

Table S1						
<b>Gene Name</b>	<b>Systematic Name</b>	<b><i>S. cerevisiae</i> ortholog (E score)</b>	<b><i>S. cerevisiae</i> gene function</b>	<b>Conserved motifs/domains</b>	<b>Domain Function</b>	<b>PHYRE</b>
<i>LIV5</i>	CNAG_02409	<i>YOP1</i> (0.00021)	ER tubulation	TB2/DP1/HVA22	unknown	none
<i>LIV6</i>	CNAG_07315	none	none	FG-GAP/VCBS	unknown; found in pathogens and integrins	lectin-like
<i>LIV7</i>	CNAG_06464	none	none	DUF3752	unknown	none
<i>LIV13</i>	CNAG_02753	<i>POM33</i> (8.3x10 <sup>-12</sup> )	nuclear pore	UPF0121	unknown; found in ER proteins	transmembrane domains
<i>MEP1</i>	CNAG_04735	none	none	peptidase M36	metalloprotease	none
<i>BLP1</i>	CNAG_06346	none	none	RlpA	lipid binding	none