



Figure S1. Structures of HDAC genes in *F. vesca* (a) and *A. thaliana* (b). UTR and CDS are indicated by yellow and green boxes, respectively. The lines indicate introns.



Figure S2. HAT genes structures of in *F. vesca* (a) and *A. thaliana* (b). UTR and CDS are indicated by yellow and green boxes, respectively. The lines indicate introns.

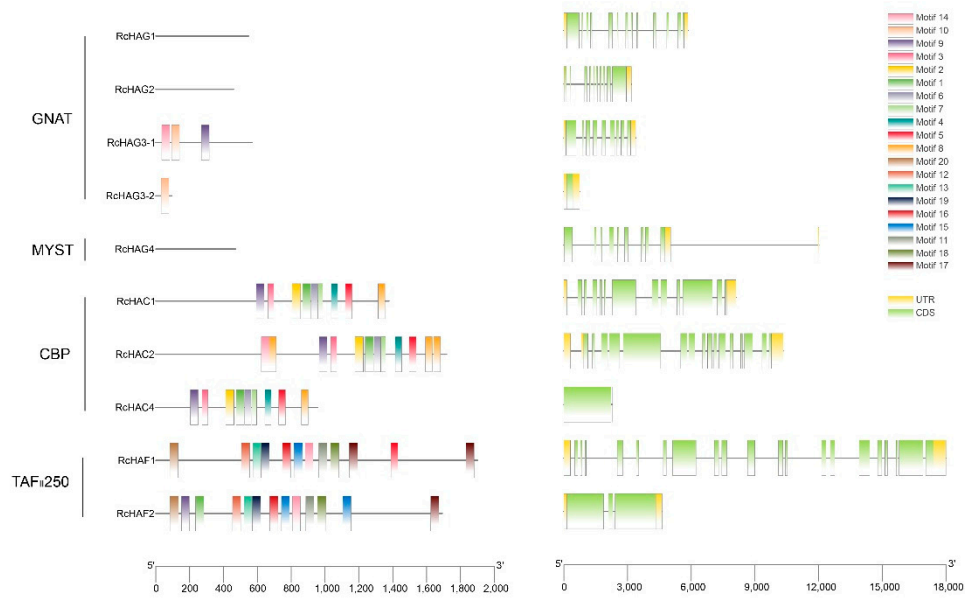


Figure S3. Conserved motifs and gene structures analysis of ten *R. chinensis* HATs. Motifs 1 to 20 are indicated by colored boxes. UTR and CDS are indicated by yellow and green boxes, respectively. The lines indicate introns.

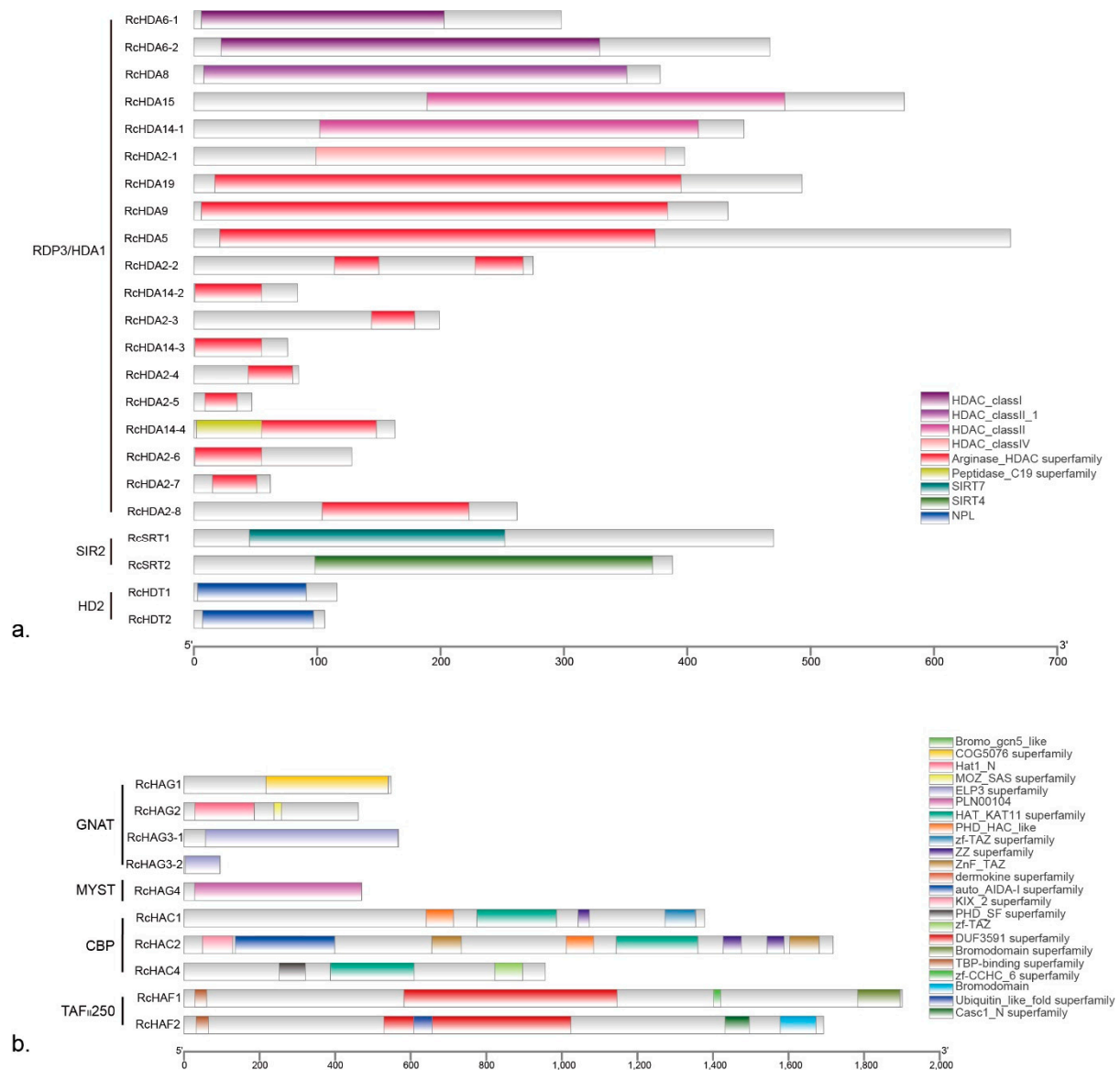


Figure S4. Conserved domains distribution in 23 HDAC proteins (**a**) and 10 HAT proteins (**b**) of *R. chinensis*. Domains are shown as colored boxes.

Table S1. HDAC and HAT genes in *A. thaliana*.

Gene subfamily	Gene ID	name
RPD3/HDA1	<i>AT5G63110.1</i>	<i>AtHDA6</i> (RPD3B)
	<i>AT5G35600.1</i>	<i>AtHDA7</i>
	<i>AT3G44680.1</i>	<i>AtHDA9</i>
	<i>AT4G38130.1</i>	<i>AtHDA19</i> (RPD3A)
	<i>AT5G61060.2</i>	<i>AtHDA5</i>
	<i>AT3G18520.2</i>	<i>AtHDA15</i>
	<i>AT5G61070.1</i>	<i>AtHDA18</i>
	<i>AT5G26040.2</i>	<i>AtHDA2</i>
	<i>AT4G33470.1</i>	<i>AtHDA14</i>
	<i>AT1G08460.1</i>	<i>AtHDA8</i>
	<i>AT3G44660.1</i>	<i>AtHDA10</i>
	<i>AT3G44490.1</i>	<i>AtHDA17</i>
SIR2	<i>AT5G55760.1</i>	<i>AtSRT1</i>
	<i>AT5G09230.7</i>	<i>AtSRT2</i>
HD2	<i>AT3G44750.1</i>	<i>AtHDT1</i>
	<i>AT5G22650.1</i>	<i>AtHDT2</i>
	<i>AT5G03740.1</i>	<i>AtHDT3</i>
	<i>AT2G27840.1</i>	<i>AtHDT4</i>
GNAT	<i>AT3G54610.1</i>	<i>AtHAG1</i> (AtGCN5)
	<i>AT5G56740.1</i>	<i>AtHAG2</i>
	<i>AT5G50320.1</i>	<i>AtHAG3</i>
MYST	<i>AT5G64610.1</i>	<i>AtHAG4</i>
	<i>AT5G09740.1</i>	<i>AtHAG5</i>
CBP	<i>AT1G79000.2</i>	<i>AtHAC1</i>
	<i>AT1G67220.1</i>	<i>AtHAC2</i>
	<i>AT1G55970.1</i>	<i>AtHAC4</i>
	<i>AT3G12980.1</i>	<i>AtHAC5</i>
	<i>AT1G16710.1</i>	<i>AtHAC12</i>
TAF _{II} 250	<i>AT1G32750.1</i>	<i>AtHAF1</i>
	<i>AT3G19040.1</i>	<i>AtHAF2</i>

Table S2. List of primers used in this study.

gene	Primer-F	Primer-R
<i>RcHDA6-1</i>	TTGCCTGACAACGACTACCAT	TATTGTCTTCCGCCTCCTCC
<i>RcHDA6-2</i>	TGTTGCTCGTTGCTGGTGCTATG	GTTGGCGGTGTTGTCTGGAAGG
<i>RcHDA19</i>	GCAGCAAGAAGAGTAAAGAAAAGAGA	TCCATAGACCCAGAGCCCATA
<i>RcHDA5</i>	ATGTGCCTGTATAGAATTACGCTCG	TGGAATGTCACGCTCCTTGC
<i>RcHDA15</i>	GGGGAGGCGGAGATAAGTC	TACTTGAAACATCAGGCAGCG
<i>RcHDA2-1</i>	ACTCCGCCGCTCAAGAACTC	CGAAGAGTAAATCAACGGCACCT
<i>RcHDA2-2</i>	GTGGAGGAAGGCAATAGAGGTA	CTGAGAGATTTGGCATCGTTTAG
<i>RcHDA2-5</i>	CATCAATGTGGGAGGACTGG	ACCCTTGAGTATGTTTAACGGC
<i>RcHDA8</i>	TACTCAGCCTATTGTCTTCAT	GATAATCGCTCGTCCTCA
<i>RcHDA14-2</i>	TATATTCTTCCTTTCAACTCACCAA	GGAGTAAACTTCAAATCTAGACTAGCA
<i>RcHDA14-3</i>	CCTTTCAACTCACCAAGTAACAAT	CTAGACTAGCATAACAAGAACATATAA
<i>RcSRT2</i>	TGTCCAAACCTCAACCCAAGT	GGATCTGAATCAGGAGCCAAC
<i>RcHDT1</i>	ACCAAGGCAATGTGGTGCA	CCCATTACGGATTGATAACCAGCA
<i>RcHDT2</i>	TCTTTCACAGGCCTGTCTGGA	TCCATGGAAGTGGACGCTCC
<i>RcHAG1</i>	CTGTACGGTGGGGCCTACTTC	CCCTGCTTCCTCCTCTCTCTT
<i>RcHAG2</i>	ATTTACCTGGTTTCTAGCAAA	GACTGTCAACAAGGGTCTCAC
<i>RcHAG4</i>	TAAACTTAGAATGGGTTGATAGG	GCCGGAGTGAGGCTTGTT
<i>RcHAC1</i>	CAGCTGGCTTCGTACTTTGGT	GCTCATTACATAGTCGTCCTCC
<i>RcHAC4</i>	CAATTTGACACCCTACGCC	TGCTGCTGCATGTCTTGTT
<i>RcHAF1</i>	CCAAATTACGTGATGCAGGAG	TTTTCAGAATCTAACGAGCCAAT
<i>RcHAF2</i>	AAGGGCTCGTAATGAGAAGGC	TTCATCACCCATAAGCAACCG
<i>RcACTIN</i>	TCAAGGATTGGTGGACTTCAGT	ACCAGAGAACAAGAATGCAAGC
<i>RcGAPDH</i>	GCTGGCAGGTATCCTTTCTG	GGCGACAATATCAGCCAAGT

Table S3. Genes encoding putative HDAC and HAT genes homologues in *R. chinensis*.

Subfamily	Gene ID	Name
RPD3/HDA1	<i>RchiOBHmChr3g0484871</i>	<i>RcHDA6-1</i>
	<i>RchiOBHmChr7g0192801</i>	<i>RcHDA6-2</i>
	<i>RchiOBHmChr5g0048241</i>	<i>RcHDA8</i>
	<i>RchiOBHmChr7g0184671</i>	<i>RcHDA15</i>
	<i>RchiOBHmChr2g0121851</i>	<i>RcHDA14-1</i>
	<i>RchiOBHmChr6g0310741</i>	<i>RcHDA2-1</i>
	<i>RchiOBHmChr6g0281731</i>	<i>RcHDA19</i>
	<i>RchiOBHmChr7g0218461</i>	<i>RcHDA9</i>
	<i>RchiOBHmChr7g0183031</i>	<i>RcHDA5</i>
	<i>RchiOBHmChr4g0398391</i>	<i>RcHDA2-2</i>
	<i>RchiOBHmChr6g0252021</i>	<i>RcHDA14-2</i>
	<i>RchiOBHmChr4g0419371</i>	<i>RcHDA2-3</i>
	<i>RchiOBHmChr1g0346631</i>	<i>RcHDA14-3</i>
	<i>RchiOBHmChr5g0034671</i>	<i>RcHDA2-4</i>
	<i>RchiOBHmChr5g0034681</i>	<i>RcHDA2-5</i>
	<i>RchiOBHmChr6g0304611</i>	<i>RcHDA14-4</i>
	<i>RchiOBHmChr6g0269961</i>	<i>RcHDA2-6</i>
	<i>RchiOBHmChr6g0269981</i>	<i>RcHDA2-7</i>
	<i>RchiOBHmChr5g0028711</i>	<i>RcHDA2-8</i>
SIR2	<i>RchiOBHmChr5g0053471</i>	<i>RcSRT1</i>
	<i>RchiOBHmChr2g0122631</i>	<i>RcSRT2</i>
HD2	<i>RchiOBHmChr5g0055321</i>	<i>RcHDT1</i>
	<i>RchiOBHmChr3g0472041</i>	<i>RcHDT2</i>
GNAT	<i>RchiOBHmChr6g0289651</i>	<i>RcHAG1</i>
	<i>RchiOBHmChr2g0092581</i>	<i>RcHAG2</i>
	<i>RchiOBHmChr7g0191201</i>	<i>RcHAG3-1</i>
	<i>RchiOBHmChr5g0026811</i>	<i>RcHAG3-2</i>
MYST	<i>RchiOBHmChr7g0240841</i>	<i>RcHAG4</i>
CBP	<i>RchiOBHmChr2g0163411</i>	<i>RcHAC1</i>
	<i>RchiOBHmChr2g0148331</i>	<i>RcHAC2</i>
	<i>RchiOBHmChr3g0448221</i>	<i>RcHAC4</i>
TAF _{II} 250	<i>RchiOBHmChr3g0492481</i>	<i>RcHAF1</i>
	<i>RchiOBHmChr5g0013481</i>	<i>RcHAF2</i>

Table S4. Genes encoding putative HDAC and HAT genes homologues in *R. multiflora*.

Subfamily	Gene ID	Name
RPD3/HDA1	<i>Rmu_sc0003880.1_g000035.1</i>	<i>RmHDA14</i>
	<i>Rmu_ssc0000289.1_g000024.1</i>	<i>RmHDA15</i>
	<i>Rmu_sc0004688.1_g000027.1</i>	<i>RmHDA2</i>
	<i>Rmu_ssc0000395.1_g000018.1</i>	<i>RmHDA2</i>
	<i>Rmu_sc0001408.1_g000004.1</i>	<i>RmHDA8</i>
	<i>Rmu_sc0002040.1_g000028.1</i>	<i>RmHDA6</i>
	<i>Rmu_sc0000014.1_g000006.1</i>	<i>RmHDA5</i>
	<i>Rmu_ssc0000126.1_g000063.1</i>	<i>RmHDA19</i>
	<i>Rmu_sc0001301.1_g000083.1</i>	<i>RmHDA9</i>
	<i>Rmu_sc0006898.1_g000006.1</i>	<i>RmHDA14</i>
	<i>Rmu_sc0010612.1_g000002.1</i>	<i>RmHDA14</i>
	<i>Rmu_sc0002351.1_g000007.1</i>	<i>RmHDA14</i>
	<i>Rmu_sc0003880.1_g000030.1</i>	<i>RmHDA2</i>
	<i>Rmu_sc0003720.1_g000019.1</i>	<i>RmHDA2</i>
	<i>Rmu_sc0003184.1_g000002.1</i>	<i>RmHDA14</i>
	<i>Rmu_sc0006653.1_g000010.1</i>	<i>RmHDA6</i>
	<i>Rmu_sc0002194.1_g000035.1</i>	<i>RmHDA14</i>
	<i>Rmu_sc0021556.1_g000004.1</i>	<i>RmHDA9</i>
SIR2	<i>Rmu_sc0005966.1_g000015.1</i>	<i>RmSRT1</i>
	<i>Rmu_sc0003133.1_g000010.1</i>	<i>RmSRT2</i>
HD2	<i>Rmu_sc0003641.1_g000018.1</i>	<i>RmHDT1</i>
	<i>Rmu_co8477099.1_g000001.1</i>	<i>RmHDT1</i>
	<i>Rmu_sc0002532.1_g000010.1</i>	<i>RmHDT1</i>
	<i>Rmu_sc0001665.1_g000047.1</i>	<i>RmHDT1</i>
	<i>Rmu_sc0011151.1_g000006.1</i>	<i>RmHDT1</i>
	<i>Rmu_sc0012467.1_g000004.1</i>	<i>RmHDT2</i>
GNAT	<i>Rmu_sc0005376.1_g000013.1</i>	<i>RmHAG1</i>
	<i>Rmu_co8234453.1_g000001.1</i>	<i>RmHAG3-1</i>
	<i>Rmu_sc0019130.1_g000001.1</i>	<i>RmHAG3-2</i>
	<i>Rmu_sc0003674.1_g000014.1</i>	<i>RmHAG3-3</i>
	<i>Rmu_ssc0000172.1_g000023.1</i>	<i>RmHAG3-4</i>
	<i>Rmu_sc0016007.1_g000009.1</i>	<i>RmHAG3-5</i>
MYST	<i>Rmu_sc0002313.1_g000023.1</i>	<i>RmHAG4</i>
	<i>Rmu_co8495669.1_g000001.1</i>	<i>RmHAG5-1</i>
	<i>Rmu_sc0004821.1_g000016.1</i>	<i>RmHAG5-2</i>
CBP	<i>Rmu_ssc0000231.1_g000004.1</i>	<i>RmHAC1</i>
	<i>Rmu_sc0005969.1_g000037.1</i>	<i>RmHAC2</i>
	<i>Rmu_sc0005969.1_g000044.1</i>	<i>RmHAC4</i>
TAF _{II} 250	<i>Rmu_sc0003458.1_g000019.1</i>	<i>RmHAF1</i>
	<i>Rmu_sc0020049.1_g000002.1</i>	<i>RmHAF2-1</i>
	<i>Rmu_sc0000971.1_g000001.1</i>	<i>RmHAF2-2</i>

Table S5. Gene encoding putative HDAC and HAT genes homologues in *F. vesca*.

Subfamily	Gene ID	Gene ID in old nomenclature	Name
RPD3/HDA1	<i>FvH4_5g06060.t1</i>	<i>gene09844</i>	<i>FvHDA6-1</i>
	<i>FvH4_1g25790.t1</i>	<i>gene12349</i>	<i>FvHDA6-2</i>
	<i>FvH4_5g13910.t1</i>	<i>gene37149</i>	<i>FvHDA5</i>
	<i>FvH4_2g17240.t1</i>	<i>gene17127</i>	<i>FvHDA1/ FvHDA 19</i>
	<i>FvH4_5g27310.t1</i>	<i>gene29263</i>	<i>FvHDA 9</i>
	<i>FvH4_3g26570.t1</i>	<i>gene40220</i>	<i>FvHDA8-1</i>
	<i>FvH4_2g32010.t1</i>	<i>gene35931</i>	<i>FvHDA2</i>
	<i>FvH4_3g26560.t1</i>	<i>gene27053</i>	<i>FvHDA8-2</i>
	<i>FvH4_1g24510.t1</i>	<i>gene16203</i>	<i>FvHDA14</i>
	<i>FvH4_5g12660.t1</i>	<i>gene26215</i>	<i>FvHDA15</i>
SIR2	<i>FvH4_1g24990.t1</i>	<i>gene16117</i>	<i>FvSRT2</i>
	<i>FvH4_3g29170.t1</i>	<i>gene15261</i>	<i>FvSRT1</i>
HD2	<i>FvH4_6g17790.t1</i>	<i>gene30136</i>	<i>FvHDT3-1</i>
	<i>FvH4_3g29940.t1</i>	<i>gene14356</i>	<i>FvHDT3-2</i>
GNAT	<i>FvH4_2g22590.t1</i>	<i>gene35776</i>	<i>FvHAG1</i>
	<i>FvH4_1g06810.t1</i>	<i>gene11375</i>	<i>FvHAG2</i>
	<i>FvH4_4g08670.t1</i>	<i>gene20524</i>	<i>FvHAG3-1</i>
	<i>FvH4_5g07450.t1</i>	<i>gene41363</i>	<i>FvHAG3-2</i>
	<i>FvH4_5g07410.t1</i>	<i>gene41358</i>	<i>FvHAG3-3</i>
	<i>FvH4_5g07340.t1</i>	<i>gene09922</i>	<i>FvHAG3-4</i>
	<i>FvH4_3g25041.t1</i>	<i>gene21768</i>	<i>FvHAG3-5</i>
MYST	<i>FvH4_5g38850.t1</i>	<i>gene02241</i>	<i>FvHAG4</i>
CBP	<i>FvH4_6g45470.t1</i>	<i>gene10338</i>	<i>FvHAC1</i>
	<i>FvH4_6g36320.t1</i>	<i>gene37806</i>	<i>FvHAC2</i>
	<i>FvH4_6g00740.t1</i>	<i>gene16783</i>	<i>FvHAC4</i>
TAF _{II} 250	<i>FvH4_1g29900.t1</i>	<i>gene30351</i>	<i>FvHAF1</i>
	<i>FvH4_3g05980.t1</i>	<i>gene30562</i>	<i>FvHAF2</i>

Table S6. Genes encoding putative HDAC and HAT genes homologues in *R. rugosa*.

Subfamily	Gene ID	name
RPD3/HDA1	<i>evm.model.Chr5.3090</i>	<i>RrHDA8</i>
	<i>evm.model.Chr6.3259</i>	<i>RrHDA14</i>
	<i>evm.model.Chr7.515</i>	<i>RrHDA5</i>
	<i>evm.model.Chr7.659</i>	<i>RrHDA15</i>
	<i>evm.model.Chr2.3097</i>	<i>RrHDA19</i>
	<i>evm.model.Chr7.1281</i>	<i>RrHDA6</i>
	<i>evm.model.Chr7.3446</i>	<i>RrHDA9-1</i>
	<i>evm.model.Chr7.3445</i>	<i>RrHDA9-2</i>
	<i>evm.model.Chr2.220</i>	<i>RrHDA2-1</i>
	<i>evm.model.Chr5.620</i>	<i>RrHDA2-2</i>
SIR2	<i>evm.model.Chr5.2852</i>	<i>RrSRT1</i>
HD2	<i>evm.model.Chr5.2728</i>	<i>RrHDT1</i>
GANT	<i>evm.model.Chr2.2236</i>	<i>RrHAG1-1</i>
	<i>evm.model.Chr2.2382</i>	<i>RrHAG1-2</i>
	<i>evm.model.Chr6.759</i>	<i>RrHAG2</i>
	<i>evm.model.Chr7.1155</i>	<i>RrHAG3-1</i>
	<i>evm.model.Chr5.413</i>	<i>RrHAG3-2</i>
MYST	<i>evm.model.Chr7.5663</i>	<i>RrHAG4</i>
CBP	<i>evm.model.Chr6.4885</i>	<i>RrHAC1</i>
	<i>evm.model.Chr6.6060</i>	<i>RrHAC2</i>
	<i>evm.model.Chr4.83</i>	<i>RrHAC4</i>
TAF _{II} 250	<i>evm.model.Chr3.1433</i>	<i>RrHAF1</i>
	<i>evm.model.Chr5.5920</i>	<i>RrHAF2</i>

Table S7. The FPKM values of HDAC and HAT genes in two *Rosa* species (*R. chinensis* ‘OB’ , *R. wichurana* ‘Rw’) and one modern rose cultivar (*R. hybrida* ‘Yesterday’ ‘Ry’).

Gene ID	Ro	Ste	Le	Sta	Ca	FB_GP	FB_CP	FB_PP	OF_PP	Rw_root	Rw_stem	Rw_leaf	Rw_bud	Ry_root	Ry_stem	Ry_leaf	Ry_bud
<i>RcHDA6-1</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA6-2</i>	68.1931	33.9198	28.3161	33.0634	40.4769	31.5418	28.0425	27.9431	28.2591	22.2996	38.1760	5.2150	21.8344	24.4309	29.8293	4.5677	4.0711
<i>RcHDA9</i>	15.7086	11.3277	12.9646	15.2004	16.3715	16.8983	14.3275	16.0481	21.2195	6.8115	7.2895	7.5479	9.5202	6.7564	5.9611	9.9143	3.0289
<i>RcHDA19</i>	33.1515	31.0477	22.9788	26.3391	45.6942	68.9842	52.4317	32.1443	28.7274	18.7022	33.0654	9.9082	56.1723	40.4236	31.7014	11.2303	11.7476
<i>RcHDA5</i>	5.3330	11.2574	7.4007	7.3819	11.6621	10.4497	8.8706	9.8802	9.5644	7.0039	4.5977	4.5117	13.6431	11.6056	4.9170	4.1314	1.1618
<i>RcHDA15</i>	14.3632	11.7600	12.1302	8.2263	16.9770	23.8132	16.8517	14.5127	14.0623	7.8336	4.9695	5.7866	13.9829	7.3094	2.7549	8.0570	3.4514
<i>RcHDA2-1</i>	7.0014	6.2643	7.1192	3.1700	7.8830	6.6625	5.8482	4.3865	2.5810	3.8068	3.8776	3.6504	3.5494	4.7202	5.0939	3.5281	0.8834
<i>RcHDA2-2</i>	0.0000	0.0000	0.0000	0.3754	0.0000	0.0641	0.0000	0.0342	0.0247	0.0000	0.0000	0.6927	1.0737	0.0000	0.0000	0.0000	0.0000
<i>RcHDA2-3</i>	0.0000	0.0000	0.0000	0.3518	0.1327	0.0235	0.1325	0.1446	0.7732	0.0000	0.1188	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA2-4</i>	0.0909	0.0000	0.0000	0.0000	0.0000	0.0195	0.0578	0.0104	0.0845	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA2-5</i>	0.2254	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0319	0.0516	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA2-6</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA2-7</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA2-8</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA8</i>	8.8498	12.3024	12.6038	4.5005	14.1289	10.8250	9.3778	5.7932	6.0205	4.6929	5.1043	4.2204	6.3255	6.9875	8.5854	8.7573	2.6562
<i>RcHDA14-1</i>	1.5716	1.8422	35.7098	0.6125	3.1743	3.2659	2.2479	1.9753	2.1350	1.0073	3.8203	33.9351	3.8945	0.2820	1.8873	19.6914	0.5048
<i>RcHDA14-2</i>	0.0000	0.0000	0.0011	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA14-3</i>	0.0000	0.0000	0.0012	0.0000	0.0000	0.0081	0.0033	0.0000	0.1842	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHDA14-4</i>	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcSRT1</i>	1.1230	2.5648	2.0542	2.0202	3.8120	6.6595	5.1210	3.4164	2.3537	1.2310	0.8315	1.7354	3.7786	1.3525	1.1302	2.9670	2.1712
<i>RcSRT2</i>	1.2859	2.0135	7.6563	6.6269	5.6303	6.6596	6.5398	13.2916	61.7715	2.7285	3.2299	9.0707	5.2049	1.9986	1.2590	10.6192	1.7019
<i>RcHDT1</i>	55.7067	39.4383	16.8726	9.8568	48.1027	75.9806	61.3818	23.1117	26.4237	19.9234	35.8015	8.0544	72.1256	32.1315	40.6580	12.0249	24.2593
<i>RcHDT2</i>	19.7365	50.8300	25.1223	37.2040	62.3613	69.4529	53.5825	50.3504	24.7683	9.2588	16.3931	18.8225	37.8389	13.3724	9.4953	27.7609	18.0468
<i>RcHAG1</i>	40.3758	18.8353	17.0497	18.3081	30.4076	28.7988	20.5563	15.5778	11.0712	13.5020	13.4019	3.7109	16.1484	12.7087	12.7984	5.0060	3.0419
<i>RcHAG2</i>	8.4054	13.1040	7.0987	4.3462	13.9784	17.9579	7.6617	5.5181	6.1029	8.6889	17.3268	2.3689	41.3577	14.0490	12.6186	4.7209	9.8482
<i>RcHAG3-1</i>	33.3840	12.5539	9.6280	6.4470	19.3447	45.0484	74.8625	33.8450	6.4529	10.4433	17.9833	2.8275	15.1442	12.1900	19.6265	1.3821	2.5073
<i>RcHAG3-2</i>	4.1221	3.4514	2.3028	0.8712	3.4352	2.7092	1.8352	0.8752	0.2171	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
<i>RcHAG4</i>	63.4138	29.7937	32.3686	31.2981	40.0903	45.1754	33.8188	33.6589	37.8126	17.2331	20.4130	15.0573	21.2715	22.3165	19.3228	14.1528	6.6573
<i>RcHAC1</i>	2.0300	0.9935	5.2661	3.3711	2.8370	5.8198	3.6232	1.7109	1.0468	0.9230	0.5309	0.1433	1.1033	0.9413	0.3669	0.0728	0.0969
<i>RcHAC2</i>	25.7755	16.6003	21.1333	16.9286	21.5600	19.7172	17.2877	18.1671	18.9509	11.0568	5.9854	1.3858	6.5107	13.4538	5.7406	0.8892	0.4081
<i>RcHAC4</i>	0.0000	0.0000	0.0000	0.1361	0.0726	0.9516	0.8626	0.4982	0.1796	0.0369	0.0000	0.0000	0.0000	0.0855	0.0353	0.0161	0.0000
<i>RcHAF1</i>	8.8430	7.1761	5.5243	10.3158	8.7373	9.3527	7.4391	9.6643	8.1126	5.3676	4.9543	0.4068	3.7509	6.3515	5.2237	0.1956	0.2868
<i>RcHAF2</i>	1.7758	2.0367	2.0384	1.7070	3.2219	3.9685	3.5418	3.4146	2.4542	1.1152	0.8675	0.0282	0.5996	1.0679	0.5825	0.0000	0.0000

Organs from *R. chinensis* ‘Old blush’ are labeled as Ro: roots; Ste: stems; Le: leaves; Sta: stamens; Ca: carpels; FB_GP: green petals in flower buds; FB_CP: petals changing colors in flower buds; FB_PP: pink petals ; and OF_PP: pink petals in open flowers. Organs from *R. wichurana* are labelled with ‘Rw’ (ex. *Rw_root* , etc.) , and those from *R. hybrida* ‘Yesterday’ are labelled with ‘Ry’ (ex. *Ry_root*, etc.)

Table S8. The expression values of selected HDAC and HAT genes in ‘CL’ roses grown under control (25°C) and high temperature (35°C) conditions.

Gene ID	25Se	25Pt	25St	25Pi	25Le	35Se	35Pt	35St	35Pi	35Le
<i>RcHDA6-1</i>	4.8506±0.3496 d	4.0044±0.4806 de	2.5522±1.0698 e	14.1843±5.4867 b	18.1732±2.5814 a	1.8529±0.1237 ef	2.1873±0.0757 e	13.4190±1.8155 c	1.2006±0.3398 ef	0.5211±0.1317 f
<i>RcHDA6-2</i>	0.6086±0.1559 d	0.8326±0.1681 c	1.2235±0.1733 b	0.8752±0.2481 c	0.3556±0.0370 e	2.0772±0.3620 a	0.8983±0.2292 c	0.4692±0.0602 e	0.4051±0.0829 e	1.2411±0.2629 b
<i>RcHDA19</i>	8.8756±1.7906 b	3.4863±0.2931 e	2.8117±0.6788 e	2.1002±0.4115 f	12.4680±1.3201 a	5.3915±0.3534 c	4.0827±0.9299 d	3.0453±0.2521 e	1.1409±0.0779 g	4.5421±1.1014 cd
<i>RcHDA5</i>	0.5122±0.1167 f	0.9359±0.1783 d	0.7973±0.0371 e	1.7458±0.2067 b	0.3883±0.1425 f	1.9893±0.1648 a	0.4993±0.0307 f	1.2431±0.3989 c	0.9272±0.2636 d	0.7287±0.1170 e
<i>RcHDA15</i>	8.2781±1.8727 a	2.4296±0.3994 c	0.2769±0.0499 e	0.3497±0.0737 e	9.0287±0.1675 a	4.3087±1.3349 b	0.4998±0.0712 de	0.9688±0.2704 d	0.2576±0.0601 e	1.0343±0.2594 d
<i>RcHDA2-1</i>	20.0741±4.3331 b	0.9844±0.1826 de	0.6382±0.0851 de	3.2011±0.2953 d	28.0703±9.6093 a	15.3868±2.5633 c	1.3153±0.1641 de	1.9210±0.3392 de	0.5115±0.0853 e	2.7652±0.5453 de
<i>RcHDA2-2</i>	7.1299±1.9705 a	0.2199±0.0219 e	0.2897±0.1016 e	1.0555±0.2472 d	5.2490±0.7321 b	4.2725±0.4489 c	0.3270±0.0202 e	0.7861±0.1833 de	0.0570±0.0110 e	0.8395±0.1067 de
<i>RcHDA2-5</i>	2.1915±0.1662 d	0.5711±0.0445 ef	2.2329±0.6074 d	5.9364±2.0183 b	8.5245±1.7927 a	1.0480±0.0369 e	0.9097±0.0732 e	3.1186±0.2843 c	0.5502±0.0079 ef	0.2158±0.0330 f
<i>RcHDA8</i>	2.1739±0.2603 de	1.7529±0.1744 e	4.1586±0.4008 c	9.0505±2.5483 a	4.8722±1.3556 b	1.0716±0.0998 ef	2.1070±0.1591 de	4.3894±2.0469 bc	2.7560±0.2036 d	0.6352±0.1090 f
<i>RcHDA14-2</i>	30.3796±3.9640 a	1.8330±0.0958 e	0.4198±0.0925 e	4.6780±1.3161 d	18.1518±1.7680 c	19.8382±3.8849 b	1.7624±0.2504 e	3.7971±2.2511 d	0.4414±0.0149 e	3.9057±0.1973 d
<i>RcHDA14-3</i>	2.2413±0.0396 a	0.0579±0.0006 f	0.0570±0.0184 f	0.4044±0.1950 d	1.2027±0.2751 c	1.3299±0.2324 b	0.1038±0.0370 f	0.2148±0.1357 e	0.0196±0.0027 f	0.2442±0.1508 e
<i>RcSTR2</i>	2.3103±0.2727 b	0.8531±0.0663 d	0.1770±0.0383 ef	0.1115±0.0227 f	11.0094±0.7852 a	1.4734±0.1468 c	0.6476±0.1798 d	0.3609±0.0382 e	0.0853±0.0176 f	0.8643±0.1583 d
<i>RcHDT1</i>	19.0941±1.7986 b	6.1130±1.5702 e	6.9274±1.6633 e	5.2706±0.4472 ef	32.8228±8.2153 a	12.9824±2.6456 c	6.9875±1.1008 e	10.2001±2.4904 d	3.6447±0.8866 f	14.5149±0.8345 c
<i>RcHDT2</i>	3.1477±0.4337 f	14.5394±2.1136 b	26.2947±4.0051 a	12.3364±0.9434 c	10.4573±2.1982 d	1.0000±0.1139 g	8.3614±1.2254 e	10.1392±1.5520 d	12.2903±0.8917 c	0.5743±0.1000 g
<i>RcHAG1</i>	280.4564±73.7220 c	374.4544±80.5126 b	120.5811±22.7445 e	58.3551±10.3943 f	1.0000±0.2309 g	183.5061±52.0257 d	164.4738±13.9708 de	429.7945±124.1338 a	103.1349±23.5513 e	396.8948±18.2811 b
<i>RcHAG2</i>	212.4227±30.9777 f	567.5547±169.4520 c	105.7994±28.8740 g	28.5742±3.9418 h	1.7770±0.4721 h	903.9821±89.8152 b	275.5408±37.6193 e	195.0845±64.7209 f	339.3324±19.4268 d	1211.4075±49.1641 a
<i>RcHAG4</i>	826.2873±27.4253 g	2645.1158±178.6772 d	677.9957±133.0009 g	318.4642±38.4116 h	248.1073±26.6545 h	4504.2930±332.9750 a	1527.1612±269.3548 e	1270.5757±502.8011 f	3666.4884±143.3607 b	3317.7079±235.6567 c
<i>RcHAC4</i>	191.5793±10.9531 a	21.0705±3.8870 f	7.0724±1.4421 g	19.0281±2.4499 fg	12.1759±1.5031 g	162.7796±16.7516 b	135.2246±7.0768 c	107.7987±25.1440 d	15.2267±2.6003 fg	96.6832±2.8881 e
<i>RcHAF2</i>	774.3281±79.4892 a	308.7874±3.3538 c	101.4640±23.4234 f	71.2960±10.7882 g	15.2515±1.8190 h	259.1747±40.4402 d	260.5073±19.1848 d	241.8952±22.5972 de	417.2425±11.6523 b	238.5693±5.1324 e

Means with different letters (a, b, c,...) indicate statistically significantly different at P<0.05, Single Factor ANOVA along with Least Significant Difference test).