Additional file 3. Classification of sRNAs in various samples.

Total reads Category	Leaf WT%	Leaf *pap2*%	Leaf OE7%	Leaf OE21%	Root WT%	Root *pap2*%	Root OE7%	Root OE21%
exon_antisense	0.87	0.99	**1.63**	**1.84**	0.25	0.23	0.29	**0.43**
exon_sense	2.33	2.39	**1.98**	2.29	1.76	1.62	1.9	1.57
intron_antisense	0.2	0.23	0.2	0.26	0.06	0.06	**0.03**	0.07
intron_sense	0.27	0.28	0.16	0.2	0.09	0.09	**0.05**	0.08
miRNA	37.5	41.02	35.24	30.77	5.95	7.03	**3.45**	6.04
rRNA	21.32	15.65	19.91	18.8	36.47	42.47	28.94	28.25
repeat	12.39	12.85	**7.77**	8.67	3.87	4.15	**1.97**	2.86
siRNA	1.78	2.68	**3.96**	**8.99**	0.39	0.54	0.57	**6.08**
snRNA	0.06	0.05	0.07	0.06	0.19	0.22	0.22	0.17
snoRNA	0.03	0.03	0.04	0.04	0.03	0.04	**0.05**	0.04
tRNA	4.47	3.6	**6.96**	3.86	32.04	21.28	47.3	32.19
unann	18.77	20.23	22.07	24.23	18.92	22.27	15.24	32.19
Total	100	100	100	100	100	100	100	100

Unique reads Category	Leaf WT%	Leaf *pap2*%	Leaf OE7%	Leaf OE21%	Root WT%	Root *pap2*%	Root OE7%	Root OE21%
exon_antisense	2.22	2.16	1.7	1.67	0.89	0.82	0.65	0.63
exon_sense	7.86	7.73	6.4	6.96	9.4	8.02	14.02	7.67
intron_antisense	0.51	0.55	0.36	0.38	0.19	0.18	0.12	0.13
intron_sense	0.56	0.57	0.42	0.43	0.28	0.24	0.23	0.18
miRNA	0.16	0.15	0.14	0.13	0.1	0.08	0.1	0.08
rRNA	6.91	6.19	7.85	6.57	13.45	12.94	12.49	11.12
repeat	30.19	30.39	19.25	19.29	11.1	9.69	6.63	6.52
siRNA	1.54	1.53	2.07	2.33	0.5	0.56	0.61	0.8
snRNA	0.15	0.13	0.17	0.13	0.31	0.3	0.4	0.25
snoRNA	0.1	0.09	0.12	0.11	0.1	0.1	0.15	0.11
tRNA	1.08	1.05	1.28	0.96	2.75	2.68	2.7	2.61
unann	48.73	49.46	60.23	61.03	60.92	64.38	61.9	69.9
Total	100	100	100	100	100	100	100	100

Numbers in bold mean significant changes in OE versus WT, p-value < 0.05 and fold change log2 (OE/WT) ≥ 1 or ≤ -1.