

**Table S3** Number of orthologous genes found with the reciprocal best blast hits (RBH) method compared with the Inparanoid method of Khoshraftar *et al.* (2013). The number of genes in each species is indicated between parentheses.

Species compared (no of genes)	RBH method	Khoshraftar <i>et al.</i> 2013
<i>Ophiostoma ulmi</i> (8639)/ <i>Neurospora crassa</i> (9730)	6276	5517
<i>O. ulmi</i> / <i>Saccharomyces cerevisiae</i> (6604)	3179	2483
<i>O. ulmi</i> / <i>O. novo-ulmi</i> (8640)	8220	NA <sup>a</sup>
<i>O. novo-ulmi</i> / <i>N. crassa</i>	6360	NA
<i>O. novo-ulmi</i> / <i>S. cerevisiae</i>	3260	NA
<i>O. novo-ulmi</i> / <i>Sporothrix schenckii</i> (8674)	7171	NA
<i>O. novo-ulmi</i> / <i>Candida albicans</i> (6218)	2774	NA
<i>O. novo-ulmi</i> / <i>Histoplasma capsulatum</i> (9233)	5292	NA
<i>H. capsulatum</i> / <i>C. albicans</i>	3391	NA

<sup>a</sup> NA : data Not Available