

Title: Environmental stress is the major cause of transcriptomic and proteomic changes in GM and non-GM plants

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Legends for Supporting information

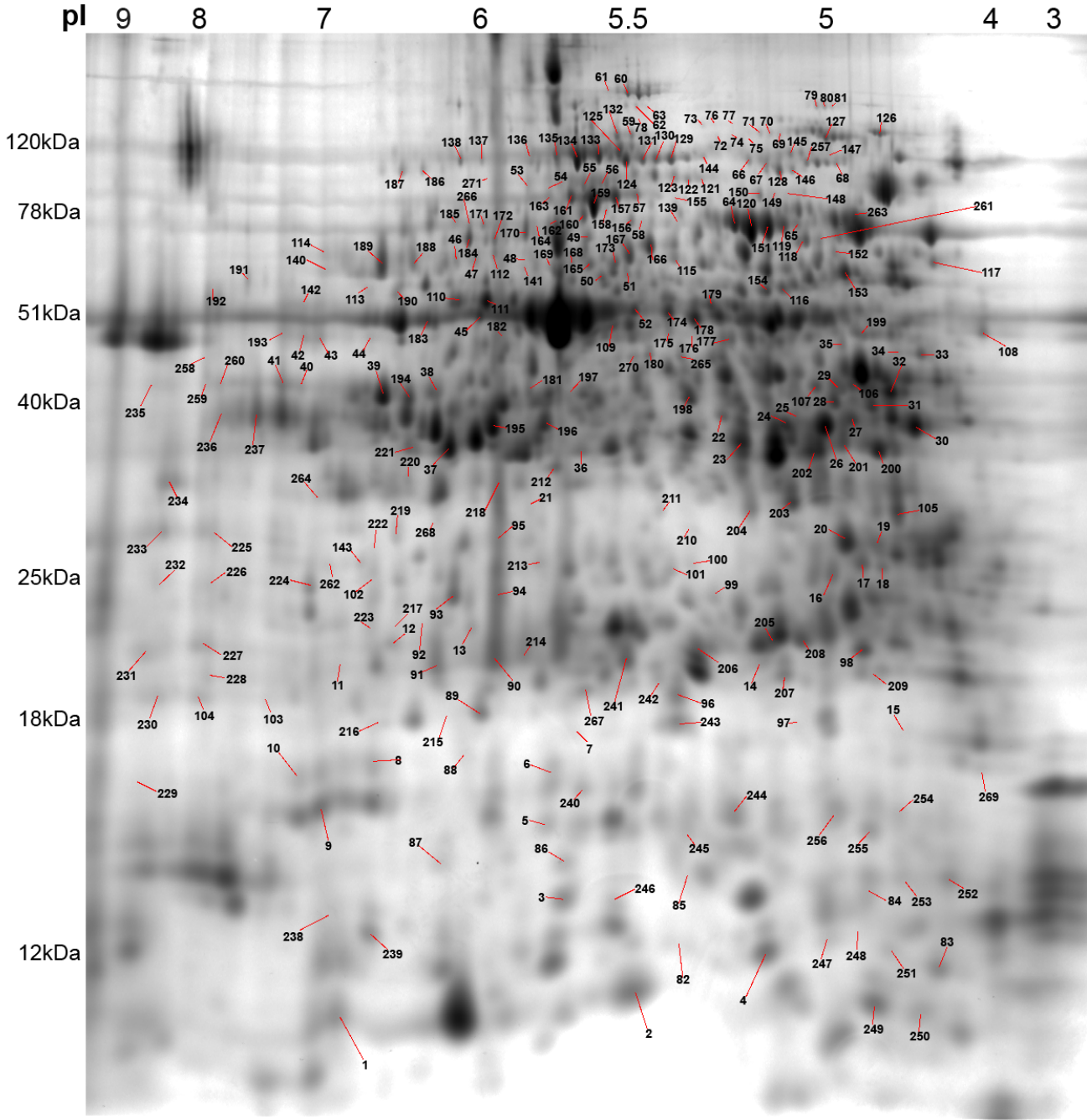
Figure S1- Representative 2D- multiplex fluorescence gel with the 271 differentially-abundant spots and 2D gel sections showing examples of different spot patterns between tested samples.

Table S1- Proteomic results.

Table S2- Microarrays results.

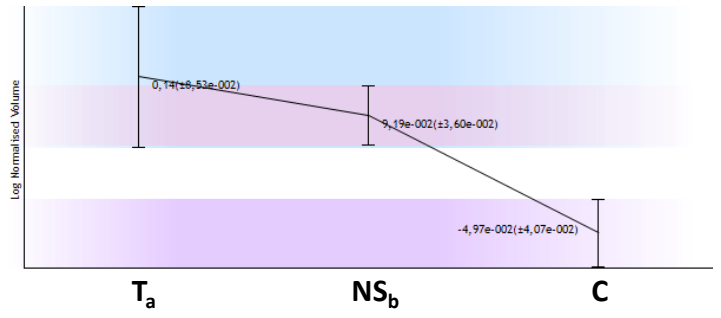
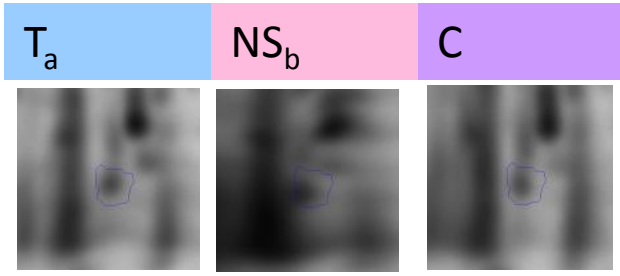
Table S3- Proteomics and Microarrays relation (salinity assay).

Figure S1- Representative 2D- multiplex fluorescence gel with the 271 differentially-abundant spots and 2D gel sections showing examples of different spot patterns between tested samples.

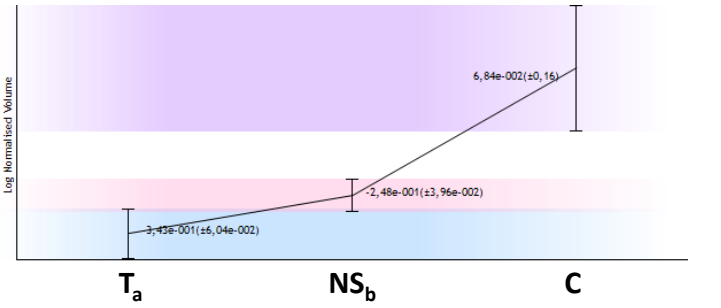
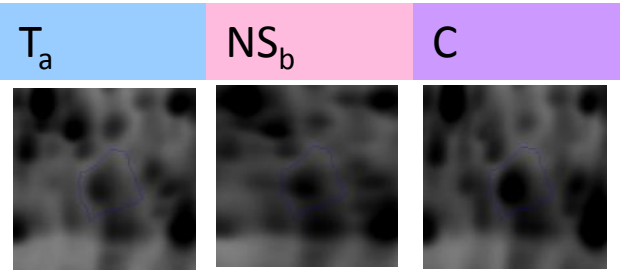


Ger F3

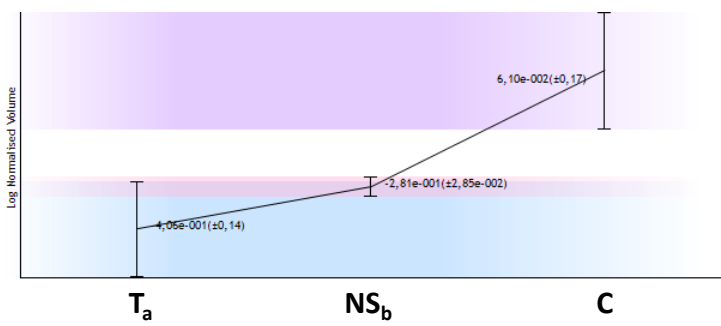
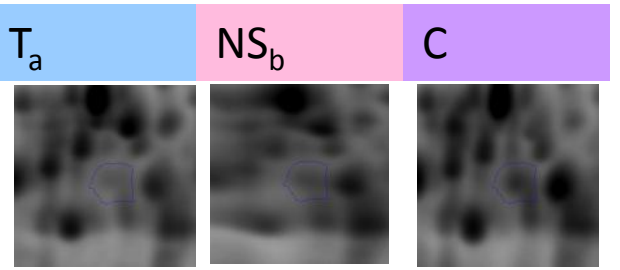
Spot 13- Ger F3



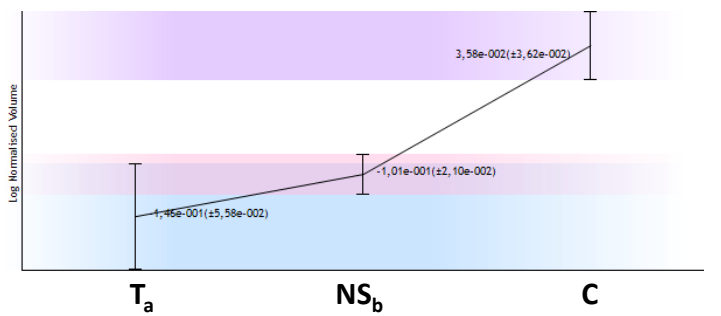
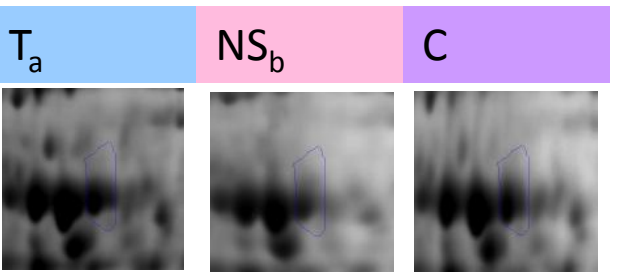
Spot 26- Ger F3



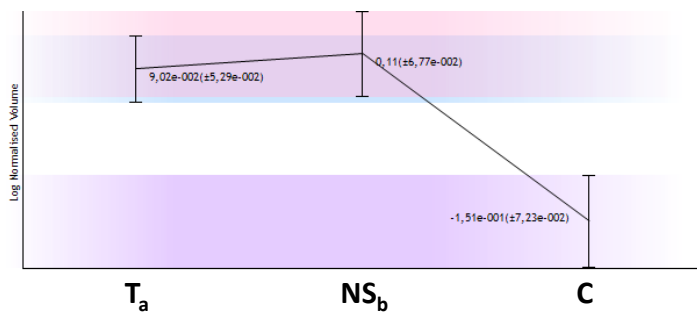
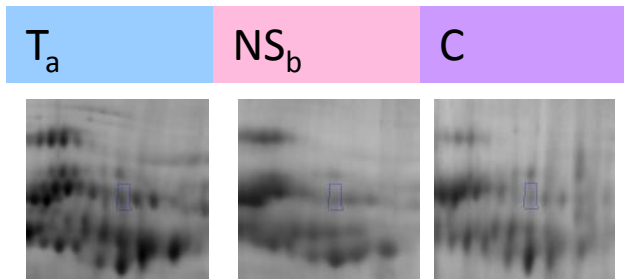
Spot 27- Ger F3



Spot 64- Ger F3

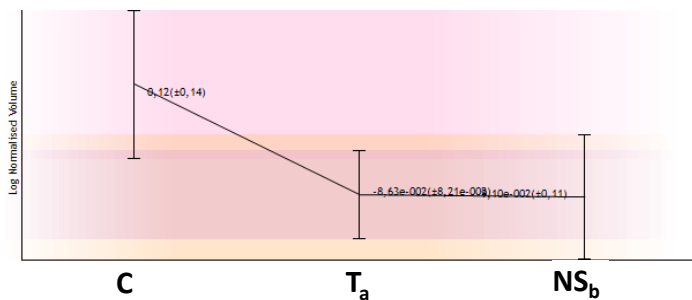
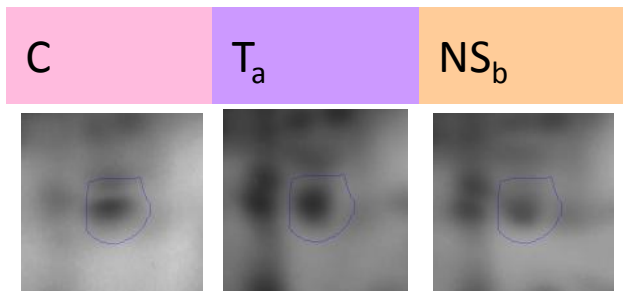


Spot 69- Ger F3

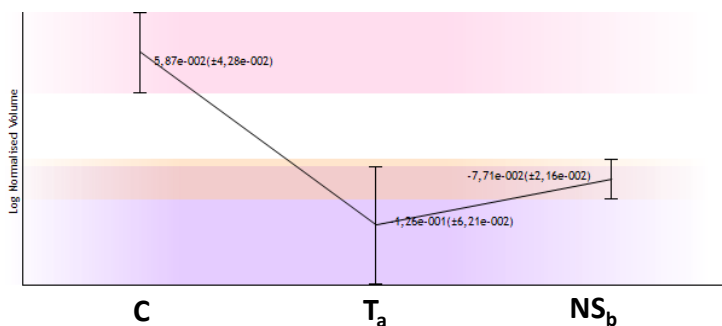
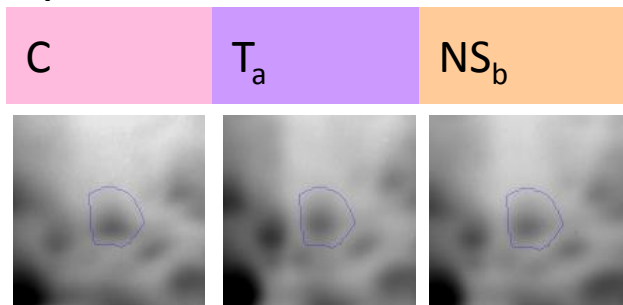


Ger F5

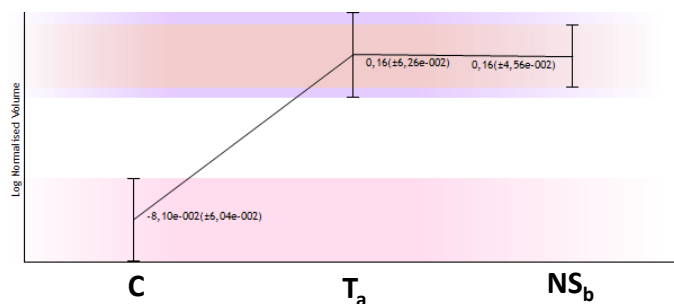
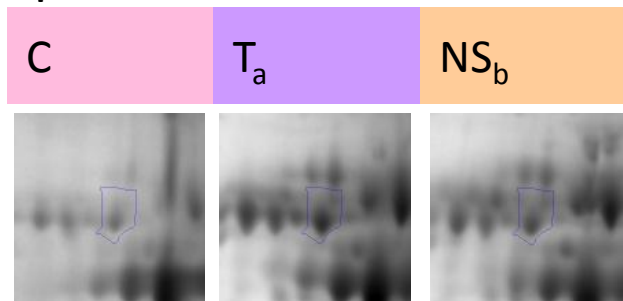
Spot 97- Ger F5



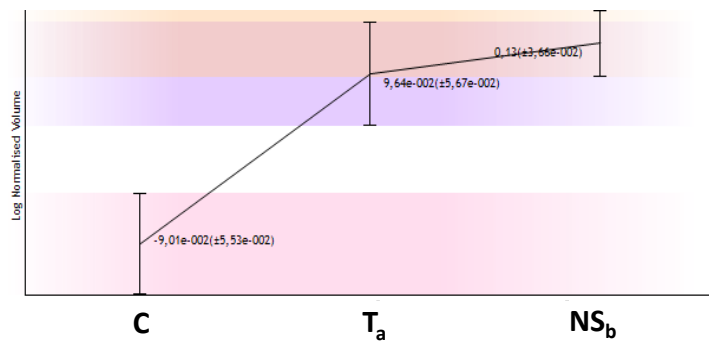
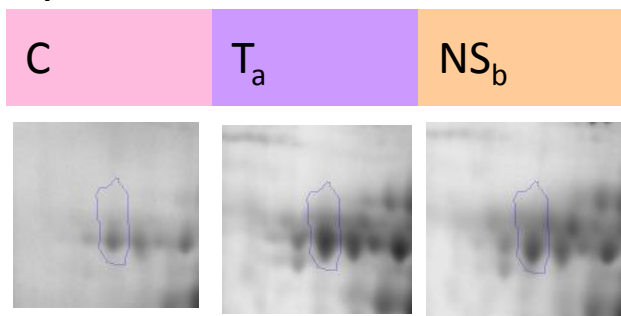
Spot 99- Ger F5



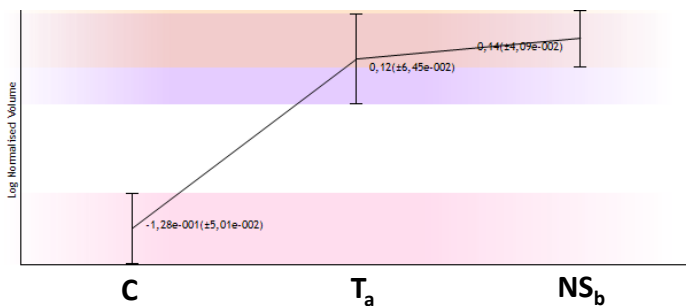
Spot 124- Ger F5



Spot 129- Ger F5

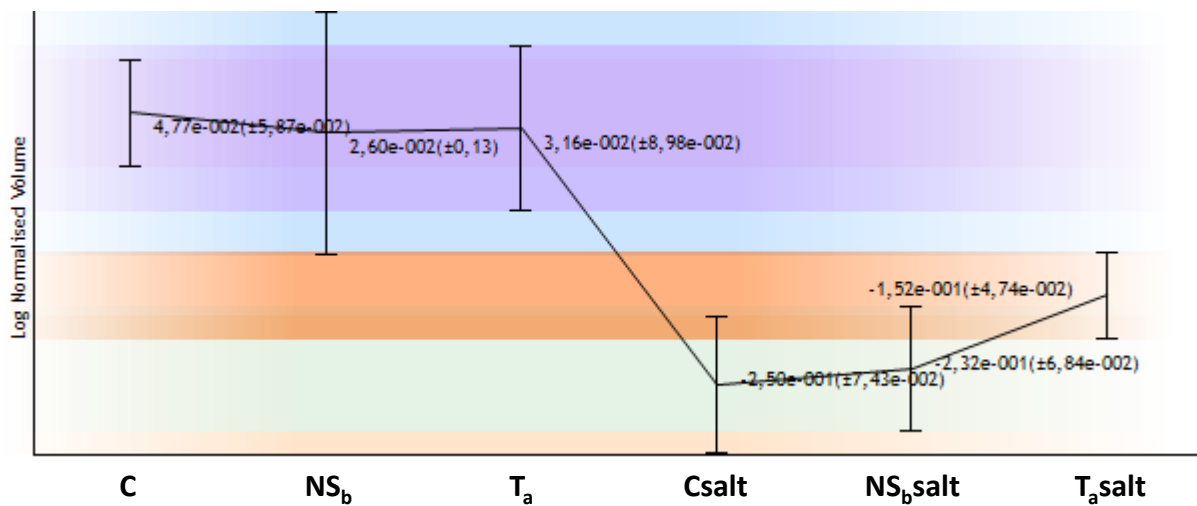
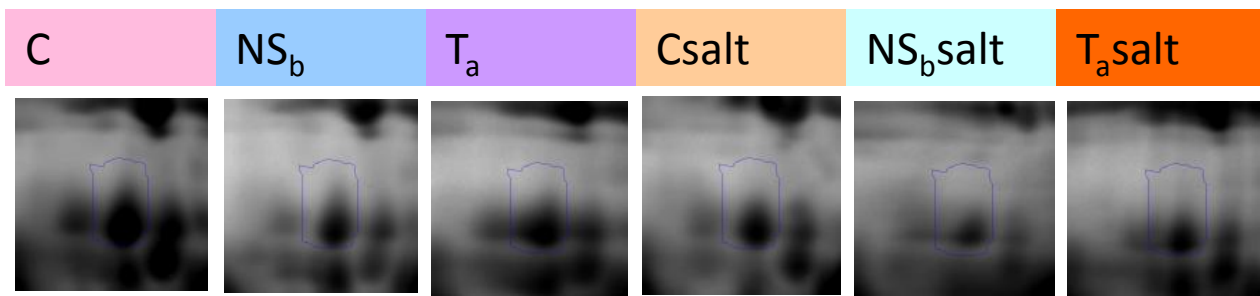


Spot 131- Ger F5

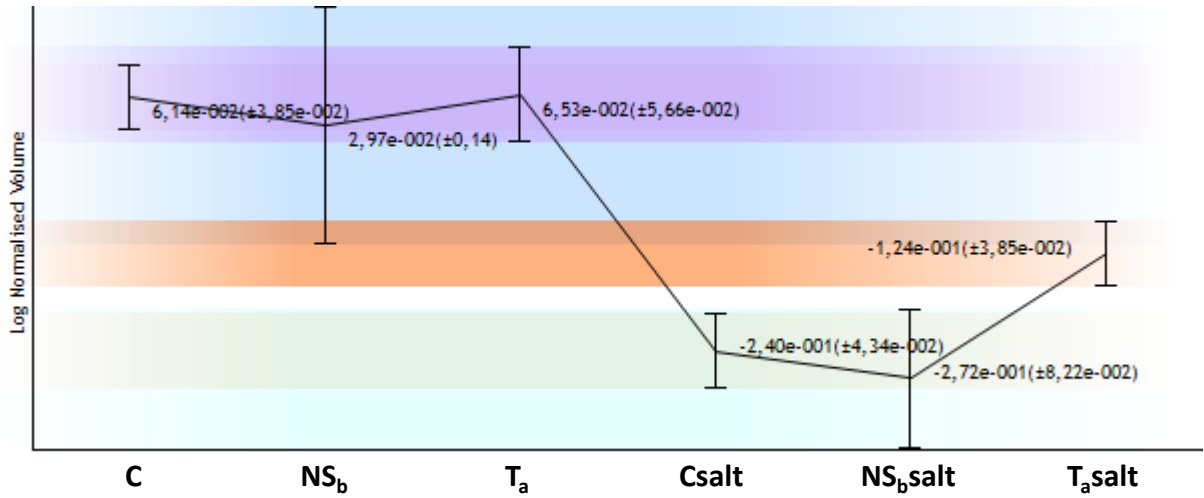
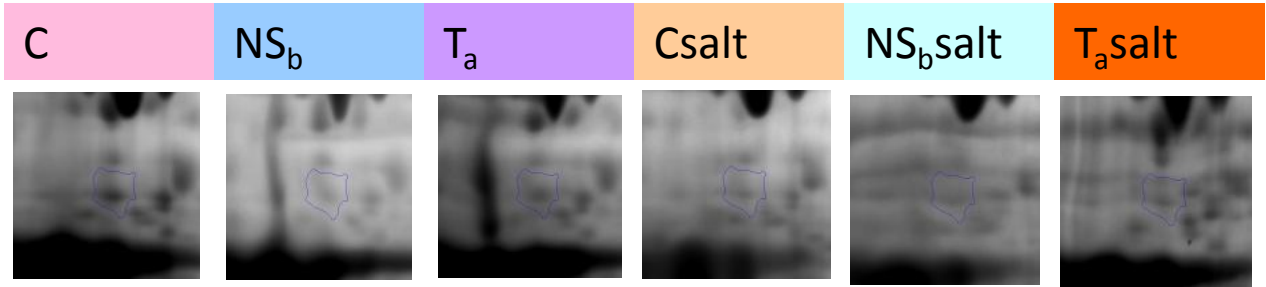


Ger F6

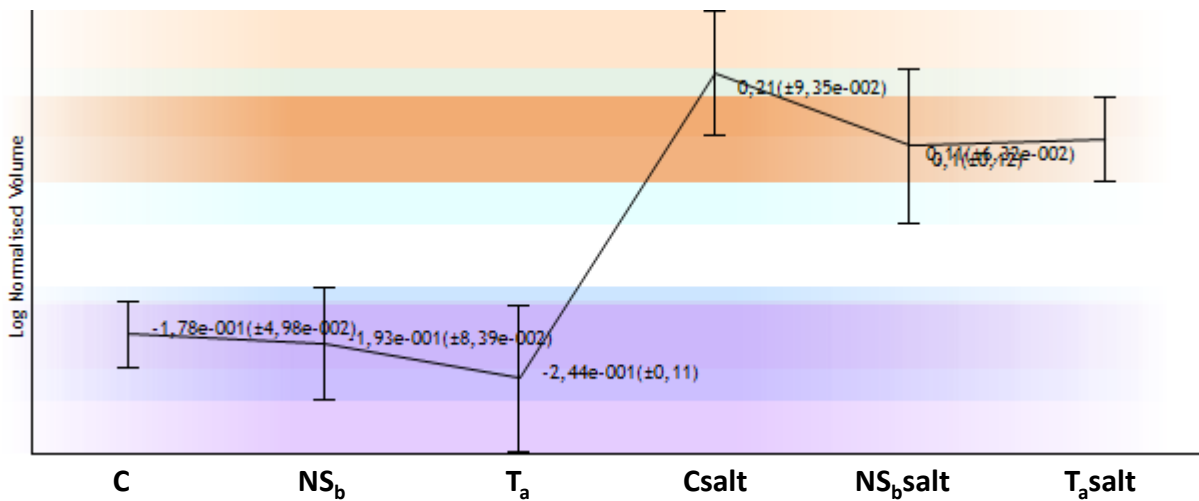
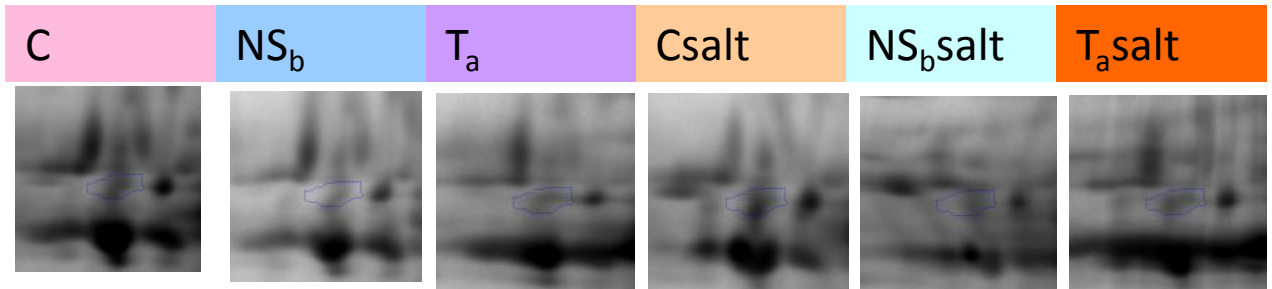
Spot 39- Ger F6



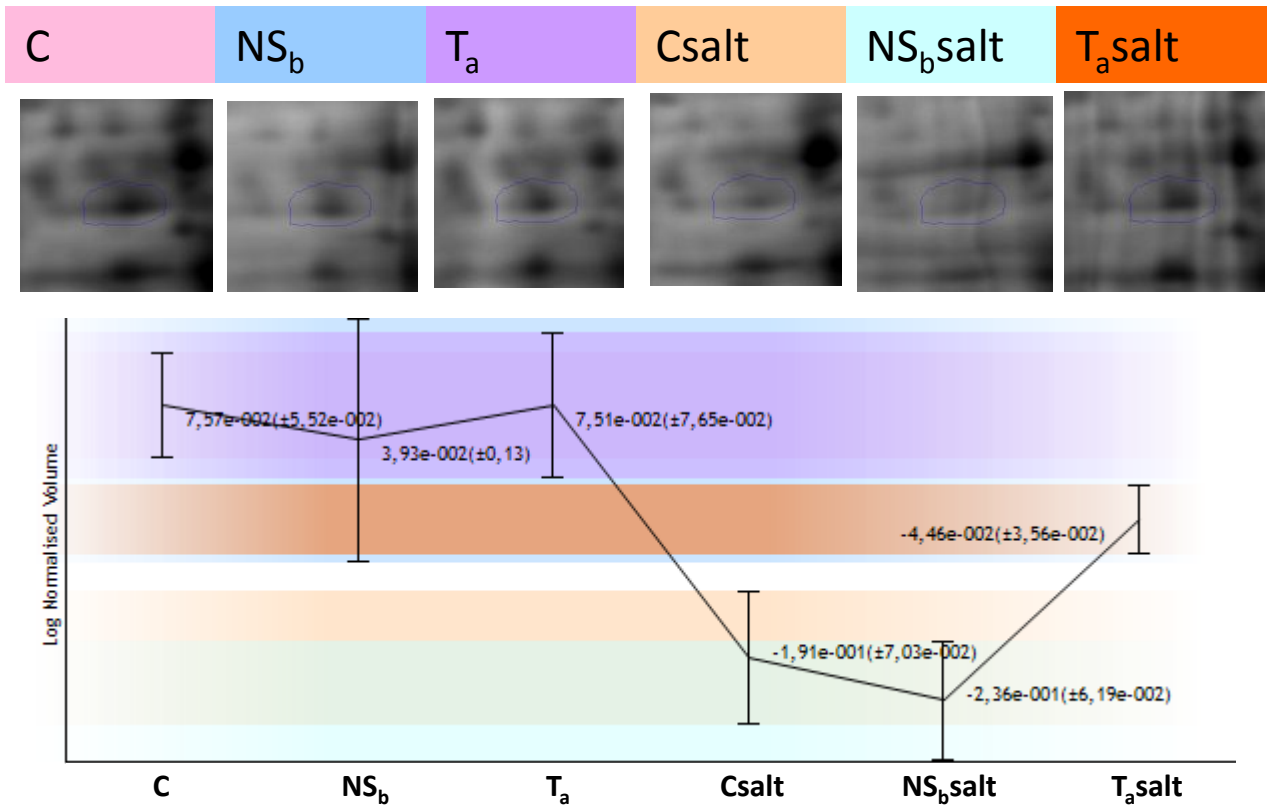
Spot 165- Ger F6



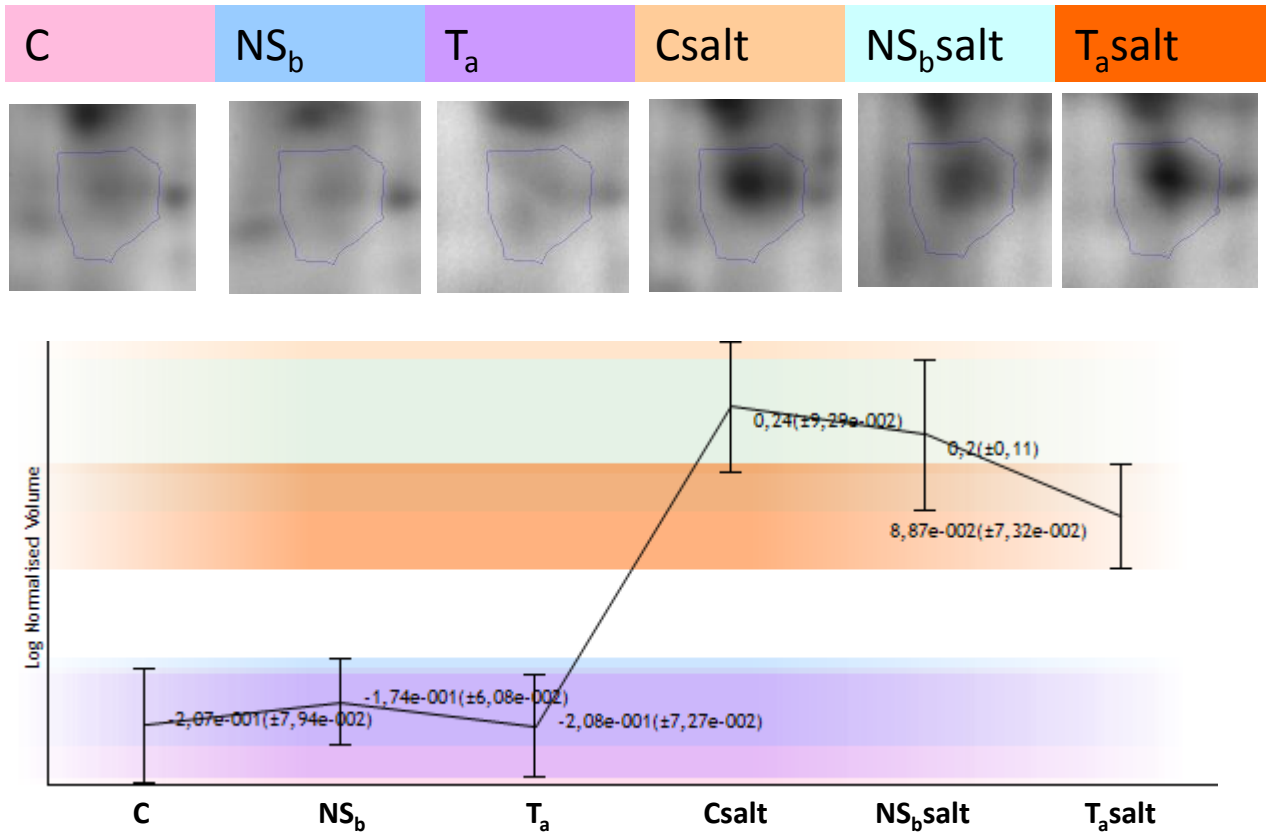
Spot 190- Ger F6



Spot 198- Ger F6

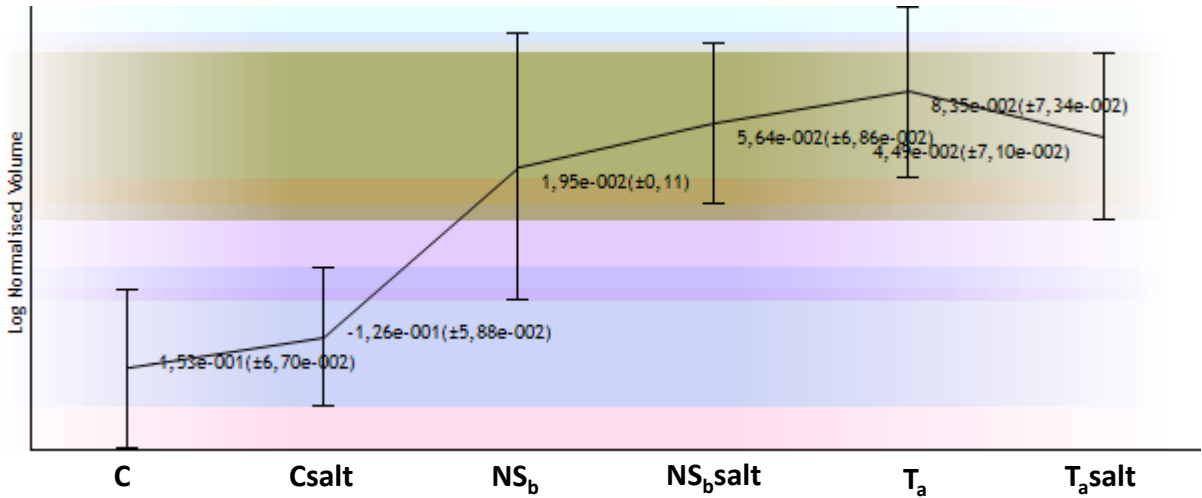
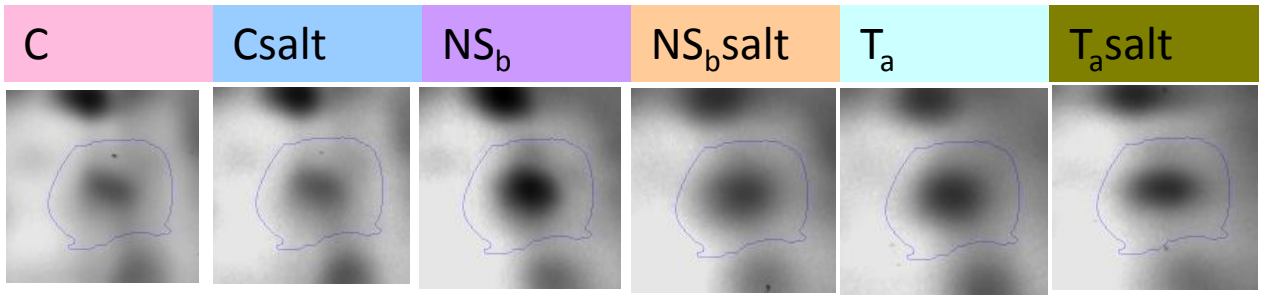


Spot 230- Ger F6

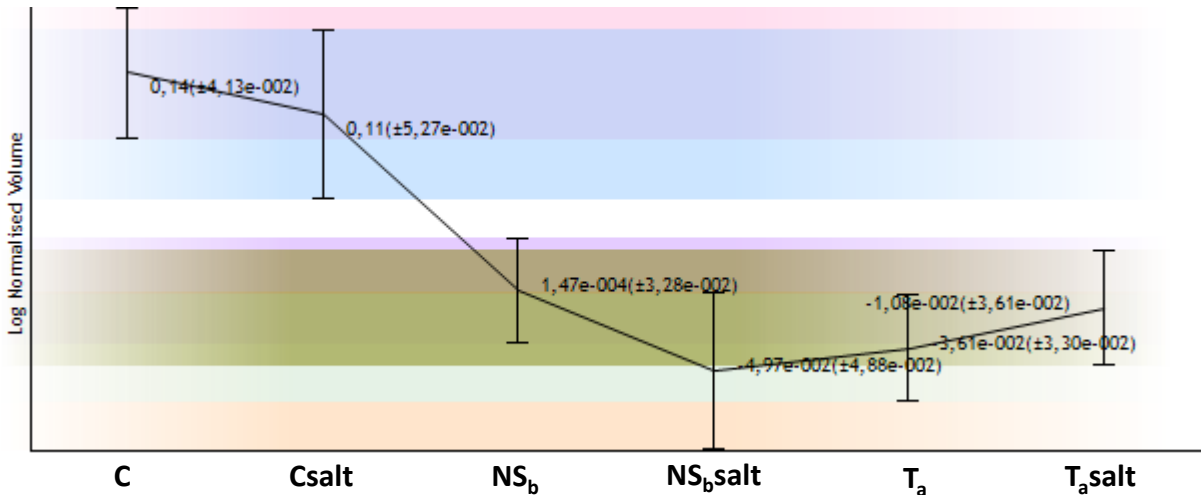
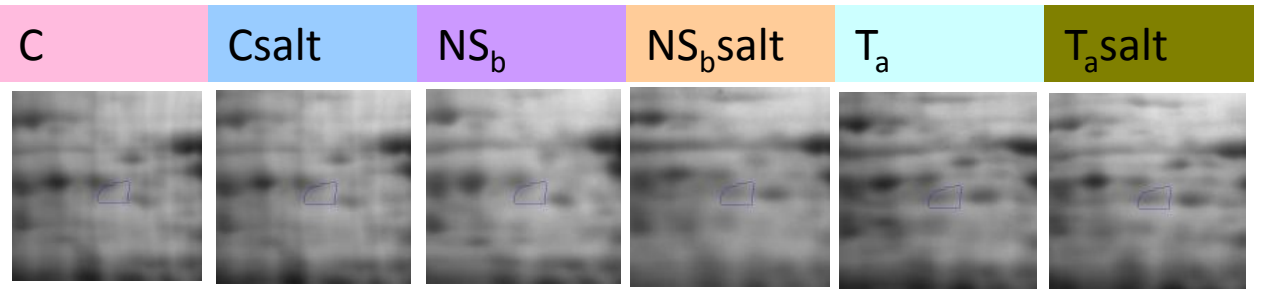


Ger F8

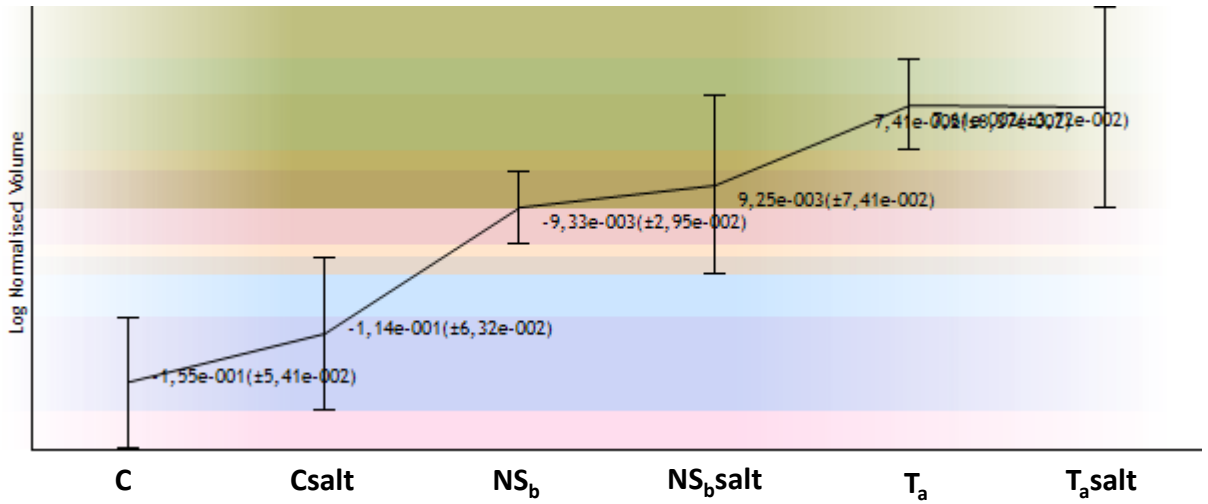
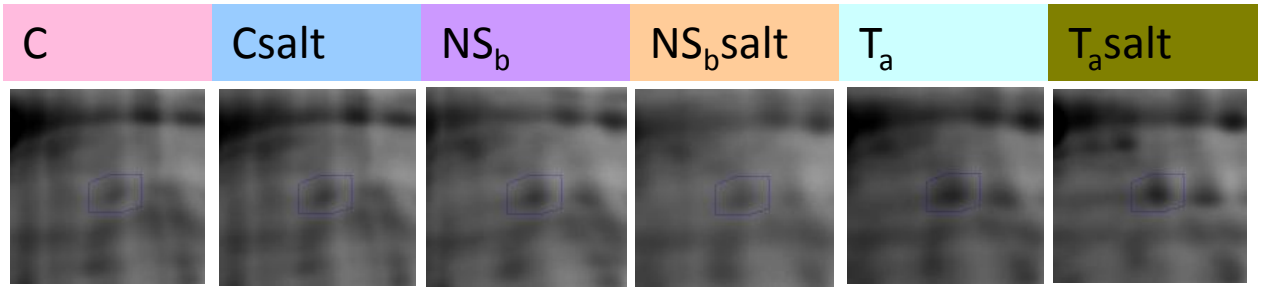
Spot 4- Ger F8



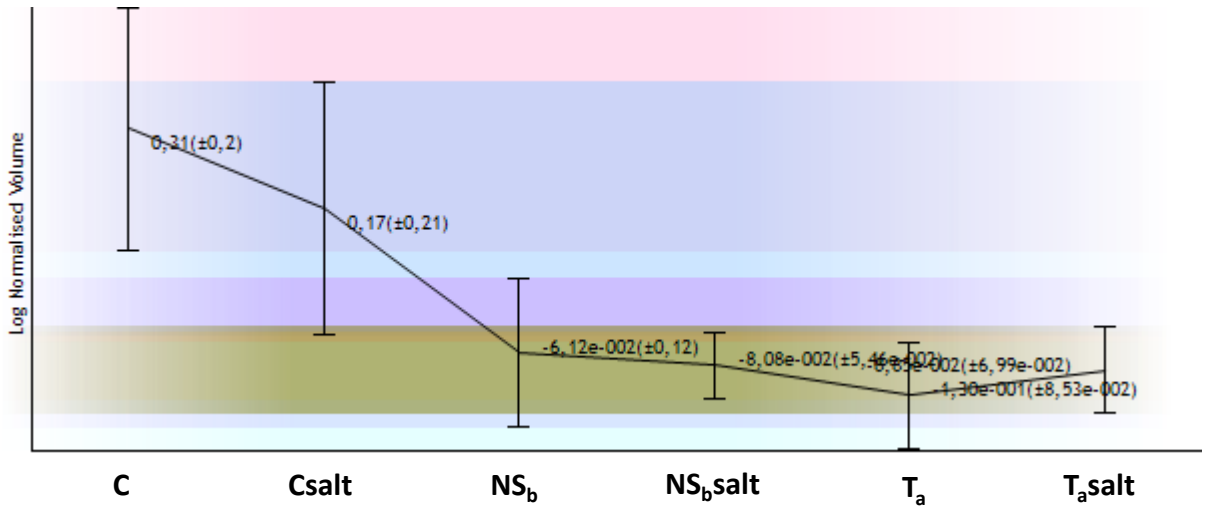
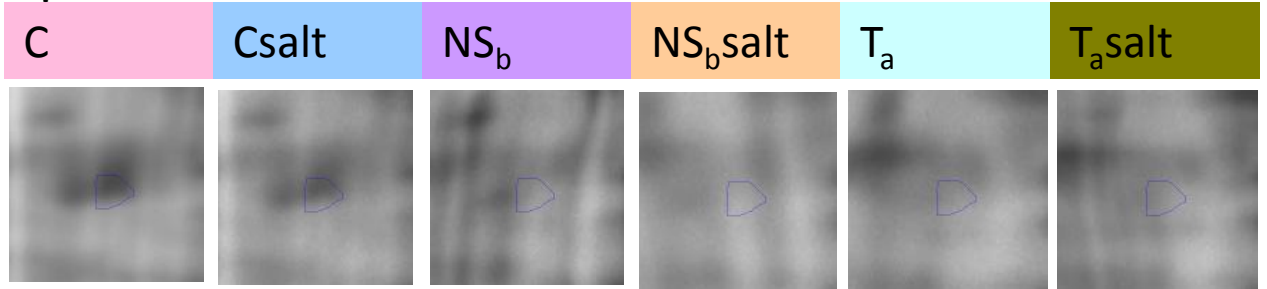
Spot 115- Ger F8



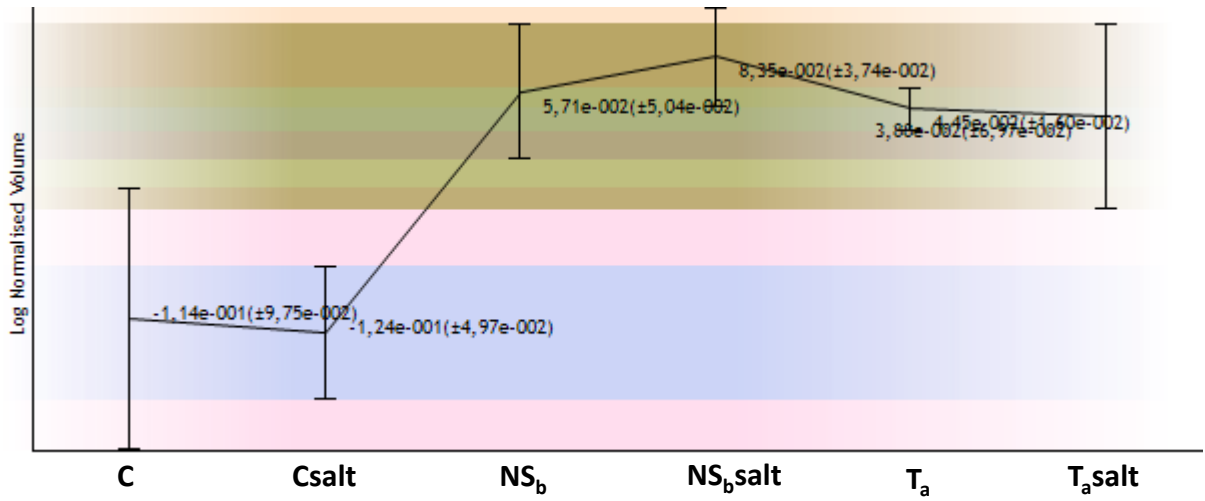
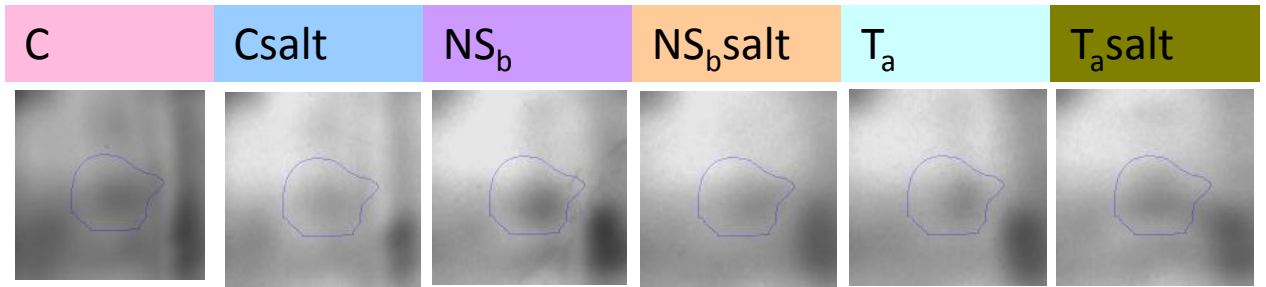
Spot 180- Ger F8



Spot 226- Ger F8



Spot 244- Ger F8



Supporting Table S3- Proteomics and Microarrays relation (salinity assay).

Proteomics					Microarrays				
Spot n°	Most probable protein identification	C vs. CSalt	T vs. Tsalt	NS vs. Nssalt	Affymetrix ID	Identification	C vs. Csalt	T vs. Tsalt	NS vs. Nssalt
Photosynthesis related					Photosynthesis related				
90	Carbonic anhydrase gi 3345477	-2.3	-1.2	-1.5	LOC_Os08g32840	bifunctional monodehydroascorbate reductase and carbonic anhydrasenelectarin-3 precursor	+3.0	+3.0	+3.0
214		-1.7							
218		-2.2	-1.2	-1.3					
207	Chloroplast 23 kDa polypeptide of photosystem II gi 164375543	+1.8		+1.6	LOC_Os11g24140	plastocyanin-like domain containing protein	+6.7	+5.3	+5.2
1	RuBisCo small chain c gi 77554383	-2.9	-2.5						
169	RuBisCo large subunit gi 290874507	-1.9		-1.6					
194	RuBisCo gi 694137368	-1.6	-1.6	-1.6					
182	RuBisCO, partial gi 440577954			-1.8					
27	RuBisCo activase gi 108864712	+1.6							
95	Phosphoglycerate kinase, chloroplastic gi 573944490 (Blast)	-1.9							
Photosynthesis and pentose phosphate pathway					Photosynthesis and pentose phosphate pathway				
119	Transketolase 1 gi 55296168	-1.5							
151	Transketolase 1 gi 55296168	-1.8		-1.8					
Photorespiration					Photorespiration				
105	Phosphoglycolate phosphatase region gi 116310328	-1.6	-1.5						
183	Glycine hydroxymethyltransferase gi 31126793	-1.6		-1.4					
Carbohydrate metabolism					Carbohydrate metabolism				
195	Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic gi 573940046 (Blast)	+1.5	+1.2	+1.2	LOC_Os03g22120	sucrose synthase	+3.7	+3.5	+5.9
196		+1.6			LOC_Os01g13570	phosphoglycerate mutase	+3.6	+3.2	+4.7
198	Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic gi 573923495 (Blast)	-1.8	-1.3	-1.9	LOC_Os03g55090	alpha-glucan phosphorylase isozyme	+2.6	+3.0	+2.9
202	Fructose-bisphosphate aldolase, chloroplastic gi 108864048	-1.6	-1.4	-1.6	LOC_Os08g02700	fructose-bisphosphate aldolase isozyme,	+2.5	+1.9	+3.2
41	Fructose-bisphosphate aldolase cytoplasmic gi 573915065 (Blast)	+2.3							
236		+1.6	+1.3						
237		+1.9	+1.3						
190	Phosphoglucose isomerase gi 639684	+2.5	+2.3	+2.0	LOC_Os08g31980	trehalose-6-phosphate synthase	+2.5	+4.1	+4.6
200	Fructokinase 1 gi 385145615	-1.6	-1.2	-1.3					
243	Adenosine diphosphate glucose pyrophosphatase	+1.5							

Cell Wall polysaccharide metabolism				
	gij21322655			
170	Glycosyl hydrolase family 38 gi 108864437	-1.5	-1.3	-1.5
188	Glycosyl hydrolase family 3 gi 108711094	-1.5	-1.2	-1.2
189	Glycosyl hydrolase family 3 gi 108711094	-1.9	-1.2	-1.4
115	Beta-D-xylosidase 4 gi 357166259 (Blast)	-1.7		-1.3
167	Beta-D-xylosidase 4 gi 573942853	-1.6		-1.3
219	RmlD substrate binding domain containing protein gi 108707480	+3.2		+1.7
TCA/ glyoxylate cycle/ respiratory chain				
181	Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial-like gi 573920524	+1.4	+1.3	+1.5
131	Aconitate hydratase, cytoplasmic gi 108706066	-1.7		
227	dihydropyridoxyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 1, mitochondrial gi 573939599	+2.1	+1.4	+1.5
165	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial gi 474445992	-2.0	-1.6	-2.0
168	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial gi 573951965 (Blast)	-1.7		-1.5
Amines metabolism and nitrogen status				
148	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase gi 108862990	-1.6		
149		-1.7		
161		-1.9	-1.2	
163	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase gi 108862992	-1.8		
155		-1.5	+1.3	
159		-1.9		-1.4
201	Cysteine synthase, chloroplastic/chromoplastic gi 573946673	-1.7	-1.4	-1.6
204		+1.8	+1.3	+1.4

Cell Wall polysaccharide metabolism						
	LOC_Os01g71340	glycosyl hydrolases family 17		+7.8	+7.2	+9.8
	LOC_Os01g71830			+6.1	+5.7	+10.4
	LOC_Os01g71670			+2.6	+2.2	+3.8
	LOC_Os01g71820			+4.2	+3.0	+3.0
	LOC_Os10g28120	glycosyl hydrolase		+3.9	+3.5	+4.9
	LOC_Os11g47500			+4.4	+4.7	+4.6
	LOC_Os11g47600			+2.9	+3.4	+3.3
	LOC_Os02g01590			-3.2	-4.1	-2.8
	LOC_Os05g15770			+9.7	+10.6	+11.6
	LOC_Os07g35560	glucan endo-1,3-beta-glucosidase precursor		+2.3	+5.3	+4.0
	LOC_Os09g31430	Os9bglu30 - beta-glucosidase		+3.2	+4.2	+3.3
	LOC_Os10g35070	alpha-galactosidase precursor		+2.6	+1.9	+3.3
	LOC_Os08g44040	rhamnogalacturonate lyase		-8.4	-5.7	-11.2
	LOC_Os07g32630	UDP-glucuronosyl and UDP-glucosyl transferase		-3.0	-2.5	-2.5
	LOC_Os02g51930	UDP-Glycosyltransferase family		+3.2	+2.6	+5.0
TCA/ glyoxylate cycle/ respiratory chain						
	LOC_Os01g41810	cytochrome P450 72A1		+3.6	+3.1	+4.8
	LOC_Os10g17260			-3.8	-3.4	-3.9
	LOC_Os02g09390			+3.1	+3.5	+2.9
	LOC_Os04g09920	cytochrome P450		+3.6	+2.0	+2.1
	LOC_Os06g37300			+3.1	+2.3	+3.7
	LOC_Os07g11739			+2.7	+2.2	+3.1
	LOC_Os08g39730			+3.6	+3.2	+4.4
	LOC_Os03g12820	ATP synthase protein 8		+5.9	+4.3	+7.0
	LOC_Os07g34520	isocitrate lyase		+2.4	+2.8	+4.3
Amines metabolism and nitrogen status						
	LOC_Os10g28350	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase		+4.3	+3.2	+4.2
	LOC_Os03g09910	aminotransferase, classes I and II, domain		+8.5	+11.1	+10.5
	LOC_Os11g42510	tyrosine aminotransferase		+3.5	+2.7	+3.4
	LOC_Os10g25130	aminotransferase, classes I and II, domain		+3.3	+3.0	+3.2
	LOC_Os08g04540	decarboxylase		+2.6	+2.7	+3.3
	LOC_Os02g54254	lysine-ketoglutarate reductase/saccharopine dehydrogenase		+4.9	+4.8	+7.1
	LOC_Os03g63330	aspartokinase		+5.1	+3.5	+4.2
	LOC_Os03g18130	asparagine synthetase		+2.8	+2.7	+3.5

178	Adenosylhomocysteinase-like gij573961524	-2.2		-1.4
179	Adenosylhomocysteinase-like gij29367605	-1.6		-1.3
154	Ketol-Acid Reductoisomerase, chain A gij226887786	-1.7	-1.5	-1.4
209	B0616E02-H0507E05.5 gij116310889	+1.6		+1.5
173	Ferredoxin--nitrite reductase, chloroplastic gij75102800	-2.3	-1.3	-1.9
85	S-adenosylmethionine synthase (MAT) gij3024122	+2.0	+1.3	+1.7
180	S-adenosylmethionine synthase (MAT) gij17529621	-1.5		
Glycine cleavage system				
39	Aminomethyltransferase, mitochondrial gij357166054 (Blast)	-2.0	-1.5	-1.8
Lipid metabolism				
113	ATP-citrate synthase beta chain protein 1 gij357131914	+1.5		
Metabolism				
184	Formate-tetrahydrofolate ligase gij51536102	-3.3		-1.4
224	NADH-cytochrome b5 reductase gij514776060 (Blast)	+1.8		+1.3
211	Esterase_lipase region gij125526544	+2.4	+1.4	+1.7
17	Soluble inorganic pyrophosphatase 1, chloroplastic gij573922996	-1.7		
220	Oxidoreductase, aldo/keto reductase family gij413924063	-1.6	-1.5	-1.5
239	Nucleoside diphosphate kinase 4 gij573946659 (Blast)	+1.8	+1.4	+1.5
210	Pyridoxine 5'-phosphate (PNP) oxidase gij218199883	+1.8		
Modifying, storing and degrading proteins				
118	DnaK-type molecular chaperone gij46805772	-1.6	-1.4	
153	Chaperonin 60 subunit beta 1, chloroplastic, gij573946766	-1.7		-1.3
262	Alpha 4 subunit of 20S proteasome, gij9186906	+1.6		
91	Proteasome subunit beta type-4-like gij573957260	-1.9	-1.2	-1.5
104	DSBA-like thioredoxin domain containing protein gij195648623 (Blast)	+1.7	+1.5	+1.6
65	Thimet oligopeptidase-like gij573921154 (Blast)	-1.3		-1.5
130	Prolyl oligopeptidase family protein gij78708638	-1.6		
257	Cytosol alanyl aminopeptidase gij565830595	-2.1		
255	Peptidyl-prolyl cis-trans isomerase gij13486733	+1.8		

LOC_Os04g58390	allantoinase	-5.2	-5.3	-5.8
LOC_Os04g40040	copper/topaquinone oxidase family	-2.7	-3.1	-3.2
LOC_Os09g25810	nodulin	-2.4	-3.0	-3.6
LOC_Os06g46740	early nodulin 20 precursor	+6.9	+3.8	+9.0
LOC_Os07g49270	AMP deaminase	+2.6	+2.3	+3.4
LOC_Os04g14690	flavin-containing monooxygenase family protein	+2.3	+5.5	+4.5
LOC_Os07g34570	Putative thiamine biosynthesis protein	+10.9	+13.3	+14.5
LOC_Os11g19840	O-methyltransferase	+11.9	+15.5	+22.8
LOC_Os04g11970	O-methyltransferase	-3.5	-2.4	-2.7
Glycine cleavage system				
Lipid metabolism				
LOC_Os12g37260	lipoxygenase 2.1, chloroplast precursor	+11.9	+14.1	+12.4
LOC_Os02g37654	lecithin:cholesterol acyltransferase	-2.7	-3.2	-3.1
LOC_Os03g52860	lipoxygenase	+4.3	+3.6	+4.8
LOC_Os03g51010	Putative lipase	+2.9	+2.2	+3.1
LOC_Os08g37210	patatin	+6.5	+4.2	+4.7
LOC_Os07g34280	CXE carboxylesterase	+2.7	+3.7	+3.5
LOC_Os04g43200	Peroxygenase	+5.7	+5.3	+9.5
Metabolism				
LOC_Os01g54030	NADP-dependent malic enzyme	+6.4	+5.0	+12.6
LOC_Os12g12590	NADP-dependent oxidoreductase	+3.4	+2.8	+2.1
LOC_Os12g27350	10-deacetylbaicatin III 10-O-acetyltransferase	+10.0	+6.2	+7.5
LOC_Os12g27220	transferase family protein	+2.6	+3.1	+3.2
LOC_Os12g27254		+13.8	+15.3	+8.9
LOC_Os08g02030		+2.6	+2.9	+3.3
Modifying, storing and degrading proteins				
LOC_Os02g32520	Chaperone protein ClpD1, chloroplastic	+3.3	+2.7	+5.6
LOC_Os01g03310	BBT11 - Bowman-Birk type bran trypsin inhibitor	+5.1	+3.6	+4.9
LOC_Os01g03320	BBT12 - Bowman-Birk type bran trypsin inhibitor	+3.8	+5.2	+6.3
LOC_Os01g03360	BBT15 - Bowman-Birk type bran trypsin inhibitor	+3.7	+3.5	+5.1
LOC_Os01g04050	BBT12 - Bowman-Birk type bran trypsin inhibitor	+3.3	+3.9	+4.3
LOC_Os10g36070	LTPL155 - Protease inhibitor/seed storage/LTP family protein	+3.6	+3.1	+3.6
LOC_Os10g36090	LTPL156 - Protease inhibitor/seed storage/LTP family protein	+3.7	+3.5	+6.7
LOC_Os04g46810	LTPL120 - Protease inhibitor/seed storage/LTP family	-3.1	-3.7	-4.2
LOC_Os10g36100	LTPL157 - Protease inhibitor/seed storage/LTP family protein	+3.5	+2.8	+2.8

	(Blast)			
139	Xaa-Pro aminopeptidase 2 gj 52076499	-1.8		-1.5
245	Immunophilin/FKBP-type peptidyl-prolyl cis-trans isomerase-like gj 34393414	+1.5		
Signal transduction, stress, defense response, apoptosis				
84	Root specific pathogenesis-related protein 10 gj 38678114	+2.8	+1.9	+2.1
223	Germin-like protein 1 gj 573912743 (Blast)	+1.8	+1.8	+1.8
6	Abscisic stress ripening protein 2 gj 149391461	+2.1		+1.3
94	Small Ras-related GTP-binding protein gj 16903082	-2.3	-1.4	-1.4
21	Chitinase Chain A, Crystal Structure Of Class I gj 146386456	+6.4	+3.1	+3.4
152	Heat shock protein 90 gj 294717842	+2.2		
246	heat shock protein B, 16.9 kDa gj 312983209	+2.6	+1.4	+1.8
171	hsp70-Hsp90 organizing protein gj 721665923 (Blast)	-2.1	-1.4	-1.5
231	Thaumatococcus, pathogenesis-related family protein gj 115489698	+1.7	+1.2	+1.4

LOC_Os04g46820	LTPL121 - Protease inhibitor/seed storage/LTP family protein	-3.0	-2.9	-3.3
LOC_Os04g33920	LTPL102 - Protease inhibitor/ seed storage/LTP family protein	+2.9	+3.3	+3.3
LOC_Os03g52390	PIII1 - Proteinase inhibitor II family	+4.3	+3.6	+4.8
LOC_Os03g54130	cysteine protease 1	-7.4	-8.3	-12.5
LOC_Os04g01710	cysteine proteinase At4g11310	+2.9	+3.1	+3.4
LOC_Os09g39070	thiol protease SEN102	-2.8	-2.4	-3.7
LOC_Os09g19800	aminopeptidase	+7.1	+4.8	+6.0
LOC_Os01g60730	RING-H2 finger protein	+2.3	+3.6	+3.3
LOC_Os11g34460	OsFBO10 - F-box and other domain containing protein	+2.4	+5.7	+3.4
LOC_Os01g58280	Subtilisin-like serine protease	+3.8	+2.7	+6.2
LOC_Os01g42860	Subtilisin-chymotrypsin inhibitor	+16.8	+12.6	+31.7
LOC_Os12g36240	Subtilisin-chymotrypsin inhibitor CI-1B	+6.2	+6.4	+10.8
LOC_Os04g03810	OsSub38 - Putative Subtilisin	+2.5	+4.2	+3.2
LOC_Os01g06740	ribosome inactivating protein	+11.5	+9.5	+12.9
LOC_Os11g08100	eukaryotic aspartyl protease	+2.4	+3.0	+3.1
LOC_Os06g16640	carboxyl-terminal peptidase	+3.1	+2.9	+3.2
Signal transduction, stress, defense response, apoptosis				
LOC_Os01g14550	pathogen-related protein	+2.3	+3.3	+3.0
LOC_Os12g36880	pathogenesis-related Bet v I family protein	+4.2	+2.7	+4.9
LOC_Os01g32780	universal stress protein domain containing protein	+4.7	+4.3	+5.5
LOC_Os02g47840	universal stress protein domain containing protein	+2.4	+2.1	+3.3
LOC_Os10g39680	CHIT14 - Chitinase family protein precursor	+3.6	+3.1	+4.8
LOC_Os04g41620	CHIT2 - Chitinase family protein precursor	+6.4	+5.6	+5.8
LOC_Os04g41680	CHIT3 - Chitinase family protein precursor	+3.1	+3.2	+3.9
LOC_Os05g33140	CHIT5 - Chitinase family protein precursor	+3.0	+2.2	+3.1
LOC_Os06g51050	CHIT7 - Chitinase family protein precursor	+6.4	+6.8	+8.0
LOC_Os06g51060	CHIT8 - Chitinase family protein precursor	+4.6	+4.1	+5.1
LOC_Os04g41640	HEV2 - Hevein family protein precursor	+3.2	+2.8	+3.2
LOC_Os11g37940	WIP2 - Wound-induced protein precursor	+5.5	+4.2	+5.6
LOC_Os11g37950	WIP3 - Wound-induced protein precursor	+5.4	+3.4	+6.6
LOC_Os11g37970	WIP5 - Wound-induced protein precursor	+5.6	+4.9	+7.2
LOC_Os04g01740	Heat shock protein	+2.8	+2.2	+3.2
LOC_Os03g15960	hsp20/alpha crystallin family protein	+3.1	+2.4	+3.1
LOC_Os03g16920	Heat shock cognate 70 kDa protein	+2.7	+2.3	+3.7
LOC_Os12g43450	Thaumatococcus	+4.0	+3.9	+4.5
LOC_Os12g43380	Thaumatococcus	+22.7	+7.4	+23.3

					LOC_Os12g43410		+3.1	+3.4	+2.7
					LOC_Os03g46070		+4.1	+3.0	+4.0
249	SalT gene product gjl2072553	+2.3		+2.2	LOC_Os11g26780	dehydrin	+6.0	+4.1	+14.4
250		+2.3			LOC_Os11g26790		+11.2	+6.1	+12.7
186	Monocopper oxidase-like protein SKU5-like gjl573959489 (Blast)	-1.6		-1.3	LOC_Os12g38170	osmotin	+3.1	+2.7	+3.8
					LOC_Os03g17790	OsRC12-5 - Putative low temperature and salt responsive protein	+4.2	+3.6	+5.4
					LOC_Os01g28450	SCP-like extracellular protein	+21.9	+7.0	+23.9
					LOC_Os01g28500		+5.3	+4.0	+4.4
					LOC_Os10g11500		+3.9	+3.2	+2.7
					LOC_Os07g03279		+3.7	+3.2	+2.9
					LOC_Os07g03319		+8.6	+8.5	+10.3
					LOC_Os07g03368		+3.6	+3.2	+2.7
					LOC_Os07g03409		+6.3	+5.3	+6.0
					LOC_Os07g03458		+3.7	+3.1	+3.0
					LOC_Os07g03499		+6.3	+5.3	+6.1
					LOC_Os07g03730		+12.3	+6.8	+9.2
					LOC_Os07g03288		+24.7	+13.2	+19.7
					LOC_Os07g03377		+24.7	+13.2	+19.7
					LOC_Os07g03467		+24.5	+13.6	+18.4
					LOC_Os07g25050		+2.6	+3.5	+2.4
					LOC_Os07g25060		+3.5	+4.7	+3.1
					LOC_Os07g24830		+5.0	+7.1	+4.3
					LOC_Os10g09850	EF hand family protein	+3.6	+3.1	+5.0
					LOC_Os01g26270	OsWAK7 - OsWAK receptor-like protein kinase	-3.0	-2.4	-2.8
					LOC_Os08g10250	SHR5-receptor-like kinase	-4.6	-3.9	-3.7
					LOC_Os08g10300	SHR5-receptor-like kinase	+2.3	+3.2	+2.7
					LOC_Os07g43570	DUF26 kinase	+3.2	+4.7	+5.5
					LOC_Os11g31540	Brassinosteroid insensitive 1-associated receptor kinase 1	+3.2	+2.5	+4.5
					LOC_Os01g62900	amino acid kinase	+3.5	+3.4	+5.1
					LOC_Os02g02780	protein kinase family protein	+4.0	+6.8	+5.0
					LOC_Os04g56430	cysteine-rich receptor-like protein kinase	+7.8	+5.6	+9.7
					LOC_Os07g36544	serine/threonine-protein kinase receptor	+2.4	+2.6	+3.9
					LOC_Os06g48300	protein phosphatase 2C	+10.5	+12.5	+20.6
					LOC_Os10g41980	RALFL26 - Rapid Alkalinization Factor RALF family	+9.5	+5.9	+8.4
					LOC_Os06g29730	RALFL28 - Rapid Alkalinization Factor RALF	+6.6	+6.1	+9.3
					LOC_Os11g02240	CAMK includes calcium/calmodulin dependent protein	+5.7	+4.2	+7.3
					LOC_Os01g24710	jacalin-like lectin domain containing protein	+3.3	+3.5	+4.6
					LOC_Os12g14440		+97.0	+86.7	+94.7
					LOC_Os12g09700		+3.9	+3.8	+3.9
					LOC_Os04g38360	wound/stress protein	+7.1	+6.1	+4.6
					LOC_Os05g46480	late embryogenesis abundant protein, group 3	+10.8	+5.9	+16.6

Glyoxalase system				
96	Lactoylglutathione lyase (Glyoxalase I) gi 341870587	-1.2	-1.4	-1.6
Phenylpropanoids metabolism and related proteins				
160	Phenylalanine/tyrosine ammonia-lyase gi 514715067	-4.4	-2.2	-2.3
164	Phenylalanine ammonia-lyase gi 573919867 (Blast)	-2.0	-1.5	-1.7
185				-1.6
Terpene biosynthesis				
Antioxidation				
3	Superoxide dismutase [Cu-Zn] gi 115473931	+2.0	+1.6	+1.8
247	Superoxide dismutase [Cu-Zn] gi 42408425	+1.9		+1.4
5	Superoxide dismutase gi 538430	+1.7		
213	Ascorbate_peroxidase gi 115458488	+1.5		
205	L-ascorbate peroxidase 1 gi 158512874 (Blast)	+1.8	+1.4	+1.4
208		+1.6	+1.2	+1.3
16	IN2-1 protein (Glutathione S-transferase GSTZ5) gi 108707532	-2.0		
241	GSH-dependent dehydroascorbate reductase 1 gi 6939839	+1.5	+1.3	+1.4
244	Peroxiredoxin-2F, mitochondrial-like gi 573912657	+1.9	+1.3	+1.7

LOC_Os03g47610	thiamine biosynthesis protein thiC	+3.8	+5.0	+7.0
LOC_Os11g37200	transmembrane BAX inhibitor motif-containing protein	+3.2	+2.3	+3.0
LOC_Os12g29400	GRAM domain containing protein	+2.8	+3.0	+4.8
LOC_Os09g08130	indole-3-glycerol phosphate synthase	+3.0	+3.3	+4.0
LOC_Os05g39250	Putative cold regulated protein	+4.7	+2.9	+4.8
LOC_Os03g48750	Germin-like protein 3-3	+6.8	+8.1	+10.6
LOC_Os03g48780	Germin-like protein 3-6	+7.7	+6.7	+7.1
LOC_Os06g19300	cadmium tolerance factor	+2.7	+3.2	+2.4
LOC_Os09g28160	Putative phosphate transport protein	+2.4	+3.1	+4.2
LOC_Os03g57640	gibberellin receptor GID1L2	+5.6	+6.8	+8.9
Glyoxalase system				
Phenylpropanoids metabolism and related proteins				
LOC_Os01g58100	polyphenol oxidase	+3.5	+4.1	+4.3
LOC_Os10g18870	dirigent	-19.0	-17.0	-17.2
LOC_Os10g18820		-3.4	-3.5	-3.3
LOC_Os01g13610	isoflavone reductase homolog IRL	+3.3	+3.3	+3.0
LOC_Os10g40934	flavonol synthase/flavanone 3-hydroxylase	+2.4	+2.8	+3.7
LOC_Os12g17160	flavonol sulfotransferase	+2.7	+2.1	+3.0
LOC_Os07g11440	chalcone synthase	+4.4	+4.0	+2.8
LOC_Os09g17560	Flavonoid 7-O-methyltransferase-like	+2.2	+2.5	+3.4
Terpene biosynthesis				
LOC_Os04g01810		+2.4	+1.7	+3.4
LOC_Os04g27430		+11.9	+10.2	+12.4
LOC_Os04g27670	terpene synthase	+4.0	+4.0	+6.8
LOC_Os08g07080		+4.3	+3.5	+3.3
LOC_Os08g04500		-2.3	-3.4	-3.2
LOC_Os04g10060	ent-kaurene synthase	+2.7	+3.1	+3.6
LOC_Os06g47130	Putative CLB1 protein	+3.3	+3.0	+4.3
Antioxidation				
LOC_Os02g53400	thioredoxin	+3.3	+5.7	+4.8
LOC_Os01g22249	Peroxidase precursor	-3.2	-1.9	-3.1
LOC_Os03g25300		-2.7	-3.2	-4.8
LOC_Os06g35520		+2.2	+3.2	+2.1
LOC_Os07g01410		-3.6	-3.3	-3.6
LOC_Os07g01420		-2.5	-2.7	-3.4

(Blast)				
Cell structure and biogenesis				
233	40S ribosomal protein S3-3-like gij573953785 (Blast)	+2.1	+1.3	+1.7
229	40S ribosomal protein S5-like gij573961547 (Blast)			+1.6
230	40S ribosomal protein S7-like gij514816665	+2.8	+2.0	+2.4
226	60S acidic ribosomal protein P0-like gij573953644	+2.7	+1.5	+1.6
4	Actin-depolymerizing factor 4 gij573926554 (Blast)	+2.0		+1.3
206	Ribosome-recycling factor, chloroplastic-like gij573952885 (Blast)	+1.3	+1.3	+1.5
147	Cell division control protein 48-A gij15232776	-1.7		
199	Alpha tubulin-1D gij90289618	-1.5	-1.4	
59	Alanyl-tRNA synthetase, mitochondrial gij110288715	-1.7		
134	Elongation factor gij119395218	-2.5		-1.9
133	Elongation factor gij119395216	-3.0		-1.7
Transport				
102	Mitochondrial outer membrane protein porin 1 gij573956673	+2.2		
232	Porin-like protein gij115451401	+3.6	+1.7	+2.1

Cell structure and biogenesis				
LOC_Os11g32880	DEAD-box ATP-dependent RNA helicase	+4.9	+4.2	+6.6
LOC_Os01g06310	glycine-rich cell wall structural protein	+4.6	+3.2	+4.2
LOC_Os09g29710	beta-expansin	+3.0	+2.5	+5.3
LOC_Os03g60580	actin-depolymerizing factor	+9.3	+10.2	+15.4
Transport				
LOC_Os01g43460	C4-dicarboxylate transporter/malic acid transport protein	+2.8	+2.6	+3.8
LOC_Os01g36720	Probable high-affinity nitrate transporter 2.4	-5.2	-5.4	-8.5
LOC_Os02g02170	High-affinity nitrate transporter 2.1	-9.9	-12.0	-8.8
LOC_Os02g38230	high affinity nitrate transporter	-5.8	-7.0	-6.1
LOC_Os10g20470	MATE efflux family protein	+2.3	+2.4	+4.1
LOC_Os04g30490	MATE efflux family protein	+2.7	+3.2	+2.5
LOC_Os10g30770	inorganic phosphate transporter	+5.6	+2.2	+4.9
LOC_Os04g10690	inorganic phosphate transporter	+4.4	+2.7	+5.6
LOC_Os04g51830	OshKT1	-3.6	-1.9	-3.6
LOC_Os06g48810	OshKT2 1 - Na+ transporter	-7.0	-4.5	-6.8
LOC_Os10g21590	transporter family protein	+3.1	+5.1	+5.3
LOC_Os04g13210	multidrug resistance-associated protein	+3.4	+3.8	+3.9
LOC_Os02g03900	metal transporter Nramp6	+3.8	+3.3	+2.7
LOC_Os01g50100	ABC transporter, ATP-binding protein	+3.1	+5.0	+4.3
LOC_Os08g29570	ABC transporter G family member 44	+2.4	+2.1	+3.4
LOC_Os07g18874	ABC transporter family protein-like	-3.4	-4.5	-3.4
LOC_Os07g33780	ABC transporter G family member 43	+2.4	+2.3	+3.0
LOC_Os03g11900	transporter family protein	+2.3	+2.4	+3.4
LOC_Os02g44080	aquaporin protein	-3.1	-3.9	-4.6
LOC_Os04g44060	aquaporin protein	-2.7	-3.1	-2.8
LOC_Os04g38680	transmembrane amino acid transporter protein	+2.7	+1.9	+3.2
LOC_Os01g50460	Bidirectional sugar transporter SWEET2b	-3.8	-4.2	-4.5
LOC_Os12g33300	integral membrane protein DUF6 containing protein	+4.8	+5.8	+5.6
LOC_Os12g31860	ureide permease	+4.6	+4.8	+5.0
LOC_Os02g09810	Putative amino acid transporter A1	+3.7	+3.9	+7.2
LOC_Os09g31478	auxin efflux carrier component	+3.7	+4.7	+5.2
LOC_Os09g29660	white-brown complex homolog protein 11	+2.6	+3.0	+3.3
LOC_Os06g03540	oligopeptide transporter	-4.0	-2.8	-3.9

Control of gene expression				
222	Methionine adenosyltransferase 2 gj 75308025	+3.0		
259	Eukaryotic translation initiation factor 3 subunit A gj 514781216 (Blast)	+3.1		+1.5
221	chloroplast stem-loop binding protein of 41 kDa b, chloroplastic-like gj 573963758	-1.4	-1.3	-1.6
RNA binding				
Transcription factors				
Unknown				
254	Expressed protein gj 108707969	+1.6		
82	NON-significant identification	-1.7	-1.6	-1.7
125	NON-significant identification	-2.1		-1.8
135	NON-significant identification			-1.5
144	NON-significant identification	+1.7		
145	NON-significant identification	-1.5		
146	NON-significant identification	-1.8		
150	NON-significant identification	-1.9	-1.2	
156	NON-significant identification	-1.8		-1.6
157	NON-significant identification	-1.6		
158	NON-significant identification	-2.5		-1.9
162	NON-significant identification	-3.2	-1.6	-2.0
166	NON-significant identification	-2.0		
172	NON-significant identification	-2.1		-1.4
174	NON-significant identification	-2.8		-1.6
175	NON-significant identification	-1.5		

LOC_Os06g07200	syntxin	+2.4	+3.0	+2.5
Control of gene expression				
LOC_Os05g31020	peptide chain release factor subunit 1	+3.8	+3.1	+4.3
LOC_Os02g36590	CPuORF19 - conserved peptide uORF	-4.0	-3.0	-3.9
RNA binding				
LOC_Os02g33610	Putative metallo beta subunit lactamase	+2.8	+3.2	+4.7
LOC_Os09g36680	Drought-induced S-like ribonuclease	+47.8	+39.7	+26.0
LOC_Os09g36700	Putative RNase S-like protein	+16.5	+17.7	+11.8
Transcription factors				
LOC_Os01g01840	helix-loop-helix DNA-binding domain containing protein	+7.1	+5.1	+6.3
LOC_Os11g02540	OsWRKY50 - Superfamily of TFs having WRKY and zinc finger domains	+6.9	+8.3	+8.1
LOC_Os12g02450	OsWRKY64 - Superfamily of TFs having WRKY and zinc finger domains	+5.6	+5.8	+6.0
LOC_Os12g02470	OsWRKY65 - Superfamily of TFs having WRKY and zinc finger domains	+7.0	+7.5	+6.0
LOC_Os05g50340	MYB family transcription factor	-3.1	-4.5	-4.1
LOC_Os06g45140	bZIP family transcription factor	-2.9	-2.7	-3.2
LOC_Os05g45410	Heat stress transcription factor A-4d	+2.0	+1.8	+3.1
Unknown				
LOC_Os05g49300	Putative iron-sulfur cluster assembly complex protein	+3.5	+2.4	+3.4
LOC_Os01g06890	leucine-rich repeat family protein	+4.7	+2.1	+4.9
LOC_Os10g34930	Putative basic secretory protein	+3.0	+2.7	+3.1
LOC_Os10g05820	POEI5 - Pollen Ole e I allergen and extensin family protein	+2.2	+2.8	+3.2
LOC_Os11g45990	von Willebrand factor type A domain containing protein	+4.1	+4.2	+4.9
LOC_Os11g46000	von Willebrand factor type A domain containing protein	+3.6	+3.1	+3.0
LOC_Os06g38080	von Willebrand factor type A domain containing protein	+3.0	+2.8	+2.2
LOC_Os04g51796	DNA repair ATPase-related	+2.8	+2.3	+3.2
LOC_Os05g28770	GCRP9 - Glycine and cysteine rich family protein	-2.3	-2.1	-3.3
LOC_Os05g29710	RING-H2 finger protein	+2.5	+3.2	+3.5
LOC_Os05g36310	zinc finger, C3HC4 type domain containing protein	+2.9	+2.6	+3.1
LOC_Os03g28990	zinc finger family protein	+2.4	+4.2	+2.9
LOC_Os07g09420	ATPase	+2.8	+2.3	+3.4
LOC_Os07g48800	VQ domain containing protein	+3.9	+3.4	+3.5
LOC_Os08g30020	membrane protein	-3.9	-3.5	-3.7
LOC_Os09g31380	jmjC domain-containing protein 5	+2.2	+4.0	+2.7

176	NON-significant identification	+1.6		
177	NON-significant identification	-1.7		-1.2
187	NON-significant identification	-2.3		
191	NOT possible to pick from the gel	+1.6	+1.4	
192	NOT possible to pick from the gel	+2.0	+1.5	+1.6
193	NOT possible to pick from the gel	+1.6		
197	NON-significant identification	+1.7		
203	NON-significant identification	+1.7	+1.4	+1.4
212	NON-significant identification	+1.8	+1.6	+1.6
215	NON-significant identification	+1.4		+1.6
216	NON-significant identification	+1.3		+1.5
217	NON-significant identification	+2.6	+1.7	+1.7
225	NOT possible to pick from the gel	+2.5	+1.3	+1.5
228	NON-significant identification	+2.8		+2.0
234	NOT possible to pick from the gel	+1.8	+1.2	+1.2
235	NON-significant identification	+1.7		
238	NON-significant identification	+1.9		
240	NON-significant identification	+1.6		
242	NON-significant identification			+1.6
248	NOT possible to pick from the gel	+1.6		+1.5
251	NOT possible to pick from the gel	+1.6		
252	NOT possible to pick from the gel	+1.8		
253	NOT possible to pick from the gel	+2.3	+1.7	+1.7
256	NON-significant identification	+1.5	+1.3	+1.4
258	NOT possible to pick from the gel	+1.9	+1.2	+1.5
260	NOT possible to pick from the gel	+2.9		+2.0
261	NON-significant identification		-1.5	

LOC_Os01g67320	expressed protein	-2.7	-3.9	-2.6
Os01g0386500	Os01g0386500 mRNA	+20.0	+13.9	+21.8
Os01g0661800	Os01g0661800 mRNA	+4.7	+3.0	+5.2
Os10g0569600	Os10g0569600 mRNA	+4.5	+4.1	+3.5
Os10g0450900	Os10g0450900 mRNA	+4.1	+3.7	+4.5
Os01g0740700	Os01g0740700 mRNA	+2.4	+2.3	+3.4
LOC_Os11g10590	hypothetical protein	+12.0	+10.7	+10.0
LOC_Os11g13750	expressed protein	-4.5	-3.0	-5.5
LOC_Os01g71624	expressed protein	+11.6	+10.1	+18.5
Os11g0303800	Os11g0303800 mRNA	+7.0	+8.6	+11.9
Os12g0257600	Os12g0257600 mRNA	+10.4	+8.5	+12.7
Os12g0431700	Os12g0431700 mRNA	+3.5	+4.7	+4.0
Os12g0440300	Os12g0440300 mRNA	+3.4	+2.0	+3.1
LOC_Os12g08700	expressed protein	+2.6	+2.2	+3.2
LOC_Os12g11990	expressed protein	+2.5	+3.5	+2.5
Os04g0650700	Os04g0650700 mRNA	-3.0	-4.9	-4.2
LOC_Os05g49940	expressed protein	+2.3	+2.1	+3.1
LOC_Os05g29160	hypothetical protein	+2.5	+2.6	+3.8
LOC_Os05g29680	hypothetical protein	+3.9	+4.8	+3.7
LOC_Os06g04480	expressed protein	+3.3	+2.3	+3.5
LOC_Os06g28630	expressed protein	-5.2	-4.0	-6.7
LOC_Os06g39120	expressed protein	+8.5	+8.5	+7.7
LOC_Os06g05420	expressed protein	+3.6	+4.7	+5.6
LOC_Os12g32610	expressed protein	+3.0	+3.2	+4.0
Os06g0199100	Os06g0199100 mRNA	+3.0	+2.7	+6.1
LOC_Os07g19540	expressed protein	+4.7	+4.2	+5.4
Os07g0431000	Os07g0431000 mRNA	+6.8	+11.7	+8.4
Os12g0222000	Os12g0222000 mRNA	+7.1	+4.8	+8.6
Os07g0418600	Os07g0418600 mRNA	+3.9	+5.6	+5.5
Os07g0457800	Os07g0457800 mRNA	+4.6	+5.0	+8.7
Os07g0468200	Os07g0468200 mRNA	+3.1	+3.0	+4.4
Os07g0678400	Os07g0678400 mRNA	-3.1	-3.1	-3.2
LOC_Os08g32930	expressed protein	+3.3	+4.2	+5.1
LOC_Os08g31860	expressed protein	+3.4	+3.0	+3.2
LOC_Os09g02180	expressed protein	+3.5	+2.5	+4.4
LOC_Os03g04080	expressed protein	+2.8	+2.1	+4.5

LOC_Os06g38660	expressed protein	+3.2	+3.9	+3.9
LOC_Os09g23590	expressed protein	+3.3	+2.4	+4.6
Os09g0513500	Os09g0513500 mRNA	+4.9	+3.6	+3.2
Os01g0124400	Os01g0124400 mRNA	+4.6	+3.2	+5.9
Os01g0695800	Os01g0695800 mRNA	+3.1	+4.3	+3.6
Os01g0944900	Os01g0944900 mRNA	+4.8	+3.3	+4.6
Os02g0155400	Os02g0155400 mRNA	+2.6	+3.6	+3.8
Os07g0418700	Os07g0418700 mRNA	+5.8	+9.3	+7.9
Os10g0515900	Os10g0515900 mRNA	+5.6	+11.2	+6.0
Os12g0562000	Os12g0562000 mRNA	+4.8	+3.9	+6.5
Os02g0494300	Os02g0494300 mRNA	+7.0	+5.1	+9.9
Os03g0120600	Os03g0120600 mRNA	+9.8	+11.1	+12.1
Os04g0600200	Os04g0600200 mRNA	+2.7	+2.8	+3.7
LOC_Os10g23240	hypothetical protein	+11.7	+9.0	+15.1
LOC_Os12g11550	hypothetical protein	+4.5	+3.5	+4.4
LOC_Os12g11620	hypothetical protein	+4.4	+6.0	+5.2
LOC_Os12g17804	hypothetical protein	+3.0	+2.0	+3.3
LOC_Os07g43604	hypothetical protein	+3.2	+1.9	+3.3

Differentially abundant spots with a fold change ≥ 1.5 at least in one of the tested circumstances were considered. Differentially expressed transcripts in the three situations and with a fold change ≥ 3 at least in one of the tested conditions were considered. Highlighted in **red** are the situations where similar identifications were found in proteomics and microarrays. **Green** means that the identification corresponds to a protein which is “non-allergen” as predicted by AlgPred software hybrid approach. **Orange** represents “allergen” proteins as predicted by AlgPred hybrid approach.