Electronic Supplementary Material (ESI) for Environmental Science: Nano.

Electronic Supplementary Information (ESI)

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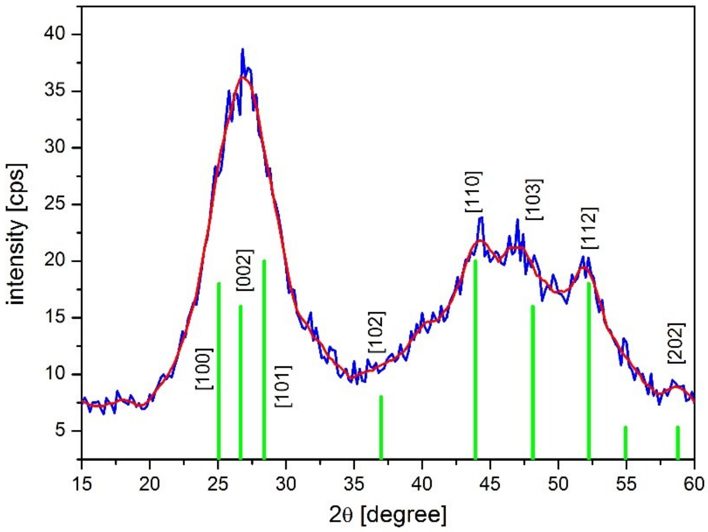


Figure S1: XRD pattern of as-grown CdS QDs. Green lines refer to hexagonal CdS (greenockite) as reported in JCPDS no. 80-0006.

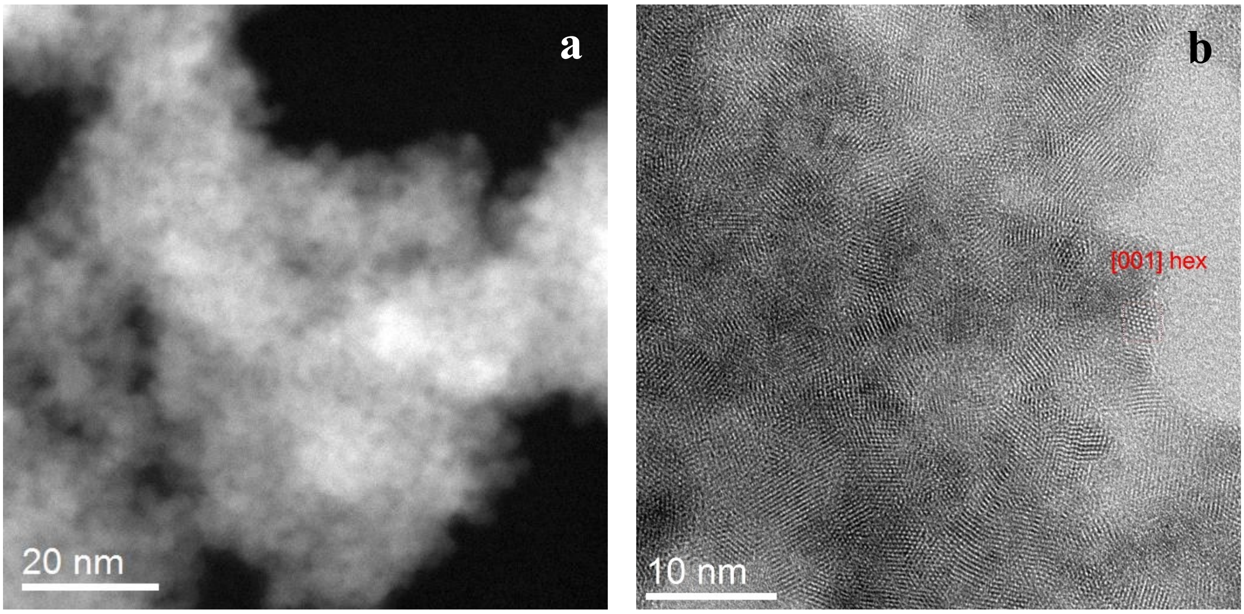


Figure S2: S/TEM (a) and HREM (b) image of as-synthesized CdS QDs.

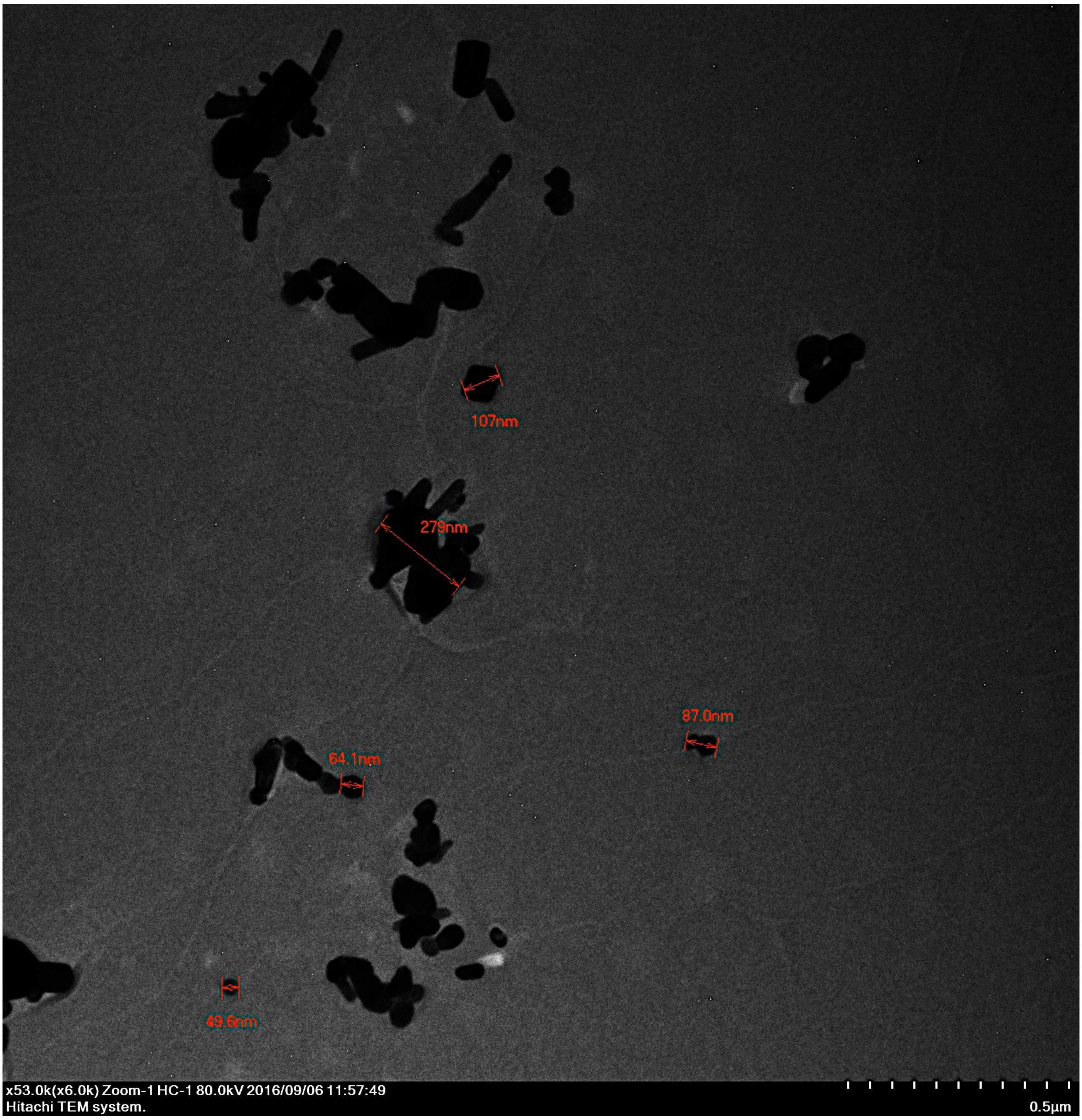


Figure S3: TEM image of ZnO NPs. TEM images related to CeO_2, La_2O_3 and CuO NPs are reported from in Pagano *et al*. (2016).[1]

Table S1: List of the 38 *C. pepo* genes used in the study (primer sequences used reported in Pagano *et. al.*, 2016).[1]

ref	**GeneID *A. thaliana***	**GeneID *C. pepo***	**gene name/function**
005u	*At1g09080*	*CUTC002577*	BIP3, Heat shock protein 70 (Hsp 70) family protein
008u	*At1g11190*	*CUTC008849*	BFN1, ENDO1, bifunctional nuclease i
013u	*At1g23730*	*CUTC008070*	ATBCA3, BCA3, beta carbonic anhydrase 3
026u	*At1g61800*	*CUTC007694*	ATGPT2, GPT2, glucose-6-phosphate/phosphate translocator 2
032u	*At1g69120*	*CUTC012366*	AGL7, AP1, K-box region and MADS-box transcription factor family protein
046u	*At2g21640*	*CUTC018024*	Encodes a protein of unknown function that is a marker for oxidative stress response.
048u	*At2g23030*	*CUTC008834*	SNRK2-9, SNRK2.9, SNF1-related protein kinase 2.9
051u	*At2g26560*	*CUTC012732*	PLA IIA, PLA2A, PLP2, PLP2, phospholipase A 2A
066u	*At3g02310*	*CUTC014559*	AGL4, SEP2, K-box region and MADS-box transcription factor family protein
070u	*At3g08860*	*CUTC004179*	PYD4, PYRIMIDINE 4
071u	*At3g12520*	*CUTC007045*	SULTR4;2, sulfate transporter 4;2
083u	*At3g54340*	*CUTC014559*	AGL4, SEP2, K-box region and MADS-box transcription factor family protein
086u	*At3g59845*	*CUTC001470*	Zinc-binding dehydrogenase family protein
090u	*At4g04460*	*CUTC002381*	PASPA3, Saposin-like aspartyl protease family protein
093u	*At4g12280*	*CUTC008356*	copper amine oxidase family protein
098u	*At4g16370*	*CUTC009101*	ATOPT3, OPT3, OPT3, oligopeptide transporter
099u	*At4g21680*	*CUTC041648*	NRT1.8, NITRATE TRANSPORTER 1.8
119u	*At5g20240*	*CUTC042444*	PI, K-box region and MADS-box transcription factor family protein
124u	*At5g24470*	*CUTC023690*	APRR5, PRR5, pseudo-response regulator 5
127u	*At5g26220*	*CUTC045405*	GGCT2;1, ChaC-like family protein
128u	*At5g26340*	*CUTC013905*	ATSTP13, MSS1, STP13, Major facilitator superfamily protein
139u	*At5g48850*	*CUTC039723*	ATSDI1, Tetratricopeptide repeat (TPR)-like superfamily protein
140u	*At5g50260*	*CUTC003431*	CEP1, Cysteine proteinases superfamily protein
143u	*At5g54960*	*CUTC034909*	PDC2, pyruvate decarboxylase-2
147u	*At5g61380*	*CUTC019875*	APRR1, AtTOC1, PRR1, TOC1, CCT motif -containing response regulator protein
150u	*AtCg00065*	*CUTC021188*	RPS12, RPS12A, ribosomal protein S12A
151u	*AtCg00360*	*CUTC004189*	YCF3, Tetratricopeptide repeat (TPR)-like superfamily protein
152u	*AtCg00590*	*CUTC036811*	ORF31, chloroplastic electron carriers
155u	*AtCg00700*	*CUTC045946*	PSBN, photosystem II reaction center protein N

ref	**GeneID *A. thaliana***	**GeneID *C. pepo***	**gene name/function**
001d	*At1g01060*	*CUTC042801*	LHY, LHY1, Homeodomain-like superfamily protein
002d	*At1g08830*	*CUTC000155*	CSD1, copper/zinc superoxide dismutase 1
004d	*At1g12520*	*CUTC013469*	ATCCS, CCS, copper chaperone for SOD1
008d	*At1g29660*	*CUTC012295*	GDSL-like Lipase/Acylhydrolase superfamily protein
011d	*At1g73010*	*CUTC016360*	ATPS2, PS2, phosphate starvation-induced gene 2
016d	*At2g11810*	*CUTC015342*	ATMGD3, MGD3, MGDC, monogalactosyldiacylglycerol synthase type C
018d	*At2g28190*	*CUTC015722*	CSD2, CZSOD2, copper/zinc superoxide dismutase 2
036d	*At5g01600*	*CUTC001028*	ATFER1, FER1, ferretin 1
037d	*At5g02540*	*CUTC012876*	NAD(P)-binding Rossmann-fold superfamily protein
043d	*At5g43350*	*CUTC049068*	ATPT1, PHT1;1, phosphate transporter 1;1
045d	*At5g43780*	*CUTC008032*	APS4, Pseudouridine synthase/archaeosine transglycosylase-like family protein

Table S2: ZnO NP and bulk and CdS QD and bulk biomass (a), moisture content (b) and root/shoot length (c) and relative Tukey's (HSD) pairwise multiple comparisons ($p < 0.05$); A represents always the lowest mean. ZnO bulk and CdS QD treatment biomass, as well as leaf moisture content of ZnO bulk and root length for CdS bulk, were significantly reduced as compared with the control untreated.

a. Biomass (g)

sample	biomass	stdev	%	HSD	
untreated	4.054	0.610	100.0	B	AB
ZnO NPs	4.640	0.537	114.5	-	B
ZnO bulk	2.134	0.459	52.6	-	A
CdS QDs	2.762	0.280	68.1	A	-
CdS bulk	3.340	0.576	82.4	AB	-

b. Moisture content (g/g)

sample	leaves	st dev	HSD		stems	st dev	HSD		roots	st dev	HSD	
untreated	19.239	7.008	A	AB	0.972	0.021	A	A	44.333	24.066	A	A
ZnO NPs	19.079	1.253	-	A	0.970	0.006	-	A	43.133	23.879	-	A
ZnO bulk	35.200	12.849	-	B	0.986	0.003	-	A	34.600	10.526	-	A
CdS QDs	25.448	5.555	A	-	0.977	0.011	A	-	31.200	9.358	A	-
CdS bulk	23.712	3.775	A	-	0.977	0.005	A	-	49.400	11.739	A	-

c. Length (cm)

sample	shoots	st dev	HSD		roots	st dev	HSD	
untreated	18.340	3.669	A	A	24.000	6.255	AB	A
ZnO NPs	18.580	3.979	-	A	33.160	2.530	-	A
ZnO bulk	14.560	2.317	-	A	24.580	6.940	-	A
CdS QDs	16.200	0.967	A	-	22.580	4.115	A	-
CdS bulk	18.620	2.435	A	-	32.000	5.962	B	-

Table S3: Nanomaterial combined treatment (NMCT) biomass (a), moisture content (b) and root/shoot length (c) and relative Tukey's (HSD) pairwise multiple comparisons ($p < 0.05$); A represents always the lowest mean.

a. Biomass (g)

sample	biomass	st dev	%	HSD
untreated	2.858	0.671	100.0	AB
CeO_2 NPs + La_2O_3 NPs	3.542	0.821	123.9	AB
CeO_2 NPs + CuO NPs	4.174	1.065	146.0	B
CeO_2 NPs + ZnO NPs	3.566	0.724	124.8	AB
CeO_2 NPs + CdS QDs	2.188	0.564	76.6	A
La_2O_3 NPs + CuO NPs	2.960	0.275	103.6	AB
La_2O_3 NPs + ZnO NPs	3.938	0.774	137.8	B
La_2O_3 NPs + CdS QDs	3.624	1.082	126.8	AB
CuO NPs + ZnO NPs	3.412	0.935	119.4	AB
CuO NPs + CdS QDs	2.540	0.824	88.9	AB
ZnO NPs + CdS QDs	3.096	0.379	108.3	AB

b. Moisture content (g/g)

sample	leaves	st dev	HSD	stems	st dev	HSD	roots	st dev	HSD
untreated	22.300	5.975	AB	0.971	0.003	A	0.944	0.017	A
CeO_2 NPs + La_2O_3 NPs	19.790	11.338	AB	0.963	0.005	A	0.953	0.013	A
CeO_2 NPs + CuO NPs	12.577	1.668	A	0.950	0.010	A	0.946	0.008	A
CeO_2 NPs + ZnO NPs	26.195	6.320	AB	0.977	0.009	A	0.968	0.014	A
CeO_2 NPs + CdS QDs	24.558	12.392	AB	0.982	0.008	A	0.970	0.004	A
La_2O_3 NPs + CuO NPs	41.633	23.288	B	0.987	0.009	A	0.981	0.003	A
La_2O_3 NPs + ZnO NPs	20.988	5.749	AB	0.972	0.004	A	0.973	0.007	A
La_2O_3 NPs + CdS QDs	26.678	11.100	AB	0.978	0.006	A	0.974	0.010	A
CuO NPs + ZnO NPs	29.327	7.102	B	0.978	0.010	A	0.977	0.009	A
CuO NPs + CdS QDs	19.973	6.575	AB	0.978	0.004	A	0.954	0.011	A
ZnO NPs + CdS QDs	38.150	17.966	B	0.976	0.006	A	0.978	0.006	A

c. Length (cm)

sample	shoots	st dev	HSD	roots	st dev	HSD
untreated	16.060	1.220	AB	29.720	7.650	A
CeO_2 NPs + La_2O_3 NPs	18.980	2.070	BC	29.740	5.700	A
CeO_2 NPs + CuO NPs	18.800	1.680	BC	31.800	3.270	A
CeO_2 NPs + ZnO NPs	18.160	1.180	AB	25.620	4.470	A
CeO_2 NPs + CdS QDs	14.840	0.970	A	24.660	5.790	A
La_2O_3 NPs + CuO NPs	17.860	2.830	BC	26.540	2.840	A
La_2O_3 NPs + ZnO NPs	20.440	1.970	C	30.120	5.630	A
La_2O_3 NPs + CdS QDs	19.460	2.280	BC	25.920	2.360	A
CuO NPs + ZnO NPs	19.540	1.260	BC	28.120	8.550	A
CuO NPs + CdS QDs	17.240	1.370	BC	24.300	4.520	A
ZnO NPs + CdS QDs	16.660	1.460	AB	23.500	2.760	A

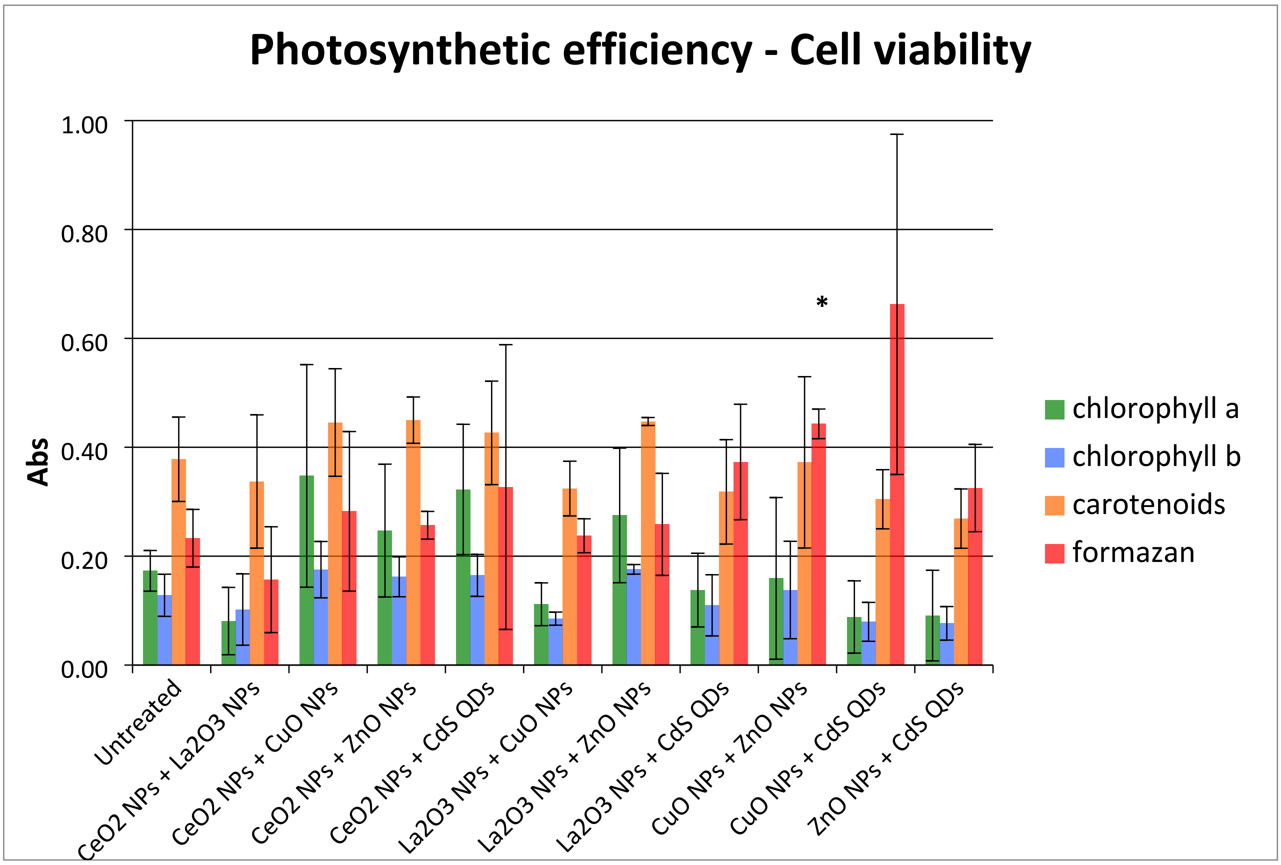


Figure S4: Nanomaterial combined treatment (NMCT) photosynthetic efficiency, expressed as absorbance of chlorophyll *a* (662 nm), *b* (645 nm) and carotenoids (470 nm), and cell viability, as absorbance of formazan (530 nm) derived from the TTC reduction. No significant differences between the control (untreated) and the treatments are evident, except in the case of formazan (CuO+ZnO NP treatment; t-test: *, $p < 0.05$; **, $p < 00.1$; ***, $p < 000.1$).

Biomass Differential Effect (BDE) index – Equations:

(α) $\text{Index}_{\text{BMT}} = \text{biomass}_{\text{bulk}} / \text{biomass}_{\text{control}}$

(β) $\text{Index}_{\text{NMCT}} = \text{biomass}_{\text{NMCT}} / \text{biomass}_{\text{control}}$

(λ) $\text{Index}_{\text{NMIT}} = \text{biomass}_{\text{NMIT}} / \text{biomass}_{\text{control}}$

(δ) $\text{BDE}_{\text{BMT}} = \text{Index}_{\text{BMT}} / \text{Index}_{\text{NMIT}}$

(ε) $\text{BDE}_{\text{NMCT}} = \text{Index}_{\text{NMCT}} / \text{Index}_{\text{NMIT}}$

Table S4: Tables (a) report values for equation (α), (b) for equation (β), (c) for equation (λ), (d) for equation (δ), (e) for equation (ε). Calculation of the Biomass Differential Effect (BDE) index for BMTs and NMCTs follow the equations reported. References reported in S5d,e represent the different materials CeO_2 NPs (A), CeO_2 bulk (bA), La_2O_3 NPs (B), La_2O_3 bulk (bB), CuO NPs (C), CuO (bC), ZnO NPs (D), ZnO bulk (bD), CdS QDs (E), CdS (bE) and their combinations, respectively.

(a)

BMT	**Index $_{\text{BMT}}$**
CeO_2 bulk	1.24753
La_2O_3 bulk	0.96476
CuO bulk	0.88612
ZnO bulk	0.52639
CdS bulk	0.82388

(b)

NMIT	**index $_{\text{NMIT}}$**
CeO_2 NPs	1.30926
La_2O_3 NPs	1.18080
CuO NPs	0.91275
ZnO NPs	1.14455
CdS QDs	0.68130

(c)

NMCT	$\text{Index}_{\text{NMCT}}$
CeO_2 NPs + La_2O_3 NPs	1.23933
CeO_2 NPs + CuO NPs	1.46046
CeO_2 NPs + ZnO NPs	1.24773
CeO_2 NPs + CdS QDs	0.76557
La_2O_3 NPs + CuO NPs	1.03569
La_2O_3 NPs + ZnO NPs	1.37789
La_2O_3 NPs + CdS QDs	1.26802
CuO NPs + ZnO NPs	1.19384
CuO NPs + CdS QDs	0.88873
ZnO NPs + CdS QDs	1.08328

(d)

ref	BMT	NMIT	BDE_{BMT}
bA vs A	CeO_2	CeO_2 NPs	1.04948
bB vs B	La_2O_3	La_2O_3 NPs	1.22393
bC vs C	CuO	CuO NPs	1.03005
bD vs D	ZnO	ZnO NPs	2.17432
bE vs E	CdS	CdS QDs	0.82695

(e)

ref	NMCT	NMIT	BDE_{NMCT}
AB vs A	CeO_2 NPs + La_2O_3 NPs	CeO_2 NPs	1.05643
AC vs A	CeO_2 NPs + CuO NPs		0.89647
AD vs A	CeO_2 NPs + ZnO NPs		1.04932
AE vs A	CeO_2 NPs + CdS QDs		1.71017
AB vs B	CeO_2 NPs + La_2O_3 NPs	La_2O_3 NPs	0.95278
BC vs B	La_2O_3 NPs + CuO NPs		1.14011
BD vs B	La_2O_3 NPs + ZnO NPs		0.85697
BE vs E	La_2O_3 NPs + CdS QDs		0.93122
AC vs C	CeO_2 NPs + CuO NPs	CuO NPs	0.62497
BC vs C	La_2O_3 NPs + CuO NPs		0.88130
CD vs C	CuO NPs + ZnO NPs		0.76455
CE vs E	CuO NPs + CdS QDs		1.02702
AD vs D	CeO_2 NPs + ZnO NPs	ZnO NPs	0.91731
BD vs D	La_2O_3 NPs + ZnO NPs		0.83066
CD vs D	CuO NPs + ZnO NPs		0.95871
DE vs D	ZnO NPs + CdS QDs		1.05656
AE vs E	CeO_2 NPs + CdS QDs	CdS QDs	0.88993
BE vs E	La_2O_3 NPs + CdS QDs		0.53730
CE vs E	CuO NPs + CdS QDs		0.76660
DE vs E	ZnO NPs + CdS QDs		0.62893

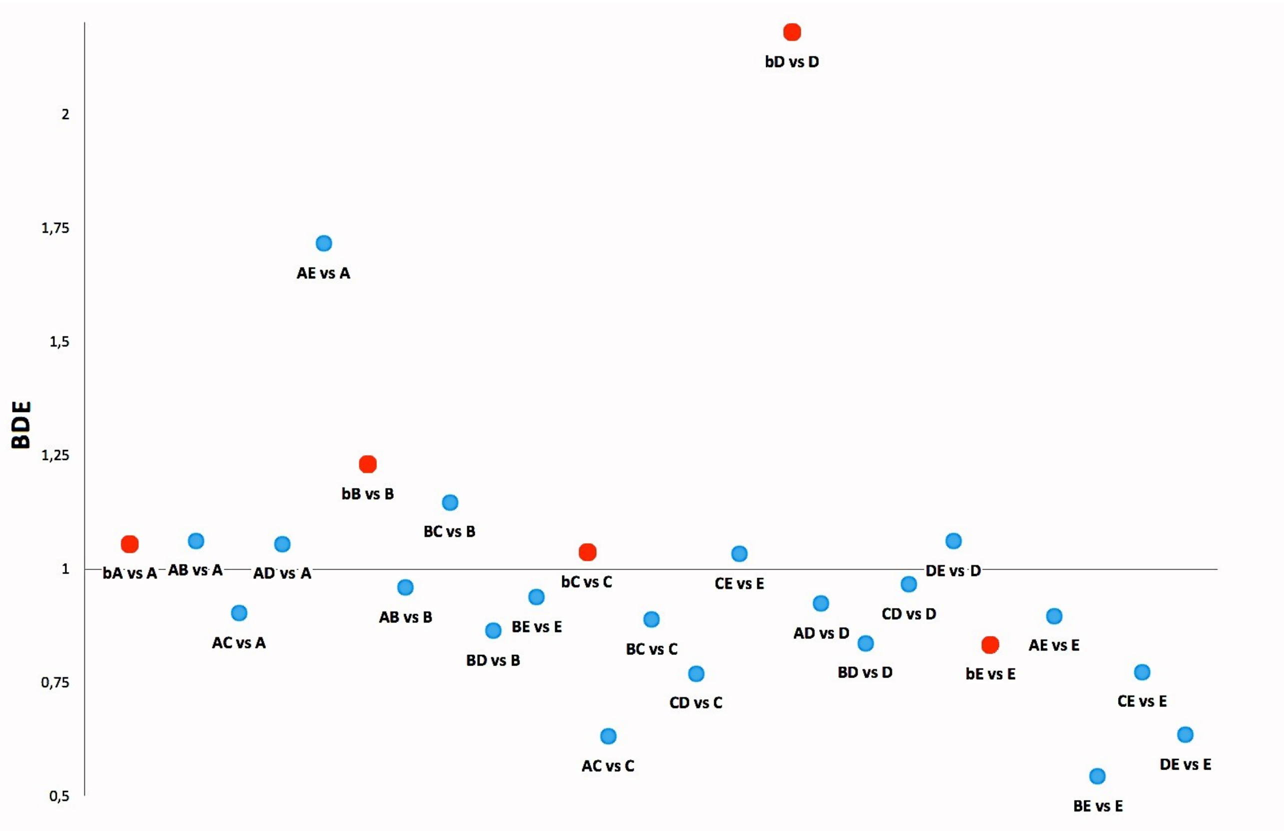


Figure S5: Graphical dispersion of the Biomass Differential Effect (BDE) index values for BMTs and NMCTs, calculated on biomass data and normalized on the untreated control, as described in Table S5. Red and blue are reported the BDE_{BMT} (following Table S5d) and BDE_{NMCT} (following Table S5e), respectively. BDE >1, the effect of the BMT or NMCT is dominant to the NMIT; BDE <1, the effect of the NMIT is dominant to the BMT or NMCT treatment. Letters reported in S8d,e represent the different materials CeO_2 NPs (A), CeO_2 bulk (bA), La_2O_3 NPs (B), La_2O_3 bulk (bB), CuO NPs (C), CuO (bC), ZnO NPs (D), ZnO bulk (bD), CdS QDs (E), CdS (bE) and their combinations. The example of CdS QDs (NMCT vs NMIT) is emblematic: in all the indexes related to NMCT that contained CdS QDs (ratios below 1), highlighting how the strongest effect was due to CdS QDs for each binary combination. On the other hand, in the case of CeO_2 NP, when combined with CdS QDs, gave opposite result (ratio higher than 1). The combination of CeO2 NP + CdS QD was more effective than the CeO2 NPs alone, suggesting that CdS QDs were more influential than the CeO2 NPs.

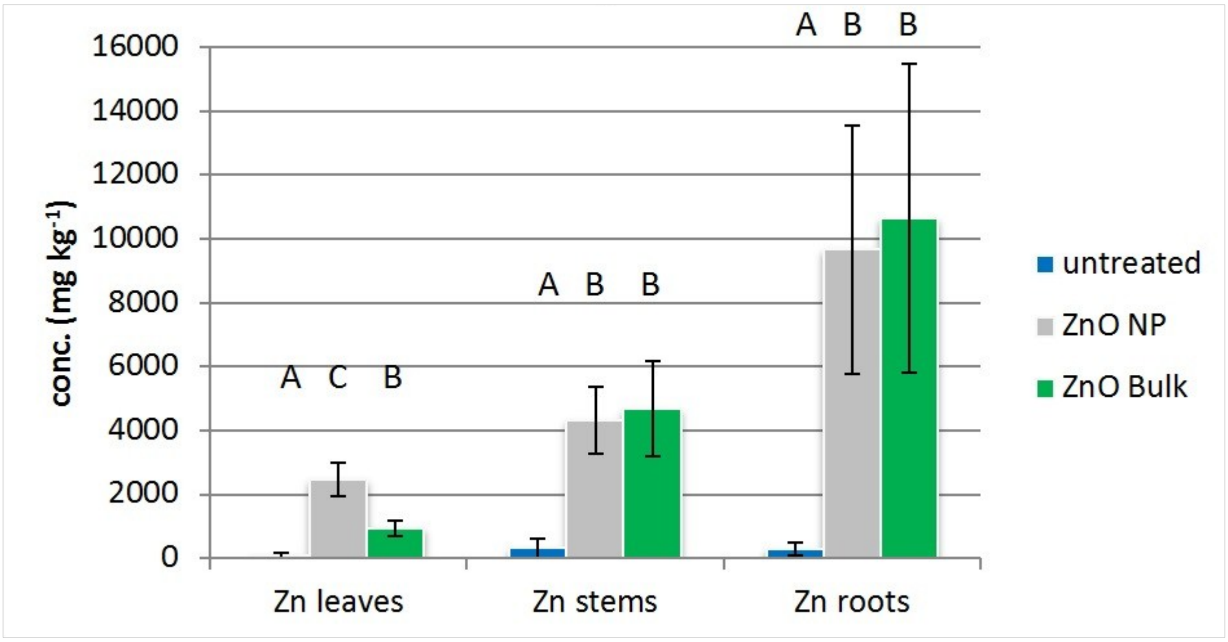


Figure S6: Zn concentrations, expressed in mg kg^{-1}, of ZnO NP and ZnO bulk (500 mg L^{-1}) and relative Tukey's (HSD) pairwise multiple comparisons ($p < 0.05$); A represents always the lowest mean.

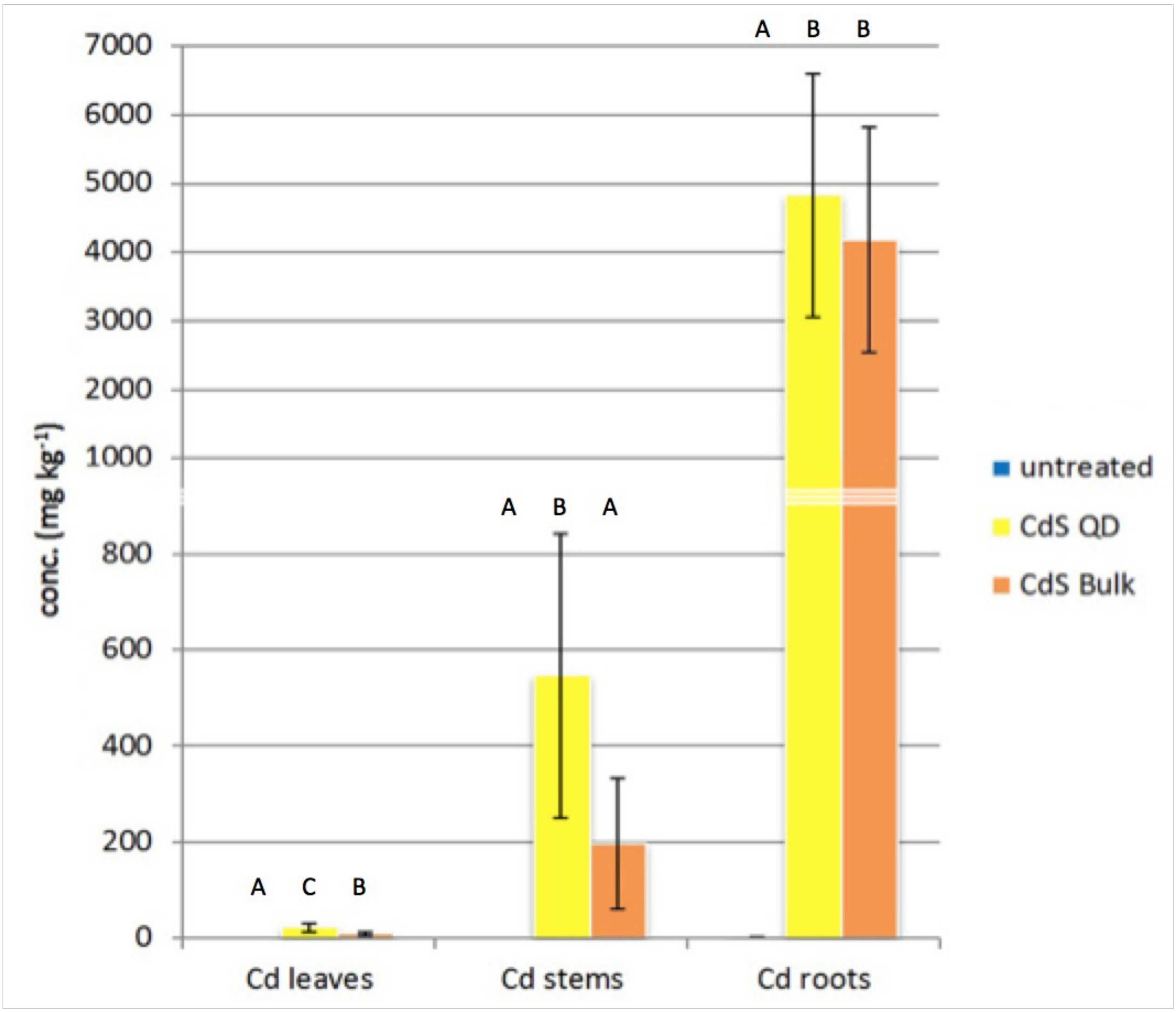


Figure S7: Cd concentrations, expressed in mg kg^{-1}, of CdS QD and CdS bulk (100 mg L^{-1}) and relative Tukey's (HSD) pairwise multiple comparisons ($p < 0.05$); A represents always the lowest mean.

Table S5: Tukey's (HSD) pairwise multiple comparisons ($p < 0.05$) related to Ce, La, Cu, Zn and Cd uptake of NMCTs in leaves (a), stems (b) and roots (c) (data reported in Figure 1); A represents always the lowest mean.

a. Metal content - Leaves	**Ce**	**La**	**Cu**	**Zn**	**Cd**
untreated	A	A	A	AB	A
CeO_2 NPs + La_2O_3 NPs	A	A	BC	B	A
CeO_2 NPs + CuO NPs	A	A	BC	B	A
CeO_2 NPs + ZnO NPs	A	A	BC	C	A
CeO_2 NPs + CdS QDs	A	A	AB	AB	A
La_2O_3 NPs + CuO NPs	A	A	BC	B	A
La_2O_3 NPs + ZnO NPs	A	A	AB	C	A
La_2O_3 NPs + CdS QDs	A	A	AB	AB	A
CuO NPs + ZnO NPs	A	A	AB	C	A
CuO NPs + CdS QDs	A	A	A	A	B
ZnO NPs + CdS QDs	A	A	A	C	B

b. Metal content - Stems	**Ce**	**La**	**Cu**	**Zn**	**Cd**
untreated	A	A	A	A	A
CeO_2 NPs + La_2O_3 NPs	BC	C	B	B	A
CeO_2 NPs + CuO NPs	C	A	BC	B	A
CeO_2 NPs + ZnO NPs	AB	A	BC	C	A
CeO_2 NPs + CdS QDs	C	A	B	AB	BC
La_2O_3 NPs + CuO NPs	A	D	BC	B	A
La_2O_3 NPs + ZnO NPs	A	B	A	CD	A
La_2O_3 NPs + CdS QDs	A	AB	A	A	B
CuO NPs + ZnO NPs	A	A	AB	CD	A
CuO NPs + CdS QDs	A	A	A	A	C
ZnO NPs + CdS QDs	A	A	A	D	B

c. Metal content - Roots	**Ce**	**La**	**Cu**	**Zn**	**Cd**
untreated	A	A	AB	AB	A
CeO_2 NPs + La_2O_3 NPs	B	B	A	A	A
CeO_2 NPs + CuO NPs	C	A	C	B	A
CeO_2 NPs + ZnO NPs	B	A	B	D	A
CeO_2 NPs + CdS QDs	B	A	BC	BC	B
La_2O_3 NPs + CuO NPs	A	C	D	C	A
La_2O_3 NPs + ZnO NPs	A	C	B	D	A
La_2O_3 NPs + CdS QDs	A	C	BC	BC	B
CuO NPs + ZnO NPs	A	A	C	D	A
CuO NPs + CdS QDs	A	A	C	BC	B
ZnO NPs + CdS QDs	A	A	BC	D	B

Table S6: Tukey's (HSD) pairwise multiple comparisons ($p < 0.05$) related to Zn (a) and Cd (b) uptake of NMCT compared to the individual treatment in leaves, stems, and roots. A represents always the lowest mean.

a. Metal content Zn	**leaves**	**stems**	**roots**
ZnO NPs	A	B	B
CeO_2 NPs + ZnO NPs	A	B	A
La_2O_3 NPs + ZnO NPs	A	AB	A
CuO NPs + ZnO NPs	A	AB	A
ZnO NPs + CdS QDs	A	A	A

b. Metal content Cd	**leaves**	**stems**	**roots**
CdS QDs	A	B	B
CeO_2 NPs + CdS QDs	A	AB	A
La_2O_3 NPs + CdS QDs	A	A	A
CuO NPs + CdS QDs	A	AB	AB
ZnO NPs + CdS QDs	A	A	A

Specific Extraction Yield ($SEY_{\%}$) index – Equation:

(ζ) $SEY_{\%} = M_{plant} / [M_{soil}]$

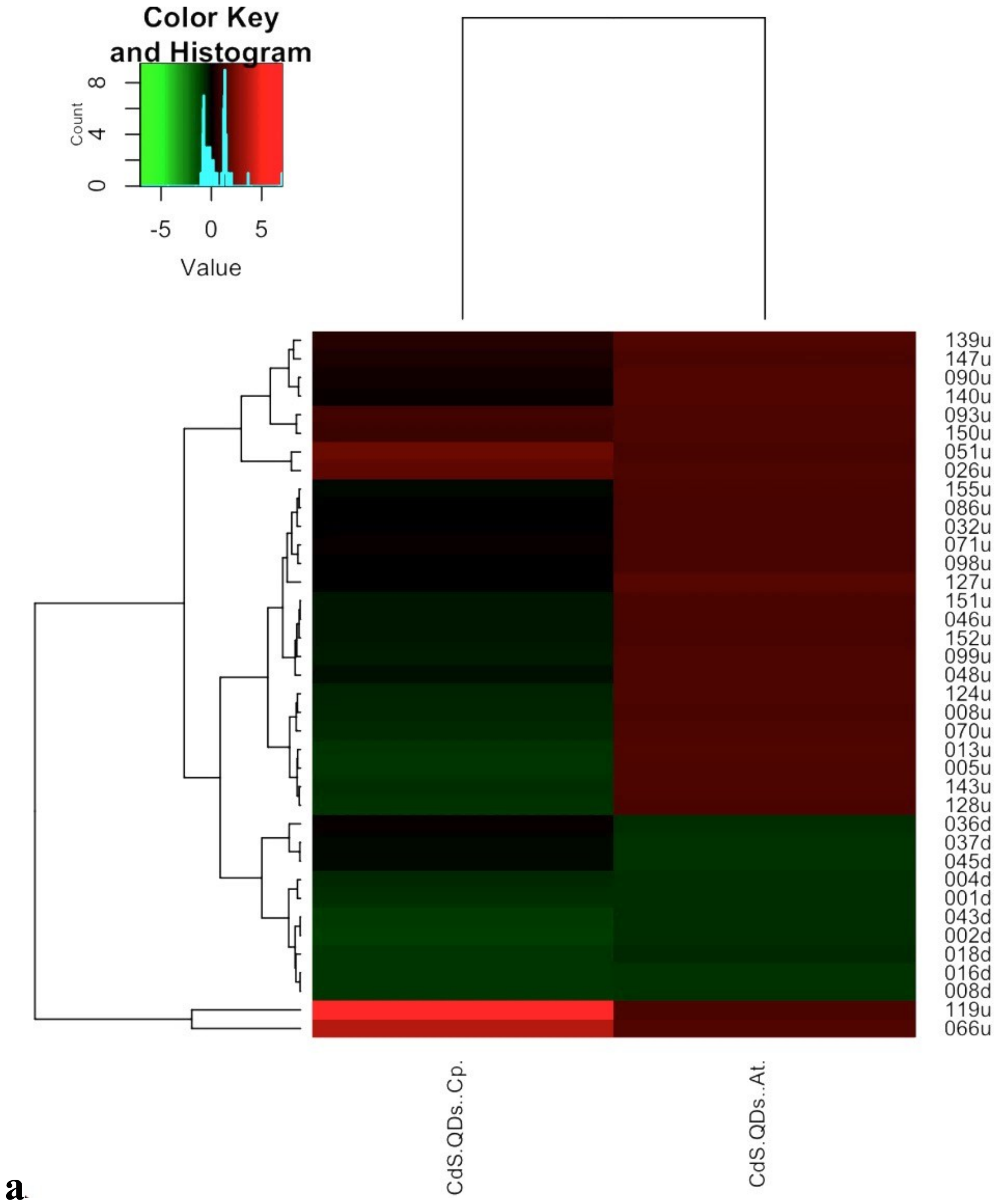
Equation (ζ) represents the $SEY_{\%}$ in the plants calculated on the ratio between M_{plant} (metal content in the different part of the plants), reported in Figure 1 and the metal concentration ($[M_{soil}]$) used in the experiment.

Table S7: Specific Extraction Yield Percentage (SEY$_{\%}$) of Ce, La, Cu, Zn and Cd derived from metal content data of NMCTs, calculated in equation (ζ), following Audet and Charest, 2007.[2] Values not reported were lower than 0.01%.

a. SEY$_{\%}$ - Leaves	**Ce**	**La**	**Cu**	**Zn**	**Cd**
untreated	-	-	0.04%	0.15%	-
CeO_2 NPs + La_2O_3 NPs	-	0.01%	0.04%	0.18%	-
CeO_2 NPs + CuO NPs	-	-	0.05%	0.13%	-
CeO_2 NPs + ZnO NPs	-	-	0.07%	2.05%	-
CeO_2 NPs + CdS QDs	-	-	0.13%	0.56%	0.08%
La_2O_3 NPs + CuO NPs	-	0.05%	0.18%	0.69%	-
La_2O_3 NPs + ZnO NPs	-	0.02%	0.04%	1.67%	-
La_2O_3 NPs + CdS QDs	-	-	0.03%	0.15%	0.02%
CuO NPs + ZnO NPs	-	-	0.05%	2.70%	-
CuO NPs + CdS QDs	-	-	0.04%	0.16%	0.12%
ZnO NPs + CdS QDs	-	-	0.04%	2.43%	0.19%

b. SEY$_{\%}$ - Stems	**Ce**	**La**	**Cu**	**Zn**	**Cd**
untreated	-	-	0.04%	0.19%	-
CeO_2 NPs + La_2O_3 NPs	0.08%	0.06%	0.04%	0.24%	-
CeO_2 NPs + CuO NPs	0.07%	-	0.05%	0.17%	-
CeO_2 NPs + ZnO NPs	0.03%	-	0.06%	5.90%	-
CeO_2 NPs + CdS QDs	0.69%	-	0.18%	1.03%	4.23%
La_2O_3 NPs + CuO NPs	-	0.36%	0.23%	1.06%	-
La_2O_3 NPs + ZnO NPs	-	0.02%	0.02%	2.72%	-
La_2O_3 NPs + CdS QDs	-	0.01%	0.03%	0.17%	0.78%
CuO NPs + ZnO NPs	-	-	0.06%	5.26%	-
CuO NPs + CdS QDs	-	-	0.07%	0.20%	3.62%
ZnO NPs + CdS QDs	-	-	0.04%	4.12%	1.14%

c. SEY$_{\%}$ - Roots	**Ce**	**La**	**Cu**	**Zn**	**Cd**
untreated	-	-	0.23%	0.28%	0.01%
CeO_2 NPs + La_2O_3 NPs	1.50%	2.09%	0.09%	0.15%	0.01%
CeO_2 NPs + CuO NPs	1.74%	-	0.61%	0.28%	-
CeO_2 NPs + ZnO NPs	3.06%	-	0.35%	16.00%	-
CeO_2 NPs + CdS QDs	9.05%	-	0.68%	1.70%	61.83%
La_2O_3 NPs + CuO NPs	-	16.92%	3.41%	1.49%	-
La_2O_3 NPs + ZnO NPs	-	4.16%	0.17%	8.18%	-
La_2O_3 NPs + CdS QDs	-	10.46%	0.29%	0.83%	20.08%
CuO NPs + ZnO NPs	-	-	0.87%	15.14%	-
CuO NPs + CdS QDs	-	-	0.90%	0.73%	33.46%
ZnO NPs + CdS QDs	-	-	0.35%	18.49%	33.00%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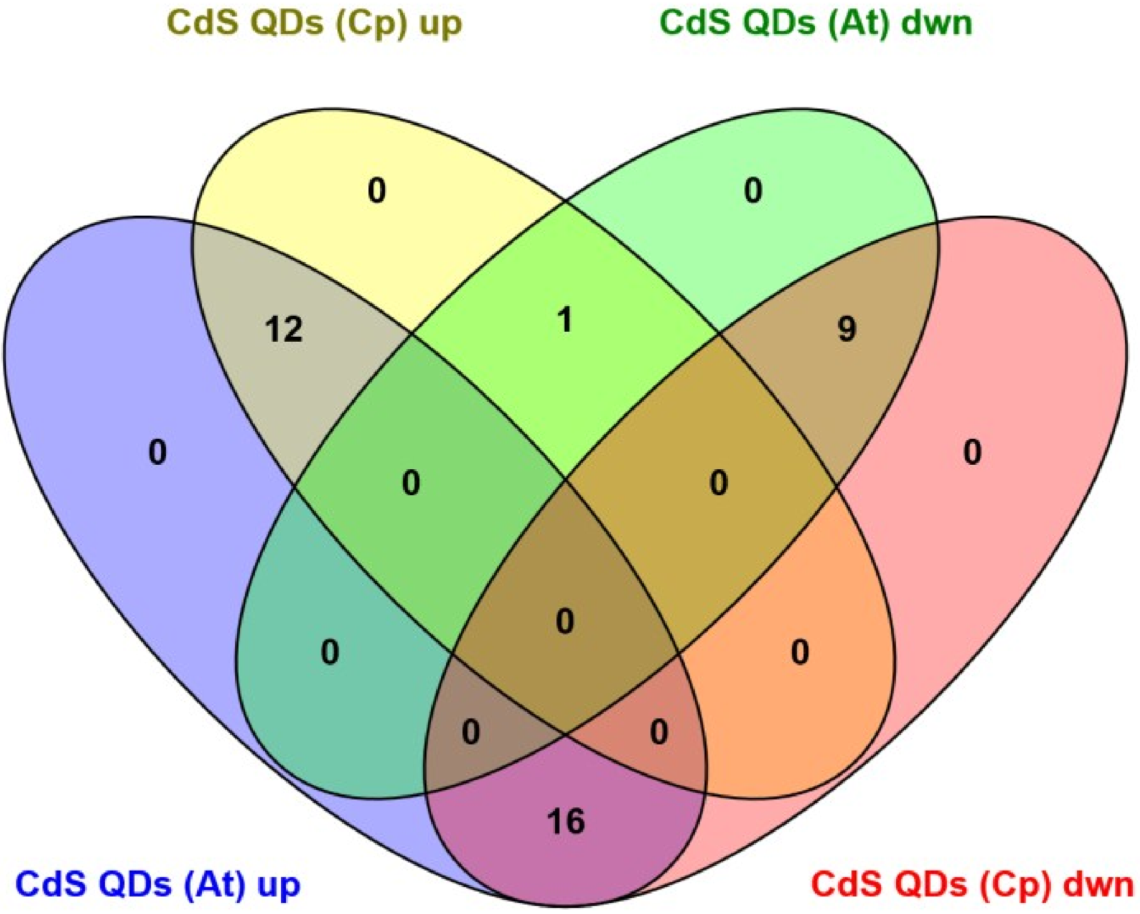
CdS.QDs..Cp.
CdS.QDs..At.
a



b

Figure S8: Heatmap (a) and Venn diagram (b) of CdS QD treatment in *A. thaliana* (At), from Marmiroli *et al*. (2014),[3] and *Cucurbita pepo* (Cp). Genes up- (red) and down-regulated (green) for both the species are reported.

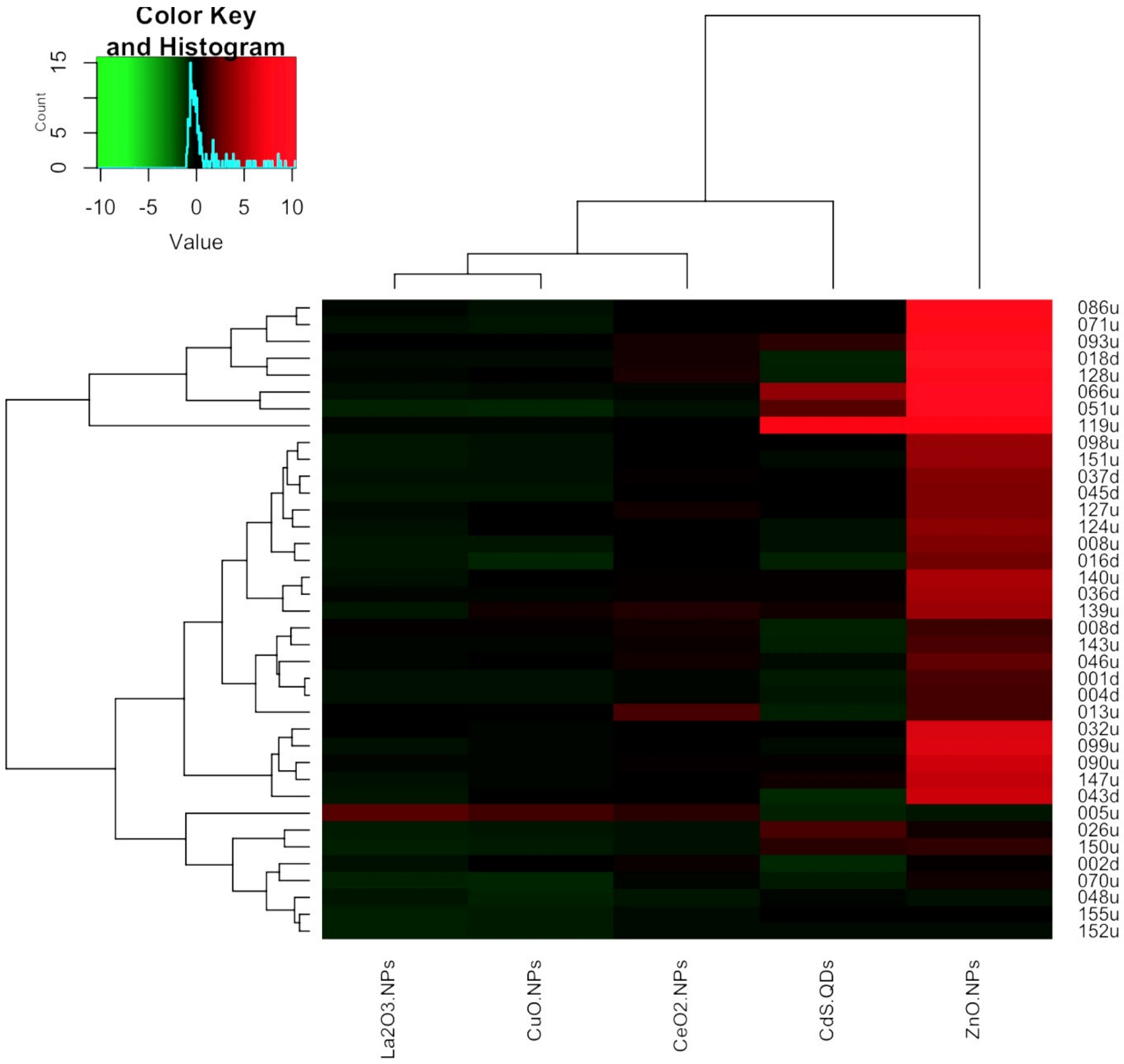
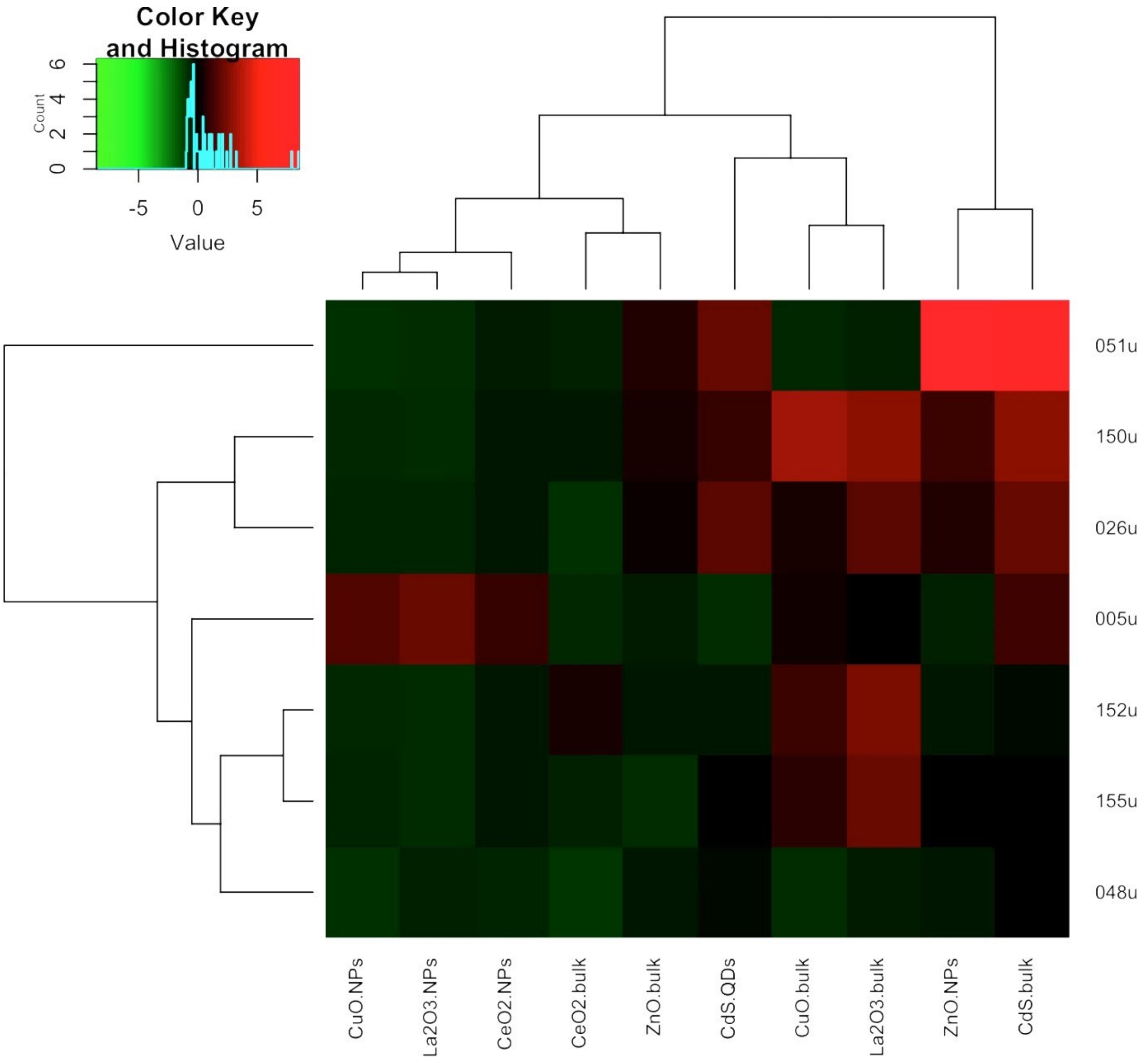


Figure S9: Heatmap of the comparison between the nanoparticle treatments in *Cucurbita pepo* (NP CeO_2, La_2O_3 and CuO results are reported from Pagano *et. al* (2016).[1] Genes up- (red) and down-regulated (green) are reported in the heatmap.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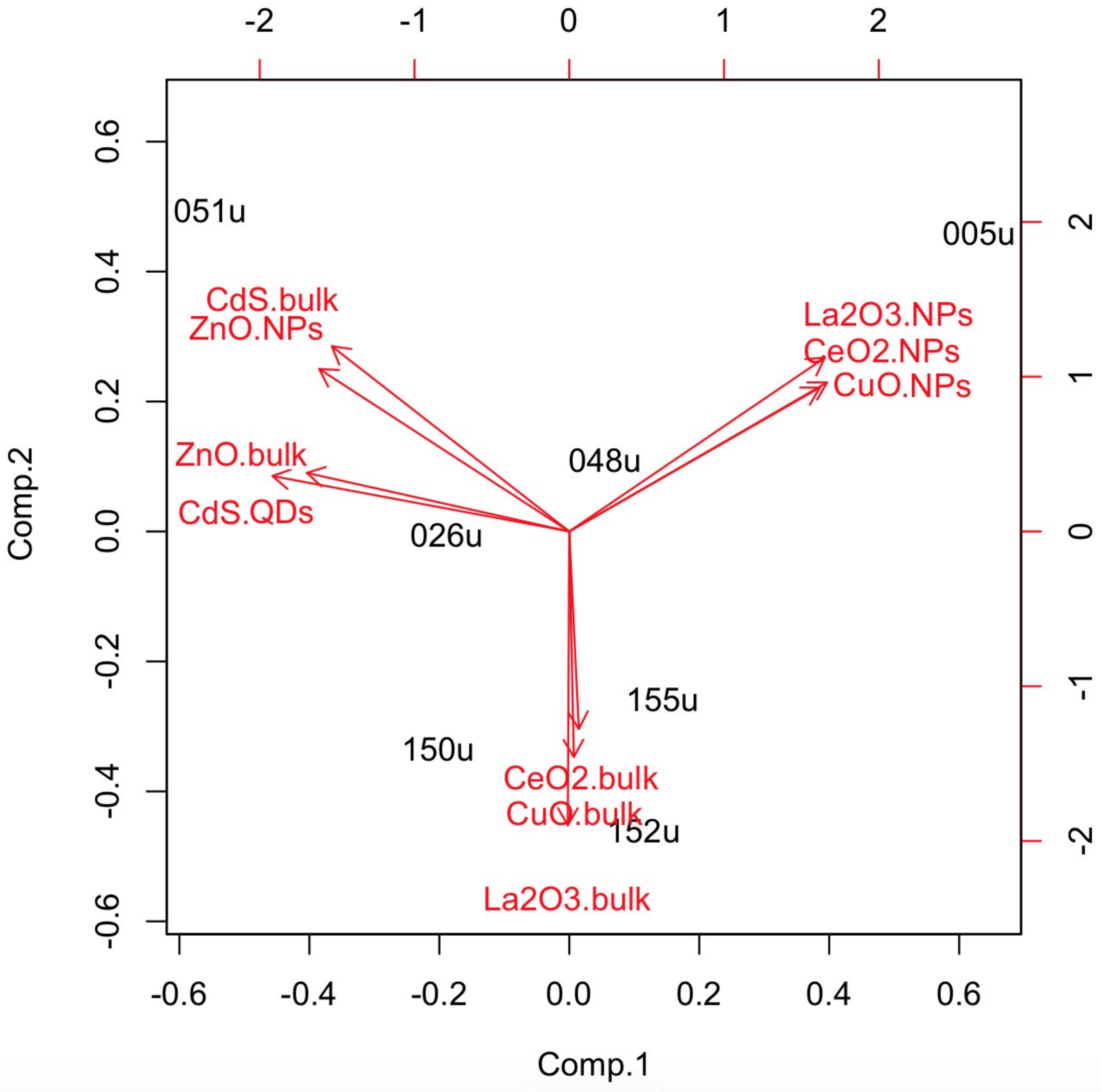
a



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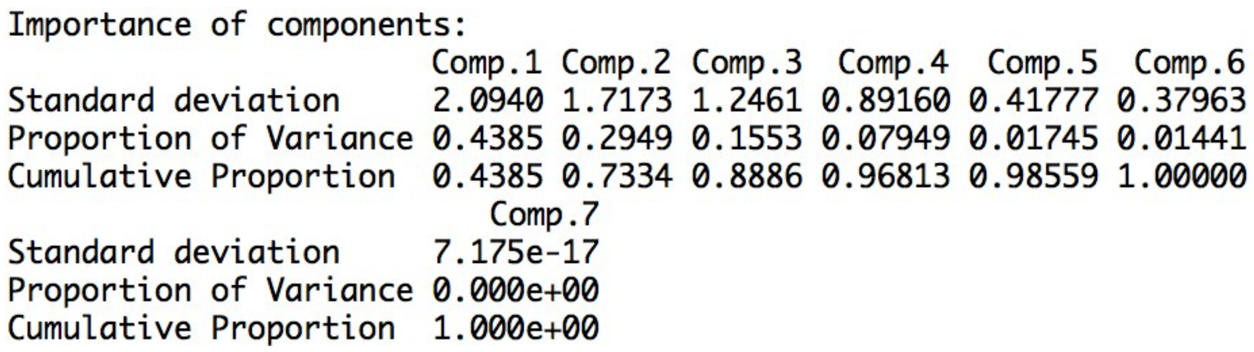


```
Importance of components:
                          Comp.1 Comp.2 Comp.3  Comp.4  Comp.5  Comp.6
Standard deviation        2.0940 1.7173 1.2461 0.89160 0.41777 0.37963
Proportion of Variance    0.4385 0.2949 0.1553 0.07949 0.01745 0.01441
Cumulative Proportion     0.4385 0.7334 0.8886 0.96813 0.98559 1.00000
                             Comp.7
Standard deviation        7.175e-17
Proportion of Variance    0.000e+00
Cumulative Proportion     1.000e+00
```

Figure S10: Heatmap (a) and PCA (b) of the gene expression of NMIT and BMT in *Cucurbita pepo* (CeO_2, La_2O_3 and CuO NP/bulk results are taken from previous paper Pagano *et. al*, 2016)[1]. Genes up- (red) and down-regulated (green) are reported in the heatmap.

Table S8: list of genes specifically modulated by ENMs treatment. Genes are divided as always up- or down-regulated in all the treatments (NMIT or NMCT) specifically for one of the nanomaterials (univocal genes, a) and for two or more nanomaterials studied (non-univocal genes, b). 152u (*ORF31*) resulted to be the only (non-univocal) gene down-regulated in all the treatments performed.

a. Univocal genes

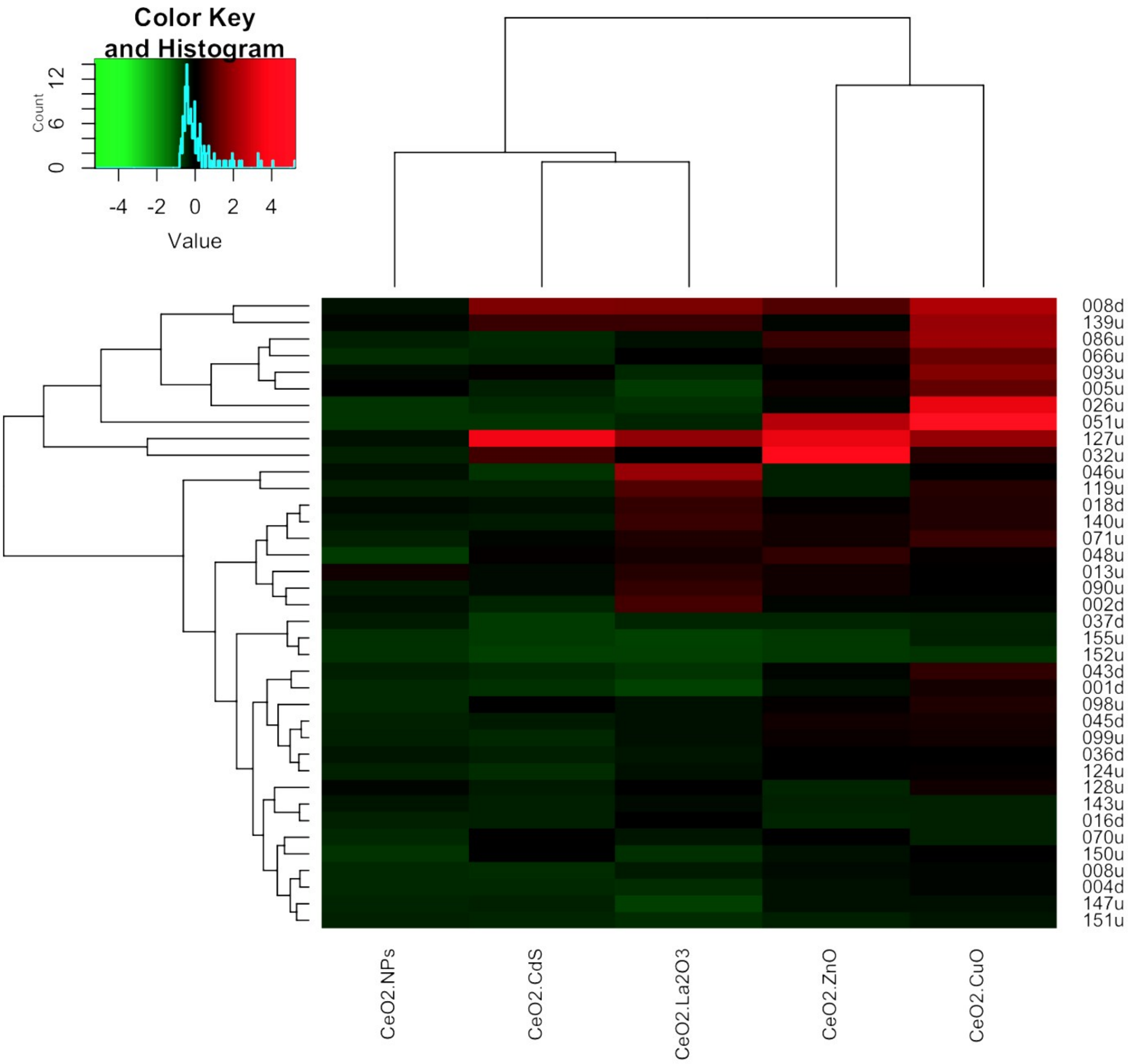
UP-REGULATED				
CeO_2 NP	**La_2O_3 NP**	**CuO NP**	**ZnO NP**	**CdS QD**
036d	-	005u	043d	150u
140u			045d	
			066u	
			093u	
			099u	

DOWN-REGULATED				
CeO_2 NP	**La_2O_3 NP**	**CuO NP**	**ZnO NP**	**CdS QD**
-	004d	-	-	124u
	147u			155u

b. Non-univocal genes

UP-REGULATED							
CeO_2 NP	**La_2O_3 NP**	**CuO NP**	**ZnO NP**	**CdS QD**	**NMIT**	**NMCT**	**NMIT+NMCT**
008d	013u	008d	013u	071u	-	-	-
013u	032u		018d	090u			
018d			032u	098u			
032u			071u	139u			
071u			090u				
090u			098u				
127u			127u				
139u							

DOWN-REGULATED							
CeO_2 NP	**La_2O_3 NP**	**CuO NP**	**ZnO NP**	**CdS QD**	**NMIT**	**NMCT**	**NMIT+NMCT**
152u	152u	152u	152u	152u	152u	152u	152u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127u
032u
046u
119u
018d
140u
071u
048u
013u
090u
002d
037d
155u
152u
043d
001d
098u
045d
099u
036d
124u
128u
143u
016d
070u
150u
008u
004d
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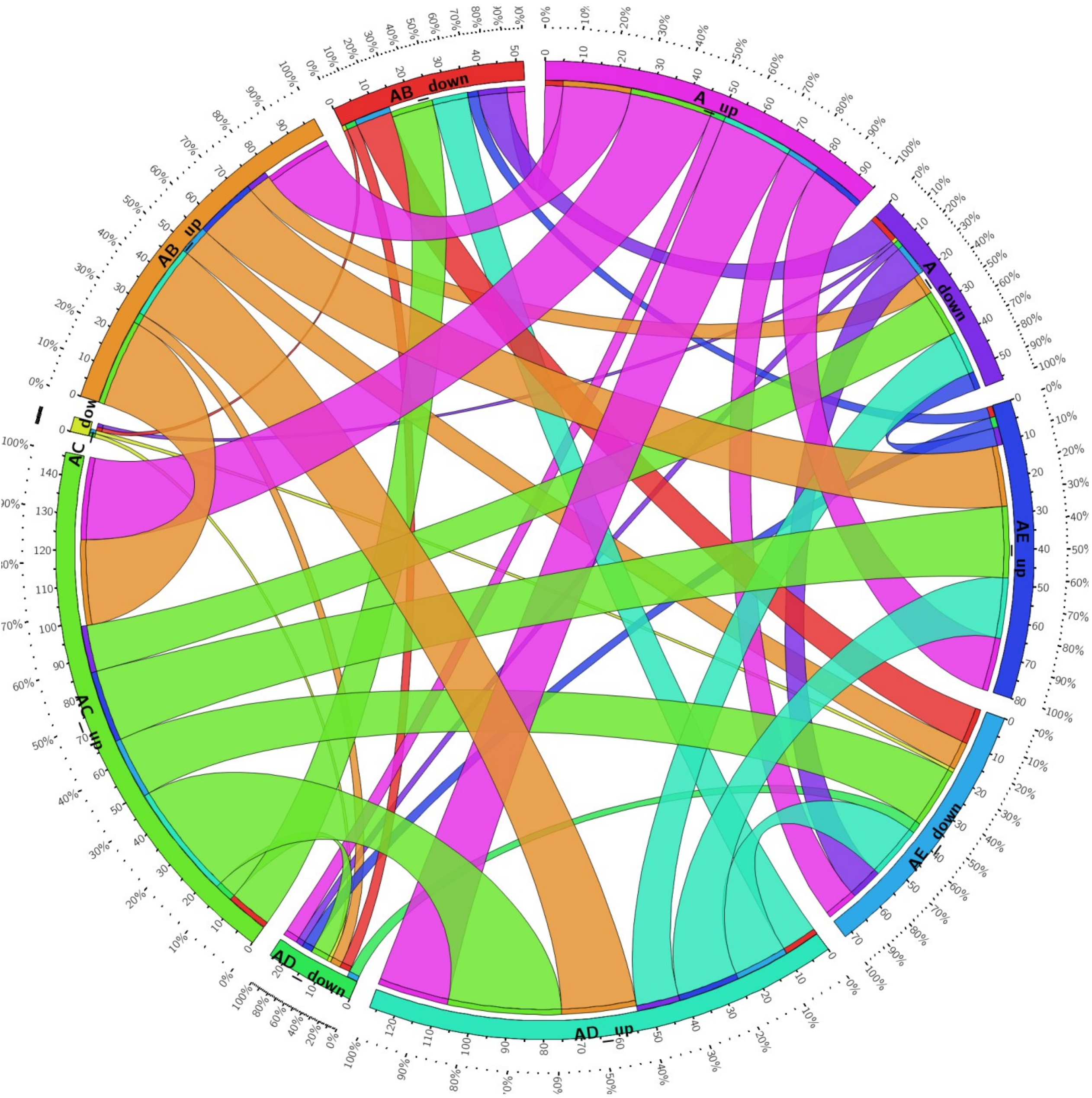
151u
CeO2.NPs
CeO2.CdS
CeO2.La2O3
CeO2.ZnO
CeO2.CuO

a



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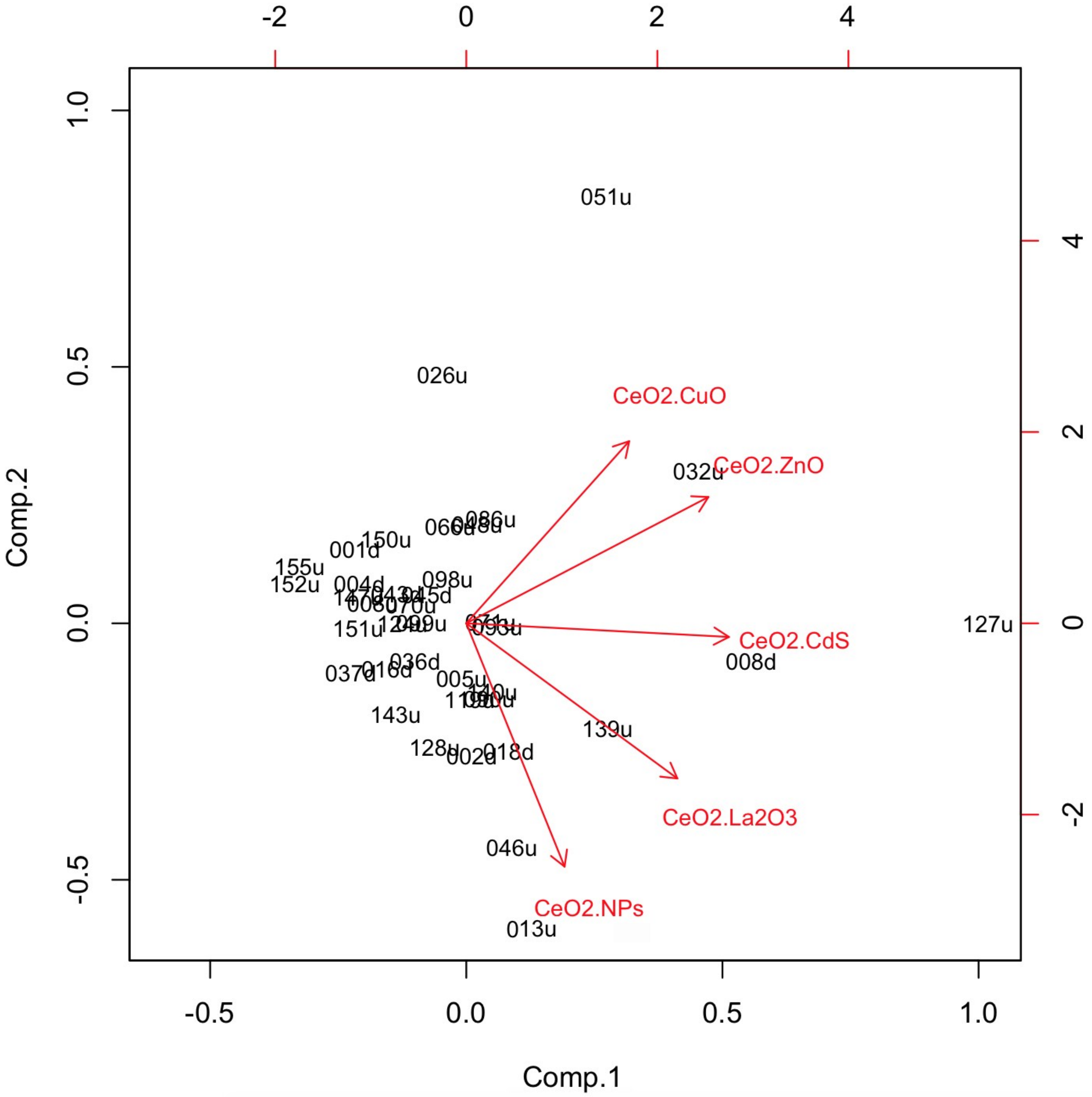

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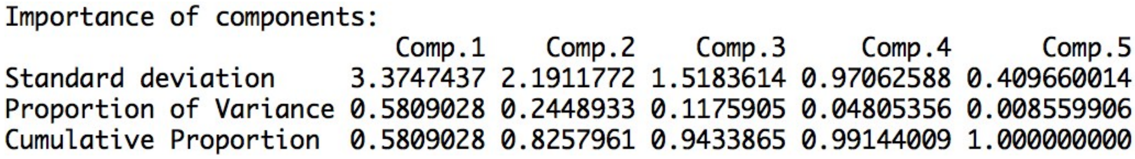
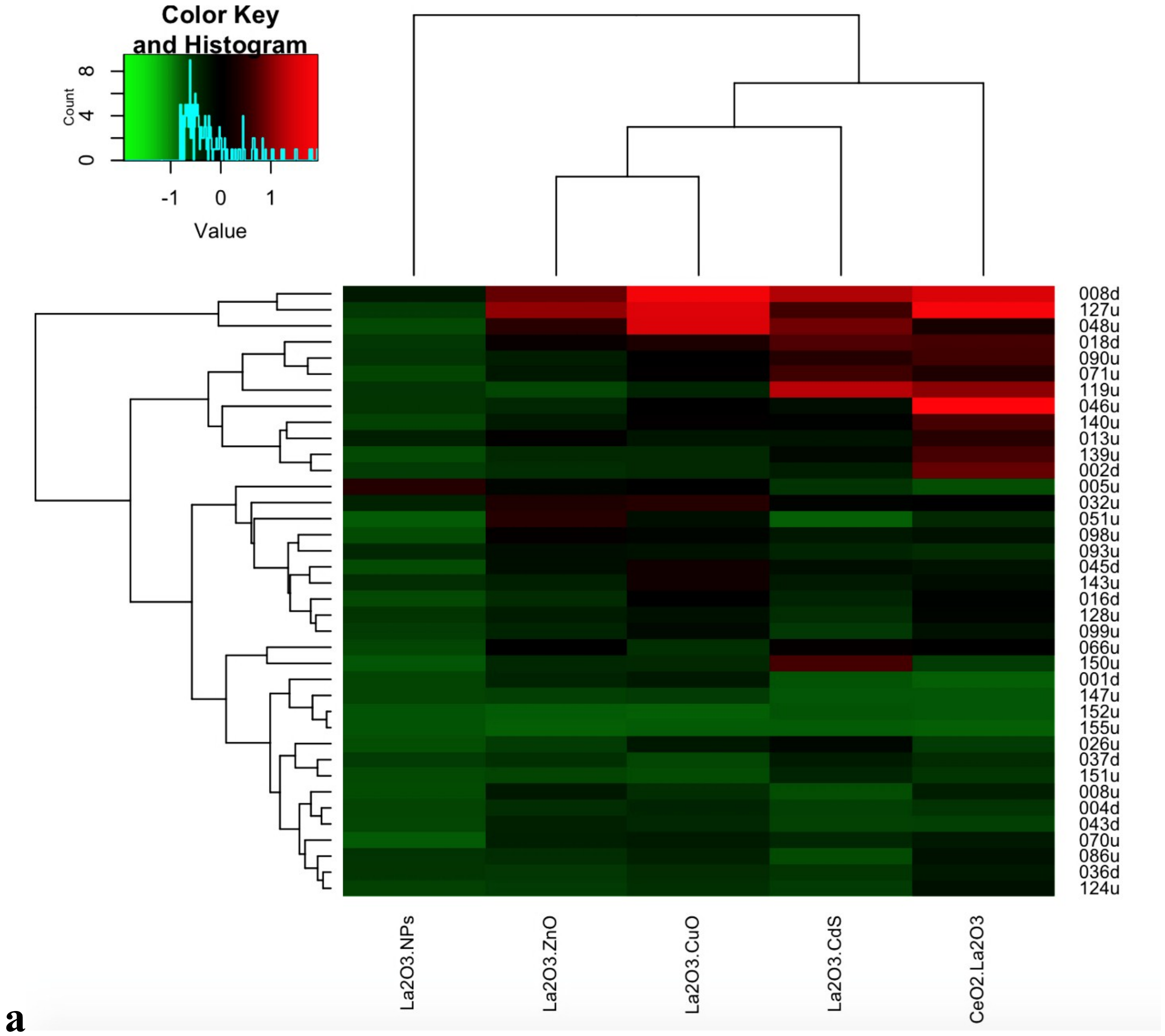
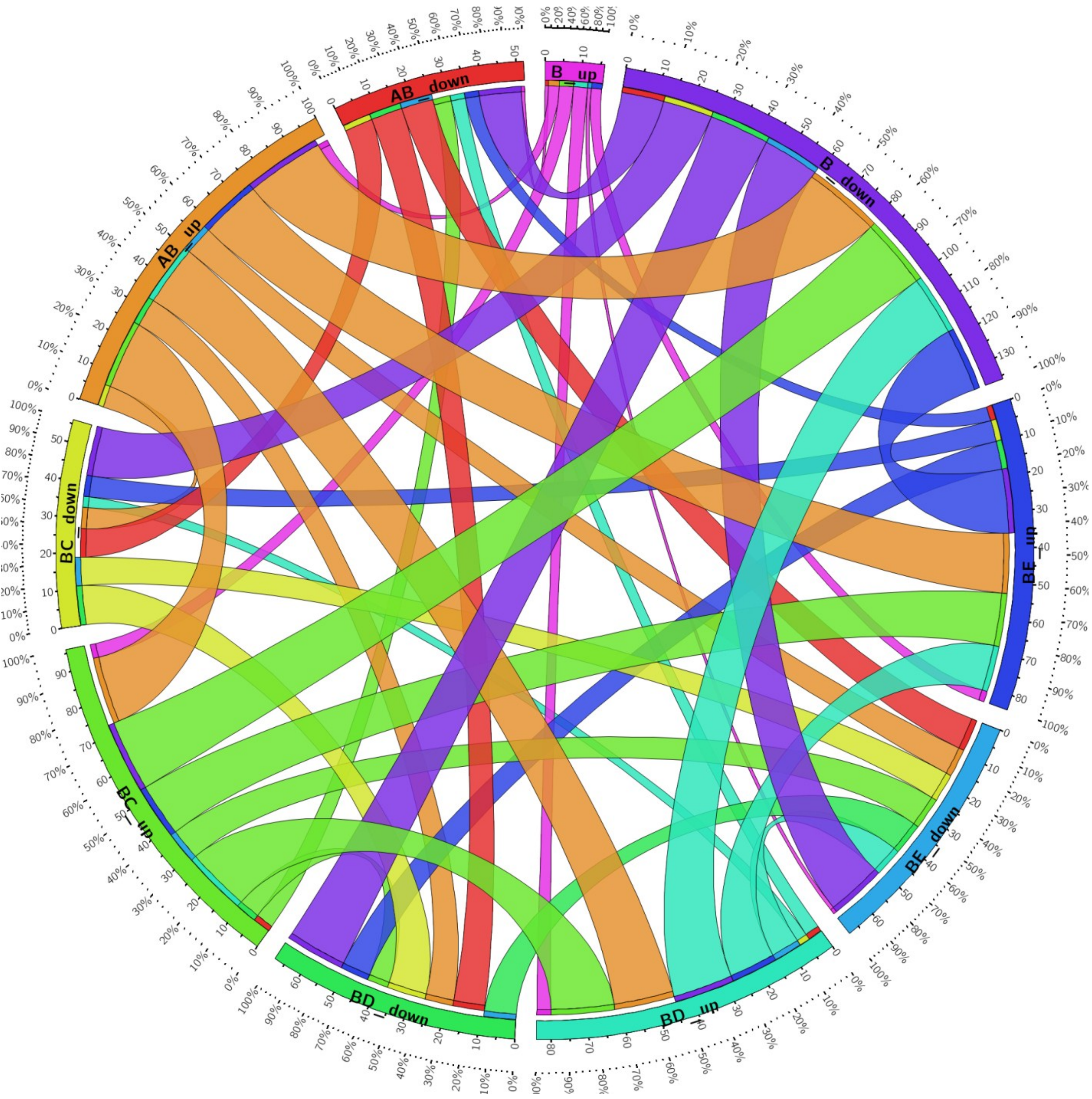


```
Importance of components:
                          Comp.1    Comp.2    Comp.3     Comp.4      Comp.5
Standard deviation     3.3747437 2.1911772 1.5183614 0.97062588 0.409660014
Proportion of Variance 0.5809028 0.2448933 0.1175905 0.04805356 0.008559906
Cumulative Proportion  0.5809028 0.8257961 0.9433865 0.99144009 1.000000000
```

Figure S11: Heatmap (a) chord diagram (b) and PCA (c) of all the CeO_2 NPs and their binary combinations with La_2O_3 NPs, CuO NPs, ZnO NPs, CdS QDs. Genes up- (red) and down-regulated (green) are reported in the heatmap. Graphic comparison between the gene expression profiles is reported in the chord diagram: ribbons show the overlap (expressed as number and percentage) between the different sets of data, reported as up- or down-regulated CeO_2 NPs (A), La_2O_3 NPs (B), CuO NPs (C), ZnO NPs (D), CdS QDs (E).





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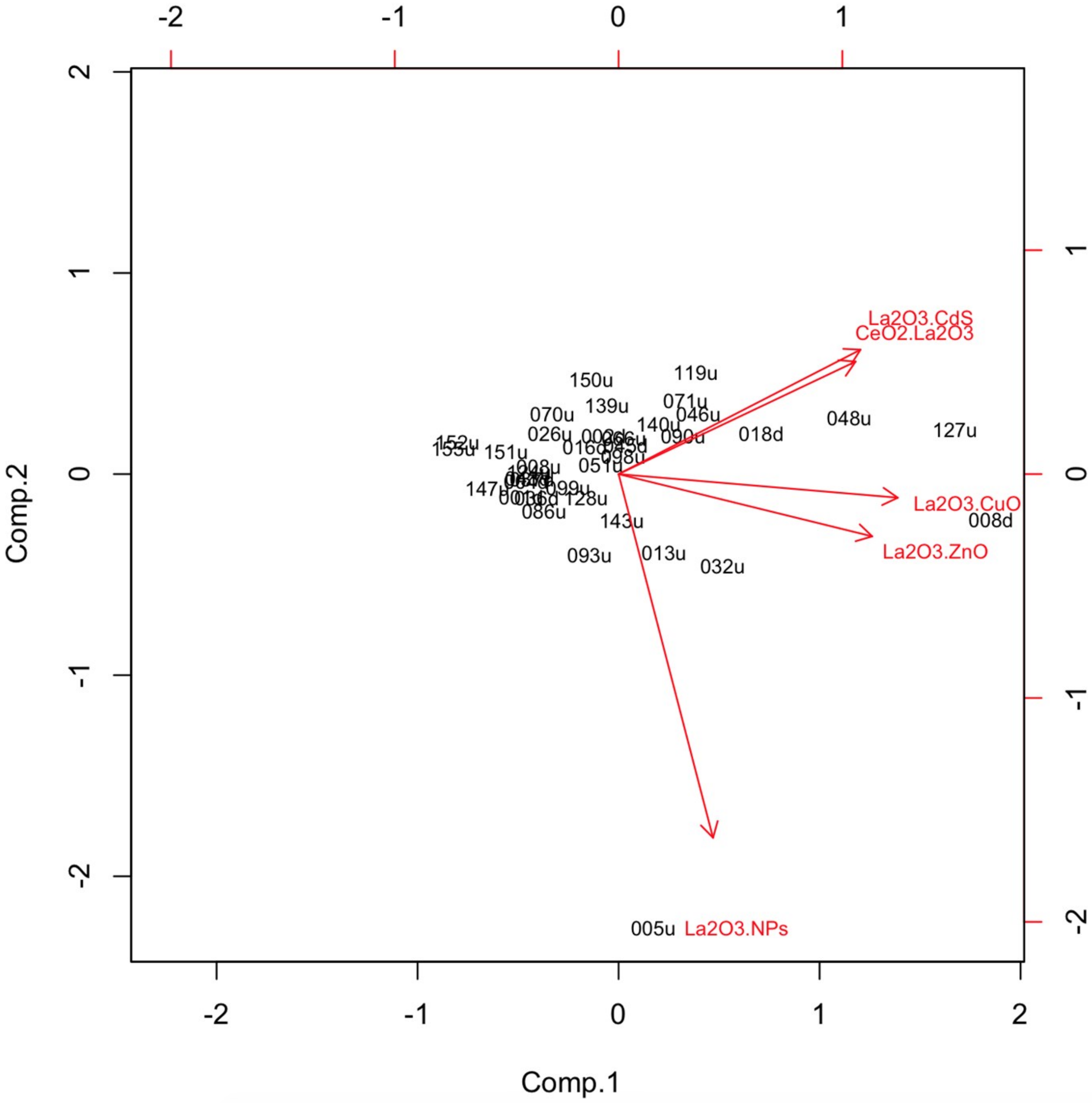

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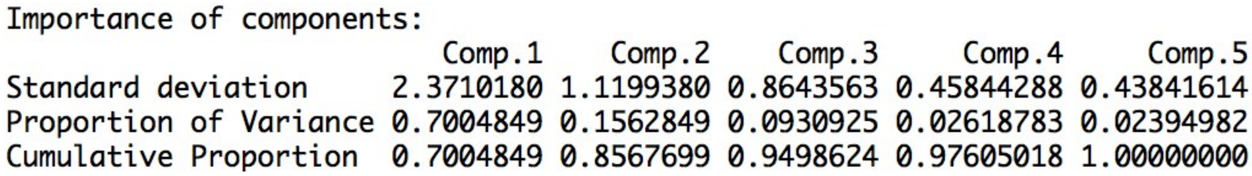
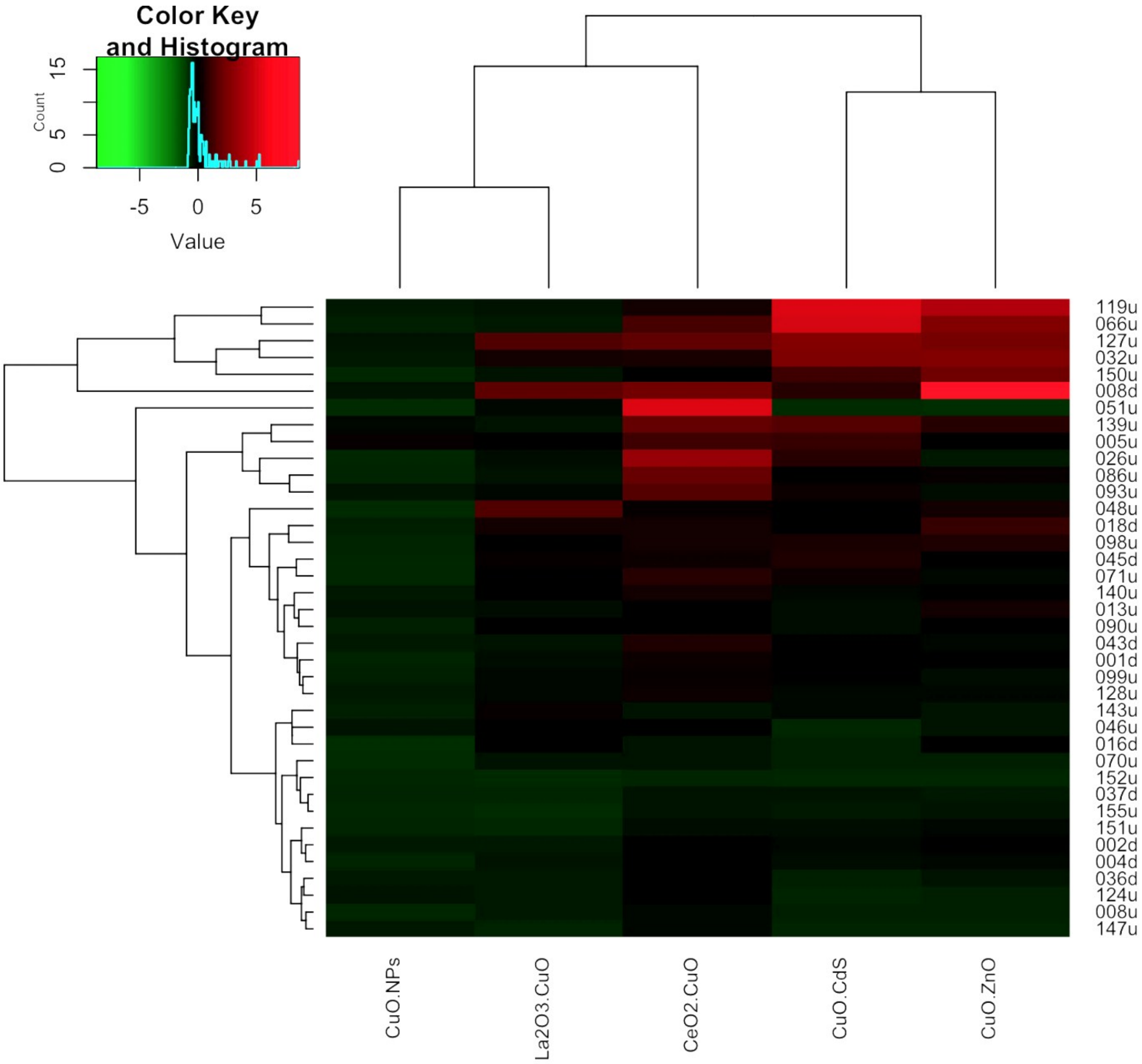


```
Importance of components:
                          Comp.1    Comp.2    Comp.3     Comp.4     Comp.5
Standard deviation     2.3710180 1.1199380 0.8643563 0.45844288 0.43841614
Proportion of Variance 0.7004849 0.1562849 0.0930925 0.02618783 0.02394982
Cumulative Proportion  0.7004849 0.8567699 0.9498624 0.97605018 1.00000000
```

Figure S12: Heatmap (a) chord diagram (b) and PCA (c) of all the La_2O_3 NPs and their binary combinations with CeO_2 NPs, CuO NPs, ZnO NPs, CdS QDs. Genes up- (red) and down-regulated (green) are reported in the heatmap. Graphic comparison between the gene expression profiles is reported in the chord diagram: ribbons show the overlap (expressed as number and percentage) between the different sets of data, reported as up- or down-regulated CeO_2 NPs (A), La_2O_3 NPs (B), CuO NPs (C), ZnO NPs (D), CdS QDs (E).



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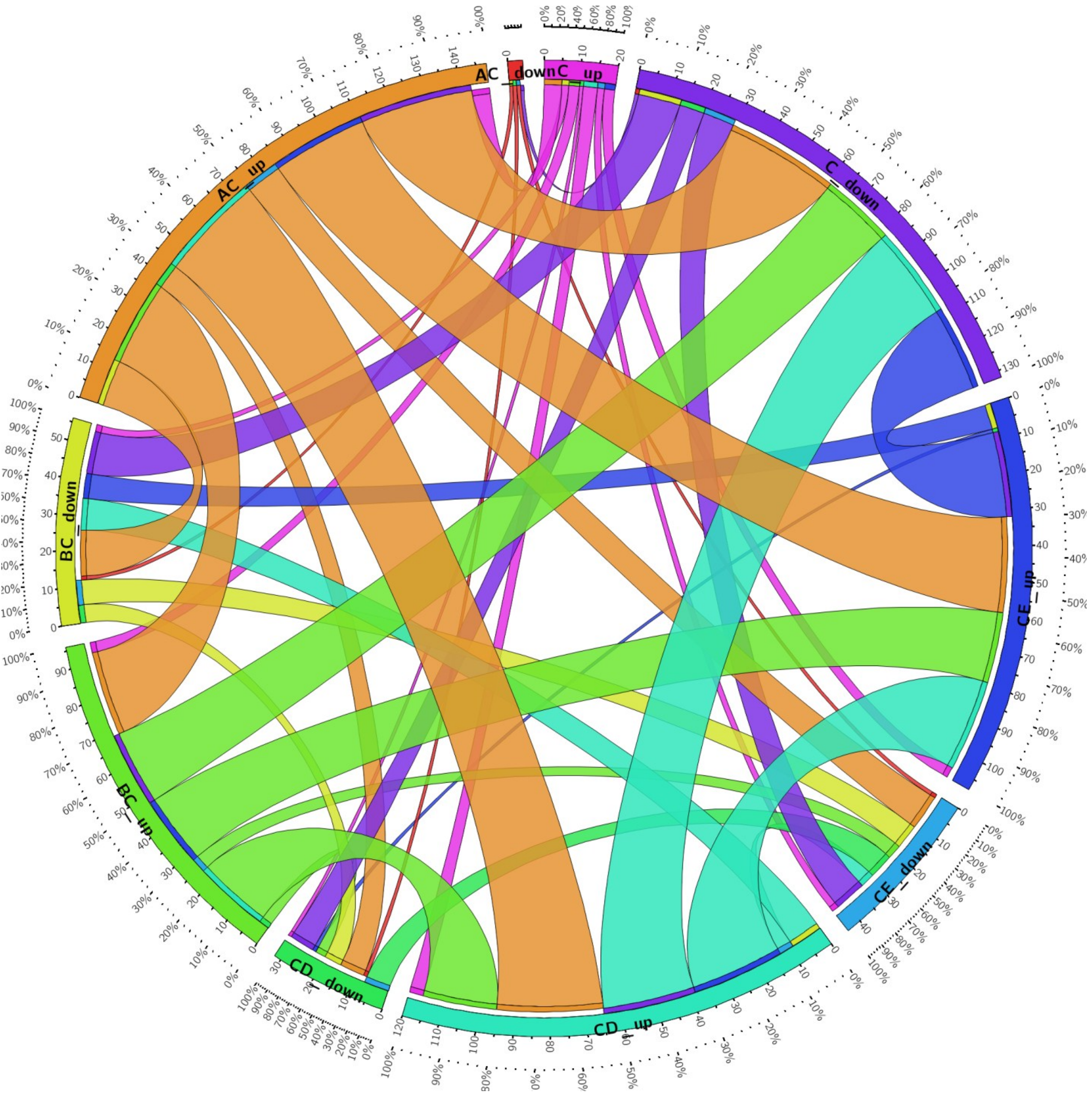

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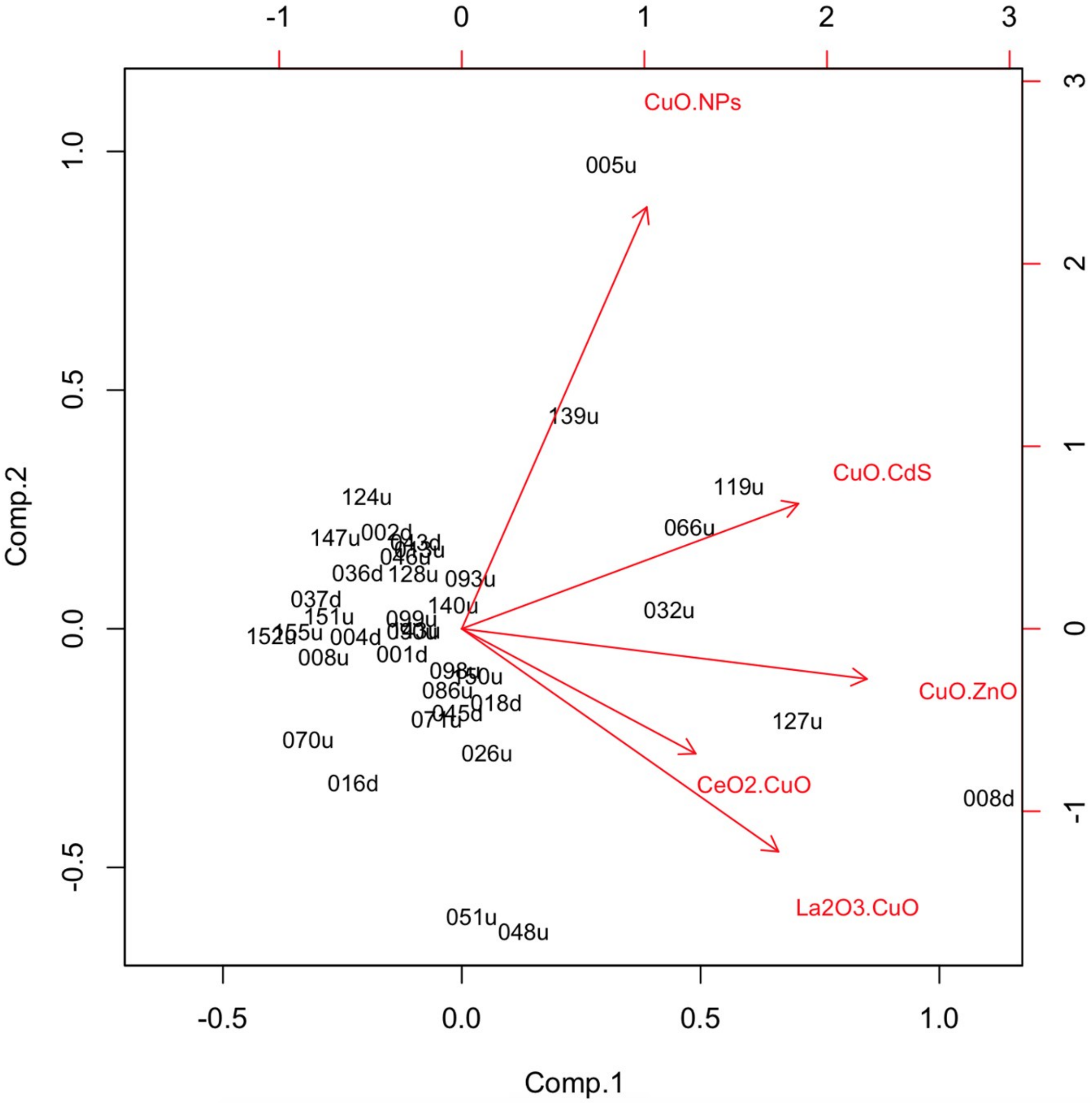

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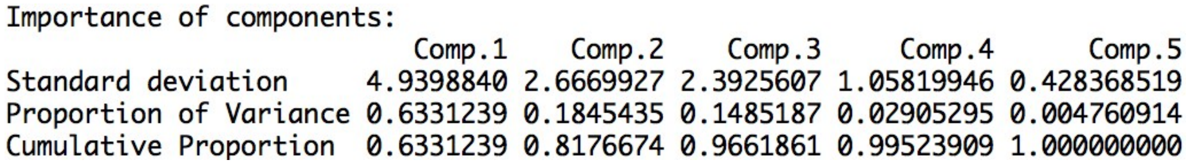
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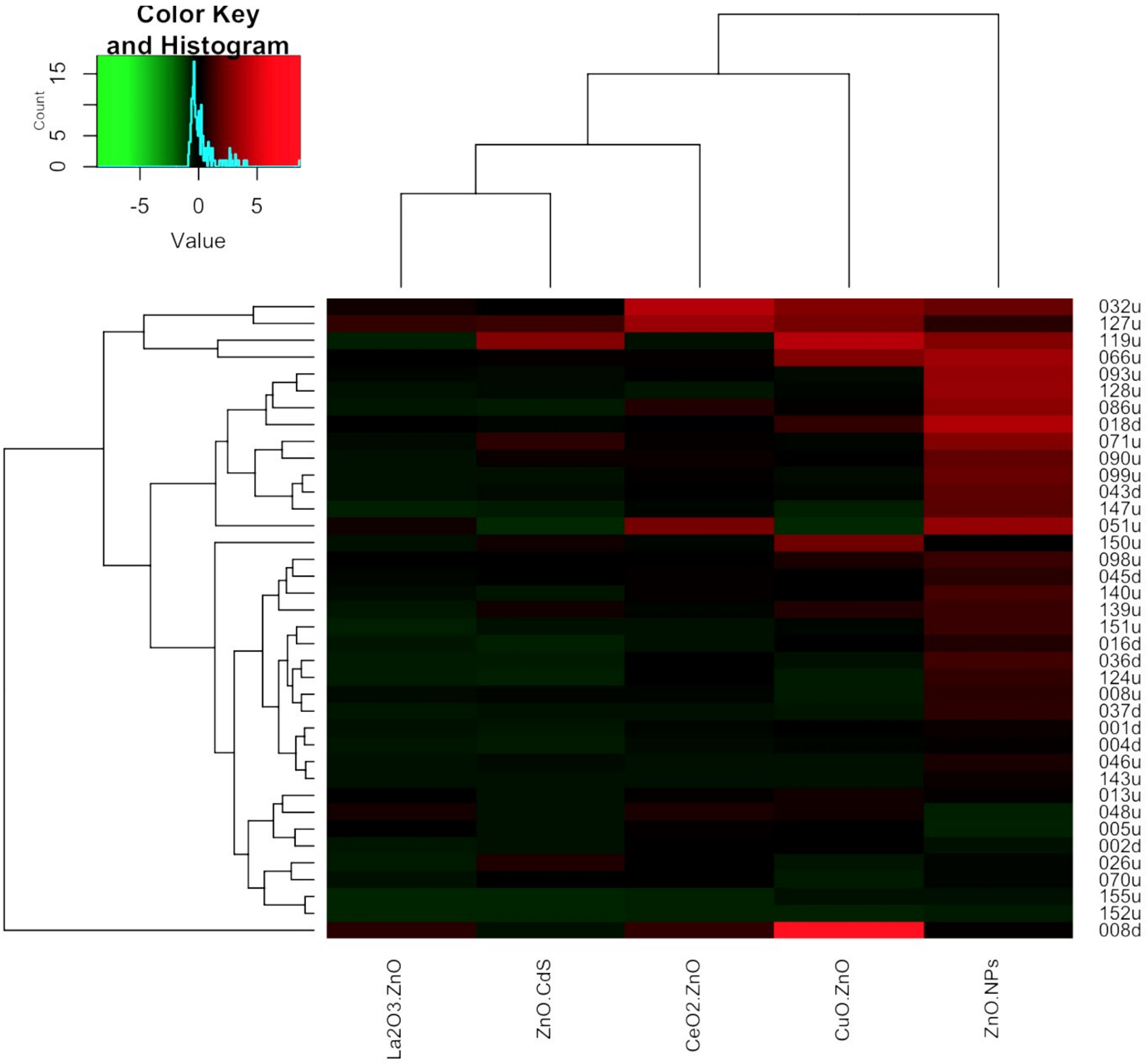
Importance of components:
                          Comp.1    Comp.2    Comp.3     Comp.4      Comp.5
Standard deviation     4.9398840 2.6669927 2.3925607 1.05819946 0.428368519
Proportion of Variance 0.6331239 0.1845435 0.1485187 0.02905295 0.004760914
Cumulative Proportion  0.6331239 0.8176674 0.9661861 0.99523909 1.000000000
```

Figure S13: Heatmap (a) chord diagram (b) and PCA (c) of all the CuO NPs and their binary combinations with CeO_2 NPs, La_2O_3 NPs, ZnO NPs, CdS QDs. Genes up- (red) and down-regulated (green) are reported in the heatmap. Graphic comparison between the gene expression profiles is reported in the chord diagram: ribbons show the overlap (expressed as number and

percentage) between the different sets of data, reported as up- or down-regulated CeO_2 NPs (A), La_2O_3 NPs (B), CuO NPs (C), ZnO NPs (D), CdS QDs (E).



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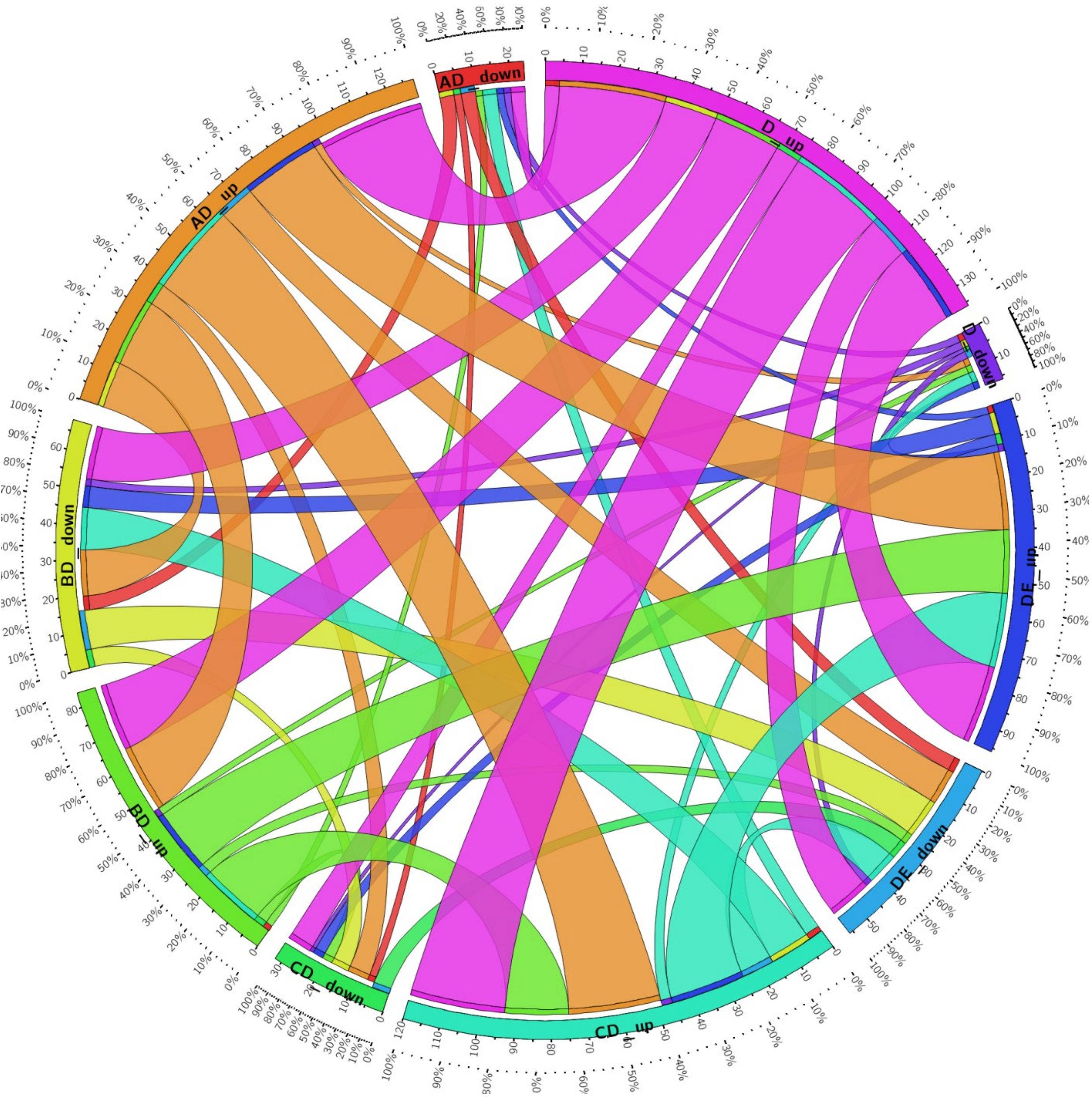

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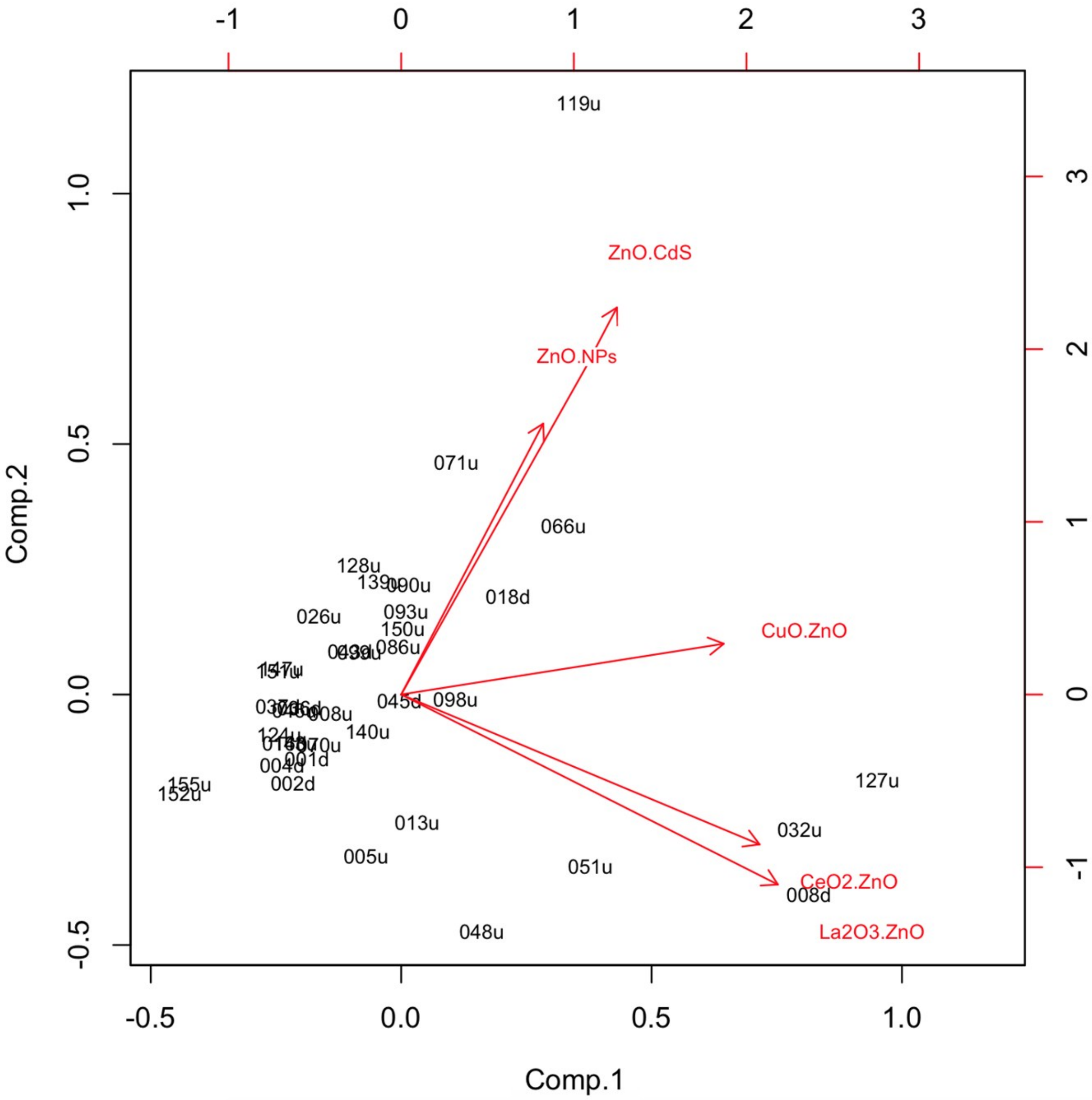

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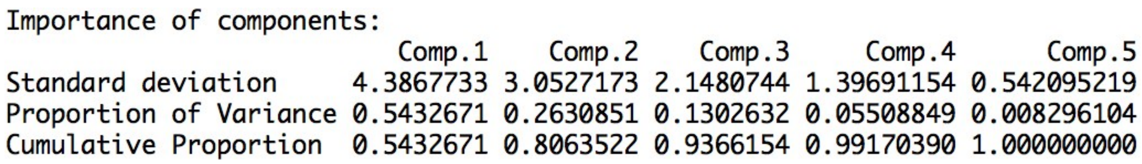

```
Importance of components:
                          Comp.1    Comp.2    Comp.3     Comp.4      Comp.5
Standard deviation     4.3867733 3.0527173 2.1480744 1.39691154 0.542095219
Proportion of Variance 0.5432671 0.2630851 0.1302632 0.05508849 0.008296104
Cumulative Proportion  0.5432671 0.8063522 0.9366154 0.99170390 1.000000000
```

Figure S14: Heatmap (a) chord diagram (b) and PCA (c) of all the ZnO NPs and their binary combinations with CeO_2 NPs, La_2O_3 NPs, CuO NPs, CdS QDs. Genes up- (red) and down-regulated (green) are reported in the heatmap. Graphic comparison between the gene expression profiles is reported in the chord diagram: ribbons showed the overlap (expressed as number and

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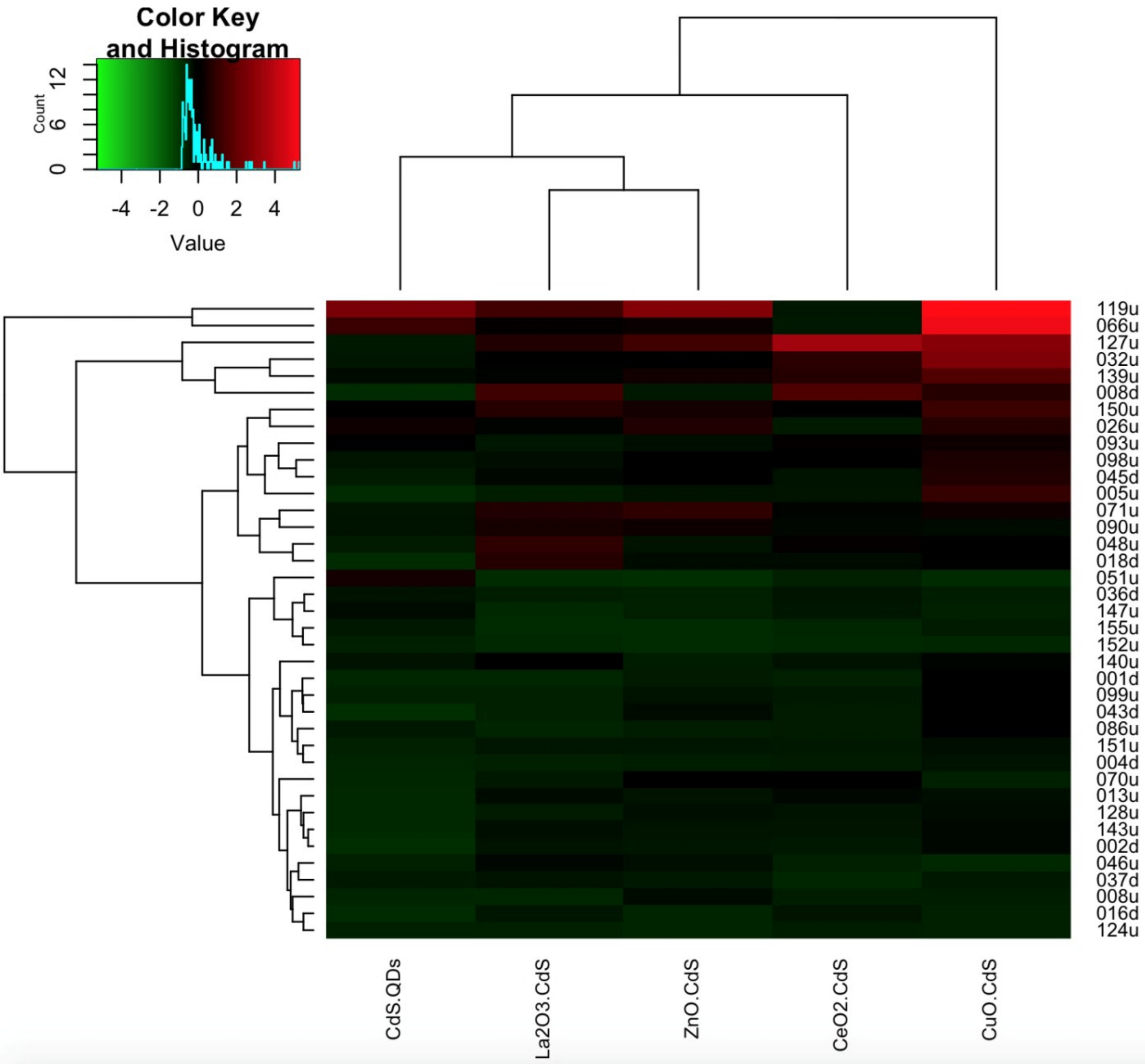

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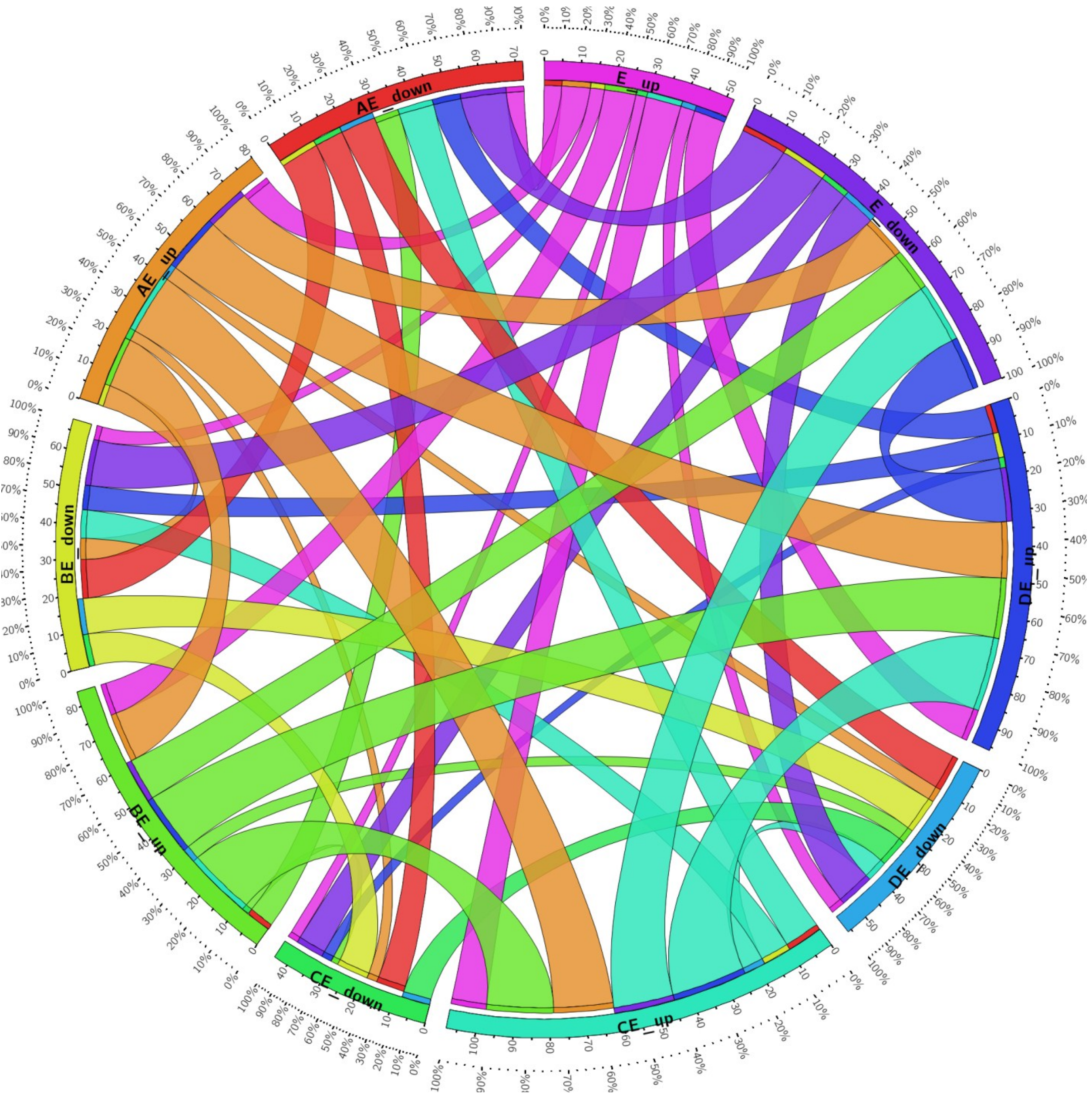

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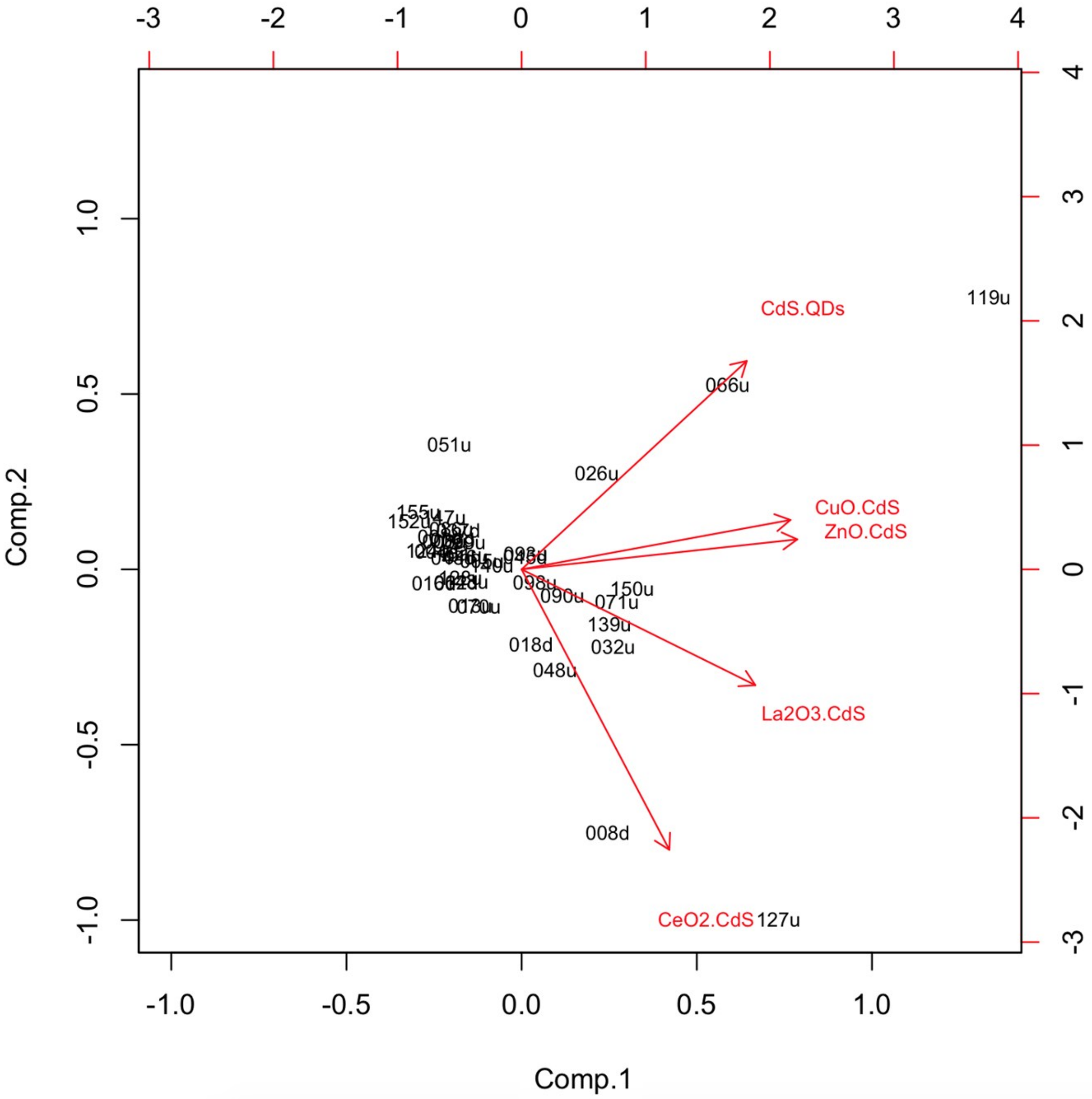

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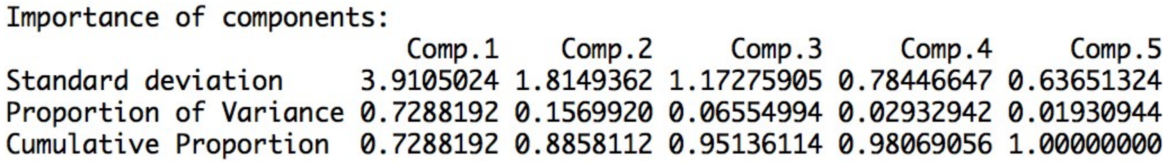

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Importance of components:
                          Comp.1    Comp.2     Comp.3     Comp.4     Comp.5
Standard deviation     3.9105024 1.8149362 1.17275905 0.78446647 0.63651324
Proportion of Variance 0.7288192 0.1569920 0.06554994 0.02932942 0.01930944
Cumulative Proportion  0.7288192 0.8858112 0.95136114 0.98069056 1.00000000
```

Figure S15: Heatmap (a) chord diagram (b) and PCA (c) of all the CdS QDs and their binary combinations with CeO_2 NPs, La_2O_3 NPs, CuO NPs, ZnO NPs. Genes up- (red) and down-regulated (green) are reported in the heatmap. Graphic comparison between the gene expression profiles is reported in the chord diagram: ribbons show the overlap (expressed as number and

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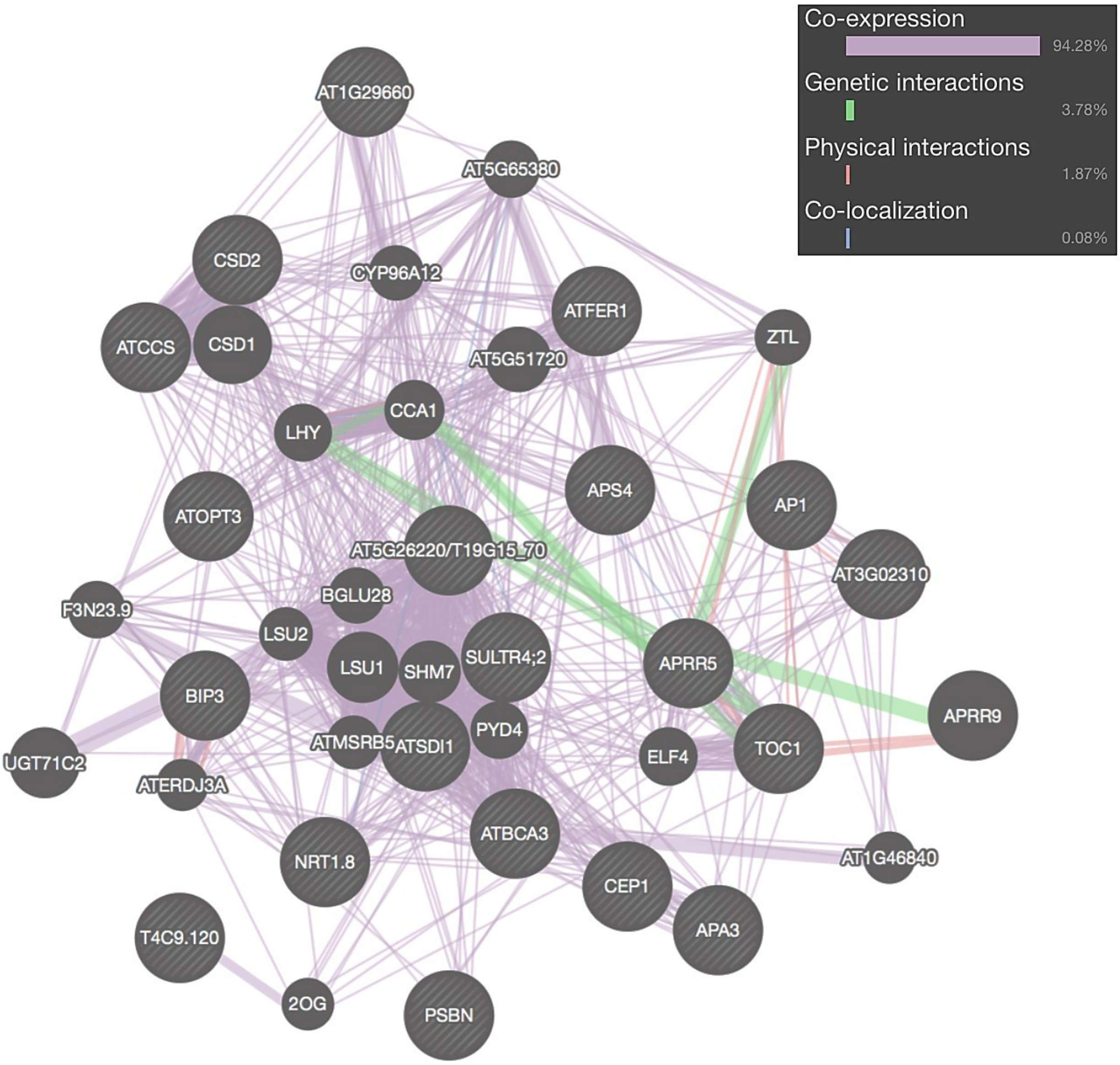

Figure S16: Gene network representing, in percentage, co-expression, co-localization, genetic and physical interaction (as reported in the legend) between the univocal and non-univocal genes related to ENM response studied. Query genes are indicated with stripes.

<u>References</u>:

1. Pagano L, Servin AD, De La Torre-Roche R, Mukherjee A, Majumdar S, Hawthorne J, Marmiroli M, Maestri E, Marra RE, Isch SM, Parkash Dhankher O, White JC, Marmiroli N. 2016. Molecular response of crop plants to engineered nanomaterials. Environ. Sci. Technol., 50 (13), 7198–7207.
2. Audet P, Charest C. 2007. Heavy metal phytoremediation from a meta-analytical perspective. Environmental Pollution. 147(1), 231-237.
3. Marmiroli M, Pagano L, Savo Sardaro ML, Villani M, Marmiroli N. 2014. Genome-wide approach in *Arabidopsis thaliana* to assess the toxicity of cadmium sulfide quantum dots. Environ. Sci. Technol. 48, 5902-5909.

Table S9: Additional references of the gene enlisted in the text.

ref	gene name	reference
004d	*CCS*	Zhou GA, Chang RZ, Qiu LJ. 2010. Overexpression of soybean ubiquitin-conjugating enzyme gene GmUBC2 confers enhanced drought and salt tolerance through modulating abiotic stress-responsive gene expression in Arabidopsis. Plant Mol Biol. 72: 357. doi:10.1007/s11103-009-9575-x
005u	*BIP3*	Maruyama D, Endo T, Nishikawa S. 2015. BiP3 supports the early stages of female gametogenesis in the absence of BiP1 and BiP2 in Arabidopsis thaliana. Plant Signal Behav. 10 (7). doi: 10.1080/15592324.2015.1035853.
008u	*BFN1*	Sakamoto W and Takami T. 2014. Nucleases in higher plants and their possible involvement in DNA degradation during leaf senescence. J. Exp. Bot. 65 (14): 3835-3843. doi: 10.1093/jxb/eru091
013u	*BCA3*	Ferreira FJ, Guo C, Coleman, JR. 2008. Reduction of plastid-localized CA activity results in reduced Arabidopsis thaliana seedling survivorship. Plant Physiol. 147 (2): 585-594.
018d	*CSD2*	Thieme CJ, Rojas-Triana M, Stecyk E, Schudoma C, Zhang W, Yang L, Minambres M, Walther D, Schulze WX, Paz-Ares J, Scheible WR, Kragler F. 2015. Endogenous Arabidopsis messenger RNA transported to distant tissues. Nature Plants 1, 15025 doi:10.1038/nplants.2015.25
032u	*AGL7*	Leal Valentim F, Mourik, SV, Posé, D., Kim, MC, Schmid M, van Ham RC, Busscher M, Sanchez-Perez GF, Molenaar J, Angenent GC, Immink RG, van Dijk AD. 2015. A quantitative and dynamic model of the Arabidopsis flowering time gene regulatory network. PLOS ONE. doi: http//dx.doi.org/10.1371/journal.pone.0116973
036d	*FER1*	Hong S, Kim SA, Guerinot ML, McClung CR. 2012. Reciprocal interaction of the circadian clock with the Fe homeostasis network in Arabidopsis thaliana. Plant Physiol 161(2): 893-903.
043d	*PHT1;1*	Ayadi A, David P, Arrighi JF, Chiarenza S, Thibaud MC, Nussaume L, Marin E. 2015. Reducing the genetic redundancy of Arabidopsis PHT1 transporters to study phosphate uptake and signaling. Plant Physiol 167 (4): 1511-1526.
045d, **093u,** **147u**	*ATPS4,* *At4g12280,* *PRR1*	Ascencio-Ibanez JT, Sozzani R, Lee T-J, Chu T-M, Wolfinger RD, Cella R, Hanley-Bowdoin L. 2008. Global Analysis of Arabidopsis Gene Expression Uncovers a Complex Array of Changes Impacting Pathogen Response and Cell Cycle during Geminivirus Infection. Plant Physiol 148(1): 436-454
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