

**Table S1. List of the unique peptides selected for analyses during vascular differentiation.**

Peptide ID (in this study)	Peptide sequence	Gene ID	Gene annotation	Reason(s) for selecting this candidate	Vascular expression*
Kratos/Peptide 1	<b>GGIGKGGGIGGGIGKGGGIG</b>	AT3G23450	unknown function	Significant difference in peptide analysis (Dataset S1). Abundant in induced wild-type but nearly absent in <i>MC9</i> -RNAi. The full protein seems to be a repeat of this peptide.	Yes
Peptide 2	<b>DSTQIHTHM</b>	AT5G17920	Methione Synthesis	Peptide abundant in induced <i>MC9</i> -RNAi but not found in wild-type.	Yes
Peptide 3	<b>AVYQRSGGAPGGAGGE</b>	AT5G28540	BIP1, Luminal-binding protein 1, HSP70	Peptide abundant in induced <i>MC9</i> -RNAi but not found in wild-type.	Yes
Peptide 4	<b>FVVTDPRDDNPVNPRPGT</b>	AT1G04680	Pectate Lyase, PLA1, lateral root emergence	Peptide abundant in induced <i>MC9</i> -RNAi but not found in wild-type. The corresponding gene is involved in lateral root emergence, a process which also involves <i>MC9</i> .	Yes
Peptide 5	<b>LVIIPAGVPRKPG</b>	AT1G53240	MITOCHONDRIAL MALATE DEHYDROGENASE 1 (mMDH1)	Peptide abundant in induced <i>MC9</i> -RNAi but not found in wild-type.	Yes
Peptide 6	<b>YVSIPIEGPYKPPH</b>	AT4G13940	HOMOLOGY-DEPENDENT GENE SILENCING 1 (HOG1)	Peptide identified in all conditions and genotypes except in induced <i>MC9</i> -RNAi.	Yes
Peptide 7	<b>TTDFPKNPPH</b>	AT2G38080	IRREGULAR XYLEM 12 (IRX12), laccase activity, Laccase-4	Peptide abundant only under the induced condition. The full protein is known to localize to the apoplast. The peptide contains 3 prolines, which is common for signaling peptides.	Yes
Peptide 8	<b>APPPMSDAHTINGKPGPL</b>	AT5G03260	LACCASE 11 (LAC11)	Peptide abundant only under the induced condition. The full protein is known to localize to the apoplast. The peptide contains 4 prolines, which is common for signaling peptides.	Yes
Peptide 9	<b>VGDVTATIVGGLNSQNGPIQK</b>	AT3G10080	RmlC-like cupins superfamily protein	Peptide abundant only under the controlled condition, mostly in the <i>MC9</i> -RNAi genotype.	Yes
Peptide 10	<b>IVNSFKTIDG</b>	AT1G04680	Pectin lyase-like superfamily protein	Peptide abundant only in the <i>MC9</i> -RNAi genotype.	Yes
Peptide 11	<b>SSAGQVDGKQ</b>	AT1G76160	SKU5 SIMILAR 5 (sks5)	Significant difference in peptide analysis (Dataset S1). Peptide identified in all conditions and genotypes except in induced <i>MC9</i> -RNAi.	Yes
Peptide 12	<b>RYSNSAGGVSGPIPGPT</b>	AT1G76160	SKU5 SIMILAR 5 (sks5)	Significant difference in peptide analysis (Dataset S1). Abundant in induced wild-type but nearly absent in <i>MC9</i> -RNAi.	Yes
Peptide 13	<b>FETEPIGKNGKGD</b>	AT2G05710	ACONITASE 3 (ACO3)	Significant difference in peptide analysis (Dataset S1). Abundant in induced wild-type but nearly absent in <i>MC9</i> -RNAi.	Yes
Bia/Peptide 14	<b>EKTAKKAAQAAAAASSGGGGKGNK</b>	AT3G24100	Uncharacterised protein family SERF	Peptide abundant in induced <i>MC9</i> -RNAi but not found in wild-type.	no data available
Peptide 15	<b>AKADVEPKAAEAETKPSQV</b>	AT3G56240	COPPER CHAPERONE (CCH)	Peptide abundant only in the induced condition. Potential <i>MC9</i> substrate	Yes
Peptide 16	<b>NAIGGRKGRIVVTPANDDPVNPRPGT</b>	AT3G27400	Pectin lyase-like superfamily protein	Peptide abundant in all conditions for all genotypes, therefore representing a potential control peptide.	Yes

\* We considered as "vascular expression" the detection of transcripts in tracheary elements (TEs) or in any cell neighboring TEs (i.e. pro-cambium, xylem-pole pericycle) in the Arabidopsis eFP Browser (Winter et al. 2007. *PLoS One* 2(8): e718) "Root" dataset, consisting of transcriptomics data from different root cell types (Brady et al. 2007. *Science* 318(5851): 801-806; Cartwright et al. 2009. *Bioinformatics* 25(19): 2581-2587).