

FIGURE S1.—Metaphase chromosomes from a root tip of an S1 allopolyploid plant, spontaneously derived from a TTR16XTQ113 F1 hybrid. The expected 42 chromosomes are shown.

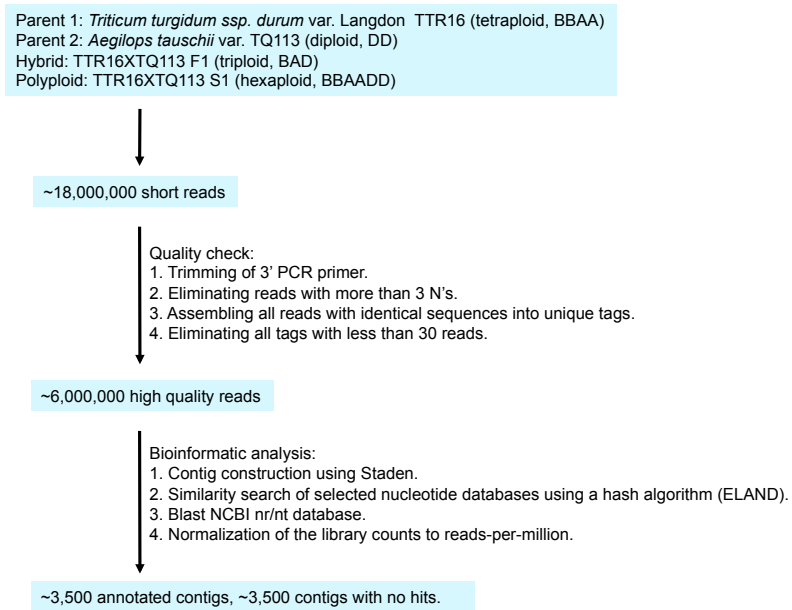


FIGURE S2.—Flow chart of small RNA high-throughput sequencing data analysis.

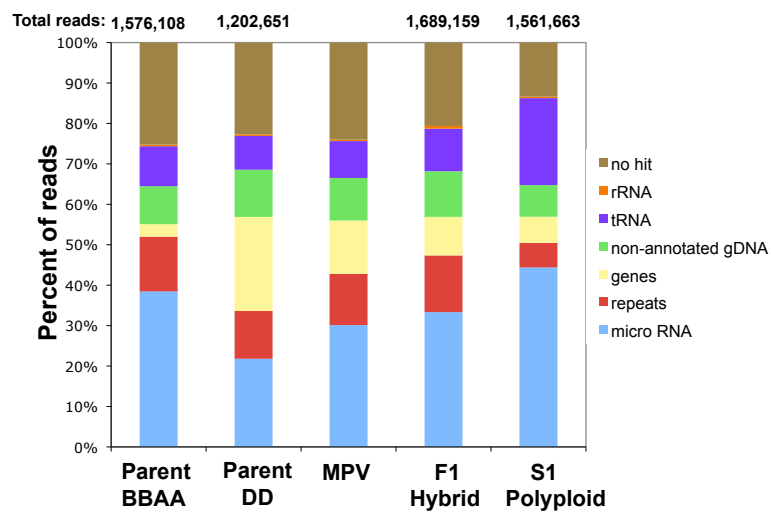


FIGURE S3.—Abundance of small RNA classes in the four analyzed libraries, namely, the tetraploid parent (genome BBAA), the diploid parent (genome DD), their hybrid and derived allopolyploid (first generation= S1), and the calculated mid-parent value (MPV). The total number of reads in each library is shown at the top of each column.

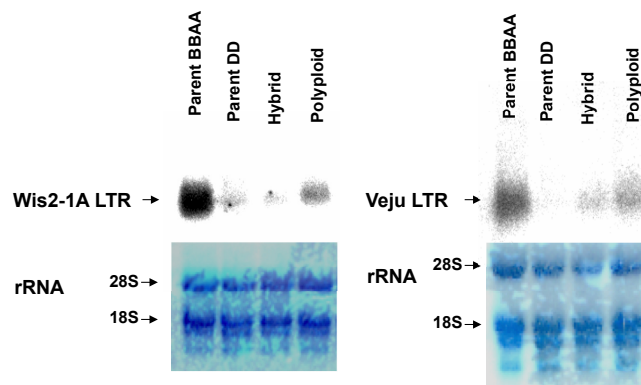


FIGURE S4.—Northern blot analyses of *Wis2-1A* (left) and *Vaju* (right) retrotransposon LTR regions in the tetraploid parent (genome BBAA), the diploid parent (genome DD), their hybrid and derived allopolyploid. Methylene blue staining of the membranes shows equal loading of RNA samples. Probes were derived from a consensus sequence from wheat *Wis2-1A* LTRs (a 354bp fragment) and from *Vaju1_TM_LTR* entry at TREP (a 339 bp fragment).

TABLE S1

Number of small RNA reads and tags in the various libraries: TTR16 –tetraploid parent (Genome BBAA), TQ113 – diploid parent (Genome DD), F1 – triploid hybrid (genome BAD), S1 – first generation of synthetic hexaploid (Genome BBAADD).

Libraries:	TTR16	TQ113	Hybrid	Polyploid	Total
Total reads	5,633,938	3,064,285	6,421,516	3,458,759	18,578,498
Total tags	3,726,879	1,879,921	3,068,481	1,092,783	-
Tags after QC ^a	991,936	2,829,480	3,423,567	1,627,189	-
Tags with >30 reads	7967	4292	6756	2772	-
Reads from tags with >30 reads	1,576,108	1,202,651	1,689,159	1,561,663	6,029,581

^aQC: Quality Control process including 1. Trimming of 3' PCR primer; 2. Elimination of reads with >3Ns; 3. Assembly of reads with identical sequences into unique tags.

TABLE S2**Micro RNAs in high-throughput small RNA sequencing data**

miRNA name	miRNA target	Libraries			
		TTR16	TQ113	Hybrid	Polyploid
ath-miR156a	SBP protein family	80003	36175	53344	140378
bna-miR156a	SBP protein family	125499	69857	101207	58
ath-miR157a	SBP protein family	0	0	0	115
osa-miR159a	GAMYB transcription factor	854	969	1142	5102
osa-miR160f	auxin reponse factor	0	0	21	56
ath-miR164a	NAC1 transcription factor	1432	595	1634	2302
ath-miR165a	classIII hd-leu zipper	43	0	40	0
ath-miR166a	class III hd-leu zipper	17463	7565	18397	8228
osa-miR166g	class III hd-leu zipper	1746	552	1378	366
osa-miR166k	class III hd-leu zipper	5983	3095	5893	1777
ath-miR167d	auxin reponse factor 8	19877	7066	12782	9790
osa-miR168a	Argonaute 1 regulation	119710	79244	126428	245051
ath-miR169b	CCAAT-binding tf	18	66	74	91
osa-miR171b	scarecrow-like protein	36	0	34	98
ath-miR172a	Apetala 2	5633	3540	4350	10126
ath-miR390a	not found	0	32	0	18
ath-miR393a	transport inhibitor protein 1	923	907	1022	1349
ath-miR396b	not found	136	136	197	258
osa-miR396d	not found	2259	1711	3771	12121
osa-miR528	not found	2020	2311	1003	2925
tae-miR1135	early light-inducible protein	312	0	186	26
Total counts		383956	213833	332913	440247

The number of reads are normalized to reads per million for comparison between the libraries. TTR16 –tetraploid parent (Genome BBAA), TQ113 – diploid parent (Genome DD), F1 – triploid hybrid (genome BAD), S1 – first generation of synthetic hexaploid (Genome BBAADD).