



1 Article

# 2 Expressions of type I and III interferons, endogenous retrovi- 3 ruses, TRIM28, and SETDB1 in children with respiratory syn- 4 cytial virus bronchiolitis

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16 **Abstract:** Interferons (IFNs) and IFN-stimulated genes (ISGs) play essential roles for the control of  
17 viral infections. Their expression in infants with respiratory syncytial virus (RSV) bronchiolitis is  
18 poorly defined. Human endogenous retroviruses (HERVs) represent 8% of our genome and mod-  
19 ulate inflammatory and immune reactions. TRIM28 and SETDB1 participate in the epigenetic reg-  
20 ulation of genes involved in the immune response, including IFNs and HERVs. No study explored  
21 the expression of HERVs, TRIM28, and SETDB1 during RSV bronchiolitis. We assessed, through a  
22 PCR real time Taqman amplification assay, the transcription levels of six IFN-I ISGs, four IFN- $\alpha$ s,  
23 pol genes of HERV-H, -K, and -W families, env genes of Syncytin (SYN)1, SYN2, and of TRIM28/  
24 SETDB1 in whole blood from 37 children hospitalized for severe RSV bronchiolitis and in Healthy  
25 children (HC). The expression of most IFN-I ISGs was significantly higher in RSV+ patients than in  
26 age-matched HC, but it was inhibited by steroid therapy. The mRNA concentrations of IFN- $\lambda$ s  
27 were comparable between patients and age-matched HC. This lack of RSV-driven IFN-III activa-  
28 tion may result in defective protection of airway mucosal surface leading to severe bronchiolitis.  
29 The expression of IFN-III showed a positive correlation with age in HC, that could account for the  
30 high susceptibility of young children to viral respiratory tract infections. The transcription levels of  
31 every HERV gene were significantly lower in RSV+ patients than in HC, while the expressions of  
32 TRIM28/SETDB1 were overlapping. Given the negative impact of HERVs and the positive effects  
33 of TRIM28/SETDB1 on innate and adaptive immune responses, the downregulation of the former  
34 and the normal expression of the latter may contribute to preserve immune functions against in-  
35 fection.

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TRIM28; SETDB1

## 1. Introduction

Respiratory syncytial virus (RSV) is one of the most frequent causes of infection during the first 2 years of life, with approximately two thirds of children infected by the end of their first year [1]. Infants and young children may develop acute bronchiolitis upon RSV infection. Most patients do not require hospitalization, however, about 3% are hospitalized because of severe clinical pictures, sometimes with admission to a pediatric intensive care unit (PICU) and support of invasive mechanical ventilation [1,2]. Prematurity, younger age, and co-morbidity were identified as risk factors for increased mor-

46 bidity and mortality [3,4]. However, nearly half of children admitted to PICU were pre-  
47 viously healthy [2]. Severe RSV bronchiolitis may predispose to childhood asthma [5,6].  
48 With increasing age, RSV episodes decrease in severity and in adults severe manifesta-  
49 tions occur only in individuals with previous pulmonary problems and in elderly [7].  
50 Most hypotheses about the particular susceptibility of infants to bronchiolitis are based  
51 on structural elements, such as small airway size, different innervation patterns, and lack  
52 of interalveolar pores and channels; however, biological factors also appear to be in-  
53 volved, such as an altered inflammatory response with increased mucus production,  
54 massive neutrophil accumulation, and prevalent Th2 responses in a genetically suscep-  
55 tible host [8].

56 Viral recognition elicits production of interferons (IFNs), which in turn induce  
57 transcription of IFN-stimulated genes (ISGs). These exert potent antiviral activities and  
58 modulate a large array of innate and adaptive immune responses. Three types of IFNs  
59 have been identified. Type I IFNs encompass several subtypes [9], which through their  
60 binding to a ubiquitous receptor (IFNAR) are able to induce a rapid transcription of  
61 thousands of genes [9,10]. Direct detection of type I interferons in biologic samples has  
62 proven to be challenging. Thus, expressions of ISGs is commonly used to calculate type I  
63 IFN signature scores [11,12]. In contrast to the type II IFN, which is mostly a lately pro-  
64 duced T-cell cytokine, the type III interferon (IFN-III) is also involved in the early phases  
65 of antiviral response. It encompasses four members, also referred to as lambdas (IFNλs).  
66 They bind to a unique receptor expressed by epithelial cells and a subset of immune cells  
67 [13]. IFNλs represent the front-line antiviral defense of the respiratory mucosa [14,15];  
68 they have less inflammatory activity than type I IFNs and fine-tune their antiviral effects  
69 [16]. Given the potent IFN-driven antiviral functions, many viruses have developed  
70 mechanisms to escape their inhibitory effects [16-18], including RSV [19,20].

71 Human endogenous retroviruses (HERVs) constitute about 8% of human genome.  
72 They originate from ancestral infections of somatic cells with subsequent stable integra-  
73 tion into the DNA of germinal cells [21]. Following deletions, multiplications, and muta-  
74 tions they cannot produce infectious virions. Some viral sequences are however trans-  
75 cribed and a few encode proteins, such as Syncytin-1 (SYN1) [22] and Syncytin-2 (SYN2)  
76 [23], that are involved in crucial physiologic functions, such as placental syncytiotroph-  
77 oblast formation and materno-fetal immune tolerance [24]. HERVs share the typical  
78 structure of retroviruses, with three major genes: group associated antigens (*gag*), poly-  
79 merase (*pol*) and envelope (*env*), flanked between two regulatory long terminal repeats  
80 (LTRs). HERVs can regulate transcription of adjacent cellular genes [25,26], their RNAs  
81 through retro-transposition may generate novel insertions into DNA or, being sensed as  
82 non-self by pattern recognition receptors (PRRs), elicit inflammatory and immune re-  
83 sponses [26-29]. Some retroviral proteins can trigger autoimmunity [30,31], while others,  
84 such as the syncytins, have intrinsic immunomodulatory properties [32-35]. Aberrant  
85 HERV expressions are associated with immune mediated and inflammatory diseases,  
86 supporting their pathogenetic role in these pathologies [25,30,31,36,37]. Exogenous viral  
87 infections can induce abnormal HERV transcription. These include human herpes sim-  
88 plex virus 1 [38-39] and 6 [39-40], Varicella-zoster virus [40], Epstein-Barr virus [41,42],  
89 human cytomegalovirus [43], HIV [44,45], hepatitis B [46] and C [47] viruses, influenza  
90 virus [48], and SARS-CoV-2 [12,49-51]. Furthermore, IFNs and inflammatory cytokines  
91 lead to an independent and synergistic activation of retroviral sequences [52]. The impact  
92 of virus-induced aberrant HERV expressions on the antiviral immune response remains  
93 poorly understood. Protective effects have been reported [50,53], but growing evidence  
94 suggests a negative action on viral control and disease progression [33,34,49,51,54-56].

95 HERV expression may be modulated by environmental factors through epigenetic  
96 mechanisms, such as DNA methylation and histone modifications. Krüppel-associated  
97 box domain zinc finger proteins (KRAB-ZFPs) represent the largest family of transcrip-  
98 tion regulators in our genome. Tripartite motif containing 28 (TRIM28), also called KAP1  
99 or TIF1-β, is a nuclear corepressor of KRAB-ZFPs [57]. SET domain bifurcated histone

lysine methyltransferase 1 (SETDB1), also called ESET, is a histone H3K9 methyltransferase that participates with TRIM28 and KRAB-ZFPs to formation of heterochromatin [58]. TRIM28 and SETDB1 were uncovered mainly through investigations on host factors regulating the transcription of endogenous retroviruses [59,60]. Recent studies have, however, drawn attention on the crucial roles of TRIM28 and SETDB1 in the epigenetic control of the immune response (60-63), including the antiviral response and IFN production [64-66].

Despite these premises, the importance of IFN signature scores in infants hospitalized with severe RSV bronchiolitis remains elusive. Furthermore, in front of the potential cross-talks between RSV infection, HERVs, and TRIM28/SETDB1, no data on their expressions in infected patients are available. To obtain targeted information on the relevance of these variables during severe RSV bronchiolitis, we compared the transcriptional levels of six IFN-I ISGs and of type III IFNs, of HERV sequences, in particular of env genes of SYN1, SYN2, and of pol genes of HERV-H, -K, -W (the three retroviral families most widely studied) as well as of TRIM28 and SETDB1 in children hospitalized for acute RSV bronchiolitis versus Healthy children (HC).

## 2. Materials and Methods

### 2.1. Study populations

Two groups of children were enrolled in the study. Group A included children who were admitted at the Regina Margherita Children's Hospital, Turin, Italy, with acute bronchiolitis due to RSV infection. These patients were also subdivided in two subgroups: Group A1 including children on steroid treatment and Group A2 including children without steroid treatment. Group B included HC tested at the same hospital for routine laboratory examinations and whose results were all within normal limits. Subjects with any confirmed or suspected disease associated with abnormal IFN production and/or HERV expression were excluded from the study. Exclusion criteria included children with confirmed or suspected immune defects (e.g. primary immunodeficiencies, born to HIV+ mothers), cancers, viral coinfections, autoimmune disorders [31], food allergy [37], prematurity [67], autism spectrum disorder [68,69].

### 2.2. Total RNA extraction

Total RNA was extracted from whole blood using the automated extractor Maxwell following the RNA Blood Kit protocol without modification (Promega, Madison, WI). This kit provides treatment with DNase during the RNA extraction process. To further exclude any contamination of genomic DNA, RNA extracts were directly amplified without reverse transcription to validate the RNA extraction protocol. RNA concentration and purity were assessed by traditional UV spectroscopy with absorbance at 260 and 280 nm. The nucleic acid concentration was calculated using the Beer-Lambert law, which predicts a linear change in absorbance with concentration. The RNA concentration range was within manufacturer specifications for the NanoDrop (Thermo Fisher Scientific, Waltham, MA USA). UV absorbance measurements were acquired using 1 µl of RNA sample in an ND-1000 spectrophotometer under the RNA-40 settings at room temperature (RT). Using this equation, an A260 reading of 1.0 is equivalent to ~40 µg/ml single-stranded RNA. The A260/A280 ratio was used to define RNA purity. An A260/A280 ratio of 1.8/2.1 is indicative of highly purified RNA. The RNAs were stored at -80° until use.

### 2.3. Reverse Transcription

Four hundred nanograms of total RNA was reverse-transcribed with 4 µl of buffer 5X, 4.8 µl of MgCl<sub>2</sub> 25 mM, 2 µl ImpromII (Promega), 1 µl of RNase inhibitor 20U/l, 0.4 µl random hexamers 250 µM (Promega), 2 µl mix dNTPs 100 mM (Promega), and dd-water in a final volume of 20 µl. The reaction mix was carried out in a GeneAmp PCR system

9700 Thermal Cycle (Applied Biosystems, Foster City, CA, USA) under the following conditions: 5 min at 25°C, 60 min at 42°C and 15 min at 70°C for the inactivation of enzyme. The cDNAs were stored at -20° until use.

#### 2.4. Transcription levels of IFNs, ISGs, TRIM28, SETDB1, pol genes of HERV-H, -K, and -W, and env genes of SYN1 and SYN2 by real-time PCR assays

GAPDH was chosen as reference gene in all determinations being one of the most stable among reference genes and already used in our previous studies [12,36,37,47,69].

Relative expression of transcription levels of IFN-I ISGs (IFI27, IFI44L, ISG15, IFIT1, RSAD2, and SIGLEC) [11], IFN-III (IFN- $\lambda$ 1, IFN- $\lambda$ 2, IFN- $\lambda$ 3, and IFN- $\lambda$ 4) [13], TRIM28, SETDB1, as well as of HERV-H-pol, HERV-K-pol, HERV-W-pol, SYN1-env, and SYN2-env was achieved as previously described in detail [12,54], using the primers and probes reported in Table 1. Briefly, 40 ng of cDNA were amplified in a 20  $\mu$ L total volume reaction, containing 2.5 U goTaQ MaterMix (Promega), 1.25 mmol/L MgCl<sub>2</sub>, 500 nmol of specific primers, and 200 nmol of specific probes.

All the amplifications were run in a 96-well plate at 95 °C for 10 min, followed by 45 cycles at 95 °C for 15 s and at 60 °C for 1 min. Each sample was run in triplicate. Relative quantification of target gene transcripts was performed according to the 2<sup>- $\Delta\Delta$ Ct</sup> method [70]. Briefly, after normalization of the PCR result of each target gene with the house-keeping gene, the method includes additional calibration using the expression of the target gene evaluated in a pool of healthy controls. The results, expressed in arbitrary units ( called relative expression, RE), show the variations of target gene transcripts relative to the standard set of controls. Since we measured Ct for every target in all samples, we argue that our methods were suitable for HERVs, IFN signatures, TRIM28 and SETDB1 detection and quantifications.

All analyses were performed in a laboratory of biosafety level 2 (BSL-2) according to the NIH [71] and WHO [72] guidelines.

Name	Primer/Probe	Sequence
<b>Type I interferon stimulated genes</b>		
IFI27	Forward	TGTCATTGCGAGGTTCTACTAGCT
	Reverse	CCCCTGGCATGGTTCTCTT
	Probe	6FAM-CCTGCCCTCGCCCTGCA-TAMRA
IFI44L	Forward	GTGACTGGCCAAGCCGTAGT
	Reverse	CACACAACATAAATGGCAGAGATT
	Probe	6FAM-TCTGATATCACCAGCATAAACCAGCGG-TAMRA
IFIT1	Forward	TGGCTGACTTCACCTAGCTCACT
	Reverse	CATGGACTGGCCAGAACCA
	Probe	6FAM-CGTAGCGCCACAGCCAGACTCCC-TAMRA
ISG15	Forward	TGGCGGGCAACGAATT
	Reverse	GGGTGATCTGCGCCTCA
	Probe	6FAM-CCTGAGCAGCTCCATGTCGGTGTC-TAMRA
RSAD2	Forward	GAGGGCCAGATGAGACCAAA
	Reverse	GTGAAGTGATAGTTGACGCTGGTT
	Probe	6FAM-AGGACCCTCCTCTGCCACCACC-TAMRA
SIGLEC1	Forward	AGGGAGACTGGGAAATGTAGTTTTTA
	Reverse	ATTCCCAACAATGTCAAAAGTCTCA
	Probe	6FAM-AGTCCAGAGGACATTTGGAATTGGAC-TAMRA
<b>Type III Interferon</b>		

IFN- $\lambda$ 1	Forward	GAGGCATCTGTACCTTC
	Reverse	GGTTGACGTTCTCAGACA
	Probe	6FAM-ACCTCTTCCGCTCCTCACG-BHQ1
IFN- $\lambda$ 2	Forward	GCCACATAGCCCAGTTCAAG
	Reverse	TCCTTCAGCAGAAGCGACTC
	Probe	6FAM-CTGTCTCCACAGGAGCTGCAGGCC-BHQ1
IFN- $\lambda$ 3	Forward	TCACCTTCAACCTCTTCC
	Reverse	GAAGGGTCAGACACACAG
	Probe	6FAM-TGGCAACACAATTCAGGTCTCG-BHQ1
IFN- $\lambda$ 4	Forward	CCTTCTACAGGGAAGAGAC
	Reverse	CTGGTAACACACAAGGA
	Probe	6FAM-CAGTTCTCCAGGAAGCCACGATA-BHQ1
<b>HERV-K pol</b>	Forward	CCACTGTAGAGCCTCCTAAACCC-
	Reverse	TTGGTAGCGGCCACTGATTT
	Probe	6FAM-CCCACACCGGTTTTTCTGTTTTCCAAGT TAA-TAMRA
<b>HERV-W pol</b>	Forward	ACMTGGAYKRTYTTRCCCAA
	Reverse	GTAAATCATCCACMTAYYGAAGGAYMA
	Probe	6FAM-TYAGGGATAGCCCYCATCTRTTGGYC AGGCA-TAMRA
<b>HERV-H pol</b>	Forward	TGGACTGTGCTGCCGCAA
	Reverse	GAAGSTCATCAATATATTGAATAAGGTGAGA
	Probe	6FAM- TTCAGGGACAGCCCTCGTTACTT- CAGCCAAGCTC-TAMRA
<b>Syncytin 1 env</b>	Forward	ACTTTGTCTCTTCCAGAATCG
	Reverse	GCGGTAGATCTTAGTCTTGG
	Probe	6FAM-TGCATCTTGGGCTCCAT-TAMRA
<b>Syncytin 2 env</b>	Forward	GCCTGCAAATAGTCTTCTTT
	Reverse	ATAGGGGCTATTCCCATTAG
	Probe	6FAM- TGATATCCGCCA- GAAACCTCCC-TAMRA
<b>TRIM28</b>	Forward	GCCTCTGTGTGAGACCTGTGTAGA
	Reverse	CCAGTAGAGCGCACAGTATGGT
	Probe	6FAM-CGCACCAGCGGGTGAAGTACACC-TAMRA
<b>SETDB1</b>	Forward	GCCGTGACTTCATAGAGGAGTATGT
	Reverse	GCTGGCCACTCTTGAGCAGTA
	Probe	6FAM-TGCCTACCCCAACCGCCCAT-TAMRA

**Table 1.** Primers and probes used to assess the transcription levels of type I interferon stimulated genes, type III interferon genes, *pol* genes of HERV-K, -W, and -H, *env* genes of Syncytin 1 and Syncytin 2, TRIM28 and SETDB1.

### 2.5. Statistical analysis

One-way ANOVA test was used to compare the transcriptional levels of IFN-I ISGs, IFN-III, TRIM28 and SETDB1, HERV-H-pol, HERV-K-pol, HERV-W-pol, SYN1-env, and SYN2-env, between Group A1 and Group A2 patients and HC. Mann-Whitney test was used to compare the transcriptional levels of each IFN-I ISG, IFN-III, TRIM28, SETDB1, HERV-H-pol, HERV-K-pol, HERV-W-pol, SYN1-env, and SYN2-env between each group of children with each other. Spearman correlation test was used to evaluate the correlations between age and mRNA concentrations of each target gene. Statistical analyses were done using the Prism software (GraphPad Software, La Jolla, CA). In all analyses,  $p < 0.05$  was taken to be statistically significant.

### 3. Results

### 3.1. Study populations

Group A included 37 children hospitalized for acute RSV bronchiolitis. Their demographics and clinical features are reported in Table 2. Three RSV+ infants with Influenza A coinfection and 1 with pre-term delivery were excluded from the study.

	<b>Patients (n = 37)</b>
Median age (IQR)	0.2 yrs (0.1 – 0.3)
Males (%)	15 (40.5)
Comorbidities, n (%)	10 (27)
Mean interval (+SD) from symptom onset and sampling	7.0 days (5.5)
Increased inflammatory markers n (%)	10 (27)
Leucocytosis, n (%)	3 (13)
Lymphopenia, n (%)	8 (21.6)
Steroid treatment, n (%)	12 (32.4)
Oxygen treatment (%)	31 (83.8)

**Table 2.** Demographics and clinical characteristics of children with acute RSV bronchiolitis. *n*: number; %: percentage; IQR: interquartile range, expressed as 25 and 75 quartile values; yrs: years; SD: standard deviation. Values upper \* or below \*\* normal limit according to age-related cutoffs.

Ten patients had comorbidities: 2 asthma, 1 metabolic disorders, 2 congenital malformations, 2 bacterial coinfections, 1 neuromuscular disease, 1 late preterm, 1 neuropsychomotor disorder. Three patients had complications: 1 had bacterial pneumonia, 1 cutaneous vasculitis, and 1 post-infective anemia. Supplemental oxygen was administered to 31 patients. One patient had been admitted to the ICU. High markers of systemic inflammation, such as C-reactive protein (CRP), erythrocyte sedimentation rate (ESR), and procalcitonin (PCT) levels, were found in 10 (27%) patients.

Patients were subdivided in two subgroups: Group A1 on steroid treatment, Group A2 without such therapy (Table 3).

At follow-up all patients recovered from the acute illness.

As detailed in Table 3, control children encompassed 4 subgroups of subjects (Group B1, B2, B3, and B4), based on the tests performed.

RSV+ Patients			Healthy Children		
Group A1	Group A2	Group B1	Group B2	Group B3	Group B4
On steroid treatment	No steroid treatment	Tested for interferon signatures	Tested for pol genes of HERV-H, -K, and -W	Tested for env genes of syncytin 1 and syncytin 2	Tested for TRIM28 and SETDB1
n. 12	n. 25	n. 46	n. 29	n. 30	n. 40
7 males, median age 0.29, IQR 0.17 - 2.25 years	16 males, median age 0.17, IQR 0.11 - 3.5 years	27 males, median age 0.7, IQR 0.2 - 2.1 years	17 males, median age 3.3, IQR 2.3 - 4.1 years	17 males, median age 1.9, IQR 1.1 - 3.8 years	23 males, median age 3.3, IQR 2.0 - 3.8 years

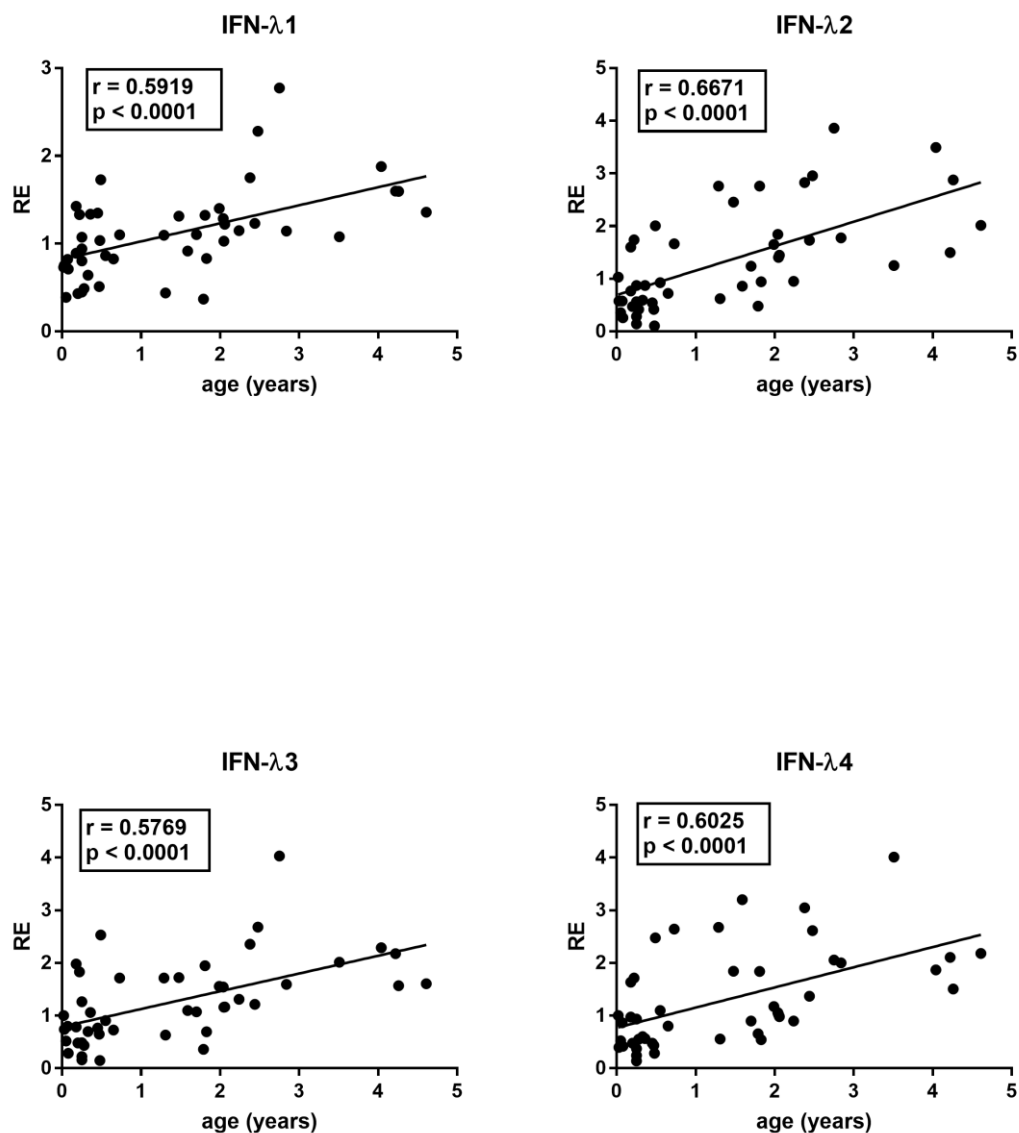
**Table 3.** Characteristics of subgroups of RSV+ patients and healthy children. IQR: interquartile range, expressed as 25 and 75 quartile values.

### 3.2. Influence of age on IFN signature scores and on expression levels of HERVs, TRIM28, and SETDB1.

The median age differed between RSV patients and control groups. In particular, Group A was significantly younger than Group B1, B2, B3, and B4 children ( $p < 0.0001$ ). However, with the exception of IFN-III, there was no significant correlation be-

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tween age and the transcriptional levels of each target gene in the control groups, even if there was a trend of negative correlation for TRIM28 and SETDB1. In contrast, there was a significantly positive correlation between the age and the mRNA levels of IFN- $\lambda$ 1, IFN- $\lambda$ 2, IFN- $\lambda$ 3, and IFN- $\lambda$ 4 in HC (Figure 1).



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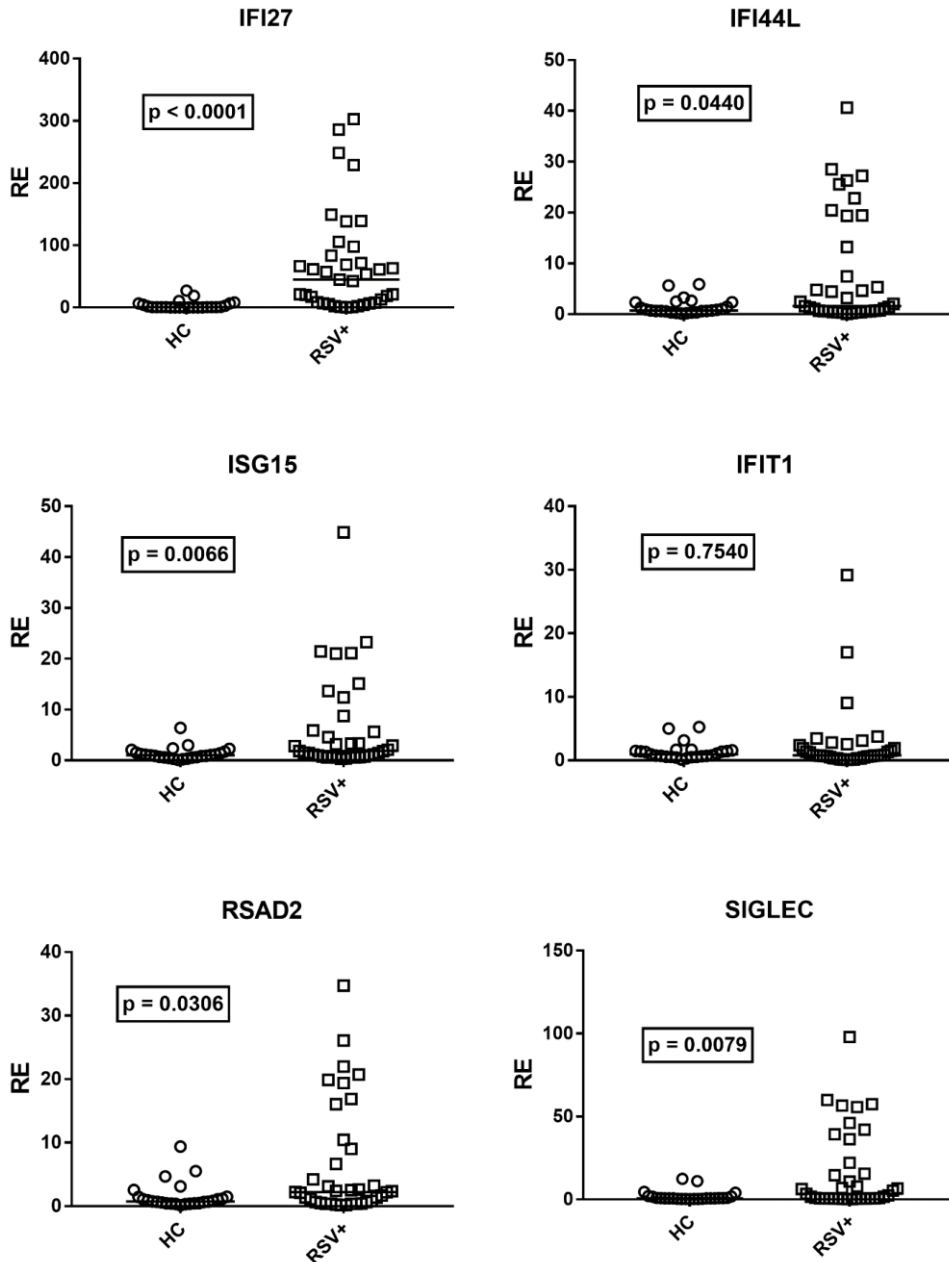
**Figure 1.** Correlations between age and transcription levels of IFN- $\lambda$ 1, IFN- $\lambda$ 2, IFN- $\lambda$ 3, and IFN- $\lambda$ 4 in whole blood from 46 healthy children of 0-5 years of age. RE: Relative Expression. Circles show the mean of three individual measurements. Line: Linear regression line. Statistical analysis: Spearman correlation test.

### 3.3. Type I IFN Signature

Although there was no correlation between age and expressions of IFN-I ISGs in HC, for analogy with IFN-III, we compared the median transcription levels of IFN-I ISGs in children with RSV bronchiolitis with the subgroup of 25 age-matched HC (median age and 25%-75% IQR: RSV+ patients: 0.2, 0.1 – 0.3; HC: 0.3, 0.2 – 0.6,  $p = 0.11$ ). Figure 2 shows that the mRNA levels of IFN-I ISGs were significantly higher in RSV+ patients than in HC for all ISGs with the exception of IFIT1.

No significant differences between males and females were found in the transcription levels of any ISG both in HC and in RSV+ patients (Supplementary figures 1 and 2).



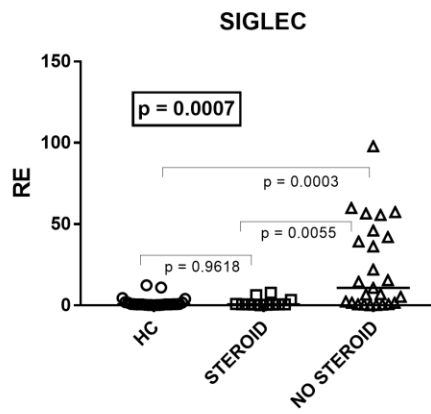
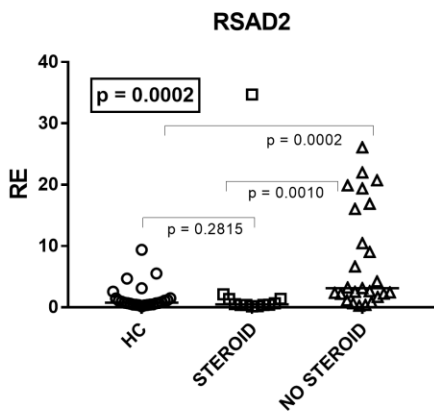
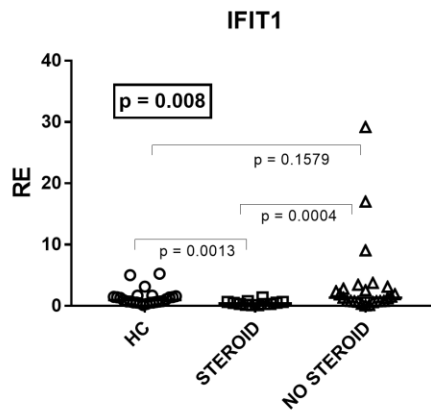
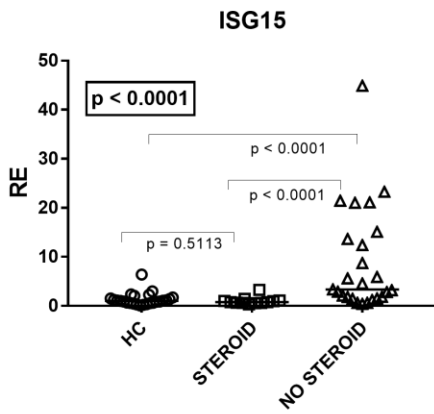
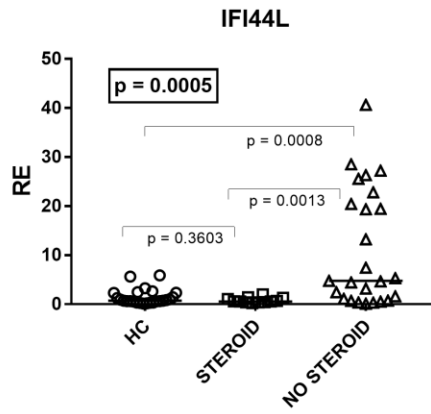
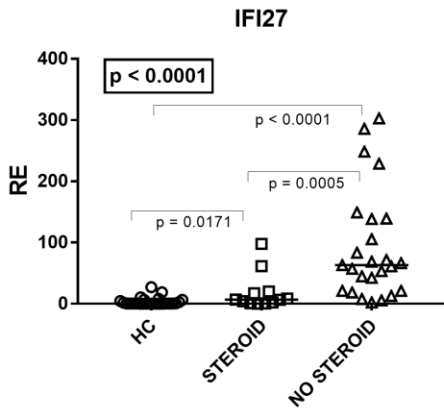


**Figure 2.** Expression of type I interferon stimulated genes (ISGs) in whole blood from 37 children with acute RSV bronchiolitis (RSV+) and 25 age-matched healthy children (HC). RE: Relative Expression. Circles and squares show the mean of three individual measurements; horizontal lines the median values. Median values and interquartile range 25%-75% of ISGs: IFI27: HC 0.55, 0.31-4.60; RSV+ 44.98, 7.90-83; IFI44L: HC 0.72, 0.54-2.36, RSV+ 1.59, 0.57-13.23; ISG15: HC: 1.02, 0.62-1.50; RSV+ 1.85, 0.78-5.89; IFIT1: HC 0.97, 0.59-1.49; RSV+ 0.79, 0.48-1.91; RSAD2: HC 0.76,

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246 0.46-1.45; RSV+ 2.21,0.66-9.02; SGLEC: HC 0.73, 0.48-1.63; RSV+ 3.43, 0.68-22.05. Statistical analysis:  
247 Mann-Whitney test was used to compare values of each group of children with each other.  
248

249 As illustrated in Figure 3, by comparing patients on steroid treatment (Group A1),  
250 untreated patients (Group A2), and HC, one-way ANOVA analysis showed significant  
251 differences in the mRNA levels of every IFN-I ISG between the three groups of children.  
252 In particular, the median transcriptional levels of IFN-I ISGs were significantly higher in  
253 untreated patients vs. HC for all genes except IFIT1. The levels of transcripts were sig-  
254 nificantly lower in treated patients vs. untreated patients for every ISG, whereas in the  
255 former vs. HC they remained significantly higher for IFI27, comparable for IFI44L, ISG15,  
256 RSAD2, and SIGLE, and reduced for IFIT1 (Figure 3).



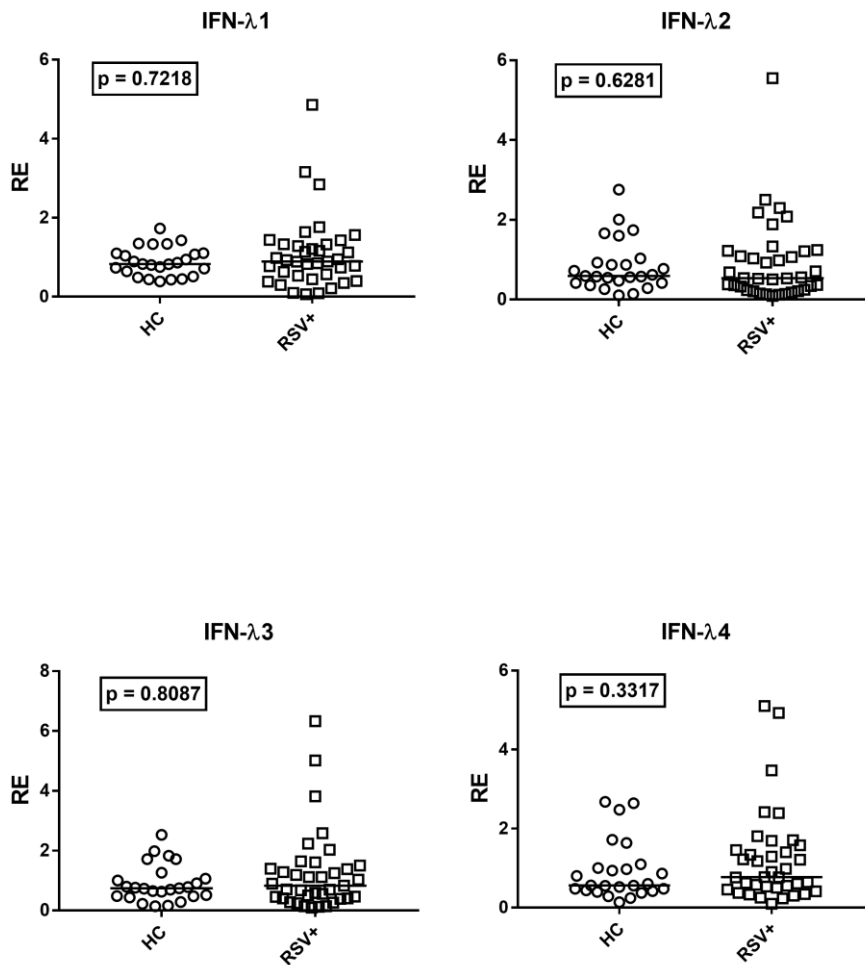
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**Figure 3.** Expression of type I interferon stimulated genes (ISGs) in whole blood from 25 age-matched healthy children (HC), 12 children with acute RSV bronchiolitis on steroid treatment (Group A1), and 25 untreated patients (Group A2). RE: Relative Expression. Horizontal lines show the median values; squares, triangles, and circles the mean of three individual measurements. Median values and interquartile range 25%-75% of six ISGs (values of HC are reported above): IFI27: Group A1 (on steroids) 6.74, 1.90–17.78; Group A2 (untreated) 63.32, 21.13–138.40; IFI44L: Group A1 0.58, 0.43–1.12; Group A2 4.78, 1.12–20.44; ISG15: Group A1 0.77, 0.59–1.05; Group A2 3.35, 1.81–13.66; IFIT1: Group A1 0.41, 0.28–0.66; Group A2 1.36, 0.75–2.82; RSAD2: Group A1 0.47, 0.39–1.36; Group A2 3.11, 2.19–16.04; SIGLEC: Group A1 0.73, 0.59–1.58; Group A2 10.76, 1.67–42.09. Statistical analysis: The transcription levels of each target between the three groups of children were compared using the one-way ANOVA test. The transcription levels of each target between each group of children with each other were compared using the Mann-Whitney test.

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3.4. Type III IFNs

Given the positive correlations between age and IFN-III levels, the transcriptional levels of every IFN- $\lambda$  in RSV infected children were compared to the subgroup of the 25 age-matched HC. The transcription levels of all IFN- $\lambda$ s were similar in RSV infected patients and age-matched HC (Figure 4)..



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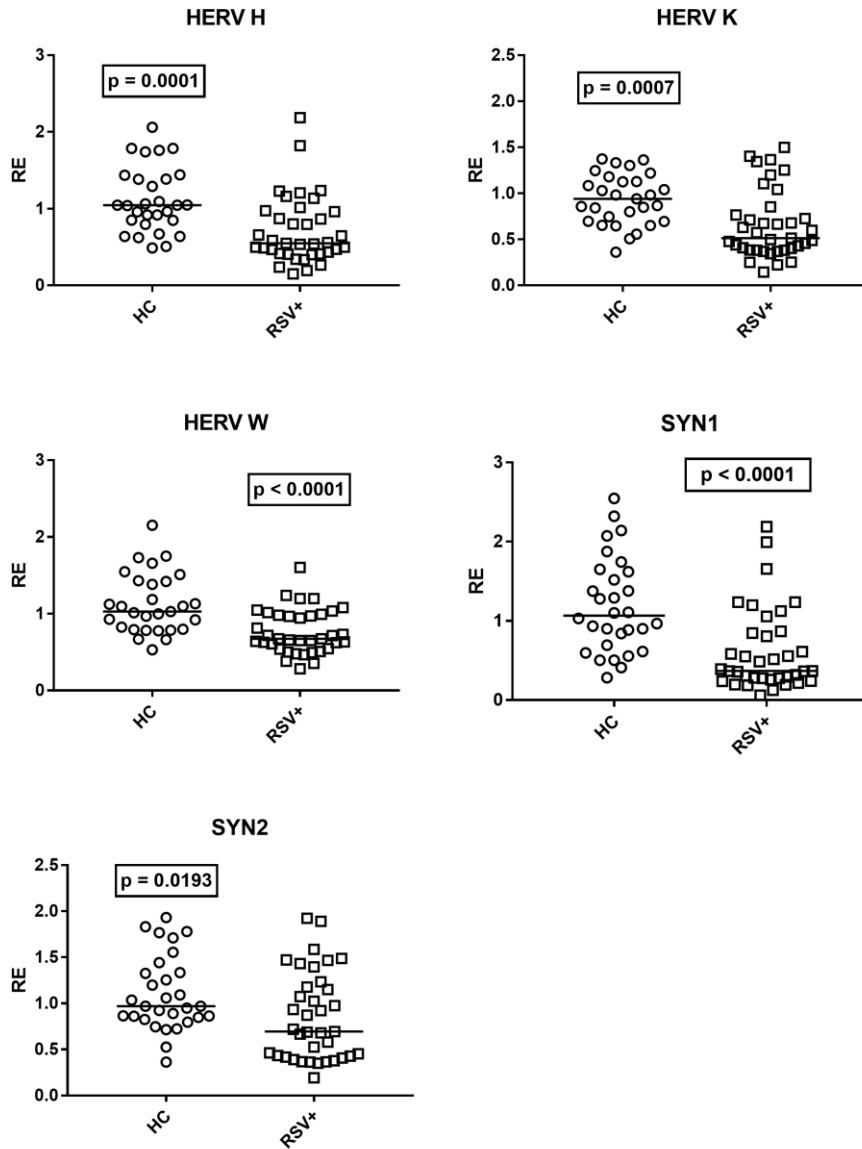
277 **Figure 4.** Expression of type III interferons in whole blood from 37 children with acute RSV bronchiolitis (RSV+) and 25 age-matched healthy children (HC). RE: Relative Expression. Circles and  
278 squares show the mean of three individual measurements, horizontal lines the median values.  
279 Median values and interquartile range 25%-75% of IFN-IIIs: IFN- $\lambda$ 1: HC 0.83, 0.64-1.10; RSV+ 0.89,  
280 0.53-1.32; IFN- $\lambda$ 2: HC 0.59, 0.42-0.93; RSV+ 0.54, 0.25- 1.21; IFN- $\lambda$ 3: HC 0.74, 0.48-1.06; RSV+ 0.83,  
281 0.41-1.39; IFN- $\lambda$ 4: HC 0.56, 0.44-1.00; RSV+ 0.77, 0.50-1.46. Statistical analysis: Mann-Whitney test  
282 was used to compare values of each group of children with each other.  
283

284 By comparing Group A1 patients (on steroid therapy) vs. Group A2 patients (un-  
285 treated) no significant difference emerged in the IFN-III transcript levels. Median values  
286 and interquartile range 25%-75% of IFN-IIIs: IFN- $\lambda$ 1: Group A1 0.81, 0.54 - 1.02; Group  
287 A2 0.93, 0.53-1.44; (p = 0.2149); IFN- $\lambda$ 2: Group A1 0.54, 0.23 - 0.77; Group A2 0.54, 0.34 -  
288 1.22; (p = 0.4909); IFN- $\lambda$ 3: Group A1: 0.77, IQR 0.45 - 1.20; Group A2 0.90, 0.41 - 1.61; (p =  
289 0.6426); IFN- $\lambda$ 4: Group A1 0.83, 0.44 - 1.27; Group A2 0.77, 0.55 - 1.46 (p = 0.5322).

290 No significant differences between genders were observed for IFN-III both in HC  
291 and RSV+ patients (Supplementary figures 3 and 4).

### 292 3.5. Expressions of *HERV-H-pol*, *HERV-K-pol*, *HERV-W-pol*, *SYN1-env*, and *SYN2-env*

293 The medians of the transcription levels of *HERV-H-pol*, *HERV-K-pol*, and  
294 *HERV-W-pol* as well as of *SYN1-env* and *SYN2-env* were significantly lower in children  
295 with RSV bronchiolitis as compared to HC (Figure 5).



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**Figure 5.** Transcription levels of pol genes of HERV-H, HERV-K, and HERV-W, and of env genes of syncytin (SYN)1 and syncytin (SYN)2 in whole blood from 37 children with acute RSV bronchiolitis (RSV+) and 29 healthy children (HC) for HERV-pols and 30 HC for SYN1-env and SYN2-env. RE: Relative Expression. Circles and squares show the median of three individual measurements, horizontal lines the median values. Median values and interquartile range 25%-75%, HERV-H-pol: HC 1.05, 0.85-1.39; RSV+ 0.55, 0.42-0.96; HERV-K-pol: HC 0.94, 0.70-1.13; RSV+ 0.51, 0.39-0.77; HER-W-pol: HC 1.03, 0.80-1.42; RSV+ 0.67, 0.55-0.98; SYN 1-env: HC 1.07, 0.73-1.60; RSV+ 0.37,0.28-0.85; SYN2-env: HC 0.97, 0.85-1.33; RSV+ 0.69, 0.43-1.18. Statistical analysis: Mann-Whitney test was used to compare values of each group of children with each other.

307 No significant differences between genders were observed in the transcription levels  
308 of HERVs both in HC and RSV+ patients (Supplementary figures 5 and 6).

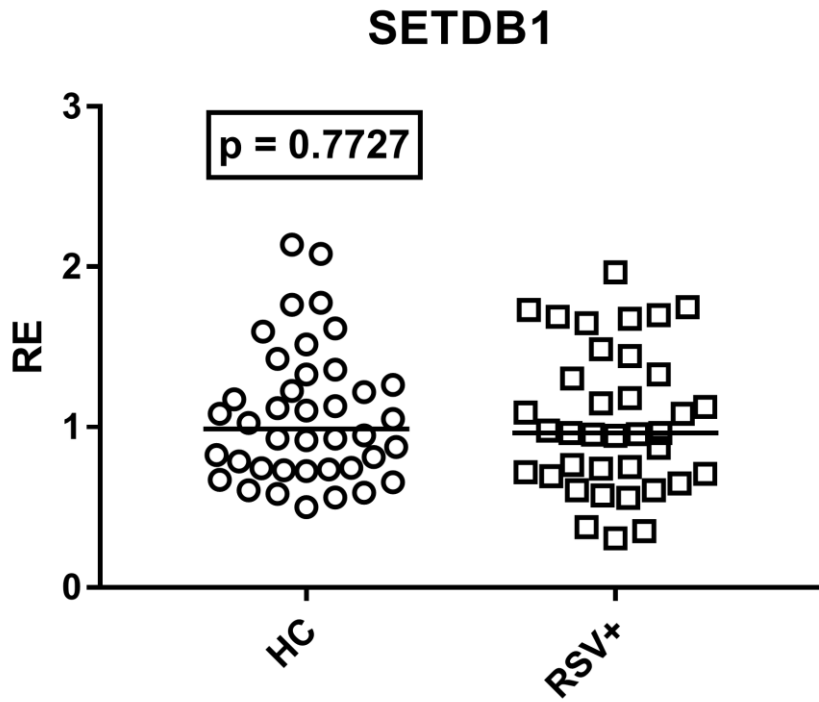
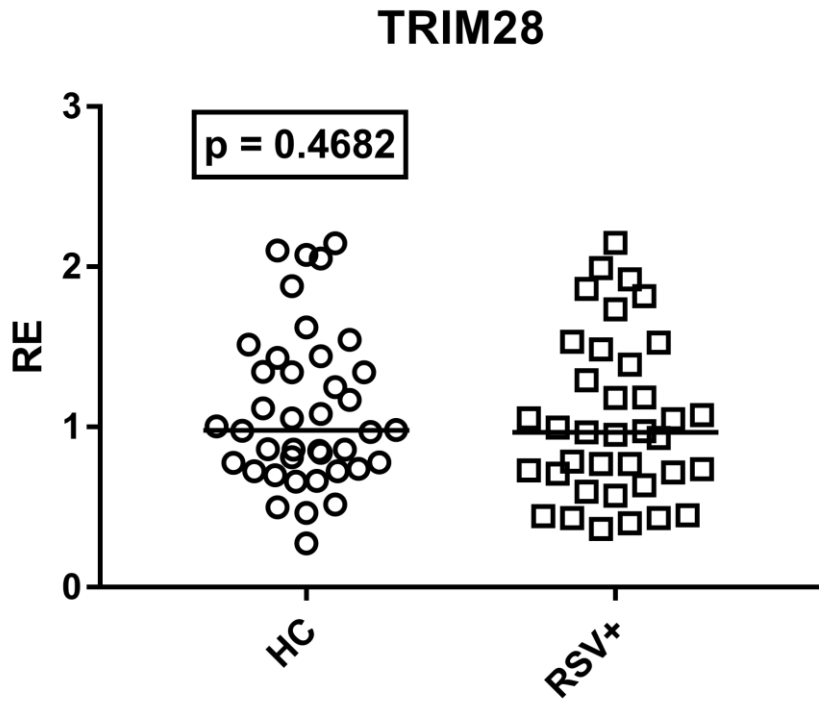
309 No difference was found between patients with (Group A1) and without (Group A2)  
310 steroid treatment. Median values and interquartile range 25%-75%, HERV-H-pol: Group  
311 A1 0.54, 0.46 - 0.84; Group A2 0.56, 0.41 - 0.97; (p = 0.9618); HERV-K-pol: Group A1 0.59,  
312 0.44 - 0.84; Group A2 0.50, 0.38 - 0.77; (p = 0.6892); HERV-W-pol: Group A1 0.70, 0.52 -  
313 1.00; Group A2 0.66, 0.61 - 0.97; (p > 0.9999); Syncytin 1-env: Group A1 0.55, 0.33 - 1.24;  
314 Group A2 0.34, 0.26 - 0.81; (p = 0.2273); Syncytin 2-env: Group A1 0.81, 0.43 - 1.24; Group  
315 A2 0.68, 0.42 - 1.15; (p = 0.9109).

### 316 3.6. Expressions of TRIM28 and SETDB1

317 As detailed in Figure 6, TRIM28 and SETDB1 expression levels were comparable  
318 between RSV infected patients and HC.

319 No difference was found between patients with (Group A1) and without (Group A2)  
320 steroid treatment. Median values and interquartile range 25%-75%: TRIM28: Group A1  
321 0.87, 0.70-1.53; Group A2 0.97, 0.71 - 1.18; (p = 0.8604); SETDB1: Group A1 1.03, 0.75 - 1.50;  
322 Group A2 0.96, 0.72 - 1.30; (p = 0.5753).

323 TRIM28 and SETDB1 expressions did not show any significant difference between  
324 males and females in HC and RSV+ patients (Supplementary figures 7 and 8).  
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**Figure 6.** Expression of TRIM28 and SETDB1 in whole blood from 40 healthy children (HC) and 37 children with acute RSV bronchiolitis. RE: Relative Expression. Circles and squares show the median of three individual measurements, horizontal lines the median values. Median values and interquartile range 25%-75%: TRIM28: HC 0.98, 0.77-1.36; RSV+ 0.97, 0.71-1.39; SETDB1: HC 0.99, 0.74-1.28; RSV+ 0.96, 0.71-1.33. Statistical analysis: Mann-Whitney test was used to compare values of each group of children with each other.

#### 4. Discussion

The key role of IFNs in controlling of viral infections is widely recognized, although their response is qualitatively and quantitatively virus specific, and their production may vary during the course and the severity of the disease. Type I and type III IFNs are thought to be main players to control the early steps of viral spread. Type I IFN production was found to be impaired in RSV infected human airway epithelial cells [73]. RSV-nonstructural protein (NS)1, -NS2, and envelope G glycoprotein inhibit IFN-I synthesis [74-77]. The suppressor of cytokine signaling (SOCS) family, through a feedback loop, inhibits IFN-I-dependent antiviral signaling pathway, and NS1 and NS2 proteins upregulate SOCS1 and SOCS3 [77]. All these findings suggest that RSV relies upon IFN-I downregulation to evade the early antiviral response. Our results, however, highlight that IFN-I signature scores were significantly higher for most ISGs in children hospitalized for acute RSV bronchiolitis without steroid treatment as compared to age-matched HC. These findings suggest that the RSV infection is actually able to trigger a significant type I IFN synthesis, although the magnitude of this response may be lower than in other acute viral infections. For instance, RSV elicited a type I IFN production in the nasal mucosa of infants, but at significantly lower amounts as compared to the robust influenza virus response [73,79]. The result may be limited protection of the spread of RSV to lower airways. The RSV-driven IFN-I production was reduced during the neonatal period in animal model [80] and in newborns and young children [20,81]. However, we did not observe any significant influence of the age on the expression of IFN-I ISGs in infants and pre-school healthy children. Furthermore, we found higher expression of IFN-I ISGs by comparing RSV+ patients with age-matched HC.

The pharmacological approach in children with bronchiolitis is still debated. Given their strong anti-inflammatory activity and the lack of side effects in the short term, the administration of steroids is not unusual. However, since there is no evidence that systemic or inhalation steroids provide a significant benefit for bronchiolitis [82,83], their administration is discouraged by several guidelines [84,85]. Nevertheless, these continue to be administered for management of RSV bronchiolitis in pediatric wards [86,87]. In line with steroid-induced suppression of IFNs [88,89], our data document that patients on steroid treatment had a significantly impaired transcription of IFN-I ISGs as compared to untreated patients. This provides a biological basis for the more prolonged viral shedding in patients treated with steroids [90], and further supports that these should not be used in RSV bronchiolitis treatment.

The type III IFN machinery seems especially implicated in the protection of mucosal surfaces from viral attacks [14,15]. A first important point emerging from our results is the positive correlation between age and transcription levels of every IFN- $\lambda$  in HC. Since IFN-III protects the respiratory and gastrointestinal tract epithelial cells from viral infections [91], impaired expression of IFN-III in the early period of life may contribute, at least in part, to the typical, high susceptibility of infants and pre-school children to viral infections of airways and gastrointestinal tract. The second point is the similar concentration of all IFN- $\lambda$  mRNAs in children with severe RSV bronchiolitis and in age-matched HC. This suggests that the IFN-III pathway remained unstimulated in RSV infected children with disease progression. TRIM28/SETDB1 and steroids exert relevant regulatory activities in induction of IFNs, but their expressions remained comparable between RSV infected patients and HC as well as between patients with and without steroid therapy. IFN-III participates in the first line defense against RSV via retinoic ac-

id-inducible gene-I-(RIG-I)-dependent pathway [92,93]. However, RSV-NS1, -NS2, G proteins, and RSV-driven high concentrations of SOCS-1 and SOCS3 are able to inhibit not only the expression of IFN-I, but also of IFN-III [77,78,94,95]. Suppression of IFN-III was also documented via RSV-induced elevated levels of prostaglandin 2 [96], activation of epidermal growth factor receptor [96], and of Rab5a [97]. Moreover, the type III IFN response was significantly lower in children with RSV bronchiolitis as compared to children with influenza infection [73]. Therefore, the impaired expression of IFN-III in the first period of life, along with the ability of RSV to downregulate its production, may account for the lack of enhanced transcription levels of IFN-III in our patients and justify the development of severe pulmonary complications. In this context, it must be underlined that blood samples were collected after a long time from symptom onset, when the role-effect of IFN-III could be exhausted. High concentrations of IFN- $\lambda$ 1 were actually found in nasal airway secretions at the onset of acute RSV respiratory illness [99]. Furthermore, we did not assess the RSV strain, which may impact the IFN-I and IFN-III expression profiles and the magnitude of the ISG response [100,101].

Present results highlight, for the first time, that in children hospitalized for acute RSV bronchiolitis the transcriptional levels of pol genes of HERV-H, -K, -W, as well as of env genes of SYN1 and SYN2 were significantly lower than in HC. The origin and the clinical significance of such reduced HERV transactivation remain to be elucidated. TRIM28 and SETDB1 are considered potent co-repressors of HERV transcription [57-60]. However, their mRNA levels were similar to those of HC, suggesting that the HERV downregulation was not sustained by abnormal expression of TRIM28 or SETDB1. Steroids can modulate the activation of retroviral elements [102,103], but we did not find any differences in HERV transcripts between treated and untreated patients. Inflammatory cytokines can stimulate activation of retroviral sequences [52]. Increased inflammatory markers or alterations in white blood cell count were however observed only in a minority of patients. Therefore, the RSV induces strong local, but poor systemic inflammation in children with severe bronchiolitis. Recently, nuclear accumulation of RSV NS1 and matrix (M) protein have been linked to global changes in host gene transcription [104,105]. Whether this induces similar alterations also in retroviral sequences remains to be investigated.

HERVs are involved in the host defense against viral infections and may trigger immune-mediated damages [25,28]. For instance, a HERV-K envelope protein inhibits the release of cytokines [54] and counteracts the tetherin-mediated antiviral activity [55]. Since HERV-K elements are highly polymorphic in the human population, interindividual variations among HERV-K-env genes may result in different immune response against the same viral infection [55,106]. A HERV-W envelope protein exerts potent pathogenic action through CD14/TLR4 stimulation [27,30]. SYN1 antagonizes antiviral responses and increases virus-induced inflammation [32,35,56,107], while SYN2 vigorously suppresses the T cell functions [34]. In general, the lower expression of HERVs in our patients may thus mirror a positive effect for the host deriving from their downregulation. These low HERV transcription levels seem antithetical to their increased activation usually elicited by exogenous viral infections. An enhanced HERV expression was noticed, however, in chronic infections, such as those due to herpesviruses [38-43], HIV [44,45], and hepatitis viruses [46,47], or *in vitro* by influenza viruses [48]. Upon an acute infection, such as SARS-CoV-2 infection, children with mild/moderate symptoms showed enhanced HERV transcription, whereas those with severe clinical pictures and long duration of disease had significant declines of their mRNA concentrations, even below the normal values [12]. Present patients were all hospitalized for a severe bronchiolitis and blood samples were collected after a long time from beginning of the infection. Taken together these findings suggest that reduced HERV expressions might characterize a severe, prolonged course of acute viral infections. This could be due to an exhaustion of the virus-driven stimulatory mechanisms and/or the upregulation of specific inhibitory checkpoints. For instance, sterile alpha motif and HD-domain-containing

434 protein 1 (SAMHD1) is able to block inflammatory responses and activation of retrovi-  
435 ruses during viral infections [108]. Based on this, children with mild forms of RSV infec-  
436 tion and/or tested in the first days of illness could exhibit normal or increased levels of  
437 HERV mRNAs, with low concentrations of transcripts being a feature of a progressive  
438 acute disease.

439 The final biologic effects of HERVs on cell homeostasis are expected to be mediated  
440 by proteins. We assessed their transcriptional profiles, not their protein-coding capacity.  
441 This is a limitation of our study, which, however, does not undermine the potential im-  
442 pact of HERVs on the evolution of RSV infection. As non-coding regulatory elements,  
443 HERVs can act as promoter and enhancer of cellular genes [25,26]. Their RNAs may be  
444 reintegrated everywhere into the DNA or recognized as non-self by viral RNA receptors  
445 triggering innate and adaptive immune responses [26-29].

446 RSV infection may induce epigenetic changes with possible clinical consequences  
447 [109,110]. Many members of the large family of TRIM proteins contribute to block viral  
448 replication [111] and growing data shed light on the pivotal roles of TRIM28/SETDB1 in  
449 epigenetic control of the immune response, including antiviral effects and T cell differ-  
450 entiation and functions [60-66]. The normal mRNA concentrations of TRIM28/SETDB1  
451 emerged in our patients, however, suggest that they are not key players in RSV-driven  
452 epigenetic variations. On the other hand, activation of TRIM28/SETDB1 is a highly dy-  
453 namic process that is removed rapidly by specific deconjugating proteases [112-113]. The  
454 prolonged time interval between symptom onset and blood collection could thus have  
455 influenced their transcription levels.

## 456 5. Conclusions

457 Our study shows enhanced expression of many IFN-I ISGs in children hospitalized  
458 for severe RSV bronchiolitis without steroid treatment. The significant suppression of  
459 ISGs following administration of steroids further points out that these should not be used  
460 in RSV bronchiolitis. The reduced expression of IFN- $\lambda$ s in the first period of life in HC  
461 and the lack of their activation in patients with disease progression may mirror an inad-  
462 equate IFN-III protection of airway mucosa surface that expose RSV infected infants to  
463 high risk of pulmonary involvement. Type III IFN is of therapeutic interest due to its low  
464 proinflammatory profile. Our data support its potential use in RSV infected at-risk in-  
465 fants to prevent the development of respiratory complications. The positive correlation  
466 between age and expression of IFN-III may account for the high frequency of viral infec-  
467 tions of the respiratory and gastrointestinal tracts in infants and pre-school children. The  
468 significantly impaired HERV transcription in children with RSV bronchiolitis was an  
469 unexpected feature. Its underlying biochemical mechanisms and clinical consequences  
470 remain to be elucidated. It does not seem imputable to inhibitory effects of corticosteroids  
471 or to alterations in TRIM28/SETDB1 repressors. The potential negative impact of HERV  
472 activation on the immune system is increasingly recognized. Their downregulation in  
473 children with severe RSV bronchiolitis may be a biomarker of disease progression, rep-  
474 resenting an attempt to limit their negative effects on the host defensive mechanisms. In  
475 contrast, given the essential role of TRIM28/SETDB1 in innate and adaptive immune re-  
476 sponses, their preserved expression may contribute to maintain an effective immune  
477 protection against infection.

479 **Supplementary Materials:** Supporting information on differences between males and females in  
480 the transcription levels of all variables studied can be downloaded in Supplementary figures 1-8 at  
481 <https://www.mdpi.com/...>

482 **Author Contributions:** P.-A.T., substantial contributions to the conception of the work, drafting the  
483 work, revising it critically for important intellectual contents and its final approval; S.G., F.S., G.P.,  
484 G.F., and E.F. enrollment and follow-up of patients, revising the work critically; V.D., M.D and I.G.  
485 performed laboratory tests, substantial contributions to analysis and interpretation of data; M.B.

substantial contributions to the conception and design of the work, analysis, and interpretation of data, and drafting of the manuscript. All authors have read and agreed to the final version of the manuscript.

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**Informed Consent Statement:** Blood samples were collected from leftovers of laboratory samples after parent's informed consent.

**Conflicts of Interest:** The authors declare no conflict of interest.

#### Abbreviations

HERVs	human endogenous retroviruses
IFN	interferon
ISGs	interferon-stimulated genes
KRAB-ZFPs	Kruppel-associated box domain zinc finger proteins
NS1	RSV-nonstructural protein 1
NS2	RSV-nonstructural protein 2
PICU	pediatric intensive care unit
PBMCs	peripheral blood mononuclear cells
PRR	pattern recognition receptor
RSV	respiratory syncytial virus
SETDB1	domain bifurcated histone lysine methyltransferase 1
SOCS	suppressor of cytokine signaling
SYN1	syncytin 1
SYN2	syncytin 2
TRIM28	tripartite motif containing 28
TLR	toll-like receptor

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