

## **Supplementary tables**

**Table S1.** Carvacrol HCGP dataset.

**Table S2.** Microarray datasets including both raw data and differentially expressed transcripts in response to carvacrol and thymol.

**Table S3.** Different genes associated to UPR and their transcript level in response to carvacrol and thymol.

Gene name	Orf19 ID	Description	Transcript level		
			Carvacrol		Thymol 30 min
			5 min	30 min	
<b>Vesicle-mediated transport</b>					
<i>ENT2</i>	orf19.1444	Protein with phosphatidylinositol-4,5-bisphosphate binding activity	1.62	1.49	1.02
<i>YSC84</i>	orf19.4127	Ortholog have actin filament binding activity	1.62	1.45	0.9
<i>UBP15</i>	orf19.1777	Ortholog have ubiquitin-specific protease activity	1.56	1.50	1.06
<i>PEP3</i>	orf19.5543	Ortholog have cell division site, cytosol localization	1.31	1.58	0.92
<i>ECM21</i>	orf19.4887	Predicted regulator of endocytosis of plasma membrane proteins	1.82	1.41	0.7
<i>OBPA</i>	orf19.3198	Similar to oxysterol binding protein	1.55	1.10	0.87
<i>RVS167</i>	orf19.1220	SH3-domain- and BAR domain-containing protein	2.11	1.36	0.93
<i>SDS24</i>	orf19.5118	Protein similar to <i>S. cerevisiae</i> Sds24 involved in cell separation	1.79	0.80	0.67
<i>SEC18</i>	orf19.4993	Functional homolog of <i>S. cerevisiae</i> Sec18p	1.91	1.82	0.94
<i>SRO77</i>	orf19.1203	Protein with a role in docking and fusion of post-Golgi vesicles	1.76	1.51	1.11
<i>VPS15</i>	orf19.130	Protein involved in retrograde endosome-to-Golgi protein transport	1.66	1.26	0.94
<i>VPS21</i>	orf19.589	Late endosomal Rab small monomeric GTPase	2.71	2.34	1.12
<i>VPS35</i>	orf19.6875	Putative role in vacuolar sorting	1.92	1.52	0.90
<i>VPS4</i>	orf19.4339	AAA-ATPase involved in transport from MVB to the vacuole	1.86	1.41	1.05
<b>Protein degradation</b>					
<i>NPL4</i>	orf19.2434	Putative ubiquitin-binding protein	1.62	1.91	1.00
<i>PR26</i>	orf19.5793	Protein proteasomal 26S regulatory subunit	1.97	2.11	1.07
<i>PRE3</i>	orf19.6991	Putative beta-1 proteasome subunit;	1.93	1.54	1.07
<i>PRE5</i>	orf19.7178	Alpha6 subunit of the 20S proteasome;	2.19	1.93	1.05
<i>PUP1</i>	orf19.7605	Putative beta 2 subunit of the 20S proteasome	2.08	2.29	1.06
<i>RPN10</i>	orf19.4102	Putative 19S regulatory particle of the 26S proteasome	1.80	1.83	1.07
<i>RPN2</i>	orf19.5260	Putative 26S proteasome subunit	1.79	1.79	1.03
<i>RPT1</i>	orf19.441	Putative 26S proteasome regulatory subunit 7	1.93	2.11	1.04
<i>VPS4</i>	orf19.4339	AAA-ATPase involved in transport from MVB to the vacuole	1.86	1.41	1.05

<b><i>UBP15</i></b>	orf19.1777	Ortholog have ubiquitin-specific protease activity	1.50	1.56	1.06
<b><i>LAP41</i></b>	orf19.1628	Putative aminopeptidase yscI precursor	1.75	1.91	1.23
<b><i>DOA4</i></b>	orf19.7207	Ubiquitin hydrolase involved in recycling ubiquitin	2.38	4.07	0.95
<b><i>DOA1</i></b>	orf19.4829	WD repeat protein; required for ubiquitin-mediated protein degradation	2.86	2.14	0.91
<b><i>CYM1</i></b>	orf19.7410	Putative metalloprotease of the mitochondrial intermembrane space	2.14	1.83	0.86
<b><i>UBP2</i></b>	orf19.457	Ortholog have ubiquitin-specific protease activity	2.46	2.08	1.07
<b><i>CDC48</i></b>	orf19.2340	Putative microsomal ATPase	1.82	1.63	1.13
<b><i>PBN1</i></b>	orf19.3447	Ortholog have mannosyltransferase activity	1.96	1.43	0.95
<b><i>PRE4</i></b>	orf19.4230	20S proteasome subunit (beta7)	2.01	1.90	1.14
<b><i>EAR1</i></b>	orf19.2703	Specificity factor required for Rsp5p-dependent ubiquitination	1.91	1.44	0.91
<b><i>SAN1</i></b>	orf19.2498	ubiquitin-protein ligase	1.68	1.65	1.03
<b><i>RQC1</i></b>	orf19.1864	Ortholog have role in ribosome-associated ubiquitin-dependent protein catabolic process and RQC complex	1.90	1.65	1.04
<b><i>PNG1</i></b>	orf19.26	Putative peptide N-glycanase	1.98	1.39	0.97
<b><i>MNL1</i></b>	orf19.834	Ortholog have carbohydrate binding, mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	2.25	1.87	0.76
<b><i>UBP14</i></b>	orf19.1516	Ortholog have ubiquitin-specific protease activity	1.70	1.72	1.04
<b><i>UBX5</i></b>	orf19.4430	Ortholog have ubiquitin binding activity	1.72	1.67	0.97
<b><i>UBP12</i></b>	orf19.6260	Ubiquitin-specific protease; cleaves ubiquitin from ubiquitinated proteins	1.20	1.54	1.12
<b><i>UBP16</i></b>	orf19.3661	Putative deubiquitinating enzyme	2.33	3.97	0.76
<b><i>PRB1</i></b>	orf19.2242	Endoprotease B	2.33	3.97	0.76
<b><i>LAP4</i></b>	orf19.6671	Aminopeptidase I	1.23	1.53	1.03
<b><i>RPN9</i></b>	orf19.1993	Protein with role in proteasome assembly	1.52	1.61	1.24
<b><i>RPN12</i></b>	orf19.213	Ortholog have role in ubiquitin-dependent protein catabolic process	2.28	2.17	0.97
<b><i>HOD1</i></b>	orf19.3122.2	Ortholog have role in exocytosis, proteasome assembly	1.62	2.01	0.97
<b><i>UBP2</i></b>	orf19.457	Ortholog have ubiquitin-specific protease activity	2.08	2.46	1.07
<b><i>ASI3</i></b>	orf19.6440	Ortholog have ubiquitin-protein ligase activity	1.57	1.16	0.83
<b><i>DDI1</i></b>	orf19.7258	Putative DNA damage inducible v-SNARE binding protein	1.62	1.16	1.03
<b><i>PIM1</i></b>	orf19.522	ATP-dependent Lon protease	1.07	1.58	1.02
<b><i>PRE1</i></b>	orf19.4025	Putative beta 4 subunit of the 20S proteasome	1.85	1.73	0.85

<i>PRE3</i>	orf19.6991	Putative beta-1 proteasome subunit	1.54	1.93	1.07
<i>PRE9</i>	orf19.350	Alpha3 (C9) subunit of the 20S proteasome	1.93	1.54	1.07
<i>PUP2</i>	orf19.709	Alpha5 subunit of the 20S proteasome	1.07	0.50	0.92
<i>RPT2</i>	orf19.5440	Putative ATPase of the 19S regulatory particle of the 26S proteasome	1.24	1.55	1.01
<b>Protein folding</b>					
<i>FMO1</i>	orf19.3307	Flavin-containing monooxygenase	1.63	1.40	1.11
<i>HSP104</i>	orf19.6387	Heat-shock protein	3.61	3.49	0.82
<i>HSP70</i>	orf19.4980	Putative hsp70 chaperone	5.81	1.66	0.60
<i>HSP78</i>	orf19.882	Heat-shock protein	4.94	4.09	0.60
<i>TRX1</i>	orf19.7611	Thioredoxin	1.67	2.16	0.90
<i>RBPI</i>	orf19.6452	Peptidyl-prolyl cis-trans isomerase	1.19	1.58	0.90
<i>JEM1</i>	orf19.3592	Protein acting with Scj1p and Kar2p (BiP) in protein folding and ER-associated degradation of misfolded proteins	1.13	1.50	1.06
<i>CYP5</i>	orf19.7421	Putative peptidyl-prolyl cis-trans isomerase	1.21	1.52	1.19
<b>Amino acid metabolism</b>					
<i>SHM2</i>	orf19.5750	Cytoplasmic serine hydroxymethyltransferase	2.20	2.32	1.20
<i>SER33</i>	orf19.5263	Predicted enzyme of amino acid biosynthesis	2.22	1.72	1.19
<i>STR2</i>	orf19.1033	Ortholog have cystathionine gamma-synthase activity	2.69	1.08	0.99
<i>TRP5</i>	orf19.4718	Predicted tryptophan synthase	2.66	1.53	1.03
<i>LYS4</i>	orf19.3846	Homoaconitase	3.66	1.98	0.61
<i>LYS1</i>	orf19.1789.1	Saccharopine dehydrogenase (biosynthetic)	3.33	1.41	1.18
<i>LYS2</i>	orf19.2970	Heterodimeric alpha-aminoadipate reductase large subunit	3.02	1.76	1.00
<i>SER1</i>	orf19.5484	Putative 3-phosphoserine aminotransferase	1.59	1.27	1.16
<i>MET15</i>	orf19.5645	O-acetylhomoserine O-acetylserine sulfhydrylase	5.54	1.10	0.49
<i>MET10</i>	orf19.4076	Sulfite reductase; role in sulfur amino acid metabolism;	1.65	2.11	0.51
<i>ARO8</i>	orf19.2098	Aromatic transaminase of the Ehrlich fusel oil	3.69	1.98	1.05
<i>ARO3</i>	orf19.1517	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	2.25	1.02	0.97
<i>ARG1</i>	orf19.7469	Argininosuccinate synthase; arginine synthesis	42.93	2.79	1.32

<i>AAT1</i>	orf19.3554	Aspartate aminotransferase	2.74	2.08	0.74
<b><i>Lipid metabolism</i></b>					
<i>LCB4</i>	orf19.5257	Putative sphingosine kinase	1.92	1.95	0.93
<i>PLC2</i>	orf19.5797	Phosphatidylinositol (PtdIns)-specific phospholipase C (PI-PLC);	1.65	1.94	1.07
<i>TGL1</i>	orf19.2050	Ortholog have sterol esterase activity	2.04	1.60	0.78
<i>ROG1</i>	orf19.3991	Ortholog have role in cellular lipid metabolic process and cytosol localization	1.84	1.13	1.09
<i>OBPA</i>	orf19.3198	Similar to oxysterol binding protein	1.55	1.10	0.87
<i>ORM1</i>	orf19.5751	Putative endoplasmic reticulum membrane protein	1.64	1.33	1.08
<i>YDC1</i>	orf19.3104	Alkaline dihydroceramidase; involved in sphingolipid metabolism	3.42	2.20	0.86
<i>VPS4</i>	orf19.4339	AAA-ATPase involved in transport from MVB to the vacuole	1.86	1.41	1.05
<i>GPII5</i>	orf19.2529	Protein involved in the synthesis of glycosylphosphatidylinositol anchors	2.36	2.87	0.84
<i>ALG13</i>	orf19.6025	Protein with N-acetylglucosaminyl-diphosphodolichol N-acetylglucosaminyl-transferase activity	1.97	2.33	1.15
<i>SMP2</i>	orf19.1462	Putative Mg <sup>2+</sup> -dependent phosphatidate phosphatase	1.52	1.07	1.36
<i>HAL22</i>	orf19.105	Putative phosphoadenosine-5'-phosphate or 3'-phosphoadenosine 5'-phosphosulfate phosphatase; possible role in sulfur recycling;	2.01	2.98	0.90
<i>POX1</i>	orf19.5723	Predicted acyl-CoA oxidase	1.89	1.45	0.95
<i>NPR1</i>	orf19.6232	Predicted serine/threonine protein kinase, involved in regulation of ammonium transport; induced in core stress response;	4.77	2.36	0.79
<i>PBN1</i>	orf19.3447	Protein with mannosyltransferase activity	1.96	1.43	0.95
<i>GPII3</i>	orf19.832	Major facilitator superfamily protein	1.87	1.23	1.08
<i>PDR16</i>	orf19.1027	Phosphatidylinositol transfer protein	4.85	2.94	0.94
<i>PEX5</i>	orf19.5640	Protein required for PTS1-mediated peroxisomal protein import	2.97	2.00	1.12
<i>SCT1</i>	orf19.1289	Putative glycerol-3-phosphate O-acyltransferase; fungal-specific	2.14	1.03	0.92
<i>HFD1</i>	orf19.6066	Hexadecenal dehydrogenase	2.14	2.09	1.02
<i>YJU3</i>	orf19.4864	Protein with acylglycerol lipase activity and serine hydrolase activity	1.55	1.51	0.90
<i>YFT2</i>	orf19.1158	Protein required for normal ER membrane biosynthesis	1.95	1.54	0.98
<i>YEH1</i>	orf19.1887	Protein with sterol esterase activity	1.34	1.75	1.06

<i>GPII5</i>	orf19.2529	Protein involved in the synthesis of glycosylphosphatidylinositol anchors	2.36	2.87	0.84
<i>IFA38</i>	orf19.3859	Putative microsomal beta-keto-reductase	1.48	2.12	1.05
<i>PEX6</i>	orf19.3573	Protein with ATPase activity, protein heterodimerization activity	1.51	1.72	1.12
<i>PLC1</i>	orf19.5506	Phosphoinositide-specific phospholipase C (PI-PLC)	1.34	1.50	1.18
<i>PLC2</i>	orf19.5797	Phosphatidylinositol (PtdIns)-specific phospholipase C (PI-PLC)	1.65	1.94	1.07
<i>RTA2</i>	orf19.24	Flippase	1.14	3.70	1.06
<i>MIT1</i>	orf19.4077	Mannosylinositol phosphorylceramide (MIPC) synthase catalytic subunit	1.22	1.50	1.01
<i>MCR1</i>	orf19.3507	NADH-cytochrome-b5 reductase	1.20	1.66	1.13
<i>ERG4</i>	orf19.5379	Protein similar to sterol C-24 reductase	1.34	2.01	1.16
<i>ERG2</i>	orf19.6026	C-8 sterol isomerase; enzyme of ergosterol biosynthesis	0.68	1.87	1.40
<b>Cellular transport</b>					
<i>CDR1</i>	orf19.6000	Multidrug transporter of ABC superfamily	4.89	2.76	0.61
<i>GAP2</i>	orf19.6993	General amino acid permease	1.22	1.73	1.34
<i>GNPI</i>	orf19.1193	Asparagine and glutamine permease	1.44	2.10	4.06
<i>AQY1</i>	orf19.2849	Aquaporin water channel	1.81	1.99	0.35
<i>ITR1</i>	orf19.3526	Inositol transporter required for uptake of exogenous inositol	1.62	1.88	1.08
<i>AGP3</i>	orf19.3795	Serine transporter with possible role in assimilation of sulfur	1.60	2.88	1.06
<i>HGT20</i>	orf19.1587	Glucose transporter of the major facilitator superfamily	1.50	1.58	0.70
<i>ATM1</i>	orf19.1077	Member of MDR subfamily of ABC family	1.53	2.03	0.83
<i>SUL2</i>	orf19.2738	Protein described as a sulfate transporter	10.63	3.45	0.30
<i>MEP1</i>	orf19.1614	Ammonium permease	5.97	4.78	0.72
<i>HIP1</i>	orf19.4940	Histidine permease	4.11	2.24	5.30
<i>HAK1</i>	orf19.6249	Putative potassium transporter	2.02	1.23	0.51
<i>CRP1</i>	orf19.4784	Copper transporter of the plasma membrane	1.87	0.65	0.44
<b>Cell wall proteins</b>					
<i>ALS1</i>	orf19.5741	Adhesin	1.65	3.82	0.43
<i>ECM29</i>	orf19.6773	Putative scaffold protein	3.62	3.03	1.01
<i>MNN4</i>	orf19.2881	Regulator of mannosylphosphorylation of N-linked mannans to cell wall	1.42	2.44	0.87

		proteins			
<b><i>ECM15</i></b>	orf19.7436.1	Protein of unknown function; predicted role in cell wall organization	2.30	1.67	0.85
<b><i>DDR48</i></b>	orf19.4082	Immunogenic stress-associated protein	1.82	4.54	0.45
<b><i>PHR1</i></b>	orf19.3829	Glycosidase of cell surface	0.94	2.25	1.20
<b><i>BMT4</i></b>	orf19.5612	Beta-mannosyltransferase	1.66	1.84	1.41