Response	AMB				AMB-LF
	Regulation	GO term	SOMs cluster	Genes	Regulation
				GPX2 + 2	
Related to		Cellular oxidant		uncharacterized	
stress	Up	detoxification	10	genes	Up
		ER-dependent		YOP1 + 2	
		peroxisome		uncharacterized	
	Up	organisation	19	genes TRX1 + 4	Up
		Glutathione		uncharacterized	
	Up	metabolic process	14	genes FHB1 + 1	Up
				uncharacterized	
	Up	Nitrosative stress	24	genes	Up
		Piecemeal		APG9 + 4	
		microautophagy of		uncharacterized	
	Up	the nucleus	20	genes	Up
	l op	the hadicus	20	genes	Op .
		Positive regulation of		2 uncharacterized	
	Up	apoptotic process	15	genes	Up
	1'	Reactive oxygen			'
		species metabolic			
	Up	process	15	TSA1, GPX2, TRR1	Up
		Regulation of		2 uncharacterized	
	Up	autophagy	20	genes	Up
		autophasy	20	Beries	
					Up
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				I
				Up
				Up
		ER-to-Golgi vesicle	5 uncharacterized	
ER related	Down	mediated transport	16 genes CHO2, PSD1 + 4	Down
		Glycerolipid	uncharacterized	
	Down	biosynthesis	12 genes RPB4, GCN3 + 24	Down
		Peptide metabolic	uncharacterized	
	Down	process	12 genes	Down
		Proteasomal ubiquitin		
		independent protein	5 uncharacterized	
	Down	catabolism	11 genes	Down
			20 uncharacterized	
	Down	Protein folding	11, 22 genes	Up
		Protein localisation to	6 uncharacterized	
	Down	the ER	11 genes	Up
		Protein localisation to	2 uncharacterized	
	Down	vacuolar membrane	12 genes 5 uncharacterized	
	Down	Protein refolding	22 genes	
		Protein transmembrane	4 uncharacterized	
	Down	transport	22 genes	
		Signal peptide	5 uncharacterized	
	Down	processing Tail anchored	11 genes	
		membrane protein		
		insertion into ER		
	Down	membrane	12 GET3, GET1	
			ZIP2, ENA1, SIT1,	
		Cation	CTR4, PMC1, ZRC1	
Metal ion		transmembrane	+ 8 uncharacterized	
related	Up	transport	14 genes	Down
	Up	Copper ion transport	10 COX17, SCO1	Up
			ZIP2, CTR4 + 3	
		Transition metal ion	uncharacterized	
	Up	transport	14 genes	Up

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	SOMs	
GO term	cluster	Genes
		APG9, HSV2 + 1
Autophagy of mitochondrion	22	uncharacterized genes
Cellular oxidant		SRX1, CAT1, GPX2 + 5
detoxification	7 16	uncharacterized genes
detoxilication	7, 10	uncharacterized genes
Cellular response to		FHB1 + 1 uncharacterized
nitrosative stress	17	genes
Cellular response to		CCP1, PIM1, TAL1, TPS1 + 5
oxidative stress	11	uncharacterized genes
Glutathione metabolic		TRX1 + 4 uncharacterized
	11	
process	11	genes
Glycoprotein biosynthetic		KRE5, KTR3 + 3
process	7	uncharacterized genes
		-
Golgi vesicle docking	1	2 uncharacterized genes
Hydrogen peroxide catabolic	1	2 uncharacterized genes
process	1	TSA1, GPX2
Late endosome vacuole	_	DDI1 + 6 uncharacterized
transport	16	genes
·		TRX1 + 7 uncharacterized
Organelle fusion	11	genes
		SEC6 + 4 uncharacterized
Organelle membrane fusion	1	genes
Protein catabolic process in		
the vacuole		3 uncharacterized genes
Protein localisation to ER	3	2 uncharacterized genes
Protein localisation to	22	4
vacuole	22	4 uncharacterized genes CIN1 + 3 uncharacterized
Regulation of actin filament polymerisation	1	
polymensation	1	genes MKK2, PTP2 + 1
Regulation of kinase activity	17	uncharacterized genes
regulation of killage delivity		anonaracterized genes
Regulation of vacuole fusion	16	4 uncharacterized genes
Pachanca to tonalogically		
Response to topologically incorrect protein	2	4 uncharacterized genes
meorrect protein	3	+ uncharacterized gelies
Stress granule disassembly	3	2 uncharacterized genes
- ,		5

Transition metal ion	YKE4, ZIP2, CTR4 + 3
transport	11 uncharacterized genes
Ubiquitin-dependent ERAD	11 difference genes
· ·	3 2 uncharacterized genes
pathway	5 2 uncharacterized genes
	ERG28, ERG26, ERG27, ERG20
Ergosterol biosynthesis	10 + 1 uncharacterized genes
GPI anchor biosynthesis	10 4 uncharacterized genes
	To it distributed believes
Iron ion transmembrane	CFT1, LAC2 + 1
	•
transport	10 uncharacterized genes
	RPB4 + 23 uncharacterized
Peptide biosynthesis	10 genes
· op and a copyright	
Doct translational protein	
Post-translational protein	
targeting to the membrane	3 2 uncharacterized genes
Proteolysis	3 4 uncharacterized genes
,	C .

Iron ion transmembrane

transport

CFT1, LAC2 + 1

10 uncharacterized genes

Copper ion transport 7 COX17, SCO1

ZIP2, FRE3, CTR4, PXA2, ENA1, PMC1, ZRC1, SIT1, PDR5-2,

AQY1 + 27 uncharacterized

Ion transport 11, 12 genes

Transition metal ion transport

YKE4, ZIP2, CTR4 + 3 11 uncharacterized genes