**Additional file 3: Table 3** Identification of TsCSAg-101 (spots 2, 4, 5) proteins identified by LC-MS/MS

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein Name | Accession no. | Theoretical Mr/*pI*(a) | Port. score | No. matched peptides | Signal peptide | Trans-Membrane domain | Subcellular localization |
| csa2 |  |  |  |  |  |  |  |
| 1. conserved hypothetical protein  | gi339235735 | 81.0/5.16 | 54 | 7 | Yes | Outside 1-744 | Extracellular |
| csa4 |  |  |  |  |  |  |  |
| 1. putative fasciclin domain protein  | gi339252024 | 66.3/5.4 | 118 | 21 | Yes | Outside 1-590 | Plasma Membrane |
| csa5 |  |  |  |  |  |  |  |
| 1. putative fasciclin domain protein  | gi339252024 | 66.3/5.4 | 123 | 25 | Yes | Outside 1-590 | Plasma Membrane |

(a) Theoretical molecular mass (kDa) and *pI*

**Table 4** Identification of TsCSAg-79 (spots 6-17) proteins identified by LC-MS/MS

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein Name | Accession no. | Theoretical Mr/*pI*(a) | Port. score | No. matched peptides | Signal peptide | Trans-Membrane domain | Subcellular localization |
| csa6 |  |  |  |  |  |  |  |
| 1. phosphoenolpyruvate carboxykinase  | gi339248807 | 71.1/6.51 | 203 | 64 | No | Outside 1-636 | Cytoplasmic |
| 2. serine proteinase  | gi13641204 | 48.0/6.33 | 54 | 9 | Yes | Outside 1-421 | Extracellular, Plasma Membrane |
| csa7 |  |  |  |  |  |  |  |
| 1. heat shockprotein A  | gi339244925 | 112.1/6.41 | 219 | 70 | No | Outside 1-1003 | Cytoplasmic |
| 2. muscle cell intermediate filament protein OV71  | gi339251730 | 188.2/7.93 | 65 | 7 | No | Outside 1-113 | Nuclear |
| csa8 |  |  |  |  |  |  |  |
| 1. heat shockprotein A  | gi339244925 | 112.1/6.41 | 738 | 125 | No | Outside 1-1003 | Cytoplasmic |
| 2. intermediate filament protein ifa-1 | gi339243637 | 73.1/5.96 | 67 | 17 | No | Outside 1-644 | Cytoplasmic, Nuclear |
| 3. muscle cell intermediate filament protein OV71  | gi339251730 | 188.2/7.93 | 59 | 12 | No | Outside 1-113 | Nuclear |

**Table 4** Identification of TsCSAg-79 (spots 6-17) proteins identified by LC-MS/MS (Cont.)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein Name | Accession no. | Theoretical Mr/*pI*(a) | Port. score | No. matched peptides | Signal peptide | Trans-Membrane domain | Subcellular localization |
| csa9 |  |  |  |  |  |  |  |
| 1. muscle cell intermediate filament protein OV71  | gi339251730 | 188.2/7.93 | 207 | 36 | No | Outside 1-113 | Nuclear |
| 2. intermediate filament protein ifa-1  | gi339243637 | 73.1/5.96 | 166 | 46 | No | Outside 1-644 | Cytoplasmic, Nuclear |
| csa10 |  |  |  |  |  |  |  |
| 1. intermediate filament protein ifa-1  | gi339243637 | 73.1/5.96 | 496 | 117 | No | Outside 1-644 | Cytoplasmic, Nuclear |
| 2. serine proteinase  | gi13641204 | 48.0/6.33 | 139 | 14 | Yes | Outside 1-421 | Extracellular, Plasma Membrane |
| csa11 |  |  |  |  |  |  |  |
| 1. serine protease  | gi168805933 | 48.0/6.33 | 181 | 28 | Yes | Outside 1-421 | Extracellular |
| csa12 |  |  |  |  |  |  |  |
| 1. serine protease  | gi168805933 | 48.0/6.33 | 345 | 35 | Yes | Outside 1-421 | Extracellular |

**Table 4** Identification of TsCSAg-79 (spots 6-17) proteins identified by LC-MS/MS (Cont.)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein Name | Accession no. | Theoretical Mr/*pI*(a) | Port. score | No. matched peptides | Signal peptide | Trans-Membrane domain | Subcellular localization |
| csa13 |  |  |  |  |  |  |  |
| 1. serine protease  | gi13641204 | 48.0/6.33 | 113 | 17 | Yes | Outside 1-421 | Extracellular |
| csa14 |  |  |  |  |  |  |  |
| 1. phosphoenolpyruvate carboxykinase  | gi339248807 | 71.1/6.51 | 107 | 50 | No | Outside 1-636 | Cytoplasmic |
| 2. serine protease  | gi13641204 | 48.0/6.33 | 51 | 6 | Yes | Outside 1-421 | Extracellular |
| csa15 |  |  |  |  |  |  |  |
| 1. phosphoenolpyruvate carboxykinase  | gi339248807 | 71.1/6.51 | 445 | 82 | No | Outside 1-636 | Cytoplasmic |
| csa16 |  |  |  |  |  |  |  |
| 1. phosphoenolpyruvate carboxykinase  | gi339248807 | 71.1/6.51 | 897 | 120 | No | Outside 1-636 | Cytoplasmic |
| csa17 |  |  |  |  |  |  |  |
| 1. phosphoenolpyruvate carboxykinase  | gi339248807 | 71.1/6.51 | 1519 | 167 | No | Outside 1-636 | Cytoplasmic |

(a) Theoretical molecular mass (kDa) and *pI*

**Table 5** Identification of TsCSAg-43 (spots 18-20) proteins identified by LC-MS/MS

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein Name | Accession no. | Theoretical Mr/*pI*(a) | Port. score | No. matched peptides | Signal peptide | Trans-Membrane domain | Subcellular localization |
| csa18 |  |  |  |  |  |  |  |
| 1. antigen targeted by protective antibodies  | gi404638 | 31.2/4.76 | 133 | 14 | Yes | Outside 1-285 | Extracellular |
| 2. DNA topoisomerase 2-alpha  | gi339241953 | 48.6/5.64 | 54 | 16 | Yes | Outside 1-404TMhelix 405-427Inside 428-436 | Plasma Membrane |
| 3. 45k antigen–trichina (fragment) | gi320992 | 2.9/8.27 | 51 | 3 | No | Outside 1-27 | Nuclear |
| 4. conserved hypothetical protein  | gi339234223 | 37.0/5.08 | 44 | 16 | Yes | Outside 1-325 | Extracellular |
| csa19 |  |  |  |  |  |  |  |
| 1. conserved hypothetical protein  | gi339234223 | 37.0/5.08 | 382 | 97 | Yes | Outside 1-325 | Extracellular |

**Table 5** Identification of TsCSAg-43 (spots 18-20) proteins identified by LC-MS/MS (Cont.)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Protein Name | Accession no. | Theoretical Mr/*pI*(a) | Port. score | No. matched peptides | Signal peptide | Trans-Membrane domain | Subcellular localization |
| 2. DNA topoisomerase 2-alpha  | gi339241953 | 48.6/5.64 | 101 | 15 | Yes | Outside 1-404TMhelix 405-427Inside 428-436 | Plasma Membrane |
| csa20 |  |  |  |  |  |  |  |
| 1. conserved hypothetical protein  | gi339234223 | 37.0/5.08 | 153 | 57 | Yes | Outside 1-325 | Extracellular |
| 2. DNA topoisomerase 2-alpha  | gi339241953 | 48.6/5.64 | 47 | 4 | Yes | Outside 1-404TMhelix 405-427Inside 428-436 | Plasma Membrane |

(a) Theoretical molecular mass (kDa) and *pI*