TBD

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2 **ABSTRACT**

3   Hello, this is the abstract.

4 **Keywords: keyword1, kw2, kw3... have to have at least 5, max 8**

1 RESULTS

5   ... a quantitative comparison of the datasets in Table 1.

Table 1. Quantitative metrics of the generated and existing functional annotation sets. C, F, P, and A refer to the aspects of the GO: Cellular Component, Biological Function, Molecular Process, and Any/All.

Genome	Genes	Dataset	Annotations[a]				Annotated Genes[b]				Median Ann. per G.[c]			
			C	F	P	**A**	C	F	P	**A**	C	F	P	**A**
maize_v3	300	GOMAP	135251	87953	291855	**515059**	34867	38099	39469	**39469**	3	2	6	**11**
		Gramene49	20072	31139	30102	**81313**	11834	18033	15800	**21926**	1	1	1	**3**
		Phytozome	4787	19098	13100	**36985**	4524	13775	11365	**16132**	0	1	1	**2**
maize_v4	320	GOMAP	88831	82849	278952	**450632**	36717	37431	39324	**39324**	2	2	6	**10**
rice	200	GOMAP	72782	64783	248713	**386278**	28619	29876	35824	**35825**	2	2	6	**9**
wheat	500	GOMAP	267742	218839	786028	**1272609**	95604	98224	107890	**107891**	2	2	6	**10**

[a] How many annotations in the C, F, and P aspect does this dataset contain? A = How many in total? $A = C + F + P$

[b] How many genes in the genome have at least one GO term from the C, F, P aspect annotated to them? A = How many at least one from any aspect? ($A = C \cup F \cup P$)

[c] Take a typical gene that is present in the annotation set. How many annotations does it have in each aspect? A = How many in total? Ask your favorite statistician why $A \neq C + F + P$