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In silico genome-wide identification and phylogenetic analysis of the WRKY transcription factor family in sweet orange (*Citrus sinensis*)

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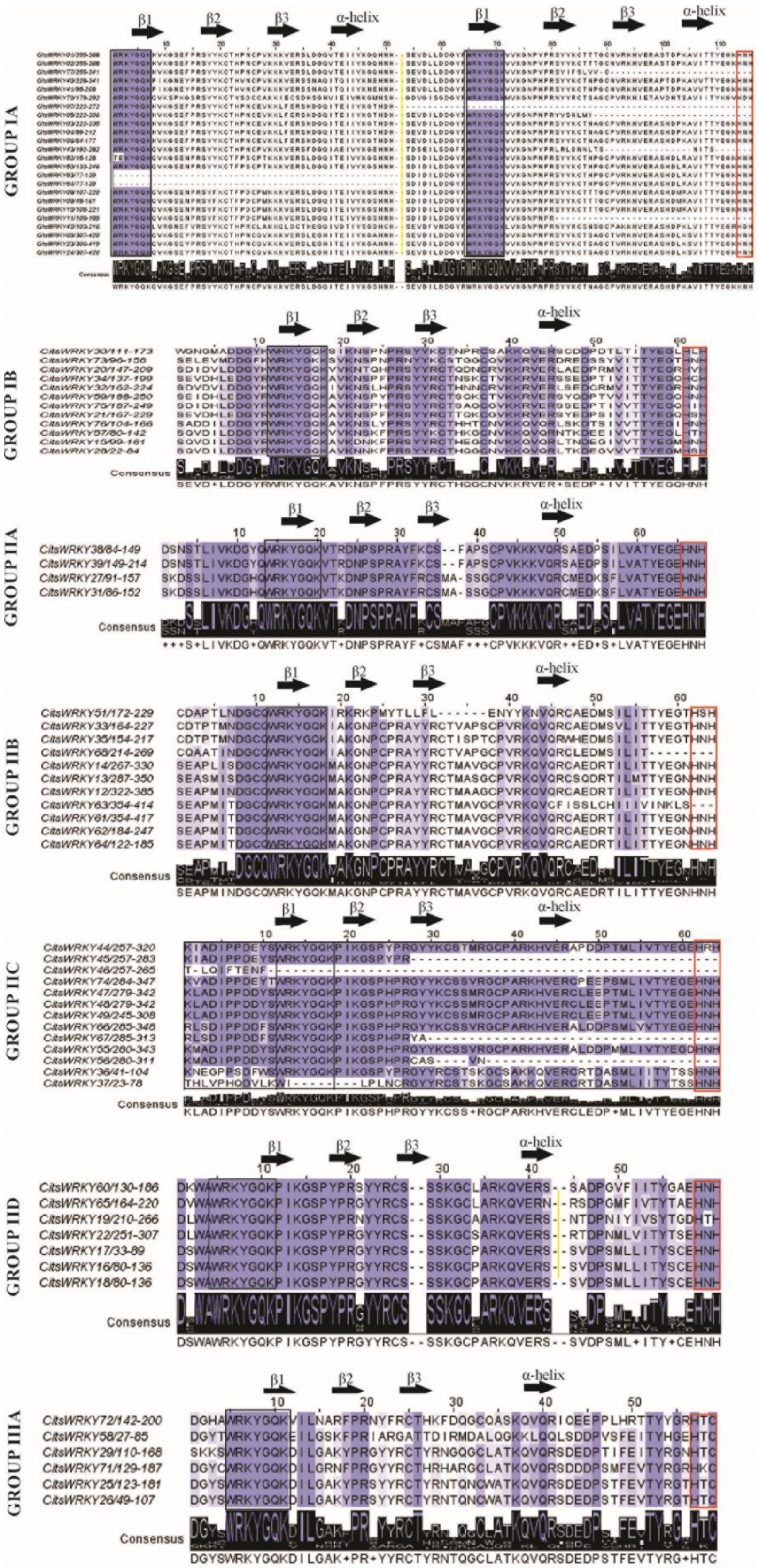
Supplementary Table S1. Physical and chemical characteristics of genes *CitsWRKY*, WRKY ID- protein identification sequence, Chr. Num/CDS.- Chromosomes, IP- isoelectric point, MW- molecular weight g/mol-, Subcellular Localization-prediction of protein localization sites in cells, AA- amino acids.

Group	CitsWRKY	WRKY ID	Chr. Num/CDS	Isoelectric Point (PI)	Molecular Weight (g/mol)	Subcellular Localization	Amino acids (aa)
I-A	*CitsWRKY01*	orange1.1g009051m	scaffold00003:3348929..3352620	8.78	59361.41	Nucleus	545
I-A	*CitsWRKY02*	orange1.1g009808m	scaffold00003:3348929..3352620	7.26	56886.49	Nucleus	525
I-A	*CitsWRKY03*	orange1.1g008501m	scaffold00049:532438..537337	6.47	60913.55	Nucleus	563
I-A	*CitsWRKY04*	orange1.1g013573m	scaffold00049:533556..537337	6.31	48087.16	Nucleus, chlo[1]	440
I-A	*CitsWRKY05*	orange1.1g015494m	scaffold00049:532438..537337	6.23	44406.63	Nucleus, cyto[2]	406
I-A	*CitsWRKY06*	orange1.1g015499m	scaffold00049:532438..537337	6.41	44249.95	Nucleus	405
I-A	*CitsWRKY07*	orange1.1g020585m	scaffold00049:532438..537337	8.01	35245.73	Nucleus, chlo, cyto	324
I-A	*CitsWRKY08*	orange1.1g013266m	scaffold00042:689265..692549	6.39	49676.99	Nucleus	446
I-A	*CitsWRKY09*	orange1.1g016551m	scaffold00042:689265..691801	7.67	42829.66	Nucleus	387
I-A	*CitsWRKY10*	orange1.1g017677m	scaffold00042:689265..692549	6.4	41766.41	Nucleus	368
I-A	*CitsWRKY11*	orange1.1g022760m	scaffold00042:689265..692549	5.4	32963.54	Nucleus	292
II-B	*CitsWRKY12*	orange1.1g007546m	scaffold00121:389458..391889	6.28	65156.91	Nucleus, mito[3]	599
II-B	*CitsWRKY13*	orange1.1g008964m	scaffold00049:126215..128926	7.06	60323.03	Nucleus, chlo, cyto	547
II-B	*CitsWRKY14*	orange1.1g040711m	scaffold00001:3810277..3813167	8.58	54409.92	Nucleus	501
I-B	*CitsWRKY15*	orange1.1g030050m	scaffold00038:626400..630108	9.08	20820.30	Cyto	183
II-D	*CitsWRKY16*	orange1.1g022353m	scaffold00007:901284..905441	5.52	33998.47	Nucleus	298
II-D	*CitsWRKY17*	orange1.1g027532m		5.57	25427.35	Nucleus, mito	222

			scaffold00007:901284..904297				
II-D	*CitsWRKY18*	orange1.1g024332m	scaffold00007:901284..904297	5.26	30568.67	Nucleus	298
II-D	*CitsWRKY19*	orange1.1g015616m	scaffold00097:230834..232265	5.12	44615.00	Nucleus	403
I-B	*CitsWRKY20*	orange1.1g026950m	scaffold01166:10456..13713	9.1	25883.18	Nucleus, chlo, cyto	230
I-B	*CitsWRKY21*	orange1.1g021142m	scaffold00007:1347875..1349215	6.8	35159.01	Nucleus	317
II-D	*CitsWRKY22*	orange1.1g012605m	scaffold00008:2345601..2348134	6.08	49778.68	Nucleus	460
I-A	*CitsWRKY23*	orange1.1g004988m	scaffold00013:1838851..1843181	5.68	77670.59	Nucleus	720
I-A	*CitsWRKY24*	orange1.1g004973m	scaffold00013:1839301..1843181	5.68	77798.72	Nucleus	721
III-A	*CitsWRKY25*	orange1.1g019737m	scaffold00009:1409048..1410893	5.2	37636.47	Nucleus	336
III-A	*CitsWRKY26*	orange1.1g024825m	scaffold00009:1409048..1410893	5.49	29619.83	Extr, chlo, vacu[4]	262
II-A	*CitsWRKY27*	orange1.1g025097m	scaffold00025:996904..999151	8.94	28812.41	Nucleus, chlo	258
I-B	*CitsWRKY28*	orange1.1g043122m	scaffold00003:164635..166589	9.89	12662.46	Nucleus, cyto	106
III-A	*CitsWRKY29*	orange1.1g045032m	scaffold00104:283550..285259	5.23	39139.06	Nucleus, cyto_nucl	354
I-B	*CitsWRKY30*	orange1.1g038951m	scaffold00189:257377..258688	4.86	33741.01	Nucleus	303
II-A	*CitsWRKY31*	orange1.1g025402m	scaffold00025:996904..998819	8.95	28274.98	Nucleus, chlo, cyto	253
I-B	*CitsWRKY32*	orange1.1g026216m	scaffold00001:354623..357157	7.05	27084.61	Nucleus, chlo	241
II-B	*CitsWRKY33*	orange1.1g009794m	scaffold00009:279247..281128	7.97	56855.02	Nucleus, mito	525
I-B	*CitsWRKY34*	orange1.1g045509m	scaffold00003:3456550..3459372	6.19	32087.38	Nucleus	291
II-B	*CitsWRKY35*	orange1.1g010903m	scaffold00003:2727603..2730035	8.22	54640.74	Nucleus	498
II-C	*CitsWRKY36*	orange1.1g023982m	scaffold00001:4402815..4404405	5.12	31079.32	Nucleus	274
II-C	*CitsWRKY37*	orange1.1g025759m	scaffold00001:4402815..4404405	5.00	28387.72	Chlo, Nucleus, Cyto_nucl, mito	248
II-A	*CitsWRKY38*	orange1.1g025216m	scaffold00025:1006589..1008372	9.01	28380.88	Nucleus, cyto_nucl	256
II-A	*CitsWRKY39*	orange1.1g020831m	scaffold00025:1006589..1008372	7.15	35783.03	Nucleus	321
I-A	*CitsWRKY40*	orange1.1g010802m	scaffold00015:1591146..1594814	6.84	55250.60	Nucleus	501
I-A	*CitsWRKY41*	orange1.1g015978m	scaffold00015:1592125..1594814	8.24	44642.93	Nucleus, chlo, vacu	397
I-A	*CitsWRKY42*	orange1.1g011340m	scaffold00077:307046..310334	6.45	53282.51	Nucleus	488
I-A	*CitsWRKY43*	orange1.1g014731m	scaffold00172:174342..178393	7.61	46350.39	Nucleus	419
II-C	*CitsWRKY44*	orange1.1g019404m	scaffold00025:483188..485204	9.54	36737.46	Nucleus	341
II-C	*CitsWRKY45*	orange1.1g023361m	scaffold00025:483188..485204	9.79	30389.32	Nucleus	283
II-C	*CitsWRKY46*	orange1.1g024631m	scaffold00025:483188..485204	9.36	28426.86	Nucleus	265
II-C	*CitsWRKY47*	orange1.1g018659m	scaffold00022:289543..292094	9.69	39494.68	Nucleus	352
II-C	*CitsWRKY48*	orange1.1g018654m	scaffold00022:289543..292222	9.69	39494.68	Nucleus	352
II-C	*CitsWRKY49*	orange1.1g021011m	scaffold00022:289543..292094	9.93	35625.34	Nucleus	318
I-A	*CitsWRKY50*	orange1.1g011483m	scaffold00626:42818..45853	7.25	53513.99	Nucleus, vacu, Cyto_nucl,	484
II-B	*CitsWRKY51*	orange1.1g045987m	scaffold00015:942103..943915	6.20	55554.2	Nucleus, cyto	510
I-A	*CitsWRKY52*	orange1.1g017783m	scaffold00626:42818..45853	6.95	39947.39	Nucleus	366
I-A	*CitsWRKY53*	orange1.1g024911m	scaffold00626:42818..45853	5.80	28221.48	Nucleus	260

I-A	*CitsWRKY54*	orange1.1g024944m	scaffold00626:42818..45853	5.80	28221.48	Nucleus	260
II-C	*CitsWRKY55*	orange1.1g018215m	scaffold00002:1863592..1865359	9.30	38791.88	Nucleus	359
II-C	*CitsWRKY56*	orange1.1g021515m	scaffold00002:1863592..1865359	9.54	33436.80	Nucleus	311
I-B	*CitsWRKY57*	orange1.1g031298m	scaffold00035:211943..212982	9.56	18204.42	Nucleus, chlo,	162
III-A	*CitsWRKY58*	orange1.1g041468m	scaffold00037:611554..612440	6.83	14184.09	Nucleus, cyto, chlo	124
I-B	*CitsWRKY59*	orange1.1g019375m	scaffold00057:464133..466331	6.66	38277.06	Nucleus	342
II-D	*CitsWRKY60*	orange1.1g021896m	scaffold00009:1025605..1026760	5.76	34128.20	Nucleus	306
II-B	*CitsWRKY61*	orange1.1g007099m	scaffold00007:1958471..1961762	5.99	67180.29	Nucleus	618
II-B	*CitsWRKY62*	orange1.1g013190m	scaffold00007:1958471..1961762	6.76	48404.95	Nucleus, chlo, cyto	448
II-B	*CitsWRKY63*	orange1.1g014735m	scaffold00007:1958471..1961762	6.08	46369.28	Nucleus, mito, chlo, plas	419
II-B	*CitsWRKY64*	orange1.1g016623m	scaffold00007:1958471..1961762	8.10	41161.97	Nucleus, chlo	386
II-D	*CitsWRKY65*	orange1.1g019126m	scaffold00001:2333743..2335147	6.32	37763.56	Nucleus	346
II-C	*CitsWRKY66*	orange1.1g017930m	scaffold00006:1346375..1348315	9.32	40160.03	Nucleus, chlo	363
II-C	*CitsWRKY67*	orange1.1g021347m	scaffold00006:1346375..1348315	9.53	34619.83	Nucleus	313
II-B	*CitsWRKY68*	orange1.1g036819m	scaffold00568:96439..97905	8.74	30705.82	Nucleus	269
I-A	*CitsWRKY69*	orange1.1g004963m	scaffold00013:1838851..1843181	5.68	77798.72	Nucleus	721
I-A	*CitsWRKY70*	orange1.1g036653m	scaffold00068:482854..486663	6.06	53543.47	Nucleus	487
III-A	*CitsWRKY71*	orange1.1g017895m	scaffold00001:2647888..2651028	5.23	41108.73	Nucleus, mito, plas	364
III-A	*CitsWRKY72*	orange1.1g020291m	scaffold00036:115494..117084	5.91	36807.72	Nucleus	328
I-B	*CitsWRKY73*	orange1.1g029257m	scaffold00362:80427..84896	6.54	22458.43	Nucleus	196
II-C	*CitsWRKY74*	orange1.1g018255m	scaffold00124:381097..383496	9.77	40539.91	Nucleus	359
I-B	*CitsWRKY75*	orange1.1g017479m	scaffold00016:1122184..1123697	6.00	40911.62	Nucleus	371
I-B	*CitsWRKY76*	orange1.1g046286m	scaffold00001:2355401..2357338	9.30	21585.46	Nucleus, chlo	188
I-A	*CitsWRKY77*	orange1.1g013055m	scaffold00003:3348929..3352620	5.90	48560.47	Nucleus	450

1:chloroplast; 2: cytoplasm; 3: mitochondria; 4:vacuole



Supplementary Fig S1. Domain alignments of *Citrus sinensis* WRKY proteins. Proteins were separately aligned and the preserved motifs are shown in the black boxes, highly preserved amino acids are presented in the red box, and the highlighted yellow lines in groups I and III indicate that the less preserved intermittent sequences are not shown.