

Paper Title: Antigen stimulation of peripheral blood mononuclear cells from *Mycobacterium bovis* infected cattle yields evidence for a novel gene expression program. Meade, K.G. *et al.*

Table S1: Green shaded rows detail 250 BOTL-5 microarray spot features that showed significant differential expression for the BTB-infected animal group ($n = 6$) between T_3 and T_0 (3h versus 0h) post stimulation with bovine tuberculin. Yellow shaded rows detail 80 BOTL-5 microarray spot features that showed significant differential expression for the BTB-infected animal group ($n = 6$) between T_{12} and T_3 (12h versus 3h) post stimulation with bovine tuberculin. [NB. Spot features are ranked by fold-change for each time point comparison].

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|---|------------------|-----------|-------------|-----------------------|
| 1 | A8.c6 | MHC class I heavy chain isoform 1 | <i>BOLA</i> | 0.0004015 | 5.58 | 3h vs 0h |
| 2 | A8.g9 | MHC class I heavy chain isoform 1 | <i>BOLA</i> | 0.0007032 | 5.28 | 3h vs 0h |
| 3 | C8.g9 | similar to chemokine CCL1/I-309 similar to chemokine CCL1/I-309 | | 0.0008610 | 5.28 | 3h vs 0h |
| 4 | C8.c6 | similar to chemokine CCL1/I-309 similar to chemokine CCL1/I-309 | | 0.0011065 | 4.98 | 3h vs 0h |
| 5 | C11.g5 | hypothetical protein | <i>LOC512361</i> | 0.0012870 | 3.94 | 3h vs 0h |
| 6 | C6.c6 | similar to GMCSFR receptor | <i>LOC511847</i> | 0.0052822 | 3.86 | 3h vs 0h |
| 7 | D11.i3 | Similar to serine/threonine protein kinase | <i>LOC514210</i> | 0.0010479 | 3.82 | 3h vs 0h |
| 8 | D11.e1 | Similar to serine/threonine protein kinase | <i>LOC514210</i> | 0.0005247 | 3.78 | 3h vs 0h |
| 9 | C11.c2 | hypothetical protein | <i>LOC512361</i> | 0.0028230 | 3.73 | 3h vs 0h |
| 10 | C6.g9 | similar to GMCSFR receptor | <i>LOC511847</i> | 0.0062652 | 3.65 | 3h vs 0h |
| 11 | B2.b5 | translocating chain-associating membrane protein | <i>TRAM</i> | 0.0029163 | 3.08 | 3h vs 0h |
| 12 | B2.f8 | translocating chain-associating membrane protein | <i>TRAM</i> | 0.0041705 | 3.03 | 3h vs 0h |
| 13 | C1.c4 | similar to MAP kinase kinase 7 gamma 1 | <i>LOC787278</i> | 0.0023537 | 3.01 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|--|---------------|-----------|-------------|-----------------------|
| 14 | B1.i7 | GATA binding protein 4 (GATA4) | | 0.0073891 | 2.77 | 3h vs 0h |
| 15 | D11.i4 | Transcribed locus, weakly similar to XP_001083311.1 similar to kinase suppressor of ras 2 [Macaca mulatta] | | 0.0002696 | 2.75 | 3h vs 0h |
| 16 | A3.c6 | CD14 molecule | <i>CD14</i> | 0.0365308 | 2.63 | 3h vs 0h |
| 17 | B3.e3 | splicing factor, arginine/serine-rich 2 | <i>SFRS2</i> | 0.0011942 | 2.56 | 3h vs 0h |
| 18 | B3.i5 | splicing factor, arginine/serine-rich 2 | <i>SFRS2</i> | 0.0052018 | 2.47 | 3h vs 0h |
| 19 | B1.e6 | GATA binding protein 4 (GATA4) | | 0.0117014 | 2.47 | 3h vs 0h |
| 20 | B9.e1 | v-akt murine thymoma viral oncogene homolog 1 | <i>AKT1</i> | 0.0065464 | 2.46 | 3h vs 0h |
| 21 | B3.i8 | ephrin-A2 | <i>ENFNA2</i> | 0.0405087 | 2.46 | 3h vs 0h |
| 22 | D1.e4 | GATA-binding protein 4 (GATA4) | | 0.0046093 | 2.42 | 3h vs 0h |
| 23 | D9.i4 | Sin3A-associated protein, 18kDa | <i>SAP18</i> | 0.0453981 | 2.39 | 3h vs 0h |
| 24 | D1.d9 | DNA fragmentation factor, 45kDa, alpha polypeptide | <i>DFFA</i> | 0.0189222 | 2.37 | 3h vs 0h |
| 25 | B6.e1 | eukaryotic translation elongation factor 1 gamma | <i>EEF1G</i> | 0.0003536 | 2.36 | 3h vs 0h |
| 26 | D5.e8 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | <i>NFKB1</i> | 0.0117779 | 2.34 | 3h vs 0h |
| 27 | A3.g9 | CD14 molecule | <i>CD14</i> | 0.0300464 | 2.33 | 3h vs 0h |
| 28 | D1.i6 | GATA-binding protein 4 (GATA4) | | 0.0024533 | 2.30 | 3h vs 0h |
| 29 | B9.i3 | v-akt murine thymoma viral oncogene homolog 1 | <i>AKT1</i> | 0.0082823 | 2.30 | 3h vs 0h |
| 30 | D5.a3 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | <i>NFKB1</i> | 0.0092788 | 2.30 | 3h vs 0h |
| 31 | B6.i4 | eukaryotic translation elongation factor 2 | <i>EEF2</i> | 0.0000402 | 2.29 | 3h vs 0h |
| 32 | D2.i2 | similar to FGFR1 protein isoform 2 | <i>FGFR1</i> | 0.0150168 | 2.27 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 33 | D2.d9 | similar to FGFR1 protein isoform 2 | <i>FGFR1</i> | 0.0152872 | 2.26 | 3h vs 0h |
| 34 | B6.e2 | eukaryotic translation elongation factor 2 | <i>EEF2</i> | 0.0000182 | 2.22 | 3h vs 0h |
| 35 | D3.e6 | ephrin-A2 (EFNA2) | | 0.0077044 | 2.21 | 3h vs 0h |
| 36 | C5.e8 | similar to Tropomyosin 3 | <i>TPM3</i> | 0.0013279 | 2.16 | 3h vs 0h |
| 37 | D9.i6 | v-akt murine thymoma viral oncogene homolog 2 | <i>AKT2</i> | 0.0146746 | 2.16 | 3h vs 0h |
| 38 | C1.g6 | similar to MAP kinase kinase 7 gamma 1 | <i>LOC787278</i> | 0.0101666 | 2.15 | 3h vs 0h |
| 39 | D11.e2 | Transcribed locus, weakly similar to XP_001083311.1 similar to kinase suppressor of ras 2 [Macaca mulatta] | | 0.0221975 | 2.14 | 3h vs 0h |
| 40 | B1.h9 | Rho guanine nucleotide exchange factor, mRNA (GEF 1) | | 0.0002962 | 2.13 | 3h vs 0h |
| 41 | D1.e6 | similar to Serum response factor (SRF) | <i>LOC533039</i> | 0.0008925 | 2.13 | 3h vs 0h |
| 42 | B6.i3 | eukaryotic translation elongation factor 1 gamma | <i>EEF1G</i> | 0.0010412 | 2.13 | 3h vs 0h |
| 43 | D9.i8 | protein kinase, cAMP-dependent, regulatory, type I, beta | <i>PRKAR2B</i> | 0.0077058 | 2.13 | 3h vs 0h |
| 44 | D9.e7 | protein kinase, cAMP-dependent, regulatory, type I, beta | <i>PRKAR2B</i> | 0.0046764 | 2.12 | 3h vs 0h |
| 45 | A8.f5 | similar to Tyrosine-protein kinase Lyn | <i>LOC534996</i> | 0.0092129 | 2.12 | 3h vs 0h |
| 46 | C2.g4 | TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa | <i>TAF6</i> | 0.0467477 | 2.12 | 3h vs 0h |
| 47 | D3.i7 | ephrin-A2 (EFNA2) | | 0.0148555 | 2.11 | 3h vs 0h |
| 48 | C5.a3 | similar to Tropomyosin 3 | <i>TPM3</i> | 0.0016879 | 2.09 | 3h vs 0h |
| 49 | D6.b8 | Transcribed locus | | 0.0043936 | 2.09 | 3h vs 0h |
| 50 | D6.f1 | DAZ associated protein 2 | <i>DAZAP2</i> | 0.0123686 | 2.09 | 3h vs 0h |
| 51 | D6.g2 | Transcribed locus | | 0.0187316 | 2.09 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 52 | B3.i2 | myelin basic protein (MBP) | | 0.0269513 | 2.09 | 3h vs 0h |
| 53 | A11.b8 | similar to death receptor 3 | <i>LOC783432</i> | 0.0153166 | 2.08 | 3h vs 0h |
| 54 | D12.i8 | GAPDH | <i>GAPDH</i> | 0.0232446 | 2.07 | 3h vs 0h |
| 55 | B6.d9 | actin, beta | <i>ACTB</i> | 0.0187244 | 2.06 | 3h vs 0h |
| 56 | D12.h1 | GAPDH | <i>GAPDH</i> | 0.0379525 | 2.06 | 3h vs 0h |
| 57 | C6.h7 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | <i>NFKB1</i> | 0.0380419 | 2.06 | 3h vs 0h |
| 58 | A1.f3 | Similar to KIAA0668 protein | <i>LOC618392</i> | 0.0000731 | 2.05 | 3h vs 0h |
| 59 | B6.i2 | actin, beta | <i>ACTB</i> | 0.0209279 | 2.05 | 3h vs 0h |
| 60 | B2.e8 | hypothetical protein | <i>LOC510651</i> | 0.0044301 | 2.04 | 3h vs 0h |
| 61 | B1.d8 | Rho guanine nucleotide exchange factor, mRNA (GEF 1) | | 0.0016250 | 2.01 | 3h vs 0h |
| 62 | A11.a3 | glioma tumor suppressor candidate region gene 2 | <i>GLTSCR2</i> | 0.0060427 | 2.01 | 3h vs 0h |
| 63 | D11.i6 | insulin receptor substrate 1, mRNA (IRS1) | | 0.0078117 | 2.01 | 3h vs 0h |
| 64 | D11.i2 | similar to p70 ribosomal S6 kinase beta | <i>LOC506083</i> | 0.0174021 | 2.01 | 3h vs 0h |
| 65 | D1.i7 | similar to Serum response factor (SRF) | <i>LOC533039</i> | 0.0016012 | 2.00 | 3h vs 0h |
| 66 | D6.a5 | DAZ associated protein 2 | <i>DAZAP2</i> | 0.0169674 | 2.00 | 3h vs 0h |
| 67 | B11.d8 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 | <i>SMARCAL1</i> | 0.0011546 | 1.98 | 3h vs 0h |
| 68 | B2.d9 | fibroblast growth factor receptor 2 | <i>FGFR2</i> | 0.0159178 | 1.98 | 3h vs 0h |
| 69 | A11.g2 | similar to death receptor 3 | <i>LOC783432</i> | 0.0162147 | 1.98 | 3h vs 0h |
| 70 | D6.i2 | similar to neuropilin-1 | <i>LOC539369</i> | 0.0349684 | 1.98 | 3h vs 0h |

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|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 71 | B3.d9 | myelin basic protein (MBP) | | 0.0434810 | 1.98 | 3h vs 0h |
| 72 | C4.d9 | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta | <i>IKKBK</i> | 0.0437243 | 1.98 | 3h vs 0h |
| 73 | A11.e8 | glioma tumor suppressor candidate region gene 2 | <i>GLTSCR2</i> | 0.0136695 | 1.95 | 3h vs 0h |
| 74 | C11.b3 | BOTL0100003XC06R | <i>AY957499</i> | 0.0091897 | 1.92 | 3h vs 0h |
| 75 | B9.d8 | similar to nuclear receptor co-repressor 1 isoform 3 | <i>NCOR1</i> | 0.0113368 | 1.90 | 3h vs 0h |
| 76 | B9.h9 | similar to nuclear receptor co-repressor 1 isoform 3 | <i>NCOR1</i> | 0.0275800 | 1.90 | 3h vs 0h |
| 77 | A7.f1 | uncoupling protein 2 (mitochondrial, proton carrier) | <i>UCP2</i> | 0.0080319 | 1.89 | 3h vs 0h |
| 78 | A1.a7 | Similar to KIAA0668 protein | <i>LOC618392</i> | 0.0031005 | 1.88 | 3h vs 0h |
| 79 | D11.e3 | lymphotoxin alpha | <i>LTA</i> | 0.0226303 | 1.88 | 3h vs 0h |
| 80 | B6.f2 | similar to Rho-related GTP-binding protein Rho6 (Rho family GTPase 1) (Rnd1) | | 0.0225457 | 1.87 | 3h vs 0h |
| 81 | A7.g1 | leukocyte receptor cluster (LRC) member 1 | <i>LENG1</i> | 0.0068147 | 1.86 | 3h vs 0h |
| 82 | A8.a8 | similar to Tyrosine-protein kinase Lyn | <i>LOC534996</i> | 0.0023238 | 1.85 | 3h vs 0h |
| 83 | B2.i2 | fibroblast growth factor receptor 2 | <i>FGFR2</i> | 0.0023800 | 1.84 | 3h vs 0h |
| 84 | B9.e2 | similar to C-terminal binding protein 1 | <i>LOC513131</i> | 0.0175062 | 1.83 | 3h vs 0h |
| 85 | D8.b7 | similar to HCF, C1, VCAF, CFF=VP16 accessory protein host cell factor | <i>LOC512908</i> | 0.0011176 | 1.82 | 3h vs 0h |
| 86 | A11.f2 | similar to Lymphocyte antigen Ly-6E precursor (Retinoic acid-induced gene E protein) (RIG-E) (Thymic shared antigen 1) (TSA-1) (Stem cell antigen 2) (SCA-2) | <i>SCA-2</i> | 0.0046485 | 1.77 | 3h vs 0h |
| 87 | A6.b8 | similar to SET binding factor 1 | <i>LOC510349</i> | 0.0054413 | 1.77 | 3h vs 0h |
| 88 | C6.d7 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | <i>NFKB1</i> | 0.0334521 | 1.77 | 3h vs 0h |

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|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 89 | A8.i3 | similar to MAP kinase-activated protein kinase 2 (MAPK-activated protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2) (MK2) | <i>LOC788091</i> | 0.0426963 | 1.77 | 3h vs 0h |
| 90 | B8.e1 | RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein) | <i>RASA3</i> | 0.0069693 | 1.76 | 3h vs 0h |
| 91 | A4.i8 | hypothetical protein | <i>LOC513497</i> | 0.0146517 | 1.76 | 3h vs 0h |
| 92 | D8.g1 | similar to HCF, C1, VCAF, CFF=VP16 accessory protein host cell factor | <i>LOC512908</i> | 0.0042541 | 1.75 | 3h vs 0h |
| 93 | D11.d9 | similar to p70 ribosomal S6 kinase beta | <i>LOC506083</i> | 0.0053191 | 1.75 | 3h vs 0h |
| 94 | A9.e9 | hypothetical protein | <i>LOC514346</i> | 0.0099714 | 1.75 | 3h vs 0h |
| 95 | C11.f7 | BOTL0100003XC06R | | 0.0123586 | 1.75 | 3h vs 0h |
| 96 | B6.b7 | similar to Syntaxin-5 | | 0.0346125 | 1.74 | 3h vs 0h |
| 97 | B8.i3 | RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein) | <i>RASA3</i> | 0.0148152 | 1.72 | 3h vs 0h |
| 98 | A11.a6 | similar to Lymphocyte antigen Ly-6E precursor (Retinoic acid-induced gene E protein) (RIG-E) (Thymic shared antigen 1) (TSA-1) (Stem cell antigen 2) (SCA-2) | <i>SCA-2</i> | 0.0013375 | 1.71 | 3h vs 0h |
| 99 | B5.i2 | NBFGC_AW659262 BRCA1associated protein-1 (ubiquitin carboxy- | | 0.0068029 | 1.71 | 3h vs 0h |
| 100 | A4.e9 | similar to SFPQ protein | <i>LOC618226</i> | 0.0050394 | 1.70 | 3h vs 0h |
| 101 | A6.a5 | similar to actin-binding LIM protein 1 isoform 3 | <i>LOC504968</i> | 0.0169954 | 1.70 | 3h vs 0h |
| 102 | A3.i6 | monocyte-chemoattractant protein-1 precursor | <i>CCL2</i> | 0.0280098 | 1.70 | 3h vs 0h |
| 103 | B9.a3 | similar to TLE3 protein | <i>LOC514326</i> | 0.0018475 | 1.69 | 3h vs 0h |
| 104 | A9.a4 | hypothetical protein | <i>LOC514346</i> | 0.0119533 | 1.69 | 3h vs 0h |
| 105 | A10.a3 | similar to G protein-coupled receptor TGR7 | <i>LOC507247</i> | 0.0006034 | 1.68 | 3h vs 0h |
| 106 | B9.e8 | similar to TLE3 protein | <i>LOC514326</i> | 0.0032038 | 1.68 | 3h vs 0h |

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|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 107 | B1.f8 | similar to Cathepsin W isoform 2 | <i>LOC510967</i> | 0.0208599 | 1.68 | 3h vs 0h |
| 108 | D5.e1 | prohibitin 2 | <i>PHB2</i> | 0.0339694 | 1.68 | 3h vs 0h |
| 109 | C5.g5 | pyruvate kinase 3 | <i>PKM3</i> | 0.0083753 | 1.67 | 3h vs 0h |
| 110 | D11.i5 | lymphotoxin alpha | <i>LTA</i> | 0.0037350 | 1.65 | 3h vs 0h |
| 111 | A8.e1 | similar to MAP kinase-activated protein kinase 2 (MAPK-activated protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2) (MK2) | <i>LOC788091</i> | 0.0042469 | 1.65 | 3h vs 0h |
| 112 | A1.g8 | endonuclease domain containing 1 | <i>ENDOD1</i> | 0.0296320 | 1.65 | 3h vs 0h |
| 113 | A2.b5 | similar to mitogen-activated protein kinase kinase kinase kinase 2 | <i>LOC520058</i> | 0.0055596 | 1.64 | 3h vs 0h |
| 114 | A4.a4 | similar to SFPQ protein | <i>LOC618226</i> | 0.0202767 | 1.63 | 3h vs 0h |
| 115 | D4.g1 | hypothetical protein | <i>LOC786280</i> | 0.0077852 | 1.62 | 3h vs 0h |
| 116 | C2.c1 | TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa | <i>TAF6</i> | 0.0226052 | 1.62 | 3h vs 0h |
| 117 | A2.f8 | similar to mitogen-activated protein kinase kinase kinase kinase 2 | <i>LOC520058</i> | 0.0004584 | 1.61 | 3h vs 0h |
| 118 | D8.e2 | similar to GCN5 general control of amino-acid synthesis 5-like 2 (yeast) | <i>LOC514420</i> | 0.0010109 | 1.61 | 3h vs 0h |
| 119 | A9.c4 | hypothetical protein | <i>LOC615329</i> | 0.0137242 | 1.61 | 3h vs 0h |
| 120 | D6.e1 | Unknown | - | 0.0150092 | 1.61 | 3h vs 0h |
| 121 | D8.d3 | ADP-ribosyltransferase (NAD+) poly (ADP-ribose) polymerase) | <i>PARP1</i> | 0.0334735 | 1.61 | 3h vs 0h |
| 122 | B7.e7 | mitogen-activated protein kinase kinase 1, RNA (MAP2K1) | | 0.0036071 | 1.59 | 3h vs 0h |
| 123 | C5.c2 | pyruvate kinase 3 | <i>PKM3</i> | 0.0353435 | 1.59 | 3h vs 0h |
| 124 | A6.g2 | similar to SET binding factor 1 | <i>LOC510349</i> | 0.0315143 | 1.58 | 3h vs 0h |
| 125 | B2.a3 | hypothetical protein | <i>LOC510651</i> | 0.0279914 | 1.57 | 3h vs 0h |

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|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 126 | A9.g6 | hypothetical protein | <i>LOC615329</i> | 0.0158345 | 1.56 | 3h vs 0h |
| 127 | C2.e2 | retinoid X receptor, beta | <i>RXRB</i> | 0.0003208 | 1.55 | 3h vs 0h |
| 128 | B3.i6 | similar to p101 protein | <i>LOC614838</i> | 0.0024366 | 1.53 | 3h vs 0h |
| 129 | A1.c1 | similar to AF-4 | <i>LOC781149</i> | 0.0024641 | 1.53 | 3h vs 0h |
| 130 | C9.b7 | similar to Eif5 protein isoform 3 | <i>LOC504752</i> | 0.0486630 | 1.53 | 3h vs 0h |
| 131 | B3.e4 | similar to p101 protein | <i>LOC614838</i> | 0.0094611 | 1.52 | 3h vs 0h |
| 132 | B1.b5 | similar to Cathepsin W isoform 2 | <i>LOC510967</i> | 0.0097576 | 1.50 | 3h vs 0h |
| 133 | D9.g1 | seryl-tRNA synthetase 2 | <i>SARS2</i> | 0.0429487 | 1.50 | 3h vs 0h |
| 134 | A1.c5 | endonuclease domain containing 1 | <i>ENDOD1</i> | 0.0313649 | 1.49 | 3h vs 0h |
| 135 | D6.f8 | BOTL0100009_A01 | | 0.0135001 | 1.48 | 3h vs 0h |
| 136 | A8.g2 | BOTL0100012_E05 | | 0.0428093 | 1.48 | 3h vs 0h |
| 137 | A6.f5 | similar to neurogranin | | 0.0409134 | 1.47 | 3h vs 0h |
| 138 | A9.f3 | hypothetical protein | <i>LOC509987</i> | 0.0232827 | 1.46 | 3h vs 0h |
| 139 | A6.a8 | similar to neurogranin | | 0.0277665 | 1.46 | 3h vs 0h |
| 140 | A6.g3 | hypothetical protein | <i>LOC506974</i> | 0.0107055 | 1.44 | 3h vs 0h |
| 141 | D6.b5 | BOTL0100009_A01 | | 0.0117410 | 1.44 | 3h vs 0h |
| 142 | A11.g5 | adenylate cyclase 7 | <i>ADCY7</i> | 0.0212583 | 1.44 | 3h vs 0h |
| 143 | C4.a4 | similar to beta-1,2-N-acetylglucosaminyltransferase II | <i>LOC790576</i> | 0.0337149 | 1.44 | 3h vs 0h |
| 144 | A3.f2 | Similar to Hexokinase 3 (white cell) | <i>HK3</i> | 0.0239656 | 1.43 | 3h vs 0h |

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|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 145 | A9.a7 | hypothetical protein | <i>LOC509987</i> | 0.0189125 | 1.42 | 3h vs 0h |
| 146 | D4.b7 | hypothetical protein | <i>LOC786280</i> | 0.0045725 | 1.41 | 3h vs 0h |
| 147 | B9.b6 | similar to human immunity associated protein 1 | <i>LOC615733</i> | 0.0481828 | 1.40 | 3h vs 0h |
| 148 | B4.d3 | chemokine (C-C motif) ligand 3-like 1 | <i>CCL3L1</i> | 0.0033673 | 1.39 | 3h vs 0h |
| 149 | D8.g3 | hypothetical protein | <i>LOC616055</i> | 0.0129208 | 1.38 | 3h vs 0h |
| 150 | C4.e9 | similar to beta-1,2-N-acetylglucosaminyltransferase II | <i>LOC790576</i> | 0.0131187 | 1.37 | 3h vs 0h |
| 151 | A6.b9 | hypothetical protein | | 0.0163643 | 1.37 | 3h vs 0h |
| 152 | C2.f1 | Unknown | | 0.0229631 | 1.37 | 3h vs 0h |
| 153 | A6.f7 | similar to Poly [ADP-ribose] polymerase 10 (PARP-10) | <i>LOC510991</i> | 0.0035098 | 1.35 | 3h vs 0h |
| 154 | D6.g1 | BOTL0100013_F10 | <i>LOC516783</i> | 0.0354595 | 1.35 | 3h vs 0h |
| 155 | D8.i4 | similar to GCN5 general control of amino-acid synthesis 5-like 2 (yeast) | <i>LOC514420</i> | 0.0318256 | 1.34 | 3h vs 0h |
| 156 | D5.a7 | strongly similar to XP_001101736.1 similar to homolog of yeast mRNA transport regulator 3 [Macaca mulatta] | | 0.0275627 | 1.32 | 3h vs 0h |
| 157 | A4.b9 | hypothetical protein | <i>LOC507577</i> | 0.0339311 | 1.30 | 3h vs 0h |
| 158 | D3.i8 | similar to caspase-2 | <i>CASP2</i> | 0.0327964 | 1.28 | 3h vs 0h |
| 159 | D8.b9 | hypothetical protein | <i>LOC616055</i> | 0.0075793 | 1.27 | 3h vs 0h |
| 160 | D8.g2 | BOTL0100013_G08 | | 0.0385722 | 1.26 | 3h vs 0h |
| 161 | D11.c1 | hypothetical protein | <i>LOC532712</i> | 0.0412314 | 1.25 | 3h vs 0h |
| 162 | B5.a7 | similar to gigaxonin | <i>GAN</i> | 0.0320668 | 1.24 | 3h vs 0h |
| 163 | D10.b5 | BOTL0100009_B10 | | 0.0342398 | 1.19 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|---|------------------|-----------|-------------|-----------------------|
| 164 | D6.i4 | similar to calcium/calmodulin-dependent protein kinase I | | 0.0375180 | 1.18 | 3h vs 0h |
| 165 | C9.a3 | similar to Dynein intermediate chain 2, cytosolic (DH IC-2) (Cytoplasmic dynein intermediate chain 2) | <i>DYNC1I2</i> | 0.0461438 | -1.17 | 3h vs 0h |
| 166 | B8.e9 | similar to Kremen2 protein | <i>LOC618527</i> | 0.0034077 | -1.20 | 3h vs 0h |
| 167 | A8.e9 | hypothetical protein | <i>LOC768044</i> | 0.0101607 | -1.20 | 3h vs 0h |
| 168 | C5.g2 | Transcribed locus | | 0.0173350 | -1.22 | 3h vs 0h |
| 169 | A10.g2 | similar to tangerin C | <i>LOC788760</i> | 0.0268463 | -1.23 | 3h vs 0h |
| 170 | C8.g5 | similar to Interleukin-1 receptor-associated kinase 4 (IRAK-4) (NY-REN-64 antigen) | | 0.0441493 | -1.24 | 3h vs 0h |
| 171 | D11.g6 | BOTL0100012_A06 | | 0.0327683 | -1.25 | 3h vs 0h |
| 172 | B5.a6 | similar to protein tyrosine phosphatase, receptor type, F | <i>LOC790379</i> | 0.0392893 | -1.26 | 3h vs 0h |
| 173 | C11.a3 | similar to ZNF786 protein | <i>LOC506408</i> | 0.0098941 | -1.27 | 3h vs 0h |
| 174 | D8.f3 | hypothetical protein | <i>LOC617688</i> | 0.0278973 | -1.28 | 3h vs 0h |
| 175 | C3.f3 | ribosomal protein, large, P1 | <i>RPLP1</i> | 0.0248478 | -1.29 | 3h vs 0h |
| 176 | B7.b3 | BOTL0100004XF08R | | 0.0325903 | -1.29 | 3h vs 0h |
| 177 | A1.e9 | hypothetical protein | <i>LOC537453</i> | 0.0487361 | -1.29 | 3h vs 0h |
| 178 | D11.f3 | ret finger protein 2 | <i>TRIM13</i> | 0.0210337 | -1.31 | 3h vs 0h |
| 179 | C3.a7 | ribosomal protein, large, P1 | <i>RPLP1</i> | 0.0293211 | -1.31 | 3h vs 0h |
| 180 | A10.b8 | similar to tangerin C | <i>LOC788760</i> | 0.0297898 | -1.31 | 3h vs 0h |
| 181 | B10.b7 | splicing factor, arginine/serine-rich 7, 35kDa | <i>SFRS7</i> | 0.0462638 | -1.32 | 3h vs 0h |
| 182 | C1.a3 | protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform | <i>PPP2R2A</i> | 0.0154861 | -1.33 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|---|--|-----------|-------------|-----------------------|
| 183 | C4.a7 | similar to Pre-mRNA cleavage complex 2 protein Pcf11 (Pre-mRNA cleavage complex II protein Pcf11) | <i>LOC510604</i> | 0.0253967 | -1.33 | 3h vs 0h |
| 184 | C4.a8 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 | <i>GNAI3</i> | 0.0332849 | -1.33 | 3h vs 0h |
| 185 | C5.e9 | similar to Serine/threonine protein phosphatase 6 (PP6) | <i>LOC608922</i> | 0.0436579 | -1.33 | 3h vs 0h |
| 186 | B9.f7 | BOTL0100004XG08R | | 0.0031473 | -1.34 | 3h vs 0h |
| 187 | D10.a3 | Transcribed locus | | 0.0135365 | -1.34 | 3h vs 0h |
| 188 | A10.f7 | similar to insulin induced gene 1 | | 0.0476418 | -1.34 | 3h vs 0h |
| 189 | C3.g3 | BOTL0100009_E08 | | 0.0036865 | -1.36 | 3h vs 0h |
| 190 | B10.a4 | hypothetical protein | <i>LOC515972</i> | 0.0045413 | -1.36 | 3h vs 0h |
| 191 | A6.i5 | similar to AXL receptor tyrosine kinase | <i>LOC516598</i> | 0.0115676 | -1.36 | 3h vs 0h |
| 192 | D11.a7 | ret finger protein 2 | <i>TRIM13</i> | 0.0151925 | -1.36 | 3h vs 0h |
| 193 | C8.g3 | BOTL0100012_E09 | | 0.0482115 | -1.36 | 3h vs 0h |
| 194 | B10.g1 | splicing factor, arginine/serine-rich 7, 35kDa | <i>SFRS7</i> | 0.0035702 | -1.38 | 3h vs 0h |
| 195 | B10.e9 | hypothetical protein | <i>LOC515972</i> | 0.0312184 | -1.38 | 3h vs 0h |
| 196 | D5.e9 | BOTL0100003XF04R | - | 0.0469598 | -1.38 | 3h vs 0h |
| 197 | D4.e9 | nuclear factor (erythroid-derived 2)-like 2 | <i>NFE2L2</i> | 0.0349485 | -1.39 | 3h vs 0h |
| 198 | C9.e3 | chemokine (C-X-C motif) ligand 2 | <i>CXCL2</i> | 0.0418240 | -1.39 | 3h vs 0h |
| 199 | C10.g1 | similar to ryanodine receptor 3 similar to cell death regulator aven | <i>LOC539899</i> <i>LOC512666</i> | 0.0367274 | -1.40 | 3h vs 0h |
| 200 | B9.b3 | BOTL0100004XG08R | | 0.0012430 | -1.41 | 3h vs 0h |
| 201 | C9.a6 | similar to Polyadenylate-binding protein-interacting protein 2 (Poly(A) binding protein-interacting protein 2) (PABP-interacting protein 2) | <i>PAIP-2</i> | 0.0350569 | -1.41 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| | | (PAIP-2) | | | | |
| 202 | A6.c5 | adaptor-related protein complex 1, sigma 1 subunit | <i>AP1S1</i> | 0.0129807 | -1.42 | 3h vs 0h |
| 203 | C10.c8 | similar to subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - human | <i>LOC524684</i> | 0.0160122 | -1.42 | 3h vs 0h |
| 204 | A12.g6 | hypothetical protein | <i>LOC509282</i> | 0.0089175 | -1.43 | 3h vs 0h |
| 205 | C9.f2 | similar to Polyadenylate-binding protein-interacting protein 2 (Poly(A) binding protein-interacting protein 2) (PABP-interacting protein 2) (PAIP-2) | <i>PAIP-2</i> | 0.0254984 | -1.43 | 3h vs 0h |
| 206 | B11.e8 | hydroxysteroid (17-beta) dehydrogenase 4 | <i>HSD17B4</i> | 0.0358533 | -1.43 | 3h vs 0h |
| 207 | D10.e8 | Transcribed locus | | 0.0025625 | -1.44 | 3h vs 0h |
| 208 | D11.e6 | Transcribed locus, strongly similar to NP_005345.3 D proto-oncogene | | 0.0161487 | -1.44 | 3h vs 0h |
| 209 | B9.f5 | BOTL0100004XG06R | | 0.0309670 | -1.44 | 3h vs 0h |
| 210 | A3.e8 | H3 histone, family 3A | <i>H3F3A</i> | 0.0320312 | -1.44 | 3h vs 0h |
| 211 | B10.b6 | hypothetical protein | <i>LOC788514</i> | 0.0151206 | -1.45 | 3h vs 0h |
| 212 | C6.e9 | BOTL0100006XA10R | | 0.0403011 | -1.45 | 3h vs 0h |
| 213 | C3.f8 | Ribosomal protein S3Ae | <i>RPS3AE</i> | 0.0213061 | -1.46 | 3h vs 0h |
| 214 | B10.f1 | small inducible cytokine subfamily E, member 1 | <i>SCYE1</i> | 0.0266269 | -1.46 | 3h vs 0h |
| 215 | C10.g8 | similar to leukocyte differentiation antigen CD84 | <i>LOC510910</i> | 0.0385931 | -1.47 | 3h vs 0h |
| 216 | A10.b3 | similar to insulin induced gene 1 | | 0.0148179 | -1.48 | 3h vs 0h |
| 217 | D5.c2 | Transcribed locus | | 0.0494607 | -1.48 | 3h vs 0h |
| 218 | B9.g3 | Transcribed locus | | 0.0044560 | -1.49 | 3h vs 0h |
| 219 | C10.h2 | similar to subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 | <i>LOC524684</i> | 0.0151789 | -1.49 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| | | precursor, splice form A - human | | | | |
| 220 | A5.f8 | hypothetical protein | <i>LOC617051</i> | 0.0434455 | -1.49 | 3h vs 0h |
| 221 | A12.c4 | hypothetical protein | <i>LOC509282</i> | 0.0019617 | -1.50 | 3h vs 0h |
| 222 | C5.a4 | similar to Serine/threonine protein phosphatase 6 (PP6) | <i>LOC608922</i> | 0.0263874 | -1.50 | 3h vs 0h |
| 223 | B10.f9 | hypothetical protein | <i>LOC788514</i> | 0.0119391 | -1.51 | 3h vs 0h |
| 224 | C3.b5 | Ribosomal protein S3Ae | <i>RPS3AE</i> | 0.0132482 | -1.51 | 3h vs 0h |
| 225 | B4.i4 | hypothetical protein isoform 4 | <i>LOC617051</i> | 0.0393397 | -1.51 | 3h vs 0h |
| 226 | B5.g4 | similar to antigen identified by monoclonal antibody Ki-67 | <i>LOC513220</i> | 0.0045181 | -1.52 | 3h vs 0h |
| 227 | C1.e8 | protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform | <i>PPP2R2A</i> | 0.0012290 | -1.55 | 3h vs 0h |
| 228 | A10.c1 | similar to jumonji domain containing 1C | <i>LOC781067</i> | 0.0093736 | -1.55 | 3h vs 0h |
| 229 | C2.c2 | ribosomal protein L6 | <i>RPL6</i> | 0.0260173 | -1.55 | 3h vs 0h |
| 230 | B9.b9 | Transcribed locus | | 0.0454385 | -1.55 | 3h vs 0h |
| 231 | B11.f2 | similar to NIR2 | <i>LOC533859</i> | 0.0377963 | -1.56 | 3h vs 0h |
| 232 | D5.g5 | Transcribed locus | | 0.0123478 | -1.57 | 3h vs 0h |
| 233 | A4.i5 | hypothetical protein | <i>LOC786378</i> | 0.0160048 | -1.58 | 3h vs 0h |
| 234 | B11.a8 | Wiskott-Aldrich syndrome protein interacting protein | <i>WIPF1</i> | 0.0136073 | -1.59 | 3h vs 0h |
| 235 | C11.e7 | similar to peptidyl-Pro cis trans isomerase isoform 1 | | 0.0497340 | -1.59 | 3h vs 0h |
| 236 | B11.e3 | Transcribed locus, moderately similar to XP_001056150.1 similar to very large G-protein coupled receptor 1 [Rattus norvegicus] | | 0.0308682 | -1.63 | 3h vs 0h |
| 237 | C7.f3 | hypothetical protein | <i>LOC788861</i> | 0.0387677 | -1.63 | 3h vs 0h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 238 | B11.a6 | similar to NIR2 | <i>LOC533859</i> | 0.0263201 | -1.64 | 3h vs 0h |
| 239 | A10.g4 | similar to jumonji domain containing 1C | <i>LOC781067</i> | 0.0388252 | -1.66 | 3h vs 0h |
| 240 | A9.c2 | similar to Conserved oligomeric Golgi complex component 4 | | 0.0071944 | -1.67 | 3h vs 0h |
| 241 | C7.a7 | hypothetical protein | <i>LOC788861</i> | 0.0347999 | -1.69 | 3h vs 0h |
| 242 | A9.c1 | similar to ornithine decarboxylase antizyme 2 | <i>LOC524677</i> | 0.0186440 | -1.73 | 3h vs 0h |
| 243 | A5.f2 | beta-2-microglobulin | <i>B2M</i> | 0.0420221 | -1.74 | 3h vs 0h |
| 244 | C11.i8 | similar to peptidyl-Pro cis trans isomerase isoform 1 | | 0.0414637 | -1.76 | 3h vs 0h |
| 245 | A7.g3 | syntaxin 7 | <i>STX7</i> | 0.0430864 | -1.77 | 3h vs 0h |
| 246 | A9.g5 | similar to Conserved oligomeric Golgi complex component 4 | | 0.0249877 | -1.78 | 3h vs 0h |
| 247 | A9.b5 | similar to carnitine O-palmitoyltransferase | <i>LOC506812</i> | 0.0044627 | -1.79 | 3h vs 0h |
| 248 | B3.a6 | similar to methionine-tRNA synthetase | <i>LOC614580</i> | 0.0061971 | -1.81 | 3h vs 0h |
| 249 | D10.f7 | hypothetical protein | <i>LOC515358</i> | 0.0138063 | -1.81 | 3h vs 0h |
| 250 | B3.f2 | similar to methionine-tRNA synthetase | <i>LOC614580</i> | 0.0060607 | -1.90 | 3h vs 0h |
| 1 | C9.f8 | similar to Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1) (Guanine nucleotide-binding protein 1) (HuGBP-1) | <i>LOC512486</i> | 0.0405088 | 2.50 | 12h vs 3h |
| 2 | C9.b5 | similar to Interferon-induced guanylate-binding protein 1 (GTP-binding protein 1) (Guanine nucleotide-binding protein 1) (HuGBP-1) | <i>LOC512486</i> | 0.0320301 | 2.46 | 12h vs 3h |
| 3 | A7.g3 | syntaxin 7 | <i>STX7</i> | 0.0296542 | 1.70 | 12h vs 3h |
| 4 | C5.h4 | collagenase | <i>MMP1</i> | 0.0027474 | 1.66 | 12h vs 3h |
| 5 | A11.g4 | similar to chromosome 17 open reading frame 27 | <i>LOC509283</i> | 0.0334622 | 1.58 | 12h vs 3h |
| 6 | B9.b9 | BOTL0100011_C03 | | 0.0056377 | 1.52 | 12h vs 3h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|---|------------------|-----------|-------------|-----------------------|
| 7 | D12.f1 | BOTL0100008_F04 | | 0.0064079 | 1.41 | 12h vs 3h |
| 8 | C10.h2 | similar to subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A - human | <i>LOC524684</i> | 0.0498153 | 1.40 | 12h vs 3h |
| 9 | C5.b8 | BOTL0100009_F06 | | 0.0447063 | 1.22 | 12h vs 3h |
| 10 | A10.g2 | similar to tangerin C | <i>LOC788760</i> | 0.0318948 | 1.10 | 12h vs 3h |
| 11 | C11.g4 | BTG family, member 3 | <i>BTG3</i> | 0.0459919 | -1.13 | 12h vs 3h |
| 12 | A4.g1 | thioredoxin-related transmembrane protein 2 | <i>TMX2</i> | 0.0363280 | -1.17 | 12h vs 3h |
| 13 | B5.g3 | hypothetical protein | <i>LOC522360</i> | 0.0450938 | -1.20 | 12h vs 3h |
| 14 | C2.f1 | Unknown | | 0.0316986 | -1.26 | 12h vs 3h |
| 15 | A2.b6 | BOTL0100012_A12 | | 0.0363306 | -1.27 | 12h vs 3h |
| 16 | D3.f8 | Hypothetical protein | <i>LOC507199</i> | 0.0062010 | -1.28 | 12h vs 3h |
| 17 | B1.f8 | similar to Cathepsin W isoform 2 | <i>LOC510967</i> | 0.0351526 | -1.29 | 12h vs 3h |
| 18 | C12.a3 | abhydrolase domain containing 8 | <i>ABHD8</i> | 0.0052133 | -1.31 | 12h vs 3h |
| 19 | C5.c4 | similar to notch 2 preproprotein | <i>LOC513730</i> | 0.0324785 | -1.32 | 12h vs 3h |
| 20 | B7.i8 | mitogen-activated protein kinase kinase 1, RNA (MAP2K1) | | 0.0088545 | -1.34 | 12h vs 3h |
| 21 | A1.c1 | similar to AF-4 | <i>LOC781149</i> | 0.0498954 | -1.34 | 12h vs 3h |
| 22 | C5.i3 | macrophage migration inhibitory factor (glycosylation-inhibiting factor) | <i>MIF</i> | 0.0379865 | -1.37 | 12h vs 3h |
| 23 | D2.g3 | similar to ribosome associated membrane protein 4 | | 0.0341231 | -1.38 | 12h vs 3h |
| 24 | D1.i8 | similar to SIT protein isoform 1 | <i>LOC512027</i> | 0.0152282 | -1.39 | 12h vs 3h |
| 25 | C7.f7 | coactosin-like 1 (Dictyostelium) | <i>COTL1</i> | 0.0336607 | -1.39 | 12h vs 3h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|---|------------------|-----------|-------------|-----------------------|
| 26 | C2.e2 | retinoid X receptor, beta | <i>RXRβ</i> | 0.0050493 | -1.40 | 12h vs 3h |
| 27 | B5.i4 | Growth hormone | <i>GH</i> | 0.0368254 | -1.46 | 12h vs 3h |
| 28 | B7.e7 | mitogen-activated protein kinase kinase 1, RNA (MAP2K1) | | 0.0025488 | -1.47 | 12h vs 3h |
| 29 | D9.b7 | seryl-tRNA synthetase 2 | <i>SARS2</i> | 0.0187143 | -1.47 | 12h vs 3h |
| 30 | D1.e6 | similar to Serum response factor (SRF) | <i>LOC533039</i> | 0.0482394 | -1.48 | 12h vs 3h |
| 31 | D1.i7 | similar to Serum response factor (SRF) | <i>LOC533039</i> | 0.0387187 | -1.49 | 12h vs 3h |
| 32 | A3.f2 | Similar to Hexokinase 3 (white cell) | <i>LOC510616</i> | 0.0302245 | -1.50 | 12h vs 3h |
| 33 | A1.g8 | endonuclease domain containing 1 | | 0.0305252 | -1.50 | 12h vs 3h |
| 34 | B1.h9 | Rho guanine nucleotide exchange factor, mRNA (GEF 1) | | 0.0330438 | -1.50 | 12h vs 3h |
| 35 | A2.f5 | Unknown | | 0.0452648 | -1.50 | 12h vs 3h |
| 36 | C12.a8 | Similar to Hexokinase 3 (white cell) | <i>LOC510616</i> | 0.0057040 | -1.51 | 12h vs 3h |
| 37 | A9.a8 | CD81 molecule | <i>CD81</i> | 0.0492306 | -1.52 | 12h vs 3h |
| 38 | D4.b7 | hypothetical protein | <i>LOC786280</i> | 0.0439083 | -1.55 | 12h vs 3h |
| 39 | D7.e6 | nitric oxide synthase 3 (endothelial cell) | <i>NOS3</i> | 0.0247806 | -1.56 | 12h vs 3h |
| 40 | C5.g5 | pyruvate kinase 3 | <i>PKM2</i> | 0.0431808 | -1.56 | 12h vs 3h |
| 41 | A9.f5 | CD81 molecule | <i>CD81</i> | 0.0309986 | -1.57 | 12h vs 3h |
| 42 | A2.f8 | similar to mitogen-activated protein kinase kinase kinase kinase 2 | <i>LOC520058</i> | 0.0029827 | -1.59 | 12h vs 3h |
| 43 | C2.g4 | TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa | <i>TAF6</i> | 0.0306969 | -1.60 | 12h vs 3h |
| 44 | A2.b5 | similar to mitogen-activated protein kinase kinase kinase kinase 2 | <i>LOC520058</i> | 0.0048977 | -1.61 | 12h vs 3h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|--|------------------|-----------|-------------|-----------------------|
| 45 | B12.a4 | hypothetical protein | <i>LOC514346</i> | 0.0221045 | -1.61 | 12h vs 3h |
| 46 | B12.a7 | similar to retinoblastoma-associated factor 600 (RBAF600) isoform 1 | <i>LOC514561</i> | 0.0326070 | -1.62 | 12h vs 3h |
| 47 | D4.g1 | hypothetical protein | <i>LOC786280</i> | 0.0123459 | -1.64 | 12h vs 3h |
| 48 | B4.b5 | similar to cyclic nucleotide phosphodiesterase | <i>LOC533323</i> | 0.0473840 | -1.64 | 12h vs 3h |
| 49 | B7.d8 | similar to KIAA2014 protein | <i>LOC540105</i> | 0.0454207 | -1.68 | 12h vs 3h |
| 50 | B12.e9 | hypothetical protein | <i>LOC514346</i> | 0.0052202 | -1.69 | 12h vs 3h |
| 51 | D1.i6 | GATA-binding protein 4 (GATA4) | | 0.0497362 | -1.69 | 12h vs 3h |
| 52 | B11.h9 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 | <i>SMARCAL1</i> | 0.0110905 | -1.71 | 12h vs 3h |
| 53 | B1.e6 | GATA binding protein 4 (GATA4) | | 0.0421441 | -1.72 | 12h vs 3h |
| 54 | A8.a8 | similar to Tyrosine-protein kinase Lyn | <i>LOC534996</i> | 0.0485333 | -1.75 | 12h vs 3h |
| 55 | B12.f3 | similar to retinoblastoma-associated factor 600 (RBAF600) isoform 1 | <i>LOC514561</i> | 0.0068731 | -1.78 | 12h vs 3h |
| 56 | B8.i3 | RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein) | <i>RASA3</i> | 0.0200022 | -1.79 | 12h vs 3h |
| 57 | B3.i2 | myelin basic protein (MBP) | | 0.0447012 | -1.82 | 12h vs 3h |
| 58 | B1.d8 | Rho guanine nucleotide exchange factor, mRNA (GEF 1) | | 0.0027317 | -1.85 | 12h vs 3h |
| 59 | C6.h7 | nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) | <i>NFKB1</i> | 0.0316886 | -1.85 | 12h vs 3h |
| 60 | B6.e1 | eukaryotic translation elongation factor 1 gamma | <i>EEF1G</i> | 0.0256508 | -1.87 | 12h vs 3h |
| 61 | D9.i8 | protein kinase, cAMP-dependent, regulatory, type I, beta | <i>PRKAR1B</i> | 0.0454800 | -1.87 | 12h vs 3h |
| 62 | B8.e1 | RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein) | <i>RASA3</i> | 0.0291039 | -1.90 | 12h vs 3h |
| 63 | A11.e8 | glioma tumor suppressor candidate region gene 2 | <i>GLTSCR2</i> | 0.0314618 | -1.99 | 12h vs 3h |

| Rank | BOTL-5 coordinates | Feature description | Gene symbol | P-value | Fold-change | Time point comparison |
|------|--------------------|---|--|-----------|-------------|-----------------------|
| 64 | A11.a3 | glioma tumor suppressor candidate region gene 2 | <i>GLTSCR2</i> | 0.0367875 | -1.99 | 12h vs 3h |
| 65 | D11.e1 | Similar to serine/threonine protein kinase | <i>LOC514210</i> | 0.0423519 | -1.99 | 12h vs 3h |
| 66 | B9.e1 | v-akt murine thymoma viral oncogene homolog 1 | <i>AKT1</i> | 0.0377055 | -2.01 | 12h vs 3h |
| 67 | A1.a7 | Similar to KIAA0668 protein | <i>LOC618392</i> | 0.0125049 | -2.02 | 12h vs 3h |
| 68 | A1.f3 | Similar to KIAA0668 protein | <i>LOC618392</i> | 0.0084437 | -2.05 | 12h vs 3h |
| 69 | D11.i3 | Similar to serine/threonine protein kinase | <i>LOC514210</i> | 0.0405599 | -2.08 | 12h vs 3h |
| 70 | A2.g6 | hypothetical protein | <i>LOC614093</i> | 0.0007606 | -2.16 | 12h vs 3h |
| 71 | A3.g9 | CD14 molecule | <i>CD14</i> | 0.0380259 | -2.24 | 12h vs 3h |
| 72 | B3.i5 | splicing factor, arginine/serine-rich 2 | <i>SFRS2</i> | 0.0107057 | -2.29 | 12h vs 3h |
| 73 | B3.e3 | splicing factor, arginine/serine-rich 2 | <i>SFRS2</i> | 0.0113258 | -2.39 | 12h vs 3h |
| 74 | C1.c4 | similar to MAP kinase kinase 7 gamma 1 | <i>LOC787278</i> | 0.0259424 | -2.60 | 12h vs 3h |
| 75 | C8.c6 | similar to chemokine CCL1/l-309 similar to chemokine CCL1/l-309 | <i>LOC786156</i> <i>LOC786204</i> | 0.0234985 | -2.65 | 12h vs 3h |
| 76 | C8.g9 | similar to chemokine CCL1/l-309 similar to chemokine CCL1/l-309 | <i>LOC786156</i> <i>LOC786204</i> | 0.0142840 | -2.75 | 12h vs 3h |
| 77 | C11.c2 | hypothetical protein | <i>LOC512361</i> | 0.0182371 | -2.78 | 12h vs 3h |
| 78 | C11.g5 | hypothetical protein | <i>LOC512361</i> | 0.0213715 | -2.82 | 12h vs 3h |
| 79 | A8.g9 | MHC class I heavy chain isoform 1 | <i>BOLA</i> | 0.0161226 | -2.93 | 12h vs 3h |
| 80 | A8.c6 | MHC class I heavy chain isoform 1 | <i>BOLA</i> | 0.0138905 | -3.06 | 12h vs 3h |