**Supplemental Table 1: Proteins co-eluting in the *S. cereviasae* Rpd3L histone deacetylation complex and their homologs in *A. thaliana*.**

| Gene | Full name | Function within the yeast complex[1] | Homologs in Arabidopsis[2] | Selected homolog(s)[3] |
|---|---|---|---|---|
| Rpd3 | Reduced Potassium Dependency 3 | Histone deacetylase, required for gene repression | 12 | HDA6, HDA19 |
| Sin3 | Switch independent 3 | Co-repressor, required for gene repression | 20 | SNL2 SNL3 |
| Ume1 | Unscheduled meiotic gene expression 1 | Unknown. Not required for gene repression. | None | |
| Sap30 | Sin3-associated protein | Unknown. Not required for gene repression. | None | |
| Pho23 | Phosphate metabolism 23 | Histone binding. Required for complex integrity. Linked to complex via Rxt2. Not required for HDAC activity or gene repression. | 8 | ING2 |
| Cti6 | CYC8-TUP-interacting protein 6 | Histone binding. Not required for gene repression. | 9 | SHL1 |
| Sds3 | Suppressor of defective silencing 3 | Unknown. Required for complex integrity. Not required for gene repression. Required for HDAC activity. | None | |
| Dep1 | Deregulated expression of phospholipid biosynthesis 1 | Unknown. Required for complex integrity, HDAC activity and gene repression | None | |
| Rxt2 | Regulator of transcription 2 | Unknown. Not required for HDAC activity or gene repression, Links Pho23 and Rxt3 to complex. Not required for HDAC activity or gene repression, | None | |
| Rxt3 | Regulator of transcription 3 | Unknown. Required for complex integrity. Linked to complex via Rxt2. Not required for HDAC activity or gene repression, | 1 | HDC1 |

[1]Summarised from (Carrozza et al., 2005). [2]E-value < 0.05 and coverage of at least 8%. [3]Included in this study.

**Supplemental Table 2: Information on selected candidates for interaction with HDC1**

| Function | Name | Yeast homolog | Binding and interaction | Domains | Physiological functions |
|---|---|---|---|---|---|
| Histone-binding protein | SHL1 | Cti6 | Binds preferentially me-H3K4[1]; interacts with HDA6 in BiFC[1] | PHD[8] BAH[9] | Multiple developmental; flowering, senescence[2] |
| Histone-binding protein | ING2 | Pho23 | Binds preferentially me-H3K4[3] | PHD | |
| Histone-binding protein | MSI1 | | Interacts with HDA19, HDC1 and SNL3 in Co-IP [7] | Hbd-RBBP4[12] WD40[13] | Multiple developmental, flowering, plant response to salt[7] |
| Co-repressor | SNL2 | Sin3 | | PAH[10] HID[11] | ABA-dependence during germination; post-ripening[4] |
| Co-repressor | SNL3 | Sin3 | Interacts with HDA19 in Y2H and pulldown[5] | PAH HID | ABA-dependence during germination[5] |
| Associated | SAP18 | | Interacts with HDA19 in Y2H and pulldown[6] | | ABA-dependence during germination[6] |

[1]Lopez-Gonzalez et al., 2014
[2](Mussig et al., 2000; Mussig and Altmann, 2003)
[3]Lee et al., 2009
[4]Wang et al., 2013
[5]Song et al., 2005
[6]Song and Galbraith 2006
[7]Mehdi et al., 2015
[8]Plant homodomain-linked zinc finger domain (histone binding)
[9]Bromo-adjacent homology motif (histone binding)
[10]Paired amphipathic helix domain (DNA binding)
[11]HDA-interaction domain (protein interaction)
[12]Histone binding domain RBBP4, N-terminal
[13]WD40 repeat

## Supplemental Table 3: Primers used for genotyping and cloning

**Primers for genotyping**

| ***Amplicon*** | **Forward Primer (5'-3')** | **Reverse Primer (5'-3')** |
|---|---|---|
| *35S promoter* | AAGGGTCTTGCGAAGGATAGTG | GGATTGATGTGATAACATGGTGGA |
| *Hygromicin* | AAGATGTTGGCGACCTCGTATT | AGTGCTTGACATTGGGGAGTTT |
| *hdc1-1 flanking* | CAAGGACTGGTGCTGAGAAAG | GCAGCCAAAATCTCAAGTAGC |
| *hdc1-1 left border* | TGATCCATGTAGATTTCCCG | pairs with hdc1-1 flanking sequence reverse primer |
| *T-DNA(pAC161)* | GCAATGAGTATGATGGTCAATATG | GGGCTACACTGAATTGGTAGCTC |

**Primers for cloning**

| ***Amplicon*** | **Forward Primer (5'-3')** | **Reverse Primer (5'-3')** |
|---|---|---|
| *RXT3like* | TAATGGCCAAACCCTCAGAGC | TTAAATCCAAGGTTCATTGC |
| *Sc RXT3* | TAATGTCGGTAAGCGAACAAG | TTAGGTCCATTTTAAATTTTTAATATAC |

**Primers for BIFC**

| ***Amplicon*** | **Forward Primer (5'-3')** | **Reverse Primer (5'-3')** |
|---|---|---|
| *HDC1 b2b3* | GGGGACAACTTTGTATAATAAAGTTGTAATGAGTGGTGTTCCAAAGAGA | GGGGACCACTTTGTACAAGAAAGCTGGGTTCTTGCTGCATGATGAAATTCT |
| *HDC1 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAGTGGTGTTCCAAAGAGA | GGGGACAACTTTGTATAGAAAAGTTGGGTTTAGTTGGGGGAGAGAAAATGAA |
| *ING2* | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAATGGCTATTGCACGAAC | GGGGACCACTTTGTACAAGAAAGCTGGGTCTACTTGCACTTGCTAG |
| *HDA6 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTAATGGAGGCAGACGAAAGC | GGGGACAACTTTGTATAGAAAAGTTGGGTTTAAGACGATGGAGGATTCAC |
| *HDA6 b2b3* | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAATGGAGGCAGACGAAAGC | GGGGACCACTTTGTACAAGAAAGCTGGGTTTAAGACGATGGAGGATTCAC |
| *HDA19* | GGGGACAAGTTTGTACAAAAAAGCAGGCTAATGGATACTGGCGGCAATTC | GGGGACAACTTTGTATAGAAAAGTTGGGTTTATGTTTTAGGAGGAAACGCCTG |
| *H3* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTCGTACCAAGCAG | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAAGCTCGTTCTCCTCTG |
| *SNL3 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTATAATGGTTGGAGGAGGAAGTG | GGGGACAACTTTGTATAGAAAAGTTGGGTTCACAAGAAGTTATTTTTGTAATATTG |
| *SNL3 b2b3* | GGGGACAACTTTGTATAATAAAGTTGTAATGGTTGGAGGAGGAAGTG | GGGGACCACTTTGTACAAGAAAGCTGGGTTCACAAGAAGTTATTTTTGTAATATTG |
| *SAP18 b2b3* | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAATGGCTGAAGCAGCGAGA | GGGGACCACTTTGTACAAGAAAGCTGGGTCTAGTAAATTGCCACATCCAG |
| *SAP18 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCTGAAGCAGCGAGA | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAGTAAATTGCCACATCCAG |
| *SHL1 b2b3* | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAATGCCCAAGCAAAAAGCTCC | GGGGACCACTTTGTACAAGAAAGCTGGGTTTAACCTGGTCGCTTAGTGTG |
| *SHL1 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCCCAAGCAAAAAGCTCC | GGGGACAACTTTGTATAGAAAAGTTGGGTTTAACCTGGTCGCTTAGTGTG |
| *SNL2* | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAATGAAGCGAATTAGGGATG | GGGGACCACTTTGTACAAGAAAGCTGGGTTCATCTTGAAGCTGAGAGAAAC |
| *RXT3like b2b3* | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAATGGCCAAACCCTCAGAGC | GGGGACCACTTTGTACAAGAAAGCTGGGTTTAAATCCAAGGTTCATTGC |
| *RXT3like b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCCAAACCCTCAGAGC | GGGGACAACTTTGTATAGAAAAGTTGGGTTTAAATCCAAGGTTCATTGC |
| *H1.1 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCAGAGGTGGAAATAG | GGGGACAACTTTGTATAGAAAAGTTGGGTTCACTTCTTAACCCTAGAAG |
| *H1.2 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCTATAGAGGAAGAAAACG | GGGGACAACTTTGTATAGAAAAGTTGGGTTCACTTCTTAGCCTTCCTAGTC |
| *H1.3 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCAGAAGACAAGATC | GGGGACAACTTTGTATAGAAAAGTTGGGTTCAAGCAGCGGAAGC |
| *H3.3 b1b4* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTTTTTTCTGTTACTG | GGGGACAACTTTGTATAGAAAAGTTGGGTTTAAGCGCGTTCACCTCTG |
| *MSI1 b2b3* | GGGGACAACTTTGTATAGAAAAGTTGGGTCTAATGGGGAAAGACGAAGAGGA | GGGGACCACTTTGTACAAGAAAGCTGGGTCTAAGAAGCTTTTGATGGTTC |

**Primers for qPCR**

| ***Amplicon*** | **Forward Primer (5'-3')** | **Reverse Primer (5'-3')** |
|---|---|---|
| *FR5* | ACAATGTCCGTTCTCGAGCATGG | AGCTGCAGCTCTGGTGGTCATAG |
| *TUB9* | AGTGTCCCTGAGCTAAC | AGTGGGAGCTATATCGC |

**Primers for protein expression**

| ***Amplicon*** | **Forward Primer (5'-3')** | **Reverse Primer (5'-3')** |
|---|---|---|
| *H1.1 B1B2* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCAGAGGTGGAAATAG | GGGGACCACTTTGTACAAGAAAGCTGGGTTCACTTCTTAACCCTAGAAG |
| *H1.2 B1B2* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCTATAGAGGAAGAAAACG | GGGGACCACTTTGTACAAGAAAGCTGGGTCCTTCTTAGCCTTCCTAGTC |
| *H1.3 B1B2* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGCAGAAGACAAGATC | GGGGACCACTTTGTACAAGAAAGCTGGGTTCAAGCAGCGGAAGC |
| *H1.2 N-ter B2* | | GGGGACCACTTTGTACAAGAAAGCTGGGTCGGAAGTTGTTTTCTTCTTCG |
| *H1.2 GD B1B2* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCTCACCCTACCTATGAAG | GGGGACCACTTTGTACAAGAAAGCTGGGTCAGGAATCTTAAAAGAAGCTTTG |
| *H1.2 C-ter B1* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGTCTGCTAGATCCGCAGCAAC | |
| *SHL1 B1B2* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGCCCAAGCAAAAAGCTCC | GGGGACCACTTTGTACAAGAAAGCTGGGTTTAACCTGGTCGCTTAGTGTG |
| *SHL1 BAH B1B2* | GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGAAGAGTATTCAAGAGGGAG | GGGGACCACTTTGTACAAGAAAGCTGGGTTTATCTGTCAGGATCAAACGCG |