

[KEGG] website <http://www.genome.jp/kegg/kegg1.html>). The genes are colored according to the transcript with the fold change in expression. Red color indicates up-regulation at onset of *Spn* infection, green down-regulation.

Fig. 2. Comparison of genes regulated as measured by microarray and qRT-PCR. The fold change of gene expression was derived by comparison of the gene expression at the onset of AOM due to *Spn* (AOM) with the pre-infection healthy stage (Preinf) in the same children with the same samples. The data from the 4 children are presented as a mean \pm SD. In all the genes studied there was no difference for the fold change between qRT-PCR and microarray ($p>0.05$).

Fig. 3. Variability of gene expression among 4 children with AOM due to Spn. Statistical package software R was used for the identification of differentially expressed genes. The profile includes 17 genes selected from the 127 immune defense response gene transcripts of PBMCs, which were >2 fold change at the comparison of the onset of AOM due to *Spn* and their pre-infection healthy stage. Shown are normalized expression (AOM stage) greater than (red), near (black), or less than (green) the mean of controls (healthy stage). Each column represents one child of healthy or AOM stage. Genes or transcripts are represented in rows.

Supplementary Table 1. *Genes differentially expressed in 4 children with AOM due to Spn versus their pre-infection healthy stage.* Genes whose relative transcription levels changed by >2 fold were considered as differentially regulated. The fold change of gene expression was derived by comparison of the normalized intensity of the signals at the time

of onset of AOM due to *Spn* with the pre-infection healthy stage in the same children. The data from the 4 children are presented as a mean.

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