

Additional file 7: Relative content of secondary metabolites obtained from seeds UPLC-QTOF-MS/MS analysis and (\log_{10}) fold change in the autopolyploid lines. Mass spectral searching utilized the algorithm incorporated in the MassLynx® data system and finally normalized by the internal standard ampicillin. Asterisks represent significant changes in metabolite content ($P < 0.01$) according to ANOVA. Fold change represents the (\log_{10}) change in the relative content of each metabolite between the autopolyploid lines and their respective control lines. The values in parentheses represent the m/z for each metabolite. NA = non-annotated

	Metabolites	2n		4n		Significance	(\log_{10}) 4n fold change	3n		6n		Significance	(\log_{10}) 6n fold change
		Average	\pm SE	Average	\pm SE			Average	\pm SE	Average	\pm SE		
Benzoic acids	Benzoic acid (123.0429)	10.04	0.36	9.99	0.38		0.00	16.86	0.31	22.42	0.50	*	0.12
	<i>p</i> -Hydrobenzoic acid (139.0386)	3.95	0.10	6.98	0.11	*	0.25	3.79	0.19	6.54	0.32	*	0.24
	Protocatechuic acid (153.0197)	6.06	0.12	19.51	0.35	*	0.51	3.66	0.56	4.22	0.34		0.06
Flavonoids	Hesperetin (303.0874)	2.79	0.07	3.84	0.10	*	0.17	2.87	0.15	5.61	0.17	*	0.29
	Quercetin (303.0508)	1.60	0.07	2.35	0.24	*	0.14	0.55	0.04	1.14	0.06	*	0.32
	Rutin (611.1613)	4.91	0.16	6.04	0.39	*	0.09	2.43	0.08	4.58	0.25	*	0.27
NA	NA (151.0308)	77.23	3.70	80.55	3.12	*	0.02	60.23	1.34	71.74	2.59	*	0.08
	NA (160.0657)	242.99	7.77	208.82	2.74	*	-0.07	234.63	7.20	124.94	5.34	*	-0.27
	NA (188.0699)	450.09	9.96	342.91	6.68	*	-0.12	425.59	12.86	229.31	7.37	*	-0.27
	NA (285.0811)	151.10	5.44	194.66	2.79	*	0.11	55.67	0.85	26.32	1.35	*	-0.33
	NA (329.9262)	359.64	9.55	377.38	9.45		0.02	338.31	11.69	366.91	4.55		0.04
	NA (365.1045)	80.32	1.48	73.15	1.50	*	-0.04	60.35	1.77	41.71	1.14	*	-0.16