

## Supplementary data:

# Rapid cloning and bioinformatic analysis of spinach Y chromosome-specific EST sequences

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**Table 1.** List of part of spinach Y chromosome-specific ESTs clones by dot blot and their size and homology to the sequences available at the GenBank database by BLASTx software.

Seq. name	Seq. description	Length	e-value	Similarity (%)
SP <sub>1</sub> -81	Hypothetical protein	192	4.21E-06	66.30
SP <sub>2</sub> -52	Hypothetical protein	389	3.74E-09	74.00
SP <sub>2</sub> -67	23S rRNA methyltransferase	139	7.78E-22	88.06
SP <sub>3</sub> -12	PREDICTED: histidine kinase 3-like	230	4.26E-38	87.64
SP <sub>3</sub> -32	PH01B031C15.18	223	9.16E-17	67.42
SP <sub>3</sub> -43	Hypothetical protein VITISV_023700	109	1.24E-07	82.94
SP <sub>3</sub> -55	Transcriptional regulator, Cro/CI family	294	6.77E-42	65.16
SP <sub>4</sub> -13	Transcription termination factor Rho	177	6.32E-32	95.08
SP <sub>4</sub> -14	Hypothetical protein	191	3.22E-06	64.83
SP <sub>4</sub> -42	Hypothetical protein NH8B_0594	394	8.56E-24	61.62
SP <sub>4</sub> -67	Hypothetical protein M301_0439	215	2.31E-06	59.29
SP <sub>4</sub> -94	Hypothetical protein	201	5.27E-23	83.58
SP <sub>5</sub> -13	PH01B031C15.18	416	4.30E-07	61.48
SP <sub>5</sub> -21	ATPase	285	4.61E-60	84.54
SP <sub>5</sub> -28	Adenosine deaminase-related growth factor	215	7.04E-17	70.16
SP <sub>5</sub> -62	S-adenosylmethionine synthase-like protein	310	2.29E-62	93.54

**Table 2.** List of part of spinach Y chromosome-specific ESTs clones by dot blot and their size and homology to the sequences available at the GenBank database by BLASTn software.

Seq. name	Seq. description	Length	e-value	Similarity (%)
SP <sub>1</sub> -3	<i>Dolomedes mizhoanus</i> isolate DMTX-401 cystine knot toxin gene, complete cds	158	2.32E-14	99.00
SP <sub>1</sub> -64	<i>Platynereis dumerilii</i> mRNA for hypothetical protein (ORF1), isolate 2	220	1.37E-63	95.75
SP <sub>1</sub> -89	<i>Platynereis dumerilii</i> mRNA for hypothetical protein (ORF1), isolate 2	233	1.21E-64	89.00
SP <sub>1</sub> -60	<i>S. oleracea</i> mRNA for peroxidase, clone PB22	173	4.12E-18	98.60
SP <sub>1</sub> -62	<i>Amborella trichopoda</i> microRNA for novel locus Atr-MIR164a	119	5.20E-08	100.00
SP <sub>2</sub> -52	<i>Arabidopsis thaliana</i> mRNA for mitochondrial half-ABC transporter (STA1 gene)	389	2.31E-13	98.96
SP <sub>3</sub> -12	<i>Betula pendula</i> histidine kinase 3 (HK3) mRNA, partial cds	230	1.27E-51	78.75
SP <sub>4</sub> -42	<i>Anguilla japonica</i> eDmc1 mRNA for RecA homolog DMC1, complete cds	394	3.48E-11	96.58
SP <sub>5</sub> -13	<i>Ricinus communis</i> mRNA for iron transport protein 2 (ipt2 gene)	416	3.02E-12	99.80
SP <sub>5</sub> -62	<i>Atriplex nummularia</i> AnSAMS4 mRNA for S-adenosyl-L-methionine synthase 4, complete cds	310	6.66E-114	81.88
SP <sub>20</sub> -26	<i>Amborella trichopoda</i> microRNA for novel locus Atr-MIR164a	240	1.25E-07	100.00
SP <sub>21</sub> -29	<i>Aegilops tauschii</i> chromosome 1Ds prolamin gene locus, complete sequence	53	1.06E-09	88.00