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Trx s1: genomic sequence with an intron of 108 bp
ATGACTACCGTCACAATAACAATGTCTTCCTTCATCTTTATAATACTTTTTCACACTCTTTCAGCATCCATGGCC
ACCGCACAACTCCTCAACGCTGCCCACTCAAGATGCTTCCAATGGAGGTTTGGTTTTAATTATTAACCTAATATTT
GTGGTTGAGATTTTGTGTTTTTATTTGTTTGCATACGAAGTGGCAATTGTATCACGATATTTTGTTTTAAATATT
GCAGTGGCTTATGTTACCGATGAAAATTTTGGTTCCCTTGTCCTTAACTCTGAGACTCTTGTGTTGGTGGAATTC
TTCGCTCCATTGTGTAGCCCCTGCAAGAATGTTGATTTCAAAATAGTTGAGCTGGCAAATGAATATGCAGGTGAG
GTCGAGTTTTTCAAACTCAATGTTGATGACAATCAACTTATTCCTTCTAAATATGGGATTAAAGGTATTCCAAAT
GTCCTTATCTTCAAAAATGGTGAACAAAGAGATACACTTTTTGGTAACTTACCCAAGGCAACGTTTATCAAACGT
ATGGAACAAAACCTATGA

Trx s1: coding region
ATGACTACCGTCACAATAACAATGTCTTCCTTCATCTTTATAATACTTTTTCACACTCTTTCAGCATCCATGGCC
ACCGCACAACTCCTCAACGCTGCCCACTCAAGATGCTTCCAATGGAGTGGCTTATGTTACCGATGAAAATTTTGGT
TCCCTTGTCCTTAACTCTGAGACTCTTGTGTTGGTGGAATTCTTCGCTCCATTGTGTAGCCCCTGCAAGAATGTT
GATTTCAAAATAGTTGAGCTGGCAAATGAATATGCAGGTGAGGTCGAGTTTTTCAAACTCAATGTTGATGACAAT
CAACTTATTCCTTCTAAATATGGGATTAAAGGTATTCCAAATGTCCTTATCTTCAAAAATGGTGAACAAAGAGAT
ACACTTTTTGGTAACTTACCCAAGGCAACGTTTATCAAACGTATGGAACAAAACCTATGA

Trx s1: protein sequence
MTTVTITMSSFIFIILFHTLSASMATAQLLNAATQDASNGVAYVTDENFGSLVLNSETLVLVEFFAPLCSPCKNV
DFKIVELANEYAGEVEFFKLNVDDNQLIPSKYGIKGIPNVLIFKNGEQRDTLFGNLPKATFIKRMEQNL
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Trx s2: genomique sequence with an intron of 146 bp
ATGGCCACCGTCACATTAGCAATGTCTTCCTTCATCATTTTAATACTTTTTCACACTCTTTCGTCATCCATGGCC
ACCGTACAACTCGAATCCTTACCAAGTTACCTCCTCAGTGCCGCCGATGCTTCCGATGGAGGTTTGGTTTTAATT
ATTAACCCAATATTTGTATTTTTTTCGTTTGCAGACGAAGTGACAAGCACCACAATATTCTGTTTTAGATTTGAT
AAAAAATGAGTTAGTGCCAGGTTAATAAAACTTTGATGTTATTATTCGATATTGTAGTGGCTCCTGTTACTGATG
AAACTTTTGGTTCCTTCGTCCCTATGTCTAAGAATCTCGTGTTGGTGGAATTCTATAATCCATGGTGTGGCCAAA
ACTGCAAAAACATACATTCCATAATGGTTGAGCTGGCAAATGATTATGCTGGTAAGGTCGATTTTTACAAACTCA
ATATTGATGAGAATCCATATATTACTAATAGATATGTGATTCAAGATCTTCCAACTGTGGTTTTCATCAAGTATG
GTATGCAGAGAGATAGACTTGTTGGTGATGTACCTAAAGCAACATTTATCGAACTTATTCAACTATCAATATGAA
CCGGGCTTCTCCTCAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTAGTGAGGGTTAATTCTGAGCTT
GGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGG
AAGCATAAAGTGTAAAGCCTGGGGTGCCTAAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCA

Trx s2: coding region
ATGGCCACCGTCACATTAGCAATGTCTTCCTTCATCATTTTAATACTTTTTCACACTCTTTCGTCATCCATGGCC
ACCGTACAACTCGAATCCTTACCAAGTTACCTCCTCAGTGCCGCCGATGCTTCCGATGGAGTGGCTCCTGTTACT
GATGAAACTTTTGGTTCCTTCGTCCCTATGTCTAAGAATCTCGTGTTGGTGGAATTCTATAATCCATGGTGTGGC
CAAAACTGCAAAAACATACATTCCATAATGGTTGAGCTGGCAAATGATTATGCTGGTAAGGTCGATTTTTACAAA
CTCAATATTGATGAGAATCCATATATTACTAATAGATATGTGATTCAAGATCTTCCAACTGTGGTTTTCATCAAG
TATGGTATGCAGAGAGATAGACTTGTTGGTGATGTACCTAAAGCAACATTTATCGAACTTATTCAACTATCAATA
TGA

Trx s2: protein sequence
MATVTLAMSSFIILILFHTLSSSMATVQLESLPSYLLSAADASDGVAPVTDETFGSFVPMSKNLVLVEFYNPWCG
QNCKNIHSIMVELANDYAGKVDFYKLNIDENPYITNRYVIQDLPTVVFIKYGMQRDRLVGDVPKATFIELIQLSI
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Supplemental Fig. 1. Genomic sequences and coding regions of *Trxs s* cloned from *M. truncatula*. Start and stop codons are indicated in red. Both isoforms of *Trxs s* have only one intron (in grey) in the coding region of their genes that separates the parts coding the putative signal peptide and the rest of the protein. The deduced protein sequences are also shown; the signal peptides that are removed in the mature proteins appear in bold.