

Table S1. PRC2 core components in different species

(Abbreviations: E(z) - Enhancer of zeste, Su(z)12 - Suppressor of zeste 12, ESC - Extra sex combs, Nurf55 - Nucleosome remodelling factor (also called p55), MSI - Multicopy Suppressor of IRA, MEZ - Maize Enhancer of zeste-like, CLF - CURLY LEAF, SWN - SWINGER, MEA - MEDEA, EMF2 - EMBRYONIC FLOWER 2, FIS2 - FERTILIZATION INDEPENDENT SEED 2, VRN2 - VERNALIZATION 2, FIE- FERTILIZATION INDEPENDENT ENDOSPERM, ESCL - ESC-like, MES- Maternal-Effect sterile, RBBP- Retinoblastoma Binding Protein, RbAp-Retinoblastoma Associated protein CAF1 - Chromatin Assembly Factor 1, NPF - *Neurospora* homolog of *Drosophila* P55 and mammalian P48.). Percentage identity/similarity (based on EMBOSS Needle[1]) to the *Drosophila melanogaster* PRC2 subunits are given in brackets (only full-length sequences available in the NCBI GenBank were used).

Supergroups	Eukaryotic group/Kingdom	Phylum or Class	Species	E(z) homolog	Su(z) homolog	Esc homolog	p55 homolog	References
Archaeplastida	Eukaryota	Rhodophyta	<i>Cyanidioschyzon merolae</i>	CmE(z) (24.3/ 37.6)	CmSu(z)12	CmESC	p55 (2) (46.3/63.0)	[2]
	Viridiplantae	Chlorophyta	<i>Ostreococcus lucimarinus</i>	OIKMT6A2 (20.1/29.8)	OIEMF2	OIFIE	OIMSI1, OIMSI4 (59.1/73.0)	[3]
			<i>Chlamydomonas reinhardtii</i>	CrE(z)/CrKMT6A2 (22.2/33.0)	CrEMF2 (12.1/21.5)	CrESC.1/2 or CrFIE (26.6/39.9)	CrMSI1 (59.6/74.5) CrMSI4	[2,3]
			<i>Volvox carteri</i>	VcKMT6A1; VcKMT6A3	-	VcFIE	VcMSI1 (61.5/74.9) VcMSI4	[3]
	Viridiplantae - Embryophyta	Bryophyta - Bryopsida	<i>Physcomitrium patens</i> (Moss)	PpCLF (22.5/31.1)	PpEMF2a, PpEMF2b, PpEMF2c (13.1/22.4)	PpFIE (31.9/50.0)	PpMSI1 (64.7/79.8), PpMSI4	[3–6]
		Lycophyte - Lycopodiopsida	<i>Selaginella moellendorffii</i> (primitive spikemoss)	SmKMT6A 1a SmKMT6A 1b (CLF like) (21.9/32.6)	SdEMF2p, SdEMF2p_1 (13.6/22.7)	SmFIE (34.5/52.1)	SmMSI1 (62.3/74.9) SmMSI2a, SmMSI2b	[3,6,7]
		Gymnosperm	<i>Picea abies</i>	E(z) (CLF)	?	?	?	[8]
		Angiosperms - Monocot	<i>Oryza sativa</i> (Rice)	OsIEZ1 (OsSWN) (21.3/32.6), OsCLF (23.8/36.4)	OsEMF2a, OsEMF2b (13.6/24.0)	OsFIE1 (32.5/47.8), OsFIE2	OsMSI1 (62.4/76.8), OsMSI2,	[7,9–12]
			<i>Triticum aestivum</i> (Bread wheat)	TaE(z)-4A1, TaE(z)-7A1.1, TaE(z)-7A1.2 (24.4/36.9)	TaSu(z)-2A1, TaSu(z)-2A2, TaSu(z)-5A1 (16.0/27.8)	TaFIE-7A1, TaFIE-7A2.1, TaFIE-7A2.2, TaFIE-4A1 (34.0/51.9)	TaMSI1-A1, TaMSI1-A2 (62.4/77.0)	[13]
			<i>Zea mays</i> (Maize)	ZmMEZ1 (CLF) (22.2/34.8), ZmMEZ2 (SWN1)	ZmEMF2a/2-1, ZmEMF2b/2-2 (15.1/26.8)	ZmFIE1, ZmFIE2 (33.7/49.2)	ZmMSI1-1 (62.4/77.4), ZmMSI1-2,	[10]

				(24.1/36.9), ZmMEZ3 (SWN2)			ZmMSI1-3, ZmMSI1-4, ZmMSI2	
			<i>Brachypodium distachyon</i> (Model grass)	BdEZL1 (CLF ortholog, BdCLF) (27.6/41.6), BdEZL2 (SWN ortholog, BdSWN)	BdEMF2a, BdEMF2b (14.8/23.6)	BdFIE1, bdFIE2, bdFIE3 (33.8/51.2)	BdMSI1a (62.1/77.4), BdMSI1b, BdMSI3, BdMSI4	[3,14,15]
			<i>Hordeum vulgare</i> (Barley)	HvCLF1, HvCLF2, HvSWN (25.6/39.4)	HvSu(z)12a (HvEMF2a), HvSu(z)12b (HvEMF2b), HvSu(z)12c (HvEMF2c) (15.6/27.5)	HvFIE (26.8/41.5)	HvMSI1 (62.4/76.8), HvMSI2	[10,16,17]
			<i>Sorghum bicolor</i>	SbCLF (20.6/32.2), SbSWN	SbEMF2a (15.2/25.3), SbEMF2b, SbEMF2c	SbFIE1, SbFIE2 (28.2/43.3)	SbMSI1 (63.0/77.4), SbMSI2	[10]
		Angiosperms - Eudicot	<i>Arabidopsis thaliana</i>	CLF (23.7/36.6), SWN (24.8/37.4), MEA (26.0/38.2)	EMF2 (15.0/26.8), FIS2 (14.4/25.0), VRN2 (10.5/17.9)	FIE (33.3/50.5)	MSI1 (62.9/77.3), MSI2, MSI3, MSI4, MSI5	[18]
Chromalveolata	SAR-Stramenopiles	Bacillariophyceae (diatoms)	<i>Phaeodactylum tricornutum</i>	Ez	Suz12	Esc	Nurf55(p55) (48.2/61.9)	[3,19]
	SAR - Alveolata	Ciliophora/ ciliates	<i>Paramecium tetraurelia</i>	Ez1p (20.3/36.0), Ez2p	-	-	Nurf55 (47.0/62.8)	[20–22]
			<i>Tetrahymena thermophila</i>	EZL1 (E(z)-like 1) (18.5/31.0)	SUZ12	ESC1	RebL1 (47.5/65.1)	[23,24]
Opisthokonta	Fungi	Basidiomycota	<i>Cryptococcus neoformans</i>	Ezh2 (20.8/30.8)	-	Eed1 (20.5/31.3)	Msl1 (51.5/67.7)	[25,26]
		Ascomycota	<i>Fusarium graminearum</i> / <i>Gibberella zeae</i>	SET-7/KMT6 (13.4/22.3)	Suz12	EED (19.5/31.0)	MSL1 (43.9/62.1), CAF1-3	[26,27]
			<i>Chaetomium thermophilum</i>	Ezh2 (11.3/19.2)	Su(z)12	EED (17.0/27.4)	p55 (45.4/66.5)	[28,29]
			<i>Neurospora crassa</i>	SET-7 (KMT6) (11.7/18.9)	SUZ12 (15.0/25.1)	EED (16.2/25.6)	NPF (p55) (44.8/64.4)	[26,30,31]
			<i>Saccharomyces cerevisiae</i>	-	-	-	-	[22,32]
	Filasterea- single- celled eukaryote	Capsaspora	<i>Capsaspora owczarzaki</i>	-	-	-	-	[33]
	Animalia/animals	Porifera	<i>Amphimedon queenslandica</i>	E(z) (4 copies)	Su(z)12 (17.0/24.7)	ESC, ESCL	Nurf55	[34]
		Cnidaria/ Hydrozoa	<i>Hydra vulgaris</i> (swiftwater hydra)	HyEZH2	Su(z)12-like (predicted) (20.5/35.3)	HyEED (42.7/62.1)	RBBP7	[35–38]

		Insecta/ insects	<i>Drosophila melanogaster</i>	E(z) (100/100)	Su(z)12 (100/100)	Esc/Escl (100/100)	p55 (Nurf55) (100/100)	[39–41]
		Nematoda/ nematodes	<i>Caenorhabditis elegans</i>	MES-2 (22.6/33.5)	-	MES-6 (23.4/36.9)	-	[42,43]
		Reptilia/ reptiles	<i>Anolis carolinensis</i> (green anole/chameleon)	AcEZH2 (52.1/62.2)	SUZ12 (26.1/38.2)	EED (46.4/63.9)	RBBP4	[44–47]
		Mammalia/ mammals	<i>Homo sapiens</i>	EZH1(50.3/63.2), EZH2 (53.5/63.8)	SUZ12 (28.8/42.6)	EED (47.8/66.6)	RBBP4/7 (RbAp48 /RbAp46) (87.8/93.8)	[48,49]
			<i>Mus musculus (Mouse)</i>	EZH1(49.9/62.9), EZH2 (54.3/64.4)	SUZ12 (28.3/42.0)	EED (48.2/66.7)	RbAp48 (87.5/93.5)	[50,51]

Table S2. A general overview at the distribution of H3K27me3 and its putative functions across various studied species.

Supergroups	Eukaryotic group/ Kingdom	Phylum or Class	Species	H3K27me3 distribution	H3K27me3 distribution related to H3K9me2/3 and/or DNA methylation	Proposed function	References
Archaeplastida	Eukaryota	Rhodophyta	<i>Cyanidioschyzon merolae</i>	Telomeric and subtelomeric regions (4% annotated genes and 50 % repetitive elements)	Unknown	Regulate gene repression especially associated with Intein-mediated splicing of proteins.	[2]
	Viridiplantae	Chlorophyta	<i>Chlamydomonas reinhardtii</i>	H3K27me3 absent or present in very low levels	No effect on K9me1/3 or DNA methylation	Repression of repetitive genomic elements	[22]
	Viridiplantae - Embryophyta	Bryophyta - Bryopsida	<i>Physcomitrium patens</i>	Genes (preference for shorter genes)	Non-overlapping	Repression of apogamy	[4,5,52]
		Marchantiophyta- Marchantiopsida	<i>Marchantia polymorpha</i>	10% annotated genes and 20 % in repetitive elements	Non-overlapping	Repression of genes and repeats (TEs)	[53]
		Pinophyta – Pinopsida (Gymnosperm)	<i>Picea abies</i>	Genes-uniformly distributed, additionally clustered in the mid arm position	Unknown	Embryogenesis, cell-fate determination	[8,54]
			<i>Pinus sylvestris</i>		Unknown		
		Angiosperms -Eudicot	<i>Arabidopsis thaliana</i>	20% – 30% annotated genes (domains <1kb)	Mutually exclusive, H3K27me3 spreading into H3K9me2-regions upon DNA demethylation	Development, phase transitions	[55–62]

Chromalveolata	SAR-Stramenopiles	Bacillariophyceae (diatoms)	<i>Phaeodactylum tricornutum</i>	7% annotated genes, 41% annotated TE and intergenic region	H3K27me3, H3K9me2/3, and DNA methylation coexist (H3K27me3 overlap with H3K9me2)	Transcriptional silencing (role in signal transduction, development and cell cycle control; morphology/cell differentiation)	[19,63]
		Ochrophyta-Phaeophyceae	<i>Ectocarpus</i>	H3K27me3 present but distribution unknown	Unknown	Unknown	[64]
	SAR - Alveolata	Cilliophora/ciliates (Chromalveolata)	<i>Tetrahymena thermophila</i>	micronucleus (K27&K9me1/2/3); macronucleus especially anlagen	Co-exist	Developmental regulation and foreign DNA elimination during somatic differentiation, macronucleus differentiation	[65,66]
			<i>Paramecium tetraurelia</i>	Newly developing macronucleus	Co-exist- H3K27me3 and H3K9me3 co-occur at TEs	Control RNAi, Transcriptional silencing of transposable elements (for the development of sexually viable progeny and the elimination of DNA)	[21]
Opisthokonta	Fungi	Basidiomycota	<i>Cryptococcus neoformans</i>	Subtelomeres - broad domains (average 41 kb). On repetitive elements cover 5% of the genome	Redistribution to centromeric H3K9me2-marked regions upon disruption of H3K27me3-marked chromatin binding; redistribution depends on H3K9me2 deposition	Dispensable for normal growth and development	[25]
		Ascomycota	<i>Neurospora crassa</i>	Subtelomeres and telomeres, including genes (broad domain-~12.5 kb)	H3K27me3 and H3K9me3 form distinct domains at telomeric regions (adjacent, but no overlap)	Developmental regulations	[30,31,67]
			<i>Saccharomyces cerevisiae</i> and <i>S. pombe</i>	Lacks H3K27 methylation	-	-	[68]
			<i>Candida albicans</i>	Lacks H3K27 methylation	-	-	[68]
	Animalia/animals	Porifera	<i>Amphimedon queenslandica</i>	Gene bodies	Unknown	Developmental regulatory genes	[34]
		Insecta/insects	<i>Drosophila melanogaster</i>	Genes (broad domains ~70kb)	H3K27me3 deposition is independent from DNA methylation. Non-overlapping or antagonistic relationship	Gene silencing or facultative heterochromatin formation (Developmental gene regulation)	[69]

					between H3K27me3 and H3K36me2/3 (De et al., 2020)		
	Nematoda/nematodes	<i>Caenorhabditis elegans</i>	X-chromosome, H3K27me3 levels are higher on arm regions compared to the centre	H3K9me3-marked chromatin coincides with H3K27me3. Antagonistic relationship between H3K27me3 and H3K36me2/3	Germline development, repression of X-chromosome	[43,70–72]	
	Mammalia/mammals	Mus musculus, Homo sapiens	Genes, telomeres (Broad domains (~43kb))	H3K27me3 and H3K9me3 distributions are mutually exclusive.	Developmental gene regulation	[73,74]	

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