Table S1. Primers used in this study.

Primer	Oligonucleotide sequence (5'→3')
SAM1-FW	AAAACCCGGGGCACAGGAAGAACACGTATC
SAM1-RV	TTTTCCCGGGCGATAGCGTAAACGAAGAAG
MUP1-FW	AAAACCCGGGGTCGGCGACAAACTAGAAG
MUP1-RV	TTTTCCCGGGGGAAGACAGCATCGTATTGT
L123M-FW	ACCAATTGCAATCTTACATTTGTTTCTGTATGCCAGCTTTCGAAG
L123M-RV	CTTCGAAAGCTGGCATACAGAAACAAATGTAAGATTGCAATTGGT
aFactor-ER	GGAATTCATGAGATTTCCTTCAATTTTTACTG
MET3p-FW	GCCCTTTTCCAAGATGATGA
MET3p-RV	AACAATGAAGTGGGAGGCAC
MET14p-FW	ACGCAAGGCATTGAGAAAAC
MET14p-RV	GCTTCATATGGGGCAGAAAT
MET17p-FW	GGTTCGCAATTGTTTGGTCT
MET17p-RV	ACAGAAGTAACCACCGGCAC
ACT1p-FW	CGTTCCAATTTACGCTGGTT
ACT1p-RV	CGGTGATTTCCTTTTGCATT

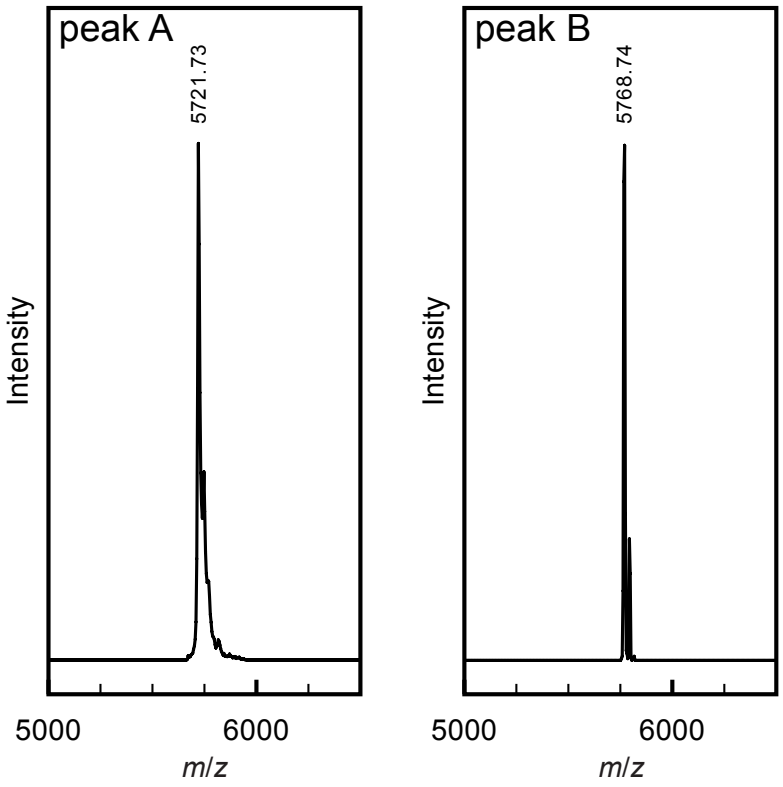

Fig. S1. Mass spectra of the Met and SeMet derivatives of the L123M EGF peptide. The eluates from reverse phase chromatography (Fig. 6, chromatogram No. 2 of SRY5-7) were analyzed by MALDI-TOF mass spectrometry as described in Materials and Methods. The average mass values of peak A (observed *m*/*z* 5721.73, left panel) and peak B (observed *m*/*z* 5768.74, right panel) corresponded closely to the L123M EGF peptide containing Met (theoretical *m*/*z* 5722.20) and SeMet (theoretical *m*/*z* 5769.11), respectively. Note that replacement of sulfur by selenium increases the mass value by 47.

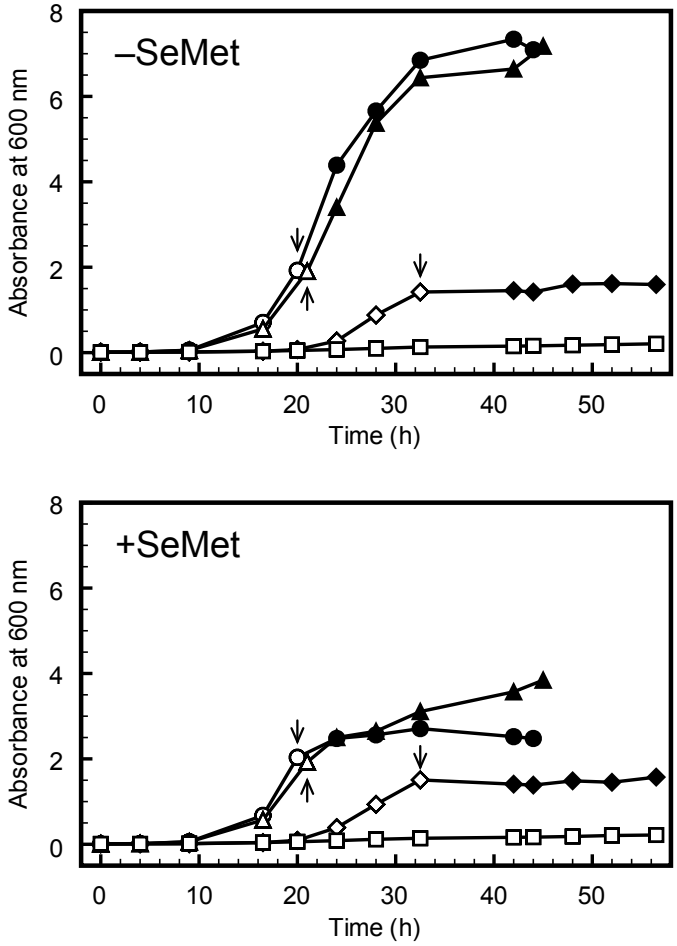

Fig. S2. Growth curves of yeast strains when induced the expression of recombinant L123M EGF peptide. The wild-type (circles), SRY5-7 (triangles), *sam1*Δ *sam2*Δ (diamonds), and *cys3*Δ (squares) strains harboring the plasmid pGAL-123M were cultured as described in Materials and Methods. To induce the L123M peptide expression, galactose was added to give a final concentration of 2% at the time points shown by arrows, and then the peptides were overexpressed in the absence (upper panel) or presence (lower panel) of 0.25 mM SeMet for 24 h. The OD_{600} values of cells before (open symbols) or after (closed symbols) addition of galactose are plotted.