

**Table S6** GO enrichment analysis of genes significantly regulated in response to *MSS11* over-expression or deletion in  $\Sigma$ 1278b (indicated as  $\Sigma$ 1278b *MSS11* and  $\Sigma$ 1278b *mss11* respectively) or over-expression in S288c (S288c *MSS11*). Shown is the number of genes identified to group in each category as selected by the use of GOEast with a Benjamini & Yekutieli calculated FDR threshold of 0.1. Categories mentioned in text are shown in bold.

GO Term	GO ID	S288c <i>MSS11</i>	Sigma <i>MSS11</i>	Sigma <i>mss11</i>
DNA binding	GO:0003677			3
L-amino acid transmembrane transporter activity	GO:0015179	2		
amine transmembrane transporter activity	GO:0005275	3		
amino acid transmembrane transporter activity	GO:0015171	3		
amino acid transport	GO:0006865	3		
<b>anchored to membrane</b>	<b>GO:0031225</b>	<b>9</b>	<b>7</b>	<b>2</b>
carbohydrate binding	GO:0030246	3	2	
carbohydrate transmembrane transporter activity	GO:0015144	4		
carbohydrate transport	GO:0008643	4		
cell	GO:0005623			7
cell growth	GO:0016049		4	3
cell part	GO:0044464			7
<b>cell periphery</b>	<b>GO:0071944</b>	<b>16</b>	<b>8</b>	
<b>cell wall</b>	<b>GO:0005618</b>	<b>10</b>	<b>7</b>	<b>2</b>
cell wall organization	GO:0071555		3	
cellular cell wall organization	GO:0007047		3	
<b>external encapsulating structure</b>	<b>GO:0030312</b>	<b>10</b>	<b>7</b>	<b>2</b>
external encapsulating structure organization	GO:0045229		3	
<b>extracellular region</b>	<b>GO:0005576</b>	<b>11</b>	<b>7</b>	<b>2</b>
<b>filamentous growth</b>	<b>GO:0030447</b>		<b>4</b>	<b>3</b>
filamentous growth of a population of unicellular organisms	GO:0044182		4	3
<b>flocculation</b>	<b>GO:0000128</b>	<b>4</b>	<b>4</b>	<b>1</b>
flocculation via cell wall protein-carbohydrate interaction	GO:0000501	2	2	
fructose transmembrane transporter activity	GO:0005353	4		
<b>fungal-type cell wall</b>	<b>GO:0009277</b>	<b>7</b>	<b>5</b>	<b>1</b>
glucose transmembrane transporter activity	GO:0005355	4		

GO Term	GO ID	S288c <i>MSS11</i>	Sigma <i>MSS11</i>	Sigma <i>mss11</i>
growth	GO:0040007		4	3
growth of unicellular organism as a thread of attached cells	GO:0070783		4	3
hexose transmembrane transporter activity	GO:0015149	4		
hexose transport	GO:0008645	4		
homoserine metabolic process	GO:0009092	2		
<b>intrinsic to membrane</b>	<b>GO:0031224</b>	<b>30</b>	<b>13</b>	
mannose transmembrane transporter activity	GO:0015578	4		
membrane	GO:0016020	30	13	
membrane part	GO:0044425	30	13	
modified amino acid transmembrane transporter activity	GO:0072349	3		
monosaccharide binding	GO:0048029	2	2	
monosaccharide transmembrane transporter activity	GO:0015145	4		
monosaccharide transport	GO:0015749	4		
<b>multi-organism process</b>	<b>GO:0051704</b>	<b>7</b>	<b>5</b>	<b>1</b>
organic substance transport	GO:0071702	8		
peptide catabolic process	GO:0043171	2		
peptide metabolic process	GO:0006518	2		
<b>plasma membrane</b>	<b>GO:0005886</b>	<b>9</b>	<b>4</b>	
pseudohyphal growth	GO:0007124		4	3
regulation of anatomical structure size	GO:0090066		4	3
regulation of biological quality	GO:0065008			3
regulation of cell size	GO:0008361		4	3
regulation of cellular component size	GO:0032535		4	3
response to stimulus	GO:0050896		10	
response to toxin	GO:0009636	2	1	
sequence-specific DNA binding	GO:0043565			2
sugar binding	GO:0005529	2	2	
sugar transmembrane transporter activity	GO:0051119	4		
sulfur amino acid metabolic process	GO:0000096	3		
sulfur amino acid transmembrane transporter activity	GO:0000099	3		

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GO Term	GO ID	S288c <i>MSS11</i>	Sigma <i>MSS11</i>	Sigma <i>mss11</i>
sulfur compound metabolic process	GO:0006790	5		
sulfur compound transport	GO:0072348	2		
transcription regulator activity	GO:0030528			2

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