S17 Table: Table containing the means of each group (Single-transgenic, single-null, triple-transgenic, triple-null) for each variable, the standard errors of the means and the p values for each comparison. The difference between Singles and Triples and the effects of transgenic vs null were compared with an ANOVA style analysis but using the REML directive in Genstat 20 in order to get predictions from the unbalanced structure. PlantID was included as a block effect (random structure) and observations within plant were considered as pseudo replication (so there were 6 true reps of Single-transgenic, single-null and triple-transgenic but only 3 true reps of triple-null. The fixed structure (treatment structure) was (Type1*Type2)/Number which gives the following four tests: Type1 – Is there a difference between singles and triples (averaged across all lines and nulls)?; Type2 – Is there a difference between transgenics and nulls (averaged across singles and triples)?; Type1.Type2 – Is the difference between transgenic and nulls (averaged across singles and triples)?; Type1.Type2 – Is the difference between transgenic structure to make sure comparisons are made against correct background variation)

	p-values				mean				SEM			
	Type1	Type2	Type1.Type2	Type1.Type2. Number	single-null	single-trans	triple-null	triple-trans	single-null	single-trans	triple-null	triple-trans
Area	0.001	0.138	0.101	0.415	20.15	20.10	23.43	21.79	0.3674	0.3674	0.5196	0.3674
Length	<0.001	0.330	0.090	0.450	6.785	6.827	7.502	7.249	0.06532	0.06532	0.09238	0.06532
Width	0.026	0.060	0.123	0.501	3.792	3.747	4.081	3.844	0.04812	0.04812	0.06805	0.04812
Hardness	<0.001	0.002	0.920	0.032	78.83	73.39	67.78	62.56	0.955	0.955	1.350	0.955
Weight	<0.001	0.085	0.055	0.564	43.85	43.67	59.78	51.99	1.427	1.427	2.018	1.427
Moisture	0.006	0.073	0.159	0.992	11.13	10.98	10.83	10.11	0.1592	0.1592	0.2251	0.1592
Diameter	<0.001	0.119	0.022	0.442	3.112	3.151	3.613	3.369	0.04006	0.04006	0.05665	0.04006