



Figure S2. Evolutionary and synteny analysis of the IPC genome. (A) Distribution plot of synonymous substitution rates (K_s) for paralogous and orthologous genes among *I. pes-capare* (*ipc*), *I. triloba* (*itr*), and *V. vinifera* (*vi*). (B) Synteny blocks between *I. pes-capare*, *I. triloba*, and *I. trifida*.