**Figure S1: Alveolar-capillary barrier co-culture model schematic.** Figure generated with BioRender. The basal side of 0.4 µm transwell inserts were coated with GelTrex LDEV-Free Reduced Growth Factor Basement Membrane Matrix and rested basal side up for 1 h at 37°C and 5% CO2. Transwell inserts were turned apical side up, the apical side coated with GelTrex, and rested for 1 h at 37°C and 5% CO2. Transwell inserts were turned basal side up, the basal side of the transwell inserts seeded with HPMEC at a concentration of 1.5 × $10^5$ cells/mL (4.5x$10^4$ cells/cm2) in a 1:1 mix of HPAEpiC and HPMEC media, and rested for 3 h at 37°C and 5% CO2. Transwell inserts were turned apical side up and HPAEpiC were seeded on the apical side at a concentration of 3 x $10^5$ cells/mL (9x $10^4$ cells/cm2) in a 1:1 mix of HPAEpiC and HPMEC media. After 24 h, media was removed from the upper compartment of the transwell insert, to allow primary epithelial cells to grow at the air-liquid interface. Media in the lower compartment was refreshed with a 1:1 mix of HPAEpiC and HPMEC media. Cells were permitted to grow to confluency for 14 days, with media in the lower compartment being refreshed every second day.

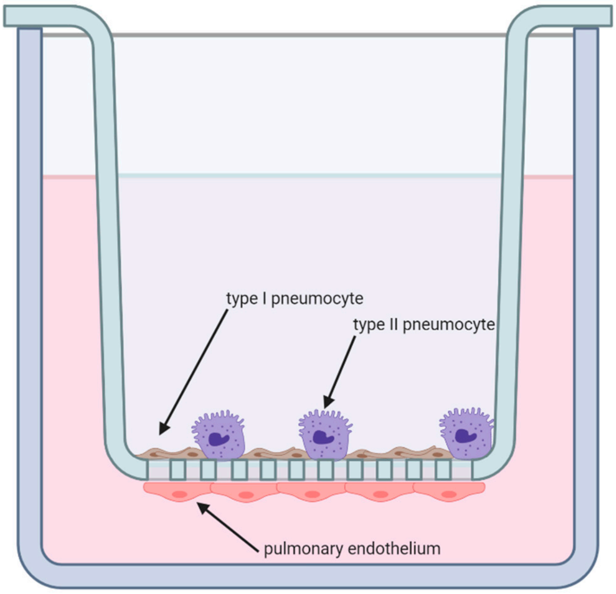

**Figure S2: Viral loads decrease during MRSA co-infection in the alveolar-capillary barrier model.** Supernatants were collected by addition of PBS to the apical surface of the alveolar epithelial cells and harvested for isolation of viral RNA prior to quantification by RT-qPCR. Error bars represent SEM calculated from at least three biological replicates.

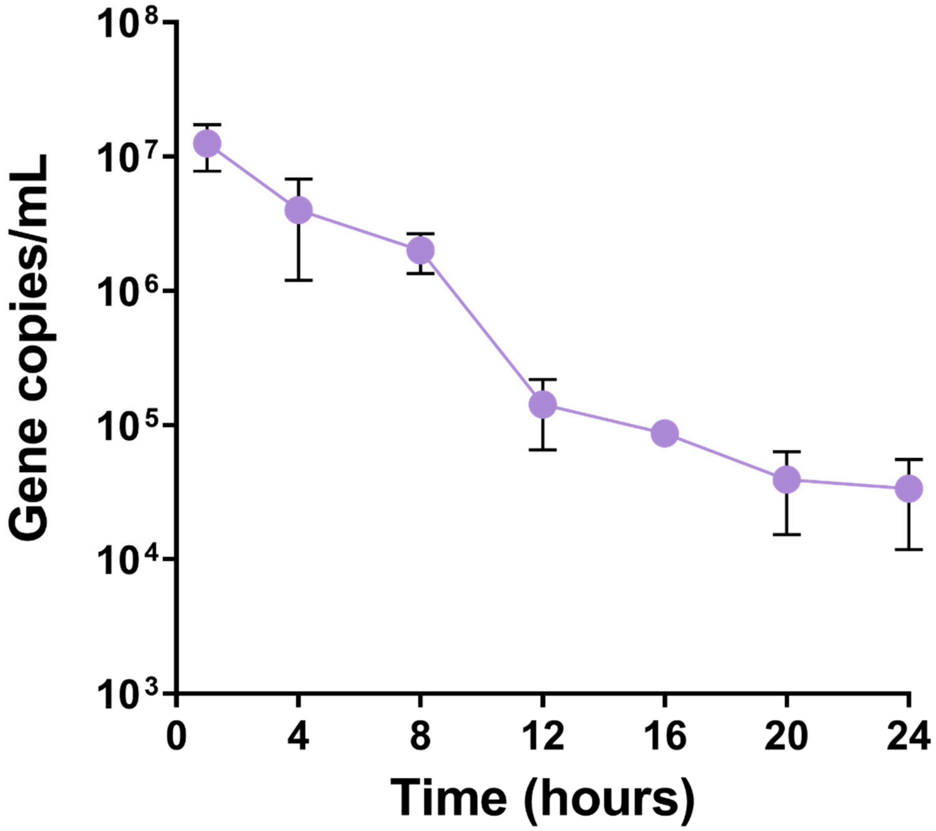

**Table S1: MRSA Virulence Factor Primer Sequences.** Primers were designed and selected using PrimerQuest.

| **Gene** | **Function** | **Primer Sequences (5′ to 3′)** |
|---|---|---|
| Coa | protects bacteria from phagocytosis by forming fibrin clots | F – TTCCACAGGGCACAATTACA<br>R-TCGGGACCTTGAACGATTTC |
| EbpS | binds elastin to facilitate colonization of injured tissues | F – GGTGAACCTGAACCGTAGTATT<br>R - CAGCAACAACAACGTCAAGG |
| Eno | forms plasmin to digest fibrin clots which keep the bacterium localized | F - TGGTTACAAACCAGGTGAAGAA<br>R - CGCCTTCGAACTTACTGTAGTC |
| FnbA | binds extracellular matrix components to mediate endothelial cell adhesion | F - CCCATTTCCGTTCGCTTTATTAC<br>R - GTAGGACATCCAGAGCAACTTTA |
| FnbB | binds fibronectin and elastin to mediate adhesion to endothelial cells | F - TGTCGCGCTGTATGATTGT<br>R - GTAGAGGAAAGTGGGAGTTCAG |
| Hla | forms pores in the cytoplasmic membrane resulting in lysis | F - CTGTAGCGAAGTCTGGTGAAA<br>R - AGATTCTTGGAACCCGGTATATG |
| HlgA | forms pores in the cytoplasmic membrane resulting in lysis | F - CCAGCAGCACGAGACTATTT<br>R - CACCTTTACCTCTTTCGTGTGA |
| IcaA | mediates intercellular adhesion and biofilm formation | F - GCAGTAGTTCTTGTCGCATTTC<br>R - GTTGGGTATTCCCTCTGTCTG |
| IcaB | mediates intercellular adhesion and biofilm formation | F - AGCCTATCCTTATGGCTTGATG<br>R - GAGTTCGGAGTGACTGCTTT |
| Sbi | mediates Fab-independent formation of IgG insoluble complexes | F - AGCCAACAAGTTTGGGTAGAA<br>R - CGTGTGGTGCTTTGTTATCTTG |
| Sek | enterotoxin with superantigen activity | F – ATCGACATCCAAATGGAATTTCTC<br>R - CTACACAGGAGATGATGGGTTAC |
| Seq | enterotoxin with superantigen activity | F -GTAGAAACCTCGTCTGTAGATATAGTG<br>R - GGAATTACGTTGGCGAATCAAA |
| Spa | forms IgG insoluble complexes to impede phagocytosis; binds airway epithelial cells | F – GCTGCACCTAAGGCTAATGATA<br>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 | Genes in InnateDB for this entity | Pathway up-regulated genes count | Pathway up-regulated p-value | Gene Symbols |
|---|---|---|---|---|---|
| Estrogen responsive protein efp controls cell cycle and breast tumors growth | 4 | 4 | 3 | 1.78E-04 | CDK1; CDK2; CDK6; CDK7; |
| Cyclin A/B1 associated events during G2/M transition | 5 | 5 | 3 | 4.35E-04 | CDC25A; CDK1; CDK2; CDK7; PPP2CA; |
| G1/S Transition | 6 | 6 | 3 | 8.50E-04 | CCNE1; CDC25A; CDK1; CDK2; CDK7; PPP2CA; |
| Cyclins and cell cycle regulation | 7 | 7 | 3 | 0.001452 | CCND1; CCNE1; CDC25A; CDK1; CDK2; CDK6; CDK7; |
| Mitotic G1-G1/S phases | 8 | 8 | 3 | 0.002268 | CCND1; CCNE1; CDC25A; CDK1; CDK2; CDK6; CDK7; PPP2CA; |
| G2/M Checkpoints | 3 | 3 | 2 | 0.003969 | CDC25A; CDK1; CDK2; |
| G2/M Transition | 10 | 10 | 3 | 0.004632 | CDC25A; CDK1; CDK2; CDK7; CSNK1D; CSNK1E; EP300; PPP1R12A; PPP2CA; PRKACA; |
| Mitotic G2-G2/M phases | 10 | 10 | 3 | 0.004632 | CDC25A; CDK1; CDK2; CDK7; CSNK1D; CSNK1E; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | EP300; PPP1R12A; PPP2CA; PRKACA; |
| Cell Cycle Checkpoints | 4 | 4 | 2 | 0.007759 | CCNE1; CDC25A; CDK1; CDK2; |
| Cyclin A:Cdk2-associated events at S phase entry | 4 | 4 | 2 | 0.007759 | CCNE1; CDC25A; CDK2; CDK7; |
| Cyclin E associated events during G1/S transition | 4 | 4 | 2 | 0.007759 | CCNE1; CDC25A; CDK2; CDK7; |
| D4gdi signaling pathway | 4 | 4 | 2 | 0.007759 | CASP1; CASP3; JUN; RHOA; |
| ERK1 activation | 4 | 4 | 2 | 0.007759 | CDK1; JAK1; JAK2; MAP2K1; |
| G0 and Early G1 | 4 | 4 | 2 | 0.007759 | CCNE1; CDC25A; CDK1; CDK2; |
| IRAK1 recruits IKK complex | 4 | 4 | 2 | 0.007759 | CHUK; PELI1; PELI2; TRAF6; |
| IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation | 4 | 4 | 2 | 0.007759 | CHUK; PELI1; PELI2; TRAF6; |
| Internal ribosome entry pathway | 4 | 4 | 2 | 0.007759 | CASP1; CASP3; CASP6; CASP8; |
| Regulation of cell cycle progression by plk3 | 4 | 4 | 2 | 0.007759 | CASP3; CASP6; CDK1; CHEK2; |
| p53 signaling pathway | 12 | 12 | 3 | 0.008093 | CASP3; CASP8; CCND1; CCNE1; CDK1; CDK2; CDK6; CHEK2; GADD45A; IGFBP3; PTEN; THBS1; |
| Cytokine Signaling in Immune system | 56 | 56 | 6 | 0.012262 | BLNK; CAMK2A; CAMK2D; CAMK2G; CASP1; CBL; CD44; CDK1; CHUK; CRK; CRKL; EIF2AK2; FYN; |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
|  |  |  |  |  | HRAS; IFNAR1; IL6ST; IL7R; IRF1; IRS1; JAK1; JAK2; LCK; LYN; MAP2K1; MAP2K2; MAP2K4; MAP3K3; MAP3K7; MAP3K8; MAPK1; NFKB1; NFKB2; PELI1; PELI2; PIK3CB; PIK3CD; PIK3R1; PIK3R2; PLCG1; PRKACA; PRKCD; PTK2B; PTPN1; RAF1; SHC1; SOCS3; SOS1; STAT1; STAT3; STAT5B; TAB1; TAB3; TOLLIP; TRAF6; YWHAB; YWHAZ; |
| E2F transcription factor network | 5 | 5 | 2 | 0.012642 | CCNE1; CDC25A; CDK1; CDK2; SIRT1; |
| Interferon alpha/beta signaling | 5 | 5 | 2 | 0.012642 | IFNAR1; IRF1; JAK1; PTPN1; SOCS3; |
| S Phase | 5 | 5 | 2 | 0.012642 | CCND1; CCNE1; CDC25A; CDK2; CDK7; |
| Signaling by Interleukins | 44 | 44 | 5 | 0.018475 | BLNK; CASP1; CBL; CDK1; CHUK; CRK; CRKL; FYN; HRAS; IL6ST; IL7R; JAK1; JAK2; LCK; LYN; MAP2K1; MAP2K2; MAP2K4; MAP3K3; MAP3K7; MAP3K8; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | MAPK1; NFKB1; NFKB2; PELI1; PELI2; PIK3CB; PIK3CD; PIK3R1; PIK3R2; PRKACA; PTK2B; RAF1; SHC1; SOCS3; SOS1; STAT3; STAT5B; TAB1; TAB3; TOLLIP; TRAF6; YWHAB; YWHAZ; |
| Degradation of the extracellular matrix | 6 | 6 | 2 | 0.018538 | CASP3; CD44; CTSB; CTSL1; CTSS; MMP8; |
| ERK activation | 6 | 6 | 2 | 0.018538 | CDK1; JAK1; JAK2; MAP2K1; MAP2K2; MAPK1; |
| TRAF6 mediated IRF7 activation | 6 | 6 | 2 | 0.018538 | EP300; IKBKE; IRF1; TBK1; TRAF2; TRAF6; |
| p73 transcription factor network | 6 | 6 | 2 | 0.018538 | ABL1; CDK2; CDK6; EP300; JAK1; SIRT1; |
| Cell cycle | 16 | 16 | 3 | 0.018709 | ABL1; CCND1; CCNE1; CDC25A; CDK1; CDK2; CDK6; CDK7; CHEK2; EP300; GADD45A; GSK3B; SMAD2; SMAD3; YWHAB; YWHAZ; |
| IFN-gamma pathway | 17 | 17 | 3 | 0.022178 | AKT1; CASP1; CBL; CEBPB; CRKL; DAPK1; IRF1; JAK1; JAK2; MAP2K1; MAP3K11; MAP3K1; MTOR; PIK3R1; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | PRKCD; STAT1; STAT3; |
| Caspase cascade in apoptosis | 7 | 7 | 2 | 0.025372 | BIRC3; CASP1; CASP3; CASP6; CASP8; PRF1; SREBF1; |
| Cell death signalling via NRAGE, NRIF and NADE | 7 | 7 | 2 | 0.025372 | CASP3; MAPK8; NGEF; NGFR; RAC1; SOS1; TRAF6; |
| Amyotrophic lateral sclerosis (ALS) | 8 | 8 | 2 | 0.033073 | CASP1; CASP3; CAT; MAP2K3; MAP3K5; MAPK14; RAB5A; RAC1; |
| FOXM1 transcription factor network | 8 | 8 | 2 | 0.033073 | CCND1; CDK1; CDK2; CHEK2; FOS; GSK3A; MAP2K1; NFATC3; |
| Retinoic acid receptors-mediated signaling | 8 | 8 | 2 | 0.033073 | AKT1; CDK1; CDK7; MAPK14; MAPK8; NCOA1; PRKACA; PRKCA; |
| MyD88 cascade initiated on plasma membrane | 35 | 35 | 4 | 0.035765 | APP; ATF2; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | RPS6KA5; TAB1; TAB3; TLR5; TRAF6; |
| Toll Like Receptor 10 (TLR10) Cascade | 35 | 35 | 4 | 0.035765 | APP; ATF2; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TLR5; TRAF6; |
| Toll Like Receptor 5 (TLR5) Cascade | 35 | 35 | 4 | 0.035765 | APP; ATF2; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TLR5; TRAF6; |

| | | | | | |
|---|---|---|---|---|---|
| MyD88 dependent cascade initiated on endosome | 36 | 36 | 4 | 0.039263 | APP; ATF2; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TLR7; TLR8; TRAF6; |
| TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation | 36 | 36 | 4 | 0.039263 | APP; ATF2; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TLR7; TLR8; TRAF6; |

| | | | | | |
|---|---|---|---|---|---|
| Toll Like Receptor 7/8 (TLR7/8) Cascade | 36 | 36 | 4 | 0.039263 | APP; ATF2; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TLR7; TLR8; TRAF6; |
| Cell cycle: g1/s check point | 9 | 9 | 2 | 0.041573 | ABL1; CCND1; CCNE1; CDC25A; CDK1; CDK2; CDK6; GSK3B; SMAD3; |
| RAF/MAP kinase cascade | 9 | 9 | 2 | 0.041573 | CDK1; HRAS; JAK1; JAK2; MAP2K1; MAP2K2; MAPK1; RAF1; YWHAB; |
| Androgen Receptor | 37 | 37 | 4 | 0.042958 | AKT1; ATF2; CASP1; CASP3; CASP8; CAV1; CCND1; CCNE1; CDC25A; CDC37; CDK1; CDK7; CDK9; CREB1; CTNNB1; EGFR; EP300; GAPDH; GSK3B; HSP90B1; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | HSPA4; HSPA5; HSPA8; HSPB1; IL6ST; JUN; NCOA1; PIK3R1; PIK3R2; PTEN; PTK2; PXN; SIRT1; SMAD3; SRC; STAT3; STUB1; |
| MyD88:Mal cascade initiated on plasma membrane | 37 | 37 | 4 | 0.042958 | APP; ATF2; BTK; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TIRAP; TLR6; TRAF6; |
| Toll Like Receptor 2 (TLR2) Cascade | 37 | 37 | 4 | 0.042958 | APP; ATF2; BTK; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
|  |  |  |  |  | NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TIRAP; TLR6; TRAF6; |
| Toll Like Receptor 9 (TLR9) Cascade | 37 | 37 | 4 | 0.042958 | APP; ATF2; CDK1; CHUK; CREB1; DUSP6; EEA1; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TLR7; TLR8; TRAF6; |
| Toll Like Receptor TLR1:TLR2 Cascade | 37 | 37 | 4 | 0.042958 | APP; ATF2; BTK; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TIRAP; TLR6; TRAF6; |
| Toll Like Receptor TLR6:TLR2 Cascade | 37 | 37 | 4 | 0.042958 | APP; ATF2; BTK; CDK1; CHUK; CREB1; DUSP6; FOS; JAK1; JAK2; JUN; MAP2K1; MAP2K2; MAP2K3; MAP2K4; MAP3K1; MAP3K7; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; NFKB1; NFKB2; NFKBIA; PELI1; PELI2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; TAB1; TAB3; TIRAP; TLR6; TRAF6; |
| Cell Cycle | 22 | 22 | 3 | 0.044538 | CCND1; CCNE1; CDC25A; CDK1; CDK2; CDK6; CDK7; CSNK1D; CSNK1E; CSNK2A1; CSNK2A2; EP300; LPIN1; LPIN2; LPIN3; MAPK1; PPP1R12A; PPP2CA; PPP2R5D; PRKACA; PRKCA; TAOK1; |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| Cell Cycle, Mitotic | 22 | 22 | 3 | 0.044538 | CCND1; CCNE1; CDC25A; CDK1; CDK2; CDK6; CDK7; CSNK1D; CSNK1E; CSNK2A1; CSNK2A2; EP300; LPIN1; LPIN2; LPIN3; MAPK1; PPP1R12A; PPP2CA; PPP2R5D; PRKACA; PRKCA; TAOK1; |

**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** | **Genes in InnateDB for this entity** | **Pathway up-regulated genes count** | **Pathway up-regulated p-value** | **Gene Symbols** |
|---|---|---|---|---|---|
| IFN-gamma pathway | 17 | 17 | 4 | 4.66E-04 | AKT1; CASP1; CBL; CEBPB; CRKL; DAPK1; IRF1; JAK1; JAK2; MAP2K1; MAP3K11; MAP3K1; MTOR; PIK3R1; PRKCD; STAT1; STAT3; |
| D4gdi signaling pathway | 4 | 4 | 2 | 0.003405 | CASP1; CASP3; JUN; RHOA; |
| Internal ribosome entry pathway | 4 | 4 | 2 | 0.003405 | CASP1; CASP3; CASP6; CASP8; |
| Cytokine Signaling in Immune system | 56 | 56 | 5 | 0.007846 | BLNK; CAMK2A; CAMK2D; CAMK2G; CASP1; CBL; CD44; CDK1; CHUK; CRK; CRKL; EIF2AK2; FYN; HRAS; IFNAR1; IL6ST; IL7R; IRF1; IRS1; JAK1; JAK2; LCK; LYN; MAP2K1; MAP2K2; MAP2K4; MAP3K3; MAP3K7; MAP3K8; MAPK1; NFKB1; NFKB2; PELI1; PELI2; PIK3CB; PIK3CD; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | PIK3R1; PIK3R2; PLCG1; PRKACA; PRKCD; PTK2B; PTPN1; RAF1; SHC1; SOCS3; SOS1; STAT1; STAT3; STAT5B; TAB1; TAB3; TOLLIP; TRAF6; YWHAB; YWHAZ; |
| Caspase cascade in apoptosis | 7 | 7 | 2 | 0.011422 | BIRC3; CASP1; CASP3; CASP6; CASP8; PRF1; SREBF1; |
| Amyotrophic lateral sclerosis (ALS) | 8 | 8 | 2 | 0.015016 | CASP1; CASP3; CAT; MAP2K3; MAP3K5; MAPK14; RAB5A; RAC1; |
| Signaling by FGFR1 mutants | 9 | 9 | 2 | 0.019035 | BCR; FGF20; FGFR1; FGFR1OP2; PIK3R1; PLCG1; STAT1; STAT3; STAT5B; |
| Oncostatin M | 27 | 27 | 3 | 0.025447 | AKT1; CASP3; CDK2; CEBPB; EP300; FOS; GRB2; HRAS; IL6ST; IRS1; JAK1; JAK2; MAPK1; MTOR; NFKB1; NFKBIA; PIK3R1; PTK2B; PXN; RAF1; SHC1; SOCS3; SOS1; SRC; STAT1; STAT3; STAT5B; |
| Factors involved in megakaryocyte | 11 | 11 | 2 | 0.02827 | ABL1; CDK2; DOCK6; EP300; IRF1; JAK2; |

| | | | | | |
|---|---|---|---|---|---|
| development and platelet production | | | | | KIF15; PRKACA; PRKAR1B; RAB5A; RAC1; |
| Pathways in cancer | 77 | 77 | 5 | 0.030483 | ABL1; AKT1; AKT3; BCR; BIRC3; BRAF; CASP3; CASP8; CBL; CCND1; CCNE1; CDK2; CDK6; CHUK; CKS2; CRK; CRKL; CSF1R; CTNNB1; DAPK1; EGFR; EP300; ETS1; FGF20; FGFR1; FGFR2; FGFR3; FLT3; FOS; FZD1; GRB2; GSK3B; HIF1A; HRAS; HSP90AB1; HSP90B1; ITGA6; JAK1; JUN; KIT; LEF1; MAP2K1; MAP2K2; MAPK1; MAPK8; MET; MTOR; NFKB1; NFKB2; NFKBIA; NOS2; PDGFRA; PDGFRB; PIK3CB; PIK3CD; PIK3CG; PIK3R1; PIK3R2; PLCG1; PLCG2; PPARG; PRKCA; PTEN; PTK2; RAC1; RAF1; RASSF5; RHOA; SMAD2; SMAD3; SOS1; STAT1; STAT3; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | STAT5B; TGFBR1; TRAF2; TRAF6; |
| Glucocorticoid receptor regulatory network | 12 | 12 | 2 | 0.033448 | AKT1; CREB1; FKBP5; FOS; GSK3B; IRF1; JUN; MAPK8; NCOA1; NFATC1; NFKB1; STAT1; |
| p53 signaling pathway | 12 | 12 | 2 | 0.033448 | CASP3; CASP8; CCND1; CCNE1; CDK1; CDK2; CDK6; CHEK2; GADD45A; IGFBP3; PTEN; THBS1; |
| Interferon Signaling | 14 | 14 | 2 | 0.044833 | CAMK2A; CAMK2D; CAMK2G; CD44; EIF2AK2; IFNAR1; IRF1; JAK1; JAK2; PLCG1; PRKCD; PTPN1; SOCS3; STAT1; |

**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** | **Genes in InnateDB for this entity** | **Pathway up-regulated genes count** | **Pathway up-regulated p-value** | **Gene Symbols** |
|---|---|---|---|---|---|
| Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | 4 | 4 | 2 | 1.59E-04 | IGFBP1; IGFBP2; IGFBP3; IGFBP5; |
| Metabolism of proteins | 20 | 20 | 2 | 0.004914 | ACO2; ATP5B; CS; EIF2AK3; EIF4EBP1; GSK3A; HSP90B1; HSPA5; HSPA9; HSPD1; IGFBP1; IGFBP2; IGFBP3; IGFBP5; PDIA3; PGM3; PROS1; RPLP2; SHC1; THBS1; |
| IGF1 signaling pathway | 22 | 22 | 2 | 0.005958 | AKT1; AKT3; BRAF; GRB2; HRAS; IGFBP1; IGFBP2; IGFBP3; IGFBP5; IRS1; MAP2K1; MAP2K2; MAPK1; PDPK1; PIK3CB; PIK3CD; PIK3R1; PIK3R2; RAF1; SHC1; SHC3; SOS1; |
| Interleukin-1 processing | 3 | 3 | 1 | 0.018828 | CASP1; NFKB1; NFKB2; |

| | | | | | |
|---|---|---|---|---|---|
| PERK regulates gene expression | 3 | 3 | 1 | 0.018828 | EIF2AK3; HSPA5; IGFBP1; |
| D4gdi signaling pathway | 4 | 4 | 1 | 0.025051 | CASP1; CASP3; JUN; RHOA; |
| Internal ribosome entry pathway | 4 | 4 | 1 | 0.025051 | CASP1; CASP3; CASP6; CASP8; |
| Cellular roles of Anthrax toxin | 5 | 5 | 1 | 0.031248 | CASP1; MAP2K1; MAP2K2; MAP2K3; MAP2K4; |
| Inflammasomes | 5 | 5 | 1 | 0.031248 | APP; CASP1; HSP90AB1; NLRP3; PSTPIP1; |
| The NLRP3 inflammasome | 5 | 5 | 1 | 0.031248 | APP; CASP1; HSP90AB1; NLRP3; PSTPIP1; |
| Cytosolic DNA-sensing pathway | 6 | 6 | 1 | 0.037418 | CASP1; CHUK; IKBKE; NFKB1; NFKBIA; TBK1; |
| Unfolded Protein Response (UPR) | 6 | 6 | 1 | 0.037418 | EIF2AK3; GSK3A; HSP90B1; HSPA5; IGFBP1; SHC1; |
| Caspase cascade in apoptosis | 7 | 7 | 1 | 0.043562 | BIRC3; CASP1; CASP3; CASP6; CASP8; PRF1; SREBF1; |
| FOXA2 and FOXA3 transcription factor networks | 7 | 7 | 1 | 0.043562 | ACADM; AKT1; ALDOB; CREB1; HADH; IGFBP1; PKLR; |
| Amyotrophic lateral sclerosis (ALS) | 8 | 8 | 1 | 0.04968 | CASP1; CASP3; CAT; MAP2K3; MAP3K5; MAPK14; RAB5A; RAC1; |

**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 | Genes in InnateDB for this entity | Pathway up-regulated genes count | Pathway up-regulated p-value | Gene Symbols |
|---|---|---|---|---|---|
| Hedgehog 'off' state | 4 | 4 | 3 | 7.05E-04 | CSNK1A1; GSK3B; PRKACA; PRKAR1B; |
| Signaling by Hedgehog | 4 | 4 | 3 | 7.05E-04 | CSNK1A1; GSK3B; PRKACA; PRKAR1B; |
| Hedgehog signaling pathway | 6 | 6 | 3 | 0.003249 | CSNK1A1; CSNK1D; CSNK1E; CSNK1G1; GSK3B; PRKACA; |
| Class I MHC mediated antigen processing & presentation | 8 | 8 | 3 | 0.008394 | CTSL1; CTSS; HSPA5; NCF1; PDIA3; SOCS3; STUB1; TRIM36; |
| Degradation of GLI2 by the proteasome | 3 | 3 | 2 | 0.009664 | CSNK1A1; GSK3B; PRKACA; |
| GLI3 is processed to GLI3R by the proteasome | 3 | 3 | 2 | 0.009664 | CSNK1A1; GSK3B; PRKACA; |
| Transcription factor creb and its extracellular signals | 17 | 17 | 4 | 0.013452 | AKT1; CAMK2A; CAMK2D; CAMK2G; CREB1; GRB2; HRAS; MAPK1; MAPK14; PDPK1; PIK3R1; PRKAR1B; PRKCA; RPS6KA1; RPS6KA5; SHC1; SOS1; |
| Cellular responses to stress | 36 | 36 | 6 | 0.013505 | CAMK2A; CAMK2D; |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
|  |  |  |  |  | CAMK2G; CAT; CCNE1; CDK2; CDK6; CEBPB; EP300; ETS1; FOS; GSK3B; HIF1A; HSP90AB1; HSPA8; IGFBP7; JUN; MAP2K3; MAP2K4; MAP3K5; MAPK1; MAPK14; MAPK8; MAPKAPK2; MAPKAPK3; MAPKAPK5; MLST8; MTOR; NFKB1; PRDX2; RPS6KA1; RPS6KA3; RPTOR; SIRT1; STAT3; TNIK; |
| VEGFR3 signaling in lymphatic endothelium | 10 | 10 | 3 | 0.016598 | AKT1; CREB1; CRK; FLT4; GRB2; MAP2K4; PIK3R1; RPS6KA1; SHC1; SOS1; |
| Antigen processing-cross presentation | 4 | 4 | 2 | 0.018624 | CTSL1; CTSS; NCF1; PDIA3; |
| Beta-catenin phosphorylation cascade | 4 | 4 | 2 | 0.018624 | CSNK1A1; GSK3B; PPP2CA; PPP2R5D; |
| Circadian Clock | 11 | 11 | 3 | 0.021926 | ATF2; CPT1A; CREB1; CSNK1D; CSNK1E; EP300; HIF1A; NCOA1; PPARA; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | PPARGC1A; SREBF1; |
| Factors involved in megakaryocyte development and platelet production | 11 | 11 | 3 | 0.021926 | ABL1; CDK2; DOCK6; EP300; IRF1; JAK2; KIF15; PRKACA; PRKAR1B; RAB5A; RAC1; |
| CREB phosphorylation | 5 | 5 | 2 | 0.029912 | CREB1; MAPKAPK2; RPS6KA1; RPS6KA3; RPS6KA5; |
| Tnfr1 signaling pathway | 5 | 5 | 2 | 0.029912 | BIRC3; CASP3; CASP8; MAP2K4; TRAF2; |
| Role of Calcineurin-dependent NFAT signaling in lymphocytes | 13 | 13 | 3 | 0.035082 | CASP3; CSNK1A1; CSNK2A1; GSK3B; MAP3K1; MAP3K8; MAPK14; MAPK8; NFATC1; NFATC2; NFATC3; PIM1; PRKACA; |
| Signaling by Wnt | 23 | 23 | 4 | 0.039044 | AKT1; AP2M1; ARRB2; CAMK2A; CAV1; CSNK1A1; CSNK1E; CSNK2A1; CSNK2A2; CTNNB1; EP300; FZD1; GSK3B; LEF1; MAP3K7; NFATC1; PLCB1; PPP2CA; PPP2R5D; PRKCA; RAC1; RHOA; YWHAZ; |

| | | | | | |
|---|---|---|---|---|---|
| MAPK targets/ Nuclear events mediated by MAP kinases | 14 | 14 | 3 | 0.042903 | ATF2; CREB1; DUSP6; FOS; JUN; MAPK1; MAPK14; MAPK8; MAPKAPK2; PPP2CA; PPP2R5D; RPS6KA1; RPS6KA3; RPS6KA5; |
| P38 mapk signaling pathway | 14 | 14 | 3 | 0.042903 | ATF2; CREB1; HRAS; HSPB1; MAP2K4; MAP3K1; MAP3K5; MAPK14; MAPKAPK2; MAPKAPK5; MKNK1; RAC1; RPS6KA5; STAT1; |
| RNF mutants show enhanced WNT signaling and proliferation | 14 | 14 | 3 | 0.042903 | AKT1; CAV1; CSNK1A1; CSNK1E; CSNK2A1; CSNK2A2; CTNNB1; EP300; FZD1; GSK3B; LEF1; PPP2CA; PPP2R5D; YWHAZ; |
| Signaling by WNT in cancer | 14 | 14 | 3 | 0.042903 | AKT1; CAV1; CSNK1A1; CSNK1E; CSNK2A1; CSNK2A2; CTNNB1; EP300; FZD1; GSK3B; LEF1; PPP2CA; PPP2R5D; YWHAZ; |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| TCF dependent signaling in response to WNT | 14 | 14 | 3 | 0.042903 | AKT1; CAV1; CSNK1A1; CSNK1E; CSNK2A1; CSNK2A2; CTNNB1; EP300; FZD1; GSK3B; LEF1; PPP2CA; PPP2R5D; YWHAZ; |
| XAV939 inhibits tankyrase, stabilizing AXIN | 14 | 14 | 3 | 0.042903 | AKT1; CAV1; CSNK1A1; CSNK1E; CSNK2A1; CSNK2A2; CTNNB1; EP300; FZD1; GSK3B; LEF1; PPP2CA; PPP2R5D; YWHAZ; |
| misspliced LRP5 mutants have enhanced beta-catenin-dependent signaling | 14 | 14 | 3 | 0.042903 | AKT1; CAV1; CSNK1A1; CSNK1E; CSNK2A1; CSNK2A2; CTNNB1; EP300; FZD1; GSK3B; LEF1; PPP2CA; PPP2R5D; YWHAZ; |
| AMER1 mutants destabilize the destruction complex | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| APC truncation mutants are not K63 polyubiquitinated | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| APC truncation mutants have impaired AXIN binding | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | LEF1; PPP2CA; PPP2R5D; |
| AXIN missense mutants destabilize the destruction complex | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| AXIN mutants destabilize the destruction complex, activating WNT signaling | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Degradation of beta-catenin by the destruction complex | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Degradation of the extracellular matrix | 6 | 6 | 2 | 0.043243 | CASP3; CD44; CTSB; CTSL1; CTSS; MMP8; |
| S33 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| S37 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| S45 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Stathmin and breast cancer resistance to antimicrotubule agents | 6 | 6 | 2 | 0.043243 | CAMK2A; CAMK2D; CAMK2G; CDK1; PRKAR1B; STMN1; |

| | | | | | |
|---|---|---|---|---|---|
| T41 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| TCF7L2 mutants don't bind CTBP | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| deletions in the AMER1 gene destabilize the destruction complex | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| deletions in the AXIN genes in hepatocellular carcinoma result in elevated WNT signaling | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| misspliced GSK3beta mutants stabilize beta-catenin | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| phosphorylation site mutants of CTNNB1 are not targeted to the proteasome by the destruction complex | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| truncated APC mutants destabilize the destruction complex | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| truncations of AMER1 destabilize the destruction complex | 6 | 6 | 2 | 0.043243 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |

**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** | **Genes in InnateDB for this entity** | **Pathway up-regulated genes count** | **Pathway up-regulated p-value** | **Gene Symbols** |
|---|---|---|---|---|---|
| Pyruvate metabolism | 4 | 4 | 2 | 0.007759 | LDHA; LDHB; PDK1; PDK4; |

**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 | Genes in InnateDB for this entity | Pathway up-regulated genes count | Pathway up-regulated p-value | Gene Symbols |
|---|---|---|---|---|---|
| Hedgehog signaling pathway | 6 | 6 | 4 | 1.78E-04 | CSNK1A1; CSNK1D; CSNK1E; CSNK1G1; GSK3B; PRKACA; |
| Hedgehog 'off' state | 4 | 4 | 3 | 8.70E-04 | CSNK1A1; GSK3B; PRKACA; PRKAR1B; |
| Signaling by Hedgehog | 4 | 4 | 3 | 8.70E-04 | CSNK1A1; GSK3B; PRKACA; PRKAR1B; |
| Degradation of GLI2 by the proteasome | 3 | 3 | 2 | 0.011089 | CSNK1A1; GSK3B; PRKACA; |
| GLI3 is processed to GLI3R by the proteasome | 3 | 3 | 2 | 0.011089 | CSNK1A1; GSK3B; PRKACA; |
| Metabolism of lipids and lipoproteins | 3 | 3 | 2 | 0.011089 | Dgat1; Fdx1; Ptgs2; |
| PKA-mediated phosphorylation of CREB | 3 | 3 | 2 | 0.011089 | CREB1; PRKACA; PRKAR1B; |
| Transcription regulation by methyltransferase of carm1 | 3 | 3 | 2 | 0.011089 | CREB1; EP300; PRKAR1B; |
| Beta-catenin phosphorylation cascade | 4 | 4 | 2 | 0.021308 | CSNK1A1; GSK3B; PPP2CA; PPP2R5D; |
| CREB phosphorylation through the activation of CaMKII | 4 | 4 | 2 | 0.021308 | CAMK2A; CAMK2D; CAMK2G; CREB1; |
| CRMPs in Sema3A signaling | 4 | 4 | 2 | 0.021308 | DPYSL2; DPYSL3; FYN; GSK3B; |
| GPCR Dopamine D1like receptor signaling pathway | 4 | 4 | 2 | 0.021308 | CREB1; PPP2R5D; PRKACA; PRKAR1B; |

| | | | | | |
|---|---|---|---|---|---|
| Metabolism | 4 | 4 | 2 | 0.021308 | Dgat1; Fdx1; Pfkfb1; Ptgs2; |
| Presenilin action in Notch and Wnt signaling | 12 | 12 | 3 | 0.033806 | CCND1; CSNK1A1; CSNK2A1; CTNNB1; FOS; FZD1; GSK3B; JUN; MAP3K7; MAPK1; PPP2R5D; TAB1; |
| Repression of pain sensation by the transcriptional regulator dream | 5 | 5 | 2 | 0.034124 | CREB1; PRKACA; PRKAR1B; PRKCA; PRKCD; |
| Vasopressin-regulated water reabsorption | 5 | 5 | 2 | 0.034124 | CREB1; PRKACA; PRKAR1B; PRKCA; PRKCD; |
| AMER1 mutants destabilize the destruction complex | 6 | 6 | 2 | 0.049193 | CREB1; FOS; JUN; PRKAR1B; RPS6KA3; |
| APC truncation mutants are not K63 polyubiquitinated | 6 | 6 | 2 | 0.049193 | CREB1; DYNC1LI1; PRKACA; RAB11A; RAB5A; |
| APC truncation mutants have impaired AXIN binding | 6 | 6 | 3 | 0.049193 | AKT1; CAMK2A; CCND1; CREB1; GRB2; GSK3B; PDPK1; PIK3R1; PLCG1; PRKCD; SHC1; SOS1; SRC; |
| AXIN missense mutants destabilize the destruction complex | 6 | 6 | 4 | 0.049193 | AKT1; AP2M1; ARRB2; CAMK2A; CAV1; CSNK1A1; CSNK1E; CSNK2A1; CSNK2A2; CTNNB1; EP300; FZD1; GSK3B; LEF1; MAP3K7; NFATC1; |

| | | | | | |
|---|---|---|---|---|---|
| | | | | | PLCB1; PPP2CA; PPP2R5D; PRKCA; RAC1; RHOA; YWHAZ; |
| AXIN mutants destabilize the destruction complex, activating WNT signaling | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Ca-calmodulin-dependent protein kinase activation | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Degradation of beta-catenin by the destruction complex | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| S33 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| S37 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| S45 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.049193 | CAMK2A; CAMK2D; CAMK2G; CAMKK1; CAMKK2; CREB1; |
| Stathmin and breast cancer resistance to antimicrotubule agents | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |

| | | | | | |
|---|---|---|---|---|---|
| T41 mutants of beta-catenin aren't phosphorylated | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| TCF7L2 mutants don't bind CTBP | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Deletions in the AMER1 gene destabilize the destruction complex | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Deletions in the AXIN genes in hepatocellular carcinoma result in elevated WNT signaling | 6 | 6 | 2 | 0.049193 | CAMK2A; CAMK2D; CAMK2G; CDK1; PRKAR1B; STMN1; |
| Misspliced GSK3beta mutants stabilize beta-catenin | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Phosphorylation site mutants of CTNNB1 are not targeted to the proteasome by the destruction complex | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Truncated APC mutants destabilize the destruction complex | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |
| Truncations of AMER1 destabilize the destruction complex | 6 | 6 | 2 | 0.049193 | CSNK1A1; CTNNB1; GSK3B; LEF1; PPP2CA; PPP2R5D; |