Table S1. *S. meliloti* metalloproteins and transition metal transporter gene transcripts induced 4-fold in nodules *vs.* growth *in vitro*, and/or enriched (≥40%) in zones of bacteroid differentiation and nitrogen fixation.

Metal[a]	**Locus**	**Description (gene name)**	**Retrived from**[b]	**Category**[c]	**Localization**[e]	**References**
Fe/Mo						
	SMa0827	Nitrogenase molybdenum-iron protein alpha chain (*nifD*)	1, 2	Energy metabolism (Nitrogen metabolism)	C	3
	SMa0829	Nitrogenase molybdenum-iron protein beta chain (*nifK*)	1, 2	Energy metabolism (Nitrogen metabolism)	C	3
Fe						
	SMa0752	Dioxygenase reductase subunit	1, 4	Unclassified	C	5
	SMa0769	Diheme c-type cytochrome (*fixP2*)	1, 2, 4	Energy metabolism (Oxidative phosphorylation)	P	6
	SMa0811	Ferredoxin (*fdxN*)	1, 2, 4	Unclassified	C	7
	SMa0814	FeMo cofactor biosynthesis protein (*nifB*)	1, 2, 4	Energy metabolism	C	8
	SMa0816	Ferredoxin-like protein (*fixX*)	1, 2, 4	Energy metabolism	C	9
	SMa0825	Nitrogenase reductase (*nifH*)	1, 4	Energy metabolism (Nitrogen metabolism)	C	10

SMa1115	Mn^{2+}/Fe^{2+} transporter NRAMP family	1, 2	Transporters	IM	11
SMa1211	Iron sulfur membrane protein (*fixG*)	1, 2, 4	Unclassified	IM	12
SMa1213	Di-heme cytochrome c (*fixP1*)	1, 2, 4	Energy metabolism (Oxidative phosphorylation)	P	6
SM_b20363	Iron ABC transporter ATP-binding protein	2	Transporters	IM	13
SM_b20364	Iron ABC transporter permease	2	Transporters	IM	13
SM_b20365	Iron ABC transporter substrate-binding protein	4	Transporters	P	14
SM_b20615	Thiamine biosynthesis protein (*thiC*)	4	Metabolism of cofactors and vitamins	C	15
SM_b20819	Ferredoxin (*mocE*)	1, 2	Amino acid metabolism	C	16
SM_b20820	Ferredoxin reductase (*mocF*)	1, 2, 4	Amino acid metabolism	C	16
SM_b20984	Nitrite reductase [NAD(P)H], large subunit protein (*nirB*)	1	Energy metabolism (Nitrogen metabolism)	C	17

SM_b20987	Siroheme synthase	2	Metabolism of cofactors and vitamins	C	18
SM_b21541	Iron ABC transporter ATP-binding protein	2	Transporters	IM	13
SM_b21542	Iron uptake ABC transporter permease	2	Transporters	IM	14
SM_b21558	Aldehyde or xanthine dehydrogenase, iron-sulfur subunit protein	2	Nucleotide metabolism	C	19
SM_b21636	Ferredoxin reductase electron transfer protein (*paaE*)	2	Amino acid metabolism	C	20
SMc00016	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (*ispH*)	2, 4	Metabolism of terpenoids and polyketides	C	21
SMc00187	Ubiquinol-cytochrome C reductase iron-sulfur subunit protein (*fbcF*)	2	Energy metabolism (Oxidative phosphorylation)	C	22
SMc00359	Erythrin-vacuolar iron transport family protein (*mbfA*)	2	Transporters	C	23
SMc00785	Iron-responsive transcriptional regulator (*rirA*)	4	Transcription factors	C	24
SMc01611	Ferrichrome receptor precursor protein (*fhuA*)	2	Transporters	OM	25

	SMc02466	Succinate dehydrogenase iron-sulfur subunit (*sdhB*)	2	Carbon metabolism	C	26
	SMc03211	4-hydroxyphenylpyruvate dioxygenase	1	Amino acid metabolism	C	27
	SMc03253	L-proline 3-hydroxylase	1, 4	Unclassified	C	28
	SMc04204	Iron transport regulator transmembrane protein (*fecR*)	1, 2	Signaling proteins	C	29
	SMc04205	Iron/heme transport protein	2	Transporters	OM	14
	SMc04316	Iron ABC transporter permease (*afuB*)	2	Transporters	IM	30
Co						
	SM_b20058	**ABC transporter, ATP-binding protein**[d]	2	Transporters	IM	31
	SMc00399	Magnesium/cobalt transporter CorA (*corA1*)	2	Transporters	C	32
	SMc01237	Vitamin B12-dependent ribonucleotide reductase (*nrdJ*)	2	Nucleotide metabolism	C	33
	SMc03189	Cobalt-precorrin-6x reductase (*cobK*)	2	Metabolism of cofactors and vitamins	C	34

	SMc03193	Cobalamin biosynthesis protein (*cobG*)	2	Metabolism of cofactors and vitamins	P	35
Cu						
	SMa0612	*cbb3*-type cytochrome c oxidase subunit I (*fixN3*)	2	Energy metabolism (Oxidative phosphorylation)	IM	36
	SMa0765	*cbb3*-type cytochrome c oxidase subunit I (*fixN2*)	2	Energy metabolism (Oxidative phosphorylation)	IM	36
	SMa1013	**Copper translocating P-type ATPase (*actP*)**	2	Transporters	IM	37
	SMa1087	Cation transport P-type ATPase (*copA3*)	1, 2	Transporters	IM	38
	SMa1182	N_2O-reductase (*nosZ*)	2	Energy metabolism (Nitrogen metabolism)	P	39
	SMa1186	Copper chaperone (*nosL*)	2	Energy metabolism (Nitrogen metabolism)	C	40
	SMa1194	Dehydrogenase (*nnrS*)	2	Defense mechanisms	IM	41
	SMa1198	Copper export protein	1, 2	Transporters	IM	42
	SMa1209	FixI1 ATPase (*copA2a*)	1, 2, 4	Transporters	IM	38

	SMa1220	*cbb3*-type cytochrome c oxidase subunit I (*fixN1*)	2	Energy metabolism (Oxidative phosphorylation)	IM	36
	SMc01754	Oxidoreductase	2	Unclassified	P	43
	SMc02282	Copper-containing oxidoreductase	2	Unclassified	P	43
	SMc02283	Copper-containing oxidoreductase signal peptide protein	2	Unclassified	C	43
	SMc02400	Probable outer membrane protein (*ropAe*)	2	Transporters	OM	44
Mn						
	SMa1711	Arginase (*argI2*)	2	Biosynthesis of amino acids	C	45
	SMc00008	3,4-dihydroxy-2-butanone-4-phosphate synthase (*ribA*)	2	Metabolism of cofactors and vitamins	C	46
	SMc00043	**Superoxide dismutase, Fe-Mn family (*sodB*)**	2	Oxidoreductase	C	47
	SMc00419	Glutathione synthetase (*gshB1*)	2	Amino acid metabolism	C	48
	SMc00472	Hypothetical protein	2	Nucleotide metabolism	C	49

	SMc00480	Isocitrate dehydrogenase (*icd*)	2	Carbohydrate metabolism	C	50
	SMc00511	D-ribulose-5-phosphate 3-epimerase (*rpe*)	2	Energy metabolism (Carbon fixation in photosynthetic organisms)	C	51
	SMc02506	Manganese/iron transport system ATP-binding protein (*sitD*)	2	Transporters	IM	52
	SMc02507	Manganese/iron transport system ATP-binding protein (*sitC*)	2	Transporters	IM	52
	SMc02508	Manganese/iron transport system ATP-binding protein (*sitB*)	2	Transporters	IM	52
	SMc02509	Manganese/iron transport system ATP-binding protein (*sitA*)	2	Transporters	P	52
Mo	SMa0873	Nitrogenase molybdenum-cofactor biosynthesis protein (*nifN*)	1, 2, 4	Energy metabolism	C	53
	SM_b21557	Aldehyde or xanthine dehydrogenase, molybdopterin binding subunit protein	2	Nucleotide metabolism	C	19
	SMc00144	Molybdenum cofactor biosynthesis protein A (*moaA*)	2	Metabolism of cofactors and vitamins	C	8

	SMc02524	Formate dehydrogenase subunit gamma (*fdsG*)	4	Carbohydrate metabolism	C	54
Zn						
	SMa0041	Zinc dependent oxidoreductase-related quinone oxidoreductase	2	Unclassified	C	55
	SMa1126	Protease	1, 4	Unclassified	IM	55
	SM_b21002	Methionine aminopeptidase (*map2*)	2	Peptidases	C	56
	SM_b21211	**Conserved putative membrane protein, metal-dependent hydrolase**	2	Unclassified	C	57
	SMc01154	Formamidopyrimidine-DNA glycosylase (*fpg*)	2	DNA replication and repair	C	58
	SMc02307	Histidinol dehydrogenase (*hisD*)	2	Amino acid metabolism	C	59
	SMc02771	Zinc-type alcohol dehydrogenase	2	Unclassified	C	55
	SMc04243	**Probable high-affinity zinc uptake system membrane ABC transporter (*znuB*)**	2	Transporters	IM	60

SMc04244	**Probable high-affinity zinc uptake system ATP-binding ABC transporter (*znuC*)**	2	Transporters	C	60
SMc04245	**Probable high-affinity zinc uptake system ABC transporter (*znuA*)**	2	Transporters	P	60

[a] Transported substrate, enyme co-factor or co-enzyme

[b] Legume-Rhizobium model: *M. truncatula* cv. Jemalongg A17 - *S. meliloti* 2011 strain GMI11495 (Roux *et al.*, 2014); *M. truncatula* cv. AS17 - *S. meliloti* Rm1021 (Barnett *et al.*, 2004); *M. truncatula* J6 - *S. meliloti* Rm1021 (Capela *et al.*, 2006)

[c] Locus and descriptions in bold indicates that the transcripts of these candidates were present in differentiation and fixation nodule zones at values between 30% and 40 % of the total counts obtained from the whole nodule

[d] Based on KEGG Orthology (https://www.genome.jp/kegg/ko.html)

[e] Localization in the bacterial cell: Outer membrane (OM), Inner membrane (IM), Cytoplasm (C), Periplasm (P)

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