Supplementary data

Human Respiratory Syncytial Virus-induced immune signature of infection revealed by transcriptome analysis of clinical pediatric nasopharyngeal swab samples

Authors

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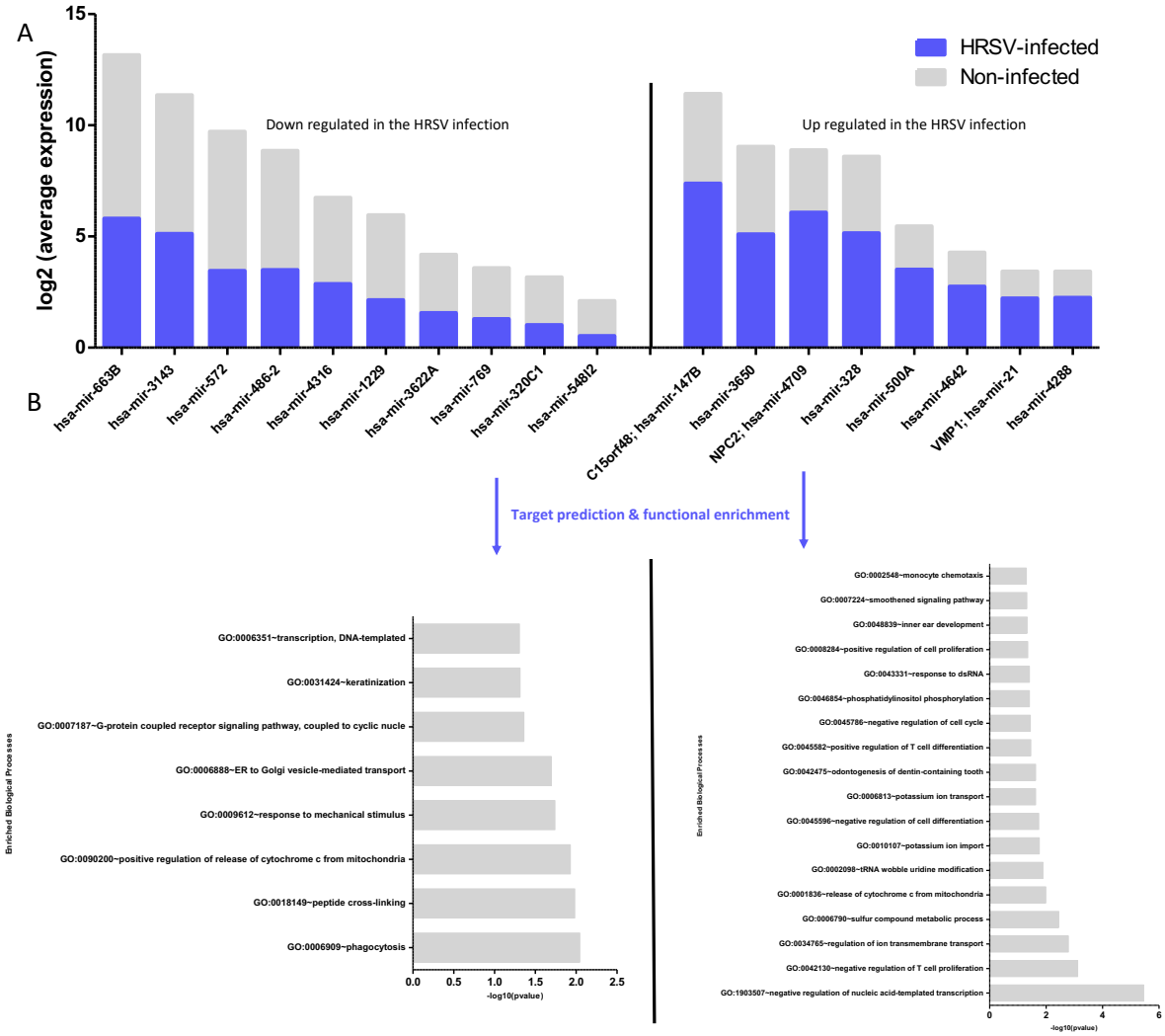
Infection Status	Sample ID	Sample type	RIN after RNA extraction	Initial concentration quantification (ng/µL)	RIN after purification	Concentration after purification (ng/ul)	cRNA quantification after amplification and purification (ug)	cDNA quantity (ng/µl) after conversion	cDNA quantification after conversion (ug)
Non-infected	1	Total RNA	2.6	0.68	1	0.11	7.835	166.78	5.3
Non-infected	2	Total RNA	2.6	0.67	1	0.27	5.225	205.78	6.6
Non-infected	3	Total RNA	2.6	1.6	1	0.084	4.92	130.11	4.2
Non-infected	4	Total RNA	1.2	0.27	Not Available	0.012	10.87	250.85	7.0
Non-infected	5	Total RNA	Not Available	40	1	1	16.54	314.3	8.8
HRSV-infected	6	Total RNA	2.6	0.790	Not Available	0.04	21.52	280.24	7.85
HRSV-infected	7	Total RNA	2.6	0.880	1	0.023	18.49	369.48	10.3
HRSV-infected	8	Total RNA	2.6	1.100	1	0.077	5.975	198.28	6.3

Suppl. Table 1: Minimal quantities requested for microarray hybridization and homogeneity between samples are respected post amplification. The 8 samples (3 infected and 5 non-infected) were quantified and qualified after total RNA extraction (Quantifluor RNA System, Promega). The low quantity/quality observed after purification determined the need for subsequent amplification of the samples for hybridization. Samples underwent 3 rounds of unbiased *in vitro* amplification and sufficient cRNA was obtained to be used as cDNA template. Minimal quantities requested for hybridization on Affymetrix Human Genechip™ 2.0 ST Array were reached for all samples after three rounds of *in vitro* transcription.

Supplementary Table 2. Gene expression results (*available upon request*)



Supp Figure 1. miRNA differential and functional analysis. (A) Log2 average expression values of both up- and down-regulated miR were extracted from the differential expression gene list (absolute fold change > 2 and p-value < 0.05). The identification of all genes targeted by at least one of the miRNAs was performed with the target prediction algorithm TargetScan 7.2. **(B)** Functional enrichment analysis (DAVID 6.8) of predicted biological targets to capture the involvement of such genes in several biological processes is show