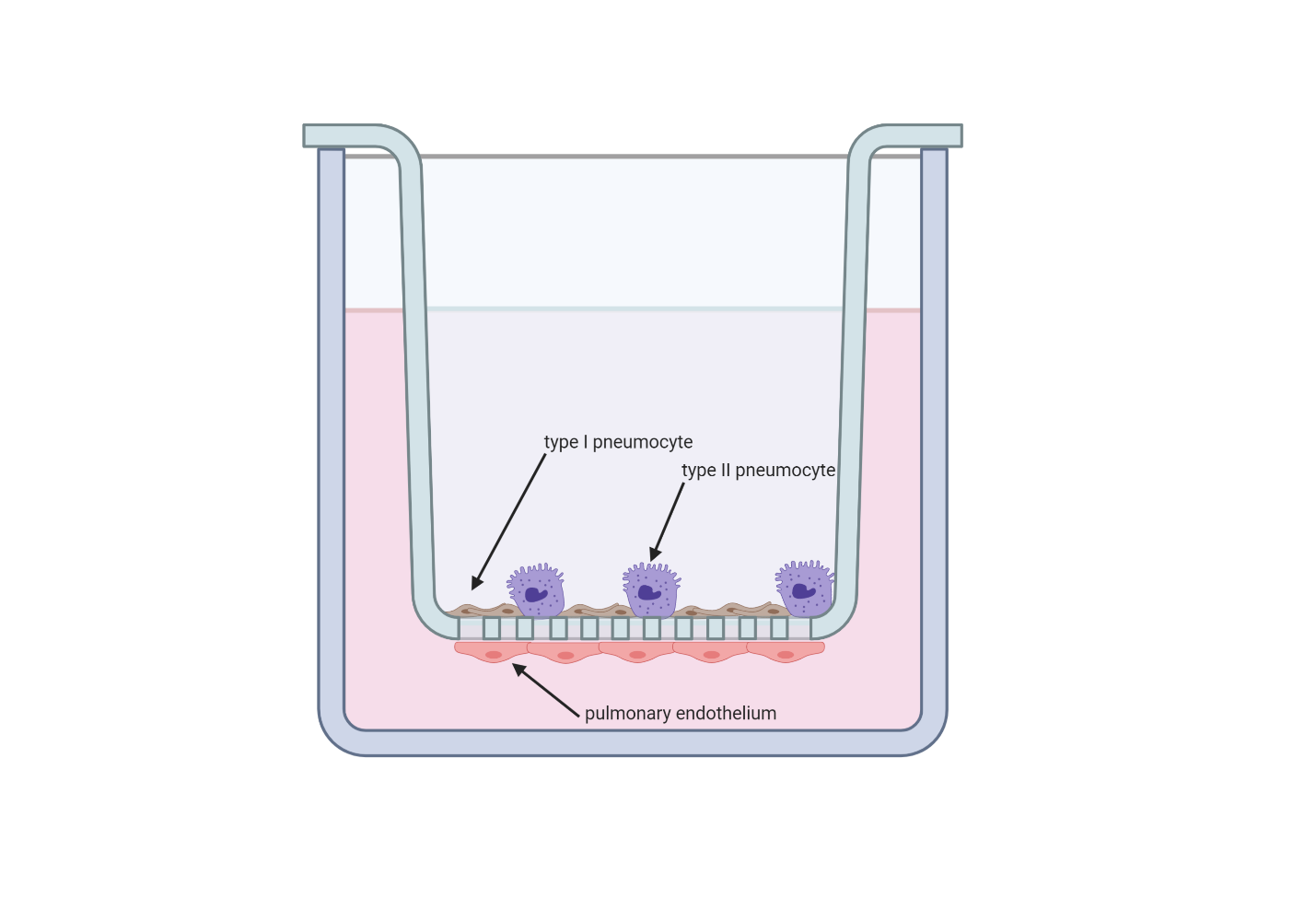
**Figure S1: Alveolar-capillary barrier co-culture model schematic.** Figure generated with BioRender.

****

**Table S1: MRSA Virulence Factor Primer Sequences.** Primers were designed and selected using PrimerQuest.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Function** | **Primer Sequences** |
| Coa | protects bacteria from phagocytosis by forming fibrin clots | F – TTCCACAGGGCACAATTACA  R-TCGGGACCTTGAACGATTTC |
| EbpS | binds elastin to facilitate colonization of injured tissues | F – GGTGAACCTGAACCGTAGTATT  R - CAGCAACAACAACGTCAAGG |
| Eno | forms plasmin to digest fibrin clots which keep the bacterium localized | F - TGGTTACAAACCAGGTGAAGAA  R - CGCCTTCGAACTTACTGTAGTC |
| FnbA | binds extracellular matrix components to mediate endothelial cell adhesion | F - CCCATTTCCGTTCGCTTTATTAC  R - GTAGGACATCCAGAGCAACTTTA |
| FnbB | binds fibronectin and elastin to mediate adhesion to endothelial cells | F - TGTCGCGCTGTATGATTGT R - GTAGAGGAAAGTGGGAGTTCAG |
| Hla | forms pores in the cytoplasmic membrane resulting in lysis | F - CTGTAGCGAAGTCTGGTGAAA R - AGATTCTTGGAACCCGGTATATG |
| HlgA | forms pores in the cytoplasmic membrane resulting in lysis | F - CCAGCAGCACGAGACTATTT R - CACCTTTACCTCTTTCGTGTGA |
| IcaA | mediates intercellular adhesion and biofilm formation | F - GCAGTAGTTCTTGTCGCATTTC R - GTTGGGTATTCCCTCTGTCTG |
| IcaB | mediates intercellular adhesion and biofilm formation | F - AGCCTATCCTTATGGCTTGATG R - GAGTTCGGAGTGACTGCTTT |
| Sbi | mediates Fab-independent formation of IgG insoluble complexes | F - AGCCAACAAGTTTGGGTAGAA  R - CGTGTGGTGCTTTGTTATCTTG |
| Sek | enterotoxin with superantigen activity | F – ATCGACATCCAAATGGAATTTCTC  R - CTACACAGGAGATGATGGGTTAC |
| Seq | enterotoxin with superantigen activity | F -GTAGAAACCTCGTCTGTAGATATAGTG  R - GGAATTACGTTGGCGAATCAAA |
| Spa | forms IgG insoluble complexes to impede phagocytosis; binds airway epithelial cells | F – GCTGCACCTAAGGCTAATGATA  R - GATAAGAAGCAACCAGCAAACC |

**Table S2: Upregulated signaling pathways in pH1N1-MRSA co-infected alveolar epithelial cells at the alveolar-capillary barrier as determined by temporal kinome analysis.** Pathways represent those that were found to be activated in pH1N1-MRSA co-infected cells as compared to mock-infected controls at 24 h post-MRSA addition. Thresholds for pathways over-representation analysis were fold-change ≥1.5, p-value ≤ 0.05.

|  |  |  |
| --- | --- | --- |
| Pathway Name | Pathway uploaded proteins | Pathway up-regulated p-value |
| Estrogen responsive protein efp controls cell cycle and breast tumors growth | 4 | 1.78E-04 |
| Cyclin A/B1 associated events during G2/M transition | 5 | 4.35E-04 |
| G1/S Transition | 6 | 8.50E-04 |
| Cyclins and cell cycle regulation | 7 | 0.001452 |
| Mitotic G1-G1/S phases | 8 | 0.002268 |
| G2/M Checkpoints | 3 | 0.003969 |
| G2/M Transition | 10 | 0.004632 |
| Mitotic G2-G2/M phases | 10 | 0.004632 |
| Cell Cycle Checkpoints | 4 | 0.007759 |
| Cyclin A:Cdk2-associated events at S phase entry | 4 | 0.007759 |
| Cyclin E associated events during G1/S transition | 4 | 0.007759 |
| D4gdi signaling pathway | 4 | 0.007759 |
| ERK1 activation | 4 | 0.007759 |
| G0 and Early G1 | 4 | 0.007759 |
| IRAK1 recruits IKK complex | 4 | 0.007759 |
| IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation | 4 | 0.007759 |
| Internal ribosome entry pathway | 4 | 0.007759 |
| Regulation of cell cycle progression by plk3 | 4 | 0.007759 |
| p53 signaling pathway | 12 | 0.008093 |
| Cytokine Signaling in Immune system | 56 | 0.012262 |
| E2F transcription factor network | 5 | 0.012642 |
| Interferon alpha/beta signaling | 5 | 0.012642 |
| S Phase | 5 | 0.012642 |
| Signaling by Interleukins | 44 | 0.018475 |
| Degradation of the extracellular matrix | 6 | 0.018538 |
| ERK activation | 6 | 0.018538 |
| TRAF6 mediated IRF7 activation | 6 | 0.018538 |
| p73 transcription factor network | 6 | 0.018538 |
| Cell cycle | 16 | 0.018709 |
| IFN-gamma pathway | 17 | 0.022178 |
| Caspase cascade in apoptosis | 7 | 0.025372 |
| Cell death signalling via NRAGE, NRIF and NADE | 7 | 0.025372 |
| Amyotrophic lateral sclerosis (ALS) | 8 | 0.033073 |
| FOXM1 transcription factor network | 8 | 0.033073 |
| Retinoic acid receptors-mediated signaling | 8 | 0.033073 |
| MyD88 cascade initiated on plasma membrane | 35 | 0.035765 |
| Toll Like Receptor 10 (TLR10) Cascade | 35 | 0.035765 |
| Toll Like Receptor 5 (TLR5) Cascade | 35 | 0.035765 |
| MyD88 dependent cascade initiated on endosome | 36 | 0.039263 |
| TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation | 36 | 0.039263 |
| Toll Like Receptor 7/8 (TLR7/8) Cascade | 36 | 0.039263 |
| Cell cycle: g1/s check point | 9 | 0.041573 |
| RAF/MAP kinase cascade | 9 | 0.041573 |
| AndrogenReceptor | 37 | 0.042958 |
| MyD88:Mal cascade initiated on plasma membrane | 37 | 0.042958 |
| Toll Like Receptor 2 (TLR2) Cascade | 37 | 0.042958 |
| Toll Like Receptor 9 (TLR9) Cascade | 37 | 0.042958 |
| Toll Like Receptor TLR1:TLR2 Cascade | 37 | 0.042958 |
| Toll Like Receptor TLR6:TLR2 Cascade | 37 | 0.042958 |
| Cell Cycle | 22 | 0.044538 |
| Cell Cycle, Mitotic | 22 | 0.044538 |
| Interferon gamma signaling | 10 | 0.050809 |
| NOD1/2 Signaling Pathway | 10 | 0.050809 |
| Signalling to p38 via RIT and RIN | 10 | 0.050809 |
| p75 NTR receptor-mediated signalling | 10 | 0.050809 |
| ARMS-mediated activation | 11 | 0.060718 |
| Factors involved in megakaryocyte development and platelet production | 11 | 0.060718 |
| GRB2 events in EGFR signaling | 11 | 0.060718 |
| GRB2 events in ERBB2 signaling | 11 | 0.060718 |
| SHC1 events in ERBB4 signaling | 11 | 0.060718 |
| SOS-mediated signalling | 11 | 0.060718 |
| p75(NTR)-mediated signaling | 11 | 0.060718 |
| Activated TLR4 signalling | 42 | 0.064408 |
| MAP kinase activation in TLR cascade | 26 | 0.068308 |
| Toll Like Receptor 4 (TLR4) Cascade | 43 | 0.069293 |
| SHC-mediated signalling | 12 | 0.071243 |
| SHC-related events triggered by IGF1R | 12 | 0.071243 |
| SHC1 events in EGFR signaling | 12 | 0.071243 |
| SHC1 events in ERBB2 signaling | 12 | 0.071243 |
| Oncostatin\_M | 27 | 0.075024 |
| Extracellular matrix organization | 13 | 0.082329 |
| FRS2-mediated cascade | 13 | 0.082329 |
| Frs2-mediated activation | 13 | 0.082329 |
| Interleukin-1 signaling | 13 | 0.082329 |
| RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways | 13 | 0.082329 |
| Signaling by Leptin | 13 | 0.082329 |
| Interferon Signaling | 14 | 0.093924 |
| NCAM signaling for neurite out-growth | 14 | 0.093924 |
| Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways | 14 | 0.093924 |
| Prolonged ERK activation events | 14 | 0.093924 |
| SHC-related events | 14 | 0.093924 |
| VEGFR2 mediated cell proliferation | 14 | 0.093924 |

**Table S3: Upregulated signaling pathways in pH1N1-infected alveolar epithelial cells at the alveolar-capillary barrier as determined by temporal kinome analysis.** Pathways represent those that were found to be activated in pH1N1 infected cells as compared to mock-infected controls at 24 h post-MRSA addition. Thresholds for pathways over-representation analysis were fold-change ≥1.5, p-value ≤ 0.05.

|  |  |  |
| --- | --- | --- |
| Pathway Name | Pathway uploaded proteins | Pathway up-regulated p-value |
| IFN-gamma pathway | 17 | 4.66E-04 |
| D4gdi signaling pathway | 4 | 0.003405 |
| Internal ribosome entry pathway | 4 | 0.003405 |
| Cytokine Signaling in Immune system | 56 | 0.007846 |
| Caspase cascade in apoptosis | 7 | 0.011422 |
| Amyotrophic lateral sclerosis (ALS) | 8 | 0.015016 |
| Signaling by FGFR1 mutants | 9 | 0.019035 |
| Oncostatin M | 27 | 0.025447 |
| Factors involved in megakaryocyte development and platelet production | 11 | 0.02827 |
| Pathways in cancer | 77 | 0.030483 |
| Glucocorticoid receptor regulatory network | 12 | 0.033448 |
| p53 signaling pathway | 12 | 0.033448 |
| Interferon Signaling | 14 | 0.044833 |
| Signaling by FGFR mutants | 15 | 0.051006 |
| EPO signaling pathway | 17 | 0.064226 |
| Inhibition of cellular proliferation by gleevec | 17 | 0.064226 |
| Immune System | 161 | 0.068943 |
| IL2-mediated signaling events | 18 | 0.071243 |
| IL6-mediated signaling events | 18 | 0.071243 |
| Alternative complement pathway | 3 | 0.073891 |
| Apoptotic signaling in response to DNA damage | 3 | 0.073891 |
| Caspase-mediated cleavage of cytoskeletal proteins | 3 | 0.073891 |
| Classical complement pathway | 3 | 0.073891 |
| G1/S DNA Damage Checkpoints | 3 | 0.073891 |
| G2/M Checkpoints | 3 | 0.073891 |
| Granzyme a mediated apoptosis pathway | 3 | 0.073891 |
| IFN gamma signaling | 3 | 0.073891 |
| IFN gamma signaling pathway | 3 | 0.073891 |
| Interleukin-1 processing | 3 | 0.073891 |
| Lectin induced complement pathway | 3 | 0.073891 |
| PERK regulates gene expression | 3 | 0.073891 |
| Regulation of Apoptosis | 3 | 0.073891 |
| Terminal pathway of complement | 3 | 0.073891 |
| The information processing pathway at the IFN beta enhancer | 3 | 0.073891 |
| BCR | 70 | 0.084334 |
| Amoebiasis | 20 | 0.086013 |
| GPCR signaling | 20 | 0.086013 |
| IL2 | 44 | 0.0898 |
| Signaling by Interleukins | 44 | 0.0898 |
| Antiviral mechanism by IFN-stimulated genes | 4 | 0.097386 |
| Cell Cycle Checkpoints | 4 | 0.097386 |
| Complement cascade | 4 | 0.097386 |
| Cyclin A:Cdk2-associated events at S phase entry | 4 | 0.097386 |
| Cyclin E associated events during G1/S transition | 4 | 0.097386 |
| Estrogen responsive protein efp controls cell cycle and breast tumors growth | 4 | 0.097386 |
| G0 and Early G1 | 4 | 0.097386 |
| IFN alpha signaling | 4 | 0.097386 |
| IRAK1 recruits IKK complex | 4 | 0.097386 |
| IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation | 4 | 0.097386 |
| ISG15 antiviral mechanism | 4 | 0.097386 |
| Ifn alpha signaling pathway | 4 | 0.097386 |
| P53 signaling pathway | 4 | 0.097386 |
| Pyruvate metabolism | 4 | 0.097386 |
| Regulation of Complement cascade | 4 | 0.097386 |
| Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 4 | 0.097386 |
| Regulation of cell cycle progression by plk3 | 4 | 0.097386 |
| SHC-mediated cascade | 4 | 0.097386 |
| Stress induction of hsp regulation | 4 | 0.097386 |
| Systemic lupus erythematosus | 4 | 0.097386 |

**Table S4: Upregulated signaling pathways in MRSA-infected alveolar epithelial cells at the alveolar-capillary barrier.** Pathways represent those that were found to be activated in MRSA infected cells as compared to mock-infected controls at 24 h post-MRSA addition. Thresholds for pathways over-representation analysis were fold-change ≥1.5, p-value ≤ 0.05.

|  |  |  |
| --- | --- | --- |
| Pathway Name | Pathway uploaded proteins | Pathway up-regulated p-value |
| Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 4 | 1.59E-04 |
| Metabolism of proteins | 20 | 0.004914 |
| IGF1 signaling pathway | 22 | 0.005958 |
| Interleukin-1 processing | 3 | 0.018828 |
| PERK regulates gene expression | 3 | 0.018828 |
| D4gdi signaling pathway | 4 | 0.025051 |
| Internal ribosome entry pathway | 4 | 0.025051 |
| Cellular roles of Anthrax toxin | 5 | 0.031248 |
| Inflammasomes | 5 | 0.031248 |
| The NLRP3 inflammasome | 5 | 0.031248 |
| Cytosolic DNA-sensing pathway | 6 | 0.037418 |
| Unfolded Protein Response (UPR) | 6 | 0.037418 |
| Caspase cascade in apoptosis | 7 | 0.043562 |
| FOXA2 and FOXA3 transcription factor networks | 7 | 0.043562 |
| Amyotrophic lateral sclerosis (ALS) | 8 | 0.04968 |
| NOD1/2 Signaling Pathway | 10 | 0.061838 |
| Direct p53 effectors | 11 | 0.067877 |
| Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways | 14 | 0.085841 |

**Table S5: Upregulated signaling pathways in pH1N1-MRSA-infected pulmonary endothelial cells at the alveolar-capillary barrier.** Pathways represent those that were found to be activated in pH1N1-MRSA co-infected endothelial cells as compared to mock-infected controls at 24 h post-MRSA addition. Thresholds for pathway over-representation analysis were fold-change ≥1.5, p-value ≤0.05.

|  |  |  |
| --- | --- | --- |
| Pathway Name | Pathway uploaded proteins | Pathway up-regulated p-value |
| Hedgehog 'off' state | 4 | 7.05E-04 |
| Signaling by Hedgehog | 4 | 7.05E-04 |
| Hedgehog signaling pathway | 6 | 0.003249 |
| Class I MHC mediated antigen processing & presentation | 8 | 0.008394 |
| Degradation of GLI2 by the proteasome | 3 | 0.009664 |
| GLI3 is processed to GLI3R by the proteasome | 3 | 0.009664 |
| Transcription factor creb and its extracellular signals | 17 | 0.013452 |
| Cellular responses to stress | 36 | 0.013505 |
| VEGFR3 signaling in lymphatic endothelium | 10 | 0.016598 |
| Antigen processing-cross presentation | 4 | 0.018624 |
| Beta-catenin phosphorylation cascade | 4 | 0.018624 |
| Circadian Clock | 11 | 0.021926 |
| Factors involved in megakaryocyte development and platelet production | 11 | 0.021926 |
| CREB phosphorylation | 5 | 0.029912 |
| Tnfr1 signaling pathway | 5 | 0.029912 |
| Role of Calcineurin-dependent NFAT signaling in lymphocytes | 13 | 0.035082 |
| Signaling by Wnt | 23 | 0.039044 |
| MAPK targets/ Nuclear events mediated by MAP kinases | 14 | 0.042903 |
| P38 mapk signaling pathway | 14 | 0.042903 |
| RNF mutants show enhanced WNT signaling and proliferation | 14 | 0.042903 |
| Signaling by WNT in cancer | 14 | 0.042903 |
| TCF dependent signaling in response to WNT | 14 | 0.042903 |
| XAV939 inhibits tankyrase, stabilizing AXIN | 14 | 0.042903 |
| misspliced LRP5 mutants have enhanced beta-catenin-dependent signaling | 14 | 0.042903 |
| AMER1 mutants destabilize the destruction complex | 6 | 0.043243 |
| APC truncation mutants are not K63 polyubiquitinated | 6 | 0.043243 |
| APC truncation mutants have impaired AXIN binding | 6 | 0.043243 |
| AXIN missense mutants destabilize the destruction complex | 6 | 0.043243 |
| AXIN mutants destabilize the destruction complex, activating WNT signaling | 6 | 0.043243 |
| Degradation of beta-catenin by the destruction complex | 6 | 0.043243 |
| Degradation of the extracellular matrix | 6 | 0.043243 |
| S33 mutants of beta-catenin aren't phosphorylated | 6 | 0.043243 |
| S37 mutants of beta-catenin aren't phosphorylated | 6 | 0.043243 |
| S45 mutants of beta-catenin aren't phosphorylated | 6 | 0.043243 |
| Stathmin and breast cancer resistance to antimicrotubule agents | 6 | 0.043243 |
| T41 mutants of beta-catenin aren't phosphorylated | 6 | 0.043243 |
| TCF7L2 mutants don't bind CTBP | 6 | 0.043243 |
| deletions in the AMER1 gene destabilize the destruction complex | 6 | 0.043243 |
| deletions in the AXIN genes in hepatocellular carcinoma result in elevated WNT signaling | 6 | 0.043243 |
| misspliced GSK3beta mutants stabilize beta-catenin | 6 | 0.043243 |
| phosphorylation site mutants of CTNNB1 are not targeted to the proteasome by the destruction complex | 6 | 0.043243 |
| truncated APC mutants destabilize the destruction complex | 6 | 0.043243 |
| truncations of AMER1 destabilize the destruction complex | 6 | 0.043243 |
| Signaling mediated by p38-alpha and p38-beta | 15 | 0.051533 |
| MAP kinase activation in TLR cascade | 26 | 0.05824 |
| Wnt signaling pathway | 26 | 0.05824 |
| Fas signaling pathway | 7 | 0.058356 |
| disassembly of the destruction complex and recruitment of AXIN to the membrane | 7 | 0.058356 |
| RAC1 signaling pathway | 17 | 0.071129 |
| Amyotrophic lateral sclerosis (ALS) | 8 | 0.075009 |
| ERK/MAPK targets | 8 | 0.075009 |
| Fas signaling pathway (cd95) | 8 | 0.075009 |
| Noncanonical Wnt signaling pathway | 8 | 0.075009 |
| Recycling pathway of L1 | 8 | 0.075009 |
| ErbB signaling pathway | 42 | 0.089179 |
| Antigen processing and presentation | 9 | 0.092985 |
| Regulation of Androgen receptor activity | 9 | 0.092985 |
| RhoA signaling pathway | 9 | 0.092985 |
| MAPK signaling pathway | 69 | 0.09367 |

**Table S6: Upregulated signaling pathways in pH1N1-infected pulmonary endothelial cells at the alveolar-capillary barrier.** Pathways represent those that were found to be activated in pH1N1 infected endothelial cells as compared to mock-infected controls at 24 h post-MRSA addition. Thresholds for pathway over-representation analysis were fold-change ≥1.5, p-value ≤0.05.

|  |  |  |
| --- | --- | --- |
| Pathway Name | Pathway uploaded proteins | Pathway up-regulated p-value |
| Pyruvate metabolism | 4 | 0.007759 |
| IL23-mediated signaling events | 11 | 0.060718 |
| Pyruvate metabolism and Citric Acid (TCA) cycle | 11 | 0.060718 |
| Jak-STAT signaling pathway | 27 | 0.075024 |
| The citric acid (TCA) cycle and respiratory electron transport | 13 | 0.082329 |

**Table S7: Upregulated signaling pathways in MRSA-infected pulmonary endothelial cells at the alveolar-capillary barrier.** Pathways represent those that were found to be activated in MRSA infected endothelial cells as compared to mock-infected controls at 24 h post-MRSA addition. Thresholds for pathway over-representation analysis were fold-change ≥1.5, p-value ≤0.05.

|  |  |  |
| --- | --- | --- |
| Pathway Name | Pathway uploaded proteins | Pathway up-regulated p-value |
| Hedgehog signaling pathway | 6 | 1.78E-04 |
| Hedgehog 'off' state | 4 | 8.70E-04 |
| Signaling by Hedgehog | 4 | 8.70E-04 |
| Degradation of GLI2 by the proteasome | 3 | 0.011089 |
| GLI3 is processed to GLI3R by the proteasome | 3 | 0.011089 |
| Metabolism of lipids and lipoproteins | 3 | 0.011089 |
| PKA-mediated phosphorylation of CREB | 3 | 0.011089 |
| Transcription regulation by methyltransferase of carm1 | 3 | 0.011089 |
| Beta-catenin phosphorylation cascade | 4 | 0.021308 |
| CREB phosphorylation through the activation of CaMKII | 4 | 0.021308 |
| CRMPs in Sema3A signaling | 4 | 0.021308 |
| GPCR Dopamine D1like receptor signaling pathway | 4 | 0.021308 |
| Metabolism | 4 | 0.021308 |
| Presenilin action in Notch and Wnt signaling | 12 | 0.033806 |
| Repression of pain sensation by the transcriptional regulator dream | 5 | 0.034124 |
| Vasopressin-regulated water reabsorption | 5 | 0.034124 |
| AMER1 mutants destabilize the destruction complex | 6 | 0.049193 |
| APC truncation mutants are not K63 polyubiquitinated | 6 | 0.049193 |
| APC truncation mutants have impaired AXIN binding | 6 | 0.049193 |
| AXIN missense mutants destabilize the destruction complex | 6 | 0.049193 |
| AXIN mutants destabilize the destruction complex, activating WNT signaling | 6 | 0.049193 |
| Ca-calmodulin-dependent protein kinase activation | 6 | 0.049193 |
| Degradation of beta-catenin by the destruction complex | 6 | 0.049193 |
| S33 mutants of beta-catenin aren't phosphorylated | 6 | 0.049193 |
| S37 mutants of beta-catenin aren't phosphorylated | 6 | 0.049193 |
| S45 mutants of beta-catenin aren't phosphorylated | 6 | 0.049193 |
| Stathmin and breast cancer resistance to antimicrotubule agents | 6 | 0.049193 |
| T41 mutants of beta-catenin aren't phosphorylated | 6 | 0.049193 |
| TCF7L2 mutants don't bind CTBP | 6 | 0.049193 |
| Deletions in the AMER1 gene destabilize the destruction complex | 6 | 0.049193 |
| Deletions in the AXIN genes in hepatocellular carcinoma result in elevated WNT signaling | 6 | 0.049193 |
| Misspliced GSK3beta mutants stabilize beta-catenin | 6 | 0.049193 |
| Phosphorylation site mutants of CTNNB1 are not targeted to the proteasome by the destruction complex | 6 | 0.049193 |
| Truncated APC mutants destabilize the destruction complex | 6 | 0.049193 |
| Truncations of AMER1 destabilize the destruction complex | 6 | 0.049193 |
| RNF mutants show enhanced WNT signaling and proliferation | 14 | 0.051314 |
| Signaling by WNT in cancer | 14 | 0.051314 |
| TCF dependent signaling in response to WNT | 14 | 0.051314 |
| XAV939 inhibits tankyrase, stabilizing AXIN | 14 | 0.051314 |
| Misspliced LRP5 mutants have enhanced beta-catenin-dependent signaling | 14 | 0.051314 |
| disassembly of the destruction complex and recruitment of AXIN to the membrane | 7 | 0.066198 |
| Wnt signaling pathway | 26 | 0.072268 |
| Noncanonical Wnt signaling pathway | 8 | 0.084852 |
| Wnt signaling pathway | 8 | 0.084852 |