

Table S7: BlastX results and functional annotation of upregulated unknown transcripts in YSMS

SeqName	Gene product	Length	#Hits	e-Value	sim mean	#GO	GO IDs	GO Names	Enzyme Codes	Enzyme Names
NW_019167849.1:16010824-16013412	ABC transporter C family member 4	582	20	6.56E-55	88.56	5	P:GO:0055085; F:GO:0005524; F:GO:0016887; F:GO:0140359; C:GO:0016020	P:transmembrane transport; F:ATP binding; F:ATP hydrolysis activity; F:ABC-type transporter activity; C:membrane	EC:3.6.1.15	Catalysing the translocation of inorganic cations; Nucleoside-triphosphate phosphatase
NW_019168015.1:15186720-15189824	ABC transporter C family member 4	1064	20	4.97E-25	89.75	5	P:GO:0055085; F:GO:0005524; F:GO:0016887; F:GO:0140359; C:GO:0016020	P:transmembrane transport; F:ATP binding; F:ATP hydrolysis activity; F:ABC-type transporter activity; C:membrane	EC:3.6.1.15	Catalysing the translocation of inorganic cations; Nucleoside-triphosphate phosphatase

NW_019167915.1:1 3785307-13786351	ABC transporter C family member 14- like	1045	20	4.08E-55	92.52	5	P:GO:0055085; F:GO:0005524; F:GO:0016887; F:GO:0140359; C:GO:0016020	P:transmembrane transport; F:ATP binding; F:ATP hydrolysis activity; F:ABC-type transporter activity; C:membrane	EC:3.6.1.1 5	Catalysing the translocation of inorganic cations; Nucleoside- triphosphate phosphatase
NW_019168159.1:4 201784-4202728	probable serine/threonine- protein kinase WNK4 isoform X2	945	20	1.56E-68	82.86	5	P:GO:0016310; P:GO:0035556; F:GO:0004674; F:GO:0005524; C:GO:0005737	P:phosphorylation; P:intracellular signal transduction; F:protein serine/threonine kinase activity; F:ATP binding; C:cytoplasm		

NW_019167993.1:1 3937795-13940351	putative reverse transcriptase/RNA- dependent DNA polymerase	1469	20	5.09E-18	49.5	9	P:GO:0006278; P:GO:0006508; F:GO:0003676; F:GO:0003677; F:GO:0003964; F:GO:0004190; F:GO:0004523; F:GO:0008270; F:GO:0046872	P:RNA-templated DNA biosynthetic process; P:proteolysis; F:nucleic acid binding; F:DNA binding; F:RNA- directed DNA polymerase activity; F:aspartic-type endopeptidase activity; F:RNA-DNA hybrid ribonuclease activity; F:zinc ion binding; F:metal ion binding		
NW_019167838.1:1 4457975-14458253	ribosomal protein L22	279	20	6.45E-12	87.33	7	P:GO:0006412; F:GO:0003723; F:GO:0003735; C:GO:0005739; C:GO:0009507; C:GO:0015934; C:GO:0015935	P:translation; F:RNA binding; F:structural constituent of ribosome; C:mitochondrion; C:chloroplast; C:large ribosomal subunit; C:small ribosomal subunit		

NW_019167849.1:6 681507-6682390	protein STABILIZED1	884	20	2.19E-94	92.98	6	P:GO:0000244; P:GO:0080188; P:GO:2000630; P:GO:2000636; C:GO:0046540; C:GO:0071013	P:spliceosomal tri- snRNP complex assembly; P:gene silencing by RNA- directed DNA methylation; P:positive regulation of miRNA metabolic process; P:positive regulation of primary miRNA processing; C:U4/U6 x U5 tri- snRNP complex; C:catalytic step 2 spliceosome		
NW_019167938.1:3 705139-3706682	autophagy-related protein 8i	935	20	2.15E-38	87.24	5	P:GO:0006914; P:GO:0006995; C:GO:0005776; C:GO:0005874; C:GO:0016020	P:autophagy; P:cellular response to nitrogen starvation; C:autophagosome; C:microtubule; C:membrane		
NW_019167827.1:1 7861127-17862950	40S ribosomal protein s2-4-like	982	20	1.54E-41	87.88	5	P:GO:0006412; F:GO:0003729; F:GO:0003735; C:GO:0015935; C:GO:0016020	P:translation; F:mRNA binding; F:structural constituent of ribosome; C:small ribosomal subunit; C:membrane		
NW_019167871.1:4 096871-4097656	cyclin-dependent protein kinase inhibitor SMR2-like	786	20	9.88E-27	72.61	2	P:GO:0032875; F:GO:0004860	P:regulation of DNA endoreduplication; F:protein kinase inhibitor activity		

NW_019167971.1:9 502348-9504531	acyl-CoA-binding domain-containing protein 3-like isoform X3	1988	20	1.09E-25	66.33	2	C:GO:0005783; C:GO:0016020	C:endoplasmic reticulum; C:membrane		
NW_019167960.1:1 8173970-18175365	cold-regulated 413 plasma membrane protein 2	647	20	2.21E-28	89.47	1	C:GO:0016020	C:membrane		
NW_019168474.1:1 07221-109931	1,4-alpha-glucan- branching enzyme 1, chloroplastic/amylo plastic-like isoform X2	1063	3	5.42E-47	88.18	1	P:GO:0005975	P:carbohydrate metabolic process		