

Table S1. Epigenetic markers in the transcriptome of potato phellogen †

Gene code	Gene name	Comment	FPKM	Sotub ID	TAIR ID
Chromatin assembly/disassembly/remodeling					
<i>SWC4*</i>	SWR1-COMPLEX 4			Sotub01g023480.1.1	At2g47210
<i>HMGB3</i>	HIGH MIBILITY GROUP B3		2117.77	Sotub02g026070.1.1	At1g20696.3
<i>HMGB3</i>	HIGH MIBILITY GROUP B3		1774.75	Sotub03g008810.1.1	At1g20696.2
<i>CHR4</i>	CHROMATIN REMODELING 19		818.05	Sotub02g014700.1.1	At5g44800.1
<i>CHR19</i>	CHROMATIN REMODELING 11		284.21	Sotub02g005500.1.1	At2g02090.1
<i>CHR11</i>	CHROMATIN REMODELING 11		6.64	Sotub01g021440.1.1	At3g06400.2
<i>EEN</i>	CHROMATIN REMODELING COMPLEX		2.57	Sotub06g006620.1.1	At4g38495.1
<i>CHC1</i>	CHROMATIN REMODELING COMPLEX ASSOCIATED WITH SWI/SNF		99.45	Sotub02g014170.1.1	At5g14170.1
<i>CHC1</i>	CHROMATIN REMODELING COMPLEX ASSOCIATED WITH SWI/SNF		1.37	Sotub03g023850.1.1	At5g14170.1
DNA methylation pathways					
<i>DRM2*</i>	DOMAINS REARRANGED METHYLTRANSFERASE		35.17	Sotub02g010360.1.1	At5g14620
<i>AGO4</i>	ARGONAUTE 4		408.96	Sotub01g009760.1.1	At2g27040.2
<i>DDM1</i>	NUCLEOSOME REMODELER		0.62	Sotub02g010390.1.1	At5g66750.1
<i>DRD1</i>	RNA-DIRECTED DNA METHYLATION 1		0.24	Sotub01g047420.1.1	At2g16390.1
<i>RDR2</i>	RNA-DEPENDENT RNA POL 2		466.40	Sotub03g027500.1.1	At4g11130.1
<i>ELF6</i>	EARLY FLOWERING 6		763.84	Sotub04g018130.1.1	At5g04240.1
DNA demethylation					
<i>DML1, ROS1</i>	DEMETER LIKE1		0.48	Sotub03g034510.1.1	At2g36490.1
Histone (de)methylation					
<i>ATX4*</i>	ARABIDOPSIS TRITHORAX	H3K4me3	3.53	Sotub01g033330.1.1	At4g27910
<i>ATXR4*</i>	ATX-Related	H3K4me3	0.68	Sotub03g011170.1.1	At5g06620
<i>SUVH4, KYP*</i>	SU(VAR)3-9 HOMOLOG, KRYPTONITE	H3K9me1	169.83	Sotub02g037730.1.1	At5g13960
<i>SUVH6*</i>			1.12	Sotub03g016470.1.1	At2g22740
<i>AL7</i>	ALFIN-LIKE 7 di- or trimethylated histone H3 (H3K4me3/2)	H3K4me3/2	1265.27	Sotub01g039670.1.1	At1g14510.1
<i>IBM1</i>	INCREASE IN BONSAI METHYLATION 1	H3mK9 demethylation	228.24	Sotub04g016780.1.1	At3g07610.1
<i>JMJ20</i>	JUMONJI DOMAIN-CONTAINING PROTEIN 20	H4-R3 demethylation	18.47	Sotub11g022090.1.1	At5g63080.1
<i>JMJ16</i>	JUMONJI DOMAIN-CONTAINING PROTEIN 16	H3K4 and H3K9 demethylation	8.29	Sotub04g009950.1.1	At1g08620.2
<i>JMJ26</i>	JUMONJI DOMAIN-CONTAINING PROTEIN 26	H3K9 demethylation	2.61	Sotub02g024130.1.1	At1g11950.1
<i>JMJ24</i>	JUMONJI DOMAIN-CONTAINING PROTEIN 24	H3K9 demethylation	1.65	Sotub02g021650.1.1	At1g09060.3
<i>JMJD5</i>	JUMONJI DOMAIN-CONTAINING PROTEIN D5	Histone demethylase	0.07	Sotub01g007240.1.1	At3g20810.1
Histone deacetylase					
<i>HDA3*</i>	HISTONE DEACETYLASE 3		8.25	Sotub11g024650.1.1	At3g44750
<i>HDA5</i>	HISTONE DEACETYLASE 5		50.12	Sotub03g028680.1.1	At5g61060.1
<i>HDA15</i>	HISTONE DEACETYLASE 15		1.41	Sotub03g033280.1.1	At3g18520.1
<i>SNL2</i>	SIN3-LIKE 2		4.52	Sotub02g035490.1.1	At5g15020.2
Histone acetyltransferase					
<i>HAC1</i>	HISTONE ACETYLASE 1		1021.46	Sotub01g008490.1.1	At1g79000.2
Known epigenetically regulated genes related to corky skin					
<i>H1.3</i>	HISTONE1.3		26.96	Sotub02g027480	At2g18050
<i>MYB1</i>	MYB TRANSCRIPTION FACTOR	Repression of lignin biosynthesis	6.84	Sotub01g048880	At4g38620

† (Vulavala et al. 2019)

* Putative regulators of *Q. suber* cork quality (Inácio et al. 2018)