGA024948	7	OsI_24642	II	WRKYGQK	1	C2H2
WRKY 30	BGIOSGA026734	7	OsI_29756	Ia	2XWRKYGQK	2	C2H2
WRKY 31	BGIOSGA020376	5	OsI_21017	II	WRKYGQK	1	C2H2
WRKY 32	BGIOSGA009118	2	OsI_09096	II	WRKYGQK	1	C2H2
WRKY 34	BGIOSGA005924	2	OsI_08301	II	WRKYGQK	1	C2H2
WRKY 35	BGIOSGA014906	4	OsI_16268	Ia	2XWRKYGQK	2	C2H2
WRKY 36	BGIOSGA014615	4	OsI_16857	II	WRKYGQK	1	C2H2
WRKY 36	BGIOSGA014617	4	OsI_16855	II	WRKYGQK	1	C2H2
WRKY 37	BGIOSGA017037	4	OsI_17230	II	WRKYGQK	1	C2H2
WRKY 38	BGIOSGA030067	9	OsI_30725	IV	WRKYGQK	1	NA

WRKY 39	BGIOSGA007926	2	OsI_06657	II	WRKYGQK	1	C2H2
WRKY 40	BGIOSGA034612	11	OsI_34881	III	WRKYGQK	1	C2HC
WRKY 41	BGIOSGA035677	11	OsI_36961	III	WRKYGQK	1	C2HC
WRKY 42	BGIOSGA008165	2	OsI_07130	II	WRKYGQK	1	C2H2
WRKY 43	BGIOSGA018854	5	OsI_18378	II	WRKYGQK	1	C2H2
WRKY 44	BGIOSGA021174	6	OsI_23123	II	WRKYGQK	1	C2H2
WRKY 45-2	BGIOSGA019621	5	OsI_19468	III	WRKYGQK	1	C2HC
WRKY 46	BGIOSGA012525	3	OsI_11354	III	WRKYGEK	1*	C2HC
WRKY 46	BGIOSGA034615	11	OsI_34877	III	WRKYGQK	1	C2HC
WRKY 46	BGIOSGA036759	11	OsI_37236	III	WRKYGEK	1*	C2HC
WRKY 47	BGIOSGA023706	7	OsI_27350	III	WRKYGQK	1	C2HC
WRKY 48	BGIOSGA030346	5	OsI_30509	III	WRKYGQK	1	C2HC
WRKY 49	BGIOSGA020371	5	OsI_21007	II	WRKYGQK	1	C2H2
WRKY 50	BGIOSGA034611	11	OsI_34882	III	WRKYGQK	1	C2HC
WRKY 51	BGIOSGA009380	4	OsI_14454	II	WRKYGQK	1	C2H2
WRKY 52	BGIOSGA034616	11	OsI_34876	III	WRKYGQK	1	C2HC
WRKY 52	BGIOSGA036760	12	OsI_37234	III	WRKYGEK	1*	C2HC
WRKY 53	BGIOSGA012571	3	OsI_11453	III	WRKYGQK	1	C2HC
WRKY 53	BGIOSGA019646	5	OsI_19532	Ia	2XWRKYGQK	2	C2H2
WRKY 54	BGIOSGA017860	5	OsI_20348	III	WRKYGQK	1	C2HC
WRKY 55	BGIOSGA012523	3	OsI_11350	III	WRKYGEK	1*	C2HC
WRKY 56	BGIOSGA000506	1	OsI_04396	II	WRKYGQK	1	C2H2
WRKY 57	BGIOSGA036823	12	OsI_37118	Ia	2XWRKYGQK	2	C2H2
WRKY 57	BGIOSGA036825	11	OsI_37112	II	WRKYGQK	1	C2H2
WRKY 58	BGIOSGA017690	5	OsI_20709	IV	WRKYGQK	1	NA
WRKY 59	BGIOSGA000921	1	OsI_03498	II	WRKYGKK	1*	C2H2
WRKY 60	BGIOSGA010118	3	OsI_12866	II	WKKYGQK	1*	C2H2
WRKY 62	BGIOSGA029757	9	OsI_31380	II	WRKYGQK	1	C2H2
WRKY 63	BGIOSGA017861	5	OsI_20347	III	WRKYGQK	1	C2HC
WRKY 64	BGIOSGA036756	12	OsI_37240	III	WRKYGQK	1	C2HC
WRKY 65	BGIOSGA013972	3	OsI_14387	II	WRKYGQK	1	C2H2
WRKY 65	BGIOSGA036755	12	OsI_37241	III	WRKYGQK	1	C2HC
WRKY 66	BGIOSGA008866	2	OsI_08576	II	WRKYGQK	1	C2H2
WRKY 67	BGIOSGA018676	5	OsI_18730	II	WRKYGQK	1	C2H2
WRKY 68	BGIOSGA017063	4	OsI_17287	II	WRKYGQK	1	C2H2
WRKY 69	BGIOSGA019117	5	OsI_18309	II	WRKYGQK	1	C2H2
WRKY 69	BGIOSGA019119	5	OsI_18313	II	WRKYGQK	1	C2H2
WRKY 69	BGIOSGA040489	8	-	III	WRKYGQK	1	C2HC
WRKY 70	BGIOSGA017556	5	OsI_21001	II	WRKYGQK	1	C2HC
WRKY 70	BGIOSGA017876	5	OsI_20320	Ia	2XWRKYGQK	2	C2H2
WRKY 71	BGIOSGA007670	2	OsI_06106	II	WRKYGQK	1	C2H2
WRKY 72	BGIOSGA002913	1	OsI_00690	II	WRKYGQK	1	C2H2
WRKY 72	BGIOSGA014175	4	OsI_17774	II	WRKYGQK	1	C2H2
WRKY 72	BGIOSGA035288	11	OsI_36153	IV	WRKYGQK	1	NA
WRKY 72	BGIOSGA035289	11	OsI_36154	II	WRKYGQK	1	C2H2
WRKY 73	BGIOSGA022298	6	OsI_21640	II	WRKYGQK	1	C2H2
WRKY 74	BGIOSGA030535	9	OsI_30936	III	WRKYGQK	1	C2HC
WRKY 75	BGIOSGA019620	5	OsI_19467	III	WRKYGQK	1	C2HC
WRKY 76	BGIOSGA029758	9	OsI_31379	II	WRKYGQK	1	C2H2
WRKY 78	BGIOSGA024007	7	OsI_26641	Ia	2XWRKYGQK	2	C2H2

WRKY 79	BGIOSGA002245	1	OsI_00664	II	WRKYGKK	1*	C2H2
WRKY 80	BGIOSGA029574	9	OsI_31794	II	WRKYGQK	1	C2H2
WRKY 81	BGIOSGA033569	11	OsI_36959	Ib	2XWRKYGQK	2	C2HC
WRKY 82	BGIOSGA027300	7	OsI_28563	Ia	2XWRKYGQK	2	C2H2
WRKY 89	BGIOSGA034613	11	OsI_34880	III	WRKYGQK	1	C2HC
WRKY 89	BGIOSGA036757	12	OsI_37239	III	WRKYGQK	1	C2HC
WRKY 98	BGIOSGA035675	11	OsI_36957	III	WRKYGQK	1	C2HC
WRKY 99	BGIOSGA003134	1	OsI_01154	II	WRKYGQK	1	C2H2
WRKY 100	BGIOSGA022355	6	OsI_21753	III	WRKYGQK	1	C2HC

(* represents variation in the domain, numbers in red represents nomenclature found using BLAST results, numbers in green represents duplicated WRKY members)

Supplementary Table 3. WRKY TF gene models in *japonica* rice

Gene symbol	Gene ID	Chromosome no.	Gene names	Group	Conserved motif	Domain number	Zinc finger
WRKY 01	LOC_Os01g14440.1	1	Os01g0246700	II	WRKYGQK	1	C2H2
WRKY 02	LOC_Os10g42850.1	10	Os10g0579400	II	WRKYGQK	1	C2H2
WRKY 03	LOC_Os03g55080.1	3	Os03g0758000	II	WRKYGQK	1	C2H2
WRKY 04	LOC_Os03g55164.1	3	Os03g0758900	I	2XWRKYGQK	2	C2H2
WRKY 05	LOC_Os05g04640.1	5	Os05g0137500	II	WRKYGQK	1	C2H2
WRKY 06	LOC_Os03g58420.1	3	Os03g0798500	II	WRKYGQK	1	C2H2
WRKY 07	LOC_Os05g46020.1	5	Os05g0537100	II	WRKYGKK	1*	C2H2
WRKY 08	LOC_Os05g50610.1	5	Os05g0583000	II	WRKYGQK	1	C2H2
WRKY 08	LOC_Os05g50610.2	5	Os05g0583000	II	WRKYGQK	1	C2H2
WRKY 09	LOC_Os01g18584.1	1	Os01g0289600	II	WRKYGQK	1	C2H2
WRKY 10	LOC_Os01g09100.1	1	Os01g0186000	II	WRKYGKK	1*	C2H2
WRKY 11	LOC_Os01g43650.1	1	Os01g0626400	II	WRKYGQK	1	C2H2
WRKY 12	LOC_Os01g43550.1	1	Os01g0624700	II	WRKYGQK	1	C2H2
WRKY 13	LOC_Os01g54600.1	1	Os01g0750100	II	WRKYGQK	1	C2H2
WRKY 14	LOC_Os01g53040.1	1	Os01g0730700	II	WRKYGQK	1	C2H2
WRKY 15	LOC_Os01g46800.1	1	Os01g0656400	II	WRKYGQK	1	C2HC
WRKY 16	LOC_Os01g47560.1	1	Os01g0665500	II	WRKYGQK	1	C2H2
WRKY 17	LOC_Os01g74140.1	1	Os01g0972800	II	WRKYGQK	1	C2H2
WRKY 18	LOC_Os10g18099.1	10	-	III	WRKYGEK	1*	C2HC
WRKY 19	LOC_Os05g49620.1	5	Os05g0571200	III	WRKYGQK	1	C2HC
WRKY 20	LOC_Os01g60540.1	1	-	III	WRKYGQK	1	C2HC
WRKY 21	LOC_Os01g60640.1	1	Os01g0821600	III	WRKYGQK	1	C2HC
WRKY 22	LOC_Os01g60490.1	1	Os01g0820400	III	WRKYGQK	1	C2HC
WRKY 23	LOC_Os01g53260.1	1	Os01g0734000	II	WRKYGQK	1	C2H2
WRKY 24	LOC_Os01g61080.1	1	Os01g0826400	I	2XWRKYGQK	2	C2H2
WRKY 25	LOC_Os08g13840.1	8	Os08g0235800	II	WRKYGQK	1	C2H2
WRKY 25	LOC_Os08g13840.2	8	Os08g0235800	II	WRKYGQK	1	C2H2
WRKY 26	LOC_Os01g51690.1	1	Os01g0714800	II	WRKYGKK	1*	C2H2
WRKY 27	LOC_Os01g40430.1	1	Os01g0586800	II	WRKYGQK	1	C2H2
WRKY 28	LOC_Os06g44010.1	6	Os06g0649000	II	WRKYGQK	1	C2H2
WRKY 29	LOC_Os07g02060.1	7	Os07g0111400	II	WRKYGQK	1	C2H2
WRKY 30	LOC_Os08g38990.1	8	Os08g0499300	I	2XWRKYGQK	2	C2H2
WRKY 31	LOC_Os06g30860.1	6	Os06g0504900	II	WRKYGQK	1	C2H2
WRKY 32	LOC_Os02g53100.1	2	Os02g0770500	II	WRKYGQK	1	C2H2
WRKY 34	LOC_Os02g43560.1	2	Os02g0652100	IV	WRKYGQK	1	-
WRKY 35	LOC_Os04g39570.1	4	Os04g0471700	I	2XWRKYGQK	2	C2H2
WRKY 36	LOC_Os04g46060.1	4	Os04g0545000	II	WRKYGQK	1	C2H2
WRKY 37	LOC_Os04g50920.1	4	Os04g0597300	II	WRKYGQK	1	C2H2
WRKY 39	LOC_Os02g16540.1	2	Os02g0265200	II	WRKYGQK	1	C2H2
WRKY 42	LOC_Os11g02530.1	11	Os11g0117500	III	WRKYGQK	1	C2HC
WRKY 43	LOC_Os05g49210.1	5	Os05g0567200	II	WRKYGQK	1	C2H2
WRKY 44	LOC_Os02g26430.1	2	Os02g0462800	II	WRKYGQK	1	C2H2
WRKY 45	LOC_Os05g25770.1	5	Os05g0322900	III	WRKYGQK	1	C2HC
WRKY 47	LOC_Os07g48260.1	7	Os07g0680400	III	WRKYGQK	1	C2HC
WRKY 48	LOC_Os05g40060.1	5	Os05g0478400	III	WRKYGQK	1	C2HC
WRKY 49	LOC_Os05g49100.1	5	Os05g0565900	II	WRKYGQK	1	C2H2
WRKY 50	LOC_Os11g02540.1	11	Os11g0117600	III	WRKYGQK	1	C2HC
WRKY 51	LOC_Os04g21950.1	4	Os04g0287400	II	WRKYGQK	1	C2H2
WRKY 52	LOC_Os11g02470.1	11	Os11g0116600	III	WRKYGEK	1*	C2HC
WRKY 53	LOC_Os05g27730.1	5	Os05g0343400	I	2XWRKYGQK	2	C2H2
WRKY 54	LOC_Os05g40080.1	5	Os05g0478800	III	WRKYGQK	1	C2HC

WRKY 55	LOC_Os03g20550.1	3	Os03g0321700	III	WRKYGEK	1*	C2HC
WRKY 56	LOC_Os01g62514.1	1	Os01g0842801	IV	WRKYGQK	1	-
WRKY 57	LOC_Os12g01180.1	12	Os12g0102300	II	WRKYGQK	1	C2H2
WRKY 58	LOC_Os05g45230.1	5	Os05g0528500	IV	WRKYGQK	1	-
WRKY 60	LOC_Os03g45450.1	3	Os03g0657400	II	WRKYGQK	1	C2H2
WRKY 61	LOC_Os11g45850.1	11	Os11g0685700	III	WKKYGQK	1*	C2HC
WRKY 62	LOC_Os09g25070.1	9	Os09g0417800	II	WRKYGQK	1	C2H2
WRKY 63	LOC_Os11g45920.1	11	Os11g0686250	III	WRKYGQK	1	C2HC
WRKY 64	LOC_Os12g02450.1	12	Os12g0116700	III	2XWRKYGQK	2	C2HC
WRKY 65	LOC_Os12g02470.1	12	Os12g0116800	III	WRKYGQK	1	C2HC
WRKY 66	LOC_Os02g47060.1	2	Os02g0698800	II	WRKYGQK	1	C2H2
WRKY 67	LOC_Os05g09020.1	5	Os05g0183100	II	WRKYGKK	1*	C2H2
WRKY 68	LOC_Os04g51560.1	4	Os04g0605100	II	WRKYGQK	1	C2H2
WRKY 69	LOC_Os08g29660.1	8	Os08g0386200	III	WRKYGQK	1	C2HC
WRKY 70	LOC_Os05g39720.1	5	Os05g0474800	II	WRKYGQK	1	C2H2
WRKY 71	LOC_Os02g08440.1	2	Os02g0181300	II	WRKYGQK	1	C2H2
WRKY 72	LOC_Os11g29870.1	11	Os11g0490900	II	WRKYGQK	1	C2H2
WRKY 73	LOC_Os06g05380.1	6	Os06g0146250	II	WRKYGQK	1	C2H2
WRKY 74	LOC_Os09g16510.1	9	Os09g0334500	III	WRKYGQK	1	C2HC
WRKY 76	LOC_Os09g25060.1	9	Os09g0417600	II	WRKYGQK	1	C2H2
WRKY 77	LOC_Os01g40260.1	1	Os01g0584900	II	WRKYGKK	1*	C2H2
WRKY 79	LOC_Os03g21710.1	3	Os03g0335200	III	WRKYGQK	1	C2HC
WRKY 80	LOC_Os03g63810.1	3	Os03g0855100	II	WRKYGQK	1	C2H2
WRKY 81	LOC_Os03g33012.1	3	Os03g0444900	I	2XWRKYGQK	2	C2H2
WRKY 82	LOC_Os05g14370.1	5	Os05g0233100	III	WRKYGQK	1	C2HC
WRKY 84	LOC_Os05g40070.1	5	Os05g0478700	III	WRKYGEK	1*	C2HC
WRKY 87	LOC_Os07g39480.1	7	Os07g0583700	II	2XWRKYGQK	2	C2H2
WRKY 88	LOC_Os07g40570.1	7	Os07g0596900	II	2XWRKYGQK	2	C2H2
WRKY 89	LOC_Os08g17400.1	8	Os08g0235800	II	2XWRKYGQK	2	C2H2
WRKY 90	LOC_Os09g30400.1	9	Os09g0481700	II	WRKYGQK	1	C2H2
WRKY 94	LOC_Os12g40570.1	12	Os12g0597700	IV	WRKYGQK	1	-
WRKY 95	LOC_Os12g02400.1	12	-	III	WRKYGQK	1	C2HC
WRKY 96	LOC_Os12g32250.1	12	Os12g0507300	II	WRKYGQK	1	C2H2
WRKY 97	LOC_Os12g02420.1	12	Os12g0116400	III	WRKYGQK	1	C2HC
WRKY 102	LOC_Os01g08710.1	1	Os01g0182700	II	WRKYGQK	1	C2H2
WRKY 104	LOC_Os11g02520.1	11	Os11g0117400	III	WRKYGQK	1	C2HC
WRKY 105	LOC_Os08g09800.1	8	Os08g0198000	II	WRMCGQK	1*	C2H2
WRKY 106	LOC_Os08g09810.1	8	Os08g0198100	II	WRMCGQK	1*	C2H2
WRKY 107	LOC_Os01g09080.1	1	Os01g0185900	II	WRKYGQK	1	C2H2
WRKY 108	LOC_Os01g60600.1	1	Os01g0821300	II	WRKYGQK	1	C2H2
WRKY 109	LOC_Os05g03900.1	5	Os05g0129800	II	WRKYGQK	1	C2H2
WRKY 111	LOC_Os05g50700.1	5	-	II	WRKYGQK	1	C2H2
WRKY 112	LOC_Os09g09630.1	9	Os08g0499300	III	WRKYGQK	1	C2HC
WRKY 113	LOC_Os06g06360.1	6	Os06g0158100	III	WRKYGQK	1	C2HC
WRKY 114	LOC_Os12g02440.1	12	Os12g0116600	III	WRKYGQK	1	C2HC
WRKY 115	LOC_Os07g27670.1	7	-	III	WRKYGQK	1	C2HC
WRKY 116	LOC_Os01g60520.1	1	Os01g0820700	III	WRKYGQK	1	C2HC
WRKY 117	LOC_Os08g09840.1	8	Os08g0198400	II	WRMCGQK	1*	C2H2
WRKY 118	LOC_Os08g09900.1	8	Os08g0198900	II	WRMCGQK	1*	C2H2
WRKY 121	LOC_Os03g53050.1	3	Os03g0741400	II	WRKYGQK	1	C2H2

(* represents variation in the domain). Numbers in red represents annotations according to the nomenclature given by Rice WRKY Working Group, numbers in green represents duplicated WRKY members

Supplementary Table 4. Motif composition of WRKY protein sequences of *indica* rice

Sequence	**Width**	**Relative entropy**	**Bayes threshold**
DGYRWRKYGQKVVKGNPYPRSYYKCT	26	90	10.7279
YRWRKYGQKAVKNNKFPRSYYRCTHQGCN	29	87.6	11.5047
VRKHVERASHDPKSVITTYEGKHNHEVPA	29	79.8	11.1915
VQRTDDDASLFDVVYHGEHTC	21	47.2	9.61962
PRFCFQTRSEVDVLD	15	46.3	10.3091
DGYQWRKYGQKQIEGAMYPRS	21	62.1	10.3709
ERSLDGQITEIVYKGTHNHAK	21	66.9	11.2771
GRCHCSKRRKNRVKRTIRVPA	21	62.6	12.1549
ELGRMNEENQRLRGMLTQVTTSYQALQMH	29	75.1	12.123
KSKVWEEFKAVLIDGKVQSAICNHCKNCLVGETTKGTSHLRRHLKSCPAK	50	184.4	13.1405
LVATNDAGLENKLEGCDQAIGSDAVVEALRGGCHCLDGFRNGNEISDCKK	50	210.1	13.2145
GCMATK	6	19.9	10.2718
GGGGGA	6	17.5	10.1623
VVETMTAAITRDPNFTTAVAAALSSIM	27	77	10.4692
ALREIARGQSLVTQLRAIVL	20	41.6	11.2097

Each motif boxes identified in WRKY proteins sequences of *indica* rice.

Supplementary Table 5. Motif composition of WRKY protein sequences of *japonica* rice

Sequence	**Width**	**Relative entropy**	**Bayes threshold**
DDGYRWRKYGQKVVK	15	50.4	9.85862
GCPARKHVERCVDDPAMLIVTYEGEHN	27	37.7	8.59115
NSPYPRSYYRC	11	35.4	9.91431
ASRAIREPRVVVQTTSEVDIL	21	55.8	10.4495
QQKDTNDPPLFSVTYFNHHTC	21	45	10.3246
GYNWRKYGQKQVKGSENPRSYYKCTFPNC	29	114.8	12.4013
NLCMVQNMPEYLIDFELERAFEFIVNSPLGSEHWTFDDSIRCEHSPICIWG*	50	228.5	14.0069
RTGFGVLKIDTSRVGYSTPIRSPVTIPPGVSPRELLESPVFLPNAIAQPS	50	190.4	8.70676
LPSPSPRTLMSSFLNEEFSSGPFSDIFCDNGSNKHQDGLGKSKAFIDSSR	50	187.6	11.5572
MHSNVKPSIPKKTEDETRHDRVFFFQPILGSKPPTCPVAEKGFSVNHQNQ	50	185.6	13.1837
LTKLSASLTTTEHAEKSVMDKQEAVDISSTLSNEEDDRVTH	41	150	12.4595
VTDNHQELSLQSSSTAAKDFTSATIVKPKTSDSMLDNDDHPSPANDQEEN	50	177.9	12.4217
GIANPYVVDTAHHSMEPINQNECNSPTLEHEAHEVQDERFE	41	177.3	13.3527
YGSAGHRPAEQFGAAAAGFSFGMLPRSIATPAPSPAIAVPA	41	122.4	9.69352
TNKLTNLVGGKRKGDKHIMDNHNLEEEAKESVSKRRKNAEHTGSTVAQAP	50	159.4	8.70676

Each motif boxes identified in WRKY proteins sequences of *japonica* rice.

Supplementary Table 6. WRKYTF network involved in rice disease resistance

RGAP7.0 Locus (RAP-DB Locus)	**Paralogs**	**Gene descriptions**	***Oryza sativa* Gramene GO biological process**	**Connected guide WRKY gene**
LOC_Os04g58810 (Os04g0684900)	No Paralog	CCR4 associated factor 1B (OsCAF1B)	Nuclear-transcribed mRNA poly(A) tail shortening; defense response to insect; defense response to bacterium; response to wounding	WRKY01 WRKY15 WRKY21 WRKY71 WRKY12 WRKY28
LOC_Os09g34250 (Os09g0518200)	No Paralog	Salicylic acid glucotransferase (OsSGT)	Metabolic process; salicylic acid metabolic process; shoot morphogenesis; benzoate metabolic process; glucosinolate biosynthetic process; cellular response to water deprivation; defense response to bacterium; para-aminobenzoic acid metabolic process; callose deposition in cell wall during defense response; cellular response to hydrogen peroxide; cellular response to abscisic acid stimulus; cellular hyperosmotic salinity response; indolebutyric acid metabolic process; auxin metabolic process	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os03g64260 (Os03g0860100)	No Paralog	Ethylene-responsive transcription factor 83 (OsERF83)	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to chitin	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os04g48850 (Os04g0578000)	No Paralog	Ethylene biosynthesis ACC synthase 2	Induction of apoptosis by oxidative stress; biosynthetic process; response to external stimulus; response to wounding; response to mechanical stimulus; response to ethylene stimulus; response to auxin stimulus; response to jasmonic acid stimulus; cellular response to iron ion; response to oxidative stress	WRKY24 WRKY71 WRKY53 WRKY28
LOC_Os03g50280 (Os03g0710700)	No Paralog	GLTP domain containing protein	Respiratory burst during defense response; protein targeting to membrane; ER-nuclear signaling pathway; salicylic acid biosynthetic process; response to ethylene stimulus; abscisic acid	WRKY01 WRKY24 WRKY71 WRKY51 WRKY48 WRKY54

			mediated signaling pathway; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; response to chitin; heat acclimation; regulation of plant-type hypersensitive response; endoplasmic reticulum unfolded protein response; negative regulation of defense response; response to endoplasmic reticulum stress; innate immune response; glycolipid transport; defense response to fungus; callose deposition during defense response	
LOC_Os01g63690 (Os01g0855600)	No Paralog	Hs1pro-1 protein	Response to oxidative stress; response to salicylic acid stimulus; defense response to bacterium, incompatible interaction	WRKY11 WRKY71 WRKY53 WRKY08 WRKY28
LOC_Os08g33940 (Os08g0437300)	LOC_Os09g24800	Typical P-type R2R3 MYB protein	Response to salicylic acid stimulus; response to gibberellin stimulus; response to chitin	WRKY21 WRKY51 WRKY48 WRKY54
LOC_Os03g57310 (Os03g0787000)	No paralog	PSY1 homolog, syntaxin	Intracellular protein transport; vesicle-mediated transport; negative regulation of cellular defense response; transpiration; regulation of stomatal movement; salicylic acid mediated signaling pathway; negative regulation of defense response; jasmonic acid mediated signaling pathway; negative regulation of programmed cell death; defense response to fungus; response to fungus; regulation of plant-type hypersensitive response; protein targeting to membrane; response to abscisic acid stimulus	WRKY21 WRKY71 WRKY53 WRKY28
LOC_Os11g47460 (Os11g0700500)	LOC_Os12g37970	Snapdragon MYB protein 305 homolog	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to salicylic acid stimulus; response to gibberellin stimulus; response to ethylene stimulus; response to chitin; response to jasmonic acid stimulus; response to cadmium ion	WRKY121 WRKY51 WRKY94

LOC_Os09g21710 (Os09g0385700)	No paralog	Stress associated protein gene 17 (SAP17)	Protein targeting to membrane; response to stress; signal transduction; toxin catabolic process; response to water deprivation; response to wounding; response to ethylene stimulus; response to auxin stimulus; response to abscisic acid stimulus; abscisic acid mediated signaling pathway; response to jasmonic acid stimulus; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; response to chitin; heat acclimation; regulation of plant-type hypersensitive response; response to cyclopentenone; hyperosmotic salinity response	WRKY11 WRKY21 WRKY8
LOC_Os06g41770 (Os06g0622700)	No paralog	bZIP50	MAPKKK cascade; respiratory burst during defense response; regulation of transcription, DNA-dependent; protein targeting to membrane; ER-nuclear signaling pathway; cell communication; response to cold; response to xenobiotic stimulus; ethylene biosynthetic process; abscisic acid mediated signaling pathway; systemic acquired resistance, salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; ethylene mediated signaling pathway; heat acclimation; regulation of plant-type hypersensitive response; negative regulation of defense response; response to endoplasmic reticulum stress; negative regulation of programmed cell death; defense response to fungus; response to chitin; endoplasmic reticulum unfolded protein response	WRKY15 WRKY71 WRKY53 WRKY113
LOC_Os02g13960 (Os02g0234300)	No paralog	Plant U-box-containing protein 4 (OsPUB4)	Plant-type hypersensitive response; defense response, incompatible interaction; defense response to fungus, incompatible interaction;	WRKY53 Peptidase C48 WRKY57 WRKY57

			protein ubiquitination	
LOC_Os10g42690 (Os10g0577600)	LOC_Os02g46930	Jumonji 706	Response to chitin	WRKY71 WRKY45 WRKY53
LOC_Os03g18150 (Os03g0292100)	No paralog	Protein phosphatase 2C32 (OsPP2C32)	Protein amino acid dephosphorylation; abscisic acid mediated signaling pathway; defense response to fungus; response to fungus; response to wounding; stomatal lineage progression	WRKY21 WRKY53
LOC_Os04g32480 (Os04g0395800)	No paralog	Tify gene 9	Signal transduction; response to water deprivation; response to fungus; jasmonic acid biosynthetic process; response to ethylene stimulus; response to auxin stimulus; abscisic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; hyperosmotic salinity response; regulation of systemic acquired resistance; response to jasmonic acid stimulus; response to wounding	WRKY13 WRKY71 WRKY28
LOC_Os05g50890 (Os05g0586200)	No paralog	Jasmonyl-l-isoleucine synthase 1 (OsJAR1)	Red, far-red light phototransduction; response to wounding; systemic acquired resistance; photomorphogenesis; jasmonic acid metabolic process; response to auxin stimulus; response to jasmonic acid stimulus; jasmonic acid and ethylene-dependent systemic resistance; induced systemic resistance, jasmonic acid mediated signaling pathway; response to mycotoxin; regulation of stomatal movement; response to ozone; response to UV-B; negative regulation of defense response; response to light stimulus; cellular response to auxin stimulus	WRKY104 WRKY95
LOC_Os01g74250 (Os01g0973600)	No paralog	Protein of unknown function DUF506	Respiratory burst during defense response; response to wounding; response to mechanical stimulus; ethylene biosynthetic process; response to chitin;	WRKY71 WRKY53 Cytochrome b5 domain containing protein

			endoplasmic reticulum unfolded protein response; callose deposition during defense response	
LOC_Os02g32590 (Os02g0527300)	No paralog	Heat stress TF a3 (OsHSfA3)	Regulation of transcription, DNA-dependent; response to heat; transcription, DNA-dependent; response to stress; response to chitin	WRKY71 Cytochrome b5 domain containing protein
LOC_Os10g39770 (Os10g0544600)	No paralog	Zinc finger, RING/FYVE/PHD-type domain containing protein	mRNA transcription; response to light stimulus; response to chitin	WRKY71 WRKY53
LOC_Os02g53320 (Os02g0773200)	No paralog	UspA domain containing protein	Response to molecule of fungal origin; response to stress	WRKY71 WRKY28
LOC_Os03g12500 (Os03g0225900)	No paralog	Allene oxide synthase 2 (OsAOS2)	Oxidation reduction; response to wounding; response to fungus; response to jasmonic acid stimulus; oxylipin metabolic process; lipid metabolic process; fatty acid metabolic process; fatty acid biosynthetic process; oxylipin biosynthetic process	WRKY14 WRKY72
LOC_Os08g44830 (Os08g0562300)	No paralog	Zinc finger, C2H2-type domain	Response to chitin	WRKY73
LOC_Os08g34800 (Os08g0448100)	No paralog	Conserved hypothetical protein	Response to chitin; cellular response to hypoxia	WRKY71 WRKY53
LOC_Os06g51390 (Os06g0730300)	No paralog	Protein of unknown function DUF829	Protein targeting to membrane; response to water deprivation; response to wounding; response to fungus; jasmonic acid biosynthetic process; response to jasmonic acid stimulus; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; response to chitin; regulation of plant-type hypersensitive response; hyperosmotic salinity response; callose deposition during defense response	WRKY71 WRKY28
LOC_Os03g32314 (Os03g0438100,Os03g0438200)	No paralog	Allene oxide cyclase (OsAOC)	Response to desiccation; response to cold; response to fungus; response to salt stress	WRKY71 WRKY28
LOC_Os02g58080 (Os02g0827200)	No paralog	Sucrose transporter 4 (OsSUT4)	Sucrose metabolic process; transport; carbohydrate transport; response to wounding; response to fungus; jasmonic acid biosynthetic process; response to jasmonic acid	WRKY94

			stimulus; response to chitin; sucrose transport; carbohydrate transmembrane transport; transmembrane transport	
LOC_Os09g01960 (Os09g0106700)	No paralog	MYB protooncogene protein (R2R3-MYB)	Response to stress; response to water deprivation; response to salt stress; response to ethylene stimulus; response to auxin stimulus; response to abscisic acid stimulus; response to gibberellin stimulus; response to salicylic acid stimulus; response to jasmonic acid stimulus; response to chitin; response to cadmium ion	WRKY51
LOC_Os05g50710 (Os05g0584200)	LOC_Os01g43530	Late embryogenesis abundant protein 8 (OsLEA8)	Response to desiccation; response to wounding; response to high light intensity; defense response to fungus	WRKY1
LOC_Os03g58580 (Os03g0800000)	LOC_Os07g09010	Nitrate and chloride transporter	Defense response to fungus	WRKY1
LOC_Os05g39930 (Os05g0476700)	LOC_Os01g60860	Plant U-box-containing protein 2 (OsPUB2)	Protein ubiquitination; response to chitin	WRKY121
LOC_Os06g12120 (Os06g0225300)	LOC_Os04g38480	Somatic embryogenesis receptor-like kinase 3 (OsSERK3)	Protein amino acid phosphorylation; phosphorylation; negative regulation of cell death; leaf senescence; cell death; brassinosteroid mediated signaling pathway; response to chitin	WRKY24
LOC_Os10g31820 (Os10g0456500)	No paralog	Glutamine synthetase	Respiratory burst during defense response; glutamine biosynthetic process; tryptophan catabolic process; nitrogen compound metabolic process; metabolic process; nitrogen fixation; indoleacetic acid biosynthetic process; response to abscisic acid stimulus; response to chitin; lateral root formation; root cap development; response to bacterium	WRKY55
LOC_Os11g35330 (Os11g0557500)	No paralog	LysM-type receptor-like kinase6 and 7 (OsLysM-RLK7, OsLYK)	Protein amino acid phosphorylation; cell wall macromolecule catabolic process; innate immune response; phosphorylation; cellular response to chitin; cellular response to molecule	WRKY1

			of bacterial origin	
LOC_Os01g71670 (Os01g0944700)	No paralog	β-1, 3-glucanase (OsGLN2)	Carbohydrate metabolic process; metabolic process; response to cold; response to bacterium; response to salt stress; defense response to fungus, incompatible interaction	WRKY53
LOC_Os09g27750 (Os09g0451000)	LOC_Os02g53180	Aminocyclopropane-1-carboxylic acid oxidase1 (OsACO1)	Response to fungus; response to salt stress; ethylene biosynthetic process; detection of ethylene stimulus; oxidation reduction; positive regulation of seed germination; cellular response to fatty acid; cellular response to iron ion	WRKY83
LOC_Os03g55800 (Os03g0767000)	No paralog	Allene oxide synthase 1	Response to wounding; response to fungus; response to jasmonic acid stimulus; oxylipin metabolic process; oxidation reduction; lipid metabolic process; Fatty acid metabolic process; fatty acid biosynthetic process; oxylipin biosynthetic process	WRKY28
LOC_Os03g04060 (Os03g0132900)	LOC_Os10g39680 LOC_Os06g51050	Pathogenesis related (PR)-3 chitinase 11	Polysaccharide catabolic process; carbohydrate metabolic process; chitin catabolic process; metabolic process; cell wall macromolecule catabolic process	WRKY47
LOC_Os01g66120 (Os01g0884300)	LOC_Os05g34830	OsNAC6	Regulation of transcription, DNA-dependent; response to wounding; negative regulation of abscisic acid mediated signaling pathway; transcription, DNA-dependent; regulation of cell size; response to salicylic acid stimulus; response to light stimulus; response to fungus; response to jasmonic acid stimulus; response to sucrose stimulus; response to hypoxia	WRKY53
LOC_Os04g37430 (Os04g0447100)	No paralog	Lipoxygenase 6 (OsLOX6)	Pollen development; response to fungus; anther dehiscence; anther development; oxidation reduction; stamen filament development; lipid metabolic process; fatty acid metabolic process; fatty acid	WRKY53

			biosynthetic process; oxylipin biosynthetic process	
LOC_Os10g42430 (Os10g0575000)	No paralog	OsMYC2	Regulation of transcription from RNA polymerase II promoter in response to oxidative stress; response to desiccation; regulation of transcription factor activity; response to chitin; positive regulation of flavonoid biosynthetic process; response to jasmonic acid stimulus; response to wounding; positive regulation of transcription, DNA-dependent; response to abscisic acid stimulus; anthocyanin biosynthetic process; defense response	WRKY71
LOC_Os02g47470 (Os02g0703600)	No paralog	Abscisic acid 8'-hydroxylase 1 (OsABA8OX1)	Response to stress; abscisic acid catabolic process; oxidation reduction; release of seed from dormancy; abscisic acid metabolic process; response to red or far red light; defense response to fungus; response to water deprivation	WRKY51
LOC_Os01g16890 (Os01g0276000)	LOC_Os01g59730 LOC_Os05g41110	60S ribosomal protein L30	Translation; response to fungus	WRKY55
LOC_Os03g60710 (Os03g0821900)	LOC_Os03g16740 LOC_Os05g02020	Receptor-like cytoplasmic kinase 118 (OsRLCK118)	Protein amino acid phosphorylation; response to fungus; phosphorylation; protein amino acid autophosphorylation; defense response to fungus	WRKY16
Loc_os06g51070 (Os06g0726300)	No paralog	OsNAC95	Regulation of transcription, DNA-dependent; inflorescence morphogenesis; negative regulation of cell size; response to chitin; leaf morphogenesis	WRKY47
LOC_Os04g43440 (Os04g0514600)	No paralog	NBS-LRR type disease resistance protein O2	MAPKKK cascade; protein targeting to membrane; defense response; detection of biotic stimulus; response to bacterium; plant-type hypersensitive response; salicylic acid biosynthetic process; systemic acquired resistance, salicylic acid mediated signaling pathway; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling	WRKY74

			pathway; positive regulation of flavonoid biosynthetic process; response to chitin; regulation of hydrogen peroxide metabolic process; regulation of plant-type hypersensitive response; detection of bacterium; regulation of defense response; negative regulation of defense response; defense response to bacterium; negative regulation of programmed cell death; regulation of multi-organism process; innate immune response; regulation of immune response; defense response to fungus; response to other organism	
LOC_Os11G06420 (Os11G0163600)	LOC_Os01G64700 LOC_Os04G59130	Tubby-like protein 6 and 13	Response to fungus	WRKY 94
LOC_Os11g35400 (Os11g0558300)	No paralog	Acyl CoA synthetase	Metabolic process; long-chain fatty acid metabolic process; defense response to insect; fatty acid metabolic process; fatty acid biosynthetic process; wax biosynthetic process; cutin biosynthetic process; lateral root formation; defense response to fungus	WRKY55
LOC_Os02g47650 (Os02g0705400)	No paralog	Pathogen induced protein 2-4	Response to molecule of fungal origin; response to stress; response to desiccation; cellular response to phosphate starvation; galactolipid biosynthetic process; cellular response to water deprivation	WRKY14
LOC_Os12g36860 (Os12g0555300)	No paralog	Pathogenesis-related gene 10 (OsPR10)	Defense response; response to biotic stimulus	WRKY77 WRKY11 WRKY72
LOC_Os09g12560 (Os09g0297000)	No paralog	Ferrochelatase 1 (OsFC1)	Porphyrin biosynthetic process; heme biosynthetic process; protein targeting to membrane; response to oxidative stress; response to wounding; regulation of plant-type hypersensitive response; methylglyoxal catabolic process to D-lactate; endoplasmic reticulum unfolded protein response; tetrapyrrole biosynthetic process; negative	WRKY71 WRKY53 WRKY28

			regulation of programmed cell death; callose deposition during defense response	
LOC_Os12g36830 (Os12g0555000)	No paralog	Root specific rice PR10 (RSOsPR10)	Defense response; response to biotic stimulus	WRKY77 WRKY67 WRKY72
LOC_Os02g54160 (Os02g0782700)	LOC_Os10g25170 LOC_Os06g09390 LOC_Os09g26420	Ethylene-Responsive Element-Binding Protein 1 (OsEREBP1)	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; defense response	WRKY11 WRKY8
LOC_Os02g47880 (Os02g0708400)	No paralog	Tetratricopeptide-like helical domain containing protein	Pollen tube growth; regulation of defense response	WRKY121 WRKY94
LOC_Os03g60650 (Os03g0821300)	LOC_Os03g16760 LOC_Os05g02110	XA21 BINDING PROTEIN 15	Defense response; metabolic process; leaf development	WRKY12 WRKY74
LOC_Os02g35490 (Os02g0562600)	LOC_Os04g36680 LOC_Os05g34550	Powdery-Mildew-resistance gene O10	Defense response	WRKY47 WRKY72
LOC_Os11g45790 (Os11g0684700)	No paralog	NB-ARC domain containing protein	Defense response	WRKY1 WRKY123
LOC_Os02g51280 (Os02g0747400)	LOC_Os06g12230	Teosinte branched/cycloidea/ proliferating cell factor 9	Inflorescence development; response to cytokinin stimulus; response to gibberellin stimulus; regulation of seed germination; regulation of defense response; cell proliferation; response to abscisic acid stimulus	WRKY51
LOC_Os06g17880 (Os06g0286500)	No paralog	NBS-LRR disease resistance protein homologue	Defense response	WRKY29 WRKY72
LOC_Os04g10160 (Os04g0180400)	No paralog	Cytochrome P450 99A2 (CYP99A2)	Defense response; oxidation reduction	WRKY77 WRKY79
LOC_Os11g13410 (Os11g0237600)	No paralog	Hypothetical conserved gene	Defense response	WRKY61
LOC_Os11g12000 (Os11g0227200)	No paralog	NBS-LRR disease resistance protein (OsLRR)	Defense response	WRKY1
LOC_Os12g36880 (Os12g0555500)	No paralog	Pathogenesis-related gene 10a	Defense response; response to biotic stimulus	WRKY77
LOC_Os11g42040 (Os11g0639600)	No paralog	NB-ARC domain containing protein	Defense response	WRKY1
LOC_Os02g39330 (Os02g0605900)	No paralog	Chitinase 6, Pathogenesis related (PR)-3	Polysaccharide catabolic process; carbohydrate metabolic process; chitin catabolic process; defense response; metabolic process; somatic embryogenesis; cell wall macromolecule catabolic process	WRKY51

LOC_Os01g18860 (Os01g0293000)	LOC_Os05g04510	S-Adenosyl-l-methionine synthetase 3 (OsSAM3)	Methionine metabolic process; s-adenosylmethionine biosynthetic process; one-carbon metabolic process; response to cold; lignin biosynthetic process; cellular response to iron ion	WRKY55
LOC_Os02g18080 (Os02g0282000)	No paralog	NB-ARC domain containing protein	Defense response	WRKY29
LOC_os01g08370 (Os01g0178900)	No paralog	Symbiosis-related disease resistance protein	Defense response	WRKY1
LOC_Os03g20840 (Os03g0324600)	No paralog	NB-ARC domain containing protein	Defense response	WRKY53
Loc_os12g36850 (os12g0555200)	No paralog	Pathogenesis-related gene 10b (OsPR10b)	Defense response; response to biotic stimulus	WRKY77
LOC_Os01g07300 (Os01g0167400)	No paralog	Protein synthesis inhibitor II	Defense response; negative regulation of translation	WRKY10
LOC_Os11g11810 (Os11g0225300)	No paralog	R-gene analog 5 (OsRGA5)	Defense response	WRKY61
LOC_Os12g37760 (Os12g0565100)	No paralog	NB-ARC domain containing protein	Defense response	WRKY53
LOC_Os03g03700 (Os03g0129100)	LOC_Os10g39520	Powdery-Mildew-resistance gene O2 and O3 (OsMLO2, OsMLO3)	Defense response; response to biotic stimulus	WRKY15
LOC_Os11g46070 (Os11g0687800)	LOC_Os12g37740	NB-ARC domain containing protein	Defense response	WRKY53
LOC_Os01g57870 (Os01g0788500)	No paralog	Disease resistance protein domain containing protein	Defense response	WRKY1
LOC_Os01g63060 (Os01g0850100)	LOC_Os05g37910	Phosphatidic acid phosphatase-like protein	Lipid metabolic process; sphingolipid metabolic process; defense response; sphingolipid biosynthetic process	WRKY108
LOC_Os11g12330 (Os11g0229400)	No paralog	NBS-LRR protein	Defense response	WRKY45
LOC_Os06g18000 (Os06g0288100)	No paralog	protein kinase	Protein amino acid phosphorylation; transmembrane receptor protein tyrosine kinase signaling pathway; positive regulation of cell death; phosphorylation; positive regulation of defense response; negative regulation of floral organ abscission	WRKY107
LOC_Os03g04110 (Os03g0133400)	No paralog	Chitin elicitor binding protein	Cell wall macromolecule catabolic process; defense response	WRKY108
LOC_Os11g07850 (Os11g0180200)	LOC_Os12g07590	Protein tyrosine phosphatase 2	Protein amino acid dephosphorylation;	WRKY94

		(OsPTP2)	dephosphorylation; peptidyl-tyrosine dephosphorylation; negative regulation of defense response	
LOC_Os07g06470 (Os07g0158500)	LOC_Os03g44540 LOC_Os12g42400	HAP2 subunit of ccaat-box binding complex (Os HAP2J)	Response to cold; lignin biosynthetic process; cellular metabolic process; steroid biosynthetic process; oxidation reduction	WRKY11 WRKY51 WRKY8 Cinnamoyl CoA reductase 20 NAD(P)-binding domain containing protein
LOC_Os11g04180 (Os11g0136800)	LOC_Os12g03990	Protein phosphatase 118 (OsPP118)	Inactivation of MAPK activity; protein amino acid dephosphorylation; dephosphorylation; peptidyl-tyrosine dephosphorylation; regulation of map kinase activity	WRKY29
LOC_Os05g04510 (Os05g0135700)	LOC_Os01g18860	S-Adenosyl-l-methionine synthetase 1 (OsSAMS1)	Methionine metabolic process; S-adenosyl methionine biosynthetic process; one-carbon metabolic process; response to cold; lignin biosynthetic process	WRKY55
LOC_os01g22010 (Os01g0323600)	No paralog	S-Adenosyl-l-methionine synthetase 2 (OsSAM2)	Methionine metabolic process; s-adenosyl methionine biosynthetic process; one-carbon metabolic process; response to cold; lignin biosynthetic process; cellular response to iron ion; response to salt stress; response to cadmium ion	WRKY55
LOC_os01g05070 (Os01g0144000)	No paralog	Conserved hypothetical protein	Pectin metabolic process; homogalacturonan metabolic process	Cytochrome b5 domain containing protein
LOC_Os05g38150 (Os05g0455500)	LOC_Os01g62900	Delta1-pyrroline-5-carboxylate synthetase (OsP5CS)	Proline biosynthetic process; response to oxidative stress; metabolic process; cellular amino acid biosynthetic process; response to desiccation; response to water deprivation; response to salt stress; response to abscisic acid stimulus; embryonic development ending in seed dormancy; hyperosmotic salinity response; root development; oxidation	WRKY 55

			reduction; phosphorylation; l-proline biosynthetic process; pollen development	
LOC_Os01g18400 (Os01g0287600)	LOC_Os05g04690	Chitinase 10, Pathogenesis related (PR)-3	Polysaccharide catabolic process; carbohydrate metabolic process; chitin catabolic process; metabolic process; cell wall macromolecule catabolic process	WRKY12
LOC_Os01g32660 (Os01g0510100)	No paralog	Mitogen-activated protein kinase kinase 6 (OsMKK6)	MAPKKK cascade; activation of MAPK activity; regulation of DNA replication; protein amino acid phosphorylation; regulation of g2/m transition of mitotic cell cycle; positive regulation of translation; phosphorylation	WRKY71
LOC_Os02g09490 (Os02g0187800)	No paralog	Protein gold hull and internode 2 (OsGH2)	Oxidation reduction; phenylpropanoid biosynthetic process; lignin biosynthetic process	WRKY15
LOC_Os05g04170 (Os05g0132100)	No paralog	long-chain acyl-CoA synthetase 1 (OsLACS1)	Metabolic process; cutin biosynthetic process; wax biosynthetic process	WRKY55
LOC_Os02g27030 (Os02g0469600)	No paralog	Cysteine proteinase 1	Proteolysis; response to osmotic stress; response to desiccation; response to salt stress; defense response to bacterium	WRKY77
LOC_Os06g01260 (Os06g0102300)	No paralog	Phytochelatin synthase	Response to metal ion; arsenite transport; indole glucosinolate catabolic process; defense response to bacterium; response to arsenic; response to cadmium ion; phytochelatin biosynthetic process; callose deposition in cell wall during defense response	WRKY53
LOC_Os07g02210 (Os07g0112800)	LOC_Os03g55150	Eukaryotic translation initiation factor 5A-4	Translational initiation; translational frameshifting; peptidyl-lysine modification to hypusine; response to wounding; response to bacterium; xylem development; programmed cell death; host programmed cell death induced by symbiont; defense response to bacterium; positive regulation of translational elongation; positive regulation of translational	WRKY8

			termination; response to cadmium ion	
LOC_Os01g56200 (Os01g0767900)	No paralog	Non-expressor of pathogenesis-related gene 2 (OsNPR2)	Defense response to bacterium, incompatible interaction; response to bacterium; defense response to bacterium; defense response to fungus, incompatible interaction; defense response to fungus; response to fungus	WRKY53
LOC_Os05g03830 (Os05g0129100)	No paralog	Acetylornithine aminotransferase, mitochondrial	Interspecies interaction between organisms; primary root development; defense response to bacterium; root development	WRKY28
LOC_Os03g46470 (Os03g0667500)	No paralog	Zinc transporter 10 (OsZIP10)	Transport; ion transport; iron ion transport; zinc ion transport; cellular iron ion homeostasis; response to bacterium; cadmium ion transport; metal ion transport; iron ion homeostasis; transmembrane transport; zinc ion transmembrane transport	WRKY16
LOC_Os09g28770 (Os09g0462400)	LOC_Os03g27610	Patatin-related phospholipase A II eta (OspPLAIIeta)	MAPKKK cascade; response to molecule of bacterial origin; respiratory burst during defense response; protein targeting to membrane; lipid metabolic process; metabolic process; cell death; detection of biotic stimulus; response to absence of light; salicylic acid biosynthetic process; response to ethylene stimulus; systemic acquired resistance, salicylic acid mediated signaling pathway; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; response to chitin; regulation of hydrogen peroxide metabolic process; regulation of plant-type hypersensitive response; negative regulation of defense response; oxylipin biosynthetic process; defense response to bacterium; negative regulation of programmed cell death; regulation of multi-organism	WRKY53

			process; defense response to fungus; defense response to virus; response to other organism; response to abscisic acid stimulus; lateral root formation	
LOC_Os10g40360 (Os10g0550900)	No paralog	Proline dehydrogenase (OsProDH)	Glutamate biosynthetic process; proline catabolic process; oxidation reduction; response to oxidative stress; defense response to bacterium; response to water deprivation; response to osmotic stress	WRKY11
LOC_Os02g47020 (Os02g0698000)	LOC_Os04g50880	Phosphoribulokinase (OsPrk)	Carbohydrate metabolic process; metabolic process; response to cold; phosphorylation; defense response to bacterium	WRKY55
LOC_Os09g23540 (Os09g0400000)	No paralog	Cinnamyl alcohol dehydrogenase 8b (CAD8B)	Response to bacterium; plant-type hypersensitive response; oxidation reduction; phenylpropanoid biosynthetic process; lignin biosynthetic process	cDNA clone:J013153 J11
LOC_Os03g57220 (Os03g0786100)	LOC_Os07g05820	Glycolate oxidase 1 (OsGLO1)	Photorespiration; oxidative photosynthetic carbon pathway; regulation of photosynthesis; virus-host interaction; oxidation reduction; defense response to bacterium; hydrogen peroxide biosynthetic process	WRKY113
LOC_Os02g43360 (Os02g0649800)	LOC_Os10g37420	Cytochrome B5 homolog	Tryptophan catabolic process; indoleacetic acid biosynthetic process; glucosinolate biosynthetic process; defense response to bacterium	WRKY70
LOC_Os04g54474 (Os04g0637000)	LOC_Os08g07970	bZIP 37	Transcription; DNA dependent; regulation of transcription, DNA-dependent; response to cold; systemic acquired resistance, salicylic acid mediated signaling pathway; defense response to bacterium	WRKY13 WRKY121 WRKY94 WRKY102
LOC_Os03g20790 (Os03g0324300)	No paralog	Ethylene insensitive 3 like 1 protein (OsEIL3)	Regulation of transcription, DNA-dependent; response to ethylene stimulus; defense response to bacterium; cellular response to iron ion	WRKY11 WRKY121 WRKY8
LOC_Os03g61740 (Os03g0833100)	No paralog	Tasselseed2 protein	Metabolic process; oxidation reduction; defense response to bacterium	WRKY66 WRKY32 WRKY37

LOC_Os08g42410 (Os08g0536000)	LOC_Os09g33500	Pyruvate dehydrogenase E1 beta subunit isoform 1	Acetyl-CoA biosynthetic process from pyruvate; metabolic process; defense response to bacterium; glycolysis; oxidation reduction	WRKY55
LOC_Os06g48300 (Os06g0698300)	LOC_Os02g05630 LOC_Os04g56450	Protein phosphatase 2C59 (OsPP2C59)	Protein amino acid dephosphorylation; defense response to bacterium; interspecies interaction between organisms	WRKY40 WRKY64
LOC_Os04g01250 (Os04g0102700)	No paralog	Fatty acid amide hydrolase (OsFAAH)	Defense response to bacterium; acylethaanolamine methabolic process	WRKY55 WRKY61
LOC_Os12g39620 (Os12g0586000)	No paralog	Disease resistance protein ADR1 (Activated disease resistance protein 1)	Defense response; response to other organism; defense response to bacterium; response to water deprivation	WRKY10 WRKY53
Loc_os08g04130 (os08g0135400)	No paralog	RING finger protein (*Os*RFPHC-2)	Protein amino acid n-linked glycosylation; calcium ion transport; response to wounding; cytokinin metabolic process; jasmonic acid mediated signaling pathway; protein ubiquitination; defense response to bacterium	WRKY15 WRKY87
LOC_Os11g09010 (Os11g0195500)	No paralog	Phytoalexin deficient 4 (OsPAD4)	MAPKKK cascade; response to hypoxia; defense response to insect; respiratory burst during defense response; regulation of transcription, DNA-dependent; protein targeting to membrane; lipid metabolic process; cell communication; response to cold; detection of external stimulus; detection of biotic stimulus; response to bacterium; response to insect; salicylic acid biosynthetic process; abscisic acid mediated signaling pathway; defense response to bacterium, incompatible interaction; systemic acquired resistance, salicylic acid mediated signaling pathway; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; leaf senescence; response to chitin; regulation of hydrogen peroxide metabolic process; regulation of plant-type hypersensitive	WRKY69

			response; aerenchyma formation; positive regulation of cell death; endoplasmic reticulum unfolded protein response; regulation of defense response; negative regulation of defense response; regulation of protein amino acid dephosphorylation; defense response to bacterium; negative regulation of programmed cell death; regulation of multi-organism process; innate immune response; regulation of innate immune response; defense response to fungus; response to other organism; systemic acquired resistance	
LOC_Os12g26290 (Os12g0448900)	No paralog	Pathogen-inducible oxygenase (OsPIOX)	Response to oxidative stress; oxidation reduction; fatty acid alpha-oxidation; long-chain fatty acid metabolic process; fatty acid metabolic process; cell death; response to salicylic acid stimulus; leaf senescence; cellular response to reactive oxygen species; cellular response to salicylic acid stimulus; defense response to bacterium; systemic acquired resistance; response to abscisic acid stimulus	WRKY11
LOC_Os02g09940 (Os02g0192700)	LOC_Os06g42000	Peroxiredoxin IIE2	Defense response to bacterium; oxidation reduction	WRKY72
LOC_Os07g48630 (Os07g0685700)	LOC_Os03g20780	Ethylene insensitive-like gene 2	Regulation of transcription, DNA-dependent; response to ethylene stimulus; defense response to bacterium	WRKY11 WRKY108 WRKY71 WRKY8
LOC_Os03g03450 (Os03g0126000)	No paralog	Phosphorybosyl anthranilate transferase 1	Tryptophan biosynthetic process; metabolic process; tryptophan catabolic process; systemic acquired resistance; indoleacetic acid biosynthetic process ;response to endoplasmic reticulum stress; defense response to bacterium	WRKY55
LOC_Os03g17700 (Os03g0285800)	No paralog	Multiple stress responsive map kinase 2	MAPKKK cascade; activation of MAPK activity involved in osmosensory signaling pathway; response to hypoxia; regulation of	WRKY108 WRKY24 WRKY71 WRKY53 WRKY07

			transcription, DNA-dependent; protein amino acid phosphorylation; protein targeting to membrane; response to osmotic stress; response to oxidative stress; signal transduction; response to cold; detection of biotic stimulus; response to wounding; response to bacterium; salicylic acid biosynthetic process; abscisic acid mediated signaling pathway; defense response, incompatible interaction; systemic acquired resistance, salicylic acid mediated signaling pathway; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; camalexin biosynthetic process; response to chitin; response to UV-B; inflorescence development; regulation of hydrogen peroxide metabolic process; regulation of plant-type hypersensitive response; stomatal complex development; phosphorylation; photosynthesis, light reaction; regulation of defense response; negative regulation of defense response; regulation of protein amino acid dephosphorylation; defense response to bacterium; negative regulation of programmed cell death; regulation of multi-organism process; ovule development; defense response to fungus; response to other organism; priming of cellular response to stress; defense response	
LOC_Os01g54510 (Os01g0748900)	No paralog	Membrane attack complex component/perforin/ complement C9 family protein	MAPKKK cascade; respiratory burst during defense response; protein targeting to membrane; immune response; cell death; plant-type hypersensitive response; systemic acquired resistance, salicylic acid	WRKY71 WRKY51 WRKY53 WRKY28

			mediated signaling pathway; jasmonic acid mediated signaling pathway; response to chitin; regulation of hydrogen peroxide metabolic process; regulation of salicylic acid metabolic process; regulation of plant-type hypersensitive response; negative regulation of defense response; defense response to bacterium; negative regulation of programmed cell death; defense response to fungus; callose deposition during defense response	
LOC_Os06g07030 (Os06g0166400)	No paralog	Ethylene response factor 7 (OsERF7)	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to cold; positive regulation of transcription, DNA-dependent; response to water deprivation; regulation of cell death; response to bacterium; defense response to bacterium; response to chitin	WRKY21 WRKY48 WRKY54
LOC_Os03g08220 (Os03g0179900, Os03g0179950)	No paralog	Lipoxygenase 2 (OsLOX0)	Pollen development; response to fungus; anther dehiscence; anther development; oxidation reduction; stamen filament development; fatty acid biosynthetic process; oxylipin biosynthetic process; lipid metabolic process; fatty acid metabolic process; lipid oxidation; response to jasmonic acid stimulus; response to high light intensity; response to wounding; response to ozone; response to bacterium	WRKY71 WRKY53 WRKY28
LOC_Os11g37950 (Os11g0592000)	No paralog	PR protein 4c (OsPR4c)	Response to virus; systemic acquired resistance; response to salt stress; response to ethylene stimulus; defense response to fungus, incompatible interaction; defense response to bacterium; defense response to fungus; response to herbivore	WRKY14
LOC_Os01g71380 (Os01g0941200)	No paralog	Glucan endo-1,3-beta-glucosidase GII precursor	Carbohydrate metabolic process; metabolic process; response to cold; response to	WRKY53

	bacterium; response to salt stress; defense response to fungus, incompatible interaction	

Locus IDs in red are from the 100 genes represented in Fig.4. Other genes are from total 2299 genes. Genes were selected based on their connectivity to either WRKY TFs already reported for disease resistance in rice or the WRKY TFs phosphorylated by MAPKs.

Supplementary Table 7. Guide genes connected to one another in RiceNet (ranked by total connectivity)

RGAP7.0 Locus (RAP-DB Locus)	Gene names	Oryza sativa Gramene GO biological process	Number of connected guide gene / number of valid guide gene	Connected WRKY guide gene
LOC_Os02g08440 (Os02g0181300)	WRKY71	Na	10/82	WRKY01 WRKY15 WRKY108 WRKY21 WRKY24 WRKY53 WRKY48 WRKY54 WRKY28 WRKY74
LOC_Os06g44010 (Os06g0649000)	WRKY28	Regulation of transcription, DNA-dependent	9/82	WRKY15 WRKY21 WRKY24 WRKY71 WRKY67 WRKY53 WRKY48 WRKY54 WRKY07
LOC_Os01g60640 (Os01g0821600)	WRKY21	Regulation of transcription, DNA-dependent	12/82	WRKY11 WRKY22 WRKY71 WRKY45 WRKY48 WRKY54 WRKY08 WRKY28 WRKY69 WRKY74 WRKY104 WRKY95
LOC_Os05g40080 (Os05g0478800)	WRKY54	Regulation of transcription, DNA-dependent	10/82	WRKY11 WRKY22 WRKY21 WRKY71 WRKY45 WRKY48 WRKY08 WRKY28 WRKY104 WRKY95

LOC_Os05g40060 (Os05g0478400)	WRKY48	Regulation of transcription, DNA-dependent	10/82	WRKY11 WRKY22 WRKY21 WRKY71 WRKY45 WRKY48 WRKY08 WRKY28 WRKY104 WRKY95
LOC_Os05g27730 (Os05g0343400)	WRKY53	Regulation of transcription, DNA-dependent; camalexin biosynthetic process; cellular heat acclimation; cellular response to heat; response to cold; response to heat; positive regulation of autophagy; defense response to bacterium; response to chitin; response to salt stress; defense response to fungus; response to water deprivation; response to osmotic stress	7/82	WRKY01 WRKY15 WRKY71 WRKY07 WRKY113 WRKY28 WRKY74
LOC_Os05g25770 (Os05g0322900)	WRKY45	Regulation of transcription, DNA-dependent	9/82	WRKY11 WRKY22 WRKY21 WRKY48 WRKY54 WRKY08 WRKY76 WRKY104 WRKY95
LOC_Os01g43650 (Os01g0626400)	WRKY11	Regulation of transcription, DNA-dependent	6/82	WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os12g02440 (Os12g0116600)	WRKY95	Regulation of transcription, DNA-dependent	5/82	WRKY21 WRKY45 WRKY48 WRKY54 WRKY104
LOC_Os11g02520 (Os11g0117400)	WRKY104	Regulation of transcription, DNA-dependent	5/82	WRKY21 WRKY45 WRKY48 WRKY54 WRKY95
LOC_Os05g46020 (Os05g0537100)	WRKY7	Regulation of transcription, DNA-dependent	5/82	WRKY16 WRKY67 WRKY53 WRKY28 WRKY87

LOC_Os05g50610 (Os05g0583000)	WRKY8	Regulation of transcription, DNA-dependent	6/82	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54
LOC_Os01g61080 (Os01g0826400)	WRKY24	Regulation of transcription, DNA-dependent	5/82	WRKY01 WRKY71 WRKY42 WRKY28 WRKY69
LOC_Os01g60490 (Os01g0820400)	WRKY22	Regulation of transcription, DNA-dependent	4/82	WRKY21 WRKY45 WRKY48 WRKY54
LOC_Os07g39480 (Os07g0583700)	WRKY87	Regulation of transcription, DNA-dependent; virus induced gene silencing; vegetative phase change; positive regulation of transcription, DNA-dependent; response to 1-aminocyclopropane-1-carboxylic acid; response to wounding	3/82	WRKY16 WRKY26 WRKY07
LOC_Os01g47560 (Os01g0665500 Os01g0665750)	WRKY16	Regulation of transcription, DNA-dependent	3/82	WRKY26 WRKY07 WRKY87
LOC_Os09g16510 (Os09g0334500)	WRKY74	Regulation of transcription, DNA-dependent	4/82	WRKY21 WRKY71 WRKY53 WRKY69
LOC_Os04g21950 (Os04g0287400)	WRKY51	Regulation of transcription, DNA-dependent; defense response to bacterium; response to chitin	3/82	WRKY10 WRKY11 WRKY08
LOC_Os01g46800 (Os01g0656400)	WRKY15	Regulation of transcription, DNA-dependent	4/82	WRKY71 WRKY53 WRKY113 WRKY28
LOC_Os08g29660 (Os08g0386200)	WRKY69	Regulation of transcription, DNA-dependent	3/82	WRKY21 WRKY24 WRKY74
LOC_Os11g29870 (Os11g0490900)	WRKY72	Regulation of transcription, DNA-dependent	3/82	WRKY77 WRKY03 WRKY 29
LOC_Os01g51690 (Os01g0714800)	WRKY26	Regulation of transcription, DNA-dependent	2/82	WRKY16 WRKY87
LOC_Os01g14440 (Os01g0246700)	WRKY 1	na	3/82	WRKY24 WRKY71 WRKY53
LOC_Os09g25060 (Os09g0417600)	WRKY76	Regulation of transcription, DNA-dependent	2/82	WRKY45 WRKY62
LOC_Os06g06360 (Os06g0158100)	WRKY113	Regulation of transcription, DNA-dependent	2/82	WRKY15 WRKY53
LOC_Os05g09020 (Os05g0183100)	WRKY67	Regulation of transcription, DNA-dependent	2/82	WRKY07 WRKY28

LOC_Os07g02060 (Os07g0111400)	WRKY29	Regulation of transcription, DNA-dependent	2/82	WRKY123 WRKY72
LOC_Os11g02530 (Os11g0117500)	WRKY40	Regulation of transcription, DNA-dependent	1/82	WRKY64
LOC_Os12g02450 (Os12g0116700)	WRKY64	Regulation of transcription, DNA-dependent	1/82	WRKY40
LOC_Os04g51560 (Os04g0605100)	WRKY68	Regulation of transcription, DNA-dependent	2/82	WRKY39 WRKY25
LOC_Os02g26430 (Os02g0462800)	WRKY42	Regulation of transcription, DNA-dependent	1/82	WRKY24
LOC_Os09g25070 (Os09g0417800)	WRKY62	Regulation of transcription, DNA-dependent	1/82	WRKY76
LOC_Os01g40260 (Os01g0584900)	WRKY77	Regulation of transcription, DNA-dependent; jasmonic acid mediated signaling pathway; defense response to bacterium; defense response to fungus	1/82	WRKY72
LOC_Os11g01180 (Os11g0102700)	Peptidase C48, SUMO/Sentrin /Ubl1 family protein	Proteolysis	1/82	WRKY57
LOC_Os12g01180 (Os12g0102300 Os12g0102350)	WRKY57	Proteolysis; regulation of transcription, DNA-dependent	1/82	Peptidase C48, SUMO/Sentrin/ Ubl1 family protein
LOC_Os02g16540 (Os02g0265200)	WRKY39	Regulation of transcription, DNA-dependent	1/82	WRKY68
LOC_Os01g09100 (Os01g0186000)	WRKY10	Regulation of transcription, DNA-dependent	1/82	WRKY51
LOC_Os01g60600 (Os01g0821300)	WRKY108	Regulation of transcription, DNA-dependent	1/82	WRKY71
LOC_Os07g17230 (Os07g0273700)	WRKY123	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; defense response	1/82	WRKY29
LOC_Os08g13840 (Os08g0235800)	WRKY25	Regulation of transcription, DNA-dependent	1/82	WRKY68
LOC_Os03g55080 (Os03g0758000 Os03g0758050)	WRKY3	Regulation of transcription, DNA-dependent; response to salt stress; response to water deprivation; response to osmotic stress	1/82	WRKY72

Supplementary Table 8. Disconnected guide gene(s) in RiceNet

RGAP7.0 Locus (RAP-DB Locus)	Gene descriptions	Oryza sativa Gramene GO biological process
LOC_Os01g43550 (Os01g0624700)	WRKY12	Regulation of transcription, DNA-dependent
LOC_Os12g02420 (Os12g0116400)	WRKY97	Regulation of transcription, DNA-dependent
LOC_Os05g04640 (Os05g0137500)	WRKY5	Regulation of transcription, DNA-dependent
LOC_Os09g30400 (Os09g0481700)	WRKY90	Regulation of transcription, DNA-dependent
LOC_Os08g38990 (Os08g0499300)	WRKY30	Regulation of transcription, DNA-dependent
LOC_Os02g47060 (Os02g0698800)	WRKY66	Regulation of transcription, DNA-dependent
LOC_Os03g58420 (Os03g0798500)	WRKY6	Na
LOC_Os03g20550 (Os03g0321700)	WRKY55	Regulation of transcription, DNA-dependent
LOC_Os05g39720 (Os05g0474800)	WRKY70	Regulation of transcription, DNA-dependent
LOC_Os03g20560 (Os03g0321800)	WRKY 55.	Sulfur amino acid metabolic process; pentose-phosphate shunt; rrna processing; protein modification process; glycine catabolic process; unsaturated fatty acid biosynthetic process; oxidoreduction coenzyme metabolic process; vitamin metabolic process; cellular amino acid biosynthetic process; aromatic amino acid family metabolic process; lipoate metabolic process; lipoate biosynthetic process; coenzyme biosynthetic process; nucleotide metabolic process; protein lipoylation; jasmonic acid biosynthetic process; chlorophyll biosynthetic process; methylglyoxal catabolic process to D-lactate; isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway; secondary metabolic process; sulfur compound biosynthetic process
LOC_Os01g54600 (Os01g0750100)	WRKY13	Regulation of transcription, DNA-dependent; brassinosteroid biosynthetic process
LOC_Os12g40570 (Os12g0597700)	WRKY94	Regulation of transcription, DNA-dependent
LOC_Os01g74140 (Os01g0972800)	WRKY17	Regulation of transcription, DNA-dependent
LOC_Os01g53040 (Os01g0730700)	WRKY14	Transition metal ion transport; regulation of transcription, DNA-dependent; iron ion transport; cellular response to iron ion starvation; response to nitrate; inorganic anion transport; nitrate transport
LOC_Os08g23754 (Os08g0326900)	cDNA clone	Na
LOC_Os01g53260 (Os01g0734000)	WRKY23	Regulation of transcription, DNA-dependent

LOC_Os04g39570 (Os04g0471700)	WRKY35	Regulation of transcription, DNA-dependent
LOC_Os02g53100 (Os02g0770500)	WRKY32	Regulation of transcription, DNA-dependent; transition metal ion transport; iron ion transport; response to zinc ion; cellular response to iron ion starvation; response to nitrate; nitrate transport
LOC_Os01g09080 (Os01g0185900)	WRKY107	Regulation of transcription, DNA-dependent
LOC_Os06g05380 (Os06g0146250)	WRKY73	Regulation of transcription, DNA-dependent
LOC_Os04g46060 (Os04g0545000)	WRKY36	Regulation of transcription, DNA-dependent
LOC_Os10g42850 (Os10g0579400)	WRKY2	Na
LOC_Os08g29669 (Os08g0386300)	cytochrome b5-like Heme/Steroid binding domain	Na
LOC_Os05g50680 (Os05g0583600)	WRKY83	Negative regulation of transcription, DNA-dependent
LOC_Os01g60650 (Os01g0821700)	Chitin-binding lectin 1 precursor (PL-I)	Na
LOC_Os03g21710 (Os03g0335200)	WRKY79	Regulation of transcription, DNA-dependent
LOC_Os03g53050 (Os03g0741400)	WRKY121	Regulation of transcription, DNA-dependent
LOC_Os07g40570 (Os07g0596900)	WRKY88	Regulation of transcription, DNA-dependent
LOC_Os11g02480 (Os11g0116900)	WRKY46,	Regulation of transcription, DNA-dependent
LOC_Os07g48260 (Os07g0680400)	WRKY47	Regulation of transcription, DNA-dependent
LOC_Os11g45850 (Os11g0685700)	WRKY61	Regulation of transcription, DNA-dependent
LOC_Os03g55164 (Os03g0758900, Os03g0758950)	WRKY4	Regulation of transcription, DNA-dependent; regulation of defense response
LOC_Os04g50920 (Os04g0597300)	WRKY37	Regulation of transcription, DNA-dependent
LOC_Os05g03900 (Os05g0129800)	WRKY109	Regulation of transcription, DNA-dependent

Supplementary Table 9. Valid *Oryza sativa* guide genes but NOT found in RiceNet

RGAP7.0 ORF_ID	**RAP-DB ID**	**RAP and MSU7**	***Oryza sativa* GO biological process**
LOC_Os01g62600	Os01g0843800	laccase precursor protein	oxidation reduction; lignin catabolic process
LOC_Os01g62514	Os01g0842801	WRKY56	regulation of transcription, DNA-dependent
LOC_Os03g63810	Os03g0855100	WRKY80	regulation of transcription, DNA-dependent
LOC_Os05g40070	Os05g0478700	WRKY84	regulation of transcription, DNA-dependent
LOC_Os11g02470	Os11g0116600	WRKY52	na
LOC_Os08g17400	Os08g0276200	WRKY89	regulation of transcription, DNA-dependent; endosperm development
LOC_Os02g43560	Os02g0652100	WRKY34	regulation of transcription, DNA-dependent

Supplementary Table 10. List of genes co-expressing along with WRKY genes obtained from direct network neighborhood analysis associated (Top 100 predictions are shown)

RGAP7.0 Locus (RAP-DB Locus)	Paralogs	Gene descriptions	*Oryza sativa* Gramene GO biological process	Connected guide WRKY gene
LOC_Os03g47280 (Os03g0676400)	No Paralog	VQ domain containing protein 13 (OsVQ13)	na	WRKY01 WRKY11 WRKY15 WRKY16 WRKY26 WRKY23 WRKY71 WRKY10 WRKY08 WRKY28 WRKY78
LOC_Os06g46950 (Os06g0683400)	No Paralog	EF-hand Ca2 -binding protein CCD1	na	WRKY11 WRKY21 WRKY24 WRKY71 WRKY42 WRKY53 WRKY08 WRKY28
LOC_Os04g58810 (Os04g0684900)	No Paralog	CCR4 associated factor 1B (OsCAF1B)	Nuclear-transcribed mRNA poly(A) tail shortening; defense response to insect; defense response to bacterium; response to wounding	WRKY01 WRKY15 WRKY21 WRKY71 WRKY12 WRKY28
LOC_Os02g21040 (Os02g0314600)	No Paralog	Peptidase A1 domain	Proteolysis	WRKY01 WRKY21 WRKY24 WRKY71 WRKY42 WRKY53 WRKY28 WRKY69
LOC_Os02g43150 (Os02g0645600)	LOC_Os04g45650	AG-motif binding protein 3	Regulation of transcription, DNA-dependent; positive regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY121 WRKY45 WRKY48 WRKY54 WRKY08 WRKY94
LOC_Os10g41230 (Os10g0561800)	LOC_Os04g46350	Homeodomain gene 1 (Oshox1)	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; shade avoidance; response to hormone stimulus; response to far red light; shoot morphogenesis; response to cytokinin stimulus; unidimensional cell growth; negative regulation of transcription, DNA-dependent; response to auxin stimulus; root	WRKY11 WRKY21 WRKY121 WRKY34 WRKY45 WRKY48 WRKY54 WRKY08 WRKY94

			development; cell proliferation; fruit septum development; reproductive developmental process; floral meristem determinacy; gynoecium development; meristem development; auxin mediated signaling pathway	
LOC_Os09g34250 (Os09g0518200)	No Paralog	Salicylic acid glucotransferase (OsSGT)	Metabolic process; salicylic acid metabolic process; shoot morphogenesis; benzoate metabolic process; glucosinolate biosynthetic process; cellular response to water deprivation; defense response to bacterium; para-aminobenzoic acid metabolic process; callose deposition in cell wall during defense response; cellular response to hydrogen peroxide; cellular response to abscisic acid stimulus; cellular hyperosmotic salinity response; indolebutyric acid metabolic process; auxin metabolic process	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os09g34214 (Os09g0517900)	No Paralog	UDP-glucoronosyl and UDP-glucosyl transferase domain	Metabolic process; salicylic acid metabolic process; shoot morphogenesis; benzoate metabolic process; cellular response to water deprivation; para-aminobenzoic acid metabolic process; cellular response to hydrogen peroxide; cellular response to abscisic acid stimulus; cellular hyperosmotic salinity response; indolebutyric acid metabolic process	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g43790 (Os02g0654700)	LOC_Os04g46220	Ethylene-responsive factor 91 (OsERF91)	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY71 WRKY53 WRKY54 WRKY28
LOC_Os08g34790 (Os08g0448000)	No Paralog	4- Coumarate: coenzyme A Ligase5	Metabolic process; phenylpropanoid metabolic process	WRKY01 WRKY108 WRKY24 WRKY71 WRKY67 WRKY45 WRKY53 WRKY07 WRKY28
LOC_Os06g36160 (Os06g0555400)	LOC_Os02g13530	40S ribosomal protein S24	Translation	WRKY22 WRKY21 WRKY48 WRKY54 Cytob$_5$ domain WRKY104 WRKY95

LOC_Os05g47650 (Os05g0549800)	LOC_Os01g49830 LOC_Os01g04750	Ethylene responsive element binding protein 96	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY01 WRKY11 WRKY21 WRKY48 WRKY54 WRKY08 WRKY29 WRKY72
LOC_Os01g52490 (Os01g0723200)	No Paralog	Ribosomal protein S24	Translation	WRKY22 WRKY21 WRKY48 WRKY54 Cytob$_5$ domain WRKY104 WRKY95
LOC_Os02g13530 (Os02g0229000)	LOC_Os06g36160	40S ribosomal protein 19 -like	Translation	WRKY22 WRKY21 WRKY48 WRKY54 Cytob$_5$ domain WRKY104 WRKY95
LOC_Os07g39220 (Os07g0580500)	No Paralog	Brassinazole resistant 1 (OsBZR1)	Brassinosteroid mediated signaling pathway; negative regulation of transcription, DNA-dependent; ovule development; seed development	WRKY11 WRKY21 WRKY36 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g57650 (Os02g0822400)	LOC_Os08g44820	NAC 70 (OsNAC70)	Regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY71 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os04g39610 (Os04g0472300)	LOC_Os02g37590 LOC_Os08g39350	phosphodiesterase family protein	Glycerol metabolic process; lipid metabolic process; cell tip growth; trichome differentiation; root epidermal cell differentiation; guard cell morphogenesis; root hair cell differentiation; plant-type cell wall cellulose metabolic process	WRKY22 WRKY21 WRKY45 WRKY48 WRKY54 WRKY104 WRKY95
LOC_Os09g34230 (Os09g0518000)	No Paralog	Indole-3-acetatae-β-glucosyltransferase	Metabolic process	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08

LOC_Os09g34270 (Os09g0518400)	No Paralog	UDP-glucoronosyl and UDP-glucosyl transferase domain	na	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os09g32040 (Os09g0493700)	No Paralog	OsNAC42	Regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os03g55540 (Os03g0764100)	LOC_Os07g39960	OsWZF1	na	WRKY01 WRKY21 WRKY71 WRKY51 WRKY53 WRKY28
LOC_Os06g10780 (na)	No Paralog	AP2 domain containg TF1	na	WRKY21 WRKY121 WRKY48 WRKY54 WRKY73 WRKY94
LOC_Os01g31370 (Os01g0498300)	No Paralog	Glycosyltransferase AER61	na	WRKY11 WRKY24 WRKY71 WRKY51 WRKY53 WRKY08 WRKY23
LOC_Os02g11070 (Os02g0205500)	LOC_Os06g39750	Fatty acid elongase 1	Fatty acid biosynthetic process; metabolic process; lipid biosynthetic process; response to cold; response to light stimulus	WRKY01 WRKY108 WRKY71 WRKY53 WRKY07 WRKY28
LOC_Os04g12980 (Os04g0206700)	No Paralog	UDP-glucoronosyl/UDP-glucosyl transferase	Metabolic process	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os01g11350 (Os01g0211800)	LOC_Os01g55150 LOC_Os02g14910	bZIP02	Regulation of transcription, DNA-dependent; positive regulation of transcription, DNA-dependent; pollen development	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os01g09850 (Os01g0195000,Os01g0195066)	No Paralog	Indeterminate domain 2 (OsIDD2)	na	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08

LOC_Os01g62130 (Os01g0838600)	LOC_Os03g17150 LOC_Os05g38600 LOC_Os05g02390	ZOS1-14 - C2H2 zinc finger protein	na	WRKY11 WRKY21 WRKY71 WRKY51 WRKY48 WRKY54 WRKY08
LOC_Os08g44820 (Os08g0562200)	LOC_Os02g57650	OsNAC40	Regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY71 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os04g12970 (Os04g0206600)	No Paralog	UDP-glucoronosyl/UDP-glucosyl transferase	Metabolic process	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os01g19130 (Os01g0295700)	LOC_Os05g04360	protein phosphatase 2C	Protein amino acid dephosphorylation	WRKY12 WRKY11 WRKY71 WRKY53 WRKY08 WRKY28
LOC_Os01g57470 (Os01g0783700)	No Paralog	EF hand family protein	Response to auxin stimulus	WRKY11 WRKY24 WRKY71 WRKY53 WRKY08 WRKY28
LOC_Os02g38130 (Os02g0594800)	LOC_Os04g40140	OsNAC50	Regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os01g36630 (Os01g0546900)	No Paralog	Jumonji 709	Regulation of transcription, DNA-dependent; N-terminal protein myristoylation; histone H4-R3 demethylation; histone H3-R2 demethylation; histone H4-R3 methylation; positive regulation of seed germination	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os10g40740 (Os10g0556200)	No Paralog	Helix-loop-helix DNA-binding domain containing protein	Regulation of transcription, DNA-dependent; double fertilization forming a zygote and endosperm	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os01g72370 (Os01g0952800)	No Paralog	Achaete-scute transcription factor related domain	na	WRKY11 WRKY16 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08

LOC_Os04g12960 (Os04g0206500)	No Paralog	UDP-glucoronosyl/UDP-glucosyl transferase	Metabolic process	WRKY11 WRKY21 WRKY51 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g03330 (Os02g0125700)	No Paralog	Lil3 protein	na	WRKY11 WRKY21 WRKY55 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os03g64260 (Os03g0860100)	No Paralog	Ethylene-responsive transcription factor 83 (OsERF83)	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to chitin	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g53410 (Os02g0774200)	LOC_Os09g27410	Conserved hypothetical protein	na	WRKY11 WRKY15 WRKY24 WRKY71 WRKY53 WRKY08 WRKY28
LOC_Os07g37400 (Os07g0561300)	No Paralog	Cyclin-like F-box (OsFBX257)	na	WRKY01 WRKY11 WRKY21 WRKY71 WRKY48 WRKY54 WRKY08
LOC_Os04g43680 (Os04g0517100)	LOC_Os02g41510 LOC_Os10g33810	OsMYB4	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to stress	WRKY01 WRKY71 WRKY51 WRKY50 WRKY28
LOC_Os05g20930 (Os05g0286100)	No Paralog	Zinc finger protein KNUCKLES	Regulation of transcription, DNA-dependent; regulation of meristem structural organization; petal development; petal morphogenesis	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os09g34860 (Os09g0520200)	No Paralog	Abhydrolase domain-containing protein 5	Triglyceride homeostasis; phospholipid homeostasis; fatty acid homeostasis; lipid homeostasis	WRKY01 WRKY11 WRKY71 WRKY51 WRKY50 WRKY08 WRKY28
LOC_Os09g32510 (Os09g0501600)	LOC_Os01g68700 LOC_Os08g41320	BHLH transcription factor, putative, expressed	na	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08

LOC_Os02g41510 (Os02g0624300)	LOC_Os10g33810 LOC_Os04g43680	OsMYB 30	Response to salt stress; response to ethylene stimulus; response to auxin stimulus; response to gibberellin stimulus; response to salicylic acid stimulus; response to jasmonic acid stimulus; response to chitin; response to cadmium ion	WRKY15 WRKY71 WRKY51 WRKY50 WRKY28
LOC_Os04g37710 (Os04g0450100)	No Paralog	Dihydroflolate reductase (DUF341 domain)	na	WRKY11 WRKY71 WRKY50 WRKY08 WRKY28
LOC_Os03g01740 (Os03g0107700)	No Paralog	EL2 protein	Response to stress; cell cycle	WRKY01 WRKY21 WRKY71 WRKY50 WRKY07 WRKY28
LOC_Os04g58850 (Os04g0685300)	LOC_Os01g64450 LOC_Os08g01210	Harpin-induced 1 domain	na	WRKY24 WRKY71 WRKY42 WRKY45 WRKY53 WRKY28
LOC_Os04g48850 (Os04g0578000)	No Paralog	Ethylene biosynthesis ACC synthase 2	Induction of apoptosis by oxidative stress; biosynthetic process; response to external stimulus; response to wounding; response to mechanical stimulus; response to ethylene stimulus; response to auxin stimulus; response to jasmonic acid stimulus; cellular response to iron ion; response to oxidative stress	WRKY24 WRKY71 WRKY53 WRKY28
LOC_Os02g37590 (Os02g0588500)	LOC_Os04g39610	Glycerophosphoryldiester phosphodiesterase family protein	Glycerol metabolic process; lipid metabolic process; cell tip growth; trichome differentiation; root epidermal cell differentiation; guard cell morphogenesis; root hair cell differentiation; plant-type cell wall cellulose metabolic process	WRKY22 WRKY21 WRKY48 WRKY54 WRKY104 WRKY95
LOC_Os01g39110 (Os01g0572300)	No Paralog	Indeterminate domain 11	na	WRKY01 WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os05g51130 (Os05g0588900)	LOC_Os01g42030	Mitochondrial chaperone BCS1	na	WRKY15 WRKY24 WRKY71 WRKY53 WRKY113 WRKY28

LOC_Os05g49420 (Os05g0569300)	LOC_Os01g46970	bZIP45	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g07450 (Os02g0170500)	LOC_Os06g45640	HAP52 subunit of CCAAT box binding complex	Regulation of transcription, DNA-dependent; positive regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY48 WRKY54 WRKY08 WRKY94
LOC_Os03g56580 (Os03g0777000)	LOC_Os07g04560	OsNAC66	Rgulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g11859 (Os02g0209300)	No Paralog	Hypothetical conserved gene	na	WRKY01 WRKY71 WRKY42 WRKY53 WRKY07 WRKY28
LOC_Os07g38240 (Os07g0569700)	No Paralog	Stress associated protein	Response to stress	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g09980 (Os02g0193200)	No Paralog	TMV response-related protein	na	WRKY01 WRKY71 WRKY51 WRKY45 WRKY53 WRKY28
LOC_Os08g41320 (Os08g0524800)	LOC_Os01g68700 LOC_Os09g32510	BHLH transcription factor	na	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os03g42370 (Os03g0621600,Os03g0621650)	No Paralog	B3 DNA binding domain	na	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os02g42380 (Os02g0635800)	LOC_Os04g44440	TCP family transcription factor	na	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os09g25760 (Os09g0425900)	LOC_Os08g34460	Senescence-associated protein DH, Tetraspanin 13	na	WRKY01 WRKY24 WRKY71 WRKY53 WRKY28

LOC_Os06g45640 (Os06g0667100)	LOC_Os02g07450	HAP5B	Regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY48 WRKY54 WRKY08 WRKY94
LOC_Os03g50280 (Os03g0710700)	No Paralog	GLTP domain containing protein	Respiratory burst during defense response; protein targeting to membrane; ER-nuclear signaling pathway; salicylic acid biosynthetic process; response to ethylene stimulus; abscisic acid mediated signaling pathway; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; response to chitin; heat acclimation; regulation of plant-type hypersensitive response; endoplasmic reticulum unfolded protein response; negative regulation of defense response; response to endoplasmic reticulum stress; innate immune response; glycolipid transport; defense response to fungus; callose deposition during defense response	WRKY01 WRKY24 WRKY71 WRKY51 WRKY48 WRKY54
LOC_Os01g46970 (Os01g0658900)	LOC_Os05g49420	bZIP8	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os08g39350 (Os08g0503200)	LOC_Os04g39610	PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	Glycerol metabolic process; lipid metabolic process; cell tip growth; trichome differentiation; root epidermal cell differentiation; guard cell morphogenesis; root hair cell differentiation; plant-type cell wall cellulose metabolic process	WRKY22 WRKY21 WRKY48 WRKY54 WRKY104 WRKY95
LOC_Os01g16240 (Os01g0267900)	No Paralog	Calmodulin 1 (OsCam1)	Pollen germination; regulation of photomorphogenesis; calcium-mediated signaling	WRKY15 WRKY121 WRKY69 WRKY94
LOC_Os03g20370 (Os03g0319300)	LOC_Os01g59530 LOC_Os11g03980 LOC_Os12g03816 LOC_Os05g41200 LOC_Os07g48780	Calmodulin1 (OsCam1)	Pollen germination; regulation of photomorphogenesis; calcium-mediated signaling	WRKY15 WRKY121 WRKY69 WRKY94
LOC_Os07g48780 (Os07g0687200)	LOC_Os03g20370 LOC_Os05g41200 LOC_Os11g03980 LOC_Os12g03816	Calmodulin B	Pollen germination; regulation of photomorphogenesis; calcium-mediated signaling	WRKY15 WRKY121 WRKY69 WRKY94

LOC_Os03g15660 (Os03g0263000)	No Paralog	Ethylene response factor 9	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY21 WRKY121 WRKY48 WRKY54 WRKY73 WRKY94
LOC_Os01g49830 (Os01g0693400)	LOC_Os01g04750 LOC_Os05g47650	Apetala2/ethylene-responsive element binding protein 127	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY53 WRKY48 WRKY54 WRKY08
LOC_Os02g09990 (Os02g0193300)	No Paralog	Conserved hypothetical protein	na	WRKY01 WRKY71 WRKY51 WRKY45 WRKY53 WRKY28
LOC_Os11g13840 (Os11g0242300)	No Paralog	Ethylene response factor 19	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY21 WRKY121 WRKY48 WRKY54 WRKY94
LOC_Os02g50460 (Os02g0738200)	LOC_Os06g13870	Plant U-box-containing protein 40	Protein ubiquitination	WRKY01 WRKY77 WRKY24 WRKY71 WRKY47 WRKY69 WRKY72
LOC_Os04g32620 (Os04g0398000)	No Paralog	Ethylene response factor 101	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY21 WRKY121 WRKY48 WRKY54 WRKY94
LOC_Os07g04560 (Os07g0138200)	LOC_Os03g56580	NAC96	na	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os10g26460 (Os10g0404300)	No Paralog	Increased leaf inclination 7	Response to light stimulus; photomorphogenesis; response to brassinosteroid stimulus; brassinosteroid mediated signaling pathway; unidimensional cell growth; embryonic root morphogenesis; regulation of timing of transition from vegetative to reproductive phase	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os04g44440 (Os04g0526000)	LOC_Os02g42380	Teosinte branched/cycloidea/proliferating cell factor 17	na	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08

LOC_Os01g44390 (Os01g0635200)	No Paralog	Homeodomain-like containing protein	na	WRKY21 WRKY121 WRKY48 WRKY54 WRKY94
LOC_Os03g11910 (Os03g0218500)	No Paralog	70 kD heat shock protein	Protein folding; heat acclimation; response to hydrogen peroxide; response to heat; response to high light intensity	WRKY11 WRKY21 WRKY48 WRKY54 WRKY08
LOC_Os03g37090 (Os03g0568500)	No Paralog	Uncharacterised protein family UPF0136	na	WRKY01 WRKY24 WRKY71 WRKY53 WRKY28 WRKY94
LOC_Os05g04210 (Os05g0132700)	LOC_Os01g19330	R2R3 Myb-like protein.	na	WRKY11 WRKY121 WRKY08 WRKY94
LOC_Os09g20220 (Os09g0367700)	No Paralog	glutathione S-transferase (GST6)	Glutathione metabolic process; response to oxidative stress; response to cold; response to herbicide; cellular response to water deprivation; response to cadmium ion	WRKY11 WRKY21 WRKY48 WRKY54 WRKY08
LOC_Os03g42230 (Os03g0619600)	LOC_Os12g40070	Transcriptional factor B3 family protein	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os03g57200 (Os03g0785900)	LOC_Os03g44170	TAU glutathione s-transferase 1	Glutathione metabolic process; response to oxidative stress; response to cold; response to herbicide; cellular response to water deprivation; response to cadmium ion	WRKY11 WRKY21 WRKY48 WRKY54 WRKY08 WRKY95
LOC_Os03g42240 (Os03g0619800)	No Paralog	Transcriptional factor B3 domain	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY11 WRKY21 WRKY45 WRKY48 WRKY54 WRKY08
LOC_Os01g72530 (Os01g0955100)	No Paralog	OsCML31 - Calmodulin-related calcium sensor protein	na	WRKY21 WRKY71 WRKY42 WRKY53 WRKY28
LOC_Os03g50210 (Os03g0710000)	LOC_Os03g15210	DUF292 domain	na	WRKY11 WRKY21 WRKY48 WRKY54 WRKY08
LOC_Os07g42740 (Os07g0619500)	No Paralog	DUF1645 domain	na	WRKY01 WRKY71 WRKY53 WRKY28 WRKY74 WRKY72

LOC_Os01g63690 (Os01g0855600)	No Paralog	Hs1pro-1 protein	Response to oxidative stress; response to salicylic acid stimulus; defense response to bacterium, incompatible interaction	WRKY11 WRKY71 WRKY53 WRKY08 WRKY28
LOC_Os05g01940 (Os05g0110000)	LOC_Os01g74040 LOC_Os03g16480	Zinc finger, RING/FYVE/PHD-type domain	na	WRKY21 WRKY71 WRKY53 WRKY28 WRKY74
LOC_Os03g08330 (Os03g0181100)	No Paralog	Jasmonate zim-domain protein	na	WRKY01 WRKY108 WRKY71 WRKY53 WRKY28
LOC_Os03g38870 (Os03g0585600)	No Paralog	DOF zinc finger domain	Regulation of transcription, DNA-dependent	WRKY16 WRKY121 WRKY51 WRKY94
LOC_Os02g33600 (Os02g0539500)	LOC_Os04g34050	VQ motif-containing protein 8	na	WRKY24 WRKY71 WRKY53
LOC_Os01g38980 (Os01g0570800)	No Paralog	IQ calmodulin-binding region domain	na	WRKY01 WRKY21 WRKY71 WRKY53
LOC_Os02g07690 (Os02g0173200)	No Paralog	VQ motif-containing protein 5	na	WRKY01 WRKY71 WRKY53 WRKY07 WRKY28
LOC_Os02g35240 (Os02g0558700)	No Paralog	Dehydration-responsive element-binding protein, putative, expressed	Transcription, DNA-dependent; regulation of transcription, DNA-dependent	WRKY21 WRKY121 WRKY48 WRKY54 WRKY94
LOC_Os02g49560 (Os02g0728001)	LOC_Os09g29820	bZIP22	Regulation of transcription, DNA-dependent	WRKY13 WRKY21 WRKY34 WRKY48 WRKY54
LOC_Os06g13870 (Os06g0248500)	LOC_Os02g50460	U-box protein CMPG1	Protein ubiquitination	WRKY24 WRKY71 WRKY53 WRKY28

Supplemetary Table 11. List of networking WRKY genes forming context associated hubs (number of enriched terms by p-values ≤ 0.01 is 100.)

RGAP locus ID (RAP-DB ID)	Paralog	Gene descriptions	Gramene annotated GO biological process term of rice	p-value
LOC_Os01g60640	LOC_Os05g40060	WRKY 21	Regulation of transcription, DNA-dependent	7.94e-15
LOC_Os05g40060	LOC_Os07g48260	WRKY47	Regulation of transcription, DNA-dependent	3.49e-13
LOC_Os03g47280		VQ motif containing protein 13	VQ domain containing protein, putative, expressed	9.24e-13
LOC_Os05g40080		WRKY45	regulation of transcription, DNA-dependent	9.64e-13
LOC_Os05g25770		WRKY 48	regulation of transcription, DNA-dependent	1.66e-12
LOC_Os06g44010		WRKY 54	regulation of transcription, DNA-dependent	2.24e-11
LOC_Os02g08440	LOC_Os06g44010	WRKY71	*Os*WRKY71 - Superfamily of TFs having WRKY and zinc finger domains, expressed	1.37e-09
LOC_Os02g50460	LOC_Os06g13870	Ubox 40	protein ubiquitination	1.39e-09
LOC_Os02g43150	LOC_Os04g45650	AG-motif binding protein-3	regulation of transcription, DNA-dependent; positive regulation of transcription, DNA-dependent	2.10e-09
LOC_Os02g21040		Peptidase A1 domain	proteolysis	7.63e-09
LOC_Os03g42240		Transcriptional factor B3 domain containing protein	transcription, DNA-dependent; regulation of transcription, DNA-dependent	7.63e-09
LOC_Os03g42230	LOC_Os12g40070	Transcriptional factor B3 family protein	transcription, DNA-dependent; regulation of transcription, DNA-dependent	1.12e-08
LOC_Os08g34790		4-coumarate--CoA ligase 1	metabolic process; phenylpropanoid metabolic process	1.15e-08
LOC_Os10g26460		Increased leaf inclination 7	response to light stimulus; photomorphogenesis; response to brassinosteroid stimulus; brassinosteroid mediated signaling pathway; unidimensional cell growth; embryonic root morphogenesis; regulation of timing of transition from vegetative to reproductive phase	1.34e-08
LOC_Os02g53410	LOC_Os09g27410	Conserved hypothetical protein	expressed protein	1.92e-08
LOC_Os01g49830	LOC_Os05g47650	Ethylene responsive factor127	transcription, DNA-dependent; regulation of transcription, DNA-dependent	2.44e-08
LOC_Os08g44820		NAC40	regulation of transcription, DNA-dependent	2.47e-08
LOC_Os04g44440		Teosinte 17	TCP family transcription factor, putative, expressed	2.86e-08
LOC_Os05g47650		Ethylene responsive factor96	transcription, DNA-dependent; regulation of transcription, DNA-dependent	3.48e-08
LOC_Os09g32040		NAC42	regulation of transcription, DNA-dependent	3.99e-08
LOC_Os07g37400		F-box domain396 (OsFBX396)	OsFBX257 - F-box domain containing protein, expressed	5.60e-08
LOC_Os01g72370		Helix loop helix domain	helix-loop-helix DNA-binding domain containing protein, expressed	5.87e-08

LOC_Os03g08330		Tify gene 11B	ZIM domain containing protein, putative, expressed	1.49e-07
LOC_Os07g39220		Brassinazole resistant 1	Brassinosteroid mediated signaling pathway; negative regulation of transcription, DNA-dependent; ovule development; seed development	1.52e-07
LOC_Os02g37590	LOC_Os04g39610	Hypothetical protein	glycerol metabolic process; lipid metabolic process; cell tip growth; trichome differentiation; root epidermal cell differentiation; guard cell morphogenesis; root hair cell differentiation; plant-type cell wall cellulose metabolic process	1.55e-07
LOC_Os10g40740		helix-loop-helix protein 113	regulation of transcription, DNA-dependent; double fertilization forming a zygote and endosperm	1.55e-07
LOC_Os07g38240		Stress associated protein gene 16	response to stress	1.84e-07
LOC_Os01g36630		Jumonji 709	regulation of transcription, DNA-dependent; N-terminal protein myristoylation; biological process; histone H4-R3 demethylation; histone H3-R2 demethylation; histone H4-R3 methylation; positive regulation of seed germination	1.84e-07
LOC_Os02g11859		Hypothetical conserved gene	expressed protein	2.43e-07
LOC_Os04g39610	LOC_Os08g39350	PLC-like phosphodiesterase, TIM beta/alpha-barrel domain	glycerol metabolic process; lipid metabolic process; cell tip growth; trichome differentiation; root epidermal cell differentiation; guard cell morphogenesis; root hair cell differentiation; plant-type cell wall cellulose metabolic process	4.31e-07
LOC_Os05g50610		WRKY8	regulation of transcription, DNA-dependent	4.49e-07
LOC_Os03g01740		EL2 protein	response to stress; cell cycle	4.71e-07
LOC_Os02g57650	LOC_Os08g44820	NAC70	regulation of transcription, DNA-dependent	5.11e-07
LOC_Os10g41230		Homeodomain leucine zipper protein (HOX1)	transcription, DNA-dependent; regulation of transcription, DNA-dependent; shade avoidance; response to hormone stimulus; response to far red light; shoot morphogenesis; response to cytokinin stimulus; unidimensional cell growth; negative regulation of transcription, DNA-dependent; response to auxin stimulus; root development; cell proliferation; fruit septum development; reproductive developmental process; floral meristem determinacy; gynoecium development; meristem development; auxin mediated signaling pathway	5.20e-07
LOC_Os02g07690		VQ domain containing protein5	VQ domain containing protein, putative, expressed	5.38e-07
LOC_Os04g58850	LOC_Os08g01210	Harpin-induced 1 domain containing protein	harpin-induced protein 1 domain containing protein, expressed	6.23e-07

LOC_Os06g46950		Small calcium binding protein with one hand motif	EF hand family protein, putative, expressed	6.39e-07
LOC_Os01g62130	LOC_Os05g02390	ZOS1-14 - C2H2 zinc finger protein	ZOS1-14 - C2H2 zinc finger protein, expressed	6.62e-07
LOC_Os05g27730	LOC_Os05g39720	WRKY53	regulation of transcription, DNA-dependent; camalexin biosynthetic process; cellular heat acclimation; cellular response to heat; response to cold; response to heat; positive regulation of autophagy; defense response to bacterium; response to chitin; response to salt stress; defense response to fungus; response to water deprivation; response to osmotic stress	7.05e-07
LOC_Os01g43650	LOC_Os05g50610	WRKY 11	regulation of transcription, DNA-dependent	7.45e-07
LOC_Os07g04560		NAC96	no apical meristem protein, putative	8.50e-07
LOC_Os03g37090		Uncharacterised protein family UPF0136	expressed protein	9.25e-07
LOC_Os03g64260		Ethylene response factor 83	transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to chitin	1.05e-06
LOC_Os02g42380	LOC_Os04g44440	Transcription factor, TCP domain	TCP family transcription factor, putative, expressed	1.19e-06
LOC_Os03g42370		Transcriptional factor B3 domain	B3 DNA binding domain containing protein	1.34e-06
LOC_Os01g61080	LOC_Os05g39720	WRKY 24	regulation of transcription, DNA-dependent	1.48e-06
LOC_Os05g20930		Zinc-finger protein KNUCKLES.	regulation of transcription, DNA-dependent; regulation of meristem structural organization; petal development; petal morphogenesis	1.51e-06
LOC_Os01g46970	LOC_Os05g49420	bZIP8	transcription, DNA-dependent; regulation of transcription, DNA-dependent	1.69e-06
LOC_Os02g11070	LOC_Os06g39750	Fatty acid elongase 1	fatty acid biosynthetic process; metabolic process; lipid biosynthetic process; response to cold; response to light stimulus	2.35e-06
LOC_Os01g31370		Glycosyltransferase AER61	glycosyltransferase, putative, expressed	2.60e-06
LOC_Os03g56580	LOC_Os07g04560	NAC66	regulation of transcription, DNA-dependent	2.62e-06
LOC_Os04g48350	LOC_Os09g35010	Dehydration responsive element binding protein (DRE) binding factor 1E	Transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to stress; response to cold; response to water deprivation ;cold acclimation	3.58e-06
LOC_Os05g51130		Mitochondrial chaperone BCS1	mitochondrial chaperone BCS1, putative, expressed	3.80e-06
LOC_Os05g49420		bZIP45	transcription, DNA-dependent; regulation of transcription, DNA-dependent	4.06e-06
LOC_Os06g45640		HAP5B subunit of CCAAT box binding complex	regulation of transcription, DNA-dependent	4.76e-06

LOC_Os01g19130	LOC_Os05g04360	Protein phosphatase-2C02	protein amino acid dephosphorylation	5.38e-06
LOC_Os03g57200		TAU Glutathione-S-transferase 1	glutathione metabolic process; response to oxidative stress; response to cold; response to herbicide; cellular response to water deprivation; response to cadmium ion	6.64e-06
LOC_Os02g45450	LOC_Os04g48350	Ethylene responsive factor 25	transcription, DNA-dependent; regulation of transcription, DNA-dependent; response to cold; response to water deprivation; cold acclimation; response to stress; positive regulation of transcription, DNA-dependent	7.19e-06
LOC_Os08g41320	LOC_Os09g32510	TA1 protein	BHLH transcription factor, putative, expressed	7.47e-06
LOC_Os03g21640	LOC_Os07g48280	Protein of unknown function DUF3133 domain	expressed protein	7.51e-06
LOC_Os01g11350	LOC_Os02g14910	bZIP02	regulation of transcription, DNA-dependent; positive regulation of transcription, DNA-dependent; pollen development	7.68e-06
LOC_Os02g03330		Lil3 protein	expressed protein	7.95e-06
LOC_Os06g13190		Conserved hypothetical protein	expressed protein	8.72e-06
LOC_Os08g37660	LOC_Os09g29390	Uclacyanin like protein 29	plastocyanin-like domain containing protein, putative, expressed	8.72e-06
LOC_Os02g07450	LOC_Os06g45640	Indeterminate domain 11	regulation of transcription, DNA-dependent; positive regulation of transcription, DNA-dependent	8.85e-06
LOC_Os01g39110		Indeterminate domain 11	ZOS1-10 - C2H2 zinc finger protein, expressed	9.02e-06
LOC_Os06g10530		Conserved hypothetical protein	expressed protein	9.37e-06
LOC_Os01g39330	LOC_Os06g37410	Helix-loop-helix protein 24	helix-loop-helix DNA-binding domain containing protein, expressed	9.37e-06
LOC_Os06g33970		VQ motif containing protein 22	VQ domain containing protein, putative, expressed	9.37e-06
LOC_Os04g46240		Ethylene responsive factor 97	AP2 domain containing protein, expressed	1.01e-05
LOC_Os07g42740		Protein of unknown function DUF1645	DUF1645 domain containing protein, putative, expressed	1.10e-05
LOC_Os02g43820		Ethylene responsive factor 95	AP2 domain containing protein, expressed	1.24e-05
LOC_Os02g44880	LOC_Os04g47450	H0211B05.7 protein	Expressed protein	1.41e-05
LOC_Os01g50420		Serine/threonine protein kinase domain	protein amino acid phosphorylation	1.41e-05
LOC_Os08g31000		Ankyrin repeat protein	expressed protein	1.50e-05
LOC_Os06g10780		AP2 domain containing protein	AP2 domain containing protein, expressed	1.66e-05
LOC_Os04g58810		CCR4 associated factor 1B	nuclear-transcribed mRNA poly(A) tail shortening; defense response to insect ;defense response to bacterium; response to wounding	1.70e-05

LOC_Os03g50280		GLTP domain	Respiratory burst during defense response; protein targeting to membrane; ER-nuclear signaling pathway; salicylic acid biosynthetic process; response to ethylene stimulus; abscisic acid mediated signaling pathway; salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; response to chitin; heat acclimation; regulation of plant-type hypersensitive response; endoplasmic reticulum unfolded protein response; negative regulation of defense response; response to endoplasmic reticulum stress; innate immune response; glycolipid transport; defense response to fungus; callose deposition during defense response	2.17e-05
LOC_Os02g32140		Ethylene responsive factor 107	AP2 domain containing protein, expressed	2.25e-05
LOC_Os01g62430		Elicitor-responsive protein 1	C2 domain containing protein, putative, expressed	2.41e-05
LOC_Os09g25760		tetraspanin protein 13	tetraspanin family protein, putative, expressed	2.41e-05
LOC_Os02g49560	LOC_Os09g29820	bZIP22	regulation of transcription, DNA-dependent	2.49e-05
LOC_Os03g15660		Ethylene responsive factor 9	transcription, DNA-dependent; regulation of transcription, DNA-dependent	2.79e-05
LOC_Os01g42030	LOC_Os05g51130	BCS1 protein-like protein	mitochondrial chaperone BCS1, putative, expressed	2.83e-05
LOC_Os07g48630		Ethylene insensitive like gene 2	regulation of transcription, DNA-dependent; response to ethylene stimulus; defense response to bacterium	2.84e-05
LOC_Os09g34270		UDP-glucosyl transferase UGT74H5	UDP-glucoronosyl and UDP-glucosyl transferase domain containing protein	2.99e-05
LOC_Os02g09990		Conserved hypothetical protein	expressed protein	3.19e-05
LOC_Os01g09850		Zinc finger, C2H2-type domain	ZOS1-04 - C2H2 zinc finger protein, expressed	3.33-05
LOC_Os05g38620		Zinc finger, C2H2 domain containing protein.	ZOS5-10 - C2H2 zinc finger protein	3.42e-05
LOC_Os09g34860		Abhydrolase domain-containing protein 5.	triglyceride homeostasis; phospholipid homeostasis; fatty acid homeostasis; lipid homeostasis	3.65e-05
LOC_Os03g55540	LOC_Os07g39960	Zinc finger transcription factor ZF1	ZOS3-18 - C2H2 zinc finger protein, expressed	3.78e-05
LOC_Os01g57470		EF-hand Ca2+ binding protein CCD1	response to auxin stimulus	3.78e-05
LOC_Os02g09980		TMV response-related protein	Expressed protein	3.86e-05

LOC_Os06g41770		bZIP50	MAPKKK cascade; respiratory burst during defense response; regulation of transcription, DNA-dependent; protein targeting to membrane; ER-nuclear signaling pathway; cell communication; response to cold; response to xenobiotic stimulus; ethylene biosynthetic process; abscisic acid mediated signaling pathway; systemic acquired resistance, salicylic acid mediated signaling pathway; jasmonic acid mediated signaling pathway; ethylene mediated signaling pathway; heat acclimation; regulation of plant-type hypersensitive response; negative regulation of defense response; response to endoplasmic reticulum stress; negative regulation of programmed cell death; defense response to fungus; response to chitin; endoplasmic reticulum unfolded protein response	3.87e-05
LOC_Os06g13870		U-box protein 39	Protein ubiquitination	3.87e-05
LOC_Os02g35240		Ethylene response factor 21	Transcription, DNA-dependent; regulation of transcription	4.34e-05
LOC_Os11g13840		Ethylene responsive factor 19	Transcription, DNA-dependent; response to stress	4.47e-05
LOC_Os04g43680	LOC_Os10g33810	OsMyb4	Transcription, DNA-dependent; response to stress	5.01e-05
LOC_Os09g29360		Basic helix-loop-helix protein 046	Helix-loop-helix DNA-binding protein, putative, expressed	5.14e-05
LOC_Os10g23050		Basic helix-loop-helix protein 045	Helix-loop-helix DNA-binding protein, putative, expressed	5.37e-05