

CORRECTION

## Correction to: “Development of SSR markers and assessment of genetic diversity of adzuki bean in the Chinese germplasm collection” [Mol Breeding (2015) 35:191]

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### Correction to: Mol Breeding (2015) 35:191

<https://doi.org/10.1007/s11032-015-0383-5>

The original version of this article unfortunately contained some mistakes in the number of unigenes reported in the Result section of Molecular Breeding article, “Development of SSR markers and assessment of genetic diversity of adzuki bean in the Chinese germplasm collection” (Mol Breeding (2015) 35:191, <https://doi.org/10.1007/s11032-015-0383-5>). The correct data is shown below.

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The online version of the original article can be found at  
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### Result

A total of 68,118 unigenes showed significant BLAST hits. Among those unigenes, 45,044 (66.1 %) showed significant similarity to known proteins in the NCBI non-redundant (Nr) sequence database. Based on Nr annotation, 31,826 (46.7 %) unigenes were assigned to gene ontology (GO) terms. The GO annotations for biological processes, cellular components and molecular functions accounted for 48.0, 28.7, and 23.3 %, respectively. Under the biological process category, the most abundant subcategory was cellular process (18,294, 22.6 %), followed by metabolic process (17,393, 21.5 %), and single-organism process (13,232, 16.3 %). Under the cellular component category, cell component (18,827, 38.9 %) and organelle component (6,274, 13.0 %) represented the majorities, whereas only a few unigenes were assigned to synapse (4) and nucleoid (1). Under the molecular function category, binding activity (18,384, 46.7 %) and catalytic activity (15,137, 38.5 %) were prominently represented.