

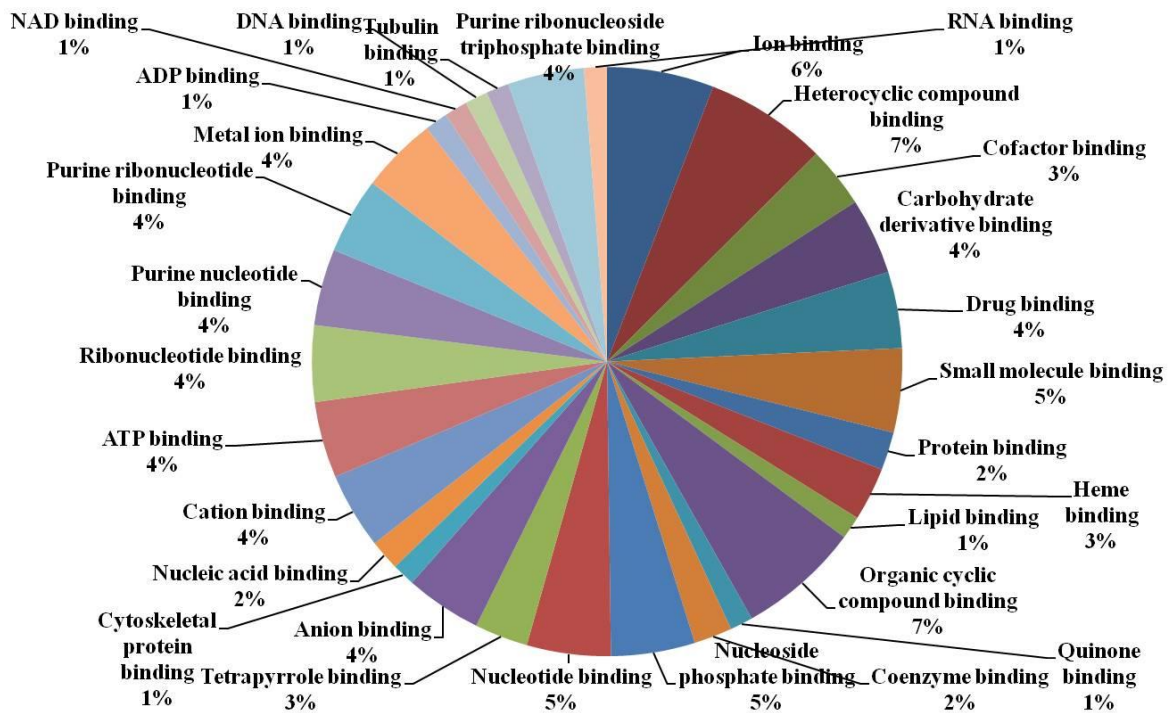
**Transcriptome sequencing assisted discovery and computational analysis of novel SNPs associated with flowering in *Raphanus sativus* in-bred lines for marker-assisted backcross breeding**

**Jin-Hee Kim<sup>1</sup>\*, Abinaya Manivannan<sup>1</sup>\*, Do-Sun Kim<sup>1</sup>, Eun-Su Lee<sup>1</sup>, and Hye-Eun Lee<sup>1</sup>\***

<sup>1</sup>Vegetable Research Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Jeonju-55365, Republic of Korea.

\*Correspondence: helee72@korea.kr; Tel.: +82-63-238-6674

\*These authors equally contributed to this work



**Supplementary Fig: 1.** Molecular binding function of SNPs identified in the radish inbred lines further annotated into different levels.