

**Supplementary Table 2. Partition of the dissected QTL regions into regions with either predominantly genic or non-genic SNPs, and the identified TAS into genic or non-genic classes across five quantitative traits.**

Trait	Region/TAS classification	HapMap			RNA-seq			merged		
		Tested SNP	Top 1 TAS	Top 5 TASs	Tested SNP	Top 1 TAS	Top 5 TASs	Tested SNP	Top 1 TAS	Top 5 TASs
Length	Genic	18	20	23	37	33*	36	36	20**	27**
	Non-genic	19	17	14	0	4*	1	1	17**	10**
Width	Genic	18	17	24	36	29**	35	33	17**	26**
	Non-genic	18	19	12	0	7**	1	3	19**	10**
Angle	Genic	9	13	10	28	23**	24	26	14**	15**
	Non-genic	19	14	18	0	5**	4	2	13**	13**
DTA	Genic	10	19**	14	32	28*	32	29	17**	22**
	Non-genic	22	13**	18	0	4*	0	3	15**	10**
DTS	Genic	12	17	13	31	24**	31	30	20**	20**
	Non-genic	19	14	18	0	7**	0	1	11**	11**

Star indicates whether the TAS is genic or non-genic (or whether more TASs coming from one class in “Top 5 TASs”) is statistically independent of whether the dissected region contains more genic or non-genic SNPs. \*  $P < 0.05$ ; \*\*  $P < 0.01$ .