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Supplemental Information

Genomes of the Venus Flytrap and Close Relatives

Unveil the Roots of Plant Carnivory

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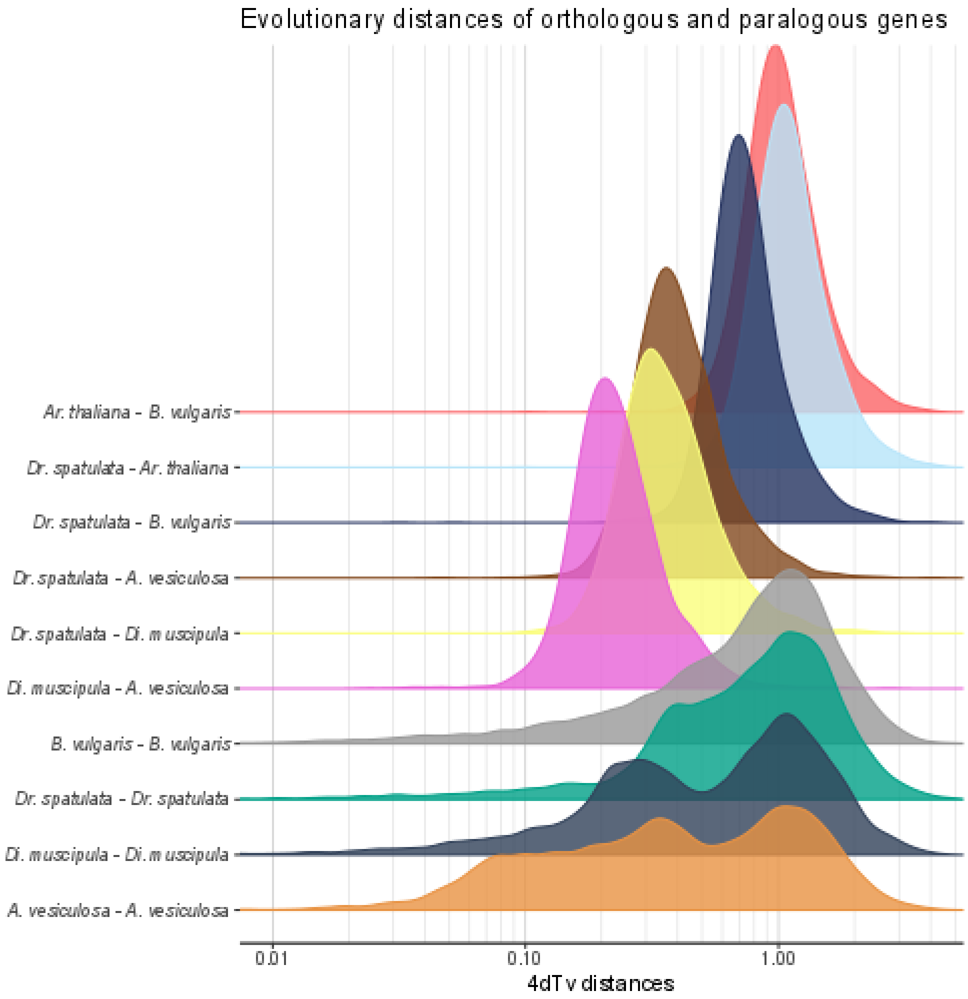


Figure S1: **4dtv distances of duplicated genes. Related to Figure 1.**

Comparison between and within the three analysed Droseracaea species and *Arabidopsis thaliana* as well as *Beta vulgaris* as an outgroup. Each peak indicates a large duplication event.

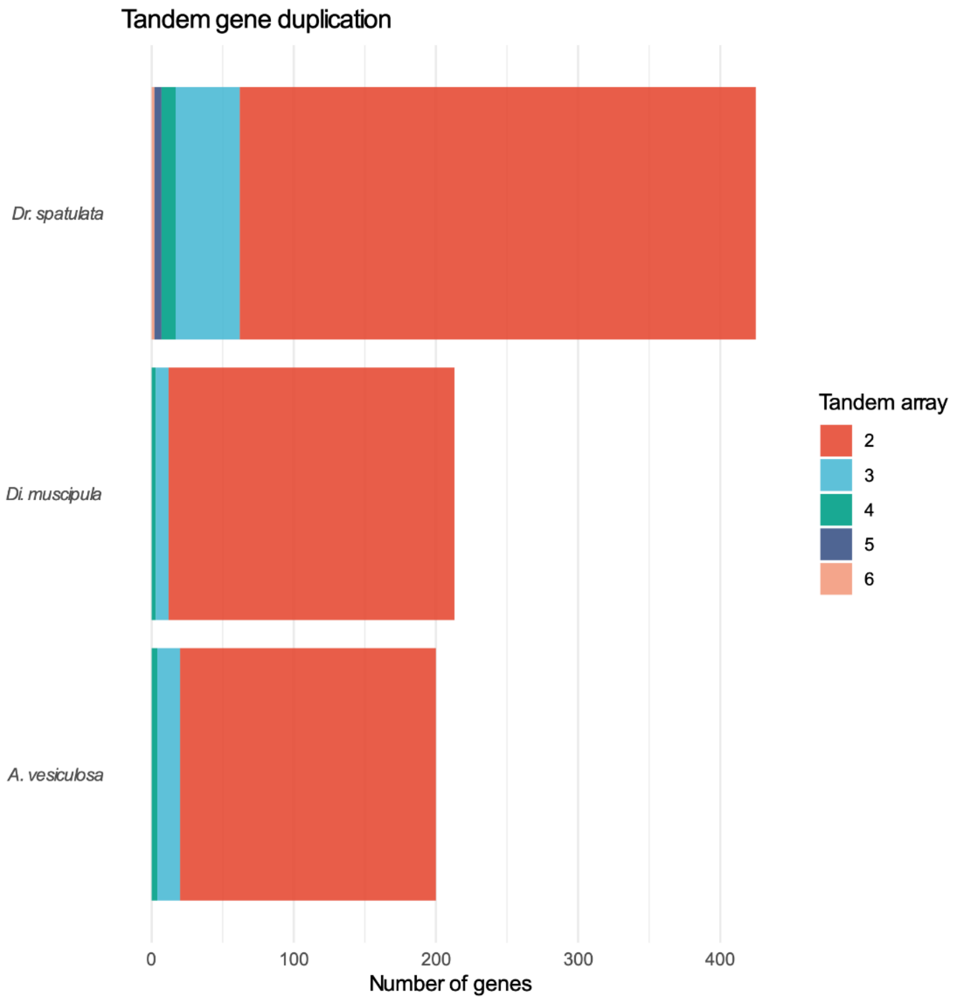


Figure S2: **Distribution of tandem duplicated genes**. **Related to Figure 4.**

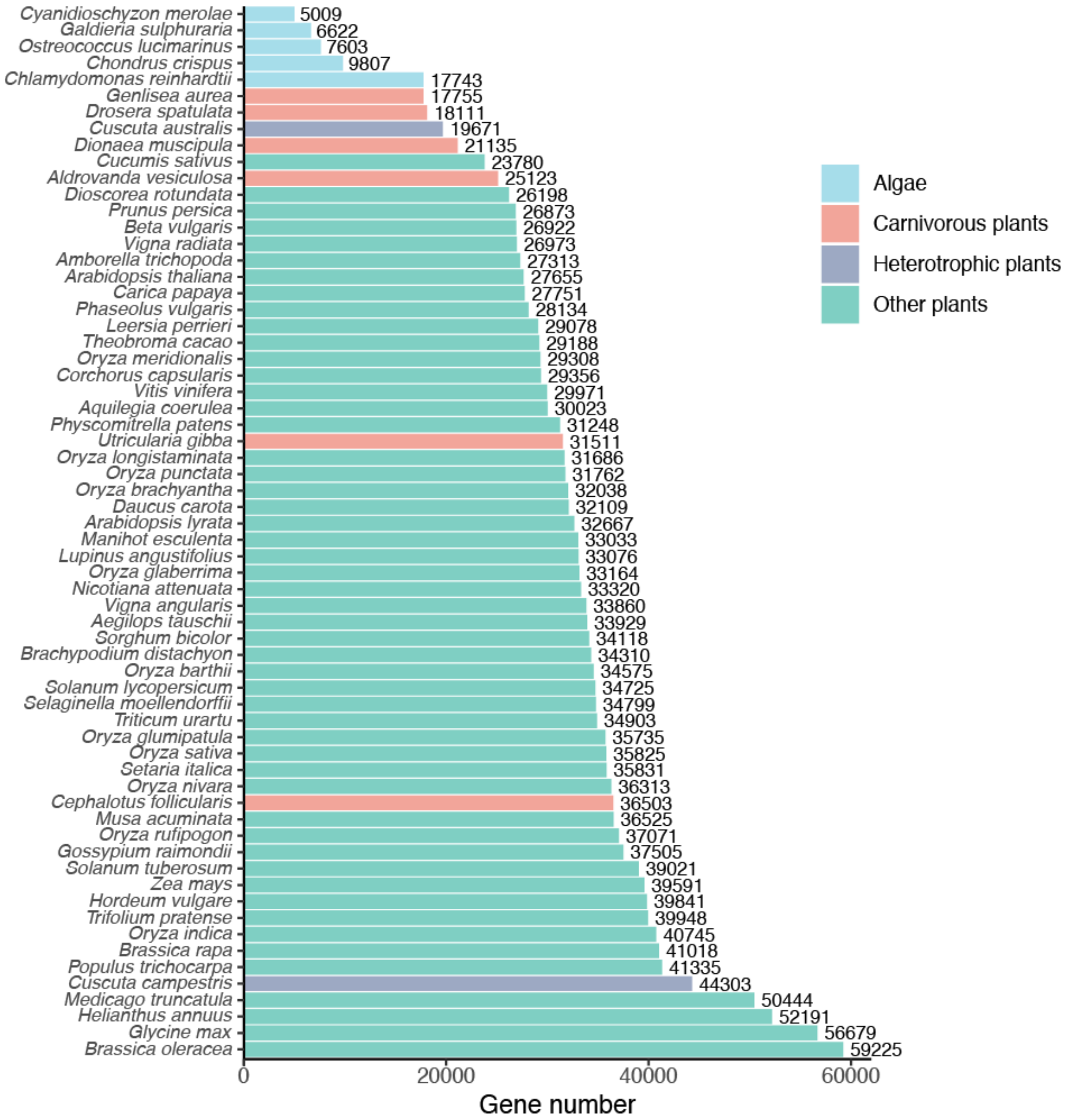


Figure S3: Comparison of gene contents for selected plant and algae genomes. Related to Figure 4.

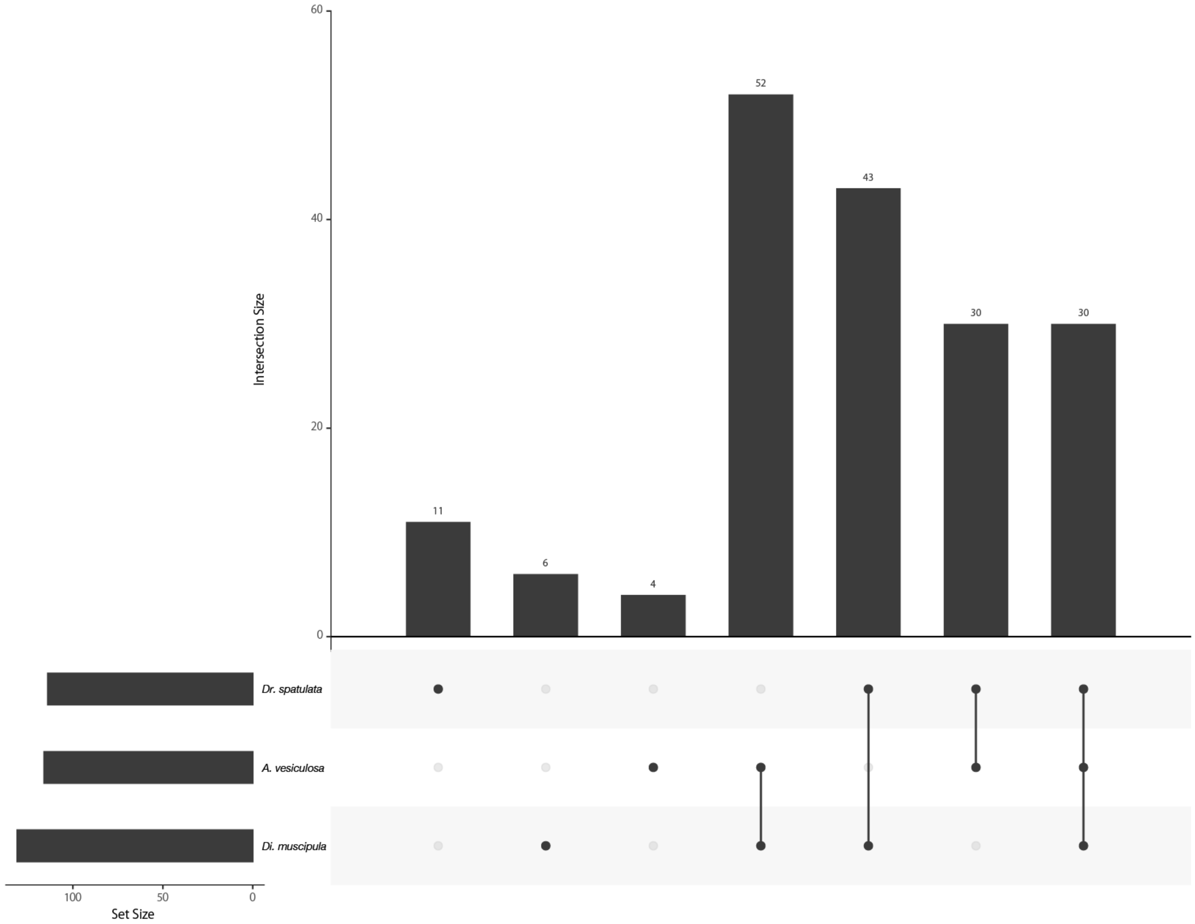
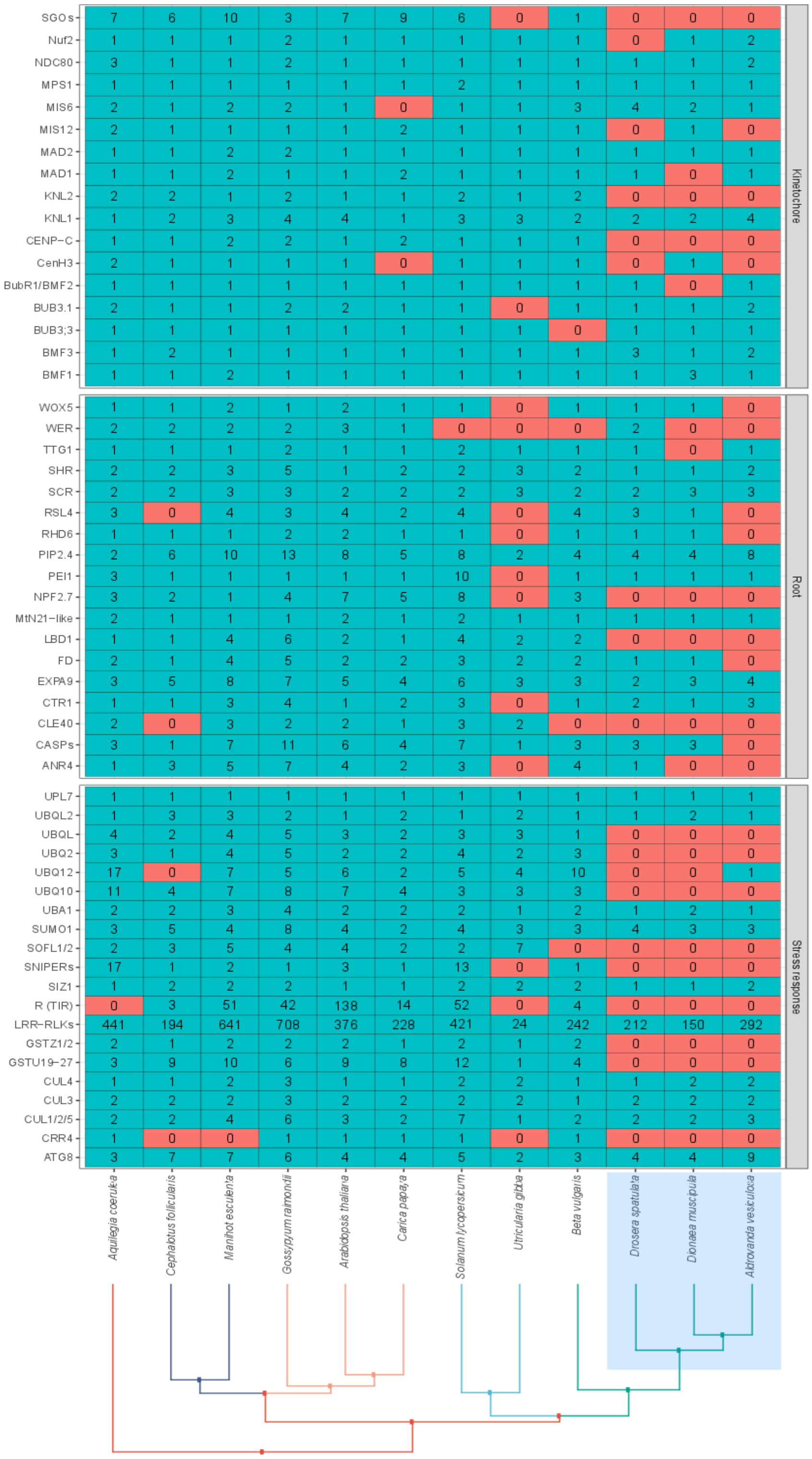


Figure S4: Orthogroups uniquely shared between the three carnivorous Droseraceae genomes.

Related to Figure 2.



		Aquilegia coerulea	*Cephalotus follicularis*	*Manihot esculenta*	*Gossypium raimondii*	*Arabidopsis thaliana*	*Carica papaya*	*Solanum lycopersicum*	*Utricularia gibba*	*Beta vulgaris*	*Drosera spatulata*	*Dionaea muscipula*	*Aldrovanda vesiculosa*
Kinetochore	SGOs	7	6	10	3	7	9	6	0	1	0	0	0
	Nuf2	1	1	1	2	1	1	1	1	1	0	1	2
	NDC80	3	1	1	2	1	1	1	1	1	1	1	2
	MPS1	1	1	1	1	1	1	2	1	1	1	1	1
	MIS6	2	1	2	2	1	0	1	1	3	4	2	1
	MIS12	2	1	1	1	1	2	1	1	1	0	1	0
	MAD2	1	1	2	2	1	1	1	1	1	1	1	1
	MAD1	1	1	2	1	1	2	1	1	1	1	0	1
	KNL2	2	2	1	2	1	1	2	1	2	0	0	0
	KNL1	1	2	3	4	4	1	3	3	2	2	2	4
	CENP−C	1	1	2	2	1	2	1	1	1	0	0	0
	CenH3	2	1	1	1	1	0	1	1	1	0	1	0
	BubR1/BMF2	1	1	1	1	1	1	1	1	1	1	0	1
	BUB3.1	2	1	1	2	2	1	1	0	1	1	1	2
	BUB3;3	1	1	1	1	1	1	1	1	0	1	1	1
	BMF3	1	2	1	1	1	1	1	1	1	3	1	2
	BMF1	1	1	2	1	1	1	1	1	1	1	3	1
Root	WOX5	1	1	2	1	2	1	1	0	1	1	1	0
	WER	2	2	2	2	3	1	0	0	0	2	0	0
	TTG1	1	1	1	2	1	1	2	1	1	1	0	1
	SHR	2	2	3	5	1	2	2	3	2	1	1	2
	SCR	2	2	3	3	2	2	2	3	2	2	3	3
	RSL4	3	0	4	3	4	2	4	0	4	3	1	0
	RHD6	1	1	1	2	2	1	1	0	1	1	1	0
	PIP2.4	2	6	10	13	8	5	8	2	4	4	4	8
	PEI1	3	1	1	1	1	1	10	0	1	1	1	1
	NPF2.7	3	2	1	4	7	5	8	0	3	0	0	0
	MtN21−like	2	1	1	1	2	1	2	1	1	1	1	1
	LBD1	1	1	4	6	2	1	4	2	2	0	0	0
	FD	2	1	4	5	2	2	3	2	2	1	1	0
	EXPA9	3	5	8	7	5	4	6	3	3	2	3	4
	CTR1	1	1	3	4	1	2	3	0	1	2	1	3
	CLE40	2	0	3	2	2	1	3	2	0	0	0	0
	CASPs	3	1	7	11	6	4	7	1	3	3	3	0
	ANR4	1	3	5	7	4	2	3	0	4	1	0	0
Stress response	UPL7	1	1	1	1	1	1	1	1	1	1	1	1
	UBQL2	1	3	3	2	1	2	1	2	1	1	2	1
	UBQL	4	2	4	5	3	2	3	3	1	0	0	0
	UBQ2	3	1	4	5	2	2	4	2	3	0	0	0
	UBQ12	17	0	7	5	6	2	5	4	10	0	0	1
	UBQ10	11	4	7	8	7	4	3	3	3	0	0	0
	UBA1	2	2	3	4	2	2	2	1	2	1	2	1
	SUMO1	3	5	4	8	4	2	4	3	3	4	3	3
	SOFL1/2	2	3	5	4	4	2	2	7	0	0	0	0
	SNIPERs	17	1	2	1	3	1	13	0	1	0	0	0
	SIZ1	1	2	2	2	1	1	2	2	2	1	1	2
	R (TIR)	0	3	51	42	138	14	52	0	4	0	0	0
	LRR−RLKs	441	194	641	708	376	228	421	24	242	212	150	292
	GSTZ1/2	2	1	2	2	2	1	2	1	2	0	0	0
	GSTU19−27	3	9	10	6	9	8	12	1	4	0	0	0
	CUL4	1	1	2	3	1	1	2	2	1	1	2	2
	CUL3	2	2	2	3	2	2	2	2	1	2	2	2
	CUL1/2/5	2	2	4	6	3	2	7	1	2	2	2	3
	CRR4	1	0	0	1	1	1	1	0	1	0	0	0
	ATG8	3	7	7	6	4	4	5	2	3	4	4	9

Figure S5: Phylogenetic distribution of lost genes associated to kinetochore, root and stress related functions. Related to Figure 4.

Plant	Cultivar/collection site	DNA content [pg/2C]	Coefficient of variance species of interest [%]	Coefficient of variance reference [%]	Haploid genome size (Mbp)
Di. muscipula	North Carolina	6.50 ± 0.02	9.1 ± 0.5	7.1 ± 0.8	3178.5
Di. muscipula	South Carolina	6.57 ± 0.06	8.2 ± 1.2	6.2 ± 1.1	3212.73
Di. muscipula	Cultivar (Type Green)	6.61 ± 0.04	7.3 ± 0.5	5.2 ± 1.3	3232.29
Di. muscipula	Cultivar (Type Red)	6.53 ± 0.04	8.4 ± 0.5	6.8 ± 0.4	3193.17
Di. muscipula	Cultivar (Type France)	6.60 ± 0.04	8.7 ± 1.2	6.6 ± 0.9	3227.4
A. vesiculosa	Cultivar	1.04 ± 0.04	9.8 ± 1.0	10.7 ± 2.1	508.1

1 pg = 978 Mbp

Table S1: Flow cytometric estimation of the DNA content *vesiculosa* genotype. Related to Figure 1.

Depth	0	1	2	3	4	5	6	7	8
A. vesiculosa	7103	6059	5136	4130	1735	740	165	43	12
Di. muscipula	20398	727	10						
Dr. spatulata	13434	3840	836						

Table S2: Coverage depth of self-syntenic regions. Related to Figure 1.

Class	*A. vesiculosa*	*Di. muscipula*	*Dr. spatulata*
LTR (total)	88,78	1236,65	16,74
LTR/Copia	26,18	327,34	10,48
LTR/Gypsy	47,29	476,25	3,52
LTR/other	15,31	433,06	2,74
LINE	-	0,11	-
SINE	0,07	0,06	-
DNA	0,22	16,82	0,25
rRNA	3,07	5,02	0,38
RC/Helitron	-	0,64	-
Retroelement	-	0,15	-
MobileElement	-	5,06	0,02
Satellite	-	0,12	-
Other	-	0,2	-
Other/Simple	-	0,67	-
not classified	24,3	299,5	5,55

Table S3: Distribution of repetitive sequences identified by on transposon assembly. Related to Figure 1

tissue	Motif
Flower	OJ1058_F05.8
Root	-
Trap	WRKY24
Trap+Cor	WRKY6
Trap+Insect	WRKY29

Table S4: Enriched transcription factor binding motifs in the 1kb upstream region of top 5% tissue specific genes. Related to Figure 3.