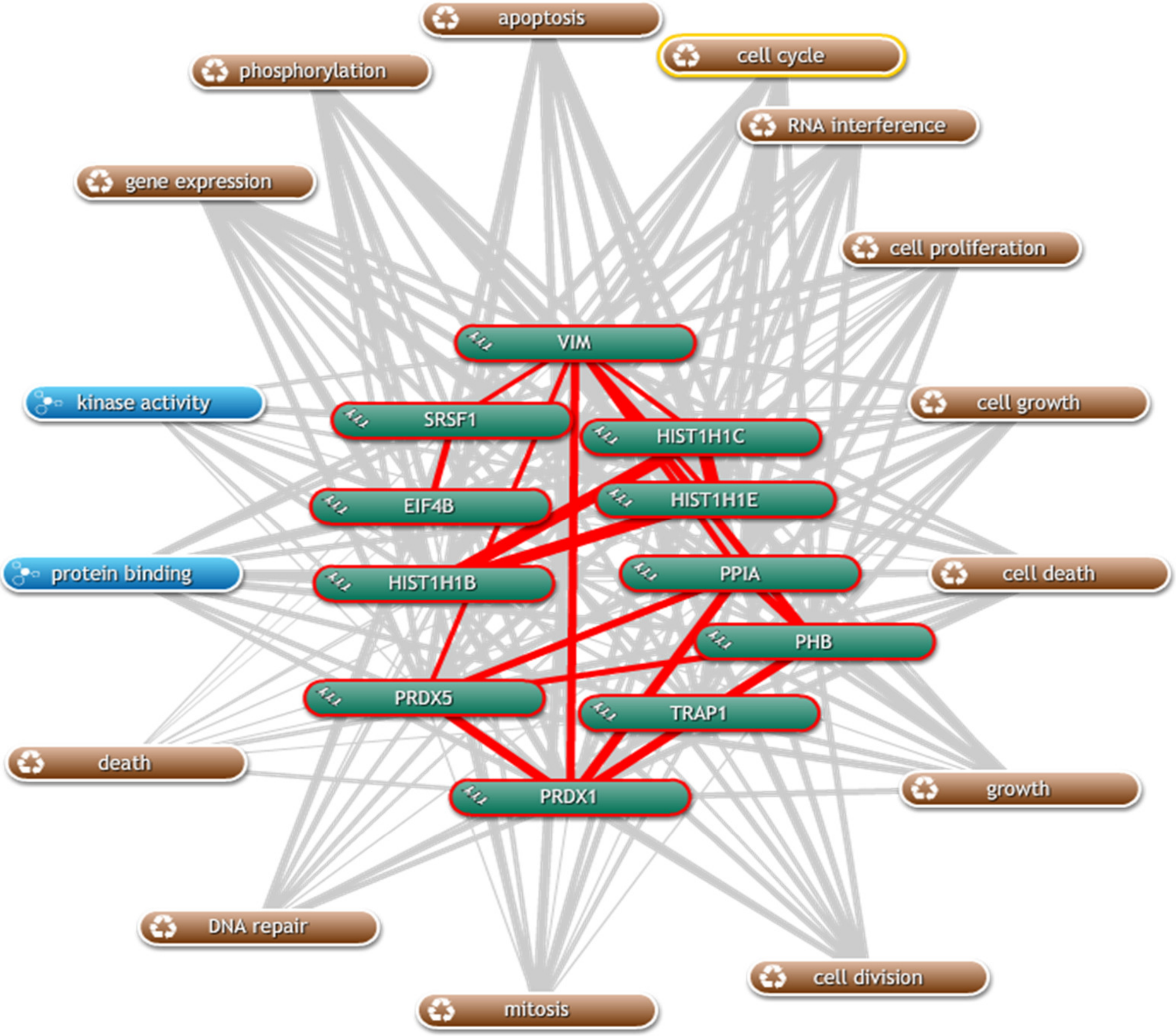
## Figure – S1

## Gene network mining of downregulated proteins during co-infection of *Filifactor alocis* with *P. gingivalis*

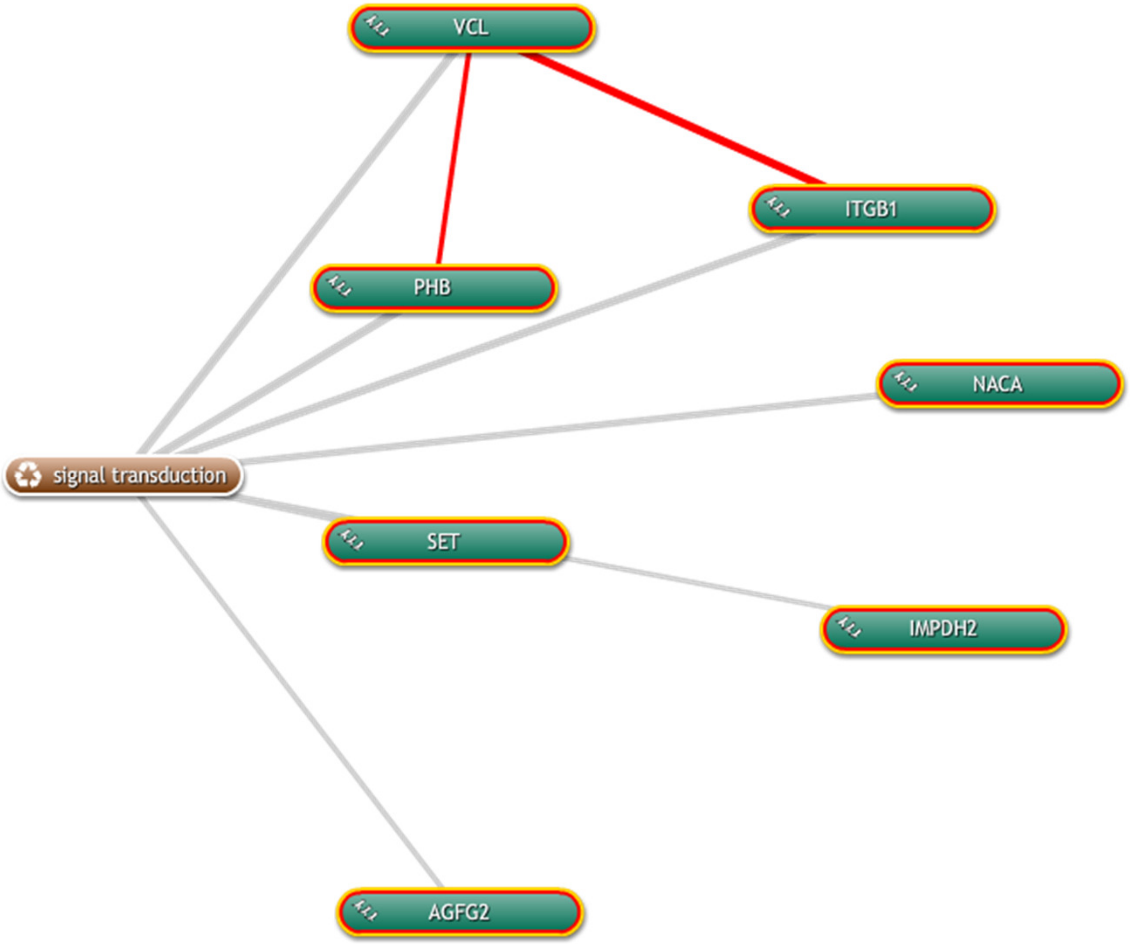


## Figure – S1
## Gene network mining of downregulated proteins during co-infection.

Gene network based host proteome data (down regulated proteins)during co-infection of *Filifactor alocis* with *P. gingivalis* mining showing modulation of vital host cellular processes.

# Figure – S2

# Gene network mining of upregulated proteins during co-infection of *Filifactor alocis* with *P. gingivalis*



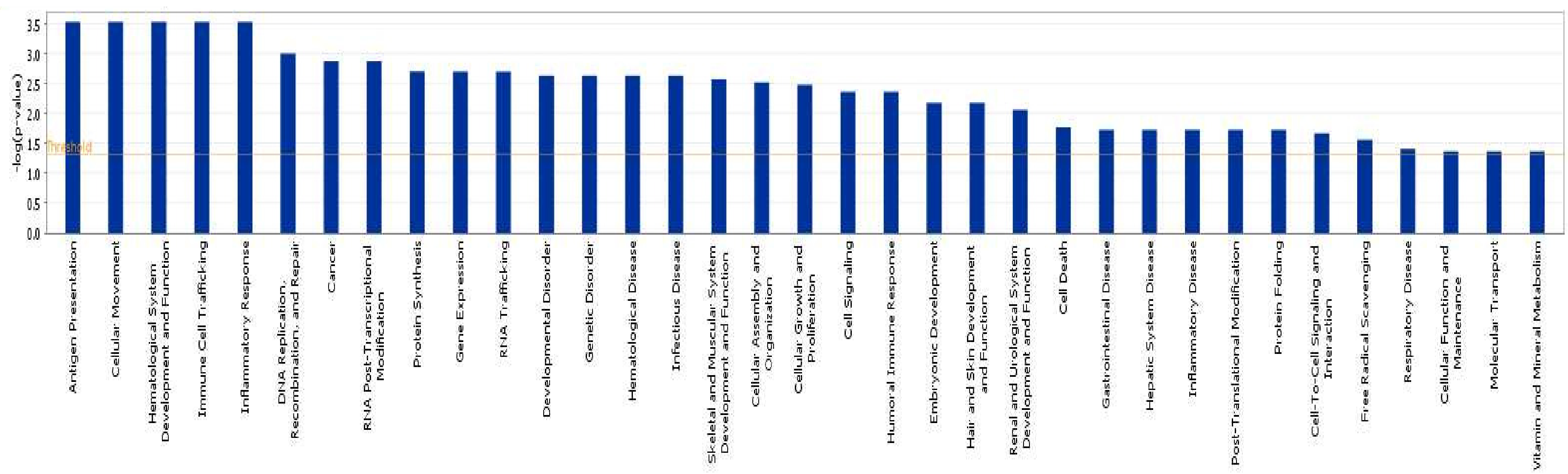
## Figure – S2

**Gene network mining of upregulated proteins during co-infection**.

Gene network based host proteome data (upregulated proteins)during co-infection of *Filifactor alocis* with *P. gingivalis* mining showing modulation of vital host cellular processes.

## Figure – S3.

## Eukaryotic proteins upregulated during *F. alocis* co culture with *P. gingivalis* Vs monoculture



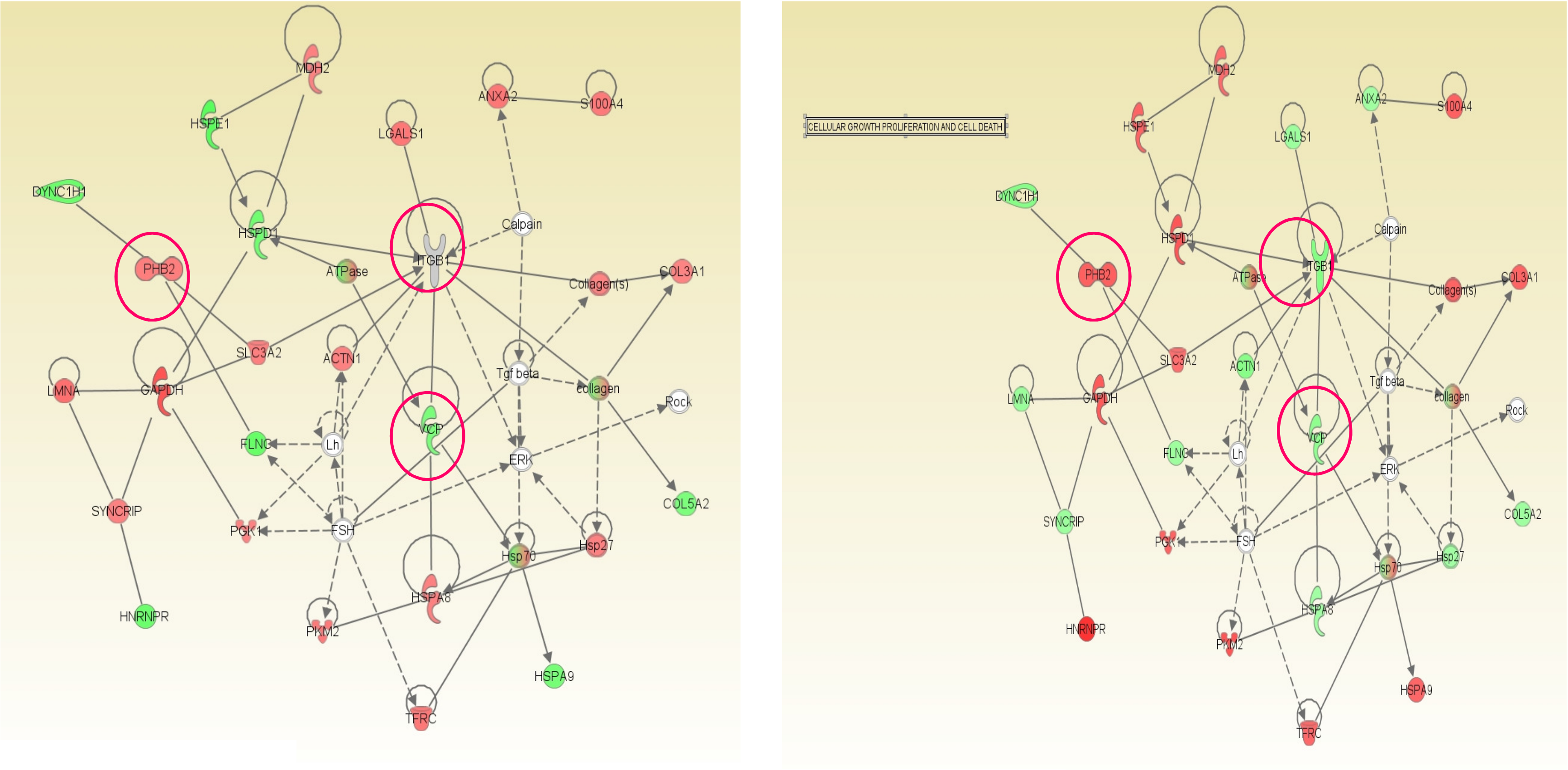
## Figure – S3.

## Eukaryotic proteins upregulated during *F. alocis* co culture with *P. gingivalis* Vs monoculture.

Ingenuity pathway analysis showed increased expression of eukaryotic genes involved in antigen presentation, cellular movement, hematological system, cell trafficking and inflammatory response

**Figure – S4**

**Co-infection of *Filifactor alocis* with *P. gingivalis* show upregulation of proteins involved in cell growth and proliferation pathway**



Monoculture

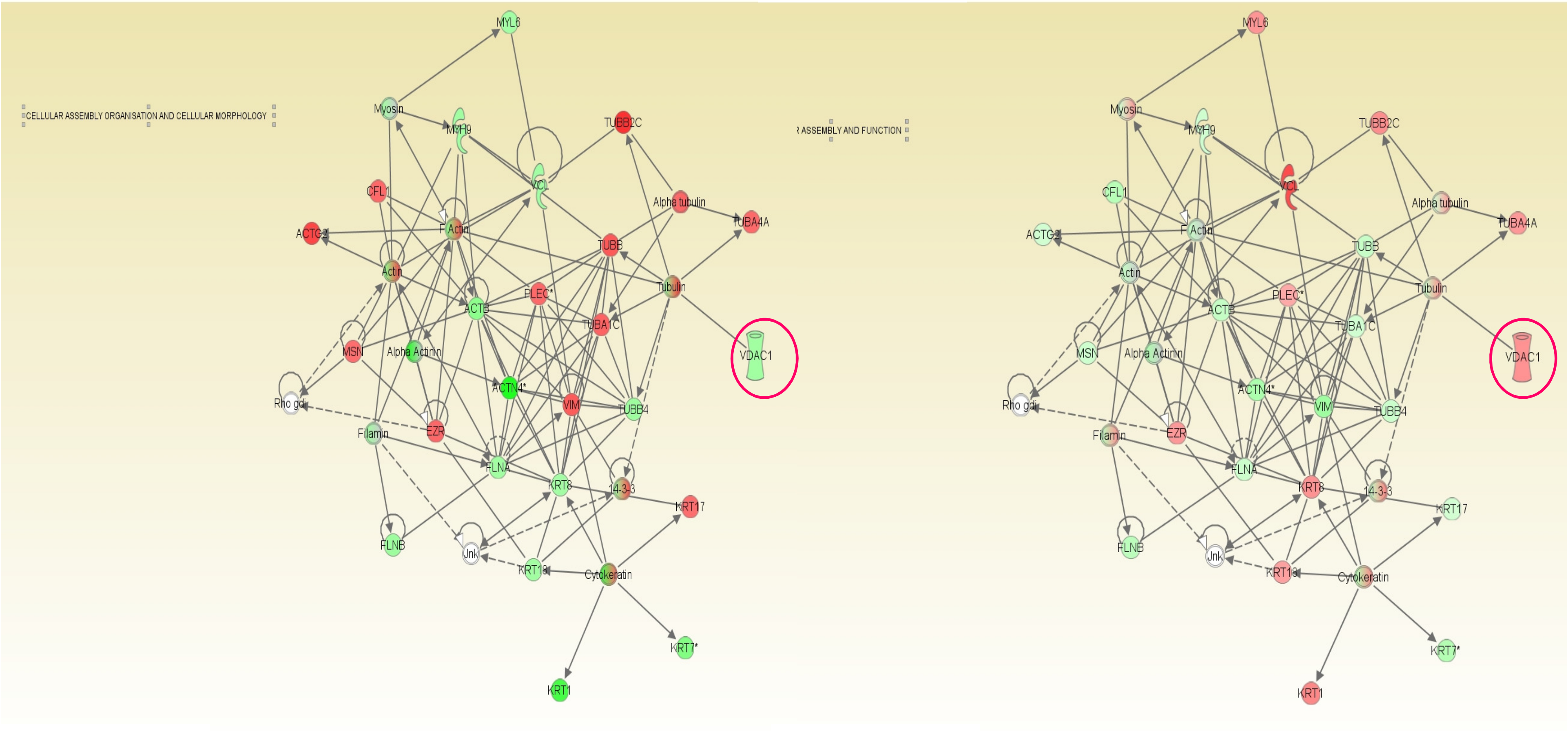
Co-culture

## Figure – S4

## Co-infection of *Filifactor alocis* with *P. gingivalis* show upregulation of proteins involved in cell growth and proliferation pathway.

Analysis of the host proteome data showed downregulation of proteins involved in cytoskeleton integrity and ubiquitin dependent protein degradation. Proteins involved in negative regulation of cell proliferation were upregulated.

## Figure – S5
## Co-infection of *Filifactor alocis* with *P. gingivalis* show modulation of proteins involved in cellular assembly and organization pathways.



Monoculture

Co-culture

**Figure – S5.**

**Co-infection of *Filifactor alocis* with *P. gingivalis* show modulation of proteins involved in cellular assembly and organization pathways**.

Analysis of the host proteome data showed modulation of many cytoskeleton proteins such as VCL, VDAC1 and downregulation of many proteins involved in actin pathway.

**Figure – S6**
**Grandzyme mediated apoptic signaling pathway**

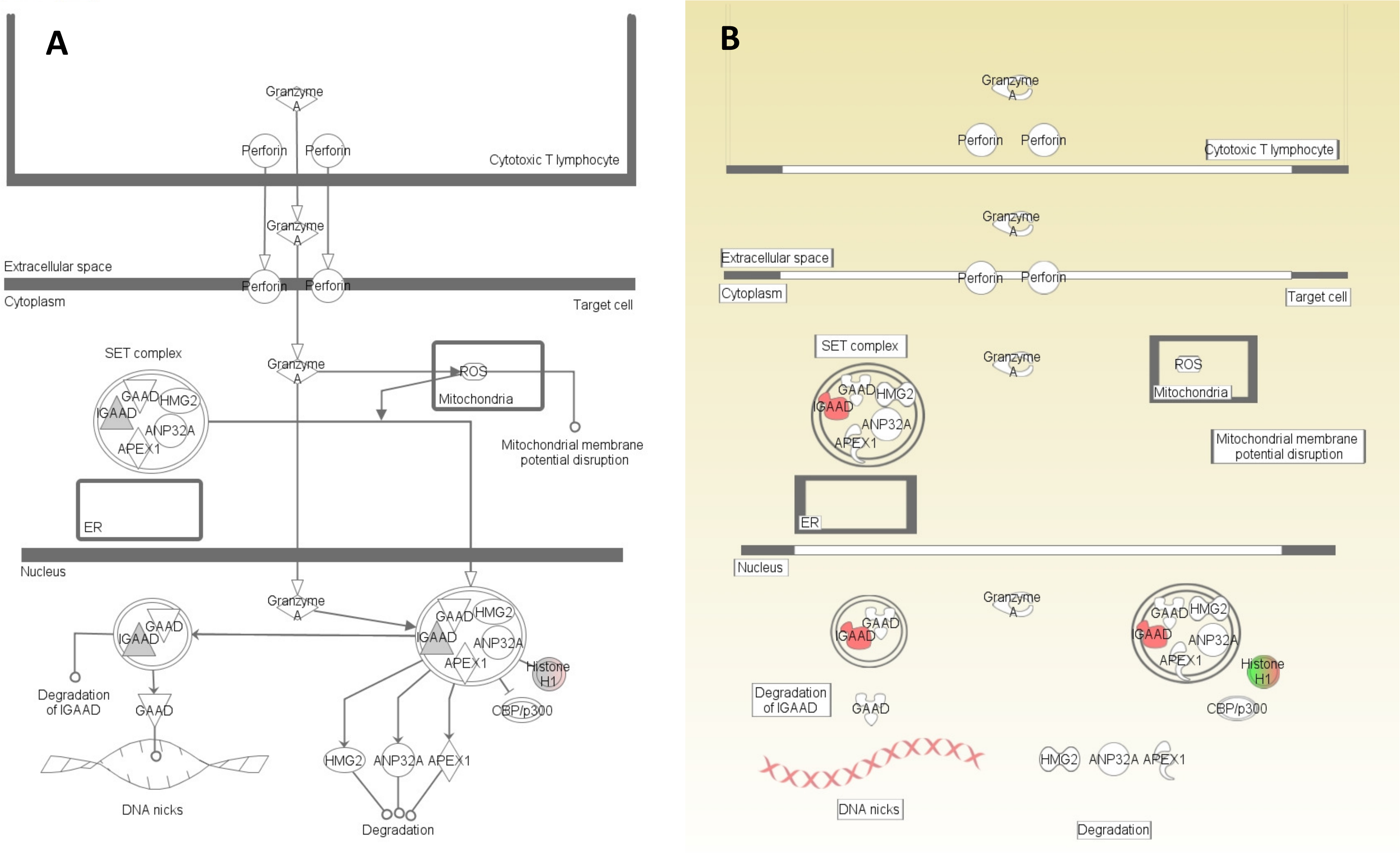


**Figure – S6**
**Grandzyme mediated apoptic signaling pathway.**

Coinfection of *F. alocis* with *P. gingivalis* showed upregulation of Grandzyme activating Dnase (GAAD) and downregulation of Histone proteins.

# Table –S1

## Fold change of host cell proteins during *F. alocis* co-infection with *P. gingivalis*.

| | Annotation |
|---:|---|
| **2.539** | HMPREF0389_01563 ABC transporter, ATP-binding protein |
| 1.446 | HMPREF0389_00656 superfamily II DNA and RNA helicase |
| **2.390** | HMPREF0389_00454 HPr(Ser) kinase/phosphatase |
| 1.493 | HMPREF0389_01289 pyridine nucleotide-disulfide oxidoreductase |
| **1.697** | HMPREF0389_00494 phosphoribosylformylglycinamidine synthase |
| **1.627** | HMPREF0389_00388 site-specific recombinase, phage integrase family |
| **1.596** | HMPREF0389_00002 pyruvate, water dikinase |
| **2.368** | HMPREF0389_00247 hypothetical protein |
| **2.730** | HMPREF0389_00647 protein=ABC transporter, ATP-binding protein |
| **3.242** | HMPREF0389_00372 protein=DNA primase |
| **1.516** | HMPREF0389_00571 DNA mismatch repair protein MutS |
| 1.254 | HMPREF0389_01226 MmcQ protein |
| 1.181 | HMPREF0389_01110 cell wall-associated serine proteinase PrtA |
| **1.642** | HMPREF0389_00174 nickase |
| 1.465 | HMPREF0389_00544 GTP pyrophosphokinase |
| 1.311 | HMPREF0389_01004 primosomal protein N' |
| **0.573** | HMPREF0389_00932 oxidoreductase, 2-nitropropane dioxygenase family |
| **1.577** | HMPREF0389_00408 hypothetical protein |
| **0.616** | HMPREF0389_01131 CTP synthase |
| 1.462 | HMPREF0389_00295 ribose ABC transporter, periplasmic ribose-binding protein |
| 0.739 | HMPREF0389_00303 penicillin-binding protein 2B |
| **0.627** | HMPREF0389_00255 membrane protein |
| 1.356 | HMPREF0389_01210 threonine--tRNA ligase |
| **2.192** | HMPREF0389_00231 DNA (cytosine-5-)-methyltransferase |
| 1.474 | HMPREF0389_01029 hypothetical protein |
| 0.751 | HMPREF0389_01580 leukotoxin translocation ATP-binding protein LktB |
| **1.963** | HMPREF0389_00966 Holliday junction resolvase |
| 1.334 | HMPREF0389_00724 ATP-dependent chaperone protein ClpB |
| **0.604** | HMPREF0389_00739 hypothetical protein |
| **0.634** | HMPREF0389_01414 transposase |
| 0.677 | HMPREF0389_00474 glutamate--ammonia ligase |
| **0.509** | HMPREF0389_00163 hypothetical protein |
| 1.477 | HMPREF0389_01037 non-structural glycoprotein |
| **1.521** | HMPREF0389_01416 DEAD/DEAH box helicase |
| 0.792 | HMPREF0389_00349 amidinotransferase family protein |
| 1.320 | HMPREF0389_00032 hypothetical protein |
| 1.436 | HMPREF0389_00553 septum site-determining protein MinD |

| | |
|---|---|
| 0.680 | HMPREF0389_01206 16S rRNA methyltransferase GidB |
| **2.066** | HMPREF0389_01347 S1 RNA binding domain protein |
| **1.559** | HMPREF0389_01031 hypothetical protein |
| **2.066** | HMPREF0389_01586 DNA replication protein DnaC |
| 1.327 | HMPREF0389_00605 dephospho-CoA kinase |
| **1.835** | HMPREF0389_00524 hypothetical protein |
| **0.630** | HMPREF0389_00439 ribulose-phosphate 3-epimerase |
| **2.188** | HMPREF0389_00707 transcription antitermination factor NusB |
| **1.519** | HMPREF0389_00807 oligopeptide ABC transporter permease OppC |
| 1.436 | HMPREF0389_00353 stage II sporulation protein E |
| 1.487 | HMPREF0389_00449 aminopeptidase, M18 family |
| **2.352** | HMPREF0389_01253 hypothetical protein |
| **0.587** | HMPREF0389_00415 fimbrial assembly protein PilN |
| **1.585** | HMPREF0389_01005 protein=hypothetical protein |
| 1.322 | HMPREF0389_00785 ABC transporter, ATP-binding protein |
| **1.506** | HMPREF0389_00123 DNA mismatch repair protein MutS |
| **1.666** | HMPREF0389_01596 electron transfer flavoprotein alpha subunit |
| **0.597** | HMPREF0389_01068 pyridoxal phosphate enzyme, YggS family |
| **0.507** | HMPREF0389_00855 50S ribosomal protein L11 |
| **0.487** | HMPREF0389_01525 tyrosine--tRNA ligase |
| **0.595** | HMPREF0389_00484 polysaccharide deacetylase family protein |
| 0.667 | HMPREF0389_00267 hypothetical protein |
| **0.574** | HMPREF0389_00246 antirestriction protein (ArdA) |
| 1.419 | HMPREF0389_00120 nitroreductase family protein |
| 1.485 | HMPREF0389_00380 NAD(FAD)-utilizing dehydrogenase |
| 0.552 | HMPREF0389_01358 leucyl aminopeptidase |
| 1.497 | HMPREF0389_00287 thiamine biosynthesis/tRNA modification protein ThiI |
| 1.095 | HMPREF0389_00901 cobalt import ATP-binding protein CbiO 1 |
| 1.367 | [gene=HMPREF0389_01246] [protein=methylated-DNA--protein-cysteine methyltransferase] [protein_id=EFE27994.1] [location=187220 |
| 1.831 | HMPREF0389_01616 cupin 2 domain-containing protein |
| 0.723 | HMPREF0389_01276 iron permease, FTR1 family |
| 0.521 | HMPREF0389_00074 membrane protein |
| 1.749 | HMPREF0389_01047 TetR family transcriptional regulator |
| 2.926 | HMPREF0389_01180 anti-anti-sigma factor RsbV |
| 1.631 | HMPREF0389_00867 ATP-dependent DNA helicase RecG |
| 1.802 | HMPREF0389_00336 translation elongation factor Ts |
| 1.471 | HMPREF0389_00527 oligoendopeptidase F |
| 0.654 | HMPREF0389_00909 group-specific protein |
| 1.437 | HMPREF0389_00861 thermonuclease |
| 1.478 | HMPREF0389_01564 ABC transporter, permease protein |
| 1.697 | HMPREF0389_00038 hypoxanthine phosphoribosyltransferase |

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|---|---|
| 0.795 | HMPREF0389_00768 peroxiredoxin |
| 0.713 | HMPREF0389_00271 cysteine--tRNA ligase |
| 0.537 | HMPREF0389_00670 hypothetical protein |
| 0.587 | HMPREF0389_00284 membrane associated protein |
| 1.317 | HMPREF0389_01258 UDP-N-acetylmuramate dehydrogenase |
| 1.316 | HMPREF0389_00479 glutamyl-tRNA(Gln) amidotransferase, A subunit |
| 0.669 | HMPREF0389_01384 oxygen-independent coproporphyrinogen III oxidase |
| 1.379 | HMPREF0389_01677 hypothetical protein |
| 0.794 | HMPREF0389_01539 translation elongation factor P |
| 1.628 | HMPREF0389_01084 hypothetical protein |
| 1.483 | HMPREF0389_01465 hypothetical protein |
| 1.443 | HMPREF0389_01627 PHP domain-containing protein |
| 1.632 | HMPREF0389_01060 GMP synthase |
| 0.673 | HMPREF0389_01369 heat shock protein HtpG |
| 0.546 | HMPREF0389_00103 hypothetical protein |
| 1.401 | HMPREF0389_01474 (R)-2-hydroxyglutaryl-CoA dehydratase, beta subunit |
| 0.617 | HMPREF0389_00373 RNA polymerase sigma factor RpoD |
| 1.681 | HMPREF0389_01081 CAAX amino protease family protein |
| 1.449 | HMPREF0389_01462 butyryl-CoA dehydrogenase |
| 1.326 | HMPREF0389_00225 transcriptional regulatory protein, AsnC family |
| 1.479 | HMPREF0389_00547 phenylalanyl-tRNA synthetase, alpha subunit |
| 0.596 | HMPREF0389_01604 glutamate--tRNA ligase |
| 1.454 | HMPREF0389_01455 hypothetical protein |
| 1.307 | HMPREF0389_00649 membrane protein |
| 1.348 | HMPREF0389_00676 glycerol dehydrogenase |
| 1.303 | HMPREF0389_01075 hypothetical protein |
| 0.280 | HMPREF0389_01322 hypothetical protein |
| 1.360 | HMPREF0389_00715 quinolinate synthetase complex, A subunit |
| 1.368 | HMPREF0389_01740 hypothetical protein |
| 0.682 | HMPREF0389_00536 leucine--tRNA ligase |
| 2.381 | HMPREF0389_00290 transcriptional regulator, LacI family |
| 0.609 | HMPREF0389_00872 hypothetical protein |
| 2.081 | HMPREF0389_01109 FeS assembly ATPase SufC |
| | HMPREF0389_01003 peptide deformylase |
| 0.750 | HMPREF0389_00639 ATP/GTP-binding protein |
| 1.544 | HMPREF0389_01606 hypothetical protein |
| 1.475 | HMPREF0389_00620 SMI1 / KNR4 family protein |
| 3.644 | HMPREF0389_00905 sodium:neurotransmitter symporter family protein |
| 0.720 | HMPREF0389_00402 DNA gyrase B subunit |
| 1.378 | HMPREF0389_01048 GTP pyrophosphokinase |
| 0.589 | HMPREF0389_00378 transporter, major facilitator family |

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|---|---|
| 1.508 | HMPREF0389_01107 iron-regulated ABC-type transporter membrane component |
| 0.765 | HMPREF0389_00655 hypothetical protein |
| 1.510 | HMPREF0389_01159 hypothetical protein |
| 0.654 | HMPREF0389_00814 RNA binding protein |
| 0.635 | HMPREF0389_00325 transcription termination factor NusA |
| 0.734 | HMPREF0389_00509 hemolysin A |
| 1.498 | HMPREF0389_00953 transcriptional regulator |
| 0.744 | HMPREF0389_01357 GntR family transcriptional regulator |
| 0.665 | HMPREF0389_00304 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase |
| 0.774 | HMPREF0389_01608 L-serine dehydratase, iron-sulfur-dependent, beta subunit |
| 1.722 | HMPREF0389_01184 DNA gyrase, B subunit |
| 0.734 | HMPREF0389_00635 tetracycline resistance protein |
| 1.331 | HMPREF0389_01012 ABC transporter, permease protein |
| 1.460 | HMPREF0389_01356 RocB protein |
| 0.780 | HMPREF0389_00117 histidinol-phosphate aminotransferase |
| 0.754 | HMPREF0389_01679 hypothetical protein |
| 0.767 | HMPREF0389_00392 ribosomal large subunit pseudouridine synthase family protein |
| 2.183 | HMPREF0389_00519 hypothetical protein |
| 1.536 | HMPREF0389_00931 malonyl CoA-acyl carrier protein transacylase |
| 1.348 | HMPREF0389_00721 copper amine oxidase N- domain protein |
| 1.299 | HMPREF0389_01165 CRISPR-associated protein Cas2 |
| 1.366 | HMPREF0389_00663 hypothetical protein |
| 0.617 | HMPREF0389_00815 30S ribosomal protein S16 |
| 0.638 | HMPREF0389_00610 hypothetical protein |
| 1.579 | HMPREF0389_00430 50S ribosomal protein L27 |
| 1.311 | HMPREF0389_00797 hypothetical protein |
| 1.519 | HMPREF0389_00849 phosphoglycerate mutase |
| 1.650 | HMPREF0389_01340 phosphoglucomutase/phosphomannomutase family protein |
| 1.340 | HMPREF0389_00308 undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase |
| 1.329 | HMPREF0389_00942 hypothetical protein |
| 2.055 | HMPREF0389_00052 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase |
| 0.767 | HMPREF0389_00800 low-density lipoprotein receptor-like protein 2 |
| 0.463 | HMPREF0389_00881 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II |
| 1.363 | HMPREF0389_01000 serine/threonine protein phosphatase |
| 1.139 | HMPREF0389_01538 Xaa-Pro dipeptidase |
| 1.350 | HMPREF0389_00116 phosphoribulokinase family protein |
| 0.782 | HMPREF0389_01484 S-adenosylmethionine:tRNA ribosyltransferase-isomerase |
| 1.541 | HMPREF0389_00789 orotidine 5'-phosphate decarboxylase |
| 1.679 | HMPREF0389_00471 single-stranded-DNA-specific exonuclease RecJ |
| 1.324 | HMPREF0389_00763 threonine synthase |
| 1.411 | HMPREF0389_01088 histidinol phosphate phosphatase HisJ family protein |

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|---|---|
| 1.951 | HMPREF0389_00948 D-3-phosphoglycerate dehydrogenase |
| 1.551 | HMPREF0389_01590 transcriptional regulator, AraC family |
| 1.830 | HMPREF0389_01398 oxygen-independent coproporphyrinogen III oxidase |
| 0.660 | HMPREF0389_00113 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase |
| 0.732 | HMPREF0389_00853 50S ribosomal protein L10d |
| 1.536 | HMPREF0389_01360 hypothetical protein |
| 0.707 | HMPREF0389_01442 aspartate transaminase |
| 1.639 | HMPREF0389_00066 PIN/TRAM domain protein |
| 0.539 | HMPREF0389_01244 DegV family protein |
| 0.670 | HMPREF0389_01280 permease domain protein |
| 1.439 | HMPREF0389_01182 hypothetical protein |
| 0.748 | HMPREF0389_01170 CRISPR-associated protein Cas5, Dvulg subtype |
| 2.281 | HMPREF0389_01164 hypothetical protein |
| 0.499 | HMPREF0389_01160 hypothetical protein |
| 0.669 | HMPREF0389_01158 hypothetical protein |
| 1.293 | HMPREF0389_00550 hypothetical protein |
| 0.742 | HMPREF0389_00521 SAM-dependent methyltransferase |
| 1.948 | HMPREF0389_00472 F420-0:Gamma-glutamyl ligase superfamily |
| 0.738 | HMPREF0389_00450 RocB protein |
| 0.723 | HMPREF0389_00431 hypothetical protein |
| 0.758 | HMPREF0389_00411 hypothetical protein |
| 0.716 | HMPREF0389_00407 excinuclease ABC subunit B |
| 1.611 | HMPREF0389_00399 phosphoribosylaminoimidazolesuccinocarboxamide synthase |
| 2.468 | HMPREF0389_00387 pyruvate kinase |
| 1.184 | HMPREF0389_00384 sensory box histidine kinase |
| 4.109 | [gene=HMPREF0389_00382] [protein=hypothetical protein |
| 1.289 | HMPREF0389_00350 membrane protein |
| 0.716 | HMPREF0389_00338 hypothetical protein |
| 1.300 | HMPREF0389_00332 riboflavin biosynthesis protein RibF |
| 6.380 | HMPREF0389_00296 PP-loop family protein |
| 1.737 | HMPREF0389_00294 ribose ABC transporter, permease protein |
| 0.477 | HMPREF0389_00258 sigma-70, region 4 superfamily |
| 1.776 | HMPREF0389_00253 ABC transporter, permease/ATP-binding protein |
| 0.787 | HMPREF0389_00222 hypothetical protein |
| 0.682 | HMPREF0389_00217 hypothetical protein |
| 2.116 | HMPREF0389_00212 CRISPR-associated protein Cas2 |
| 1.374 | HMPREF0389_00211 CRISPR-associated protein Cas1 |
| 1.504 | HMPREF0389_00209 transposase |
| 0.738 | HMPREF0389_00206 sigma-70, region 4 subfamily |
| 1.337 | HMPREF0389_00203 sensor protein ResE |
| 1.375 | HMPREF0389_00201 toxin-antitoxin system, antitoxin component, Xre family |

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|---|---|
| 1.351 | HMPREF0389_00198 integrase-recombinase |
| 1.336 | HMPREF0389_00181 hypothetical protein |
| 0.658 | HMPREF0389_00168hypothetical protein |
| 1.401 | HMPREF0389_00165 TraG family protein |
| 1.356 | HMPREF0389_00159 modification methylase LlaDCHIA |
| 0.740 | HMPREF0389_00152 protein=hypothetical protein |
| 0.757 | HMPREF0389_00147 protein=lysine--tRNA ligase |
| 0.735 | HMPREF0389_00110 di-trans,poly-cis-decaprenylcistransferase |
| 0.607 | HMPREF0389_00107 UMP kinase |
| 0.766 | HMPREF0389_00105 dCTP deaminase |
| 1.455 | HMPREF0389_00104 radical SAM domain protein |
| 0.755 | HMPREF0389_00101 nicotinate phosphoribosyltransferase |
| 0.740 | HMPREF0389_01688 copper-sensing transcriptional repressor CsoR |
| 1.793 | HMPREF0389_00068 hypothetical protein |
| 0.631 | HMPREF0389_00063 phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase |
| 2.083 | HMPREF0389_00044 glutamate synthase (NADPH), homotetrameric |
| 1.088 | HMPREF0389_00042 fructose-bisphosphate aldolase, class I |
| 0.608 | HMPREF0389_00041 indole-3-acetyl-L-aspartic acid hydrolase |
| 0.535 | HMPREF0389_00040 chaperonin HslO |
| 1.222 | HMPREF0389_00039 S-adenosylmethionine-dependent methyltransferase |
| 1.249 | HMPREF0389_00034 pseudouridine synthase, RluA family |
| 1.287 | HMPREF0389_00020 ComE operon protein |
| 2.344 | HMPREF0389_00019 outer membrane protein |
| 0.792 | HMPREF0389_00016 translation elongation factor G |
| 0.790 | HMPREF0389_00004 phosphatidylserine decarboxylase proenzyme 2 |
| 1.456 | HMPREF0389_01654 neutrophil-activating protein A |
| 1.913 | HMPREF0389_01649 NAD-specific glutamate dehydrogenase |
| 0.220 | HMPREF0389_01637 lipoprotein |
| 0.649 | HMPREF0389_01626 methionine adenosyltransferase |
| 0.668 | HMPREF0389_01589 hypothetical protein |
| 1.036 | HMPREF0389_01584 arginine deiminase |
| 1.319 | HMPREF0389_01549 group 1 family glycosyl transferase |
| 1.420 | HMPREF0389_01497 ATP synthase F1, alpha subunit |
| 1.592 | HMPREF0389_01460 serine protease HtrA |
| 0.607 | HMPREF0389_01458 serine--tRNA ligase |
| 0.355 | HMPREF0389_01457 D-methionine-binding lipoprotein MetQ |
| 0.620 | HMPREF0389_01444 ribosomal-protein-alanine acetyltransferase |
| 0.699 | HMPREF0389_01428 hypothetical protein |
| 1.413 | HMPREF0389_01425 hypothetical protein |
| 0.303 | HMPREF0389_01702 hypothetical protein |
| 0.716 | HMPREF0389_01410 phosphoenolpyruvate carboxykinase (ATP) |

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|---|---|
| 1.562 | HMPREF0389_01382 hypothetical protein |
| 0.745 | HMPREF0389_01376 alanine racemase |
| 1.423 | HMPREF0389_01373 membrane protein |
| 1.206 | HMPREF0389_01353 amidinotransferase superfamily] |
| 0.712 | HMPREF0389_01351 YihY family protein |
| 2.651 | HMPREF0389_01346 radical SAM domain protein |
| 1.447 | HMPREF0389_00565 protein=triose-phosphate isomerase |
| 1.827 | HMPREF0389_00569 protein=tRNA delta(2)-isopentenylpyrophosphate transferase |
| 0.762 | HMPREF0389_00577 protein=UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase |
| 1.657 | HMPREF0389_00586 DNA polymerase III |
| 0.987 | HMPREF0389_00590 CAAX amino protease family protein |
| 0.755 | HMPREF0389_00596 UDP-N-acetylmuramyl-tripeptide synthetase |
| 0.755 | HMPREF0389_00643 transcriptional regulator |
| 1.443 | HMPREF0389_00645 hypothetical protein |
| 1.391 | HMPREF0389_00657 DNA topoisomerase III |
| 0.756 | HMPREF0389_00708 alkaline shock protein |
| 1.398 | HMPREF0389_00712 RmuC domain protein |
| 1.701 | HMPREF0389_00756 cytidylate kinase |
| 1.365 | HMPREF0389_00786 orotate phosphoribosyltransferase |
| 0.762 | HMPREF0389_00816 signal recognition particle protein |
| 1.561 | HMPREF0389_00825 methionine aminopeptidase, type I |
| 2.008 | HMPREF0389_00838 30S ribosomal protein S17 |
| 0.695 | HMPREF0389_00880 riboflavin synthase, alpha subunit |
| 1.550 | HMPREF0389_00886 hypothetical protein |
| 0.342 | HMPREF0389_00893 hypothetical protein |
| 1.513 | HMPREF0389_00908 hypothetical protein |
| 0.608 | HMPREF0389_00916 anaerobic ribonucleoside-triphosphate reductase activating protein |
| 1.271 | HMPREF0389_00930 3-oxoacyl-acyl-carrier-protein |
| 0.791 | HMPREF0389_00933 enoyl-(acyl-carrier-protein) reductase II |
| 0.673 | HMPREF0389_00949 TRAP dicarboxylate transporter, DctP subunit |
| 1.287 | HMPREF0389_00959 NADH oxidase, water-forming |
| 3.102 | HMPREF0389_00967 hypothetical protein |
| 0.628 | HMPREF0389_00969 formate/nitrite transporter family protein |
| 1.300 | HMPREF0389_01001 neutral zinc metallopeptidase family protein |
| 0.543 | HMPREF0389_01017 hypothetical protein |
| 0.665 | HMPREF0389_01021 cyclase |
| 0.503 | HMPREF0389_01026 hypothetical protein |
| 0.650 | HMPREF0389_01741 hypothetical protein |
| 0.756 | HMPREF0389_01065 S4 domain protein |
| 1.296 | HMPREF0389_0107 UDP-N-acetyl-D-mannosamine transferase |
| 1.376 | HMPREF0389_01104 hypothetical protein |

| | |
|---|---|
| 1.310 | HMPREF0389_01329 hypothetical protein |
| 0.663 | HMPREF0389_01292 alginate O-acetyltransferase AlgI |
| 0.670 | HMPREF0389_01271 hypothetical protein |
| 1.347 | HMPREF0389_01264 protein=phosphocarrier protein HPr |
| 0.706 | HMPREF0389_01252 protein=hypothetical protein |
| 3.858 | HMPREF0389_01236 30S ribosomal protein S18 |
| 1.271 | HMPREF0389_01223 transcriptional regulator, MarR family |
| 0.789 | HMPREF0389_01214 sensory box histidine kinase YycG |
| 1.311 | HMPREF0389_01204 hypothetical protein |

## Table –S2

## Fold change of host cell proteins during *F. alocis* co-infection with *P. gingivalis*.

| IPI Accession* | Description | Fold change during co-infection |
|---|---|---|
| IPI00784154.1 | 60 kDa heat shock protein, mitochondrial precursor | 1.226 |
| IPI00418471.6 | Vimentin | 0.463 |
| IPI00018534.4 | Histone H2B type 1-L | 0.358 |
| IPI00003935.6 | Histone H2B type 2-E | |
| IPI00219018.7 | Glyceraldehyde-3-phosphate dehydrogenase | 0.798 |
| IPI00414676.6 | Heat shock protein HSP 90-beta | 0.663 |
| IPI00784295.2 | Heat shock protein HSP 90-alpha | 0.724 |
| IPI00450768.7 | Keratin, type I cytoskeletal 17 | 0.999 |
| IPI00021439.1 | Actin, cytoplasmic 1 | 0.758 |
| IPI00455315.4 | Annexin A2 | 1.302 |
| IPI00025416.3 | Actin, gamma-enteric smooth muscle | 0.988 |
| IPI00306959.10 | Keratin, type II cytoskeletal 7 | 1.046 |
| IPI00465248.5 | Isoform alpha-enolase of Alpha-enolase | 0.761 |
| IPI00218918.5 | Annexin A1 | 1.214 |
| IPI00792677.1 | 46 kDa protein | |
| IPI00220362.5 | 10 kDa heat shock protein, mitochondrial | 2.160 |
| IPI00011654.2 | Tubulin beta chain | 0.800 |
| IPI00554648.3 | Keratin, type II cytoskeletal 8 | 1.335 |
| IPI00644576.1 | Filamin A, alpha | 0.887 |
| IPI00655639.1 | Hypothetical protein (Fragment) | 0.588 |
| IPI00465439.5 | Fructose-bisphosphate aldolase A | 0.669 |
| IPI00555610.3 | 313 kDa protein | 1.313 |
| IPI00218343.4 | Tubulin alpha-6 chain | 0.980 |
| IPI00303476.1 | ATP synthase subunit beta, mitochondrial precursor | 1.329 |

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|---|---|---|
| IPI00783284.2 | Aspartyl/asparaginyl beta-hydroxylase | 0.735 |
| IPI00019502.3 | Myosin-9 | 0.943 |
| IPI00003362.2 | HSPA5 protein | 1.109 |
| IPI00789157.1 | Protein | 1.351 |
| IPI00169383.3 | Phosphoglycerate kinase 1 | 0.679 |
| IPI00217467.3 | Histone H1.4 | 0.378 |
| IPI00398777.3 | plectin 1 isoform 8 | 1.056 |
| IPI00217465.5 | Histone H1.2 | 0.365 |
| IPI00794663.1 | 48 kDa protein | 1.255 |
| IPI00215943.1 | Isoform 3 of Plectin-1 | |
| IPI00748943.1 | Similar to tubulin, beta polypeptide paralog | |
| IPI00640741.1 | 19 kDa protein | 0.738 |
| IPI00217966.7 | Isoform 1 of L-lactate dehydrogenase A chain | 1.516 |
| IPI00299024.9 | Brain acid soluble protein 1 | 1.023 |
| IPI00027252.6 | Prohibitin-2 | 1.205 |
| IPI00396485.3 | Elongation factor 1-alpha 1 | 0.996 |
| IPI00644989.2 | Isoform 1 of Protein disulfide-isomerase A6 precursor | 1.223 |
| IPI00479186.5 | Isoform M2 of Pyruvate kinase isozymes M1/M2 | 0.973 |
| IPI00025491.1 | Eukaryotic initiation factor 4A-I | 0.896 |
| IPI00328328.3 | Isoform 1 of Eukaryotic initiation factor 4A-II | 0.812 |
| IPI00735709.1 | similar to Signal peptidase complex subunit 2 (Microsomal signal peptidase 25 kDa subunit) (SPase 25 kDa subunit) isoform 3 | |
| IPI00003269.1 | hypothetical protein LOC345651 | 0.972 |
| IPI00003918.6 | 60S ribosomal protein L4 | 1.176 |
| IPI00419585.9 | Peptidyl-prolyl cis-trans isomerase A | 0.302 |
| IPI00024920.1 | ATP synthase delta chain, mitochondrial precursor | 1.384 |
| IPI00737435.1 | similar to actin, alpha 2, smooth muscle, aorta | 0.823 |
| IPI00384444.5 | Keratin, type I cytoskeletal 14 | |
| IPI00807545.1 | Isoform 3 of Heterogeneous nuclear ribonucleoprotein K | 1.016 |
| IPI00291175.7 | Isoform 1 of Vinculin | 2.189 |
| IPI00186290.6 | Elongation factor 2 | 0.844 |
| IPI00745933.1 | 18 kDa protein | 0.769 |
| IPI00008530.1 | 60S acidic ribosomal protein P0 | 1.136 |
| IPI00216691.5 | Profilin-1 | 0.877 |
| IPI00013683.2 | Tubulin beta-3 chain | |
| IPI00216952.1 | Isoform C of Lamin-A/C | 0.519 |
| IPI00013895.1 | Protein S100-A11 | 0.903 |
| IPI00003865.1 | Isoform 1 of Heat shock cognate 71 kDa protein | 0.659 |
| IPI00007765.5 | Stress-70 protein, mitochondrial precursor | 1.371 |

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|---|---|---|
| IPI00007752.1 | Tubulin beta-2C chain | 1.383 |
| IPI00010720.1 | T-complex protein 1 subunit epsilon | 0.849 |
| IPI00304925.4 | Heat shock 70 kDa protein 1 | 1.137 |
| IPI00740238.1 | similar to 40S ribosomal protein S16 isoform 2 | 0.842 |
| IPI00003734.1 | Putative S100 calcium-binding protein H_NH0456N16.1 | |
| IPI00218592.5 | Isoform ASF-3 of Splicing factor, arginine/serine-rich 1 | 0.247 |
| IPI00025512.2 | Heat-shock protein beta-1 | 0.562 |
| IPI00747497.1 | 50 kDa protein | 0.856 |
| IPI00478896.2 | Ribosomal protein L7a | 0.899 |
| IPI00215780.5 | 40S ribosomal protein S19 | 1.198 |
| IPI00646055.1 | 57 kDa protein | 0.720 |
| IPI00219217.3 | L-lactate dehydrogenase B chain | 1.452 |
| IPI00008529.1 | 60S acidic ribosomal protein P2 | 1.103 |
| IPI00023598.2 | Tubulin beta-4 chain | 0.860 |
| IPI00550363.3 | Transgelin-2 | 0.956 |
| IPI00657680.1 | 55 kDa protein | 1.139 |
| IPI00217468.3 | Histone H1.5 | 0.758 |
| IPI00304612.9 | 60S ribosomal protein L13a | 1.157 |
| IPI00797044.1 | 54 kDa protein | 0.973 |
| IPI00384653.1 | Prothymosin a14 | |
| IPI00412977.1 | Prothymosin alpha | 0.786 |
| IPI00646304.4 | peptidylprolyl isomerase B precursor | 0.564 |
| IPI00291006.1 | Malate dehydrogenase, mitochondrial precursor | 1.081 |
| IPI00010796.1 | Protein disulfide-isomerase precursor | 1.074 |
| IPI00470509.2 | PCBP2 protein | 0.939 |
| IPI00017334.1 | Prohibitin | 1.178 |
| IPI00301277.1 | Heat shock 70 kDa protein 1L | |
| IPI00022977.1 | Creatine kinase B-type | 0.815 |
| IPI00216308.5 | Voltage-dependent anion-selective channel protein 1 | 1.336 |
| IPI00293616.3 | ATP-dependent RNA helicase DDX3Y | 0.620 |
| IPI00339269.1 | Heat shock 70 kDa protein 6 | |
| IPI00645385.1 | Copine I | 1.160 |
| IPI00641706.1 | 46 kDa protein | 1.512 |
| IPI00007188.5 | ADP/ATP translocase 2 | 1.204 |
| IPI00639797.1 | Hydroxyacyl-Coenzyme A dehydrogenase, type II | 1.122 |
| IPI00784347.2 | Keratin, type I cytoskeletal 18 | 1.150 |
| IPI00027230.3 | Endoplasmin precursor | 1.165 |
| IPI00008433.4 | 40S ribosomal protein S5 | 0.658 |
| IPI00413108.4 | Ribosomal protein SA | 0.769 |

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|---|---|---|
| IPI00453473.6 | Histone H4 | 1.394 |
| IPI00816097.1 | Ribosomal protein L28 variant (Fragment) | 1.393 |
| IPI00795527.1 | 21 kDa protein | 1.202 |
| IPI00787573.1 | similar to Ubiquitin-63E CG11624-PA, isoform A | 0.778 |
| IPI00790768.1 | 26 kDa protein | 1.907 |
| IPI00397498.1 | Isoform 2 of Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor | 1.152 |
| IPI00007471.2 | nascent-polypeptide-associated complex alpha polypeptide-like | |
| IPI00797126.1 | Similar to Nascent polypeptide associated complex alpha subunit | 2.310 |
| IPI00641719.1 | Surfeit 4 | 1.136 |
| IPI00012011.6 | Cofilin-1 | 0.622 |
| IPI00759596.1 | Isoform 4 of Heterogeneous nuclear ribonucleoproteins C1/C2 | 0.832 |
| IPI00329801.12 | Annexin A5 | 1.226 |
| IPI00554722.1 | solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform e | 0.897 |
| IPI00794894.1 | Protein | 0.480 |
| IPI00041625.1 | similar to 60S ribosomal protein L23a | |
| IPI00446017.3 | LOC649946 protein | |
| IPI00549248.4 | Isoform 1 of Nucleophosmin | 0.807 |
| IPI00784090.2 | T-complex protein 1 subunit theta | 1.003 |
| IPI00171611.7 | Histone H3.2 | 1.454 |
| IPI00217030.10 | 40S ribosomal protein S4, X isoform | 0.827 |
| IPI00793344.1 | 22 kDa protein | 1.193 |
| IPI00792424.1 | 9 kDa protein | 1.082 |
| IPI00025874.2 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor | 1.186 |
| IPI00792641.1 | Hypothetical protein DKFZp686J13123 | 1.201 |
| IPI00005490.1 | Golgi phosphoprotein 3 | 0.773 |
| IPI00419880.6 | 40S ribosomal protein S3a | 1.120 |
| IPI00081836.3 | Histone H2A type 1-H | 0.755 |
| IPI00024933.3 | 60S ribosomal protein L12 | 0.857 |
| IPI00478310.3 | similar to 60S ribosomal protein L12 | 1.056 |
| IPI00794205.1 | 26 kDa protein | 1.334 |
| IPI00216613.1 | Isoform Short of Splicing factor, proline- and glutamine-rich | 0.732 |
| IPI00646059.1 | SET translocation | 0.987 |
| IPI00001639.2 | Importin beta-1 subunit | 0.824 |
| IPI00789577.1 | 12 kDa protein | 0.898 |

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|---|---|---|
| IPI00008438.1 | 40S ribosomal protein S10 | 1.039 |
| IPI00382699.1 | Isoform 5 of Filamin-B | 0.662 |
| IPI00413958.3 | Isoform 2 of Filamin-C | 1.329 |
| IPI00024993.4 | Enoyl-CoA hydratase, mitochondrial precursor | 1.328 |
| IPI00016513.5 | Ras-related protein Rab-10 | 0.787 |
| IPI00220327.3 | Keratin, type II cytoskeletal 1 | 1.461 |
| IPI00794340.1 | 273 kDa protein | 1.087 |
| IPI00297779.7 | T-complex protein 1 subunit beta | 1.249 |
| IPI00552590.1 | chaperonin containing TCP1, subunit 6A isoform b | 1.007 |
| IPI00790892.1 | 6 kDa protein | |
| IPI00797983.1 | Ribosomal protein L5 | 1.113 |
| IPI00398806.2 | H2A histone family, member V isoform 5 | 2.509 |
| IPI00011253.3 | 40S ribosomal protein S3 | 1.190 |
| IPI00220642.7 | 14-3-3 protein gamma | 1.578 |
| IPI00439415.6 | eukaryotic translation initiation factor 4B | 0.272 |
| IPI00793285.1 | 39 kDa protein | 0.534 |
| IPI00013808.1 | Alpha-actinin-4 | 0.966 |
| IPI00032313.1 | Protein S100-A4 | 0.678 |
| IPI00645194.1 | integrin beta 1 isoform 1A precursor | 1.167 |
| IPI00791426.1 | 13 kDa protein | 0.432 |
| IPI00394838.2 | ATP citrate lyase isoform 2 | 0.730 |
| IPI00021033.2 | Isoform 1 of Collagen alpha-1(III) chain precursor | 0.445 |
| IPI00645078.1 | Ubiquitin-activating enzyme E1 | 1.100 |
| IPI00402185.4 | Isoform 5 of Heterogeneous nuclear ribonucleoprotein Q | 1.066 |
| IPI00027107.5 | Tu translation elongation factor, mitochondrial | 1.286 |
| IPI00159072.3 | ROD1 regulator of differentiation 1 | 1.171 |
| IPI00413922.5 | 11 kDa protein | 0.429 |
| IPI00796366.1 | 16 kDa protein | 1.300 |
| IPI00064086.5 | EEF1D protein | 0.794 |
| IPI00216694.3 | plastin 3 | 1.061 |
| IPI00219219.3 | Galectin-1 | 0.571 |
| IPI00012074.3 | Heterogeneous nuclear ribonucleoprotein R | 1.728 |
| IPI00029623.1 | Proteasome subunit alpha type 6 | 0.794 |
| IPI00291510.3 | Inosine-5'-monophosphate dehydrogenase 2 | 2.472 |
| IPI00796210.1 | 28 kDa protein | 1.204 |
| IPI00798321.1 | 10 kDa protein | 0.877 |
| IPI00550020.3 | Parathymosin | 0.524 |
| IPI00022462.2 | Transferrin receptor protein 1 | 0.768 |
| IPI00028055.4 | Transmembrane emp24 domain-containing protein 10 precursor | 1.002 |

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|---|---|---|
| IPI00022774.3 | Transitional endoplasmic reticulum ATPase | 0.854 |
| IPI00030179.3 | 60S ribosomal protein L7 | 0.991 |
| IPI00456969.1 | Dynein heavy chain, cytosolic | 1.148 |
| IPI00651653.1 | Isoform 3 of Probable ATP-dependent RNA helicase DDX17 | 1.942 |
| IPI00219365.3 | Moesin | 0.905 |
| IPI00337736.1 | Isoform 2 of Kinectin | 0.981 |
| IPI00796633.1 | 22 kDa protein | 1.176 |
| IPI00020599.1 | Calreticulin precursor | 1.073 |
| IPI00011200.5 | D-3-phosphoglycerate dehydrogenase | 1.110 |
| IPI00013164.4 | Isoform 1 of Peripherin | 0.197 |
| IPI00739539.2 | similar to Prostate, ovary, testis expressed protein on chromosome 2 | |
| IPI00009655.3 | zinc finger, BED-type containing 5 | 1.114 |
| IPI00375307.1 | peroxiredoxin 5 precursor, isoform c | 1.470 |
| IPI00018146.1 | 14-3-3 protein theta | 0.762 |
| IPI00414696.1 | Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1 | 0.349 |
| IPI00827743.1 | 31 kDa protein | 1.397 |
| IPI00743867.1 | Similar to Pyruvate kinase, isozymes M1/M2 | 0.731 |
| IPI00016342.1 | Ras-related protein Rab-7 | 0.898 |
| IPI00746388.1 | Ezrin | 1.251 |
| IPI00394732.4 | Isoform 2 of Transformation/transcription domain-associated protein | 0.555 |
| IPI00554711.2 | Junction plakoglobin | 0.942 |
| IPI00798040.1 | 46 kDa protein | 0.963 |
| IPI00294578.1 | Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2 | 0.840 |
| IPI00013508.5 | Alpha-actinin-1 | 0.875 |
| IPI00020956.1 | Hepatoma-derived growth factor | 0.843 |
| IPI00739099.1 | Collagen alpha-2(V) chain precursor | 1.218 |
| IPI00410017.1 | Isoform 2 of Polyadenylate-binding protein 1 | 0.926 |
| IPI00465430.5 | 70 kDa protein | 0.491 |
| IPI00445123.1 | CDNA FLJ44592 fis, clone BLADE2002310, highly similar to Homo sapiens SH3-domain binding protein 1 (Fragment) | 0.304 |
| IPI00010810.1 | Electron transfer flavoprotein subunit alpha, mitochondrial precursor | 1.195 |
| IPI00740545.1 | similar to Prostate, ovary, testis expressed protein on chromosome 2 isoform 2 | |
| IPI00001091.4 | AFG3-like protein 2 | 1.774 |

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|---|---|---|
| IPI00024911.1 | Endoplasmic reticulum protein ERp29 precursor | 1.601 |
| IPI00795919.1 | Pseudogene candidate | 1.286 |

*- IPI – International protein index accession number

## Supporting Information

## Supplemental Figures

**Figure – S1**

**Gene network mining of downregulated proteins during co-infection.**

Gene network based host proteome data (down regulated proteins)during co-infection of *Filifactor alocis* with *P. gingivalis* mining showing modulation of vital host cellular processes.

**Figure – S2**

**Gene network mining of upregulated proteins during co-infection**.

Gene network based host proteome data (upregulated proteins)during co-infection of *Filifactor alocis* with *P. gingivalis* mining showing modulation of vital host cellular processes.

**Figure – S3.**

**Eukaryotic proteins upregulated during *F. alocis* co culture with *P. gingivalis* Vs monoculture.**

Ingenuity pathway analysis showed increased expression of eukaryotic genes involved in antigen presentation, cellular movement, and hematological system, cell trafficking and inflammatory response

**Figure – S4**

**Co-infection of *Filifactor alocis* with *P. gingivalis* show upregulation of proteins involved in cell growth and proliferation pathway.**

Analysis of the host proteome data showed downregulation of proteins involved in cytoskeleton integrity and ubiquitin dependent protein degradation. Proteins involved in negative regulation of cell proliferation were upregulated.

**Figure – S5.**

**Co-infection of *Filifactor alocis* with *P. gingivalis* show modulation of proteins involved in cellular assembly and organization pathways**.

Analysis of the host proteome data showed modulation of many cytoskeleton proteins such as VCL, VDAC1 and downregulation of many proteins involved in actin pathway.

**Figure – S6**

**Grandzyme mediated apoptic signaling pathway.**

Coinfection of *F. alocis* with *P. gingivalis* showed upregulation of Grandzyme activating Dnase (GAAD) and downregulation of Histone proteins.

## Tables

**Table –S1**

**Fold change of host cell proteins during *F. alocis* co-infection with *P. gingivalis*.**

**Table –S2**

**Fold change of host cell proteins during *F. alocis* co-infection with *P. gingivalis*.**