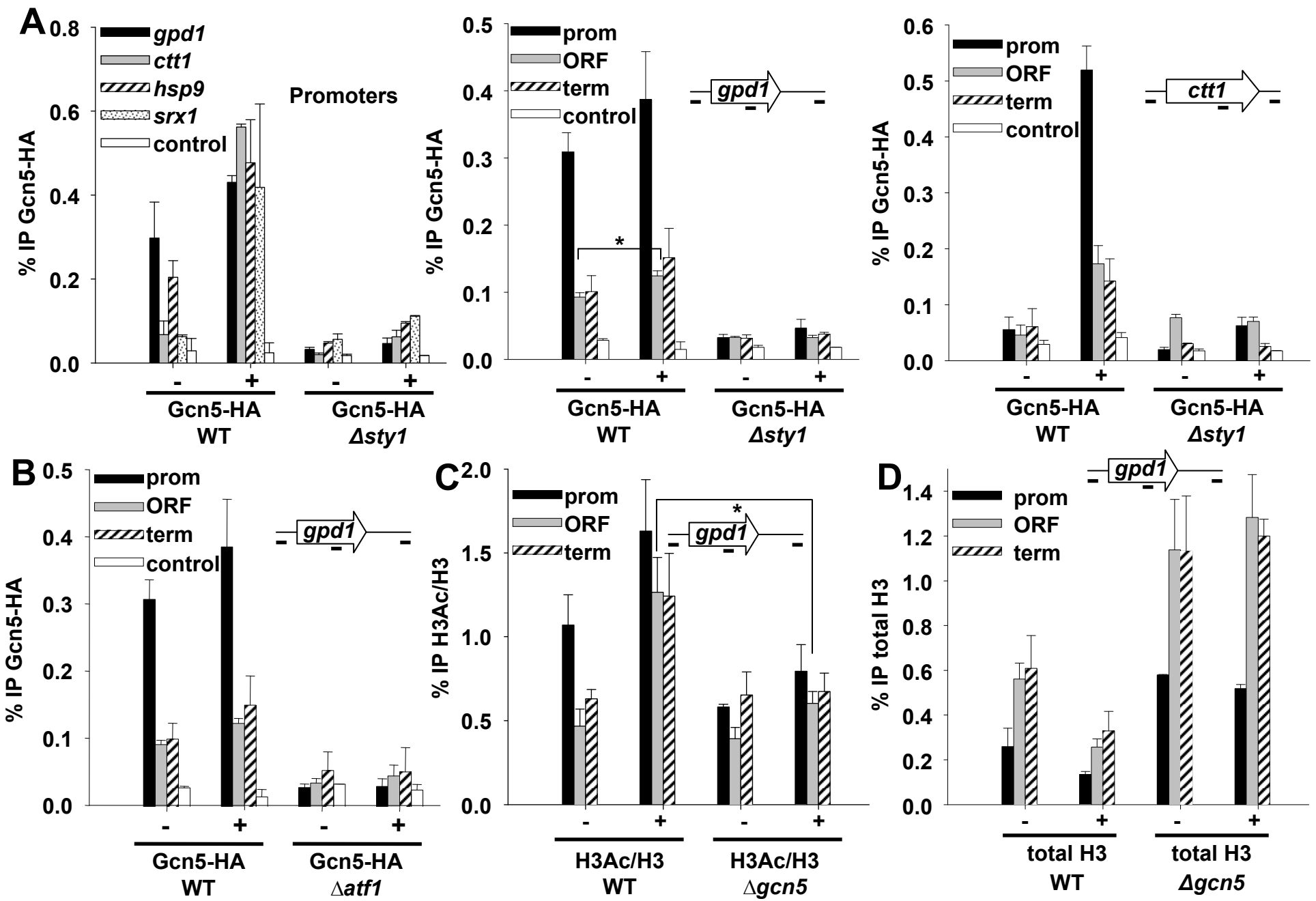
SUPPLEMENTARY FIGURE LEGENDS – Sansó et al. 2011

Supplementary Figure S1. Atf1-dependent Gcn5 recruitment to stress promoters induces histone acetylation and nucleosome eviction along the *gpd1* gene. (**A**) Gcn5 recruitment depends on Sty1. Cultures of strains HMP47 (*gcn5-HA*) and MS208 (*gcn5-HA* Δ*sty1)* were treated (+) or not (-) with 1 mM H_2O_2 for 15 min. ChIP experiments using anti-HA antibodies, coupled to quantification by real-time PCR, were performed using primers covering only promoter regions (*gpd1, ctt1, hsp9* and *srx1* promoters; left panel), or promoter (prom), coding (ORF) and termination (term) sequences of the *gpd1* (central panel) or *ctt1* (right panel) genes. Primers of an intergenic region were used as a negative control (control). Error bars for all ChIP experiments were calculated from biological triplicates. Significant difference between Gcn5-HA binding to ORF before and after stress in wild-type cells was determined by the Student's t-test (*P<0.05). (**B**) Gcn5 is physically recruited to *gpd1* in an Atf1-dependent manner. Cultures of strains HMP47 (*gcn5-HA*) and MS176 (*gcn5-HA* Δ*atf1*) were treated (+) or not (-) with 1 mM H_2O_2 for 15 min. ChIP experiments using anti-HA antibodies were performed as described above, using primer pairs corresponding to the promoter (prom), coding (ORF) and terminal region (term) of the *gpd1* gene. (**C**) Gcn5 promotes histone H3 acetylation upon stress imposition in coding region of the *gpd1* gene. Cultures of strains 972 (WT) and MS112 (Δ*gcn5*) were treated (+) or not (-) with 1 mM H_2O_2 for 15 min. ChIP experiments using antibodies specific for acetylated lysines 9 and 14 of histone H3 (H3Ac) or against unmodified C-terminal domain of H3 (H3) were performed as described above, using primers covering promoter (prom), coding (ORF) and termination (term) sequences of the *gpd1* gene. The percentage of immunoprecipitation of acetylated H3 *versus* total H3 is indicated (% IP H3Ac/H3). Significant difference between wild-type versus Δ*gcn5* cells at ORF upon stress was determined by the Student's t-test (*P<0.05). (**D**) Gcn5 promotes nucleosome eviction at the *gpd1* locus. The same experiment as in Supplementary Figure S1C is represented here as the percentage of total H3 immunoprecipitated (% IP H3).

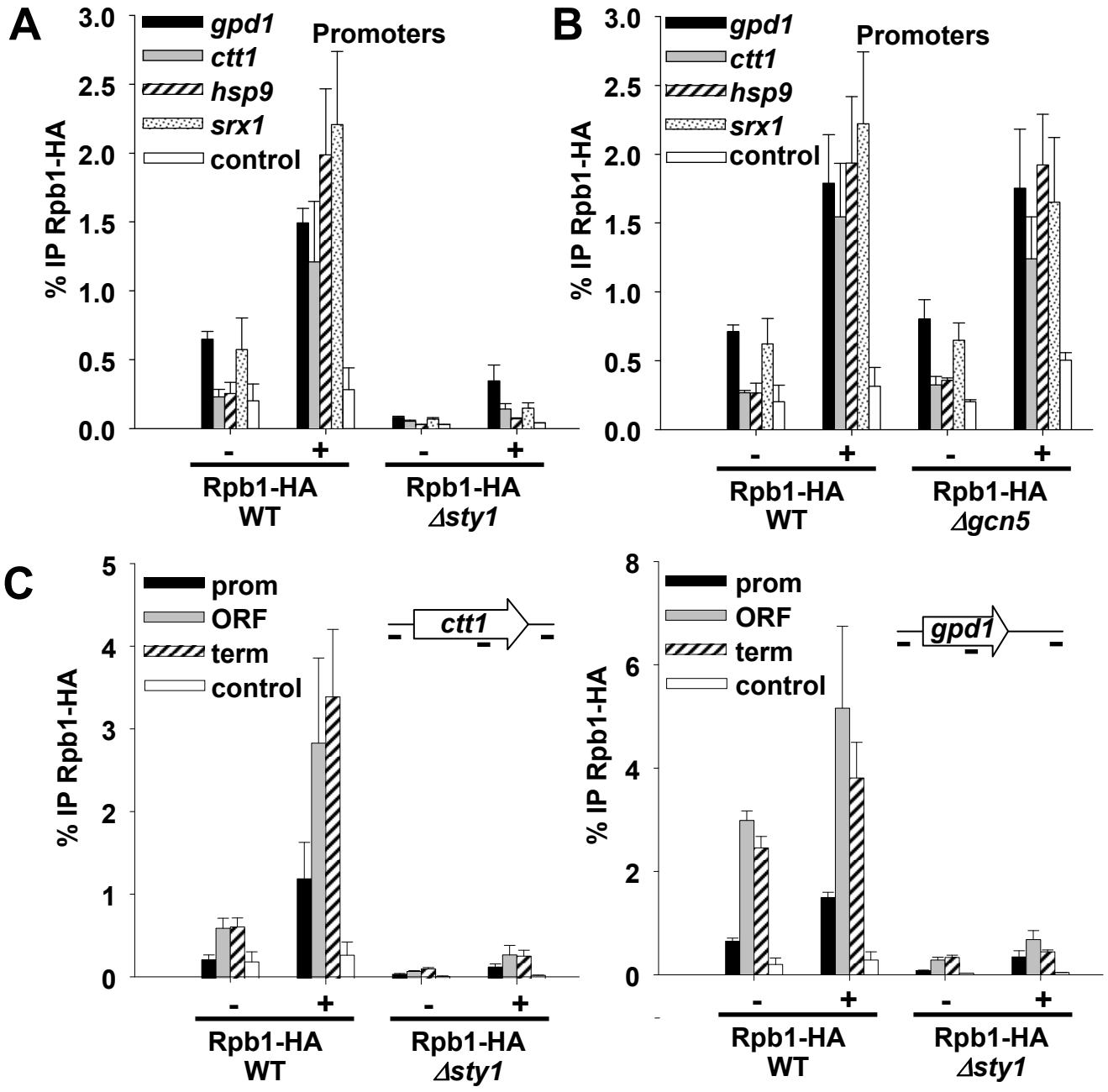
Supplementary Figure S2. Lack of Gcn5 impairs Pol II progression, but not Pol II recruitment to promoters. (**A**) Pol II recruitment to promoters depends on Sty1. Strains CN011 (*rpb1-HA*

WT) and CN009 (*rpb1-HA* Δ*sty1*), expressing Rpb1-HA, were cultured and treated (+) or not (-) with 1 mM H_2O_2 for 15 min. ChIP experiments were performed as in Supplementary Figure S1A using primers of promoter regions. (**B**) Pol II recruitment to promoters is not affected in cells lacking Gcn5. Cultures of strains CN011 (*rpb1-HA*) and MS52 (*rpb1-HA* Δ*gcn5*) were treated (+) or not (-) with 1 mM H_2O_2 for 15 min. ChIP experiments with anti-HA antibodies were performed as described in Supplementary Figure S1A, using primers covering promoter regions. (**C**) Pol II recruitment to coding sequences depends on Sty1. Strains and conditions as in (A), using primers of the *ctt1* gene. (**D**) Pol II recruitment to coding sequences is significantly affected in cells lacking Gcn5. Strains and conditions as in (B), using primers of the *gpd1* gene. (**E**) Phosphorylation at Ser5 of the CTD of the large Pol II subunit Rpb1. Strains 972 (WT) and MS161 (Δ*gcn5*) were cultured and treated (+) or not (-) with 1 mM H_2O_2 for 15 min. ChIP experiments with specific antibodies for phosphorylated Ser5 (Ser5-CTD) were performed as described in Supplementary Figure S1A, using primers covering the *gpd1* gene. (**F**) Phosphorylation at Ser2 of the CTD of the large Pol II subunit Rpb1. Strains and conditions as in (E), using specific antibodies for phosphorylated Ser2 (Ser2-CTD). Significant difference between wild-type *versus* Δ*gcn5* cells at terminator (term) upon stress was determined by the Student's t-test (*P<0.05).

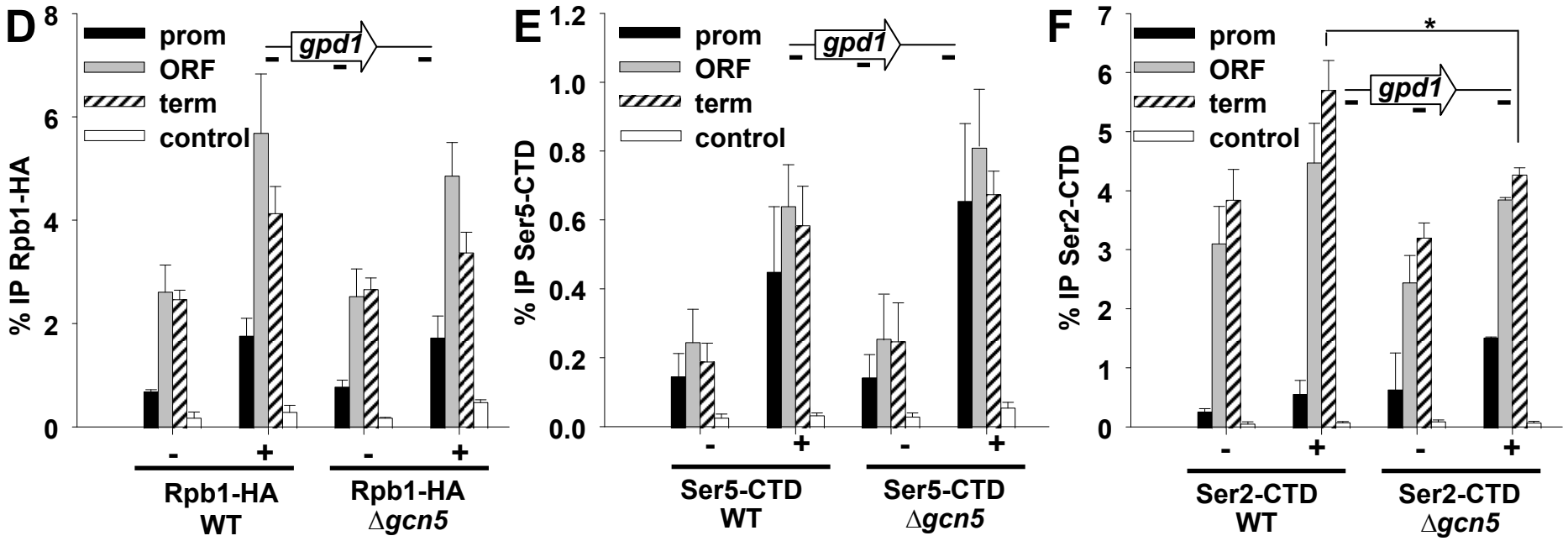
Supplementary Figure S3. Short-time kinetics of Pol II progression along the *gpd1* gene: Gcn5 mediates promoter escape. Strains CN011 (*rpb1-HA*) and MS52 (*rpb1-HA* Δ*gcn5*), expressing the large Pol II subunit Rpb1-HA, were cultured and treated or not with 1 mM H_2O_2 for the time in seconds indicated in the figure. ChIP experiments with anti-HA antibodies were performed as described in Supplementary Figure S1A, using primers covering promoter (prom), coding (ORF) and termination (term) sequences of the *gpd1* gene.



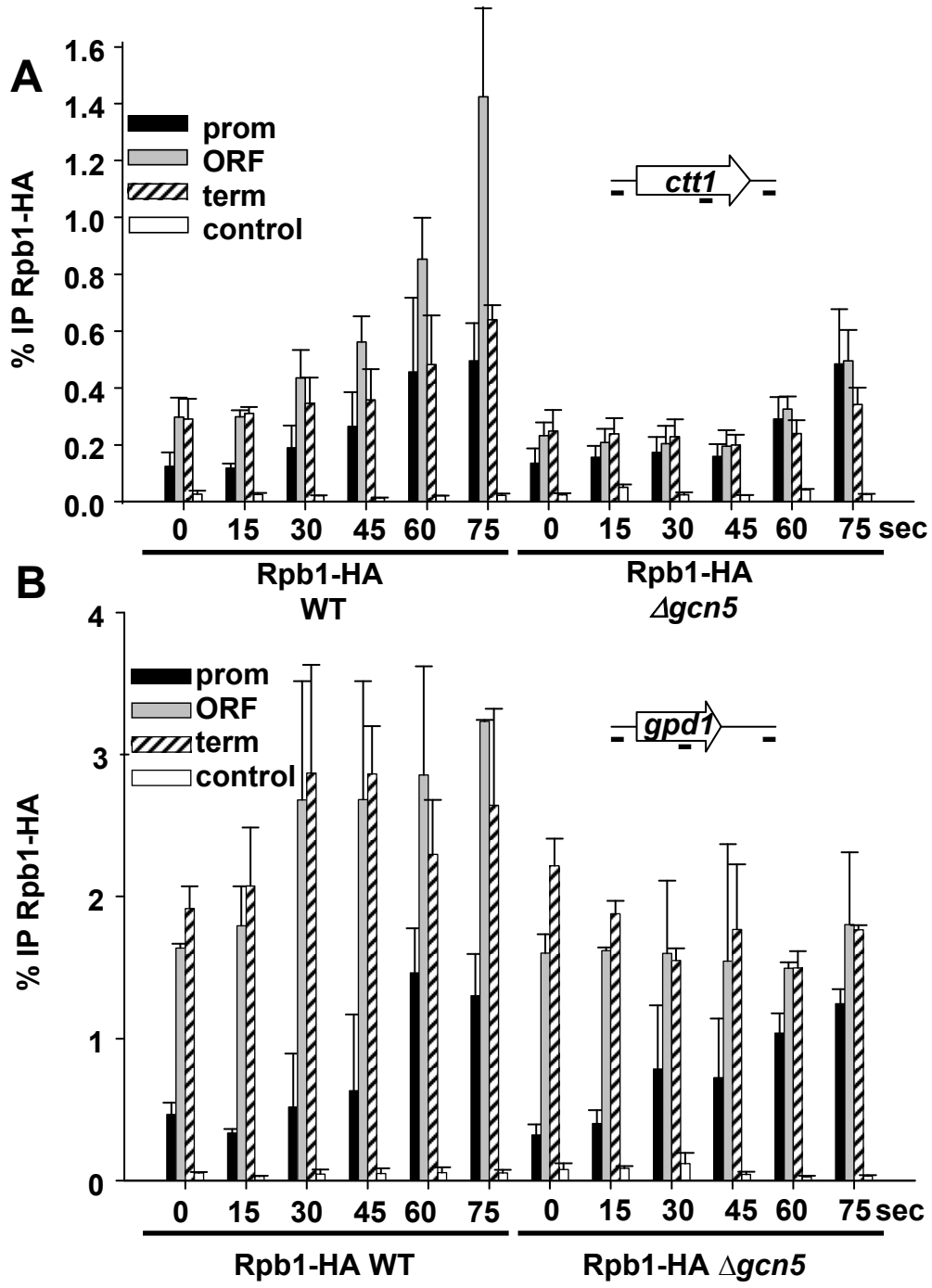
Sansó et al. Supplementary Figure S1



Sansó et al. Supplementary Figure S2A-C



Sansó et al. Supplementary Figure S2D-F



Sansó et al. Supplementary Figure S3

Supplementary Table S1. List of the top 50 genes up-regulated in response to 0.5 mM H_2O_2

Genes names	Genomic microarrays[a]	Expression microarrays[b]	PCR microarrays[c]	Chromosome	Strand	ORF left position[d]	ORF right position[d]	TSS[d]	NDR[e]
SPBC660.05	5.6	5.5	5.4	II	+	202536	202967	202302	YES
SPAC23H3.15c:SPAC25H1.01c	5.4	5.7	6.6	I	-	2523629	2524606	2524622	YES
SPBC24C6.09c	5.1	5.8	6.8	II	-	2335262	2337739	2337900	YES
SPCC794.04c	5.1	5.5	0.8	III	-	248551	250194	nd	YES
SPAC513.02	4.9	5.2	4.3	I	+				NO
SPAC4H3.03c	4.7	4.7	4.8	I	-	3826640	3828589	3829200	YES
lsd90:SPBC16E9.16c	4.6	4.5	6.5	II	-	1947985	1950255	nd	YES
gut2:SPCC1223.03c	4.6	4.2	4.8	I	-				NO
SPCC70.12c:ecl1	4.5			III	-	2355545	2355787	nd	YES
SPAC637.03	4.4	3.5	4.0	I	+				NO
pyp2:SPAC19D5.01	4.3	5.0	5.0	I	+	5202823	5204958	5202024	YES
SPCC757.03c	4.1	4.2	4.7	III	-	47741	48475	48486	YES
ish1:SPBC365.12c	4.0	3.8	4.7	II	-	2516249	2518303	2518722	YES
SPAC2H10.01	3.9	4.6	0.6	I	+	5274171	5275613	5273084	YES
SPAC22F8.05	3.9	3.4	3.9	I	+	4792308	4794983	4791890	YES
SPBC725.03	3.9	4.1	5.0	II	+	1207040	1207813	1207813	YES
oca2:SPCC1020.10	3.7	3.6	2.5	III	-	758901	760853	762606	YES
srx1:SPBC106.02c	3.5	2.3	4.6	II	-	376462	376836	376983	YES
SPCC1739.08c	3.4	2.8	4.2	III	-	2043282	2044067	nd	YES
SPAC23G3.13c:SPAC22H12.01c:mug35	3.3	2.8	1.2	I	-	893719	894423	894476	YES
SPBC725.10	3.2	3.3	3.0	II	+	1224974	1225462	1224587	YES
SPAC15E1.02c	3.2	2.7	4.6	I	-				NO
ctt1:cta1:SPCC757.07c	3.2	3.0	4.7	III	-	56927	58465	58825	YES
SPCC417.13:SPCC191.01	3.1	3.4	2.8	III	+	1706461	1706997	1705835	YES
SPAPB1A10.05	3.1	3.3	-0.2	I	+				NO
rsv2:SPBC1105.14	3.1	3.3	2.4	II	+	3532931	3534844	3532931	YES
SPCP31B10.06:mug190	3.0	3.7	3.5	III	+	533322	536888	532541	YES
SPBC1105.13c	3.0	3.4	1.0	II	-	3531760	3532188	3532400	YES
SPAC32A11.02c	3.0	2.9	4.3	I	-	2447948	2450503	2451032	YES
SPBC11C11.06c	2.9	2.3	3.7	II	-	3359360	3359896	3359940	YES
SPBC21C3.19	2.9	2.8	4.3	II	+	3830167	3830487	3830083	YES
SPAC17G6.13	2.9	1.9	0.5	I	+				NO
SPBPB2B2.12c	2.9	2.7	1.6	II	-				NO
SPAC23C11.06c	2.9	2.7	3.6	I	-				NO
srk1:mkp1:SPCC1322.08	2.9	3.4	3.6	III	+	1302900	1304865	1301970	YES
SPAC16A10.01	2.8	2.6	2.0	I	+	3077676	3080168	nd	YES

SPAC26F1.04c:etr1	2.8	2.4	2.4	I	+				NO
SPAC13C5.04	2.7	2.1		I	+				NO
SPAC57A7.02c:SPAC167.06c:mug143	2.7	2.9	3.4	I	+	1550133	1550498	1550076	YES
SPCC338.12	2.7	1.5	3.2	III	-	1355276	1355509	1355596	YES
SPBC20F10.03	2.7	2.7	2.5	II	+	3287750	3289090	3287725	YES
ssa1:SPAC13G7.02c	2.6	2.8	-0.7	I	-	2295819	2297753	2297965	YES
SPBC428.10	2.6	2.5	3.1	II	+	461306	463561	460856	YES
SPCC4G3.03	2.6	2.1	2.3	III	-	466796	467839	468100	YES
SPAC57A7.05	2.6	2.5	2.7	I	-	1534588	1538601	1540300	YES
hsp16:SPBC3E7.02c	2.6	1.5	0.1	II	-	2660490	2660921	2660948	YES
SPCC16A11.15c	2.6	2.8	4.1	III	-	896182	896535	896915	YES
cgs1:SPAC8C9.03	2.5	2.3	2.4	I	+	3643239	3644742	3643046	YES
ntp1:SPBC660.07	2.5	1.8	1.9	II	+	207078	209285	206592	YES
SPBC16D10.08c	2.4	1.8	0.1	II	-	3612359	3615076	3615254	YES

log2 gene inductions after 30 min in 0.5 mM H_2O_2 measured by genomic[a] or expression[b] microarrays (Quintales et al. 2010, BMC Bioinformatics 11:136), or by PCR fragments-based microarrays[c] (Chen et al. 2008, Mol. Biol. Cell 19:308)

[d]Data for 5' UTR, 3' UTR, and TSS were extracted from Lantermann et al. 2010, Nature Struct. Mol. Biol. 17:251 and Quintales et al. 2010, BMC Bioinformatics 11:136

[e]The presence of NDRs was determined from data in Lantermann et al. 2010, Nature Struct. Mol. Biol. 17:251