Supplemental information

Mediator phosphorylation prevents stress response transcription during non-stress conditions

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I. Supplemental Figures and Tables

Supplemental Figure S1: Comparison of phosphosite mutants *D7P* and *D30P* to the Med15 knock-out.

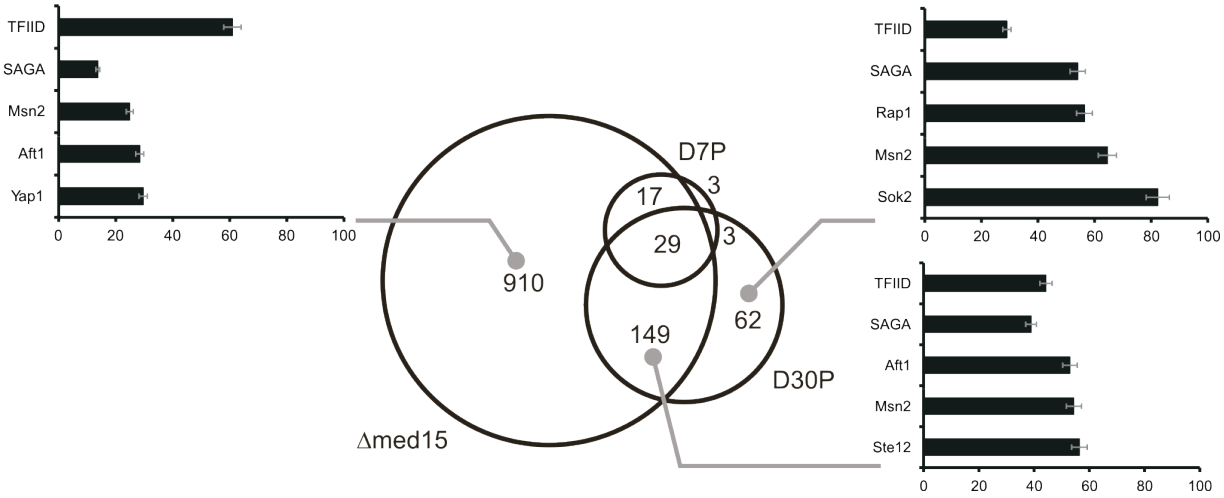

Figure S1: The *D30P* phosphosites act on different genes as *Δmed15*. Venn diagram of the induced datasets of *D7P*, *D30P* and *Δmed15* under normal growth conditions. The mutation of the 30 phosphosites induce expression of 62 genes, which are not induced in the Med15 knock-out. Bar plots represent the relative enrichment (fisher's exact test) of transcription factor targets from a total set of 110 transcription factors (1,2) and TFIID, SAGA (3). The length of the bars represent the percentage of genes in the subset regulated by the respective factor.

Supplemental Figure S2: Individual contribution of datasets to the response to osmotic stress

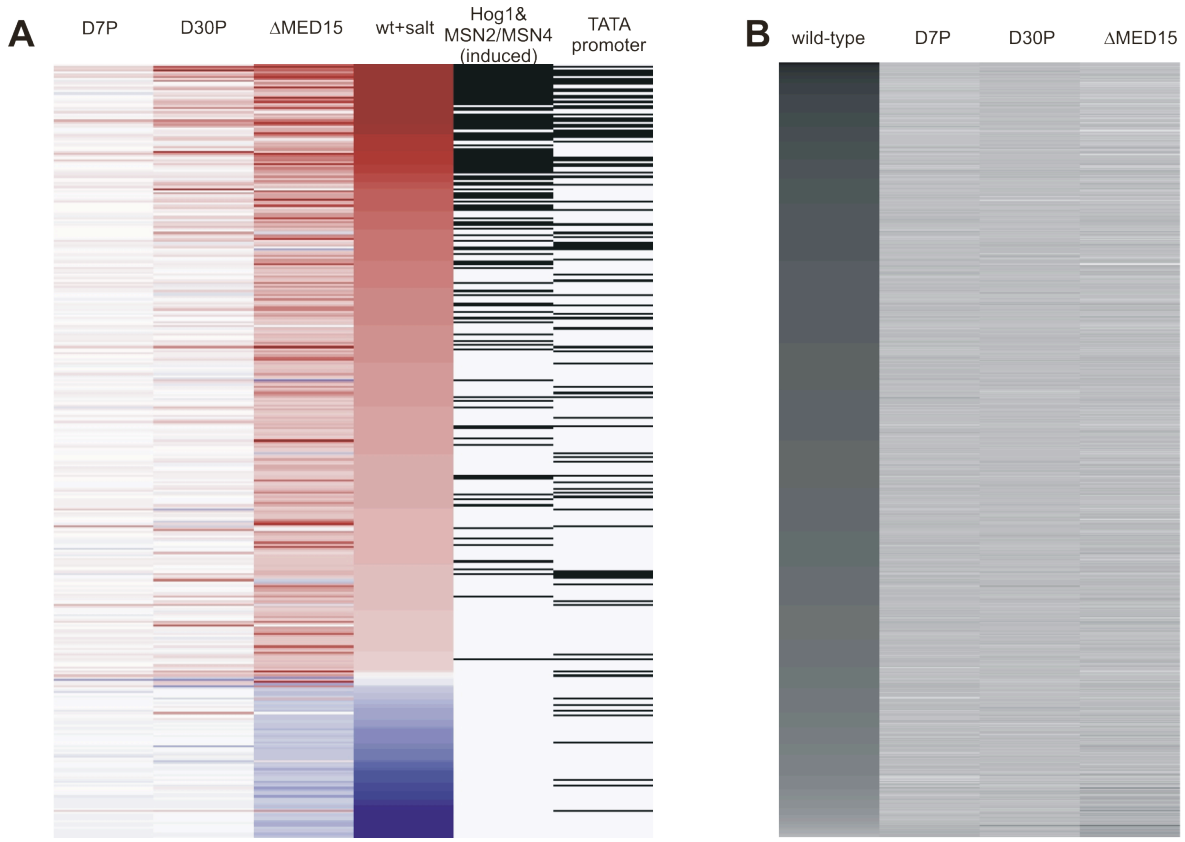

Figure S2: Linear regression analysis: Effect of Med15 phosphosite mutants on osmotic stress response. **A)** Global changes in labeled mRNA expression under normal conditions and response to osmotic stress. Heatmap illustrating the effect of the mutated phosphosites on global gene expression (labeled mRNA fraction, 6 min labeling time). The horizontal lines represent genes, which are differentially expressed at least 1.5 fold in at least one of the datasets. Red color indicate genes, which are relative induced compared to the wild-type control. Blue color indicate relative repressed genes. Black bars mark the genes, which are regulated by Msn2/4 (p-value: 6.32E-42) (second right column) or TATA containing promoter genes (p-value: 6.25E-11) (25) (right column). **B)** linear regression analysis to decipher the influences of the mutation (*D7P* & *D30P*) and *Δmed15* strains under non-stress and salt stress conditions.

Supplemental Table S1: Phospho peptides from Mediator identified by mass spectrometry

Mediator subunit	Phosphorylated amino acid	Relative position	Phospho-peptide sequence	Number of phospho (STY)	pSTY-class	Localization p-value	PTM Score	Literature (5,6)
Med1	148	S	S(1)LDSSNASFNNQGK	1	I	0,999997	256,36	
Med1	151	S	S(0.002)LDS(0.869)S(0.129)NAS(0.001)FNNQGK	1	I	0,868889	256,36	
Med1	152	S	S(0.001)LDS(0.018)S(0.981)NAS(1)FNNQGK	2	I	0,980961	278,37	
Med1	155	S	SLDSSNAS(1)FNNQGK	1	I	0,999764	256,36	Albuquerque, 2008 (7)
Med1	363	S	LVS(0.069)T(0.069)PS(0.315)S(0.315)NS(0.315)NS(0.458) S(0.458)ELEPDYQAPFSTSTK	2	II	0,315399	154,07	
Med1	364	S	LVS(0.069)T(0.069)PS(0.315)S(0.315)NS(0.315)NS(0.458) S(0.458)ELEPDYQAPFSTSTK	2	II	0,315399	154,07	
Med1	366	S	LVS(0.001)T(0.003)PS(0.02)S(0.142)NS(0.793)NS(0.02) S(0.02)ELEPDYQAPFSTSTK	1	I	0,793442	225,11	
Med1	368	S	LVS(0.069)T(0.069)PS(0.315)S(0.315)NS(0.315)NS(0.458) S(0.458)ELEPDYQAPFSTSTK	2	II	0,458234	154,07	
Med1	369	S	LVS(0.021)T(0.07)PS(0.281)S(0.281)NS(0.309)NS(0.313) S(0.717)ELEPDY(0.005)QAPFSTSTK	2	II	0,717215	154,07	
Med1	389	S	NS(0.077)S(0.855)T(0.059)S(0.008)NTEPIPR	1	I	0,855457	139,39	
Med1	391	S	NS(0.025)S(0.116)T(0.096)S(0.382)NT(0.382)EPIPR	1	II	0,381914	139,39	
Med1	393	T	NS(0.025)S(0.116)T(0.096)S(0.382)NT(0.382)EPIPR	1	II	0,381914	139,39	
Med1	404	S	HGS(1)VVEASR	1	I	1	149,55	Albuquerque, 2008 Smolka, 2007 (7,8)
Med1	419	S	S(1)KRPS(0.999)IT(0.001)EAMMLK	2	I	1	238,08	
Med1	423	S	RPS(0.998)IT(0.002)EAMMLK	1	I	0,998231	212,14	Li, 2007 Soufi, 2009 (9,10)
Med2	6	S	VVQNS(0.989)PVS(0.002)S(0.009)VHTANFSER	1	I	0,989191	298,44	Albuquerque, 2008 (7)
Med2	9	S	VVQNS(0.206)PVS(0.703)S(0.26)VHT(0.831)ANFS(0.001) ER	2	II	0,702841	243,05	
Med2	10	S	VVQNS(0.985)PVS(0.154)S(0.859)VHT(0.002)ANFSER	2	I	0,858722	243,05	
Med2	13	T	VVQNS(0.206)PVS(0.703)S(0.26)VHT(0.831)ANFS(0.001) ER	2	I	0,830722	243,05	
Med2	208	S	ENYQELGSLQSSSQTQLENANAANNGAAFS(0.999)PLT (0.001)TTR	1	I	0,999232	235,08	Van de Peppel, 2005 Hallberg, 2004 (11,12)
Med2	266	S	GFDDNDS(0.995)GNNY(0.005)NDINISSIENNINNNINST K	1	I	0,995136	346,28	

Med3	189	S	S(0.796)GS(0.193)T(0.011)MGTPTVHNSTAAAPIAAPK	1	I	0,795633	246,24	
Med3	191	S	S(0.09)GS(0.807)T(0.104)MGTPTVHNSTAAAPIAAPK	1	I	0,806632	246,24	
Med3	192	T	S(0.145)GS(0.799)T(0.526)MGT(0.526)PT(0.004)VHNSTA AAPIAAPK	2	II	0,525873	174,85	
Med3	195	T	S(0.02)GS(0.024)T(0.024)MGT(0.925)PT(0.007)VHNSTAA APIAAPK	1	I	0,924891	246,24	
Med3	197	T	S(0.145)GS(0.173)T(0.035)MGT(0.035)PT(0.611)VHNSTA AAPIAAPK	1	II	0,611461	246,24	

Med4	18	S	S(0.73)S(0.131)S(0.131)VS(0.007)LVAEATSNTNSEDK	1	II	0,729971	269,14	
Med4	19	S	S(0.094)S(0.764)S(0.118)VS(0.024)LVAEATSNTNSEDK	1	I	0,764367	269,14	
Med4	20	S	S(0.597)S(0.597)S(0.597)VS(0.189)LVAEAT(0.01)S(0.003) NT(0.003)NS(0.003)EDK	2	II	0,596842	234,73	
Med4	22	S	S(0.334)S(0.334)S(0.333)VS(0.998)LVAEATSNTNSEDK	2	I	0,99797	234,73	
Med4	222	S	IPGEEVEETEVPTVPPS(0.5)QS(0.5)EEQK	1	II	0,499999	161,68	Albuquerque, 2008 (7)
Med4	224	S	IPGEEVEETEVPTVPPS(0.163)QS(0.837)EEQK	1	I	0,837069	161,68	
Med4	237	T	EGT(1)PKTDSFIFDGTAK	1	I	0,99957	246,71	Albuquerque, 2008 (7) Guidi, 2004 (13) Li, 2007 (9) Chi, 2007 (14) Smolka, 2007 (8) Hallberg, 2004 (12) Soufi, 2009 (10)
Med4	240	T	KEGT(0.004)PKT(0.969)DS(0.026)FIFDGT(0.001)AK	1	I	0,968929	246,71	
Med4	242	S	T(0.019)DS(0.981)FIFDGTAK	1	I	0,980673	246,71	Albuquerque, 2008 (7) Chi, 2007 (14) Smolka, 2007 (8) Soufi, 2009 (10)
Med4	248	T	KEGT(0.001)PKTDSFIFDGT(0.999)AK	1	I	0,998687	246,71	

Med5	64	T	ASDLVDT(0.978)PS(0.021)NNTAATADTTHLHEALDIVC SDFVK	1	I	0,978365	275,96	Albuquerque, 2008 (7)
Med5	66	S	KAS(0.001)DLVDT(0.499)PS(0.499)NNT(0.001)AATADT THLHEALDIVCSDFVK	1	II	0,498934	275,96	
Med5	257	S	DS(0.031)T(0.031)NEFVGS(0.773)PS(0.092)LT(0.031) S(0.031)PQY(0.01)IPSPLSSTKPPGSVNSAAK	1	I	0,772976	253,18	
Med5	259	S	DS(0.024)T(0.024)NEFVGS(0.183)PS(0.587)LT(0.069) S(0.069)PQY(0.024)IPS(0.005)PLS(0.004)S(0.005)T(0.005) KPPGS(0.001)VNS(0.001)AAK	1	II	0,586881	253,18	
Med5	262	S	DS(0.001)T(0.001)NEFVGS(0.977)PS(0.147)LT(0.147) S(0.725)PQY(0.002)IPSPLSSTKPPGSVNSAAK	2	I	0,724792	215,35	Albuquerque, 2008 (7)
Med5	268	S	DSTNEFVGSPSLTSPQY(0.001)IPS(0.967)PLS(0.012) S(0.01)T(0.01)KPPGSVNSAAK	1	I	0,966826	253,18	Albuquerque, 2008 (7)
Med5	271	S	DSTNEFVGS(0.952)PS(0.051)LT(0.147)S(0.147) PQY(0.146)IPS(0.573)PLS(0.662)S(0.16)T(0.16) KPPGS(0.001)VNSAAK	3	II	0,662499	195,1	

Med5	278	S	DS(0.033)T(0.033)NEFVGS(0.429)PS(0.429)LT(0.036)S(0.034)PQY(0.018)IPS(0.071)PLS(0.179)S(0.179)T(0.18)KPPGS(0.186)VNS(0.192)AAK	2	III	0,185502	215,35	
Med5	281	S	DS(0.033)T(0.033)NEFVGS(0.429)PS(0.429)LT(0.036)S(0.034)PQY(0.018)IPS(0.071)PLS(0.179)S(0.179)T(0.18)KPPGS(0.186)VNS(0.192)AAK	2	III	0,191816	215,35	
Med5	682	S	YYLEESNVNDS(0.996)DMLT(0.004)K	1	I	0,995628	286,16	
Med5	838	S	VQSQS(0.002)NY(0.002)GIY(0.044)S(0.476)S(0.476)DAQGDPNLEPLIAK	1	II	0,476154	256,79	
Med5	839	S	VQSQS(0.002)NY(0.002)GIY(0.044)S(0.476)S(0.476)DAQGDPNLEPLIAK	1	II	0,476154	256,79	
Med5	1014	S	NDS(1)AEVRQETQPK	1	I	1	154,46	

Med6	225	S	VPTDTSTTATAATNGNNAGGGS(1)NK	1	I	1	341,32	
Med6	228	S	S(0.181)S(0.181)VRPT(0.181)GGANMAT(0.184)VPS(0.187)T(0.187)T(0.187)NVNMT(0.23)VNT(0.228)MGT(0.242)GGQT(0.011)IDNGT(0.002)GR	2	III	0,181253	209,5	
Med6	229	S	S(0.181)S(0.181)VRPT(0.181)GGANMAT(0.184)VPS(0.187)T(0.187)T(0.187)NVNMT(0.23)VNT(0.228)MGT(0.242)GGQT(0.011)IDNGT(0.002)GR	2	III	0,181253	209,5	
Med6	233	T	S(0.181)S(0.181)VRPT(0.181)GGANMAT(0.184)VPS(0.187)T(0.187)T(0.187)NVNMT(0.23)VNT(0.228)MGT(0.242)GGQT(0.011)IDNGT(0.002)GR	2	III	0,181253	209,5	
Med6	240	T	S(0.005)S(0.005)VRPT(0.012)GGANMAT(0.864)VPS(0.576)T(0.175)T(0.186)NVNMT(0.052)VNT(0.056)MGT(0.055)GGQT(0.013)IDNGT(0.001)GR	2	I	0,863718	209,5	
Med6	243	S	S(0.005)S(0.005)VRPT(0.007)GGANMAT(0.013)VPS(0.593)T(0.593)T(0.568)NVNMT(0.462)VNT(0.46)MGT(0.198)GGQT(0.094)IDNGT(0.002)GR	3	II	0,592586	171,88	
Med6	244	T	S(0.005)S(0.005)VRPT(0.007)GGANMAT(0.013)VPS(0.593)T(0.593)T(0.568)NVNMT(0.462)VNT(0.46)MGT(0.198)GGQT(0.094)IDNGT(0.002)GR	3	II	0,592586	171,88	
Med6	250	T	S(0.005)S(0.005)VRPT(0.007)GGANMAT(0.013)VPS(0.593)T(0.593)T(0.568)NVNMT(0.462)VNT(0.46)MGT(0.198)GGQT(0.094)IDNGT(0.002)GR	3	II	0,461857	171,88	
Med6	253	T	SSVRPTGGANMATVPS(0.004)T(0.003)T(0.004)NVNMT(0.077)VNT(0.926)MGT(0.969)GGQT(0.017)IDNGTGR	2	I	0,925921	209,5	
Med6	256	T	SSVRPTGGANMATVPSTTNVNMTVNT(0.009)MGT(0.939)GGQT(0.052)IDNGTGR	1	I	0,938822	214,26	Albuquerque, 2008 (7)
Med6	260	T	SSVRPTGGANMATVPSTTNVNMT(0.041)VNT(0.036)MGT(0.145)GGQT(0.773)IDNGT(0.005)GR	1	I	0,773043	214,26	

Med7	214	S	LTSIQDTLRT(0.249)GS(0.751)QS(0.999)PPS(0.001)SSQ	2	I	0,751232	239,75	
Med7	219	S	LT(0.001)S(0.001)IQDT(0.028)LRT(0.106)GS(0.251)QS(0.805)PPS(0.55)S(0.481)S(0.776)Q	3	II	0,550011	240,65	
Med7	220	S	LT(0.001)S(0.001)IQDT(0.028)LRT(0.106)GS(0.251)QS(0.805)PPS(0.55)S(0.481)S(0.776)Q	3	II	0,481251	240,65	
Med7	221	S	LTSIQDTLRTGSQS(0.999)PPS(0.002)S(0.037)S(0.961)Q	2	I	0,961147	239,75	

Med8	220	S	FTFTGEKPIITGSTST(0.001)S(0.45)S(0.45)S(0.098)N	1	II	0,450021	210,67	
Med8	221	S	FTFTGEKPIITGSTST(0.001)S(0.45)S(0.45)S(0.098)N	1	II	0,450021	210,67	

Med9	118	S	S(1)PSEWQDIIHQR	1	I	0,999948	279,51	
Med9	120	S	DLLS(0.084)KS(0.097)PS(0.819)EWQDIIHQR	1	I	0,819416	279,51	

Med10	147	T	RT(0.949)S(0.051)PIDNVSNTH	1	I	0,949122	180,17	
Med10	148	S	RT(0.187)S(0.813)PIDNVSNTH	1	I	0,813052	180,17	
Med10	156	T	RTSPIDNVS(0.024)NT(0.976)H	1	I	0,975873	180,17	

Med13	425	S	QTTVSNDLENS(1)PLK	1	I	1	159,17	Albuquerque, 2008 Smolka, 2007 (7,8)
Med13	472	S	EQNENLPS(1)DKS(0.997)DS(0.003)MVDK	2	I	0,999986	162,71	
Med13	475	S	EQNENLPS(1)DKS(0.997)DS(0.003)MVDK	2	I	0,997092	162,71	
Med13	477	S	EQNENLPS(0.095)DKS(0.948)DS(0.957)MVDK	2	I	0,956694	162,71	
Med13	746	T	IPQNDIPQT(0.569)ES(0.431)PLK	1	II	0,568941	176,38	

Med14	2	T	T(0.456)T(0.102)T(0.102)IGS(0.34)PQMLANEER	1	II	0,455663	314,92	
Med14	3	T	T(0.279)T(0.32)T(0.32)IGS(0.08)PQMLANEERLS(0.001) NEMHALK	1	II	0,320262	314,92	
Med14	4	T	T(0.279)T(0.32)T(0.32)IGS(0.08)PQMLANEERLS(0.001) EMHALK	1	II	0,320262	314,92	
Med14	7	S	TTTIGS(1)PQMLANEER	1	I	1	314,92	Albuquerque, 2008 (7)
Med14	18	S	T(0.075)T(0.086)T(0.086)IGS(0.319)PQMLANEERLS (0.434)NEMHALK	1	II	0,434133	170,08	
Med14	48	S	NTQLHGPS(0.499)AT(0.499)DPET(0.002)TATQK	1	II	0,498769	132,93	

Med15	163	T	RQLT(1)PQQQQLVNQMK	1	I	1	193,14	Albuquerque, 2008 (7)
Med15	398	T	AQNVPMNIIQQQQQQNT(0.004)NNNDT(0.001)IAT (0.014)S(0.05)AT(0.926)PNAAAFS(0.004)QQQNAS(0.001) S(0.001)K	1	I	0,925814	203,97	
Med15	728	T	NT(0.462)S(0.076)S(0.462)MDFLNSMENTPK	1	II	0,462191	245,93	
Med15	729	S	NT(0.158)S(0.727)S(0.115)MDFLNSMENTPK	1	II	0,727063	245,93	
Med15	730	S	NT(0.013)S(0.104)S(0.883)MDFLNSMENTPK	1	I	0,882932	245,93	Albuquerque, 2008 (7)
Med15	746	S	VPVS(1)AAATPSLNK	1	I	0,999759	205,99	Albuquerque, 2008 (7)
Med15	750	T	VPVS(0.999)AAAT(0.997)PS(0.004)LNK	2	I	0,997081	178,35	Albuquerque, 2008 (7)
Med15	752	S	VPVSAAAT(0.008)PS(0.992)LNK	1	I	0,991966	205,99	Albuquerque, 2008 (7)
Med15	767	S	S(0.997)NT(0.003)IPVTSIPSTNKK	1	I	0,996723	154,81	Soufi, 2009 (10)
Med15	783	S	KLS(0.998)IS(0.002)NAASQQPTPRSASNTAK	1	I	0,998448	238,32	Albuquerque, 2008 (7) Gruhler, 2005 (15)
Med15	785	S	KLSIS(1)NAAS(1)QQPTPR	2	I	1	293,6	Smolka, 2007 (8) Albuquerque, 2008 (7) Soufi, 2009 (10)

Med15	789	S	KLSISNAAS(1)QQPTPR	1	I	0,999996	238,32	
Med15	793	T	LSISNAASQQPT(1)PR	1	I	0,999998	238,32	Albuquerque, 2008 (7)
Med15	796	S	S(0.847)AS(0.17)NT(0.901)AKS(0.086)T(0.206)PNT(0.738) NPS(0.052)PLK	3	I	0,847316	223,49	
Med15	798	S	KLS(0.132)IS(0.014)NAAS(0.543)QQPT(0.194)PRS(0.266) AS(0.665)NT(0.188)AK	2	II	0,664764	203,01	
Med15	800	T	S(0.028)AS(0.189)NT(0.785)AKS(0.841)T(0.156) PNT(0.001)NPSPLK	2	I	0,785459	203,01	
Med15	803	S	SASNTAKS(1)T(0.992)PNT(0.008)NPSPLK	2	I	0,999583	203,01	Albuquerque, 2008 (7) Soufi, 2009 (10)
Med15	804	T	SASNTAKS(1)T(0.992)PNT(0.008)NPSPLK	2	I	0,99188	203,01	Albuquerque, 2008 (7)
Med15	810	S	STPNTNPS(1)PLK	1	I	0,99995	140,69	Soufi, 2009 (10)
Med15	820	T	NGT(1)PNPNNMK	1	I	1	194,11	
Med15	828	T	T(0.934)VQS(0.066)PMGAQPSYNSAIIENAFRK	1	I	0,933878	248,59	Albuquerque, 2008 (7) Soufi, 2009 (10)
Med15	831	S	T(0.094)VQS(0.906)PMGAQPSYNSAIIENAFR	1	I	0,906148	248,59	Albuquerque, 2008 (7) Soufi, 2009 (10)
Med15	978	S	DLS(0.399)T(0.399)LVHS(0.067)S(0.067)S(0.067)PS(0.027) T(0.022)S(0.476)S(0.476)NMDVGNPR	2	II	0,399447	220,7	
Med15	983	S	DLS(0.003)T(0.003)LVHS(0.926)S(0.525)S(0.525)PS(0.009) T(0.009)SSNMDVGNPR	2	I	0,925609	220,7	Albuquerque, 2008 (7)
Med15	984	S	DLSTLVHS(0.001)S(0.994)S(0.976)PS(0.027)T(0.001)SSN MDVGNPR	2	I	0,994309	220,7	Albuquerque, 2008 (7)
Med15	985	S	DLSTLVHS(0.001)S(0.994)S(0.976)PS(0.027)T(0.001)SSN MDVGNPR	2	I	0,975761	220,7	Gruhler, 2005 (15) Smolka, 2007 (8) Albuquerque, 2008 (7)
Med15	987	S	DLS(0.016)T(0.034)LVHS(0.107)S(0.742)S(0.121)PS(0.978) T(0.002)SSNMDVGNPR	2	I	0,978318	220,7	Albuquerque, 2008 (7)
Med15	1003	S	RKAS(1)VLEISPQDSIASVLSPDSNIMSDSK	1	I	0,999833	279,49	Smolka, 2007 (8) Albuquerque, 2008 (7)
Med15	1008	S	ASVLEIS(0.956)PQDS(0.042)IAS(0.004)VLS(0.975) PDS(0.014)NIMS(0.008)DS(0.002)KK	2	I	0,955844	275,02	
Med15	1018	S	ASVLEISPQDSIASVLS(0.973)PDS(0.027)NIMSDSKK	1	I	0,97272	279,49	Smolka, 2007 (8)
Med15	1021	S	ASVLEISPQDSIASVLS(0.011)PDS(0.976)NIMS(0.011) DS(0.002)K	1	I	0,975597	279,49	
Med15	1034	S	VDS(1)PDDPFMTK	1	I	1	235,28	Smolka, 2007 (8) Li, 2007 (9) Chi, 2007 (14) Albuquerque, 2008 (7)

Med17	56	T	ADT(0.879)S(0.121)IRLEGDELENK	1	I	0,87863	194,24	

Med17	57	S	ADT(0.003)S(0.997)IRLEGDELENK	1	I	0,997496	194,24	Smolka, 2007 (8) Albuquerque, 2008 (7)

Med18	129	S	NILHNTVPQVTNFNSTNEDQNNS(1)K	1	I	1	258,12	

Med19	197	S	S(0.611)S(0.611)GS(0.362)S(0.362)MAT(0.044)PT(0.007) HS(0.003)DS(0.001)HEDMK	2	II	0,610692	199,85	
Med19	198	S	S(0.611)S(0.611)GS(0.362)S(0.362)MAT(0.044)PT(0.007) HS(0.003)DS(0.001)HEDMK	2	II	0,610692	199,85	
Med19	200	S	S(0.049)S(0.056)GS(0.747)S(0.146)MAT(0.002)PT(0.001) HSDSHEDMK	1	II	0,746841	220,76	
Med19	201	S	S(0.447)S(0.447)GS(0.451)S(0.447)MAT(0.021)PT(0.085) HS(0.1)DS(0.002)HEDMK	2	II	0,44693	199,85	
Med19	204	T	SSGSS(0.003)MAT(0.813)PT(0.172)HS(0.01)DS(0.002) HEDMK	1	I	0,81314	220,76	
Med19	206	T	S(0.001)S(0.001)GS(0.005)S(0.005)MAT(0.113)PT(0.763) HS(0.113)DSHEDMK	1	I	0,763434	220,76	
Med19	208	S	S(0.016)S(0.016)GS(0.013)S(0.02)MAT(0.435)PT(0.558) HS(0.941)DS(0.001)HEDMK	2	I	0,940917	199,85	
Med19	210	S	SSGSSMAT(0.004)PT(0.15)HS(0.032)DS(0.814)HEDMK	1	I	0,814275	220,76	

Med31	11	T	SSTNGNAPAT(0.851)PS(0.149)SDQNPLPTR	1	I	0,850876	182,11	

Supplemental Table S2: Phospho peptides from endogenous Mediator (SILAC) identified by quantitative mass spectrometry

Subunit	Phosphorylated Amino acid	Relative position	Phosphopeptide sequence	Number of phospho (STY)	pSTY-class	Localization p-value	PTM Score	Ratio H/L normalized by protiens	Ratio H/L Protein	Experiment (replicate)
Med1	S	155	LDSSNASFNNQGK	1	I	0,999988	113,1	1,1403	0,93111	[8]
Med2	S	266	GFDDNDSGNNYND	1	I	0,999916	91,06	1,2889	1,0173	[8]
Med3	S	189	GKRGPKSGSTMGT	2	II	0,520948	110,2	0,67404		[5]
Med3	T	195	SGSTMGTPTVHNS	2	II	0,483304	110,2	0,67404		[5]
Med3	T	197	STMGTPTVHNSTA	2	I	1	110,2	0,67404		[5]
Med4	S	2	MSVQDTKA	2	II	0,375866	42,7	0,89538		[5]
Med4	S	29	LVAEATSNTNSED	2	II	0,427697	42,7	0,89538		[5]
Med4	T	237	MAKKEGTPKTDSF	1	I	0,895187	63,90	0,88859	0,97272	[8]
Med4	T	240	KEGTPKTDSFIFD	1	II	0,466767	63,90	0,87087	0,97272	[8]
Med5	T	64	ASDLVDTPSNNTA	1	I	0,711911	44,01	0,75578	0,96689	[8]
Med5	S	66	DLVDTPSNNTAAT	1	II	0,414839	44,01	0,75578	0,96689	[8]
Med5	S	257	TNEFVGSPSLTSP	1	II	0,594324	59,16	1,0164	0,96689	[8]
Med5	S	257	TNEFVGSPSLTSP	2	II	0,504487	35,82	0,60258		[5]
Med5	S	259	EFVGSPSLTSPQY	3	II	0,349267	35,82	0,60258		[5]
Med5	T	261	VGSPSLTSPQYIP	3	II	0,351505	35,82	0,60258		[5]
Med5	S	262	GSPSLTSPQYIPS	3	II	0,728166	35,82	0,60258		[5]
Med5	S	268	SPQYIPSPLSSTK	1	II	0,554887	59,16	1,0164	0,96689	[8]
Med5	S	268	SPQYIPSPLSSTK	3	III	0,188482	35,82	0,60258		[5]
Med5	S	271	YIPSPLSSTKPPG	3	III	0,190959	35,82	0,60258		[5]
Med5	S	272	IPSPLSSTKPPGS	2	II	0,306	35,82	0,60258		[5]
Med5	T	273	PSPLSSTKPPGSV	2	II	0,306287	35,82	0,60258		[5]
Med5	S	1014	LHEKNDSAEVRQE	1	I	1	108,8	1,1616	0,96689	[8]
Med6	S	225	NNAGGGSNKSSVR	1	I	0,999975	68,61	0,75332		[5]
Med6	S	225	NNAGGGSNKSSVR	1	I	1	245,8	0,98941	0,96518	[8]
Med7	S	214	DTLRTGSQSPPSS	1	I	0,965933	162,7			[8]
Med7	S	214	DTLRTGSQSPPSS	1	I	0,999754	112,6			[5]

Med7	S	216	DTLRTGSQSPPSS	1	I	1	162,7			[8]
Med7	S	216	LRTGSQSPPSSSQ	2	I	0,999821	112,6			[5]
Med7	S	219	GSQSPPSSSQ	3	II	0,591076	152,58			[5]
Med7	S	221	QSPPSSSQ	3	II	0,745165	152,58			[5]
Med14	S	7	MTTTIGSPQMLAN	1	I	0,981906	59,61	1,0028	0,93638	[8]
Med14	T	1036	DTKRLGTPESVKP	1	I	0,999212	40,65	1,4734	0,93638	[8]
Med15	S	746	TPKVPVSAAATPS	2	I	1	139,73	0,59134		[5]
Med15	T	750	PVSAAATPSLNKT	2	I	0,75299	139,73	0,59134		[5]
Med15	S	767	VNGRTKSNTIPVT	1	I	0,997779	108,8	0,7847	1,0152	[8]
Med15	S	767	VNGRTKSNTIPVT	2	I	1	121,83	0,23904		[5]
Med15	T	769	GRTKSNTIPVTSI	2	I	0,999999	121,83	0,23904		[5]
Med15	S	783	STNKKLSISNAAS	1	I	0,930035	62,19	1,3327	1,0152	[8]
Med15	S	796	QQPTPRSASNTAK	1	II	0,431756	62,19	0,28888	1,0152	[8]
Med15	S	798	PTPRSASNTAKST	1	II	0,431756	62,19	0,28888	1,0152	[8]
Med15	T	800	PRSASNTAKSTPN	1	II	0,328631	62,18	0,28888	1,0152	[8]
Med15	S	803	ASNTAKSTPNTNP	1	II	0,506016	31,18	0,77543	1,0152	[8]
Med15	T	804	SNTAKSTPNTNPS	1	I	0,821598	31,19	0,62814	1,0152	[8]
Med15	T	820	TQTKNGTPNPNNM	1	I	1	63,85	1,1509	1,0152	[8]
Med15	T	820	TQTKNGTPNPNNM	1	I	1	96,19	0,67499		[5]
Med15	S	831	NMKTVQSPMGAQP	1	I	0,952246	86,1	1,1016	1,0152	[8]
Med15	S	983	LSTLVHSSSPSTS	1	II	0,319945	128,3	0,98032	1,0152	[8]
Med15	S	983	LSTLVHSSSPSTS	1	II	0,467627	100,57	0,80973		[5]
Med15	S	984	STLVHSSSPSTSS	1	II	0,335819	128,3	0,98032	1,0152	[8]
Med15	S	984	STLVHSSSPSTSS	1	II	0,467627	100,57	0,80973		[5]
Med15	S	987	VHSSSPSTSSNMD	1	II	0,335819	128,3	0,98032	1,0152	[8]
Med15	S	1008	ASVLEISPQDSIA	2	I	0,759731	74,54	1		[5]
Med15	S	1018	SIASVLSPDSNIM	2	I	0,974119	74,54	1,0		[5]
Med15	S	1034	KKIKVDSPDDPFM	1	I	1	242,1	1,0116	1,0152	[8]
Med15	S	1034	KKIKVDSPDDPFM	1	I	1	164,05	0,75937		[5]
Med17	S	57	AGKADTSIRLEGD	1	I	0,926108	106,6	1,0224	0,96252	[8]
Med17	T	56	SAGKADTSIRLEG	1	II	0,5	106,6	0,94258	0,96252	[8]

Supplemental Table-S3: Genomic point mutations in *D7P* mutant strain

	Relative amino-acid position	Point mutation
Med15	746	S →A
Med15	750	T →A
Med15	796	S →A
Med15	798	S →A
Med15	769	T →A
Med15	767	S →A
Med15	800	S →A

Supplemental Table-S4: Genomic point mutations in *D30P* mutant strain

	Relative amino-acid position	Point mutation
Med15	728	T →A
Med15	729	S →A
Med15	730	S →A
Med15	746	S →A
Med15	750	T →A
Med15	752	S →A
Med15	767	S →A
Med15	769	T →A
Med15	783	S →A
Med15	785	S →A
Med15	789	S →A
Med15	793	T →A
Med15	796	S →A
Med15	798	S →A
Med15	800	T →A
Med15	803	S →A
Med15	804	T →A
Med15	810	S →A
Med15	820	T →A
Med15	828	T →A
Med15	831	S →A
Med15	978	S →A
Med15	983	S →A
Med15	984	S →A
Med15	985	S →A
Med15	987	S →A
Med15	1003	S →A
Med15	1008	S →A
Med15	1018	S →A
Med15	1034	S →A

II. Supplemental Text and additional Figures

1.0 Quantitative mass-spectrometry of Mediator phosphosites during osmotic stress

1.1 Sequence coverage

Stable isotope labeling of amino acids in cell culture (SILAC) and preparation of mediator proteins was performed as described in Material & Methods section. To elucidate the completeness of the analysis, we calculated the sequence coverage of the detected peptides in relation to the sequence length of each Mediator protein. The analysis of the detected peptides covers more than 53% of the complete mediator core sequence (Fig.S2-A).

1.2 SILAC experiment: data processing

Combination of SILAC with high performance LQ-MS/MS analysis enables the simultaneous quantification of heavy and light peptides and the phosphosites. This experimental strategy allows the observation of the mediator phophosite dynamics in response to osmotic stress. We defined the protein ratio (ratio H/L proteins) as ratio between intensities of heavy peptides originated from the hyperosmotic stress sample and light peptides from the control sample. The protein ratio of a single protein was normalized against all peptide ratios identified. For calculation of phosphosite ratios (ratio H/L), we calculated the relative difference of heavy- and light phosphopeptides originated from the same protein. The phosphosite ratios were normalized against the protein ratios from the same protein. We defined an increase or decrease in phosphorylation, respectively, as alteration of the normalized phosphosite ratio by a factor of 1.5, whereas the normalized protein ratio remained constant. We detected 21 mediator subunits, whereas normalized protein ratios of 20 Mediator subunits remained constant which were used as basis for quantitative analysis of phosphorylated sites (Fig. S2B).

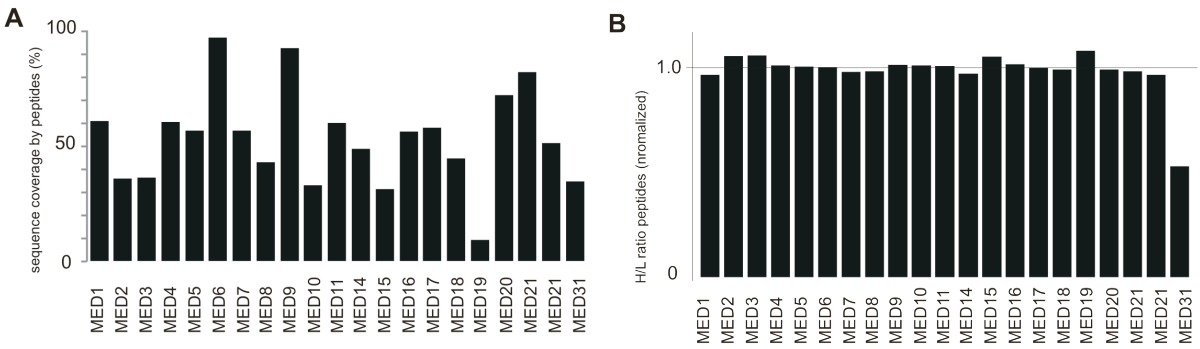

Figure S3: Statistics of osmotic stress SILAC experiment; **A)** Histogram illustrating the sequence coverage of Mediator proteins by peptides. **B)** Histogram illustrating normalized heavy/light ratio of peptides.

2.0 Location of dynamically phosphorylated sites in secondary structure of Med5 and Med15

Secondary structure prediction of Med5 and Med15 was performed by HHpred and I-Tasser (16-19); (Fig. S3).

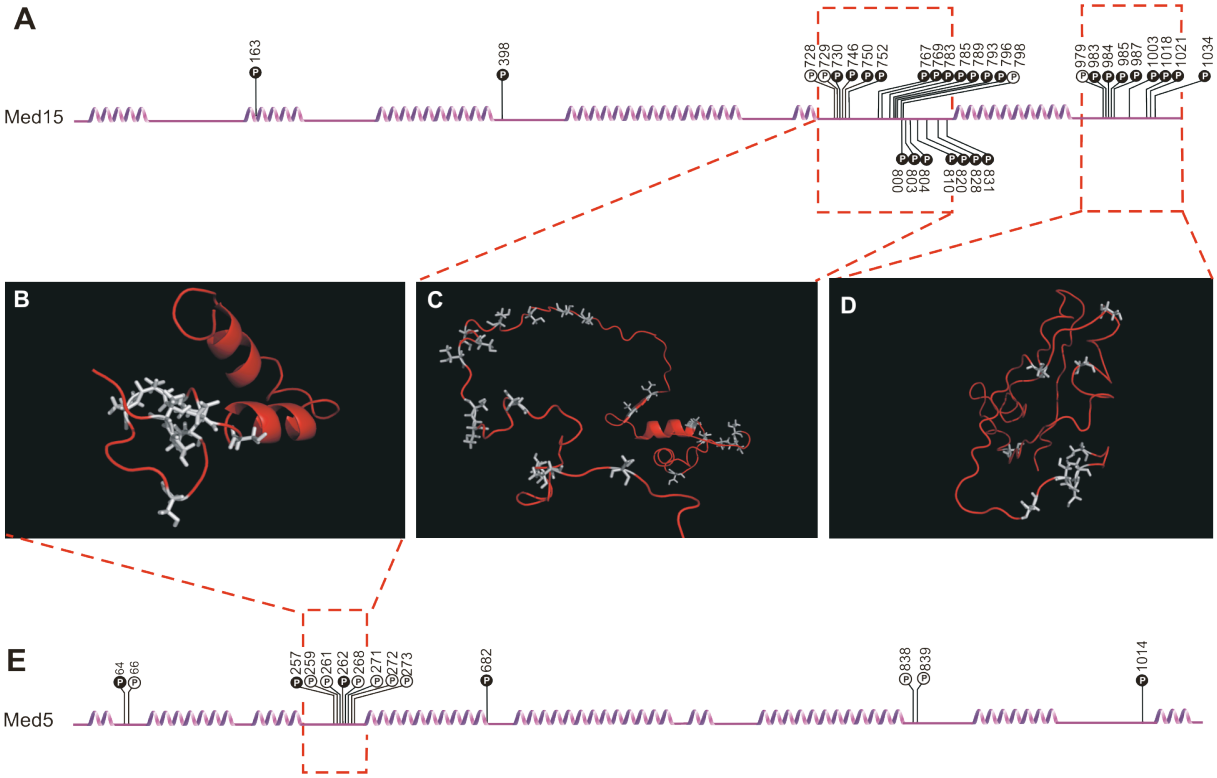

Figure S4: Dynamically phosphorylated sites in Med5 and Med15 are located in loops. **(A)** Schematic view of Med15 secondary structure prediction (HHpred, Soeding, et al., 2005) and localization of phosphosites identified under normal- and osmotic stress conditions. Dynamically phosphorylated sites are colored in orange. Phosphorylated sites which are unchanged or phosphorylated in YPD are colored in black. Phosphositepositions are given by numbers above the phosphor-symbols. **(B)** Model by I-TASSER (Roy, et al., 2010; Zhang, 2008) of Med5 phospho-loop (residues: 227 to 276). Phosphosites are high-lighted as stick models in grey. **(C)** Model by I-TASSER of Med15 phospho-loop (residues: 721 to 835). Phosphosites are high-lighted as stick models in grey. **(D)** Model by I-TASSER of Med15 phospho-loop (residues: 978 to 1081). Phosphosites are high-lighted as stick models in grey. **(E)** Schematic view of Med15 secondary structure prediction (HHpred) and localization of phosphosites identified under normal- and osmotic stress conditions. Dynamically phosphorylated sites are colored in orange. Phosphorylated sites which are unchanged or phosphorylated under normal growth conditions are colored in black. Phosphositepositions are given by numbers above the phosphor-symbols.

3.0 Phenotyping of *med15* deletion mutant

We tested the *med15* deletion mutant (Δ*med15*) for different stress conditions. The experiment was performed as described in the Materials and Methods section. The (Δ*med15*) deletion mutant show a growth defect on high salt concentrations and on high- as well as on low temperatures. From this observation we concluded that Med15 is involved in temperature- and salt induced stress response (Fig. S4).

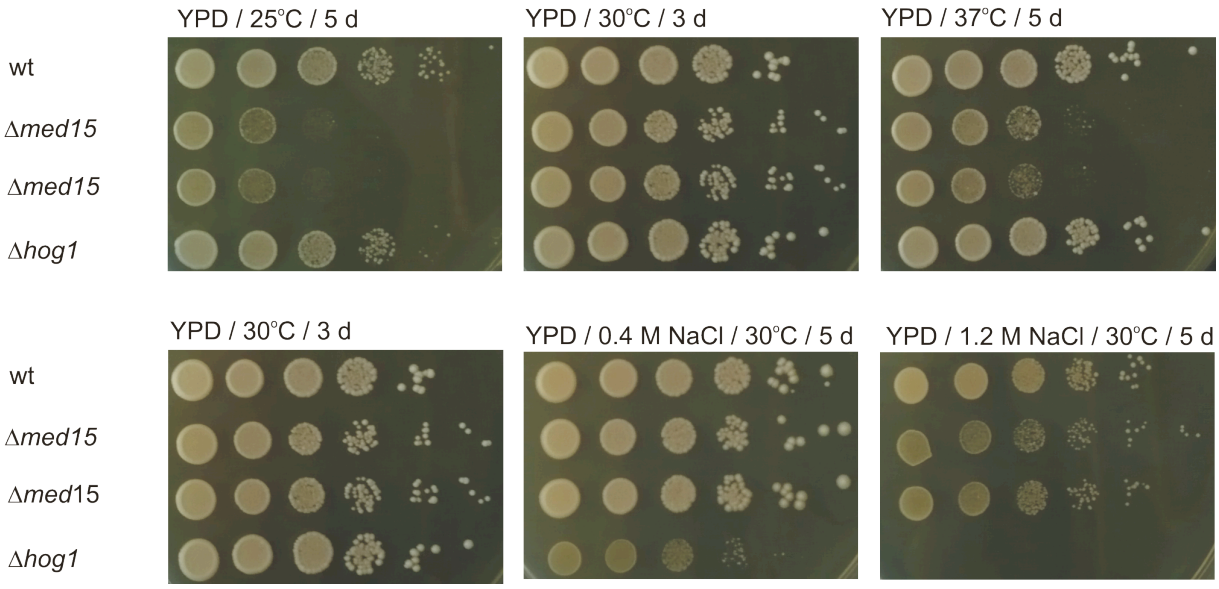

Figure S5: Phenotyping of *med15* deletion mutant; **(upper panel):** Cells were grown on YPD agar media at 25ºC, 30ºC and 37ºC 3 days or 5 days, respectively. Cells were spotted in different dilutions (from left to right): 1, 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}. *med15* deletion mutant show a growth defect at low (25ºC) and high (37ºC) temperatures. **(lower panel):** Cells were grown on YPD agar media containing 0 M , 0.4 M and 1.2 M sodium chloride at 30ºC for 3 days or 5 days, respectively. Cells were spotted in different dilutions (from left to right): 1, 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}. Δ*med15* deletion mutant show a growth defect on high salt concentrations.

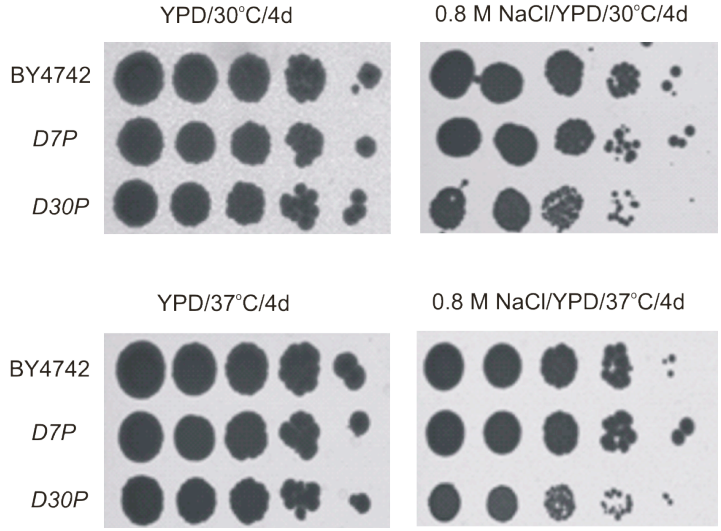

Figure S6: Phenotyping of *D7P* and *D30P* mutant; **(upper panel):** Cells were grown on YPD agar media containing 0 M and 0.8 M sodium chloride at 30ºC for 4 days. Cells were spotted in different dilutions (from left to right): 1, 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}. *D30P* mutant show a weak growth defect at high salt concentrations. **(lower panel):** Cells were grown on YPD agar media containing 0 M and 0.8 M sodium chloride at 37ºC for 4 days. Cells were spotted in different dilutions (from left to right): 1, 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}. *D30P* deletion mutant show a weak growth defect on high salt concentrations at 37ºC.

Supplemental Table-S5: Overview to all gene expression arrays used in this study

Profile name column: file name of the corresponding CEL file. **Fraction column:** (L) for analysis of labeled mRNA; (T) for analysis of total mRNA; **Time window column:** start and end of the labeling period (4-sU) after osmotic stress was induced; **Labeling time column:** incubation time with 4-sU; **Osmotic stress column:** Addition of sodium chloride to a final concentration of 0.8 M; **Bio.rep column:** number of the biological replicate. **Day column:** Indicator of the experiment date. **Exp.series column:** abbreviation of for the experiment series (WT: wildtype; GA: *med15* mutant; SS: osmotic stress; NO: normal growth conditions);

	profile name	fraction	time window	labeling time	osmotic stress	bio. rep.	day	exp. Series
1	L D07P xxxx 01 B +00-+06 ssss tt WILD PM GA2	L	------	6	-	1	1	*D7P*
2	L D07P xxxx 02 B +00-+06 ssss tt WILD PM GA2	L	------	6	-	2	1	*D7P*
3	L D07P xxxx 01 B +18-+24 SALT 24 WILD PM GA2	L	18-24	6	+	1	1	*D7P*
4	L D07P xxxx 02 B +18-+24 SALT 24 WILD PM GA2	L	18-24	6	+	2	1	*D7P*
5	L D30P xxxx 01 n +00-+06 ssss tt rrrr PM GA1	L	------	6	-	1	1	*D30P*
6	L D30P xxxx 02 n +00-+06 ssss tt rrrr PM GA1	L	------	6	-	2	1	*D30P*
7	L D30P xxxx 01 n +18-+24 SALT 24 WILD PM GA1	L	18-24	6	+	1	1	*D30P*
8	L D30P xxxx 02 n +18-+24 SALT 24 WILD PM GA1	L	18-24	6	+	2	1	*D30P*
9	L MD15 xxxx 01 B +00-+06 ssss tt WILD KO GA2	L	------	6	-	1	1	*Δmed15*
10	L MD15 xxxx 02 B +00-+06 ssss tt WILD KO GA2	L	------	6	-	2	1	*Δmed15*
11	L MD15 xxxx 01 B +18-+24 SALT 24 WILD KO GA2	L	18-24	6	+	1	1	*Δmed15*
12	L MD15 xxxx 02 B +18-+24 SALT 24 WILD KO GA2	L	18-24	6	+	2	1	*Δmed15*
13	L WILD xxxx 01 B +00-+06 ssss tt rrrr CO GA2	L	------	6	-	1	1	WT-2
14	L WILD xxxx 02 B +00-+06 ssss tt rrrr CO GA2	L	------	6	-	2	1	WT-2
15	L WILD xxxx 01 n +00-+06 ssss tt rrrr CO GA1	L	------	6	-	1	1	WT-1
16	L WILD xxxx 02 n +00-+06 ssss tt rrrr CO GA1	L	------	6	-	2	1	WT-1
17	L WILD xxxx 01 B +18-+24 SALT 24 rrrr CO GA2	L	18-24	6	+	1	1	WT-2
18	L WILD xxxx 02 B +18-+24 SALT 24 rrrr CO GA2	L	18-24	6	+	2	1	WT-2
19	L WILD xxxx 01 n +18-+24 SALT 24 WILD CO GA1	L	18-24	6	+	1	1	WT-1

20	L WILD xxxx 02 n +18-+24 SALT 24 WILD CO GA1	L	18-24	6	+	2	1	WT-1
21	T D07P xxxx 01 B +00-+06 ssss tt WILD PM GA2	T	------	6	-	1	1	D7P
22	T D07P xxxx 02 B +00-+06 ssss tt WILD PM GA2	T	------	6	-	2	1	D7P
23	T D07P xxxx 01 B +18-+24 SALT 24 WILD PM GA2	T	18-24	6	+	1	1	D7P
24	T D07P xxxx 02 B +18-+24 SALT 24 WILD PM GA2	T	18-24	6	+	2	1	D7P
25	T D30P xxxx 01 n +00-+06 ssss tt rrrr PM GA1	T	------	6	-	1	1	D30P
26	T D30P xxxx 02 n +00-+06 ssss tt rrrr PM GA1	T	------	6	-	2	1	D30P
27	T D30P xxxx 01 n +18-+24 SALT 24 WILD PM GA1	T	18-24	6	+	1	1	D30P
28	T D30P xxxx 02 n +18-+24 SALT 24 WILD PM GA1	T	18-24	6	+	2	1	D30P
29	T MD15 xxxx 01 B +00-+06 ssss tt WILD KO GA2	T	------	6	-	1	1	*Δmed15*
30	T MD15 xxxx 02 B +00-+06 ssss tt WILD KO GA2	T	------	6	-	2	1	*Δmed15*
31	T MD15 xxxx 01 B +18-+24 SALT 24 WILD KO GA2	T	18-24	6	+	1	1	*Δmed15*
32	T MD15 xxxx 02 B +18-+24 SALT 24 WILD KO GA2	T	18-24	6	+	2	1	*Δmed15*
33	T WILD xxxx 01 B +00-+06 ssss tt rrrr CO GA2	T	------	6	-	1	1	WT-2
34	T WILD xxxx 02 B +00-+06 ssss tt rrrr CO GA2	T	------	6	-	2	1	WT-2
35	T WILD xxxx 01 n +00-+06 ssss tt rrrr CO GA1	T	------	6	-	1	1	WT-1
36	T WILD xxxx 02 n +00-+06 ssss tt rrrr CO GA1	T	------	6	-	2	1	WT-1
37	T WILD xxxx 01 B +18-+24 SALT 24 rrrr CO GA2	T	18-24	6	+	1	1	WT-2
38	T WILD xxxx 02 B +18-+24 SALT 24 rrrr CO GA2	T	18-24	6	+	2	1	WT-2
39	T WILD xxxx 01 n +18-+24 SALT 24 WILD CO GA1	T	18-24	6	+	1	1	WT-1
40	T WILD xxxx 02 n +18-+24 SALT 24 WILD CO GA1	T	18-24	6	+	2	1	WT-1

4.0 Dynamic transcriptome analysis of inactive Med15 phosphosites

4.1 Experimental datasets

DTA experiment was performed as described in Material & methods section. We obtained duplicate samples each from wild-type and *med15* mutant under normal growth conditions and under osmotic stress conditions. The RNA from each sample were isolated and each were split into 3 fractions: Total RNA, labeled RNA (4sU incorporated into newly transcribed transcripts) and unlabeled RNA (pre-existing transcripts) as described previously (20). Total and labeled mRNA extracts were hybridized on GeneChip Yeast Genome 2.0 microarrays (Affymetrix). A listing of arrays can be found in (Supplementary Table S4).

4.2 Data processing

Probe signals from the GeneChip Yeast Genome 2.0 microarrays (Affymetrix) were captured and processed with GeneChip Operating Software (Affymetrix) and the resulting CEL files were pre-processed using the GC Robust Multi-array Average (GCRMA) method, with exception of the quantile normalization (21). Since we aim to identify genes which behave differentially in comparison of two data sets, we processed the data as previously described in (4,20).

4.2.1 Subset of reliable genes for DTA

To identify a set of reliable genes for DTA analysis, we considered only genes which are annotated as verified or uncharacterized ORFs in SGD database (Saccharomyces Genome Database, (22). We excluded all 137 ribosomal protein genes identified in (23), because of their high expression level. Therefore, we defined a set of 5331 reliable genes.

4.5 GO enrichment analysis

Data processing was performed by using the cytoscape-plugin BINGO (24). The top 20 GO terms of dataset is illustrated in Fig. 5C (Supplemental table S-5).

Supplemental Table-S6: *Δmed15* (induced): GO term

GO-ID	p-value	x	n	X	N	Description
7039	3,48E-39	73	118	732	6208	vacuolar protein catabolic process (autophagy)
9056	1,06E-26	190	775	732	6208	catabolic process
44248	3,28E-24	169	680	732	6208	cellular catabolic process
6914	3,68E-15	57	163	732	6208	autophagy
30163	6,10E-14	84	314	732	6208	protein catabolic process
55114	1,19E-13	92	363	732	6208	oxidation reduction
44257	1,27E-13	81	301	732	6208	cellular protein catabolic process
5975	8,80E-11	79	326	732	6208	carbohydrate metabolic process
44262	1,24E-10	73	293	732	6208	cellular carbohydrate metabolic process
44281	2,49E-10	167	912	732	6208	small molecule metabolic process
44282	6,83E-10	45	148	732	6208	small molecule catabolic process
9057	1,20E-08	92	442	732	6208	macromolecule catabolic process
6066	1,43E-08	59	240	732	6208	alcohol metabolic process
5984	2,71E-08	13	20	732	6208	disaccharide metabolic process
44265	4,47E-08	87	421	732	6208	cellular macromolecule catabolic process
5996	7,69E-08	38	132	732	6208	monosaccharide metabolic process
19318	1,12E-07	35	118	732	6208	hexose metabolic process
6112	2,29E-07	18	41	732	6208	energy reserve metabolic process
9266	5,09E-07	19	47	732	6208	response to temperature stimulus
51187	5,52E-07	16	35	732	6208	cofactor catabolic process

Supplemental Table-S7: *Δmed15* (repressed): GO term

GO-ID	p-value	x	n	X	N	Description
42254	1,83E-125	237	372	818	6208	ribosome biogenesis
22613	7,44E-111	240	423	818	6208	ribonucleoprotein complex biogenesis
6364	1,47E-97	173	252	818	6208	rRNA processing
16072	2,02E-94	174	262	818	6208	rRNA metabolic process
34470	1,19E-92	201	350	818	6208	ncRNA processing
34660	2,49E-90	216	409	818	6208	ncRNA metabolic process
6396	8,45E-61	213	532	818	6208	RNA processing
16070	3,16E-56	271	837	818	6208	RNA metabolic process
462	9,41E-55	78	93	818	6208	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5,8S rRNA, LSU-rRNA)
10467	4,98E-54	451	1921	818	6208	gene expression
30490	1,14E-53	80	99	818	6208	maturation of SSU-rRNA
44085	1,07E-52	278	903	818	6208	cellular component biogenesis
6417	3,07E-45	106	192	818	6208	regulation of translation
32268	1,19E-42	110	215	818	6208	regulation of cellular protein metabolic process
10608	2,20E-41	106	206	818	6208	posttranscriptional regulation of gene expression
42273	4,76E-40	61	77	818	6208	ribosomal large subunit biogenesis
42255	6,83E-38	56	69	818	6208	ribosome assembly
466	4,95E-32	53	72	818	6208	maturation of 5,8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5,8S rRNA, LSU-rRNA)
460	4,95E-32	53	72	818	6208	maturation of 5,8S rRNA
51246	5,45E-31	112	279	818	6208	regulation of protein metabolic process

Supplemental Table-S8: *D30P* (induced): GO term

GO-ID	p-value	x	n	X	N	Description
7039	5,92E-23	32	118	183	6208	vacuolar protein catabolic process (autophagy)
9266	2,65E-16	18	47	183	6208	response to temperature stimulus
44257	2,70E-11	33	301	183	6208	cellular protein catabolic process
30163	8,54E-11	33	314	183	6208	protein catabolic process
9628	1,97E-09	22	165	183	6208	response to abiotic stimulus
16052	2,69E-09	16	86	183	6208	carbohydrate catabolic process
44275	5,35E-09	15	78	183	6208	cellular carbohydrate catabolic process
44282	8,92E-09	20	148	183	6208	small molecule catabolic process
9056	1,11E-08	51	775	183	6208	catabolic process
44248	9,11E-08	45	680	183	6208	cellular catabolic process
44265	1,49E-07	33	421	183	6208	cellular macromolecule catabolic process
46164	3,68E-07	12	66	183	6208	alcohol catabolic process
9057	4,66E-07	33	442	183	6208	macromolecule catabolic process
46365	1,25E-06	11	61	183	6208	monosaccharide catabolic process
19320	5,03E-06	10	57	183	6208	hexose catabolic process
6091	6,20E-06	22	259	183	6208	generation of precursor metabolites and energy
44262	1,40E-05	23	293	183	6208	cellular carbohydrate metabolic process
6007	1,44E-05	9	51	183	6208	glucose catabolic process
6066	2,24E-05	20	240	183	6208	alcohol metabolic process
6006	2,66E-05	12	98	183	6208	glucose metabolic process

Supplemental Table-S9: *D30P* (repressed): GO term

GO-ID	p-value	x	n	X	N	Description
42180	6,55E-08	17	391	59	6208	cellular ketone metabolic process
19752	2,46E-07	16	377	59	6208	carboxylic acid metabolic process
43436	2,46E-07	16	377	59	6208	oxoacid metabolic process
6082	4,81E-07	16	396	59	6208	organic acid metabolic process
44281	3,87E-06	23	912	59	6208	small molecule metabolic process
44271	2,61E-05	12	310	59	6208	cellular nitrogen compound biosynthetic process
16053	2,98E-05	9	172	59	6208	organic acid biosynthetic process
46394	2,98E-05	9	172	59	6208	carboxylic acid biosynthetic process
32787	3,54E-05	8	135	59	6208	monocarboxylic acid metabolic process
44283	5,54E-05	13	390	59	6208	small molecule biosynthetic process
6519	1,51E-04	11	315	59	6208	cellular amino acid and derivative metabolic process
44106	1,95E-04	10	270	59	6208	cellular amine metabolic process
6767	3,01E-04	5	63	59	6208	water-soluble vitamin metabolic process
6766	4,02E-04	5	67	59	6208	vitamin metabolic process
6520	4,75E-04	9	247	59	6208	cellular amino acid metabolic process
9308	4,93E-04	10	303	59	6208	amine metabolic process
46942	5,26E-04	5	71	59	6208	carboxylic acid transport
19541	8,72E-04	2	5	59	6208	propionate metabolic process
6865	1,13E-03	4	49	59	6208	amino acid transport
15849	1,20E-03	5	85	59	6208	organic acid transport

Supplemental Table-S10: *D7P* (induced): GO term

GO-ID	p-value	x	n	X	N	Description
7039	2,78E-08	7,98E-06	10	118	51	vacuolar protein catabolic process (autophagy)
9266	8,08E-08	1,16E-05	7	47	51	response to temperature stimulus
6006	1,05E-06	6,64E-05	8	98	51	glucose metabolic process
15749	1,16E-06	6,64E-05	5	24	51	monosaccharide transport
8645	1,16E-06	6,64E-05	5	24	51	hexose transport
6066	2,77E-06	1,33E-04	11	240	51	alcohol metabolic process
19318	4,32E-06	1,77E-04	8	118	51	hexose metabolic process
5996	9,97E-06	3,58E-04	8	132	51	monosaccharide metabolic process
6112	1,84E-05	5,27E-04	5	41	51	energy reserve metabolic process
8643	1,84E-05	5,27E-04	5	41	51	carbohydrate transport
34637	2,97E-05	7,11E-04	6	75	51	cellular carbohydrate biosynthetic process
160	8,91E-05	1,83E-03	6	91	51	carbohydrate biosynthetic process
44257	1,34E-04	2,26E-03	10	301	51	cellular protein catabolic process
30163	1,90E-04	2,98E-03	10	314	51	protein catabolic process
46323	1,97E-04	2,98E-03	2	3	51	glucose import
6091	2,17E-04	3,12E-03	9	259	51	generation of precursor metabolites and energy
5975	2,58E-04	3,53E-03	10	326	51	carbohydrate metabolic process
9628	3,57E-04	4,26E-03	7	165	51	response to abiotic stimulus
44265	4,90E-04	5,41E-03	11	421	51	cellular macromolecule catabolic process
7039	2,78E-08	7,98E-06	10	118	51	vacuolar protein catabolic process

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