Supplementary Table 6. Comparison of gene numbers and features of three grass genomes and the dicot Arabidopsis. Gene and exon statistics are shown for gene complements of rice (IRGSP version RAP2), *Brachypodium* (version 1.0) sorghum (version 1.4) and Arabidopsis (TAIR8).

Feature	Rice	*Brachypodium*	Sorghum	Arabidopsis (TAIR8)
	(RAP2)	(v1.0)	(v1.4)	
Genome assembly size (bp)	382,150,945	271,923,306	738,540,932	119,186,497
Assembled chromosomes (bp)	382,150,945	271,148,425	659,229,367	119,186,497
Unanchored Sequence (bp)	---	774,881	79,311,565	---
Protein coding loci	28,236	25,532 [1]	27,640 [1,2]	26,990[1]
Exons	134,812	140,142	136,658	142,267
Mean exons per gene	4.77	5.49	4.94	5.27
Mean exon size [bp]	364	268	297	280
Median exon size [bp]	165	140	154	155
Mean intron size [bp]	440	391	444	163
Median intron size [bp]	161	146	147	99
Mean gene size with UTR [bp]	3,403	3,336	3,218	2,174
Median gene size with UTR[bp]	2,807	2,643	2,448	1,889
Mean gene size without UTR[bp]	2,467	2,956	2,927	1,857
Median gene size without UTR[bp]	1,812	2,233	2,154	1,553
Mean intergenic region [bp]	10,339	7,311	17,002[2]	2,266
Median intergenic region [bp]	4,349	3,310	4,238[2]	928
Mean Locus density per 100 kb	7.39	9.39	3.74	22.64

[1] For loci comprising predicted alternative splice variants, the longest representative has been selected.
[2] Only *bona fide* gene models of sorghum were considered for this table [20].