Supporting Word file S1

Zn accumulation in contrasting barley lines: search for candidate genes explaining natural variation

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Metal gene search:

1. Ensembl search key words
2. Bins potentially related to metal homeostasis
3. Gene Ontology search based on search term `metal`
4. *Arabidopsis thaliana* metal genes list (based on manually curated list of MapMan transition metal homeostasis genes of *A. thaliana*" in Suryawanshi, *et al*. (2016) Between-species differences in gene copy number are enriched among functions critical for adaptive evolution in *Arabidopsis halleri*. BMC genomics 17)

1. Search at Ensembl (http://plants.ensembl.org/Hordeum_vulgare/Info/Index) **platform with following key words:**

- ABC, ABC transporter
- ATPase, transporting ATPase
- Cation
- CDF (Cation diffusion)
- Cobalt
- Copper
- Ferric reductase
- Ferrritin
- Ion
- Iron
- Lead
- Magnesium
- MATE, MATE efflux

- Metal, heavy metal, metal ion, metal ion transport, metal tolerance, metal tolerance protein
- Metallothionein
- natural resistence
- Nickel
- Nicotianamine, aminotransferase, synthase
- Nramp
- Phytochelatin, synthase
- Transport, ion transport, metal ion transport
- YSL, phytosiderophore, yellow-stripe-like
- Zinc
- ZIP

2. Bins with potential connection to metal homeostatis:

- 20 stress
    - 20.1 stress.biotic
    - 20.1 stress.biotic AND 29.5.11.4.2 protein.degradation.ubiquitin.E3.RING
    - 20.1 stress.biotic AND 34.16 **transport.ABC transporters** and multidrug resistance systems
        - 20.1.1 stress.biotic.respiratory burst
    - 20.2 stress.abiotic
        - 20.2.1 stress.abiotic.heat
        - 20.2.1 stress.abiotic.heat AND 27.3.23 RNA.regulation of transcription.HSF,Heat-shock transcription factor family
        - 20.2.1 stress.abiotic.heat AND 29.4 protein.postranslational modification
        - 20.2.1 stress.abiotic.heat AND 29.6 protein.folding
        - 20.2.2 stress.abiotic.cold
        - 20.2.2 stress.abiotic.cold AND 20.2.3 stress.abiotic.drought/salt
        - 20.2.2 stress.abiotic.cold AND 33.99 development.unspecified
        - 20.2.3 stress.abiotic.drought/**salt**
        - 20.2.3 stress.abiotic.drought/**salt** AND 20.2.3 stress.abiotic.drought/salt
        - 20.2.3 stress.abiotic.drought/**salt** AND 27.3.3 RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family
        - 20.2.4 stress.abiotic.touch/wounding
        - 20.2.4 stress.abiotic.touch/wounding AND 30.2.99 signalling.receptor kinases.misc
        - 20.2.4 stress.abiotic.touch/wounding AND 30.2.99 signalling.receptor kinases.misc
        - 20.2.4 stress.abiotic.touch/wounding AND 31.3 cell.cycle

        - 20.2.5 stress.abiotic.light
        - 20.2.5 stress.abiotic.light AND 29.5.11.4.6 protein.degradation.ubiquitin.E3.DCX
        - 20.2.5 stress.abiotic.light AND 30.11 signalling.light
        - 20.2.5 stress.abiotic.light AND 31.2 cell.division
        - 20.2.99 stress.abiotic.unspecified
        - 20.2.99 stress.abiotic.unspecified AND 30.11 signalling.light
        - 20.2.99 stress.abiotic.unspecified AND 30.3 **signalling.calcium**
    - 28.99 DNA.unspecified AND 34.99 **transport.misc**
    - 30.3 signalling.**calcium**
    - 30.3 signalling.**calcium** AND 34.21 transport.calcium
    - 33.1 development.**storage proteins**
    - 33.2 development.late embryogenesis abundant
        - 33.30.1 development.multitarget.target of rapamycin
    - 33.50 development.inhibitor proteins
    - 33.99 development.unspecified
    - 33.99 development.unspecified AND 34.16 **transport.ABC transporters** and multidrug resistance systems
    - 33.99 development.unspecified AND 35.2 not assigned.unknown
    - 34.1 **transport.p- and v-ATPases**
    - 34.10 transport.nucleotides
    - 34.11 transport.NDP-sugars at the ER
    - 34.12 **transport.metal**
    - 34.12 **transport.metal** AND 34.21 **transport.calcium**
    - 34.13 transport.peptides and oligopeptides
    - 34.14 transport.unspecified **cations**
    - 34.14 transport.unspecified **cations** AND 34.18 **transport.unspecified** anions
    - 34.15 **transport.potassium**
    - 34.16 **transport.ABC transporters** and multidrug resistance systems
    - 34.18 **transport.unspecified anions**
        - 34.19.1 transport.Major Intrinsic Proteins.PIP
        - 34.19.2 transport.Major Intrinsic Proteins.TIP
    - 34.2 transporter.sugars
        - 34.2.1 transporter.sugars.sucrose
    - 34.20 transport.porins
    - 34.21 transport.**calcium**
    - 34.22 transport.cyclic nucleotide or calcium regulated channels
    - 34.3 transport.amino acids
    - 34.3 transport.amino acids AND 34.13 transport.peptides and oligopeptides
    - 34.4 transport.**nitrate**
    - 34.5 transport.**ammonium**
    - 34.6 transport.**sulphate**
    - 34.7 transport.**phosphate**
    - 34.8 transport.metabolite transporters at the envelope membrane
    - 34.9 transport.metabolite transporters at the mitochondrial membrane

- 34.9 transport.metabolite transporters at the mitochondrial membrane AND 34.21 transport.**calcium**
- 34.98 **transporter.membrane system unknown**
- 34.99 **transport.misc**

3. Results from key word search at Gene Ontology Platform:

- http://www.ebi.ac.uk/QuickGO/GSearch?q=metal&what=GO&limit=1000
- Search term: „metal“

spect	ID	Name
Component	GO:1902695	metallochaperone complex
Component	GO:0031942	i-AAA complex
Component	GO:0043234	protein complex
Component	GO:0017090	meprin A complex
Component	GO:1990850	H-gal-GP complex
Component	GO:0016610	nitrogenase complex
Component	GO:1990660	calprotectin complex
Component	GO:0071052	alpha9-beta1 integrin-ADAM1 complex
Component	GO:0071053	alpha9-beta1 integrin-ADAM2 complex
Component	GO:0071054	alpha9-beta1 integrin-ADAM3 complex
Component	GO:0071055	alpha9-beta1 integrin-ADAM9 complex
Component	GO:0071133	alpha9-beta1 integrin-ADAM8 complex
Component	GO:0071056	alpha9-beta1 integrin-ADAM15 complex
Component	GO:0071057	alphav-beta3 integrin-ADAM15 complex
Component	GO:0071067	alphav-beta3 integrin-ADAM23 complex
Component	GO:0071068	alpha9-beta1 integrin-ADAM12 complex
Component	GO:0071100	alphaV-beta8 integrin-MMP14-TGFbeta-1 complex
Function	GO:0046872	metal ion binding
Function	GO:0051540	metal cluster binding
Function	GO:0031420	alkali metal ion binding
Function	GO:0046911	metal chelating activity
Function	GO:0008237	metallopeptidase activity
Function	GO:0016530	metallochaperone activity
Function	GO:0070573	metallodipeptidase activity
Function	GO:0005505	obsolete heavy metal binding
Function	GO:0008235	metalloexopeptidase activity
Function	GO:0046914	transition metal ion binding
Function	GO:0004222	metalloendopeptidase activity
Function	GO:0070006	metalloaminopeptidase activity
Function	GO:0004181	metallocarboxypeptidase activity
Function	GO:0051139	metal ion:proton antiporter activity
Function	GO:0008191	metalloendopeptidase inhibitor activity
Function	GO:0005373	obsolete heavy metal ion porter activity
Function	GO:0008472	obsolete metallocarboxypeptidase D activity
Function	GO:0046873	metal ion transmembrane transporter activity
Function	GO:0015076	obsolete heavy metal ion transporter activity
Function	GO:0016722	oxidoreductase activity, oxidizing metal ions
Function	GO:0030405	obsolete matrix metalloproteinase 19 activity
Function	GO:0030406	obsolete matrix metalloproteinase 25 activity
Function	GO:0004007	obsolete heavy metal-exporting ATPase activity
Function	GO:0031368	obsolete Pro-X metallocarboxypeptidase activity
Function	GO:0015335	obsolete heavy metal ion:hydrogen symporter activity
Function	GO:0004023	alcohol dehydrogenase activity, metal ion-independent
Function	GO:0030946	protein tyrosine phosphatase activity, metal-dependent
Function	GO:0046915	transition metal ion transmembrane transporter activity
Function	GO:0015337	obsolete low affinity metal ion uptake transporter activity
Function	GO:0015336	obsolete high affinity metal ion uptake transporter activity
Function	GO:0016724	oxidoreductase activity, oxidizing metal ions, oxygen as acceptor
Function	GO:0043783	oxidoreductase activity, oxidizing metal ions with flavin as acceptor

Function	GO:1990908	obsolete Lys63-specific zinc metallopeptidase deubiquitinase activity
Function	GO:0016723	oxidoreductase activity, oxidizing metal ions, NAD or NADP as acceptor
Function	GO:0001199	transcription factor activity, metal ion regulated sequence-specific DNA binding
Function	GO:0001209	transcriptional activator activity, metal ion regulated sequence-specific DNA binding
Function	GO:0001210	transcriptional repressor activity, metal ion regulated sequence-specific DNA binding
Function	GO:1902945	metalloendopeptidase activity involved in amyloid precursor protein catabolic process
Function	GO:0001200	RNA polymerase II transcription factor activity, metal ion regulated sequence-specific DNA binding
Function	GO:0001204	bacterial-type RNA polymerase transcription factor activity, metal ion regulated sequence-specific DNA binding
Function	GO:0001215	bacterial-type RNA polymerase transcriptional activator activity, metal ion regulated sequence-specific DNA binding
Function	GO:0001218	bacterial-type RNA polymerase transcriptional repressor activity, metal ion regulated sequence-specific DNA binding
Function	GO:0001201	RNA polymerase II transcription factor activity, metal ion regulated core promoter proximal region sequence-specific binding
Function	GO:0001213	RNA polymerase II transcriptional activator activity, metal ion regulated core promoter proximal region sequence-specific binding
Function	GO:0001214	RNA polymerase II transcriptional repressor activity, metal ion regulated core promoter proximal region sequence-specific binding
Function	GO:0004857	enzyme inhibitor activity
Function	GO:0008047	enzyme activator activity
Function	GO:0030234	enzyme regulator activity
Function	GO:0004231	obsolete insulysin activity
Function	GO:0042029	obsolete fibrolase activity
Function	GO:0004235	obsolete matrilysin activity
Function	GO:0004245	obsolete neprilysin activity
Function	GO:0008975	obsolete pitrilysin activity
Function	GO:0004228	obsolete gelatinase A activity
Function	GO:0004229	obsolete gelatinase B activity
Function	GO:0030402	obsolete matrilysin-2 activity
Function	GO:0004248	obsolete stromelysin 1 activity
Function	GO:0004249	obsolete stromelysin 3 activity
Function	GO:0030303	obsolete stromelysin 2 activity
Function	GO:0030403	obsolete collagenase 4 activity
Function	GO:0030404	obsolete collagenase 3 activity
Function	GO:0015295	solute:proton symporter activity
Function	GO:0004234	obsolete macrophage elastase activity
Function	GO:0051405	obsolete microbial collagenase activity
Function	GO:0008130	obsolete neutrophil collagenase activity
Function	GO:0004232	obsolete interstitial collagenase activity
Function	GO:0015291	secondary active transmembrane transporter activity
Function	GO:0048037	cofactor binding
Function	GO:0098769	TIMP family protein binding
Function	GO:0071991	phytochelatin transporter activity
Function	GO:0015115	silicate transmembrane transporter activity
Function	GO:0051002	ligase activity, forming nitrogen-metal bonds
Function	GO:0015603	iron chelate transmembrane transporter activity
Function	GO:0071992	phytochelatin transmembrane transporter activity
Function	GO:0051981	copper chelate transmembrane transporter activity
Process	GO:0030001	metal ion transport
Process	GO:0010038	response to metal ion
Process	GO:0055065	metal ion homeostasis
Process	GO:0051238	sequestering of metal ion
Process	GO:0070839	divalent metal ion export
Process	GO:0070838	divalent metal ion transport
Process	GO:0097501	stress response to metal ion
Process	GO:0000041	transition metal ion transport
Process	GO:0006875	cellular metal ion homeostasis
Process	GO:0042142	obsolete heavy metal chelation
Process	GO:0071248	cellular response to metal ion
Process	GO:0031163	metallo-sulfur cluster assembly
Process	GO:0009412	obsolete response to heavy metal
Process	GO:0055076	transition metal ion homeostasis
Process	GO:0010959	regulation of metal ion transport

Process	GO:1990773	matrix metallopeptidase secretion
Process	GO:0006823	obsolete heavy metal ion transport
Process	GO:1990419	obsolete response to elemental metal
Process	GO:1905048	regulation of metallopeptidase activity
Process	GO:0046916	cellular transition metal ion homeostasis
Process	GO:1990267	response to transition metal nanoparticle
Process	GO:0009634	obsolete heavy metal sensitivity/resistance
Process	GO:1904683	regulation of metalloendopeptidase activity
Process	GO:0030006	obsolete heavy cellular metal ion homeostasis
Process	GO:0018283	iron incorporation into metallo-sulfur cluster
Process	GO:0018282	metal incorporation into metallo-sulfur cluster
Process	GO:0030923	metal incorporation into metallo-oxygen cluster
Process	GO:1904464	regulation of matrix metallopeptidase secretion
Process	GO:0018414	nickel incorporation into metallo-sulfur cluster
Process	GO:0018427	copper incorporation into metallo-sulfur cluster
Process	GO:0031162	sulfur incorporation into metallo-sulfur cluster
Process	GO:1905049	negative regulation of metallopeptidase activity
Process	GO:1905050	positive regulation of metallopeptidase activity
Process	GO:0030925	calcium incorporation into metallo-oxygen cluster
Process	GO:0042039	vanadium incorporation into metallo-sulfur cluster
Process	GO:0051221	tungsten incorporation into metallo-sulfur cluster
Process	GO:0030924	manganese incorporation into metallo-oxygen cluster
Process	GO:0018289	molybdenum incorporation into metallo-sulfur cluster
Process	GO:1904684	negative regulation of metalloendopeptidase activity
Process	GO:1904685	positive regulation of metalloendopeptidase activity
Process	GO:0042040	metal incorporation into metallo-molybdopterin complex
Process	GO:1904465	negative regulation of matrix metallopeptidase secretion
Process	GO:1904466	positive regulation of matrix metallopeptidase secretion
Process	GO:1902962	regulation of metalloendopeptidase activity involved in amyloid precursor protein catabolic process
Process	GO:1902963	negative regulation of metalloendopeptidase activity involved in amyloid precursor protein catabolic process
Process	GO:1902964	positive regulation of metalloendopeptidase activity involved in amyloid precursor protein catabolic process
Process	GO:0030926	calcium incorporation into metallo-oxygen cluster via bis-L-aspartato tris-L-glutamato L-histidino calcium tetramanganese tetroxide
Process	GO:0030927	manganese incorporation into metallo-oxygen cluster via bis-L-aspartato tris-L-glutamato L-histidino calcium tetramanganese tetroxide
Process	GO:0050790	regulation of catalytic activity
Process	GO:0043085	positive regulation of catalytic activity
Process	GO:0043086	negative regulation of catalytic activity
Process	GO:0018315	molybdenum incorporation into molybdenum-molybdopterin complex
Process	GO:0046713	borate transport
Process	GO:0071836	nectar secretion
Process	GO:0015708	silicate transport
Process	GO:0015688	iron chelate transport
Process	GO:0071993	phytochelatin transport
Process	GO:0051186	cofactor metabolic process
Process	GO:0051206	silicate metabolic process
Process	GO:0043241	protein complex disassembly
Process	GO:0016226	iron-sulfur cluster assembly
Process	GO:0018942	organometal metabolic process
Process	GO:0050787	detoxification of mercury ion
Process	GO:0035445	borate transmembrane transport
Process	GO:0061007	hepaticobiliary system process
Process	GO:0046937	phytochelatin metabolic process
Process	GO:0071995	phytochelatin import into vacuole
Process	GO:0046938	phytochelatin biosynthetic process
Process	GO:0061008	hepaticobiliary system development
Process	GO:0018934	nitrilotriacetate metabolic process
Process	GO:0018979	trichloroethylene metabolic process
Process	GO:0050696	trichloroethylene catabolic process
Process	GO:0043624	cellular protein complex disassembly
Process	GO:0071994	phytochelatin transmembrane transport
Process	GO:0090423	phytochelatin-metal complex formation
Process	GO:0090424	phytochelatin-metal-sulfur complex formation

4. *Arabidopsis thaliana* metal genes list:

ID	Genesymbol	Function	QueryLength
At1g30400	ABCC1	vacuolar phytochelatin transporter, also MRP1	1622
At2g34660	ABCC2	vacuolar phytochelatin transporter, also MRP2	1623
At1g75830	AFP1	antifungal protein 1	
At2g43510	AFP10	distantly related to antifungal protein	
At2g26010	AFP2	putative antifungal protein	
At5g44430	AFP3	putative antifungal protein	
At5g44420	AFP4	putative antifungal protein	
At2g26020	AFP5	distantly related to antifungal protein; PDF1.2b	
At1g19610	AFP6	distantly related to antifungal protein	
At2g02140	AFP7	distantly related to antifungal protein	73
At2g02130	AFP8	distantly related to antifungal protein	77
At2g43550	AFP9	distantly related to antifungal protein	
At4g19070	AS8	Cadmium-induced protein AS8 [Source:UniProtKB/Swiss-Prot;Acc:P42735]	171
At4g28630	ATM1	Half-molecule ABC transporter, Fe-S cluster biogenesis	678
At4g28620	ATM2	Half-molecule ABC transporter, Fe-S cluster biogenesis	680
At5g58270	ATM3	Half-molecule ABC transporter, Fe-S cluster biogenesis	728
At1g66240	ATX1	copper chaperone, interacts with HMA5?	106
At2g41240	bHLH100	Functions as a key regulator of iron-deficiency responses independent of the master regulator FIT. Likely regulates genes involved in the distribution of iron within the plant.Encodes a member of the basic helix-loop-helix transcription factor family protein.	242
At5g04150	bHLH101	Functions as a key regulator of iron-deficiency responses independent of the master regulator FIT.	240

		Likely regulates genes involved in the distribution of iron within the plant.Encodes a member of the basic helix-loop-helix transcription factor family protein.	
At1g51070	bHLH115	interactor of POPEYE, Fe deficiency response	292
At3g56970	bHLH38	bHLH transcription factor, interactor of FIT1	253
At3g56980	bHLH39	bHLH transcription factor, interactor of FIT1	258
At3g18290	BTS	BRUTUS, E3 ubiquitin ligase containing hemerythrin motifs, important in Fe deficiency response, ko lethal	1254
At4g35040	bZIP19	regulator of Zn deficiency response, redundant with AtbZIP23	261
At2g16770	bZIP23	regulator of Zn deficiency response, redundant with AtbZIP19	249
At2g38170	CAX1	Ca2+/H+ exchangers	475
At1g54110	CAX10	Ca2+/H+ exchangers	236
At1g08960	CAX11	Ca2+/H+ exchangers	546
At3g13320	CAX2	Ca2+/H+ exchangers	441
At3g51860	CAX3	Ca2+/H+ exchangers	459
At5g01490	CAX4	Ca2+/H+ exchangers	454
At1g55730	CAX5	Ca2+/H+ exchangers	441
At1g55720	CAX6	Ca2+/H+ exchangers	467
At5g17860	CAX7	Ca2+/H+ exchangers	570
At5g17850	CAX8	Ca2+/H+ exchangers	559
At3g14070	CAX9	Ca2+/H+ exchangers	643
At2g01770	CCC1/VIT1	similar to yeast Fe transporter CCC1 originally thought to transport Ca and Mn	250
At3g43660	CCCl1	a little similar to AtCCC1; annotated as nodulin	198
At1g21140	CCCl2	a little similar to AtCCC1; annotated as nodulin	200
At3g43630	CCCl3	a little similar to AtCCC1; annotated as nodulin	200
At1g76800	CCCl4	a little similar to AtCCC1; annotated as nodulin	196
At3g25190	CCCl5	a little similar to AtCCC1; annotated as nodulin	219
At3g56240	CCH, HIPP45	copper chaperone	121
At5g37860	CCH-like	putative Cu chaperone (Zachgo)	262
At1g12520	CCS	copper chaperone	320

At2g46800	CDF1	cation diffusion facitlitator or metal transport protein family (MTP)	398
At3g58060	CDF10	cation diffusion facitlitator or metal transport protein family (MTP)	411
At3g12100	CDF11	cation diffusion facitlitator or metal transport protein family (MTP)	393
At1g51610	CDF12	cation diffusion facitlitator or metal transport protein family (MTP)	457
At3g61940	CDF2	cation diffusion facitlitator or metal transport protein family (MTP)	334
At3g58810	CDF3	cation diffusion facitlitator or metal transport protein family (MTP)	432
At2g29410	CDF4	cation diffusion facitlitator or metal transport protein family (MTP)	375
At2g04620	CDF5	cation diffusion facitlitator or metal transport protein family (MTP)	798
At2g47830	CDF6	cation diffusion facitlitator or metal transport protein family (MTP)	471
At2g39450	CDF7	cation diffusion facitlitator or metal transport protein family (MTP)	394
At1g16310	CDF8	cation diffusion facitlitator or metal transport protein family (MTP)	428
At1g79520	CDF9	cation diffusion facitlitator or metal transport protein family (MTP)	414
At1g16380	CHX1	cation/H+ exchanger of unknown specificity - CPA2 family	785
At3g44930	CHX10	cation/H+ exchanger of unknown specificity - CPA2 family	783
At3g44920	CHX11	cation/H+ exchanger of unknown specificity - CPA2 family	783
At3g44910	CHX12	cation/H+ exchanger of unknown specificity - CPA2 family	770
At2g30240	CHX13	cation/H+ exchanger of unknown specificity - CPA2 family	831
At1g06970	CHX14	cation/H+ exchanger of unknown specificity - CPA2 family	829
At2g13620	CHX15	cation/H+ exchanger of unknown specificity - CPA2 family	821

At1g64170	CHX16	cation/H+ exchanger of unknown specificity - CPA2 family	811
At4g23700	CHX17	cation/H+ exchanger of unknown specificity - CPA2 family	820
At5g41610	CHX18	cation/H+ exchanger of unknown specificity - CPA2 family	810
At3g17630	CHX19	cation/H+ exchanger of unknown specificity - CPA2 family	800
At1g79400	CHX2	cation/H+ exchanger of unknown specificity - CPA2 family	783
At3g53720	CHX20	cation/H+ exchanger of unknown specificity - CPA2 family	842
At2g31910	CHX21	cation/H+ exchanger of unknown specificity - CPA2 family	832
At1g05580	CHX23	cation/H+ exchanger of unknown specificity - CPA2 family	867
At5g37060	CHX24	cation/H+ exchanger of unknown specificity - CPA2 family	859
At5g58460	CHX25	cation/H+ exchanger of unknown specificity - CPA2 family	857
At5g01680	CHX26	cation/H+ exchanger of unknown specificity - CPA2 family	784
At5g01690	CHX27	cation/H+ exchanger of unknown specificity - CPA2 family	745
At3g52080	CHX28	cation/H+ exchanger of unknown specificity - CPA2 family	801
At5g22900	CHX3	cation/H+ exchanger of unknown specificity - CPA2 family	822
At3g44900	CHX4	cation/H+ exchanger of unknown specificity - CPA2 family	817
At1g08150	CHX5	cation/H+ exchanger of unknown specificity - CPA2 family	815
At1g08140	CHX6	cation/H+ exchanger of unknown specificity - CPA2 family	818
At2g28170	CHX7	cation/H+ exchanger of unknown specificity - CPA2 family	801
At2g28180	CHX8	cation/H+ exchanger of unknown specificity - CPA2 family	847

At5g22910	CHX9	cation/H+ exchanger of unknown specificity - CPA2 family	800
At5g50920	CLPC1	NA	929
At5g59030	COPT1	copper transporter	170
At3g46900	COPT2	copper transporter	158
At5g59040	COPT3	copper transporter	151
At2g37920	COPT4	copper transporter, new 37925	251
At5g20650	COPT5	copper transporter	146
At2g26975	COPT6	copper transporter	145
At3g15352	COX17-1	copper chaperone	74
At1g53030	COX17-2	copper chaperone	72
At3g15640	COX5b-1	subunit of the mitochondrial cytochrome c oxidase	176
At5g20720	CPN20	Chaperonin 20, metallochaperone that delivers Fe to FeSOD in chloroplast	253
At1g66810	CTH1	related to ScCTH1	310
At1g68200	CTH2	related to ScCTH2, Fe metabolism regulator	308
At2g33740	CUTA	chloroplast copper-binding protein	182
At5g03280	EIN2	Nramp family	1294
At5g01600	FER1	ferritin 1 precursor (chloroplast protein)	255
At3g11050	FER2	putative ferritin	253
At3g56090	FER3	putative ferritin	259
At2g40300	FER4	putative ferritin	259
At4g03240	FH	frataxin homologue of A. thaliana; delivers Fe for heme and Fe-S cluster biosynthesis in mitochondrium	187
At2g28160	FIT1/bHKH029	Fe-deficiency Induced Transcription Factor 1	318
At3g08040	FRD3	ferric reductase deficient 3 gene, MATE family; transports citrate into root xylem to maintain root-to-shoot Fe mobility	526
At1g01590	FRO1	putative ferric chelate reductase	704
At1g01580	FRO2	ferric chelate reductase "the one" FRD1	725
At1g23020	FRO3	ferric chelate reductase, putative	717
At5g23980	FRO4	cupric chelate reductase	699
At5g23990	FRO5	cupric chelate reductase, putative	657

At5g49730	FRO6	ferric chelate reductase, putative	738
At5g49740	FRO7	ferric chelate reductase, essential for Fe import into leaf chloroplast	747
At5g50160	FRO8	ferric chelate reductase, putative	728
At3g08950	HCC1	electron transport SCO1/SenC family protein	334
At4g39740	HCC2	electron transport SCO1/SenC family protein	276
At5g52750	HIPP13	putative metallochaperone-like protein; Heavy metal transport/detoxification superfamily protein	139
At5g52760	HIPP14	putative metallochaperone-like protein; Copper transport protein family	126
At4g13380	HIPP18, MEE56	maternal effect embryo arrest 56	195
At1g71050	HIPP20	putative copper chaperone	152
At5g17450	HIPP21	putative copper chaperone	149
At1g22990	HIPP22	putative copper chaperone (Zachgo)	152
At4g39700	HIPP23	putative copper chaperone	158
At4g08570	HIPP24	putative copper chaperone	150
At4g35060	HIPP25	putative copper chaperone	153
At4g38580	HIPP26	putative metallochaperone-like protein;putative farnesylated protein (At4g38580) mRNA, complete	153
At5g66110	HIPP27	putative metallochaperone-like protein; Heavy metal transport/detoxification superfamily protein	147
At4g10465	HIPP32	putative metallochaperone-like protein; Heavy metal transport/detoxification superfamily protein	183
At1g56210	HIPP35	putative copper chaperone	364
At1g49420	HIPP38	putative metallochaperone-like protein; Heavy metal transport/detoxification superfamily protein	
At1g01490	HIPP39	putative metallochaperone-like protein; Heavy metal transport/detoxification superfamily protein	177
At3g05920	HIPP43	putative metallochaperone-like protein; Heavy metal	126

		transport/detoxification superfamily protein	
At2g36950	HIPP5	putative metallochaperone-like protein; Heavy metal transport/detoxification superfamily protein	386
At5g03380	HIPP6	putative metallochaperone-like protein; Heavy metal transport/detoxification superfamily protein	392
At5g63530	HIPP7	putative metallochaperone-like protein; Farnesylated protein that binds metals	355
At4g37270	HMA1	P1B CPX metal ATPase, CPX motif similar to bacterial Co pumps; suggested to be chloroplast Cu importer and/or chloroplast Zn exporter	819
At4g30110	HMA2	P1B CPX metal ATPase, Zn/Cd/Pb pump	951
At4g30120	HMA3	P1B CPX metal ATPase, Zn/Cd/Pb pump	542
At2g19110	HMA4	P1B CPX metal ATPase, Zn/Cd/Pb pump	1172
At1g63440	HMA5	P1B CPX metal ATPase, Cu pump?	995
At1g68100	IAR1	IAA-alanine resistance protein	469
At3g18485	ILR2	IAA-leucine resistant mutant; encodes inhibitor of ATP-dependent Mn transport	
At5g54680	ILR3	bHLH transcription factor, interactor of POPEYE in Fe deficiency response	234
At2g38460	IREG1	plasma membrane/stele localization	524
At5g03570	IREG2	vacuolar localization, Fe-deficiency-induced immobilization of Ni, Co in root cortex and epidermis	512
At5g26820	IREG3	less sim. to human IREG, identical to MAR1, or kanamycin resistance locus	598
At4g19690	IRT1	ZIP family	347
At4g19680	IRT2	ZIP family	350
At1g60960	IRT3	ZIP family	425
At1g54410	ITP2	similar to Ricinus iron transport protein ITP2	
At1g07030	Mfm1	Mitoferrin-related of MITOCHONDRIAL SOLUTE CARRIER (MSC) family, putative iron transporter across inner mitochondrail membrane related to ScMrs3p and ScMrs4p	326

At2g30160	Mfm2	Mitoferrin-related of MITOCHONDRIAL SOLUTE CARRIER (MSC) family, putative iron transporter across inner mitochondrail membrane related to ScMrs3p and ScMrs4p	331
At2g47600	MHX1	Mg2+/H+ antiporter; Zn/H+ antiporter	539
At4g05105	mir397a	mir397 microRNA family	
At4g13555	mir397b	mir397 microRNA family	
At2g03445	mir398a	mir398 microRNA family	
At5g14545	mir398b	mir398 microRNA family	
At5g14565	mir398c	mir398 microRNA family	
At2g47015	mir408	mir408 microRNA family	
At4g13554	mir857	mir857 microRNA family	
At1g07025	MIT	Mitoferrin of MITOCHONDRIAL SOLUTE CARRIER (MSC) family, putative iron transporter across inner mitochondrail membrane related to ScMrs3p and ScMrs4p	166
At1g07600	MT1a	metallothionein 1a	
At1g07610	MT1c	metallothionein 1c	
At3g09390	MT2a	metallothionein 2 a	81
At5g02380	MT2b	metallothionein 2 b	77
At3g15353	MT3	metallothionein 3	69
At2g42000	MT4a	metallothionein 4 a	120
At2g23240	MT4b	metallothionein 4 b	85
At4g27940	MTM1	AtMTM1 of the MITOCHONDRIAL SOLUTE CARRIER (MSC) superfamily, can restore mitochondrial Mn-SOD activation in yeast Mtm1p mutant	413
At2g46320	MTM1-like	AtMTM1-like member of the MSC superfamily	361
At1g15730	NA	COG0523-domain containing plastid protein, CobW-like cobalamin biosynthesis protein, putative Zn metallochaperone	448
At1g80480	NA	COG0523-domain containing plastid protein, CobW-like cobalamin biosynthesis protein, putative Zn metallochaperone	444
At5g04950	NAS1	nicotianamine synthase	320
At5g56080	NAS2	nicotianamine synthase	320

At1g09240	NAS3	nicotianamine synthase	320
At1g56430	NAS4	putative nicotianamine synthase	324
At4g26480	NAS-like	protein with NAS domain and KH domain	308
At5g51720	NEET	NEET protein acting in chloroplast Fe homeostasis containing a redox-active labile 2Fe-2S cluster binding domain	108
At1g80830	NRAMP1	Nramp family	532
At1g47240	NRAMP2	Nramp family	530
At2g23150	NRAMP3	Nramp family	509
At5g67330	NRAMP4	Nramp family	512
At4g18790	NRAMP5	Nramp family	530
At1g15960	NRAMP6	Nramp family	527
At3g03630	OAS-TL	O-acetylserine thiol lyase	404
At3g22460	OAS-TL	putative O-acetylserine thiol lyase	305
At4g14880	OAS-TL	O-acetylserine thiol lyase	322
At4g16370	OPT3	oligopeptide transporter (OPT) family	737
At4g33520	PAA1	responsible for Cu import into chloroplasts, also HMA6, P1B CPX metal ATPase	949
At5g21930	PAA2	P1B CPX P-type ATPase; Cu transport into thylakoid lumen; also AtHMA8	883
At1g14880	Pcr1	Cys-rich protein, probably plasma membrane Cd exporter conferring Cd tolerance (see publ. Lee and Martinoia)	151
At2g40935	Pcr10	related to AtPcr1, Cd exporter conferring Cd tolerance	190
At1g14870	Pcr2	related to AtPcr1, Zn exporter in root-to-shoot Zn transport and Zn export from root epidermis	152
At5g35525	Pcr3	related to AtPcr1, Cd exporter conferring Cd tolerance	152
At3g18460	Pcr4	related to AtPcr1, Cd exporter conferring Cd tolerance	184
At3g18450	Pcr5	related to AtPcr1, Cd exporter conferring Cd tolerance	184
At1g49030	Pcr6	related to AtPcr1, Cd exporter conferring Cd tolerance	224
At3g18470	Pcr7	related to AtPcr1, Cd exporter conferring Cd tolerance	133

At1g52200	Pcr8	related to AtPcr1, Cd exporter conferring Cd tolerance	190
At1g58320	Pcr9	related to AtPcr1, Cd exporter conferring Cd tolerance	148
At5g44070	PCS1	phytochelatin synthase as first cloned	485
At1g03980	PCS2	phytochelatin synthase	452
At2g15290	PIC1	chloroplast Fe/Zn/Mg importer?	296
At3g14310	PME3	Overly Zinc Sensitive 2	592
At3g47640	PYE	POPEYE, bHLH transcription factor important in root Fe deficiency response in pericycle	240
At5g44790	RAN1	P1B CPX metal ATPase, Cu Transporter, also HMA7	1001
At1g02500	SAMS	S-adenosylmethionine synthetase	393
At2g36880	SAMS	S-adenosylmethionine synthetase	390
At3g17390	SAMS	S-adenosylmethionine synthetase	393
At4g01850	SAMS2	S-adenosylmethionine synthetase 2	393
At1g55920	SAT	serine acetyl transferase	314
At1g78330	SAT?	pseudogene; putative serine acetyl transferase	
At3g13110	SAT1	serine acetyl transferase 1	391
At5g56760	SAT52	serine acetyl transferase 52	312
At5g18830	SPL7	Squamosa-promoter binding-like protein family member, regulator of Cu deficiency response	818
At2g28660	unknown	Chloroplast-targeted copper chaperone protein	265
At4g24120	YSL1	Yellow stripe like transporter 1, role in metal mobility within plant, iron and NA seed loading	673
At5g24380	YSL2	Yellow stripe like transporter 2 in Zn and Fe homeostasis, plasma membrane localization in root endodermis and pericycle facing xylem	664
At5g53550	YSL3	Yellow stripe like transporter 3, role in metal mobility within plant	675
At5g41000	YSL4	Yellow stripe like transporter 4	670
At3g17650	YSL5	Yellow stripe like transporter 5	714
At3g27020	YSL6	Yellow stripe like transporter 6	676

At1g65730	YSL7	Yellow stripe like transporter 7	688
At1g48370	YSL8	Yellow stripe like transporter 8	724
At5g13740	ZIF1	ZINC-INDUCED FACILITATOR1, vacuolar NA or Zn-NA transporter	486
At5g13750	ZIFl1	ZINC-INDUCED FACILITATOR-linke 1	478
At3g43790	ZIFl2	ZINC-INDUCED FACILITATOR-linke 2	484
At3g12750	ZIP1	ZIP family	355
At1g31260	ZIP10	ZIP family	364
At1g55910	ZIP11	ZIP family	326
At5g62160	ZIP12	ZIP family	355
At5g59520	ZIP2	ZIP family	353
At2g32270	ZIP3	ZIP family	339
At1g10970	ZIP4	ZIP family	408
At1g05300	ZIP5	ZIP family	360
At2g30080	ZIP6	ZIP family	341
At2g04032	ZIP7	ZIP family	365
At5g45105	ZIP8	ZIP family	299
At4g33020	ZIP9	ZIP family	344
At2g16800	ZN1	ZEBRA-NECROSIS 1; high-affinity nickel transport protein family member	372
At4g35080	ZN2	ZEBRA-NECROSIS 2; high-affinity nickel transport protein family member	389
At3g20870	ZTP29	ZINC TRANSPORTER 29	276
At3g08650	ZTP50; GufA	ZINC TRANSPORTER 50, putative ZIP family transporter of the ZTP50 subfamily related to CrZIP7; only A. thaliana member of GufA subfamily of ZIP family	619