



pg/mL



15

10

2 hours

Jm/gd



control AcaR

2 hours

Acap control

24 hours

20

lm/gc

N.







IP-10 AcaR control N. 2 hours 24 hours

AcaR control

24 hours

CHEMOKINES

'n.





The concentrations of several cytokines and chemokines were increased in B. pseudomallei-

infected human OECs at 24 hours post-infection when compared to non-infected control cells. However, infection with the WT strain was not associated with significantly higher levels of any analytes tested compared to the acapsular mutant. Higher concentrations of cytokines and chemokines were detected at 24 hours post-infection when compared to 2 hours postinfection (direct statistical comparisons not shown). Data were analysed by one-way analysis of variance followed by Tukey's multiple comparison test. *p < 0.05, **p < 0.01. IH = inhalation; IN = intra-nasal; WT = MSHR520 wild type strain; $\Delta cap = MSHR520 \Delta cap$ strain.



Top two OEC canonical pathways underlying antimicrobial gene networks as identified using

IPA and ranked using z-score. The top pathways at 24 hours post-infection are (A) Role of

pattern recognition receptors in recognition of bacteria and viruses and (B) TREM1 signalling.

IPA Legend defining molecule shapes, relationship types, colors and fonts available at

http://ingenuity.force.com/ipa/IPATutorials?id=kA25000000TN2wCAG.

Supplementary Table I.

Primers used in this study.

<u>Target</u> Genes	<u>Assay ID</u>	Forward Primer (5' - 3')	<u>Reverse Primer (5' - 3')</u>	<u>Probe</u> (UPL#)	<u>Amplicon</u> <u>Size (bp)</u>
ACTB	143636	TCCTCCCTGGAGAAGAGCTA	CGTGGATGCCACAGGACT	27	127
CCL3	136214	GCTGACTACTTTGAGACGAGCA	GCTTCGCTTGGTTAGGAAGA	125	66
CSF2	110860	TCTCAGAAATGTTTGACCTCCA	GCCCTTGAGCTTGGTGAG	1	98
CSF3	140545	ACTTTGCCACCACCATCTG	TGGAAAGCAGAGGCGAAG	48	100
CXCL1	105522	TCCTGCATCCCCCATAGTTA	CTTCAGGAACAGCCACCAGT	52	105
GAPDH	141139	AGCCACATCGCTCAGACAC	GCCCAATACGACCAAATCC	60	66
IFNG	110609	GGCATTTTGAAGAATTGGAAAG	TTTGGATGCTCTGGTCATCTT	21	112
IL12A	112242	CACTCCCAAAACCTGCTGAG	TCTCTTCAGAAGTGCAAGGGTA	50	88
IL12B	137378	AGATGGAATTTGGTCCACTGA	GCAGGTGAAACGTCCAGAAT	142	103
IL1A	145628	CAAAAGGCGAAGAAGACTGAC	GGAACTTTGGCCATCTTGAC	20	102
IL1B	100950	AGCTGATGGCCCTAAACAGA	TCGGAGATTCGTAGCTGGAT	85	87
IL6	144013	ACCGGGAACGAAAGAGAAG	GAAGGCAACTGGACCGAAG	133	88
TNF	141083	CGGTGCTTGTTCCTCAGC	GCCAGAGGGCTGATTAGAGA	12	137
IL17A	147091	CCACCTCACCTTGGAATCTC	GGTAGTCCACGTTCCCATCA	117	117
CCL11	140075	GCCTCCAACATGAAGGTCTC	AGGTGGTTGGGACAGAAGC	8	103
CCL4	147090	CTTCCTCGCAACTTTGTGGT	TGCTTGCTTCTTTTGGTTTG	32	89

Supplementary Table I

Primers used in this study.

Supplementary Table II.

Human OEC transcriptional responses triggered by B. pseudomallei 2 h and 24 h post-infection. The lists represent (A) OECs in infection and control conditions at 2 h; (B) OECs in infection and control conditions at 24 h; (C) IPA Canonical Pathways activated by infection at 24 h; and (D) InnateDB ORA pathway data, ranked according to P value. Red and Green, up- and down-regulated, respectively.

A. Bp infected versus Ctrl OECs at 2h

Genes in Bp-induced	Fold Change (FC)	P-value (for FC)
Transcriptional Signature	Bp infected OECs vs. Ctrl	
in OECs at 2h (n= 24	OECs at 2h	
genes)		
MIR137, MIR137HG, MIR268	5.652781113	5.00E-05
CCL20	3.430175952	5.00E-05
SNORA76, SNORD104	2.967677461	5.00E-05
S100A4	2.259031921	5.00E-05
CSF2	2.037536868	5.00E-05
TNFAIP3	1.934154286	5.00E-05
CXCL1	1.742127526	5.00E-05
CXCL2	1.731748513	5.00E-05
IL8	1.72990009	5.00E-05
CXCL3	1.579544987	5.00E-05
REL	1.573096051	0.00035
PTX3	1.452809496	0.00025
NFKBIA	1.448702006	5.00E-05
PTGS2	1.400184623	5.00E-05
PDE4B	1.379874441	0.00015
NR4A1	1.339597211	0.0004
IL6	1.325164999	0.0003
ANGPTL4	1.316247672	0.0004
KRT14,KRT16,KRT17	-1.649713624	5.00E-05
REXO1	-2.443106786	5.00E-05
SFN	-2.497949063	5.00E-05
KRT13,KRT15	-3.21776659	5.00E-05
KRT19	-3.792060619	0.00035
HEATR6	-31.4366563	5.00E-05

B. Bp infected versus Ctrl OECs at 24h

Genes in Bp-induced	Fold Change (FC)	<i>P</i> -value (for FC)
Transcriptional Signature	Bp infected OECs vs.	
<u>in OECs at 24h (n= 378</u>	Ctrl OECs at 24h	
genes)		
RPS18	-Infinity	5.00E-05
SNORD116-4	23.71770404	5.00E-05
MMP12	20.29615046	0.0002
MX1	17.44594595	5.00E-05
CXCL1	16.05578982	5.00E-05
CXCL5	15.7706868	0.0001
HEATR6	13.44046057	5.00E-05
CXCL10	11.20260175	5.00E-05
C3	10.44253078	5.00E-05
IL8	10.24452768	5.00E-05
CXCL3	8.387213849	5.00E-05
MX2	8.248084743	5.00E-05
OAS1	7.339406888	5.00E-05
IFI27	6.620541205	5.00E-05
IFI44I	6 576332991	5.00E-05
CSE2	6 553482677	5.00E-05
BST2	6 226941618	5.00E-05
116	6 215662394	5.00E-05
	E 077100012	5.002-05
	5.027100015	5.002-05
	5.525400220	5.00E-05
	5.273408459	5.00E-05
	5.042920948	5.00E-05
	4.984519195	0.0002
SERPINB2	4.852668213	5.00E-05
XAF1	4.803312995	5.00E-05
IFITM1	4.608580171	5.00E-05
TNFAIP3	4.536568023	5.00E-05
IL1B	4.102599922	5.00E-05
OAS2	4.081146047	5.00E-05
C15orf48	3.713966677	5.00E-05
MMP10	3.671708981	5.00E-05
SOD2	3.422624307	5.00E-05
CCL2	3.268283292	5.00E-05
PTX3	3.182244925	5.00E-05
BATF2	3.094321463	5.00E-05
USP18	3.061559881	5.00E-05
GBP4	3.015317697	5.00E-05
TNFRSF9	2.951737029	5.00E-05
ICAM1	2.932922788	5.00E-05
TRIM22	2.860187957	5.00E-05
TNFSF13B	2.853596803	5.00E-05
IFIT1	2.832952678	5.00E-05
IFI6	2.806345711	5.00E-05
LRRN3	2.771555517	5.00E-05

C1S	2.678224798	5.00E-05
CLDN1	2.631143076	5.00E-05
EFNA1	2.524965592	5.00E-05
MMP13	2.518036518	5.00E-05
DCN	2.447508409	5.00E-05
IFIH1	2.39966601	5.00E-05
KYNU	2.349839953	5.00E-05
BIRC3	2.342267648	5.00E-05
TRAF1	2.28513357	5.00E-05
TNC	2.224068045	5.00E-05
LIF	2.220873451	5.00E-05
IRAK2	2.192783834	5.00E-05
ESM1	2.160272531	5.00E-05
CTSS	2,137500656	5.00F-05
SEMA3D	2.085013974	5.00E-05
SAMD9I	2 084497339	5.00E-05
INHBA	2.056657596	5.00E-05
NEKBIA	2.028895201	5.00E-05
117	1 983070516	0.00015
	1 977967197	5 00F-05
OAS3	1 9680678/9	5.00E-05
	1,96003963	
	1.955715420	5.00E_05
	1.052751665	5.00L-05
GRD1	1.953751005	5.00L-05
	1.949411919	5.00L-05
	1.940837408	
	1.912308133	5.00L-05
	1.91238703	5.00E-05
	1.909020513	5.00E-05
RTP4	1.898370284	5.00E-05
	1.89/5332/4	5.00E-05
PSIVIB8	1.886750195	0.00065
BDKKB2	1.850192011	5.00E-05
GBP2	1.838178054	5.00E-05
EREG	1.827846912	5.00E-05
ROBO4	1.823272914	5.00E-05
KLRC2,KLRC3	1.804227181	0.00095
PLA2G4A	1.803747247	5.00E-05
HERC6	1.800907495	5.00E-05
RELB	1.789687182	5.00E-05
FAM198B	1.7868103	5.00E-05
IFI44	1.783959925	5.00E-05
HLA-C	1.781028523	0.00075
HAS2	1.778265433	5.00E-05
PTGS2	1.776740121	5.00E-05
CCL5	1.775779092	5.00E-05
ABI3BP	1.761400044	5.00E-05
ZC3H12A	1.754686552	5.00E-05
ATP8B4	1.743969873	0.00015
WISP1	1.740726345	5.00E-05

REL	1.738057063	0.00015
ANXA10	1.734990321	5.00E-05
RPPH1	1.733260615	5.00E-05
TFPI2	1.73059503	5.00E-05
OASL	1.728320162	5.00E-05
TGM2	1.7250694	5.00E-05
EPSTI1	1.723354449	5.00E-05
KLHL38	1.720512084	0.0009
PLSCR1	1.70333004	5.00E-05
DTX3L	1.701119444	5.00E-05
KCNJ15	1.697820046	0.0008
WNT5A	1.689886506	5.00E-05
LCP1	1.68537015	0.0001
FIF3C FIF3CI	1,677981843	5.00F-05
STAT1	1.657945824	5.00E-05
RMRP	1.651062423	5.00E-05
KIAA1107	1 650948469	0 0008
DHX58	1 63726249	5 00F-05
IFIT3	1 634384734	5.00E-05
SAMHD1	1 629852941	5.00E-05
ΔΤΡ2Β1	1 62625563	5.00E-05
	1 623997942	0.0002
	1 618353501	0.0002
	1 61//18852	5 00F-05
FGF2	1 612905426	5.00E-05
	1 503338082	5.00E-05
NRD2	1 587/2161	5.00E-05
	1.586086278	0.00105
	1.580580578	5.00105 E 00E 0E
	1.501050451	5.00E-05
	1.5799752	5.00E-05
	1.509225559	5.00E-05
	1.507800028	5.00E-05
	1.558000073	5.00E-05
	1.555874987	5.00E-05
HLA-B	1.555343254	5.00E-05
IRF9,RNF31	1.553166562	5.00E-05
IFI15	1.54/834361	5.00E-05
SP110	1.544436349	5.00E-05
C1R	1.544292575	5.00E-05
DDX60L	1.539900678	0.001
SEMA3C	1.537114972	5.00E-05
ACO1	1.535253197	5.00E-05
POSTN	1.534049934	0.0001
CD274	1.527375898	5.00E-05
IKBKE	1.523834478	5.00E-05
TRPM3	1.521054532	0.00055
NEGR1	1.519470811	5.00E-05
G0S2	1.519417139	0.0006
SLFN5	1.516336838	0.0001
KLHL5	1.514337055	5.00E-05

IFI16	1.510738094	5.00E-05
SLC39A14	1.504905873	5.00E-05
ANGPT1	1.503708339	0.0009
EDNRA	1.498672406	5.00E-05
НІРК2	1.498230021	5.00E-05
NPR3	1.49806135	5.00E-05
KLF9	1.496789512	5.00E-05
FTH1	1.495263332	5.00E-05
SIRPB1	1.493269689	0.0004
KCNJ2	1.491235529	5.00E-05
SLC4A7	1.486697736	5.00E-05
AMPD3	1.486494848	5.00E-05
IKZF2	1.486440485	0.00105
ZC3H12C	1.48558371	5.00E-05
EIF2AK2	1.484419902	0.00025
DIAPH2	1.484243573	0.00015
UBE2L6	1.477722772	5.00E-05
PNPT1	1.472021475	5.00F-05
DDX58.TOPORS	1.471587533	5.00F-05
LRWD1	1 470304154	5.00E-05
HFI72	1 470073693	5.00E-05
НК2	1 469382122	5.00E-05
F3	1 467390573	5.00E-05
	1 464269076	5.00E-05
RNF144B	1 462676516	5.00E-05
TRPCA	1 462249421	0.00075
IFIT2	1 460841692	5 00F-05
15615	1 460702254	5.00E-05
RASGRP3	1 460459934	0.0008
NAMPT	1 /58762763	5 00F-05
	1.457062165	5.00E-05
GPC6	1.457002105	0.00015
SORDI	1.450515701	5.00F-05
	1,450561483	5.00E-05
15620	1.430301483	0.0005
SAT1	1.449520890	5.00E_05
MCTD1	1.440385052	0.00105
	1.440475054	5 00E 0E
	1.439433114	5.00E-05
	1.436497630	5.00E-05
	1.433020736	0.0001
	1,433790349	
BCATI	1.433247701	5.00E-05
	1.433030825	
	1.432362748	5.00E-05
HDAC9	1.430864554	0.00045
	1.428678534	5.00E-05
NFKBIZ,NXPE3	1.42431958	0.00015
	1.422962441	5.00E-05
	1.418598876	0.0001
RNF213	1.414981252	0.00105

EDN1	1.414853306	0.00105
BMPER	1.409403125	0.0007
PTGFR	1.407959185	0.00015
NR1D2	1.406995672	5.00E-05
LPAR1	1.404362893	5.00E-05
LHFPL2	1.403360687	5.00E-05
STC1	1.401712497	0.00035
PDE3A	1.400949657	5.00E-05
GTF2I	1.400848804	0.00045
GLIS3	1.394500859	0.00035
KIAA1644	1.392630443	0.0001
FAM126A	1.392589303	5.00E-05
APOL6	1.39199648	5.00E-05
ITGAV	1.390890518	0.00025
TFPI	1.390704624	5.00E-05
TNFAIP2	1.388464563	0.00025
SP100	1.387865248	0.0005
CYP1B1	1.384234482	0.00015
NAB1	1.384155928	0.0003
ETS1	1.380814872	5.00E-05
ASPH	1.38017299	0.00025
HECW2	1.37924765	0.00085
HLA-B	1.378110978	0.0007
SEC22B	1.375545713	0.0003
MYOCD	1.372065295	0.0005
FER	1.371371454	0.00035
DNAJB14	1.370170103	0.0006
CEP170	1.366905132	5.00E-05
ADAMTS1	1.366747253	5.00E-05
SEMA5A	1.36655313	0.00095
SLIT2	1.364530521	0.0005
NEDD4	1.364375102	0.00025
РІКЗСА	1.363146159	0.00085
RNF138	1.360689077	0.0005
RIPK2	1.36032989	0.0003
PRKAA1	1.359172957	0.0003
HLA-B	1.358055708	0.00055
CDK6	1.357966827	0.00055
ELOVL2	1.357404885	0.001
TGFBR1	1.35255569	0.00015
ARHGAP31	1.350096793	0.00045
PPFIBP1,REP15	1.348624427	0.00045
IL11	1.347950774	0.0001
TMEM171	1.347501832	0.00085
CD82	1.346875618	0.0006
MTR	1.345124917	0.0007
ARRDC3	1.344808784	0.00105
KRAS	1.343986261	0.00035
NOTCH2	1.343789848	0.00055
ADAM9	1.340150675	0.00025

RICTOR	1.338991368	0.00045
AOX1	1.338660969	0.00035
UEVLD	1.336727604	0.0009
ADAM12	1.335532349	0.0006
OTUD4	1.333136238	0.0005
TRIM25	1.332736913	0.0003
TRANK1	1.330423398	0.00075
NEDD1	1.330422739	0.00085
PDE4D	1.329070906	0.0006
TRIM21	1.325982863	0.00075
UQCRB	1.324990812	0.00065
P4HA1	1.324125775	0.00035
SOCS5	1.322009586	0.0009
UBASH3B	1.321909573	0.00045
PKN2	1.320472695	0.00085
LNPEP	1.319631566	0.0012
SERPINB8	1,318971305	0.0007
PPAP2B	1.317827701	0.00085
	1 317624209	0.000
TOP2B	1 317514419	0.0007
ABCF1	1 316416922	0.0007
	1 315836355	0.00105
	1 31525557	0.00043
	1 21//2717	0.0004
	1 200252284	0.00113
	1 207126754	0.0012
	1 306202026	0.0012
	1.306056865	0.0011
	1.202962969	0.00003
	1.303602606	0.00125
	1.299053134	0.0008
	1.297664535	0.00125
PDCD5	1.293538847	0.001
	1.292883055	0.0011
SLC9A3R1	-1.286936962	0.0012
	-1.306589877	0.00115
IER5L	-1.307960658	0.00035
I HEM6	-1.31495834	0.0007
SOLH	-1.315195802	0.00105
EVA1B	-1.317711115	0.0011
CCNL2	-1.318476351	0.00095
H2AFX	-1.319890399	0.0008
SLC6A9	-1.329154936	0.0009
TINAGL1	-1.336918785	0.00055
RAMP1	-1.341004359	0.00105
SMCR7	-1.341711647	0.00085
MFAP2	-1.342634601	0.0011
MVD	-1.348848901	0.0004
RTN4R	-1.349209257	0.00115
RBP4	-1.349466571	0.00055
GIGYF1	-1.352334406	0.0004

ARHGAP33	-1.354233508	0.00105
HIC1	-1.35687479	0.00085
C17orf59	-1.357599263	0.00055
CACFD1	-1.36205543	0.00045
DDX12P	-1.362576964	0.00095
NPTX2	-1.362767787	0.00025
PIF1	-1.364144518	0.00075
ABCA7	-1.366830931	0.00025
SCARF2	-1.368243302	0.00055
EPHB3	-1.36849374	0.0006
SLC6A8	-1.37355833	5.00E-05
ASNS	-1.37450164	0.00025
PCSK9	-1.379298342	0.0002
PHGDH	-1.382052476	5.00F-05
TRIB3	-1.382934751	0.0002
SI C9A3R2	-1.39466246	0.0002
	-1 401194458	5 00F-05
	-1 406537012	0.0005
	-1 410770388	5 00F-05
	-1 414830492	0.00015
GDE15	-1 41523432	0.0012
	-1 /29539123	5 00F-05
SH2B2	-1 /30/113/9	0.00015
FIRCD1	-1 /3071/355	5 00F-05
FAM222A	-1.430714333	0.000
	-1.437154040	0.0001
IGEN1	-1.441050012	0.001
	-1.442259524	0.00095
	1 443133330	0.0007
	-1.447362254	
		5.00E-05
	-1.457953824	
GPRCSC	-1.461/88184	5.00E-05
RCNQ2	-1.4/3800/03	0.0003
APOE	-1.4/9215805	0.00035
ISC22D3	-1.482623051	5.00E-05
IIGB4	-1.500901028	5.00E-05
CYS1	-1.505443606	0.00055
VIPR1	-1.507523434	0.00015
HDAC10	-1.509504801	0.00015
PLEKHH3	-1.514302768	5.00E-05
GOLGA8B	-1.514523165	5.00E-05
ADRA2C	-1.516722316	0.00015
INHBB	-1.520265703	5.00E-05
EPS8L2	-1.522438321	0.0009
ISYNA1	-1.522738183	0.0001
RASGRP2	-1.526536313	0.00015
WNT9A	-1.530185417	0.0007
ADCY5	-1.5333824	5.00E-05
HES6	-1.533466971	5.00E-05
IL17RE	-1.536004079	0.0004

ZGLP1	-1.561488998	0.00035
TSSK6	-1.561504372	0.00075
KCNK15	-1.567535728	0.0004
SLC18A3	-1.581551697	0.0007
TSPAN10	-1.585258526	0.0002
LINC00324	-1.585775505	0.00035
HAP1	-1.586688418	0.00025
ADM2	-1.595866487	0.00015
ARC	-1.612568493	0.00045
SEC31B	-1.615127166	5.00E-05
HSD11B2	-1.624954536	0.00015
MROH6	-1.675010512	5.00E-05
CHRD	-1.681640425	0.00045
NUPR1	-1.717948262	5.00E-05
NGFR	-1.73273877	0.0001
INHBE	-1.733571935	0.00075
KRT14,KRT16,KRT17	-1.736221702	5.00E-05
ADAM33	-1.762341221	5.00E-05
CHAC1	-1.828254848	5.00E-05
SCNN1D	-1.841324016	5.00E-05
LPAR5	-1.868746198	5.00E-05
PRRG2	-1.967163529	0.0011
GRM4	-2.107222843	5.00E-05
REXO1	-2.247529463	5.00E-05
RHBDL1	-2.351888992	0.00095
CPSF1	-2.449056883	5.00E-05
CRYAB	-3.066037064	0.0003
SCRIB	-4.120263072	5.00E-05
TNNC1	-4.970938804	5.00E-05
TNNI3	-5.136855034	5.00E-05
MYL3	-7.049604028	0.0001
SNORA76,SNORD104	-14.07978218	5.00E-05
ACTC1	-17.93718055	5.00E-05
MIR1204,PVT1	-60.4901186	5.00E-05

C. IPA Canonical Pathways for Bp infected versus Ctrl OECs at 24h

Ingenuity Canonical Pathways	-log (p-	Ratio	z-score
	value)		
Agranulocyte Adhesion and Diapedesis	2.25E01	1.11E-01	
Granulocyte Adhesion and Diapedesis	1.86E01	1.02E-01	
Role of IL-17F in Allergic Inflammatory Airway Diseases	1.23E01	2.05E-01	
Role of IL-17A in Arthritis	1.14E01	1.67E-01	
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	9.89E00	4.7E-02	
Hepatic Fibrosis / Hepatic Stellate Cell Activation	9.82E00	6.09E-02	
Differential Regulation of Cytokine Production in Macrophages and T Helper Cells by IL-17A and IL-17F	9.77E00	3.33E-01	
Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	9.34E00	7.87E-02	2.000
IL-17 Signaling	8.76E00	1.11E-01	
Role of IL-17A in Psoriasis	8.58E00	3.85E-01	
TREM1 Signaling	7.19E00	9.33E-02	2.646
Differential Regulation of Cytokine Production in Intestinal Epithelial Cells by IL-17A and IL-17F	7.18E00	2.17E-01	
IL-17A Signaling in Gastric Cells	6.98E00	2E-01	
Atherosclerosis Signaling	6.91E00	6.5E-02	
Role of Cytokines in Mediating Communication between Immune Cells	6.59E00	1.07E-01	
IL-17A Signaling in Airway Cells	6.24E00	9.38E-02	
IL-17A Signaling in Fibroblasts	6.21E00	1.43E-01	
Inhibition of Matrix Metalloproteases	5.97E00	1.28E-01	
HMGB1 Signaling	5.79E00	5.83E-02	2.646
Role of Hypercytokinemia/hyperchemokinemia in the Pathogenesis of Influenza	5.65E00	1.11E-01	
Bladder Cancer Signaling	5.45E00	6.9E-02	
Glucocorticoid Receptor Signaling	5.39E00	3.45E-02	
Hematopoiesis from Pluripotent Stem Cells	5.38E00	9.8E-02	
Leukocyte Extravasation Signaling	5.35E00	4.04E-02	1.890
Communication between Innate and Adaptive Immune Cells	5.34E00	6.59E-02	
Airway Pathology in Chronic Obstructive Pulmonary Disease	5.25E00	3.75E-01	
Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	5.03E00	3.65E-02	
TNFR2 Signaling	4.99E00	1.38E-01	
Hepatic Cholestasis	4.93E00	4.32E-02	
Role of Tissue Factor in Cancer	4.86E00	5.45E-02	
Acute Phase Response Signaling	4.81E00	4.14E-02	2.236

Interferon Signaling	4.71E00	1.18E-01	2.000
Calcium Signaling	4.66E00	3.93E-02	
Toll-like Receptor Signaling	4.58E00	6.76E-02	1.000
HIF1α Signaling	3.91E00	4.9E-02	
Tight Junction Signaling	3.85E00	3.59E-02	
Dendritic Cell Maturation	3.68E00	3.35E-02	
CD40 Signaling	3.59E00	6.15E-02	
4-1BB Signaling in T Lymphocytes	3.38E00	9.68E-02	
Oncostatin M Signaling	3.26E00	8.82E-02	
TWEAK Signaling	3.26E00	8.82E-02	
Pathogenesis of Multiple Sclerosis	3.11E00	2.22E-01	
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	3.09E00	4.55E-02	
B Cell Activating Factor Signaling	3.05E00	7.5E-02	
Colorectal Cancer Metastasis Signaling	3.05E00	2.54E-02	2.449
Hematopoiesis from Multipotent Stem Cells	2.85E00	1.67E-01	
TNFR1 Signaling	2.79E00	6.12E-02	
Lymphotoxin β Receptor Signaling	2.67E00	5.56E-02	
IL-6 Signaling	2.65E00	3.45E-02	2.000
LXR/RXR Activation	2.58E00	3.31E-02	-1.000
Induction of Apoptosis by HIV1	2.54E00	5E-02	
Cellular Effects of Sildenafil (Viagra)	2.48E00	3.1E-02	
Activation of IRF by Cytosolic Pattern Recognition Receptors	2.46E00	4.69E-02	
IL-15 Signaling	2.42E00	4.55E-02	
IL-10 Signaling	2.39E00	4.41E-02	
Epithelial Adherens Junction Signaling	2.29E00	2.74E-02	
Crosstalk between Dendritic Cells and Natural Killer Cells	2.06E00	3.37E-02	
NF-ĸB Signaling	2.04E00	2.31E-02	0.000
Death Receptor Signaling	2.02E00	3.26E-02	
IL-8 Signaling	1.95E00	2.19E-02	2.000
ILK Signaling	1.93E00	2.15E-02	-2.000
Complement System	1.88E00	5.41E-02	
April Mediated Signaling	1.86E00	5.26E-02	
Thyroid Cancer Signaling	1.81E00	5E-02	
Axonal Guidance Signaling	1.77E00	1.39E-02	

iNOS Signaling	1.74E00	4.55E-02
Role of RIG1-like Receptors in Antiviral Innate Immunity	1.72E00	4.44E-02
Actin Cytoskeleton Signaling	1.71E00	1.84E-02
MSP-RON Signaling Pathway	1.7E00	4.35E-02
Systemic Lupus Erythematosus Signaling	1.69E00	1.82E-02
Graft-versus-Host Disease Signaling	1.66E00	4.17E-02
Tetrahydrofolate Salvage from 5,10-methenyltetrahydrofolate	1.63E00	2E-01
Superoxide Radicals Degradation	1.55E00	1.67E-01
Protein Ubiquitination Pathway	1.48E00	1.57E-02
Histidine Degradation III	1.43E00	1.25E-01
Tryptophan Degradation to 2-amino-3-carboxymuconate Semialdehyde	1.43E00	1.25E-01
Role of MAPK Signaling in the Pathogenesis of Influenza	1.39E00	2.94E-02
Folate Transformations I	1.38E00	1.11E-01
Small Cell Lung Cancer Signaling	1.35E00	2.82E-02
PEDF Signaling	1.35E00	2.82E-02
VDR/RXR Activation	1.28E00	2.56E-02
PPARa/RXRa Activation	1.28E00	1.68E-02
Cleavage and Polyadenylation of Pre-mRNA	1.26E00	8.33E-02
RANK Signaling in Osteoclasts	1.19E00	2.27E-02
Apoptosis Signaling	1.18E00	2.25E-02
NAD biosynthesis II (from tryptophan)	1.16E00	6.67E-02
Regulation of Actin-based Motility by Rho	1.16E00	2.2E-02
IL-1 Signaling	1.16E00	2.2E-02
Fcy Receptor-mediated Phagocytosis in Macrophages and Monocytes	1.14E00	2.15E-02
PPAR Signaling	1.14E00	2.13E-02
Antioxidant Action of Vitamin C	1.11E00	2.06E-02
Cardiomyocyte Differentiation via BMP Receptors	1.04E00	5E-02
Tryptophan Degradation III (Eukaryotic)	1.04E00	5E-02
Type I Diabetes Mellitus Signaling	1.02E00	1.82E-02
Ga12/13 Signaling	9.75E-01	1.71E-02
p38 MAPK Signaling	9.75E-01	1.71E-02
Tumoricidal Function of Hepatic Natural Killer Cells	9.68E-01	4.17E-02
Role of Lipids/Lipid Rafts in the Pathogenesis of Influenza	9.52E-01	4E-02
Role of JAK family kinases in IL-6-type Cytokine Signaling	9.52E-01	4E-02

RhoA Signaling	9.45E-01	1.64E-02
IL-15 Production	9.2E-01	3.7E-02
FXR/RXR Activation	9.16E-01	1.57E-02
PI3K Signaling in B Lymphocytes	9.11E-01	1.56E-02
Aryl Hydrocarbon Receptor Signaling	8.48E-01	1.43E-02
MIF-mediated Glucocorticoid Regulation	8.39E-01	3.03E-02
Aldosterone Signaling in Epithelial Cells	7.91E-01	1.32E-02
Docosahexaenoic Acid (DHA) Signaling	7.72E-01	2.56E-02
Role of PKR in Interferon Induction and Antiviral Response	7.62E-01	2.5E-02
MIF Regulation of Innate Immunity	7.53E-01	2.44E-02
Mechanisms of Viral Exit from Host Cells	7.53E-01	2.44E-02
RhoGDI Signaling	7.05E-01	1.16E-02
RAR Activation	6.94E-01	1.14E-02
Ephrin A Signaling	6.91E-01	2.08E-02
Sertoli Cell-Sertoli Cell Junction Signaling	6.87E-01	1.12E-02
Role of NFAT in Cardiac Hypertrophy	6.83E-01	1.12E-02
NRF2-mediated Oxidative Stress Response	6.79E-01	1.11E-02
CD27 Signaling in Lymphocytes	6.6E-01	1.92E-02
Glutamate Receptor Signaling	6.25E-01	1.75E-02
ATM Signaling	6.12E-01	1.69E-02
GM-CSF Signaling	5.94E-01	1.61E-02
ERK5 Signaling	5.88E-01	1.59E-02
Retinoic acid Mediated Apoptosis Signaling	5.82E-01	1.56E-02
Hypoxia Signaling in the Cardiovascular System	5.76E-01	1.54E-02
Angiopoietin Signaling	5.7E-01	1.52E-02
Role of PI3K/AKT Signaling in the Pathogenesis of Influenza	5.7E-01	1.52E-02
PXR/RXR Activation	5.65E-01	1.49E-02
Erythropoietin Signaling	5.65E-01	1.49E-02
Protein Kinase A Signaling	5.6E-01	7.77E-03
Remodeling of Epithelial Adherens Junctions	5.59E-01	1.47E-02
Agrin Interactions at Neuromuscular Junction	5.54E-01	1.45E-02
Cardiac Hypertrophy Signaling	5.46E-01	8.97E-03
T Helper Cell Differentiation	5.43E-01	1.41E-02
Chemokine Signaling	5.43E-01	1.41E-02

Caveolar-mediated Endocytosis Signaling	5.38E-01	1.39E-02
JAK/Stat Signaling	5.38E-01	1.39E-02
LPS-stimulated MAPK Signaling	5.33E-01	1.37E-02
NF-ĸB Activation by Viruses	5.33E-01	1.37E-02
Signaling by Rho Family GTPases	5.18E-01	8.55E-03
Regulation of IL-2 Expression in Activated and Anergic T Lymphocytes	5.05E-01	1.27E-02
Prostate Cancer Signaling	4.91E-01	1.22E-02
HIPPO signaling	4.75E-01	1.16E-02
FAK Signaling	4.71E-01	1.15E-02
TGF-β Signaling	4.71E-01	1.15E-02
Neuregulin Signaling	4.67E-01	1.14E-02
G-Protein Coupled Receptor Signaling	4.66E-01	7.81E-03
Virus Entry via Endocytic Pathways	4.63E-01	1.12E-02
PAK Signaling	4.63E-01	1.12E-02
OX40 Signaling Pathway	4.63E-01	1.12E-02
VEGF Signaling	4.55E-01	1.1E-02
Factors Promoting Cardiogenesis in Vertebrates	4.51E-01	1.09E-02
Mouse Embryonic Stem Cell Pluripotency	4.4E-01	1.05E-02
Xenobiotic Metabolism Signaling	4.35E-01	7.38E-03
T Cell Receptor Signaling	4.33E-01	1.03E-02
Amyotrophic Lateral Sclerosis Signaling	4.29E-01	1.02E-02
Neuropathic Pain Signaling In Dorsal Horn Neurons	4.22E-01	1E-02
Cholecystokinin/Gastrin-mediated Signaling	4.19E-01	9.9E-03
Paxillin Signaling	4.16E-01	9.8E-03
HGF Signaling	4.06E-01	9.52E-03
fMLP Signaling in Neutrophils	3.96E-01	9.26E-03
iCOS-iCOSL Signaling in T Helper Cells	3.96E-01	9.26E-03
Fc Epsilon RI Signaling	3.93E-01	9.17E-03
Renin-Angiotensin Signaling	3.93E-01	9.17E-03
Role of NANOG in Mammalian Embryonic Stem Cell Pluripotency	3.87E-01	9.01E-03
Type II Diabetes Mellitus Signaling	3.7E-01	8.55E-03
CD28 Signaling in T Helper Cells	3.67E-01	8.47E-03
PKC0 Signaling in T Lymphocytes	3.67E-01	8.47E-03
Synaptic Long Term Potentiation	3.65E-01	8.4E-03

Gai Signaling	3.62E-01	8.33E-03
PI3K/AKT Signaling	3.54E-01	8.13E-03
Human Embryonic Stem Cell Pluripotency	3.27E-01	7.46E-03
Relaxin Signaling	3.24E-01	7.41E-03
Synaptic Long Term Depression	3.11E-01	7.09E-03
Regulation of eIF4 and p70S6K Signaling	3E-01	6.85E-03
Gaq Signaling	2.98E-01	6.8E-03
CXCR4 Signaling	2.88E-01	6.58E-03
Molecular Mechanisms of Cancer	2.86E-01	5.48E-03
Gap Junction Signaling	2.83E-01	6.45E-03
Tec Kinase Signaling	2.77E-01	6.33E-03
Germ Cell-Sertoli Cell Junction Signaling	2.73E-01	6.25E-03
Cdc42 Signaling	2.61E-01	5.99E-03
Mitochondrial Dysfunction	2.54E-01	5.85E-03
Role of NFAT in Regulation of the Immune Response	2.54E-01	5.85E-03
CREB Signaling in Neurons	2.54E-01	5.85E-03
Ephrin Receptor Signaling	2.49E-01	5.75E-03
B Cell Receptor Signaling	2.46E-01	5.68E-03
Production of Nitric Oxide and Reactive Oxygen Species in Macrophages	2.4E-01	5.56E-03
Clathrin-mediated Endocytosis Signaling	2.32E-01	5.41E-03
EIF2 Signaling	2.32E-01	5.41E-03
mTOR Signaling	2.28E-01	5.32E-03
Thrombin Signaling	2.24E-01	5.24E-03
Integrin Signaling	2.09E-01	4.95E-03

D. Pathway Over-representation Analysis for Bp infected vs Ctrl OECs at 24h

Pathway Name	Path.	Source	Org.	Pathway up-	Genes in	Pathway up-	Pathway up-	Pathway	Pathway	Pathway
(Red is Up-regulated, Green is Down-regulated,	Id	Name		regulated	InnateDB	regulated p-	regulated p-	down-	down-	down-
Pathways with P values of <0.05 shown sorted				genes count		value	value	regulated	regulated	regulated p-
according to most significant)							(corrected)	genes	p-value	value
	_							count		(corrected)
Cytokine-cytokine receptor interaction	515	KEGG	9606	17	247	5.16E-15	1.20E-11	0	1	1
Chemokine receptors bind chemokines	13243	REACTOME	9606	9	49	3.42E-12	2.65E-09	0	1	1
Cytokine Signaling in Immune system	17418	REACTOME	9606	15	256	2.96E-12	3.44E-09	0	1	1
NOD-like receptor signaling pathway	8112	KEGG	9606	9	54	8.68E-12	5.03E-09	0	1	1
Interferon alpha/beta signaling	13074	REACTOME	9606	9	59	2.01E-11	9.33E-09	0	1	1
Interferon Signaling	18059	REACTOME	9606	11	151	3.53E-10	1.37E-07	0	1	1
Striated Muscle Contraction	13920	REACTOME	9606	0	33	1	1	5	1.08E-10	2.51E-07
Immune System	18444	REACTOME	9606	22	1081	9.95E-09	3.30E-06	0	1	1
Cardiac muscle contraction	4399	KEGG	9606	0	73	1	1	5	6.73E-09	5.21E-06
Muscle contraction	19261	REACTOME	9606	0	53	1	1	5	1.30E-09	1.51E-06
Chemokine signaling pathway	4389	KEGG	9606	10	173	2.31E-08	6.71E-06	0	1	1
Validated transcriptional targets of AP1 family m	14994	PID NCI	9606	6	35	2.74E-08	7.08E-06	0	1	1
Peptide ligand-binding receptors	13249	REACTOME	9606	10	179	3.21E-08	7.44E-06	0	1	1
Hypertrophic cardiomyopathy (HCM)	4395	KEGG	9606	1	83	0.3655193	1	5	1.30E-08	7.52E-06
Dilated cardiomyopathy	5714	KEGG	9606	0	90	1	1	5	1.95E-08	9.07E-06
Malaria	10359	KEGG	9606	6	46	1.51E-07	3.19E-05	0	1	1
IL23-mediated signaling events	15427	PID NCI	9606	5	37	1.49E-06	2.88E-04	0	1	1
G alpha (i) signalling events	13220	REACTOME	9606	9	223	2.62E-06	4.68E-04	1	0.21794	1
Class A/1 (Rhodopsin-like receptors)	13250	REACTOME	9606	10	296	3.39E-06	5.62E-04	0	1	1
CD40/CD40L signaling	14909	PID NCI	9606	4	26	1.06E-05	0.00164362	0	1	1
Toll-like receptor signaling pathway	564	KEGG	9606	6	98	1.37E-05	0.00199153	0	1	1
Chagas disease (American trypanosomiasis)	10366	KEGG	9606	6	101	1.63E-05	0.00222902	0	1	1
Activation of Matrix Metalloproteinases	13391	REACTOME	9606	4	32	2.49E-05	0.00289466	0	1	1
Amoebiasis	10358	KEGG	9606	6	107	2.27E-05	0.00292877	0	1	1
Tnfr2 signaling pathway	4004	PID BIOCART	9606	3	11	2.43E-05	0.00296442	0	1	1

AP-1 transcription factor network	15318 PID NCI	9606	5	67	2.91E-05	0.00322007	0	1	1
Signal transduction through il1r	4064 PID BIOCAR1	9606	4	34	3.19E-05	0.00322029	0	1	1
Glucocorticoid receptor regulatory network	15321 PID NCI	9606	5	68	3.13E-05	0.00330413	0	1	1
Degradation of the extracellular matrix	17498 REACTOME	9606	6	116	3.59E-05	0.00347521	0	1	1
GPCR ligand binding	19266 REACTOME	9606	10	420	7.10E-05	0.00658846	1	0.373828	1
Hepatitis C	10404 KEGG	9606	6	132	7.42E-05	0.00662703	0	1	1
Extracellular matrix organization	17095 REACTOME	9606	8	264	7.87E-05	0.00676875	0	1	1
Cytosolic DNA-sensing pathway	8117 KEGG	9606	4	58	2.65E-04	0.02198396	0	1	1
Antiviral mechanism by IFN-stimulated genes	17226 REACTOME	9606	4	62	3.43E-04	0.02489101	0	1	1
ISG15 antiviral mechanism	13075 REACTOME	9606	4	62	3.43E-04	0.02489101	0	1	1
Interferon gamma signaling	13077 REACTOME	9606	4	62	3.43E-04	0.02489101	0	1	1
Collagen degradation	13392 REACTOME	9606	4	61	3.22E-04	0.02579683	0	1	1
Nfkb activation by nontypeable hemophilus influ	4159 PID BIOCAR1	9606	3	28	4.51E-04	0.03174895	0	1	1
RIG-I-like receptor signaling pathway	5713 KEGG	9606	4	69	5.17E-04	0.03530383	0	1	1
JAK STAT pathway and regulation	16125 INOH	9606	7	267	5.54E-04	0.03676622	0	1	1
NOD1/2 Signaling Pathway	13056 REACTOME	9606	3	31	6.12E-04	0.03947658	0	1	1
HIV-1 Nef: Negative effector of Fas and TNF-alph	15863 PID NCI	9606	3	33	7.38E-04	0.04626598	0	1	1
Toll-Like Receptors Cascades	17767 REACTOME	9606	5	136	8.19E-04	0.04876558	0	1	1
TNF receptor signaling pathway	15154 PID NCI	9606	3	34	8.06E-04	0.04921935	0	1	1
African trypanosomiasis	10384 KEGG	9606	3	35	8.78E-04	0.05094678	0	1	1
GPCR signaling	16218 INOH	9606	7	291	9.23E-04	0.05226469	1	0.275303	1
Cd40l signaling pathway	4093 PID BIOCAR1	9606	2	9	0.0010197	0.05635109	0	1	1
Apoptosis	485 KEGG	9606	4	85	0.0011363	0.05994233	0	1	1
Hematopoietic cell lineage	415 KEGG	9606	4	85	0.0011363	0.05994233	0	1	1
MyD88-independent cascade	13030 REACTOME	9606	4	94	0.0016511	0.08153795	0	1	1
TRIF-mediated TLR3/TLR4 signaling	19507 REACTOME	9606	4	94	0.0016511	0.08153795	0	1	1
Toll Like Receptor 3 (TLR3) Cascade	13031 REACTOME	9606	4	94	0.0016511	0.08153795	0	1	1
Nucleotide-binding domain, leucine rich repeat of	18305 REACTOME	9606	3	46	0.0019526	0.09248964	0	1	1
Signaling by GPCR	17449 REACTOME	9606	13	991	0.0019477	0.09417882	1	0.680786	1
Innate Immune System	17476 REACTOME	9606	9	534	0.0020844	0.09675847	0	1	1
Erythropoietin mediated neuroprotection throug	4161 PID BIOCART	9606	2	13	0.0021788	0.09915848	0	1	1
Activated TLR4 signalling	19190 REACTOME	9606	4	106	0.0025642	0.11021468	0	1	1

Signaling by Interleukins	18744 REACTOME	9606	4	105	0.0024773	0.11057384	0	1	1
Staphylococcus aureus infection	10357 KEGG	9606	3	51	0.0026281	0.1109064	0	1	1
Classical complement pathway	3972 PID BIOCAR1	9606	2	14	0.0025332	0.11093317	0	1	1
Hiv-1 nef: negative effector of fas and tnf	4101 PID BIOCART	9606	3	52	0.0027784	0.11313475	0	1	1
Keratinocyte differentiation	4032 PID BIOCART	9606	3	52	0.0027784	0.11313475	0	1	1
Assembly of collagen fibrils and other multimeric	13386 REACTOME	9606	3	54	0.0030947	0.12384027	0	1	1
Toll Like Receptor 4 (TLR4) Cascade	13046 REACTOME	9606	4	118	0.0037765	0.14856411	0	1	1
Initial triggering of complement	13054 REACTOME	9606	2	18	0.0042003	0.15981765	0	1	1
Immunoregulatory interactions between a Lymp	13066 REACTOME	9606	3	60	0.004173	0.16142583	0	1	1
IL1	15917 NETPATH	9606	3	66	0.0054543	0.20418604	0	1	1
CXCR3-mediated signaling events	15621 PID NCI	9606	2	21	0.0057054	0.20691104	0	1	1
Epithelial cell signaling in Helicobacter pylori infe	457 KEGG	9606	3	67	0.0056884	0.2095661	0	1	1
GMCSF-mediated signaling events	15598 PID NCI	9606	2	22	0.0062543	0.21994153	0	1	1
Leishmaniasis	10355 KEGG	9606	3	69	0.0061743	0.22046919	0	1	1
ATF4 activates genes	13379 REACTOME	9606	2	23	0.0068262	0.22961804	0	1	1
Canonical NF-kappaB pathway	15469 PID NCI	9606	2	23	0.0068262	0.22961804	0	1	1
TRAF6 mediated NF-kB activation	13015 REACTOME	9606	2	23	0.0068262	0.22961804	0	1	1
RIG-I/MDA5 mediated induction of IFN-alpha/be	13017 REACTOME	9606	3	75	0.0077781	0.25789974	0	1	1
Pathways in cancer	4397 KEGG	9606	6	324	0.0078936	0.25804168	0	1	1
Alpha9 beta1 integrin signaling events	15241 PID NCI	9606	2	25	0.0080385	0.25912886	0	1	1
IL27-mediated signaling events	15133 PID NCI	9606	2	26	0.0086783	0.27219223	0	1	1
PERK regulates gene expression	13380 REACTOME	9606	2	26	0.0086783	0.27219223	0	1	1
Polyadenylation of mrna	4158 PID BIOCART	9606	0	8	1	1	1	0.008677	1
Transport of Mature mRNA Derived from an Intr	13750 REACTOME	9606	0	8	1	1	1	0.008677	1
Transport of Mature mRNAs Derived from Intror	19048 REACTOME	9606	0	9	1	1	1	0.009757	1
Jak-STAT signaling pathway	568 KEGG	9606	4	153	0.0094009	0.27973755	0	1	1
MyD88 cascade initiated on plasma membrane	13043 REACTOME	9606	3	80	0.0092861	0.27990895	0	1	1
Toll Like Receptor 10 (TLR10) Cascade	13044 REACTOME	9606	3	80	0.0092861	0.27990895	0	1	1
Toll Like Receptor 5 (TLR5) Cascade	13048 REACTOME	9606	3	80	0.0092861	0.27990895	0	1	1
TRAF6 mediated induction of NFkB and MAP kina	13040 REACTOME	9606	3	81	0.0096067	0.28224376	0	1	1
MyD88 dependent cascade initiated on endoson	13041 REACTOME	9606	3	83	0.0102674	0.28711523	0	1	1
Toll Like Receptor 7/8 (TLR7/8) Cascade	16831 REACTOME	9606	3	83	0.0102674	0.28711523	0	1	1

Beta2 integrin cell surface interactions	15182 PID NCI	9606	2	28	0.0100239	0.28722791	0	1	1
TAK1 activates NFkB by phosphorylation and act	13027 REACTOME	9606	2	28	0.0100239	0.28722791	0	1	1
Syndecan-2-mediated signaling events	14896 PID NCI	9606	2	29	0.0107293	0.28956507	0	1	1
amb2 Integrin signaling	15836 PID NCI	9606	2	29	0.0107293	0.28956507	0	1	1
Collagen formation	19746 REACTOME	9606	3	84	0.0106074	0.29309189	0	1	1
Import of palmitoyl-CoA into the mitochondrial r	13521 REACTOME	9606	0	11	1	1	1	0.011914	1
Small cell lung cancer	527 KEGG	9606	3	86	0.0113069	0.29821935	0	1	1
Toll Like Receptor 9 (TLR9) Cascade	13042 REACTOME	9606	3	86	0.0113069	0.29821935	0	1	1
Negative regulators of RIG-I/MDA5 signaling	13013 REACTOME	9606	2	30	0.011456	0.29875633	0	1	1
MyD88:Mal cascade initiated on plasma membra	13034 REACTOME	9606	3	88	0.0120326	0.30689662	0	1	1
Toll Like Receptor TLR6:TLR2 Cascade	13036 REACTOME	9606	3	88	0.0120326	0.30689662	0	1	1
Toll Like Receptor 2 (TLR2) Cascade	17710 REACTOME	9606	3	91	0.0131705	0.32519854	0	1	1
Toll Like Receptor TLR1:TLR2 Cascade	13035 REACTOME	9606	3	91	0.0131705	0.32519854	0	1	1
Ceramide signaling pathway	4149 PID BIOCART	9606	2	32	0.0129725	0.32727434	0	1	1
Processing of Intronless Pre-mRNAs	13664 REACTOME	9606	0	13	1	1	1	0.014066	1
TWEAK	15930 NETPATH	9606	2	34	0.0145716	0.35600807	0	1	1
Complement cascade	19237 REACTOME	9606	2	35	0.0154016	0.37236462	0	1	1
Bladder cancer	514 KEGG	9606	2	36	0.0162514	0.3848928	0	1	1
Prion diseases	4396 KEGG	9606	2	36	0.0162514	0.3848928	0	1	1
Regulation of pyruvate dehydrogenase (PDH) cor	13591 REACTOME	9606	0	16	1	1	1	0.017287	1
Graft-versus-host disease	2807 KEGG	9606	2	37	0.0171209	0.40139093	0	1	1
IL-1 signaling pathway	16110 INOH	9606	2	38	0.0180099	0.41387219	0	1	1
Urokinase-type plasminogen activator (uPA) and	15219 PID NCI	9606	2	38	0.0180099	0.41387219	0	1	1
GPCR downstream signaling	18003 REACTOME	9606	10	884	0.018972	0.43170633	1	0.636556	1
Interleukin-1 signaling	13078 REACTOME	9606	2	40	0.0198455	0.44719702	0	1	1
Antagonism of Activin by Follistatin	13272 REACTOME	9606	1	4	0.021594	0.48191948	0	1	1
Calcineurin-regulated NFAT-dependent transcrip	15231 PID NCI	9606	2	44	0.0237401	0.5101926	0	1	1
Processing of Capped Intronless Pre-mRNA	18842 REACTOME	9606	0	22	1	1	1	0.023699	1
Ceramide signaling pathway	14925 PID NCI	9606	2	44	0.0237401	0.5101926	0	1	1
Interleukin-2 signaling	13083 REACTOME	9606	2	44	0.0237401	0.5101926	0	1	1
Intestinal immune network for IgA production	8118 KEGG	9606	2	44	0.0237401	0.5101926	0	1	1
Pyruvate metabolism	13592 REACTOME	9606	0	24	1	1	1	0.025829	1

LPA receptor mediated events	15008 PID NCI	9606	2	46	0.0257957	0.54928363	0	1	1
Acetylation and deacetylation of rela in nucleus	4016 PID BIOCART	9606	1	5	0.0269207	0.56290872	0	1	1
Alternative complement activation	13053 REACTOME	9606	1	5	0.0269207	0.56290872	0	1	1
Transport of Mature Transcript to Cytoplasm	18637 REACTOME	9606	0	25	1	1	1	0.026892	1
Asthma	2818 KEGG	9606	0	28	1	1	1	0.030075	1
mRNA 3'-end processing	13667 REACTOME	9606	0	30	1	1	1	0.032191	1
Activation of C3 and C5	13049 REACTOME	9606	1	6	0.0322189	0.65026209	0	1	1
Classical antibody-mediated complement activat	13051 REACTOME	9606	1	6	0.0322189	0.65026209	0	1	1
IL-6 signaling	16155 INOH	9606	1	6	0.0322189	0.65026209	0	1	1
Interleukin-1 processing	13085 REACTOME	9606	1	6	0.0322189	0.65026209	0	1	1
ATF-2 transcription factor network	15253 PID NCI	9606	2	55	0.0358868	0.71804501	0	1	1
EGFR Transactivation by Gastrin	13218 REACTOME	9606	1	7	0.0374889	0.73738804	0	1	1
Yaci and bcma stimulation of b cell immune resp	4151 PID BIOCAR1	9606	1	7	0.0374889	0.73738804	0	1	1
MAP kinase activation in TLR cascade	18088 REACTOME	9606	2	57	0.0383062	0.74713272	0	1	1
Class C/3 (Metabotropic glutamate/pheromone	13227 REACTOME	9606	0	39	1	1	1	0.041665	1
Cleavage of Growing Transcript in the Terminatic	13761 REACTOME	9606	0	39	1	1	1	0.041665	1
RNA Polymerase II Transcription Termination	17068 REACTOME	9606	0	39	1	1	1	0.041665	1
ERK2 activation	13001 REACTOME	9606	1	8	0.0427308	0.80632647	0	1	1
IRAK2 mediated activation of TAK1 complex	13033 REACTOME	9606	1	8	0.0427308	0.80632647	0	1	1
IRAK2 mediated activation of TAK1 complex upo	13038 REACTOME	9606	1	8	0.0427308	0.80632647	0	1	1
Pertussis toxin-insensitive ccr5 signaling in macro	4060 PID BIOCAR1	9606	1	8	0.0427308	0.80632647	0	1	1
Shigellosis	10374 KEGG	9606	2	61	0.0433263	0.81097117	0	1	1
Pyruvate metabolism and Citric Acid (TCA) cycle	17168 REACTOME	9606	0	45	1	1	1	0.047934	1
ERK1 activation	13000 REACTOME	9606	1	9	0.0479447	0.88317128	0	1	1
Sodd/tnfr1 signaling pathway	4139 PID BIOCART	9606	1	9	0.0479447	0.88317128	0	1	1

Human OEC transcriptional responses triggered by B. pseudomallei 2 hours and 24 hours

post-infection. The lists represent (A) OECs in infection and control conditions at 2 hours; (B)

OECs in infection and control conditions at 24 hours; (C) IPA Canonical Pathways activated

by infection at 24 hours; and (D) InnateDB ORA pathway data, ranked according to P value.

Red and Green indicate up- and down-regulated pathways, respectively.