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3 **Supplementary files to the manuscript “The global effect of IL-10 on the**
4 **transcriptional profile induced by *N. meningitidis* in human monocytes” by**

5 **Unni Gopinathan and colleagues**

6 **Tables**

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Table S1. Genes up-regulated by <i>N. meningitidis</i> which were down-regulated by interleukin-10^a						
Probe Set ID	Gene Symbol	Molecular function^b	Fold change			
			Nm vs control^c	Nm + IL-10 vs control^c	IL-10 vs control^c	Nm + IL-10 vs Nm^d
8083690	IL12A	Cytokine activity	13.0	2.0	-1.2	-6.5
7917875	F3	Phospholipid binding	7.1	1.6	-2.2	-4.4
8101131	CXCL11	Chemokine activity	23.6	5.5	-2.2	-4.3
8109649	MIR146A	Post-transcriptional regulation	2.4	-1.6	-1.9	-3.9
8116921	EDN1	Patterning of blood vessels	14.7	3.8	-1.8	-3.9
8107887	CSF2	Immune response	3.3	-1.0	-1.3	-3.5
7972217	SPRY2	Cell-cell signaling	3.5	1.1	-2.9	-3.1
8179263	TNF	Cytokine activity	6.2	2.0	-2.3	-3.0
8054712	IL1A	Cytokine activity	2.2	-1.4	-4.0	-3.0
8116992	EST	N/A	2.9	-1.0	1.0	-3.0
7930299	C10orf78	Protein binding	6.7	2.3	-1.2	-3.0
7956251	IL23A	Cytokine activity	4.4	1.5	-1.0	-2.9
8172268	MIR222	Post-transcriptional regulation	3.2	1.1	-1.8	-2.9
8138542	IL6	Cytokine activity	6.4	2.2	-1.1	-2.9
8172266	MIR221	Post-transcriptional regulation	2.0	-1.4	-2.4	-2.8
8100984	CXCL3	Chemokine activity	2.1	-1.3	-2.8	-2.8
7964787	IFNG	Cytokine activity	16.9	6.5	1.7	-2.6
8147206	RIPK2	CARD domain binding	3.7	1.4	-2.4	-2.6
8105828	CCNB1	Histone kinase activity	6.9	2.7	-1.1	-2.5
8100994	CXCL2	Chemokine activity	2.9	1.1	-2.7	-2.5
8096301	SPP1	Extracellular matrix binding	1.9	-1.4	-1.3	-2.5
8120967	NT5E	5'-nucleotidase activity	3.4	1.4	1.1	-2.5
8044541	IL1F9	Interleukin-1 receptor antagonist activity	9.6	3.8	-2.0	-2.5

7954434	EST	N/A	4.5	1.9	1.1	-2.4
7932985	NRP1	Co-receptor activity	1.9	-1.2	-2.0	-2.4
8097098	USP53	Ubiquitin thiolesterase activity	2.0	-1.2	-1.2	-2.4
7951259	MMP10	Calcium ion binding	11.8	5.0	-1.3	-2.4
8047125	EST	N/A	4.2	1.8	1.1	-2.4
8180376	EST	N/A	3.3	1.5	-1.7	-2.3
7953878	CLEC2D	Transmembrane signaling receptor activity	4.4	1.9	1.2	-2.3
8151816	GEM	Calmodulin binding	3.3	1.5	-1.7	-2.2
7908388	RGS1	Calmodulin binding	3.0	1.4	-1.2	-2.2
8143471	CLEC5A	Protein binding	1.5	-1.4	-2.7	-2.2
8172270	EST	N/A	1.9	-1.2	-1.7	-2.2
8050503	TTC32	Protein binding	2.0	-1.1	-1.1	-2.1
8129937	CITED2	Chromatin binding	2.3	1.1	-1.5	-2.1
8092390	EST	N/A	2.0	-1.0	-1.1	-2.1
7957271	EST	N/A	1.9	-1.1	-1.3	-2.1
7994161	RBBP6	Ligase activity	3.1	1.5	-1.1	-2.1
8130539	TAGAP	Guanyl-nucleotide exchange factor activity	4.9	2.3	-1.3	-2.1
8098261	EST	N/A	2.5	1.2	-1.1	-2.1
7917514	EST	N/A	5.3	2.6	1.0	-2.0
7912157	ERRFI1	Protein kinase binding	2.1	1.0	-1.7	-2.0
8156848	NR4A3	Nucleic acid binding	3.3	1.6	-1.2	-2.0
8081488	HHLA2	N/A	1.9	-1.1	-1.6	-2.0
8141016	TFPI2	Peptidase inhibitor activity	5.2	2.6	-1.6	-2.0
8048723	EST	N/A	2.0	-1.0	-1.1	-2.0
7919556	EST	N/A	3.3	1.7	-1.3	-1.9
7951271	MMP1	Calcium ion binding	7.9	4.1	-1.4	-1.9
7919560	EST	N/A	3.3	1.7	-1.3	-1.9
8112668	GCNT4	Acetylglucosaminyltransferase activity	7.5	3.9	-1.0	-1.9
8105267	ITGA2	Cell adhesion molecule binding	2.8	1.4	1.1	-1.9
8004694	CYB5D1	Heme binding	2.4	1.3	1.1	-1.9
7931832	AKR1C2	Aldo-keto reductase (NADP) activity	3.0	1.6	1.1	-1.9
7932862	EST	N/A	2.2	1.2	-1.1	-1.9
7911178	NLRP3	Nucleotide binding	3.5	1.8	-1.7	-1.9
7902495	NEXN	Actin binding	3.8	2.0	-1.1	-1.9
7983922	EST	N/A	2.7	1.4	-1.0	-1.9
8045695	EST	N/A	3.8	2.1	-1.1	-1.9
7972867	PCID2	Transcription regulator	1.5	-1.2	-1.8	-1.9
8021376	NEDD4L	Acid-amino acid ligase activity	3.0	1.6	-1.5	-1.9
7981427	CKB	ATP binding	2.2	1.2	-1.3	-1.8
7965249	C12orf50	N/A	4.1	2.2	-1.2	-1.8
8136662	MGAM	Alpha-glucosidase activity	7.8	4.3	-1.6	-1.8
8004691	TMEM88	N/A	1.6	-1.2	-1.1	-1.8
7899502	RNU11	N/A	2.3	1.3	-1.1	-1.8
8139207	INHBA	Cytokine activity	15.0	8.3	-1.1	-1.8

8017964	ABCA6	ATPase activity	2.8	1.6	-1.1	-1.8
8017096	EST	N/A	4.0	2.3	-1.1	-1.8
8041447	CRIM1	Enzyme inhibitor activity	1.7	-1.0	-1.4	-1.8
8006999	CSF3	Cytokine activity	3.7	2.1	-1.1	-1.8
8178435	IER3	Protein binding	1.5	-1.2	-1.2	-1.7
7965094	E2F7	Nucleic acid binding	2.9	1.7	1.0	-1.7
8096032	PRDM8	Nucleic acid binding	4.1	2.4	1.2	-1.7
7976065	EST	N/A	2.0	1.2	-1.1	-1.7
8013987	EST	N/A	1.9	1.1	1.2	-1.7
7926821	MASTL	ATP binding	5.4	3.2	-1.1	-1.7
7964736	HMGA2	5'-deoxyribose-5-phosphate lyase activity	1.8	1.1	-1.0	-1.7
7933008	EST	N/A	1.6	-1.1	-1.2	-1.7
7903786	CSF1	Macrophage colony-stimulating factor receptor binding	1.8	1.1	-1.4	-1.7
8101118	CXCL9	chemokine activity	3.9	2.3	-1.0	-1.7
8017098	EST	N/A	3.4	2.0	-1.2	-1.7
7961371	DUSP16	Hydrolase activity	1.7	1.0	-1.3	-1.7
8048717	SGPP2	Catalytic activity	1.9	1.1	-2.2	-1.7
7925480	FH	Catalytic activity	1.8	1.1	-1.6	-1.7
8120431	PTP4A1	Hydrolase activity	1.9	1.2	-1.3	-1.7
8023598	RNF152	Ligase activity	1.8	1.1	-1.1	-1.7
7922523	LOC730167	N/A	2.1	1.3	-1.2	-1.6
8071134	C22orf37	N/A	1.8	1.1	-1.1	-1.6
8048761	EST	N/A	2.7	1.6	1.0	-1.6
8147746	EST	N/A	11.3	6.9	-1.1	-1.6
8084206	B3GNT5	Galactosyltransferase activity	1.9	1.2	-1.5	-1.6
8057990	ANKRD44	Protein binding	1.6	1.0	-1.0	-1.6
8094169	CPEB2	Nucleic acid binding	2.0	1.2	-1.6	-1.6
7970441	GJB2	Gap junction channel activity	2.2	1.4	-1.2	-1.6
8021645	SERPINB10	Peptidase inhibitor activity	1.9	1.2	1.0	-1.6
7931281	FANK1	Transcription regulator	2.1	1.3	-1.2	-1.6
8105300	EST	N/A	2.4	1.5	1.1	-1.6
7985257	EST	N/A	2.3	1.5	1.1	-1.6
8113358	ST8SIA4	Sialic acid binding	2.3	1.4	-1.3	-1.6
8057898	HECW2	Acid-amino acid ligase activity	2.5	1.6	1.0	-1.6
8069612	NCRNA00158	N/A	2.3	1.4	1.0	-1.6
7918457	KCNA3	Ion channel activity	1.8	1.1	1.1	-1.6
8162276	NFIL3	Nucleic acid binding	1.8	1.1	-1.2	-1.6
7991283	RHCG	Ammonia transmembrane transporter activity	3.3	2.1	-1.1	-1.6
8068361	SLC5A3	Myo-inositol:sodium symporter activity;	4.0	2.6	-1.1	-1.6
7929012	STAMBPL1	Hydrolase activity	3.2	2.0	1.2	-1.6
8015796	EST	N/A	2.7	1.7	-1.1	-1.6
7951977	FXYD6	Ion channel activity	2.2	1.4	-1.7	-1.6
8047272	SPATS2L	N/A	1.8	1.2	-1.4	-1.6
8123232	SLC22A1	Transmembrane	8.4	5.4	-1.2	-1.6

		transporter activity				
7902104	PDE4B	Hydrolase activity	1.8	1.2	-1.2	-1.6
8023043	PSTPIP2	Actin binding	2.3	1.5	-1.3	-1.6
8081405	EST	N/A	1.9	1.2	-1.0	-1.6
8057416	EST	N/A	1.7	1.1	-1.0	-1.6
8069565	BTG3	Protein binding	1.8	1.2	-1.7	-1.5
7951413	CARD17	Cysteine-type endopeptidase activity	2.6	1.7	-1.2	-1.5
8120061	ENPP4	Catalytic activity	1.7	1.1	-1.1	-1.5
8113759	EST	N/A	1.6	1.1	-1.2	-1.5
7911049	C1orf100	N/A	1.7	1.1	-1.1	-1.5
8023059	EST	N/A	2.0	1.3	-1.2	-1.5
8052669	SERTAD2	Transcription coactivator activity	1.6	1.1	-1.2	-1.5
8169995	FAM122C	N/A	2.0	1.3	-1.0	-1.5
8068353	MRPS6	rRNA binding	3.2	2.1	-1.2	-1.5
8114964	SPINK1	Endopeptidase inhibitor activity	4.1	2.7	-1.0	-1.5

1 **Table S1 legend**

2 ^aListed according to the column “Nm + IL-10 vs Nm”.

3 ^bMolecular function was identified by searching gene ontology annotations in the Ingenuity Knowledge

4 Base. N/A denotes that annotations were not available. EST denotes expressed sequence tags, which are

5 partially sequenced cDNA fragments that may represent gene transcripts.

6 ^cThe presented FCs are in comparison to unstimulated monocytes.

7 ^dThe presented FCs are in comparison to monocytes stimulated by *N. meningitidis*.

Probe Set ID	Gene Symbol	Molecular function ^b	Fold change			
			Nm vs contro ^c	Nm + IL-10 vs control ^c	IL-10 vs control ^c	Nm + IL-10 vs Nm ^d
8030860	FPR2	G-protein coupled receptor activity	-3,6	2,4	2,6	8,8
8022393	PTPN2	Nucleic acid binding	-1,6	3,2	3,4	5,2
7946559	GNG10	GTPase activity	-1,9	2,6	2,5	5,0
7960794	CD163	Scavenger receptor activity	-1,5	3,0	3,6	4,6
8140840	STEAP4	Electron carrier activity	-1,9	2,3	1,8	4,4
8038899	FPR1	G-protein coupled receptor activity	-2,0	2,1	2,4	4,2
7975799	FLVCR2	Heme binding	-2,1	1,8	2,0	3,8
8068266	IFNAR1	Interferon receptor activity	-2,0	1,9	1,7	3,8
8099834	TLR1	Lipopeptide binding	-2,7	1,4	3,2	3,7
8025076	VAV1	Guanyl-nucleotide exchange factor activity	-2,1	1,7	2,1	3,6

7986092	FURIN	Endopeptidase activity	-2,5	1,4	1,7	3,5
8061668	HCK	ATP binding; kinase activity	-1,9	1,8	1,6	3,4
7971486	C13orf18	N/A	-1,7	2,0	1,8	3,4
8017212	USP32	Calcium ion binding	-1,6	2,0	2,6	3,2
8030782	SIGLEC9	Monosaccharide binding	-3,9	-1,2	1,1	3,2
8031223	LILRB1	MHC class I receptor activity	-2,4	1,3	1,8	3,1
8121515	SLC16A10	Amino acid transport activity	-2,1	1,5	4,8	3,1
7938370	SWAP70	ATP binding	-2,6	1,2	1,2	3,1
8031712	ZNF805	Nucleic acid binding	-2,9	1,1	-1,0	3,1
8114612	CD14	Lipopolysaccharide binding	-3,7	-1,2	1,4	3,0
8099897	UGDH	Electron carrier activity	-1,6	1,8	1,7	3,0
8158123	FPGS	ATP binding	-1,6	1,8	1,3	2,9
8032839	SEMA6B	Semaphorin receptor binding	-3,2	-1,1	1,5	2,9
8139500	TNS3	Metal ion binding	-2,0	1,5	2,2	2,9
8084794	IL1RAP	Interleukin-1 receptor activity	-1,7	1,7	2,5	2,8
7908097	SMG7	Protein phosphatase 2A binding	-1,7	1,7	1,3	2,8
8154305	SELT	Selenium binding	-1,7	1,6	1,3	2,8
8157761	NEK6	ATP binding	-3,5	-1,3	1,5	2,8
8039257	LAIR1	Protein binding	-3,2	-1,2	1,1	2,7
8034873	EMR2	Calcium ion binding	-1,7	1,6	1,8	2,7
8065607	PLAGL2	Nucleic acid binding	-1,9	1,4	1,5	2,7
8031213	LILRA1	Transmembrane signaling receptor activity	-2,9	-1,1	1,5	2,7
7962869	DDX23	ATP binding	-2,0	1,3	1,1	2,6
8035456	LRRC25	N/A	-5,0	-2,0	1,2	2,6
8060772	CDS2	Nucleotidyltransferase activity	-1,6	1,6	1,6	2,6
7981111	DICER1	ATP-dependent helicase activity	-1,8	1,4	1,7	2,5
7954527	ARNTL2	Nucleic acid binding	-1,7	1,5	1,7	2,5
8032909	PLIN3	Protein binding	-2,3	1,1	1,8	2,5
8070819	PTTG1P	Nuclear translocation activity	-2,4	1,1	1,5	2,5
7955535	ACVR1B	Activin-activated receptor activity	-1,7	1,5	1,5	2,5
8039236	LILRA5	Receptor activity	-1,7	1,4	1,8	2,5
8024111	CNN2	Actin binding	-1,8	1,4	1,6	2,5
7933659	CSTF2T	Nucleic acid binding	-1,7	1,5	1,2	2,4
7995448	TMEM188	N/A	-2,4	-1,0	1,4	2,4
8180196	EST	N/A	-2,1	1,1	1,4	2,4
8039196	LILRB3	Transmembrane signaling receptor activity	-1,7	1,4	1,4	2,4
8144516	ERI1	3'-5' exonuclease activity	-1,7	1,3	2,0	2,3
8003903	ARRB2	G-protein coupled receptor binding	-2,6	-1,1	1,1	2,3
7953211	C12orf5	Catalytic activity	-3,1	-1,3	1,1	2,3
8038885	SIGLEC14	Sugar binding	-1,6	1,5	1,4	2,3
7904086	LRIG2	EST	-1,6	1,4	-1,0	2,3
8024572	GNA15	G-protein coupled receptor binding	-2,7	-1,2	1,1	2,3
8025421	MARCH2	Ligase activity	-1,6	1,4	2,0	2,2

8157270	SLC31A1	Copper ion transmembrane transporter activity	-2,3	-1,1	1,3	2,2
8039212	LILRB2	Cell adhesion molecule binding	-2,0	1,1	1,2	2,2
8149749	TNFRSF10D	Transmembrane signaling receptor activity	-1,6	1,4	1,6	2,2
8091432	COMMD2	Protein binding	-2,5	-1,1	1,1	2,2
7924760	ITPKB	ATP binding	-1,5	1,4	1,5	2,2
8158112	CDK9	Cyclin-dependent protein kinase activity	-2,0	1,1	1,2	2,2
8180405	EST	N/A	-2,2	-1,0	1,0	2,1
8169603	LONRF3	ATP-dependent peptidase activity	-2,0	1,1	1,5	2,1
8129590	STX7	SNAP receptor activity	-2,8	-1,3	1,0	2,1
8029465	BCL3	Nucleic acid binding	-1,8	1,2	1,5	2,1
7904018	CTTNBP2NL	Protein binding	-2,2	-1,1	-1,0	2,1
8035477	ELL	Phosphatase binding	-1,5	1,4	1,2	2,1
7938777	LDHA	Catalytic activity	-1,7	1,2	1,4	2,1
8091120	GK5	ATP binding	-1,7	1,2	2,1	2,1
8020919	C18orf21	N/A	-2,1	-1,0	1,1	2,0
8148694	GRINA	Cation channel activity	-1,6	1,3	1,4	2,0
8107691	PHAX	RNA binding	-2,7	-1,4	-1,1	2,0
8025285	C19orf59	N/A	-2,3	-1,1	2,0	2,0
8122144	SNORA33	N/A	-1,9	1,1	-1,4	2,0
7960411	C12orf4	N/A	-1,6	1,3	1,1	2,0
8037408	KCNN4	Calcium-activated potassium channel activity	-1,7	1,2	1,0	2,0
8031207	LILRA2	Antigen binding	-3,3	-1,6	1,2	2,0
7964246	SNORD59B	N/A	-2,5	-1,2	-1,1	2,0
7931216	FAM175B	Polyubiquitin binding	-1,8	1,1	1,0	2,0
7986350	ARRDC4	Signal transduction	-3,5	-1,8	1,1	2,0
8052622	LOC388955	N/A	-2,1	-1,1	1,2	1,9
8015835	DUSP3	Hydrolase activity	-1,8	1,1	1,3	1,9
8160016	RANBP6	Protein transport	-1,9	1,0	1,3	1,9
7906703	NDUFS2	Electron carrier activity	-2,0	-1,1	-1,0	1,9
8112967	TMEM167A	N/A	-2,1	-1,1	1,2	1,9
8017186	HEATR6	N/A	-1,7	1,1	-1,2	1,9
7976571	C14orf129	N/A	-2,3	-1,2	1,0	1,9
8050255	NOL10	N/A	-1,9	-1,0	1,1	1,9
8110318	PRELID1	N/A	-1,9	-1,0	1,3	1,9
7960518	TNFRSF1A	Tumor necrosis factor-activated receptor activity	-2,0	-1,1	1,3	1,9
8113591	PGGT1B	Catalytic activity	-2,3	-1,2	1,1	1,9
7928019	HK1	ATPase activity	-1,5	1,2	1,3	1,9
8001651	ZNF319	Nucleic acid binding	-1,8	1,0	1,7	1,8
7930450	EST	N/A	-1,9	-1,0	1,2	1,8
8024228	MIDN	N/A	-1,6	1,1	1,2	1,8
8155883	OSTF1	SH3 domain binding	-2,1	-1,2	1,1	1,8
7900009	EIF2C4	Nucleic acid binding	-1,9	-1,1	1,4	1,8
8032127	C19orf22	N/A	-1,7	1,1	1,1	1,8
8180261	EST	N/A	-1,6	1,1	1,2	1,8

8031690	ZNF264	Nucleic acid binding	-1,7	1,0	1,2	1,8
7928944	PAPSS2	Adenylylsulfate kinase activity	-1,6	1,1	1,5	1,8
8010161	SEPT9	GTPase activity	-2,0	-1,1	1,3	1,8
8081740	ATP6V1A	ATP binding	-2,2	-1,3	1,4	1,8
8020110	RAB31	GTPase activity	-2,0	-1,1	1,4	1,8
8046346	HAT1	Histone acetyltransferase activity	-1,6	1,1	1,3	1,8
8047228	MOBK3	Metal ion binding	-2,2	-1,3	1,0	1,8
8179575	TRIM27	Nucleic acid binding	-1,7	1,0	-1,0	1,8
8030978	ZNF845	Metal ion binding	-2,6	-1,5	-1,1	1,8
8011018	CRK	Protein phosphorylated amino acid binding	-1,6	1,1	1,1	1,8
7945803	CARS	Aminoacyl-tRNA ligase activity	-1,9	-1,1	1,2	1,7
8003962	PLD2	Catalytic activity	-1,7	-1,0	1,4	1,7
8107578	SRFBP1	Transcription regulator	-2,0	-1,1	-1,3	1,7
8011713	CXCL16	Chemokine activity	-2,5	-1,4	1,3	1,7
8111772	DAB2	Protein C-terminus binding	-3,3	-1,9	1,6	1,7
8081953	GTF2E1	Metal ion binding	-1,9	-1,1	-1,1	1,7
7939329	PDHX	Transferase activity	-1,6	1,1	-1,0	1,7
8051396	NLRC4	Protein homodimerization activity	-2,4	-1,4	1,0	1,7
7936091	USMG5	N/A	-1,8	-1,0	-1,1	1,7
8007505	DHX8	ATP-dependent helicase activity	-2,1	-1,2	1,0	1,7
7943577	RAB39	GTP binding	-1,9	-1,1	1,1	1,7
7995040	BCKDK	Protein serine/threonine kinase activity	-2,3	-1,3	-1,1	1,7
7952522	PUS3	Isomerase activity	-1,9	-1,1	-1,1	1,7
7954969	IRAK4	Protein serine/threonine kinase activity	-1,6	1,1	1,4	1,7
8146930	TMEM70	Mitochondrial proton-transporting ATP synthase complex assembly	-1,6	1,1	1,1	1,7
8001496	NUDT21	Histone deacetylase binding	-3,0	-1,8	-1,1	1,7
8053046	DUSP11	Phosphatase activity	-3,0	-1,8	-1,1	1,7
8149330	CTSB	Cysteine-type endopeptidase activity	-1,7	-1,0	1,5	1,7
7979906	COX16	N/A	-2,0	-1,2	-1,3	1,7
8169617	PGRMC1	Heme binding	-1,6	1,1	1,3	1,7
8128123	RRAGD	GTP binding	-1,8	-1,1	1,1	1,7
8136045	IRF5	Sequence-specific Nucleic acid binding transcription factor activity	-1,7	-1,0	1,0	1,7
8045736	FMNL2	Rho GTPase binding	-1,6	1,0	1,2	1,7
8068254	IL10RB	Interleukin-10 receptor activity	-1,8	-1,1	1,1	1,7
7962783	ASB8	Transcription regulator	-1,6	1,1	1,1	1,7
8116848	PAK1IP1	Signal transduction	-2,0	-1,2	-1,4	1,7
7990033	TLE3	Protein binding	-2,2	-1,3	-1,1	1,7
8052721	PPP3R1	Calcium-dependent protein serine/threonine phosphatase activity	-1,7	1,0	1,1	1,7

8014047	C17orf42	Crossover junction endodeoxyribonuclease activity	-1,7	1,0	1,2	1,7
7989735	CLPX	ATP-dependent peptidase activity	-3,2	-1,9	-1,1	1,7
7984190	TRIP4	Ligand-dependent nuclear receptor binding	-1,8	-1,1	1,0	1,7
8018352	SLC25A19	Deoxynucleotide transmembrane transporter activity	-2,2	-1,3	1,2	1,7
8051413	FAM98A	N/A	-2,6	-1,6	-1,6	1,7
8050695	SF3B14	Nucleic acid binding	-1,5	1,1	-1,0	1,7
8048835	MFF	N/A	-1,6	1,0	1,2	1,7
7977571	OSGEP	Metalloendopeptidase activity	-1,7	-1,0	1,0	1,7
8088526	THOC7	RNA binding	-1,9	-1,1	-1,0	1,7
8079368	EST	N/A	-2,0	-1,2	-1,0	1,7
7929677	PI4K2A	1-phosphatidylinositol 4-kinase activity	-2,8	-1,7	-1,3	1,7
7960730	LPCAT3	Transferase activity	-1,9	-1,2	1,2	1,7
8075423	DUSP18	Hydrolase activity	-3,1	-1,9	1,1	1,7
7923173	MIR181B1	Post-transcriptional regulation	-2,9	-1,7	1,1	1,6
8001552	CIAPIN1	Protein binding	-1,9	-1,2	-1,1	1,6
8063607	RAB22A	GTPase activity	-1,6	1,0	1,1	1,6
8130765	FAM103A1	Protein binding	-1,7	-1,0	1,1	1,6
7951422	KIAA1826	N/A	-3,0	-1,8	-1,3	1,6
8121461	CDC40	Catalytic activity	-1,8	-1,1	1,2	1,6
8070269	DSCR3	Vacuolar transport	-2,9	-1,8	-1,1	1,6
7916130	KTI12	ATP binding	-2,3	-1,4	-1,5	1,6
8159006	SNORD36B	N/A	-2,7	-1,6	-1,6	1,6
8036908	SERTAD3	Protein binding	-2,8	-1,7	1,3	1,6
8065353	THBD	Transmembrane signaling receptor activity	-3,9	-2,4	1,3	1,6
8075089	TFIP11	Nucleic acid binding	-1,7	-1,1	-1,1	1,6
8156263	SPIN1	Methylated histone residue binding	-2,4	-1,5	1,3	1,6
7941243	DPF2	Nucleic acid binding	-2,2	-1,4	-1,1	1,6
7936706	C10orf119	Chromatin binding	-1,7	-1,0	-1,1	1,6
8055890	STAM2	Protein binding	-1,8	-1,1	1,0	1,6
8158714	EXOSC2	3'-5'-exoribonuclease activity	-2,8	-1,7	-1,7	1,6
7915516	MED8	RNA polymerase II transcription cofactor activity	-2,9	-1,8	-1,2	1,6
7943552	AASDHPPT	Holo-[acyl-carrier-protein] synthase activity	-2,5	-1,5	-1,2	1,6
8049574	UBE2F	Acid-amino acid ligase activity	-2,4	-1,5	-1,0	1,6
8031815	ZNF776	Nucleic acid binding	-1,7	-1,1	1,1	1,6
8031784	ZNF134	Sequence-specific DNA binding transcription factor activity	-2,1	-1,3	-1,2	1,6
7921868	FCGR3A	IgG binding	-2,7	-1,6	1,2	1,6
8003116	HSDL1	Cxidoreductase activity	-1,5	1,1	-1,1	1,6
8084947	FBXO45	Protein binding	-2,5	-1,5	-1,4	1,6
8163999	ZBTB6	Nucleic acid binding	-1,7	-1,0	-1,0	1,6

7935746	BLOC1S2	Gamma-tubulin binding	-2,1	-1,3	1,0	1,6
8155192	GLIPR2	N/A	-2,4	-1,5	1,0	1,6
8147864	TTC35	N/A	-1,8	-1,1	1,1	1,6
8106784	RASA1	GTPase activator activity	-2,7	-1,7	-1,3	1,6
8009205	DDX42	ATP-dependent helicase activity	-2,5	-1,5	1,1	1,6
7950644	NDUFC2	NADH dehydrogenase (ubiquinone) activity	-2,0	-1,2	-1,0	1,6
7897620	PGD	Phosphogluconate 2-dehydrogenase activity	-2,2	-1,4	1,0	1,6
7950197	ARAP1	GTPase activator activity	-2,4	-1,5	-1,0	1,6
7985488	FAM103A1	RNA binding	-1,7	-1,1	1,1	1,6
7899377	PPP1R8	Protein phosphatase inhibitor activity	-2,1	-1,3	-1,2	1,6
8150175	C8orf41	N/A	-2,0	-1,2	-1,1	1,6
8135250	PSMC2	Nucleoside-triphosphatase activity	-2,4	-1,5	-1,1	1,6
7996012	ARL2BP	GTPase activator activity	-2,4	-1,5	-1,1	1,6
8096905	AP1AR	Protein transporter	-1,6	-1,0	1,1	1,6
7961865	KRAS	GTPase activity	-1,7	-1,1	1,2	1,6
7944375	TRAPPC4	Protein binding	-2,2	-1,4	-1,1	1,6
8152863	EST	N/A	-2,4	-1,5	1,2	1,6
8120428	FKBP1A	Isomerase activity	-2,4	-1,5	-1,0	1,6
8140859	MTERF	Double-stranded DNA binding	-1,7	-1,1	1,1	1,6
7945058	FAM118B	N/A	-1,7	-1,1	-1,1	1,6
8041257	SLC30A6	Cation transmembrane transporter activity	-2,1	-1,3	1,0	1,6
8124022	DTNBP1	Protein binding	-1,5	1,0	1,2	1,6
8040639	HADHB	3-hydroxyacyl-CoA dehydrogenase activity	-1,7	-1,1	1,1	1,6
8108603	HARS2	aminoacyl-tRNA ligase activity	-1,6	-1,0	1,1	1,6
8151842	KIAA1429	RNA splicing	-2,0	-1,3	1,1	1,6
7956658	SLC16A7	Monocarboxylic acid transmembrane transporter activity	-1,7	-1,1	1,8	1,6
8083630	GFM1	GTPase activity	-1,9	-1,2	-1,1	1,6
7967473	EIF2B1	Enzyme regulator activity	-2,3	-1,5	-1,3	1,6
8011875	DERL2	Protein binding	-1,8	-1,2	1,1	1,6
7905355	SCNM1	Metal ion binding	-1,9	-1,2	1,0	1,6
8044793	STEAP3	Electron carrier activity	-1,7	-1,1	1,1	1,6
8161242	EXOSC3	3'-5'-exoribonuclease activity	-2,3	-1,5	-1,3	1,6
7909527	EST	N/A	-1,6	-1,0	1,1	1,6
7914996	MEAF6	Protein binding	-2,7	-1,7	-1,3	1,6
8071069	IL17RA	Interleukin-17 receptor activity	-2,0	-1,3	-1,1	1,6
7918955	GDAP2	N/A	-2,0	-1,3	-1,0	1,6
8108163	C5orf24	N/A	-2,7	-1,7	-1,2	1,6
7912198	ENO1	Protein homodimerization activity	-2,0	-1,3	-1,1	1,6
8058985	RNF25	Ubiquitin-protein ligase activity	-2,3	-1,5	-1,1	1,6
8019523	WDR45L	Phosphatidylinositol-3,5-bisphosphate binding	-2,8	-1,8	-1,1	1,6

8055060	WDR33	Signal transduction	-2,4	-1,6	-1,1	1,6
7921873	FCGR3A	IgG binding	-2,5	-1,6	1,1	1,6
7904364	WDR3	Signal transduction	-2,8	-1,8	-1,9	1,6
7979698	ATP6V1D	ATPase activity	-1,8	-1,2	1,2	1,6
8011093	SLC43A2	L-amino acid transmembrane transporter activity	-3,9	-2,5	-1,1	1,6
7958147	TDG	Damaged DNA binding	-2,1	-1,3	-1,1	1,6
8097704	TMEM184C	N/A	-2,0	-1,3	-1,1	1,5
8054217	TXNDC9	Protein binding	-1,9	-1,3	1,2	1,5
8064438	NSFL1C	ATPase binding	-1,8	-1,2	1,1	1,5
7963577	SPRYD3	N/A	-1,6	-1,1	-1,1	1,5
8067295	SLMO2	N/A	-2,0	-1,3	-1,1	1,5
7925062	SIPA1L2	GTPase activator activity	-1,7	-1,1	1,1	1,5
8053036	TPRKB	Protein kinase binding	-2,0	-1,3	-1,1	1,5
7972180	RNF219	Metal ion binding	-2,3	-1,5	-1,1	1,5
7954503	MED21	DNA-directed RNA polymerase activity	-2,9	-1,9	-1,1	1,5
8090546	CNBP	Sequence-specific DNA binding transcription factor activity	-2,4	-1,6	-1,1	1,5
7971967	DIS3	3'-5'-exoribonuclease activity	-1,6	-1,0	1,1	1,5
7948898	SNORD31	N/A	-2,3	-1,5	-1,3	1,5
8003627	TIMM22	Protein channel activity	-1,9	-1,2	-1,1	1,5
8084345	AP2M1	Transporter activity	-2,2	-1,5	-1,1	1,5
7977693	CHD8	DNA helicase activity	-2,2	-1,4	1,0	1,5
7983469	SPATA5L1	Nucleoside-triphosphatase activity	-1,6	-1,0	-1,0	1,5
8157947	ZBTB34	Nucleic acid binding	-1,8	-1,2	1,1	1,5
7934513	AP3M1	Protein binding	-2,3	-1,5	-1,0	1,5
8079346	SACM1L	Phosphoric ester hydrolase activity	-2,0	-1,3	1,1	1,5
8031720	ZNF543	Nucleic acid binding	-1,5	-1,0	1,0	1,5
7970347	CDC16	Protein binding	-2,1	-1,4	-1,1	1,5
7910539	C1orf124	Nucleic acid binding	-1,6	-1,0	1,1	1,5
8163964	PDCL	Protein complex binding	-1,7	-1,1	1,0	1,5
8007976	NPEPPS	Aminopeptidase activity	-1,9	-1,3	1,1	1,5
7906128	SLC25A44	Transmembrane transporter	-2,1	-1,4	1,0	1,5
8110499	RUFY1	Protein transporter activity	-1,6	-1,1	1,1	1,5
8052925	TEX261	N/A	-2,5	-1,6	-1,2	1,5
8042468	ANXA4	Calcium-dependent phospholipid binding	-1,8	-1,2	-1,3	1,5
7971550	MED4	Ligand-dependent nuclear receptor transcription coactivator activity	-1,6	-1,0	1,0	1,5
8146544	UBXN2B	N/A	-2,2	-1,5	1,3	1,5
8124459	ZNF322A	Nucleic acid binding	-2,0	-1,3	-1,0	1,5
8112302	C5orf43	N/A	-2,7	-1,8	-1,2	1,5
7953321	LTBR	Receptor activity	-1,8	-1,2	1,2	1,5
7979732	VTI1B	Protein binding	-2,5	-1,7	-1,2	1,5
7991581	CHSY1	Transferase activity	-2,0	-1,3	1,4	1,5
8083272	GYG1	Transferase activity	-1,8	-1,2	1,1	1,5

8016088	CCDC43	N/A	-1,9	-1,3	-1,1	1,5
7966738	C12orf49	N/A	-2,1	-1,4	-1,1	1,5
8110920	FASTKD3	Protein kinase activity	-2,0	-1,3	-1,1	1,5
8164883	SURF4	Cytochrome-c oxidase activity	-1,5	-1,0	1,1	1,5
7920401	SLC39A1	Metal ion transmembrane transporter activity	-1,7	-1,1	1,1	1,5
8026541	FAM32A	N/A	-2,1	-1,4	-1,2	1,5
8005857	TMEM199	N/A	-1,7	-1,1	-1,1	1,5
7964466	DCTN2	Protein binding	-2,0	-1,3	-1,1	1,5
8060379	PSMF1	Endopeptidase inhibitor activity	-2,1	-1,4	-1,1	1,5
8164587	TOR1A	Nucleotide binding	-2,8	-1,9	-1,2	1,5
8013581	IFT20	Protein binding	-1,6	-1,1	1,3	1,5
7994102	DCTN5	Transferase activity	-2,3	-1,5	-1,1	1,5
8106743	VCAN	Hyaluronic acid binding	-1,9	-1,3	2,0	1,5
8142663	NDUFA5	NADH dehydrogenase (ubiquinone) activity	-1,8	-1,2	1,0	1,5

1 **Table S2 legend**

2
3 ^aListed according to the column "Nm + IL-10 vs Nm".

4 ^bMolecular function was identified by searching gene ontology annotations in the Ingenuity Knowledge

5 Base. N/A denotes that annotations were not available. EST denotes expressed sequence tags, which are
6 partially sequenced cDNA fragments that may represent gene transcripts.

7 ^cThe presented FCs are in comparison to unstimulated monocytes.

8 ^dThe presented FCs are in comparison to monocytes stimulated by *N. meningitidis*.

9 **Table S3. Genes up-regulated in synergy by *N. meningitidis* and interleukin-10^a**

Probe Set ID	Gene Symbol	Molecular function ^c	Fold change		
			Nm vs control ^c	Nm + IL-10 vs control ^c	IL-10 vs control ^c
7921652	SLAMF1	Transmembrane signaling receptor activity	7.4	54.5	9.3
8091411	TM4SF1	Signal transduction	7.6	28.7	5.5
7934898	ANKRD22	Transcription regulator	4.6	22.8	3.3
7921434	AIM2	Double-stranded Nucleic acid binding	9.9	18.3	2.5
7931914	IL2RA	Interleukin-2 receptor activity	4.3	16.5	2.0
8178115	CFB	Catalytic activity	11.5	16.5	1.2
7939314	EHF	Nucleic acid binding	2.7	11.8	2.0
8102594	TNIP3	N/A	3.4	10.7	7.0
8107706	LMNB1	Phospholipase binding	2.0	10.6	7.6
8082673	ACPP	Acid phosphatase activity	1.4	9.9	4.9
7951385	CASP5	Cysteine-type endopeptidase activity	1.6	9.6	4.4
8103508	MARCH1	Ligase activity	1.0	9.1	6.8
8163896	STOM	Protein homooligomerization	1.2	8.5	4.4

8126839	TNFRSF21	Protein binding	1.9	8.3	3.7
8094743	RHOH	GTPase inhibitor activity	3.2	8.2	1.5
8128939	TRAF3IP2	Protein binding	4.5	7.2	2.1
8136115	FAM40B	N/A	1.6	6.9	3.9
7908351	PLA2G4A	Calcium-dependent phospholipid binding	4.8	6.5	1.2
8124307	CMAH	Iron-sulfur cluster binding	3.6	6.3	1.7
8145317	ADAMDEC1	Metalloendopeptidase activity	2.9	6.2	1.7
8129627	VNN3	Pantetheine hydrolase activity	1.8	6.1	2.5
8083594	PTX3	(1->3)-beta-D-glucan binding	2.1	6.1	1.2
7953651	PEX5	Peroxisome targeting sequence binding	1.0	5.4	2.4
7962884	RND1	GTPase activity	1.6	5.0	1.3
8083569	TIPARP	Transferase activity	2.4	5.0	1.5
8023688	SERPINB4	Peptidase inhibitor activity	1.7	4.9	1.3
7953749	CLEC4D	Sugar binding	1.5	4.8	1.8
8097461	CCRN4L	Sequence-specific Nucleic acid binding transcription factor activity	2.9	4.8	1.6
7998940	MEFV	Actin binding	1.7	4.6	2.8
7993800	LYRM1	N/A	2.9	4.6	1.5
8072735	APOL1	Chloride channel activity	2.1	4.6	1.4
8056222	DPP4	Aminopeptidase activity	2.7	4.5	1.2
8109326	C5orf62	N/A	2.0	4.3	1.6
7908409	RGS2	GTPase activator activity	1.8	3.8	1.5
8103911	IRF2	Sequence-specific Nucleic acid binding transcription factor activity	1.8	3.7	1.8
7999423	SOCS1	N/A	2.0	3.7	1.4
7985285	ARNT2	Protein heterodimerization activity	1.3	3.7	1.6
8000028	DCUN1D3	N/A	1.9	3.6	1.5
7928999	LIPN	Hydrolase activity	2.2	3.4	1.2
7922162	SLC19A2	Folic acid transporter activity	1.3	3.4	1.3
8102839	NDUFC1	NADH dehydrogenase (ubiquinone) activity	1.4	3.2	1.1
7900426	SMAP2	GTPase activator activity	1.1	3.2	2.1
8130939	DLL1	Calcium ion binding	1.3	3.2	1.6
7924166	BATF3	Protein heterodimerization activity	1.2	3.1	1.5
7953243	NDUFA9	NADH dehydrogenase (ubiquinone) activity	1.3	3.1	1.4
8171418	PIGA	Phosphatidylinositol N-acetylglucosaminyltransferase activity	1.7	3.0	1.2
8147766	FZD6	G-protein coupled receptor activity	1.8	2.9	1.1
8154721	IFNK	Interferon-alpha/beta receptor binding	1.5	2.9	1.2
8025058	TRIP10	Identical protein binding	1.1	2.8	1.7
8040960	GCKR	Enzyme inhibitor activity	1.2	2.7	1.4
8042119	PAPOLG	Nucleotidyltransferase activity	1.0	2.6	1.2

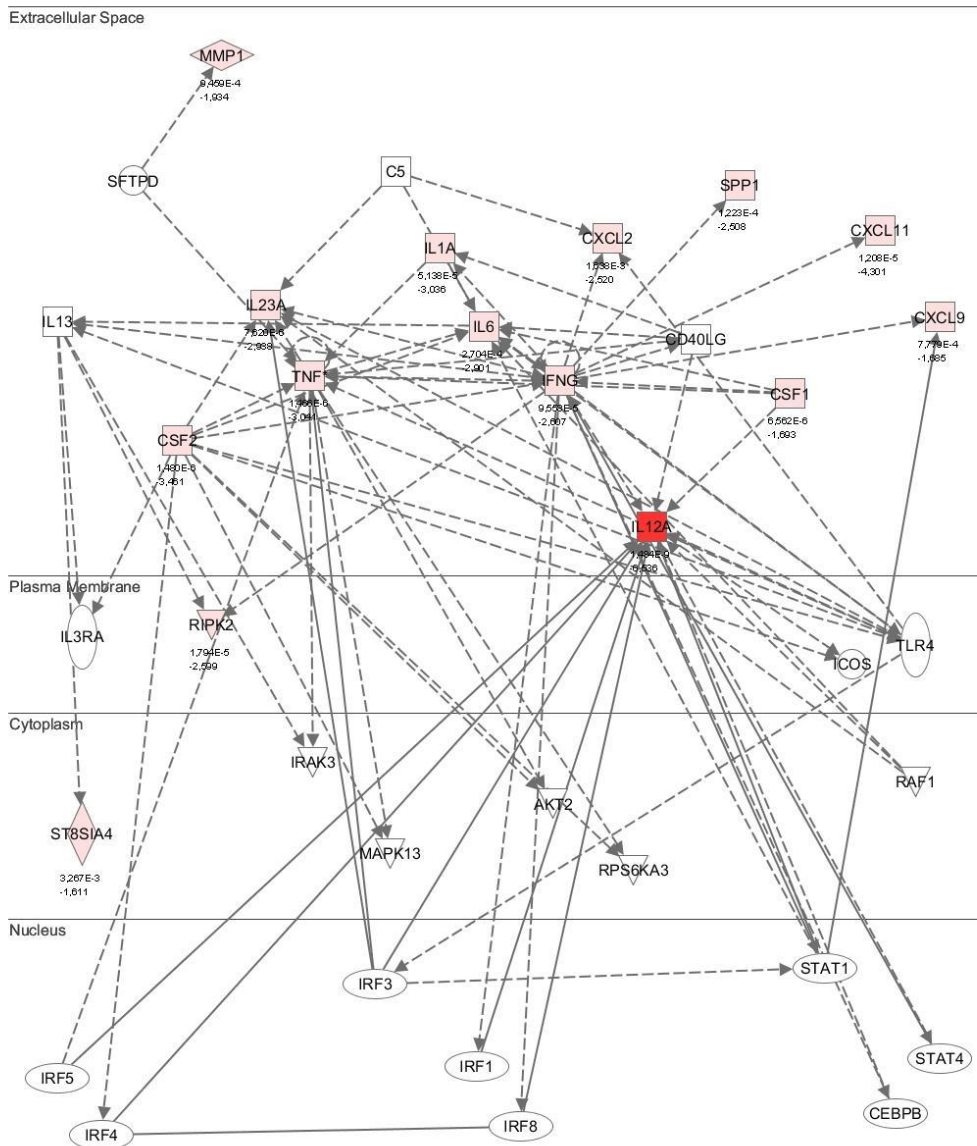
7980537	STON2	Protein binding	1.3	2.6	1.1
7899361	STX12	SNAP receptor activity	1.0	2.4	1.3

1
2 **Table S3 legend**
3
4 ^aListed according to the column “Nm + IL-10 vs control”.
5 ^bMolecular function was identified by searching gene ontology annotations in the Ingenuity Knowledge
6 Base. N/A denotes that annotations were not available. EST denotes expressed sequence tags, which are
7 partially sequenced cDNA fragments that may represent gene transcripts.
8 ^cThe presented FCs are in comparison to unstimulated monocytes.

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Figure S2: Network 1 generated from the genes up-regulated by *N. meningitidis* and down-regulated by IL-10



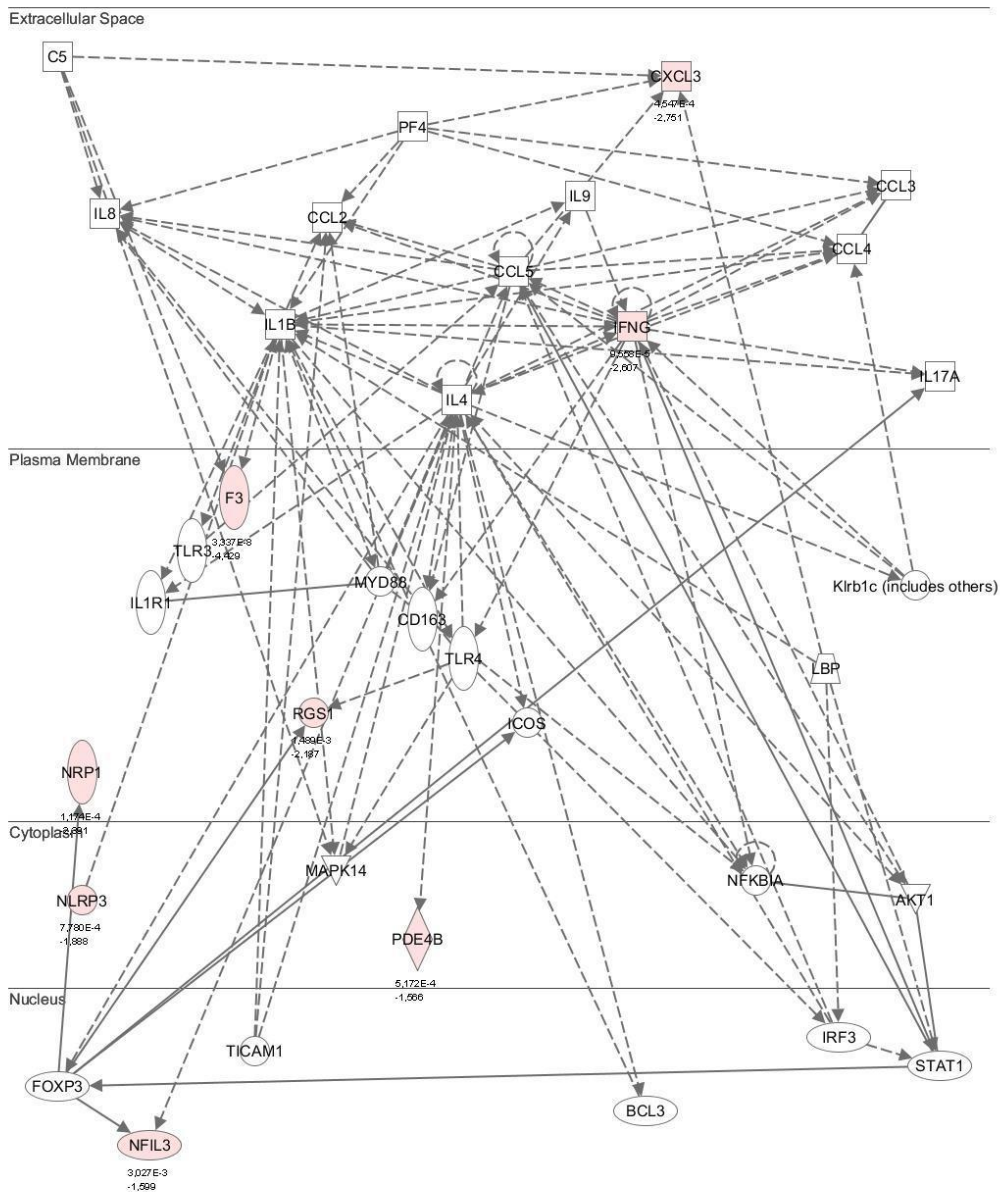
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7 **Figure S2 legend**

1 Figure S2 displays network 1 from Table 3. The color red indicates that the gene has
2 been down-regulated by IL-10, and the tone of the color indicates the extent to which the
3 gene has been down-regulated. Ingenuity Pathway Analysis has located the genes to
4 the nucleus, cytoplasm, plasma membrane and extracellular space. Solid lines imply
5 direct relationships between the proteins encoded by the genes, while dashed lines
6 represent indirect relationships.

7

8 **Figure S3: Network 2 generated from genes up-regulated by *N. meningitidis* and**
9 **down-regulated by IL-10**



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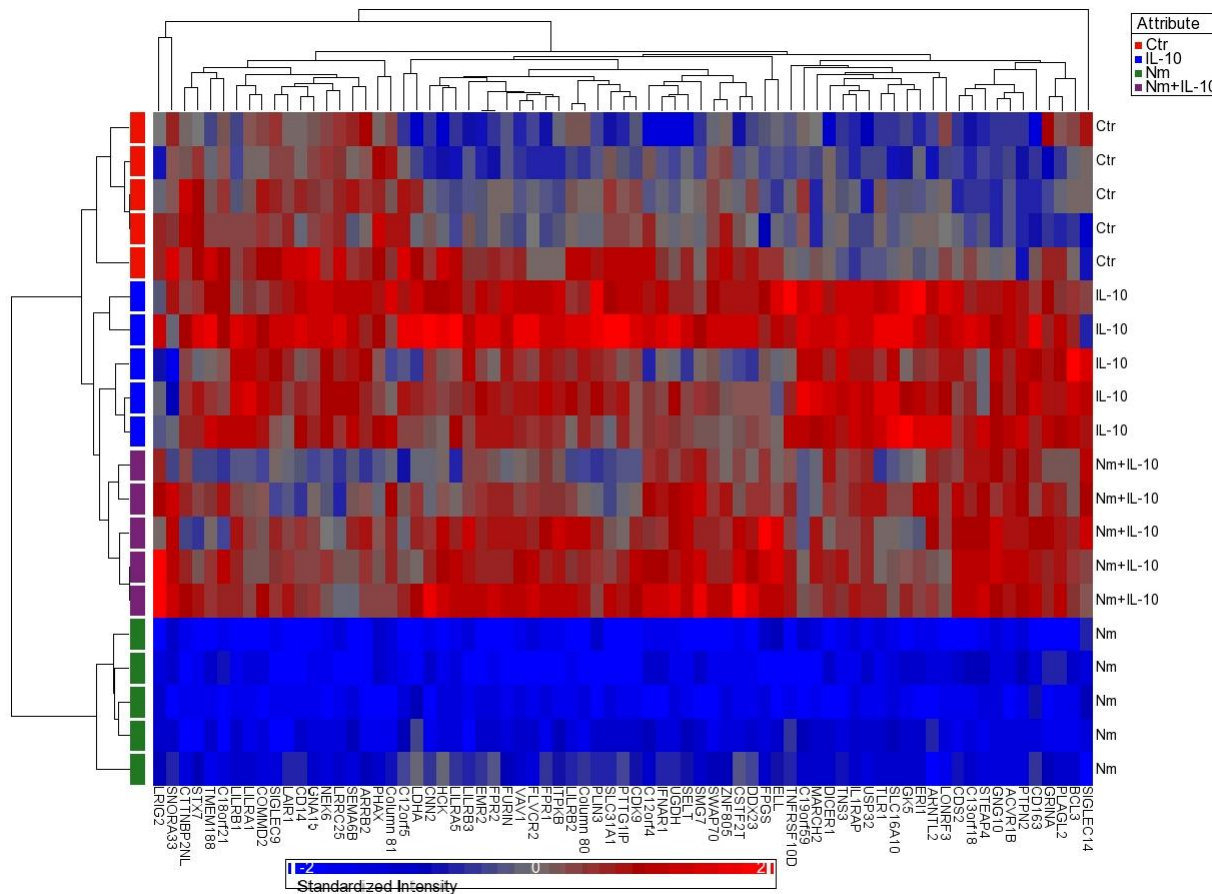
2 **Figure S3 legend**

3 Figure S3 displays network 2 from Table 3. The color red indicates that the gene has
 4 been down-regulated by IL-10, and the tone of the color indicates the extent to which the
 5 gene has been down-regulated. Ingenuity Pathway Analysis has located the genes to
 6 the nucleus, cytoplasm, plasma membrane and extracellular space. Solid lines imply

1 direct relationships between the proteins encoded by the genes, while dashed lines
 2 represent indirect relationships.

3

4 **Figure S4: Heatmap of genes down-regulated by *N. meningitidis* and up-regulated**
 5 **by IL-10**



6

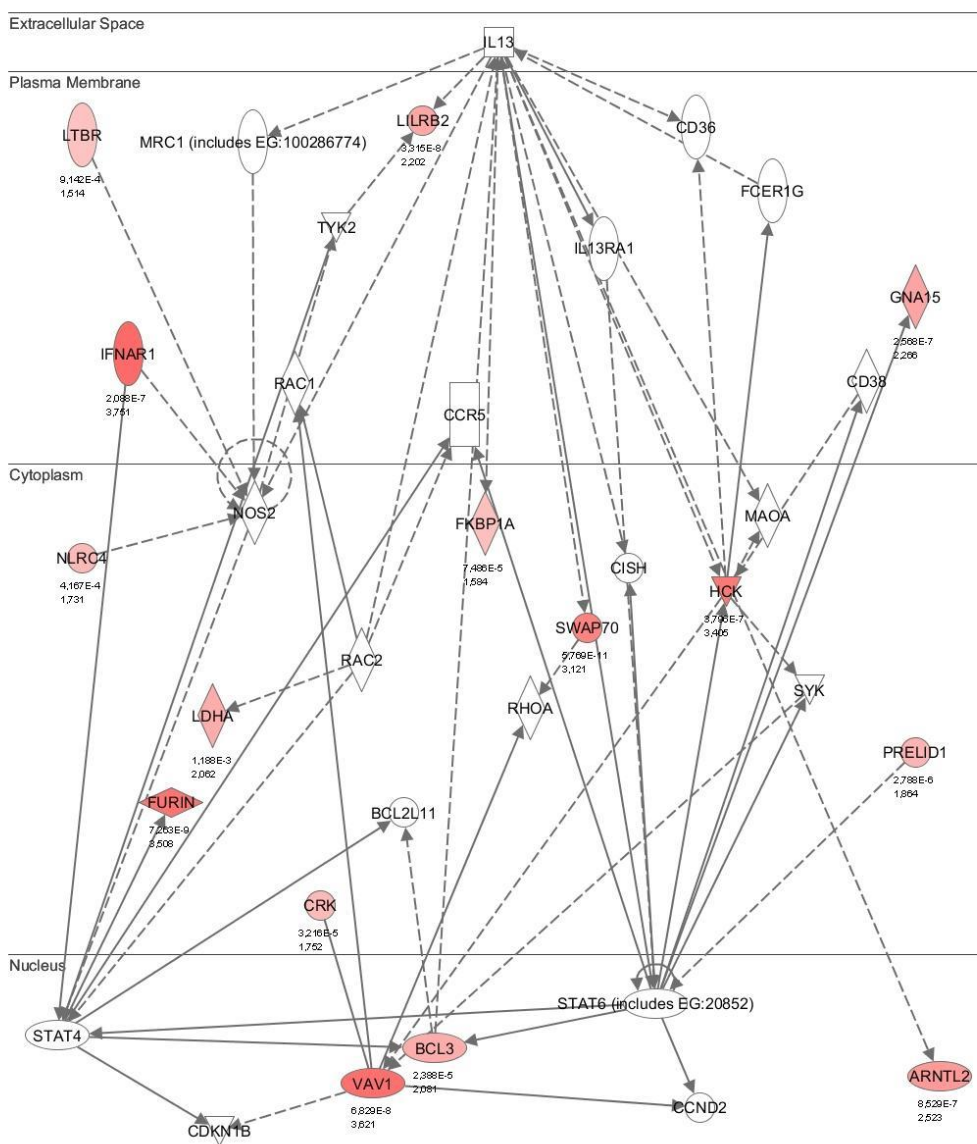
7 **Figure S4 legend**

8 The heatmap displays the expression of genes in unstimulated monocytes (Ctr) and
 9 monocytes stimulated by IL-10 (IL-10) alone, *N. meningitidis* (Nm) alone and *N.*
 10 *meningitidis* in combination with IL-10 (Nm + IL-10). The signal intensity for each gene
 11 is compared to the average intensity detected for the gene over the 20 microarrays.
 12 Grey color indicates that the signal intensity for the gene in the array is close to this

1 average signal intensity level. The color red indicates up-regulation and signal intensity
 2 above the average level, while blue indicates down-regulation and signal intensity below
 3 the average level.

4

5 **Figure S5: Network 1 generated from genes down-regulated by *N. meningitidis***
 6 **and up-regulated by IL-10**



7

1 **Figure S5 legend**

2 Figure S5 displays network 1 from Table 4. The color red indicates that the gene has
3 been up-regulated IL-10, and the tone of the color indicates the extent to which the gene
4 has been up-regulated. Ingenuity Pathway Analysis has located the genes to the
5 nucleus, cytoplasm, plasma membrane and extracellular space. Solid lines imply direct
6 relationships between the proteins encoded by the genes, while dashed lines represent
7 indirect relationships.

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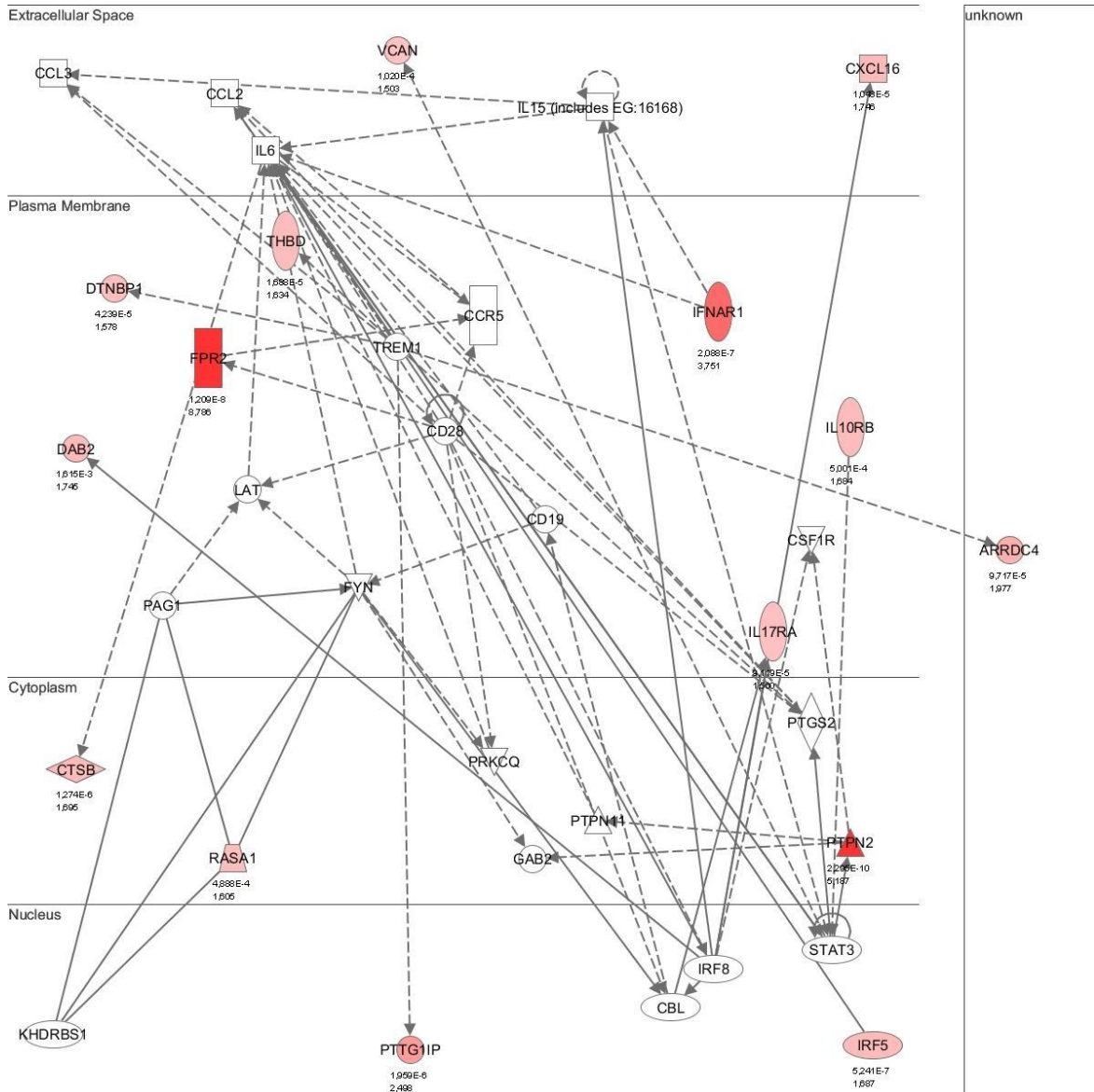
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1 **Figure S6: Network 2 generated from genes down-regulated by *N. meningitidis***
 2 **and up-regulated by IL-10**



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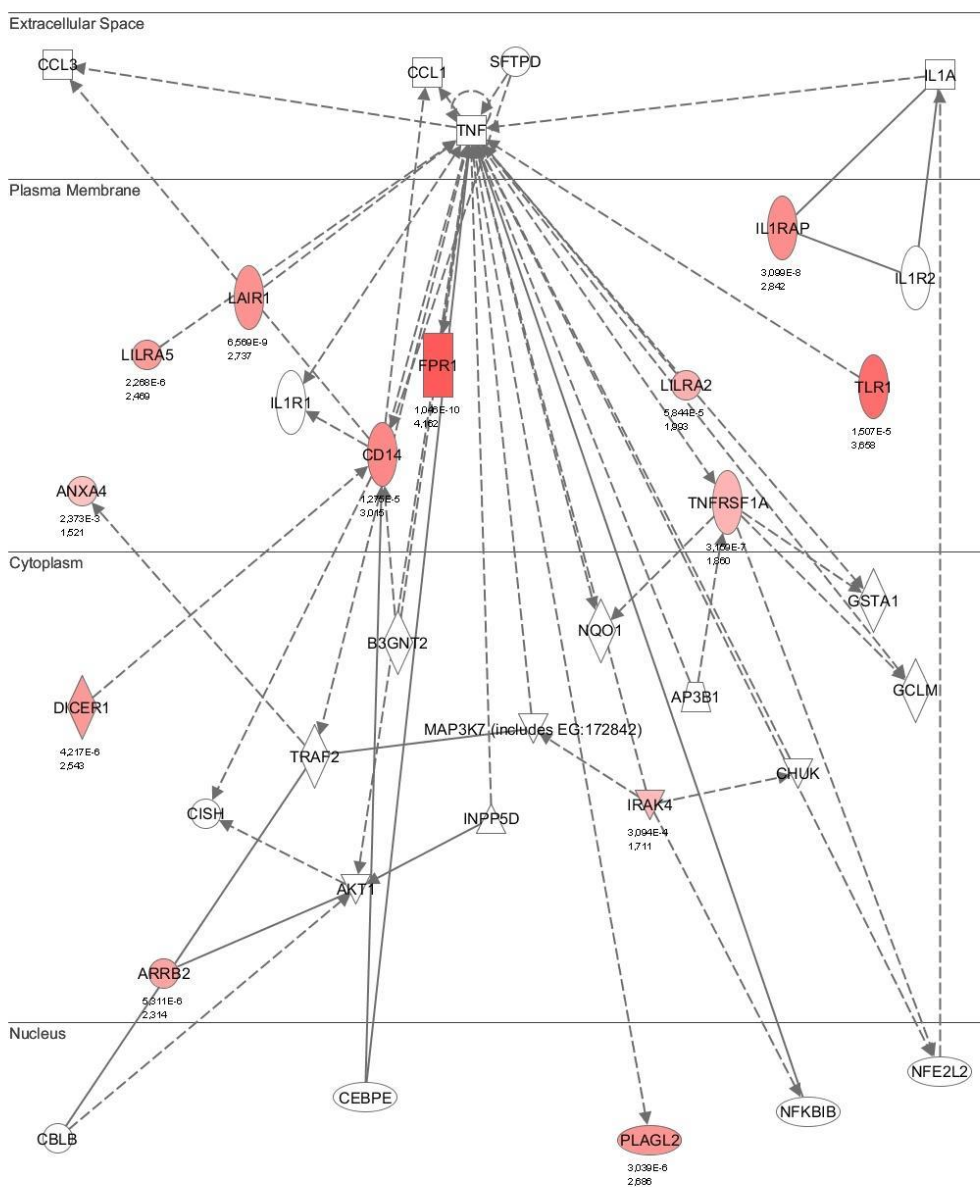
4 **Figure S6 legend**

5 Figure S6 displays network 2 from Table 4. The color red indicates that the gene has
 6 been up-regulated by IL-10, and the tone of the color indicates the extent to which the
 7 gene has been up-regulated. Ingenuity Pathway Analysis has located the genes to the

1 nucleus, cytoplasm, plasma membrane and extracellular space. Solid lines imply direct
 2 relationships between the proteins encoded by the genes, while dashed lines represent
 3 indirect relationships.

4

5 **Figure S7: Network 3 generated from genes down-regulated by *N. meningitidis***
 6 **and up-regulated by IL-10**



7

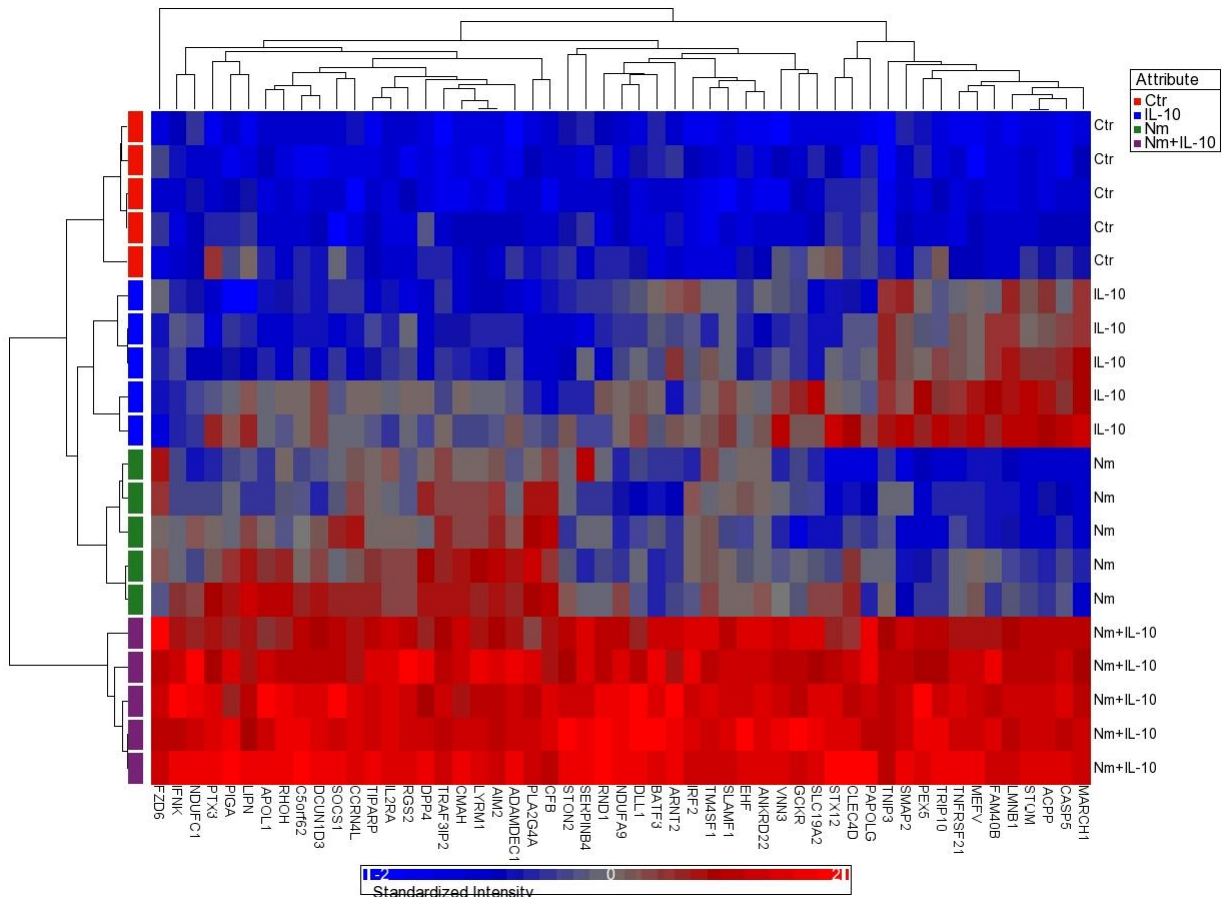
1 **Figure S7 legend**

2 Figure S7 displays network 3 from Table 4. The color red indicates that the gene has
3 been up-regulated by IL-10, and the tone of the color indicates the extent to which the
4 gene has been up-regulated. Ingenuity Pathway Analysis has located the genes to the
5 nucleus, cytoplasm, plasma membrane and extracellular space. Solid lines imply direct
6 relationships between the proteins encoded by the genes, while dashed lines represent
7 indirect relationships.

8

9 **Figure S8: Heatmap of genes synergistically up-regulated by *N. meningitidis* and**

10 **IL-10.**



11

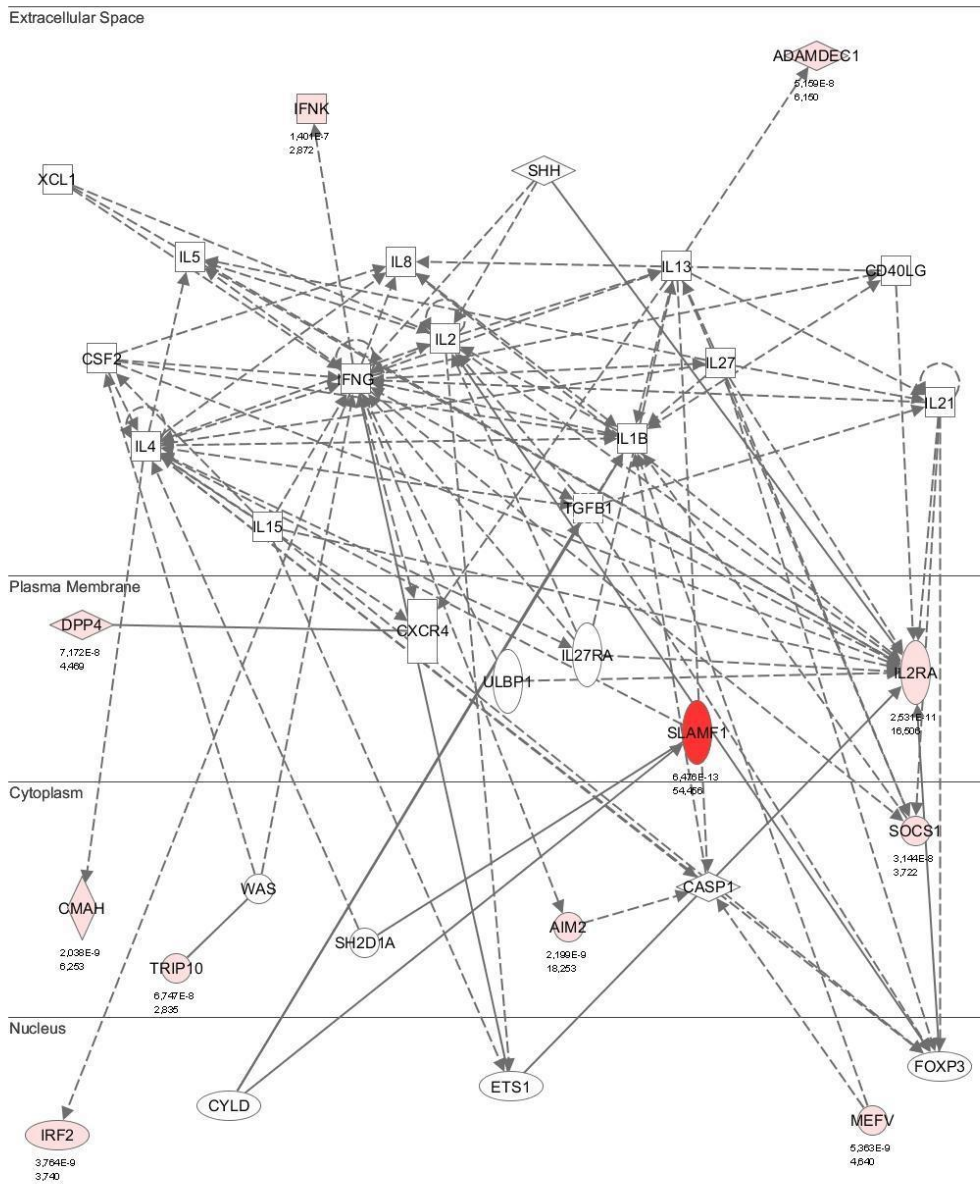
12

1 **Figure S8 legend**

2 Heatmap displaying genes synergistically up-regulated by *N. meningitidis* in combination
3 with IL-10. The heatmap displays the expression of genes in unstimulated monocytes
4 (Ctr) and monocytes stimulated by IL-10 (IL-10), *N. meningitidis* (Nm) and *N.*
5 *meningitidis* in combination with IL-10 (Nm + IL-10). The signal intensity for each gene
6 is compared to the average intensity detected for the gene over the 20 microarrays.
7 Grey color indicates that the signal intensity for the gene in the array is close to this
8 average signal intensity level. The color red indicates up-regulation and signal intensity
9 above the average level, while blue indicates down-regulation and signal intensity below
10 the average level.

11

12 **Figure S9: Network 1 generated from genes synergistically up-regulated by *N.***
13 ***meningitidis* and IL-10.**



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2 **Figure S9 legend**

3 Figure S9 displays network 1 from Table 5. The color red indicates that the gene has
 4 been synergistically up-regulated by *N. meningitidis* and IL-10, and the tone of the color
 5 indicates the extent to which the gene has been up-regulated. Ingenuity Pathway
 6 Analysis has located the genes to the nucleus, cytoplasm, plasma membrane and

- 1 extracellular space. Solid lines imply direct relationships between the proteins encoded
- 2 by the genes, while dashed lines represent indirect relationships.