Cite as: D. Lee *et al.*, *Science* 10.1126/science.abo3627 (2022).

Inborn errors of OAS–RNase L in SARS-CoV-2–related multisystem inflammatory syndrome in children

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Multisystem inflammatory syndrome in children (MIS-C) is a rare and severe condition that follows benign COVID-19. We report autosomal recessive deficiencies of *OAS1*, *OAS2*, or *RNASEL* in five unrelated children with MIS-C. The cytosolic dsRNA-sensing OAS1 and OAS2 generate 2′-5′-linked oligoadenylates (2-5A) that activate the ssRNA-degrading RNase L. Monocytic cell lines and primary myeloid cells with *OAS1*, *OAS2*, or *RNASEL* deficiencies produce excessive amounts of inflammatory cytokines upon dsRNA or SARS-CoV-2 stimulation. Exogenous 2-5A suppresses cytokine production in OAS1- but not RNase L-deficient cells. Cytokine production in RNase L-deficient cells is impaired by MDA5 or RIG-I deficiency and abolished by MAVS deficiency. Recessive OAS–RNase L deficiencies in these patients unleash the production of SARS-CoV-2–triggered, MAVS-mediated inflammatory cytokines by mononuclear phagocytes, thereby underlying MIS-C.

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Interindividual clinical variability in the course of primary infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is immense in unvaccinated individuals (*1*–*4*). We have shown that inborn errors of type I interferon (IFN) immunity and their phenocopies—autoantibodies against type I IFNs—collectively underlie at least 15% of cases of critical COVID-19 pneumonia in unvaccinated patients (*5*–*9*). Common genetic variants act as more modest risk factors (*10*–*13*). Children were initially thought to be rarely affected by COVID-19, as only 0.001 to 0.005% of infected children had critical pneumonia (*2*). However, another severe SARS-CoV-2–related phenotype, multisystem inflammatory syndrome in children (MIS-C), occurs predominantly in children, typically 4 weeks after infection (*14*–*16*). Its prevalence is estimated at about 1 per 10,000 infected children (*17*–*19*). Children with MIS-C do not suffer from hypoxemic pneumonia and typically display no detectable viral infection of the upper respiratory tract at disease onset. However, most MIS-C cases test positive for anti-SARS-CoV-2 antibodies and almost all cases have a history of exposure to SARS-CoV-2 (*17*, *20*). Initial reports of MIS-C described it as an atypical form of Kawasaki disease (KD) (*16*, *21*–*25*), as its clinical features included fever,

rash, abdominal pain, myocarditis, lymphadenopathy, coronary aneurysm, and elevated biological markers of acute inflammation.

The elevated markers frequently detected in MIS-C patients suggest that inflammation occurs in various organs (*21*, *22*, *26*–*36*). These include surrogates of cardiovascular endothelial injury [e.g., troponin and B-type natriuretic peptide (BNP)] and gastrointestinal epithelial injury [e.g., LPS-binding protein (LBP) and soluble CD14] (*36*). Various leukocyte subsets are also affected. Sustained monocyte activation has been consistently reported as a key immunological feature of MIS-C, with high levels of pro-inflammatory markers, including ferritin, IL-1RA, IL-6, IL-10, IL-18, MCP1 (CCL2), and TNF (*21*, *22*, *26*–*36*). In addition, the levels of biomarkers related to type II IFN (IFN-γ) signaling, which are not necessarily specific to monocyte activation, often increase during the early phase of disease (*22*, *31*–*36*). An immunological phenotype unique to MIS-C, observed in ~75% of patients, is the polyclonal expansion of $CD4^+$ and $CD8^+$ T cells bearing the Vβ21.3 segment (*32*, *34*, *36*–*38*). In this multitude of molecular, cellular, and clinical abnormalities, the root cause of MIS-C remains unknown (*39*). We hypothesized that monogenic inborn errors of immunity (IEI) to SARS-CoV-2 may underlie MIS-C in some children and that the identification of these inborn errors may clarify the molecular, cellular, and immunological basis of disease (*15*, *40*).

Results

Identification of homozygous rare predicted loss-of-function variants of OAS1 *or* RNASEL *in two MIS-C patients*

We performed whole-exome or whole-genome sequencing for 558 patients with MIS-C from the international COVID Human Genetic Effort (CHGE) cohort (https://www.covidhge.com/) (fig. S1, A to C). We first searched for homozygous or hemizygous rare variants predicted to be loss-of-function (pLOF) with a high degree of confidence in human genes with a gene damage index (GDI) below 13.83 (*41*). We then restricted the list to genes involved in host response to viruses (Gene Ontology term "response to virus", GO:0009615). We identified two unrelated patients homozygous for stop–gain variants, of *OAS1* in one patient (P1, p.R47*) and *RNASEL* in the other (P5, p.E265*) (Fig. 1A, fig. S2A, and Table 1). 2′-5′-oligoadenylate synthetase 1 (OAS1) is one of the four members of the OAS family (OAS1, OAS2, OAS3, and the catalytically inactive OASL). These proteins are type I IFN–inducible cytosolic proteins that produce 2′-5′-linked oligoadenylates (2-5A) upon binding to double-stranded RNA (dsRNA). The 2-5A, in turn, induce the dimerization and activation of the latent endoribonuclease RNase L, which degrades single-stranded RNA (ssRNA) of viral or human origin (*42*, *43*). No homozygous variants fulfilling these criteria were identified in any of the 1288 subjects with asymptomatic/mild SARS-CoV-2 infection (SARS-CoV-2–infected controls) in the CHGE database (fig. S1A to C). MIS-C patients therefore display significant enrichment (P = 0.013) in homozygous pLOF variants of the *OAS1* and *RNASEL* genes, suggesting that these loci are probably relevant to MIS-C pathogenesis. Moreover, although OAS1, OAS2, OAS3, and RNase L are expressed in various cell types in mice and humans, their levels are particularly high in myeloid cells, including monocytes and macrophages (*44*–*46*). Thus, autosomal recessive (AR) deficiencies of the OAS–RNase L pathway may underlie MIS-C by impairing the restriction of viral replication and/or enhancing the virus-triggered inflammatory response in monocytes, macrophages, dendritic cells, or other cell types.

Identification of biallelic rare experimentally deleterious variants of OAS1, OAS2, *or* RNASEL *in five MIS-C patients*

OAS1, *OAS2*, *OAS3*, and *RNASEL* have CoNeS scores for negative selection of 2.25, 0.79, 1.46, and 0.66, respectively, consistent with findings for known monogenic IEI with an AR mode of inheritance (*47*). We therefore extended our search to all homozygous or potential compound heterozygous nonsynonymous or essential splicing site variants with a MAF < 0.01 at these four loci in our MIS-C cohort. We identified a total of 12 unrelated patients and 16 different variants of *OAS1*, *OAS2*, *OAS3*, and *RNASEL* (Table 1). To study the expression and function of these 16 variants in vitro, we first analyzed RNase L-mediated rRNA degradation after the cotransfection of RNase L-deficient HeLa M cells with the corresponding *OAS1*, *OAS2*, *OAS3*, or *RNASEL* cDNAs (*48*–*51*) (Fig. 1, B to D, and fig. S2, B and C). The p.R47* OAS1 (homozygous in P1) mutant protein was not produced and LOF (Fig. 1B and fig. S2D). The three mutant OAS2 proteins detected (p.R535Q, p.Q258L, and p.V290I) were produced in normal amounts, but p.R535Q (homozygous in P2 and P3) had minimal activity and p.Q258L and p.V290I (both found in P4) had lower levels of activity than the wild-type (WT) protein (Fig. 1, A and C). All the *OAS3* variants were produced in normal amounts and all but one (p.R932Q, found in the heterozygous state in one patient) of these variants had normal levels of activity (fig. S2C). The *RNASEL* p.E265* variant (homozygous in P5) was expressed as a truncated protein and was LOF (Fig. 1D and fig. S2E), whereas the p.I264V variant was neutral in expression and function (Fig. 1D). We also quantified the function of the OAS1 and OAS2 mutants in a FRET assay, which confirmed that P1's *OAS1* variant was LOF and that the *OAS2* variants of P2, P3 and P4 were hypomorphic (21% to 43%, 32% to 76%, and 36% to 75% of WT OAS2 activity for p.Q258L, p.V290I, and p.R535Q, respectively) (Fig. 1, E and F). Thus, we identified five unrelated MIS-C patients

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homozygous or compound heterozygous for rare and deleterious alleles of three of the four genes controlling the OAS–RNase L pathway (Fig. 1A and fig. S2A). The patients' genotypes were confirmed by Sanger sequencing and familial segregation. Their clinical and immunological features were consistent with those previously reported for other MIS-C patients (*21*, *22*, *26*–*36*, *52*) (Fig. 1, G to I, and Table 2).

Enrichment in homozygous deleterious OAS1, OAS2, *and* RNASEL *variants in MIS-C patients*

We found no homozygous rare (MAF < 0.01) deleterious variants of the three genes in the 1288 SARS-CoV-2–infected controls or in a control cohort of 334 patients under the age of 21 years with asymptomatic/mild infection or COVID-19 pneumonia (fig. S1, A to C). Thus, there was a significant enrichment in such homozygotes among MIS-C patients relative to infected controls ($P = 0.001$) or controls under 21 years old ($P = 0.046$), suggesting that AR deficiencies of three genes of the OAS–RNase L pathway (*OAS1*, *OAS2*, and *RNASEL*) specifically underlie MIS-C. We further assessed the probability of AR deficiencies of these three gene products being causal for MIS-C, by evaluating the expression and function of all non-synonymous variants of *OAS1*, *OAS2*, and *RNASEL* for which homozygotes were reported in gnomAD (v2.1.1 and v3.1.1, 28 variants in total) in our RNase L-mediated rRNA degradation assay (fig. S2, F to H, and table S1). In total, 13 *OAS1*, *OAS2* or *RNASEL* variants were deleterious and present in the homozygous state in 18 individuals in the gnomAD database (Fig. 1, J to L). The estimated cumulative frequency of homozygous carriers of LOF variants at the three loci was ~0.00013 (95% CI: 7.2 – 20 × 10^{-5}) in the general population. The rarity of AR OAS–RNase L deficiencies in the general population is therefore consistent with that of MIS-C. Moreover, the enrichment in these deficiencies observed in MIS-C patients relative to the individuals included in gnomAD was highly significant ($P = 2 \times 10^{-6}$). These findings suggest that AR deficiencies of OAS1, OAS2, and RNase L are genetic etiologies of MIS-C.

The expression pattern for the OAS–RNase L pathway implicates mononuclear phagocytes

We studied the basal expression of *OAS1*, *OAS2*, *OAS3*, and *RNASEL* in cells from different tissues. Consistent with data from public databases (*44*), our in-house human cell RNA-seq and RT-qPCR data showed that myeloid blood cells had higher basal mRNA levels for the four genes than the tissue-resident cells tested (Fig. 2, A and B). In all cell types studied, both type I and type II IFN treatments up-regulated the levels of mRNA for *OAS1*, *OAS2*, and *OAS3*, whereas the levels of *RNASEL* mRNA were not influenced by these IFNs (fig. S3A). Previous studies reported a relationship between cell type-dependent activation of the OAS–RNase L pathway and basal levels of expression in mice (*45*, *46*). MIS-C occurs 3 to 6 weeks after SARS-CoV-2 infection, but the virus and/or viral proteins may still be detectable in non-respiratory tissues, such as the intestine or heart, at disease onset in some patients (*32*, *34*, *37*). In addition, $CD4^+$ and $CD8^+$ T cells carrying Vβ21.3 expand, which implies a superantigen-like viral driver of MIS-C (*32*, *34*, *36*–*38*) and suggests that the virus or its antigens persist. Thus, AR deficiencies of the OAS–RNase L pathway may underlie MIS-C by impairing SARS-CoV-2 restriction and/or enhancing virus-triggered inflammatory responses in monocytes and other mononuclear phagocytes.

OAS–RNase L deficiencies have no impact on SARS-CoV-2 replication in A549 epithelial cells and fibroblasts

Previous studies have shown that the overproduction of exogenous OAS1 can result in the restriction of SARS-CoV-2 replication in A549 lung epithelial cells in the absence of exogenous type I IFN (*53*, *54*). However, the five OAS–RNase L–deficient patients had MIS-C without pneumonia. We assessed SARS-CoV-2 replication in A549 cells rendered permissive to SARS-CoV-2 by the stable expression of ACE2 and TMPRSS2, which facilitates viral entry. Knockouts (KO) of OAS1 or OAS2 did not increase the proportion of SARS-CoV-2–infected cells at 24 hours or 48 hours relative to that for the parental WT A549 cells, regardless of the presence or absence of exogenous IFN-α2b (Fig. 2, C and D, and fig. S3B). Only RNase L-KO cells resulted in a mild increase in susceptibility to SARS-CoV-2 relative to WT cells in the absence of IFN-α2b, consistent with previous findings (*55*). We also used patient-specific SV40-transduced human dermal fibroblasts (SV40-fibroblasts) stably expressing ACE2 as a surrogate cell type for studying the impact of OAS–RNase L deficiencies on tissue-resident cell-intrinsic defenses against SARS-CoV-2 (*5*). Consistent with the lack of pneumonia in these patients, no increase in SARS-CoV-2 susceptibility was observed in any of the fibroblasts with *OAS1* (from P1), *OAS2* (P3 and P4) or *RNASEL* (P5) mutations up to 72 hours after infection in the presence or absence of exogenous IFN-α2b, despite the complete loss of expression of OAS1 or RNase L in the cells of P1 and P5, respectively (Fig. 2, E and F). This contrasted with the increased susceptibility reported for fibroblasts from a patient with AR complete IFNAR1 deficiency (*56*) and critical COVID-19 pneumonia.

OAS–RNase L deficiencies have no impact on SARS-CoV-2 replication in THP-1 cells

Only abortive SARS-CoV-2 infection has been reported in human mononuclear phagocytes, including monocytes and macrophages, which express very little to no ACE2 (*57*–*59*). However, basal *Oas* and *Rnasel* expression levels have previously been correlated with murine coronavirus or VSV

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restriction in mouse macrophages (*60*). We tested the hypothesis that deficiencies of OAS–RNase L might result in productive SARS-CoV-2 infection in mononuclear phagocytes by assessing the replication of SARS-CoV-2. Unlike WT A549 cells stably transduced with ACE2/TMPRSS2, in which SARS-CoV-2 can be detected 24 hours after infection, no SARS-CoV-2 was detected in THP-1–derived macrophages (*61*), whether parental, or with a KO of OAS1, OAS2, or RNase L (Fig. 2, G and H, and fig. S3C). Thus, no myeloid SARS-CoV-2 replication was detected in the presence or absence of deficiencies of the OAS–RNase L pathway, at least in this cellular model of mononuclear phagocytes (*60*).

OAS–RNase L deficiencies result in an exaggerated inflammatory response to intracellular dsRNA in THP-1 cells

Sustained monocyte activation has repeatedly been reported to be a key immunological feature of MIS-C (*22*, *31*–*36*). We studied the impact of OAS–RNase L deficiencies on cellular responses to intracellular (cytosolic) or extracellular (endosomal) stimulation with dsRNA in THP-1 cells. Consistent with a previous study (*62*), THP-1 cells and THP-1–derived macrophages with a KO for OAS1, OAS2, or RNase L displayed enhanced activation, as demonstrated by their higher levels of IFN-λ1, IFN-β, IL-1β, IL-6, CXCL9, CXCL10, and TNF secretion 24 hours after stimulation with various doses of intracellular poly(I:C) (Fig. 3A and fig. S4A), as well as higher mRNA induction for *IL6* and *CXCL9* 8 hours after stimulation (fig. S4, B and C). Cell viability was similar to that of WT THP-1 cells following intracellular poly(I:C) stimulation (fig. S4D). ShRNA-mediated knockdown (KDn) of the expression of *OAS1*, *OAS2*, and *RNASEL* in THP-1 cells confirmed these findings (fig. S4E). The transduction of THP-1 cells with a KO of the corresponding gene with the WT cDNA of *OAS1*, *OAS2*, or *RNASEL*, respectively, resulted in cytokine secretion levels similar to those observed in parental cells, whereas transduction with mutant cDNAs corresponding to the patients' variants had no such effect (*OAS1* variant of P1 and *RNASEL* variant of P5) or a lesser effect (*OAS2* variants of P2-P4) (Fig. 3B and fig. S5, A to C). Thus, OAS–RNase L deficiencies result in exaggerated inflammatory responses to intracellular dsRNA stimulation in THP-1 cells. Enhanced responses may also occur in the mononuclear phagocytes of our patients, underlying MIS-C.

The inflammatory response to intracellular dsRNA in THP-1 cells is MAVS-dependent

Intracellular dsRNA is known to stimulate the RIG-I/MDA5-MAVS pathway, inducing type I IFNs and other cytokines in various cell types (*63*), in addition to the OAS–RNase L pathway (*42*, *64*). Indeed, unlike WT THP-1 cells, MAVS KO THP-1 cells did not respond to intracellular poly(I:C) stimulation and *RNASEL* gene KDn did not result in enhanced activation (Fig. 3C and fig. S5, D and E), confirming that the response to poly(I:C) is dependent on MAVS-mediated signaling in these cells. The enhancement of the intracellular poly(I:C) response following *RNASEL* KDn was partially attenuated in RIG-I or MDA5 KO THP-1 cells (Fig. 3C and fig. S5, D and E), suggesting that both dsRNA sensors may be involved. Another dsRNA agonist that specifically activates RIG-I, 5′ppp-dsRNA, induced enhanced responses in RNase L KO THP-1 cells similar to those seen with poly(I:C) (Fig. 3D). By contrast, the activation of other sensing pathways, including the extracellular ssRNA-sensing TLR7 and TLR8 (R848) pathways, the TLR4 pathway (LPS), and the intracellular DNA agonist-sensing DAI pathway (ISD), resulted in responses in RNase L KO or KDn THP-1 cells that were like those of the parental WT cells (Fig. 3D and fig. S5F). Thus, the exaggerated inflammatory responses to cytosolic dsRNA observed in THP-1 cells deficient for OAS–RNase L appear to require RIG-I/MDA5 sensing and MAVS activation.

Activation of the OAS–RNase L pathway can suppress inflammatory responses in THP-1 cells

Intracellular dsRNA stimulates both the RIG-I/MDA5–MAVS and OAS–RNase L pathways (*42*, *63*, *64*). We therefore investigated whether the dsRNA-sensing MAVS-dependent signaling pathway was itself hyperactivated due to OAS–RNase L deficiency. Following intracellular poly(I:C) stimulation, IRF3 and NF-κB phosphorylation levels were similar in RNase L-KO and WT THP-1 cells (Fig. 3E). Thus, the molecular mechanisms by which OAS–RNase L deficiency results in an exaggerated inflammatory response appears to involve an impairment of RNase L activation resulting in a lack of host RNA transcriptional and/or translational inhibition (*65*–*68*), rather than a hyperactivation of the MAVS-dependent pathways. Consistent with this hypothesis, treatment with exogenous 2-5A, which is normally generated by OASs upon dsRNA sensing and activates RNase L (*42*, *43*), rescued the inflammatory phenotype in OAS1 KO THP-1 cells following intracellular poly(I:C) stimulation (Fig. 3F). By contrast, dephosphorylated 2-5A, which is unable to activate RNase L (*69*, *70*), had no such effect (fig. S5G). Moreover, exogenous 2-5A treatment decreased the response to TLR7/8 activation in WT THP-1 cells (Fig. 3G). Treatment with 2-5A had a much weaker effect or even no suppressive effect in RNase L-KDn or -KO THP-1 cells (Fig. 3F and fig. S5, G and H). Thus, the exaggerated inflammatory response in OAS–RNase L-deficient mononuclear cells appears to result from the activation of the MAVS-dependent pathway (but not of other nucleic acid-sensing pathways) and an impairment of RNase L activation by OAS1– or OAS2–derived 2-5A following dsRNA-sensing. This imbalance creates a phenotype that is probably a consequence of an impairment of the posttranscriptional

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activities of RNase L (*65*–*68*).

OAS–RNase L deficiencies result in an exaggerated inflammatory response to SARS-CoV-2 in THP-1 cells

We investigated whether OAS–RNase L deficiencies resulted in exaggerated inflammatory responses to SARS-CoV-2 in mononuclear phagocytes. Bulk RNA-seq on THP-1 cells with KO of OAS1, OAS2, or RNase L stimulated with intracellular poly(I:C) or SARS-CoV-2 revealed transcriptomic profiles different from those of the parental cells (Fig. 4, A and B, and fig. S6A). Gene-set enrichment analysis (GSEA) against Hallmark gene sets (*71*) revealed an enrichment in genes relating to inflammatory responses and IFN-γ signaling in OAS–RNase L–deficient cells, showing that these cells displayed an exacerbated inflammatory response not only to synthetic dsRNA, but also to SARS-CoV-2 (Fig. 4, C and D). Moreover, RNase L KO THP-1 cells had higher levels of IL-6 and CXCL10 secretion than WT cells when cocultured with SARS-CoV-2–infected Vero cells, which support SARS-CoV-2 replication (*72*, *73*) (Fig. 4E and fig. S6, B and C). Bulk RNA-seq further confirmed this observation at the transcriptome level (Fig. 4F and fig. S6D), revealing an enrichment in the expression of genes relating to inflammatory responses and IFN-α signaling in RNase L KO cells relative to WT cells (Fig. 4G). In addition, transfection with total RNA from SARS-CoV-2–infected Vero cells, but not from uninfected Vero cells, also induced enhanced responses in RNase L KO THP-1 cells relative to parental WT cells, with an enrichment in genes relating to inflammatory responses and IFN-γ signaling (Fig. 4H and fig. S6E). These findings suggest that OAS-RNase L deficiency results in excessive inflammatory responses in mononuclear phagocytes following both abortive SARS-CoV-2 infection and coculture with SARS-CoV-2–replicating cell types. This is likely due to defective activation of the OAS-RNase L pathway following the engulfment of the virus or infection-related by-products, leading to the release of dsRNA into the cytosol (*73*).

OAS–RNase L deficiencies result in an enhanced inflammatory response to intracellular dsRNA in primary mononuclear cells

We then studied the impact of OAS–RNase L deficiencies on the response to intracellular poly(I:C) stimulation in human PBMCs. Routine blood-cell counts and immunotyping for the five patients revealed no significant abnormalities in blood leukocyte subsets, a result confirmed by deep immunophenotyping by mass cytometry (CyTOF) (fig. S7A and table S2). Following intracellular poly(I:C) stimulation, PBMCs from P2 (OAS2-deficient), P3 (OAS2-deficient), and P5 (RNase L-deficient) secreted larger amounts of the inflammatory cytokines studied than cells from healthy controls (Fig. 5A and fig. S7B). This enhanced inflammatory response to intracellular poly(I:C) stimulation was monocyte-dependent, as the depletion of monocytes from the PBMCs of healthy controls strongly decreased this response (fig. S7C). Moreover, the shRNA-mediated KDn of *OAS1*, *OAS2*, or *RNASEL* in monocyte-derived dendritic cells (MDDCs) from healthy controls resulted in an enhanced inflammatory response to intracellular poly(I:C) stimulation, as shown by the higher levels of inflammatory cytokines, including IFN-λ1, IL-6, TNF, and IL-12, than were observed with WT parental cells (Fig. 5B). Thus, deficiencies of the OAS–RNase L pathway also result in exaggerated inflammatory responses to intracellular dsRNA stimulation in primary mononuclear phagocytes, or at least in monocytes and MDDCs.

Enhanced myeloid cell activation by SARS-CoV-2 in patient PBMCs

We studied the impact of OAS–RNase L deficiencies on the responses of the various PBMC populations to SARS-CoV-2 by performing single-cell RNA sequencing (scRNA-seq) on PBMCs from P1 (OAS1), P2 (OAS2), P3 (OAS2), and P5 (RNase L), and comparing the results with those for healthy controls. Regardless of genotype, 6 hours of stimulation with SARS-CoV-2 induced a strong immune response across all five major immune cell types including myeloid, B, $CD4^+$ T, $CD8^+$ T, and natural killer (NK) cells (Fig. 5C), with 1301 unique differentially expressed genes (DEGs) (data S1). OAS–RNase L deficiency significantly changed the response of 48 to 94% of the DEGs in each lineage, with myeloid cells the most affected. Cellular responses were generally stronger in the OAS–RNase L-deficient patients and were essentially limited to the IFN-α and IFN-γ response pathways. Myeloid cell responses were characterized by a distinct pro-inflammatory component, such as *IL1B* and *CCL3*, that was stronger in OAS–RNase L-deficient cells (Fig. 5D and data S2). We then calculated pseudobulk estimates by cell type. Consistent with the single-cell observations, genes strongly up-regulated by SARS-CoV-2 in OAS–RNase L-deficient myeloid cells were enriched in type I and II IFN signature genes and TNF signature genes, whereas those strongly up-regulated in $CD4^+$ T cells were enriched in type I IFN signature genes (Fig. 5E). Thus, there is an exaggerated inflammatory response to intracellular dsRNA or extracellular SARS-CoV-2 stimulation in primary monocytes and other mononuclear phagocytes with deficiencies of the OAS–RNase L pathway cultured alone or with other PBMC populations. This provides a plausible pathogenic mechanism for MIS-C, in which this condition is driven by the exacerbated activation of mononuclear phagocytes. This hypothesis is also supported by scRNA-seq on PBMCs from P5 (RNase L-deficient) collected during MIS-C and the convalescence period. Enhanced expression levels were observed for IFN-α, IFN-γ, or TNF signature genes in monocytes, myeloid dendritic cells (mDCs), B lymphocytes,

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plasmacytoid dendritic cells (pDCs), and activated T cells of P5 relative to healthy pediatric controls (Fig. 5, F and G, and fig. S8, A to D). Quantitatively inferred cell–cell communications (*74*) revealed that MIS-C in the RNase L-deficient patient was probably driven by a signal from hyperactivated monocytes and mDCs directed at $CD8^+$ αβ T cells (Fig. 5, H and I, and fig. S8, E to G). This situation differs from that observed in patients with COVID-19 pneumonia without MIS-C, but is similar to reports for previously described MIS-C patients (fig. S9, A to C) (*33*, *34*, *36*), identifying exaggerated myeloid cell activation due to OAS–RNase L deficiency as the core driver of the immunological and clinical phenotypes of MIS-C in our patients.

Discussion

We report AR deficiencies of *OAS1*, *OAS2*, and *RNASEL* as genetic etiologies of MIS-C in five unrelated children, corresponding to about 1% of the international cohort of patients studied. OAS–RNase L–deficient monocytic cell lines, monocyte-derived dendritic cells modeling patient genotypes, and primary monocytes from patients displayed excessive inflammatory responses to intracellular dsRNA, SARS-CoV-2, SARS-CoV-2–infected cells, and their RNA, providing a plausible mechanism for MIS-C. In these patients, MIS-C may result primarily from an excessive response of monocytes and other mononuclear phagocytes to SARS-CoV-2 dsRNA intermediates or by-products, followed by the presentation of a viral superantigen to T cells, resulting in the activation and expansion of $V\beta21.3^+$ $CD4^+$ and $CD8^+$ T cells. The molecular basis of the exacerbated inflammatory response to SARS-CoV-2 due to OAS–RNase L deficiency in mononuclear phagocytes involves an impairment of the activation of RNase L via the dsRNA-sensing molecules OAS1 and OAS2, probably resulting in defective posttranscriptional RNase L activity (*67*, *68*) and the unchecked RIG-I/MDA5–MAVS-mediated production of inflammatory cytokines. Alternative molecular mechanisms cannot be excluded (*64*, *75*). The SARS-CoV-2–related RNA products that trigger phagocyte activation, the viral superantigen(s) that activate T cells, and the HLA restriction elements all remain to be discovered. Our findings also do not exclude the possibility that AR OAS–RNase L deficiency additionally affects antiviral responses in cells of other tissues injured during MIS-C, such as cardiomyocytes, enterocytes, and endothelial cells. The role of this pathway in T cells themselves merits further investigation. MIS-C in other patients may result from IEIs that may or may not be related to the OAS–RNase L pathway. Our findings also suggest that other forms of KD may be caused by other virus-specific IEI in other patients (*15*).

The notion that the OAS–RNase L pathway is essential for antiviral immunity in mononuclear phagocytic cells was first proposed nearly 40 years ago (*60*). Intriguingly, the OAS–RNase L pathway is apparently dispensable for protective immunity to SARS-CoV-2 in the respiratory tract. Indeed, none of the five MIS-C patients had a pulmonary phenotype, and no viral replication was detectable in the upper respiratory tract of any of the five children at the onset of MIS-C. Nevertheless, genome-wide association studies (GWAS) have suggested that common variants in the vicinity of *OAS1* may be weakly associated with COVID-19 severity (*10*, *11*, *53*, *76–79*). Our finding that the human OAS–RNase L pathway is crucial for regulation of the mononuclear phagocyte response to SARS-CoV-2, but not for SARS-CoV-2 restriction in the respiratory tract, suggests that the main protective action of this pathway is mediated by the control of phagocyte-driven systemic inflammation at a later stage of disease rather than viral restriction in the respiratory tract early on. These findings are also consistent with the discovery of germline gain-of-function *OAS1* mutations in humans with an autoinflammatory syndrome involving myeloid cells (*80*, *81*).

The five patients, now aged 1 to 15 years, are normally resistant to diseases caused by other common viruses. Since the discovery of the OAS–RNase L pathway in the 1970s (*65*, *82*, *83*), this pathway has been one of the most intensively studied type I IFN-inducible pathways (*42*, *84*). Biochemically, the three OAS have different subcellular distributions, different dsRNA optima for activation, they synthesize 2-5A of different lengths (*42*, *85*), and they appear to have antiviral activity against different viruses (*86–88*). The only well-established function of 2-5A is the activation of RNase L (*66*) and any of the three OAS appears to be sufficient for the biochemical activation of RNase L in human cells in vitro. RNase L has been shown to have antiviral activity against certain viruses (dengue virus and Sindbis virus), but not others (Zika virus), in murine and human cells in vitro (*85*, *89*). In vivo RNase L deficiency in mice drives susceptibility to various viruses (e.g., encephalomyocarditis virus, coxsackievirus B4, murine coronavirus, etc.) (*45*, *85*). Our data suggest that human OAS1, OAS2, and RNase L are each essential for the correct regulation of immunity to SARS-CoV-2, but otherwise largely redundant in natural conditions of infection. It is also clear that the RNase L-dependent functions of OAS1 and OAS2 are crucial for the regulation of immunity to SARS-CoV-2 within the same cells, as the genetic deficiency of any of these three components results in the same immunological and clinical phenotype, namely MIS-C.

Materials and methods

Patients

We enrolled an international cohort of 558 MIS-C patients (aged 3 months to 19 years, 60.4% boys and 39.6% girls) originating from Europe, Africa, Asia, and America, and living in 16 different countries. All patients met the WHO diagnostic criteria for MIS-C (*52*). We focus here on five of these patients

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(P1-P5). Written informed consent was obtained in the country of residence of each patient, in accordance with local regulations and with institutional review board (IRB) approval. Experiments were conducted in the United States and in France, in accordance with local regulations and with the approval of the IRB of the Rockefeller University and the Institut National de la Santé et de la Recherche Médicale, respectively. Approval was obtained from the French Ethics Committee (Comité de Protection des Personnes), the French National Agency for Medicine and Health Product Safety, the Institut National de la Santé et de la Recherche Médicale in Paris, France (protocol no. C10-13), and the Rockefeller University Institutional Review Board in New York, USA (protocol no. JCA-0700). For patients sequenced by NIAID through TAGC other than the five patients described in this paper, written informed consent was obtained in the country of residence of each patient, in accordance with local regulations and with institutional review board (IRB) approval: Ethics Committee of the Fondazione IRCCS Policlinico San Matteo, Pavia, Italy (protocol 20200037677); Comitato Etico Interaziendale A.O.U. Città della Salute e della Scienza di Torino, Turin, Italy (protocol 00282/2020); and IRB at CHOP (protocol 18-014863).

The five patients with MIS-C and AR deficiencies of the OAS–RNase L pathway—two boys and three girls—were aged from 3 months to 14 years at the time of diagnosis and all fulfilled the WHO criteria for MIS-C (Table 2) (*52*). They originated from the Philippines (P1), Spain (P2), Turkey (P3 and P4), and Canada (of French descent) (P5) and lived in Spain, Turkey, and Canada. P1 (*OAS1* mutation) (*29*), P3 (*OAS2*), and P4 (*OAS2*) had a severe course of MIS-C, with coronary aneurysm, myocarditis, and polyneuropathy, respectively. P2 (*OAS2*) and P5 (*RNASEL*) had a milder course of MIS-C, with a typical KD presentation. None of these patients presented any clinical or radiological evidence of pneumonia. Cytokine profiling of serum obtained from P1, P2, and P5 during MIS-C revealed high levels of IFN-γ, soluble CD25, IL-18, IL-1RA, and MCP1 (CCL2) (Fig. 1G), consistent with previously published immune profiles of MIS-C and in contrast to those for pulmonary COVID-19 (*21*). Bulk mRNA sequencing (RNA-seq) of whole-blood RNA from P1 and P2 collected during the MIS-C phase revealed transcriptomic signatures clearly different from those of healthy controls and a pediatric case of acute COVID-19 pneumonia, but similar to those of previously reported MIS-C patients (Fig. 1H) (*33*). TCR Vβ repertoire analysis confirmed the expansion of *TRBV 11-2* (encoding Vβ21.3) in one of the three MIS-C-phase samples available (P5, with AR RNase L deficiency) (Fig. 1I). The clinical and immunological features of the five patients were, therefore, consistent with those previously reported for other MIS-C patients (*21*, *22*, *26*–*36*).

Whole-exome, whole-genome, and Sanger sequencing

Genomic DNA was extracted from whole blood. Whole-exome sequencing (WES) or whole-genome sequencing (WGS) was performed at several sequencing centers, including the Genomics Core Facility of the Imagine Institute (Paris, France), the Yale Center for Genome Analysis (USA), the New-York Genome Center (NY, USA), the American Genome Center (TAGC, USUHS, Bethesda, USA), and the Genomics Division-ITER of the Canarian Health System sequencing hub (Canary Islands, Spain). More technical details are provided in the supplementary materials. For the Sanger sequencing of *OAS1*, *OAS2*, and *RNASEL* variants, the relevant regions of *OAS1*, *OAS2*, and *RNASEL* were amplified by PCR, purified by ultracentrifugation through Sephadex G-50 Superfine resin (Amersham-Pharmacia-Biotech), and sequenced with the Big Dye Terminator Cycle Sequencing Kit on an ABI Prism 3700 apparatus (Applied Biosystems).

Whole-exome sequencing data analysis

We performed an enrichment analysis focusing on the three candidate genes in our cohort of 558 MIS-C patients and 1288 children and adults with asymptomatic or paucisymptomatic SARS-CoV-2 infection (controls). We considered variants that were predicted to be loss-of-function or missense, with a highest population minor allele frequency (MAF)<0.01, not included in segmental duplication regions (gnomAD v2.1.1). We considered genes corresponding to the Gene Ontology term "response to virus" (GO:0009615), with a gene damage index (GDI) below 13.83 (*41*), corresponding to the 90% least damaged genes. We searched for all homozygous variants in MIS-C patients, SARS-CoV-2–infected controls, and the gnomAD database. We compared the proportions of patients and controls carrying experimentally confirmed deleterious homozygous variants by means of a logistic regression model, accounting for the ethnic heterogeneity of the cohorts by including the first five principal components of the principal component analysis (PCA), and for data heterogeneity (WGS and WES with various kits and calling processes) by including the two first PCs of a PCA on individual sequence-quality parameters, as previously described (*9*). The PCA for ethnic heterogeneity was performed with PLINK (v1.9) on WES and WGS data, with the 1000 Genomes (1kG) Project phase 3 public database as a reference, using >15,000 exonic variants with a minor allele frequency > 0.01 and a call rate > 0.99. The PCA for data heterogeneity was performed with the R FactoMineR package and the following individual sequence quality parameters calculated with bcftools stats: number of alleles, number of ALT alleles, number of heterozygous variants, Ts/Tv ratio, number of indels, mean depth of coverage, number of singletons and number of missing genotypes, We also compared the frequency of experimentally confirmed deleterious homozygous variants of the three genes between

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our MIS-C cohort and gnomAD, in Fisher's exact test.

Cell culture

Primary cultures of human fibroblasts were established from skin biopsy specimens from patients or healthy controls. They were transformed with an SV40 vector, as previously described (*56*), to create immortalized SV40-fibroblast cell lines. SV40-fibroblasts, HEK293T cells, and A549 cells were cultured in DMEM medium (GIBCO) with 10% fetal bovine serum (FBS) (GIBCO). THP-1 cells were cultured in RPMI 1640 medium (GIBCO) with 10% FBS. For the generation of phorbol-12-myristate-13-acetate (PMA)-primed THP-1-derived macrophages, THP-1 cells were incubated with 50 ng/ml of PMA for 48 hours, then left without PMA overnight before stimulation. PBMCs were cultured in RPMI 1640 medium (GIBCO) with 10% FBS. For intracellular poly(I:C) or SARS-CoV-2 stimulation of the PBMCs, blood samples were obtained from the OAS–RNase L-deficient patients 2 months to 1 year after acute-phase MIS-C and from five healthy controls with (two pediatric controls and one adult control) or without (one pediatric control and one adult control) prior asymptomatic/mild SARS-CoV-2 infection about 6 months before sample collection. For the differentiation of monocyte-derived dendritic cells, monocytes were isolated from PBMCs with the Pan Monocyte Isolation kit (Miltenyi Biotec) and cultured with 50 ng/ml of recombinant human GM-CSF (PeproTech) and 20 ng/ml of recombinant human IL-13 (PeproTech) for 7 days before cell stimulation experiments.

Plasmids

For overexpression studies in HEK293T cells, wild-type (WT) cDNAs for *OAS1* and *RNASEL* in a pCMV6 backbone were purchased from Origene. For rRNA degradation assays, human *OAS1* (GenBank accession no. BC071981.1), *OAS2* (GenBank accession no. BC049215.1), *OAS3* (GenBank accession no. BC113746), and *RNASEL* (GenBank accession no. L10381.1) cDNAs were inserted into p3X-FLAG-CMV-10 (Sigma) as previously described (*75*, *88*). Patient-specific variants or variants from the gnomAD database were generated by site-directed mutagenesis PCR with the Super Pfx DNA Polymerase (CWbio). For stable lentivirus-mediated transduction with *ACE2* and *RNASEL*, cDNAs for WT and patient-specific *ACE2* or *RNASEL* variants were inserted into pTRIP-SFFV-CD271-P2A, a modified pTRIP-SFFV-mtagBFP-2A (Addgene #102585) in which mtagBFP is replaced with CD271, with InFusion (Takara Bio), according to the manufacturer's instructions. We used the XhoI and BamHI restriction sites. For stable lentivirus-mediated transduction with *OAS1* and *OAS2*, cDNAs for WT and patient-specific *OAS1* or *OAS2* variants were inserted into a modified pSCRPSY vector (KT368137.1) with a PaqCI cutting site expressing BFP. The PaqCI site was used for cDNA insertion with InFusion. We checked the entire sequences of the *OAS1*, *OAS2*, *OAS3*, and *RNASEL* cDNAs in the plasmids by Sanger sequencing.

Cell-free system assays of OAS and RNase L activity

Assays for OAS and RNase L activity were performed with a modified cell-free system assay based on HeLa M cells (*49*, *50*). The HeLa M cells were cultured in DMEM with 10% FBS and their identity was confirmed by the presence of short tandem repeat loci with a 94.12% match to HeLa cells (ATCC CCL2, Genetica, Burlington, NC). We previously reported that HeLa M cells have no RNase L expression (*51*). Cells were plated in 24-well dishes (6×10^4 cells per well) with empty vector (p3X-FLAG-CMV-10), or vector containing WT or mutant human *OAS1* (GenBank accession no. BC071981.1), *OAS2* (GenBank accession no. BC049215.1), *OAS3* (GenBank accession no. BC113746), or *RNASEL* (GenBank accession no. L10381.1) cDNAs. HeLa M cells were cotransfected with cDNAs in the presence of Lipofectamine 2000 for 20 hours. Conditions were optimized for each type of enzyme assayed. RNase L assays were performed on cells cotransfected with 300 ng of WT or mutant *RNASEL* cDNA and 100 ng of WT *OAS3* cDNA. *OAS1* assays were performed with 300 ng of *OAS1* cDNA and 100 ng of *RNASEL* cDNA. OAS2 assays were performed with 300 ng (condition 1) or 600 ng (condition 2) of *OAS2* cDNA and 100 ng of *RNASEL* cDNA, and *OAS3* assays were performed with 300 ng of *OAS3* cDNA and 100 ng of *RNASEL* cDNA. The lysis-activation-reaction (LAR) buffer contained 0.1% (by volume) Nonidet P-40, 50 mM Tris-HCl pH 7.5, 0.15 M NaCl, 2 mM EDTA, 10 mM $MgCl_2$, 2 mM ATP, 400 U/ml of RNaseOUT (Thermo Fisher Scientific), and 2.5 μg/ml of poly(I):poly(C) (Millipore catalog number 528906). LAR buffer (75 μl) was added to each well of cells on ice and the contents of the wells were then transferred to tubes on ice. The lysates were then incubated at 30°C for 30 min, except in OAS2 assays, for which lysates were incubated at 37°C (condition 1) or 30°C (condition 2) for 40 min and 50 min, respectively. Total RNA was isolated with RLT buffer supplemented with guanidinium isothiocyanate and the EZ-10 Spin Columns Total RNA Minipreps Super kit (BIO BASIC). RNA was separated on RNA chips with an Agilent Bioanalyzer 2000, from which images and RNA integrity numbers (RINs) were obtained. For immunoblots, aliquots of the lysates (10 μg of protein) were separated by SDS-PAGE in a 7% acrylamide gel. Immunoblots were probed with a monoclonal antibody against the Flag epitope or β-actin (Sigma-Aldrich).

FRET-based OAS enzyme assays

FRET assays of the amount of 2-5A synthesized by WT and mutant isoforms of OAS2 were performed with lysates of transfected HeLa M cells (*90*). Cells were plated in 24-well dishes (6×10^4 cells per well), cultured for 24 hours and transfected for 20 hours with Lipofectamine 2000 transfection

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reagent (Thermo Fisher Scientific) and 0.5 μg empty vector (p3X-FLAG-CMV-10), or 500 ng of vector containing WT or mutant OAS1 or OAS2. Cells were washed with cold PBS and then lysed with 100 μl of LAR buffer [containing ATP and poly(I:C)] per well on ice. The lysates were transferred to tubes on ice and incubated at 30°C for 50 min before heating at 95°C for 10 min (to stop the reaction and denature proteins) and vortexing twice. The lysates were centrifuged at 12,000*g* for 10 min. The supernatants were then collected and diluted 10-fold in H_2O. Diluted samples (2 μl) were added to 45 μl of cleavage buffer (25 mM Tris-HCl, pH 7.4, 0.1 M KCl, 10 mM $MgCl_2$, 50 μM ATP pH 7.4, and 7 mM β-mercaptoethanol) containing 40 nM RNase L and 135 nM FRET probe in 96-well plates. The probe used was a 36-nucleotide synthetic oligoribonucleotide probe with multiple RNase L cleavage sites, a fluorophore (6-FAM or 6-carboxyfluorescein) at the 5′-terminus, and the black hole quencher-1 (BHQ1) at the 3′-terminus (IDT, Inc.) (*90*). FRET assays were performed at room temperature, every 5 min, for 30 min. Fluorescence was measured in relative fluorescence units (RFU), with excitation at 485 nm and emission at 535 nm, with a Varioskan LUX multimode microplate reader and Skanit version 6.0.1 software (Thermo Fisher Scientific). There were six biological replicates for each treatment group. Standard curves were plotted in triplicate with 0.1 to 30 nM ppp5′A2′p5′A2′p5′A (trimer 2-5A) synthesized with isolated OAS1 and purified by HPLC (*70*).

Cytokine quantification in plasma samples

Cytokine quantification in plasma samples was performed as previously described (*32*). Briefly, whole blood was sampled into EDTA tubes. The plasma concentrations of IFN-γ, IL-1RA, IL-10, IL-18, IL-6, MCP-1, soluble CD25, and TNF were then determined with Simpleplex technology and an ELLA instrument (Protein Simple) according to the manufacturer's instructions. Plasma IFN-α concentrations were determined with a single-molecule array (Simoa) on an HD-1 Analyzer (Quanterix) with a commercial kit for IFN-α2 quantification (Quanterix). Blood samples from P1, P2, and P5 were obtained on days 7, 4, and 9 after symptom onset, respectively.

TRBV 11-2 *relative expression levels*

Whole blood was collected into PAXgene (BD Biosciences) or Tempus (Thermo Fisher Scientific) blood RNA tubes or EDTA tubes. RNA was extracted with the corresponding RNA extraction kits or with the Maxwell 16 LEV Blood RNA kit and a Maxwell extractor (Promega) and quantified by spectrometry (Nanovue). For P5, RNA was extracted from sorted T cells with the RNeasy Plus microkit (Qiagen). Relative expression levels were determined for *TRBV 11-2* with nCounter analysis technology (NanoString Technologies), by calculating *TRBV 11-2* mRNA levels relative to other *TRBV* mRNA levels and normalizing against the median value for the healthy volunteer group. Blood samples from P1, P2, and P5 were obtained on days 7, 4, and 9 after symptom onset, respectively.

Immunoblots

Total cell extracts were prepared from SV40-fibroblasts and THP-1 cells. Cells were lysed in NP40 lysis buffer (150 mM NaCl, 50 mM Tris pH 8.0, and 1.0% NP40) supplemented with cOmplete Protease Inhibitor cocktail (Roche, Mannheim, Germany). Equal amounts of protein from each sample were subjected to SDS-PAGE, and the proteins were blotted onto polyvinylidene difluoride membranes (Bio-Rad). The membranes were then probed with the desired primary antibody followed by the appropriate secondary antibody. Primary antibodies against the following targets were used: Flag tag (Sigma-Aldrich, cat: F1804), human OAS1 (Cell Signaling, cat: 14498), OAS2 (Proteintech, cat: 19279-1-AP), RNase L (Cell Signaling, cat: 27281), RIG-I (Cell Signaling, cat: 3743), MDA5 (Cell Signaling, cat: 5321), MAVS (Cell Signaling, cat: 3993), phospho-IRF3 (Cell Signaling, cat: 4947), total IRF3 (Cell Signaling, cat: 11904), phospho-p65 (Cell Signaling, cat: 3033), and total p65 (Santa Cruz, cat: sc-372). Membranes were probed with a horseradish peroxidase (HRP)-conjugated antibody against GAPDH (Proteintech, cat: HRP-60004), as a protein loading control. Antibody binding was detected by enhanced chemiluminescence (Thermo Fisher Scientific).

RT-qPCR

Total RNA was extracted from THP-1 cells and various other cell types with the Quick-RNA MicroPrep kit (Zymo Research). RNA was reverse-transcribed with random hexamers and the Superscript III first-strand cDNA synthesis system (Invitrogen). Quantitative real-time PCR was then performed with the TaqMan universal PCR master mix (Applied Biosystems). For gene expression assays, TaqMan probes for *OAS1*, *OAS2*, *OAS3*, *RNASEL*, *IL6*, and *CXCL9* were used (Thermo Fisher Scientific). We used β-glucuronidase (*GUSB*) for normalization (Applied Biosystems). The results were analyzed with the ΔCt or ΔΔCt method. For SARS-CoV-2 genomic RNA quantification, RNA was extracted from 3×10^5 THP-1 cells infected with SARS-CoV-2 for 24 hours. Cells were washed three times with PBS and lysed for RNA extraction. Equal amounts of total RNA were reverse-transcribed with random hexamers and the Superscript III first-strand cDNA synthesis kit (Invitrogen). Equal amounts of cDNA were used for the qPCR reaction. Primers and probes for the N gene (N2 region), the RdRP gene, and their respective standards were purchased from IDT technologies. All qPCR reactions were analyzed with the QuantStudio 3 system.

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Gene knockout

OAS1 and OAS3 knockout THP-1 cells and the parental WT cells were kindly provided by Wook-bin Lee (*62*). The THP-1 cells with knockouts for RIG-I, MDA5, and MAVS were purchased from Invivogen. A549 KO cells were kindly provided by S. Weiss (*55*). For the generation of OAS2 and RNase L KO THP-1 cells, a set of three single-guide RNAs for *OAS2* or *RNASEL* (Synthego) were combined with TrueCut Cas9 protein v2 (Invitrogen) and used for the nucleofection of the cells with Cell Line Nucleofection kit V (Lonza) and AMAXA Nucleofector 2b (Lonza), according to the manufacturer's instructions. The cells were cultured for several days and then plated at clonal density in 96-well plates and amplified. Genomic DNA was extracted from multiple clones, and genomic regions of about 450 bp around the *OAS2* or *RNASEL* single guide RNAs were subjected to Sanger sequencing. The absence of the protein was confirmed by immunoblotting. The loss of RNase L activity in RNase L KO THP-1 cells was confirmed in an rRNA degradation assay. The sequences of the guide RNAs for OAS2 and RNase L knockout were 5′-AGCUGAGAGCAAUGGGAAAU-3′, 5′-UCAGACACUGAUCGACGAGA-3′, and 5′-UGCACCAGGGGGAACUGUUC-3′ (*OAS2*), 5′-GCAGUGGAGAAGAAGCACUU-3′, 5′-GCAGGUGGCAUUUACCGUCA-3′, and 5′-UUUGACCUUACCAUACACAG-3′ (*RNASEL*). The sequencing primers were 5′-CAGTTTCAGTTTCCTGGCTCTGG-3′ and 5′-GCACATAATAGGCACCCAGCAC-3′ for *OAS2*, 5′-CTCTGTTGCCAGAGAATCCCAATTTAC-3′, 5′-CAATCGCTGCGAGGATAAAAGG-3′, 5′-GAGCGTGAAGCTGCTGAAAC-3′, and 5′-TGTACTGGCTCCACGTTTG-3′ for *RNASEL*.

Gene knockdown

The shRNA-mediated silencing experiments were performed with GIPZ (Horizon Discovery) lentiviral vectors encoding microRNA-adapted shRNAs targeting the open reading frame of OAS1 (Catalog numbers #200201641 and #200293786), OAS2 (#200260991 and #200255637), and RNASEL (#200226261 and #200226578), or a non-silencing control shRNA (#RHS4346). Lentiviral particles encoding shRNA were generated by the transient transfection of HEK293T cells with lentiviral GIPZ vectors and a mixture of packaging plasmids with XtremeGENE9 transfection reagent, used according to the manufacturer's instructions. Briefly, HEK293T cells at 80 to 90% confluence in a six-well plate were transfected with 1.5 μg of the lentiviral vector GIPZ, 1 μg of the packaging plasmid (psPAX2, Addgene), and 0.5 μg of the envelope plasmid (pMD2G, Addgene). The medium was changed the following day and the virus-containing supernatant was collected 48 hours after transfection, passed through a filter with 0.45-μm pores and used directly for cell transduction or stored at −80°C.

For the transduction of THP-1 cells, the cells were incubated with supernatants containing the lentiviral particles. The medium was replaced with fresh medium the following day and puromycin was added three days after transduction, to a final concentration of 2 μg/ml. Protein production was analyzed by immunoblotting after four days of selection. All the experiments were performed between days 7 and 14 post-transduction.

For shRNA-mediated knockdown experiments in primary monocyte-derived dendritic cells (MDDCs), a high transduction efficiency (>60% GFP^+ cells) was achieved by cotransduction with shRNA-encoding lentiviral particles and virion-like particles (VLPs) carrying the SIV viral protein Vpx (VLP-Vpx). Vpx suppresses the SAMHD1-mediated restriction of lentiviral reverse transcription in myeloid cells. VLP-Vpx were produced by transfecting HEK293T cells with 1.5 μg of the packaging vector SIV3+ (derived from SIVmac251) and 0.5 μg of the envelope plasmid pMD2G with XtremeGENE9. Monocytes were isolated from peripheral blood mononuclear cells (PBMCs) from healthy donors by negative selection with the Pan Monocyte Isolation Kit (Miltenyi Biotec). Freshly purified monocytes were transduced with shRNA-encoding lentiviral particles and VLP-Vpx in the presence of protamine (8 μg/ml). Transduced cells were allowed to differentiate into MDDCs in the presence of recombinant human GM-CSF (10 ng/ml) and IL-4 (25 ng/ml) for 5 days.

Lentiviral transduction

HEK293T cells were dispensed into a six-well plate at a density of 8×10^5 cells per well. The next day, cells were transfected with pCMV-VSV-G (0.2 μg), pHXB2-env (0.2 μg; NIH-AIDS Reagent Program; 1069), psPAX2 (1 μg; Addgene plasmid no. 12260), and either pTRIP-SFFV-CD271-P2A empty vector or encoding the protein of interest (1.6 μg) in Opti-MEM (Gibco; 300 μl) containing XtremeGene-9 (Sigma Aldrich; 10 μl), according to the manufacturer's instructions. After 6 hours, the medium was replaced with 3 ml of fresh culture medium and the cells were incubated for a further 24 hours for lentiviral particle production. The viral supernatant was collected and passed through a syringe filter with 0.2-μm pores (Pall) to remove debris. Protamine sulfate (Sigma; 10 μg/ml) was added to the supernatant, which was then used immediately or stored at −80°C until use.

For the transduction of THP-1 cells with *OAS1*, *OAS2*, or *RNASEL*, the corresponding gene KO THP-1 cells were dispensed into a 12-well plate at a density of 1×10^6 cells per well, in 500 μl of culture medium per well. Viral supernatant was added (500 μl per well). For the transduction of SV40-fibroblasts with ACE2, healthy control or patient-specific SV40-fibroblasts were used to seed six-well plates at a density of 5×10^5 cells per well. Viral supernatant was then added

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(500 μl per well). The cells were then incubated for a further 48 hours at 37°C. Transduction efficiency was evaluated by surface staining for CD271 (Miltenyi Biotec) for the pTRIP vector, or by flow cytometry to evaluate BFP expression levels for the pSCRPSY vector. MACS column separation was performed with selection beads for CD271-positive cells (Miltenyi Biotec) if the proportion of CD271-positive cells was below 80%. Cells transduced with the pSCRPSY vector were selected with puromycin or by flow cytometry. Protein production was subsequently validated by immunoblotting.

SARS-CoV-2 infection

The SARS-CoV-2 NYC isolate was obtained from the saliva of a deidentified patient on 28 July 2020. The sequence of the virus is publicly available (GenBank OM345241). The virus isolate was initially amplified in Caco-2 cells (passage 1, or P#1 stock). For the generation of P#2 and P#3 working stocks, Caco-2 cells were infected with the P#1 and P#2 viruses, respectively, at a multiplicity of infection (MOI) of 0.05 plaque-forming units (PFU)/cell and incubated for 6 days and 7 days, respectively, at 37°C. The virus-containing supernatant was then harvested, clarified by centrifugation (3000*g* for 10 min), and filtered through a disposable vacuum filter system with 0.22-μm pores. The P3 stock used in this study had a titer of 3.4×10^6 PFU/ml determined on Vero E6 cells with a 1% methylcellulose overlay, as previously described (*72*).

A549 + ACE2/TMPSS2 cells, human SV40-fibroblasts + ACE2, or THP-1 cells were used to seed 96-well plates at a density of 1.5×10^4 cells per well, 4×10^3 cells per well, and 1×10^5 cells per well, respectively, in the presence or absence of IFN-α2b at a concentration of 1000 IU/ml. The cells were infected with SARS-CoV-2 24 hours later by directly adding 10 μl of virus stock at various dilutions to the wells (final volume: 110 μl). Cells were infected for 24 hours, 48 hours, or 72 hours. The cells were fixed with neutral buffered formalin at a final concentration of 10% and stained for SARS-CoV-2 with an anti-N antibody (catalog no. GTX135357; GeneTex). An Alexa Fluor 488- or Alexa Fluor 647-conjugated secondary antibody (Invitrogen) was used. Plates were imaged with an ImageXpress micro XL and analyzed with MetaXpress (Molecular Devices).

Cell stimulation

THP-1 cells were used to coat a 96-well plate at a density of 1×10^6 cells per 100 μl of culture medium. For stimulations of PBMCs and MDDCs, we used 1×10^5 cells and 5×10^5 cells per 100 μl of culture medium, respectively. The cells were stimulated with the indicated stimulus at the specified concentrations, with or without lipofectamine 2000 (Invitrogen), according to the manufacturer's instructions. Poly(I:C), 5′ppp-dsRNA, 5′ppp-dsRNA control (Invivogen), ISD, ISD control (Invivogen), R848, CPG-ODN2006, and LPS were purchased from Invivogen. For exogenous 2′5′-linked oligoadenylate (2-5A) or dephosphorylated 2-5A, we used 20 μM of 2-5A for transfection in the presence of lipofectamine simultaneously with the other stimuli (poly(I:C), R848 or LPS). Dephosphorylated 2-5A (A2′p5′A2′p5′A) was prepared by treating 2-5A with shrimp alkaline phosphatase (Thermo Fisher Science) to remove the 5′-triphosphoryl group from 2-5A, rendering it unable to activate RNase L (*69*, *70*). The dephosphorylation reaction mixture contained 5 mM 2-5A incubated with 5 units of SAP at 37°C for 1 hour, according to the manufacturer's protocol. Samples were denatured by incubation at 95°C for 5 min. Supernatants containing dephosphorylated 2′,5′-A3 were removed after centrifugation at 18,000*g* for 15 min at 4°C. Dephosphorylated 2-5A was then validated by HPLC and FRET assays for RNase L activity. Following cell stimulation, the cells or supernatants were harvested, and their cytokine mRNA and protein levels were assessed by quantitative RT-PCR (RT-qPCR) and with a multiplex bead assay (BioLegend), respectively.

Detection of secreted cytokines in a multiplex bead assay

The harvested supernatants of stimulated THP-1 cells, PBMCs, and other types of cells were prepared and used for the LEGENDplex multiplex bead assay (BioLegend), according to the manufacturer's instructions. Samples were analyzed by flow cytometry on an Attune NxT flow cytometer, according to the manufacturer's instructions. Data were analyzed with LEGENDplex Cloud-based Data Analysis Software.

Luciferase assay

THP-1 cells expressing an ISRE-lucia luciferase reporter gene were purchased from Invivogen (THP1-Dual). Cells were stimulated according to the conditions specified above. The supernatant was collected and used for the luciferase assay in accordance with the manufacturer's instructions.

Coculture of THP-1 and SARS-CoV-2–infected cells

Vero cells were plated in a six-well plate and infected at a MOI of 0.05 (as determined by plaque assay on Vero E6 cells) for a total of 48 hours. The supernatant of the infected cells was carefully removed, and the infected cells were then transferred to fresh THP-1 culture medium. A fixed volume of the resulting cell suspension was then dispensed onto WT or RNase L-KO THP-1 cells plated in a 96-well plate at a density of 1×10^5 cells in 100 μl. THP-1 cells stimulated with SARS-CoV-2 only were stimulated in parallel for 24 hours. THP-1 cells were stimulated for a total of 24 hours before collection of the supernatant for cytokine determinations and cells for total RNA extraction.

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Transfection of THP-1 cells with RNA from SARS-CoV-2–infected cells

Total RNA was extracted from mock-infected Vero cells or Vero cells infected with SARS-CoV-2 at a MOI of 0.05 for a total of 72 hours. THP-1 cells were transfected with 2 μg/ml of total RNA extract for 8 hours. THP-1 cells were then collected for total RNA extraction.

Deep immunophenotyping by mass cytometry (CyTOF)

CyTOF was performed on whole blood with the Maxpar Direct Immune Profiling Assay (Fluidigm), according to the manufacturer's instructions, as previously described (*7*). Cells were frozen at −80°C after overnight staining to eliminate dead cells, and acquisition was performed on a Helios machine (Fluidigm). The antibodies used for staining are listed in table S3. All the samples were processed within 24 hours of sampling. Data analysis was performed with OMIQ software.

Bulk RNA sequencing (RNA-seq)

Total RNA was extracted from THP-1 cells or sorted blood-cell populations. Cells were left untreated or were stimulated with poly(I:C) in the presence of lipofectamine or infected with SARS-CoV-2. RNA was extracted with the Quick-RNA MicroPrep kit (Zymo Research) or the RNeasy Micro Kit (Qiagen) and treated with DNase I (Zymo Research and Qiagen) to remove residual genomic DNA. RNA-Seq libraries were prepared with the Illumina RiboZero TruSeq Stranded Total RNA Library Prep Kit (Illumina) and sequenced on the Illumina NovaSeq platform in the 100 nt, paired-end configuration. Each library was sequenced twice.

The RNA-seq FASTQ files were first inspected with fastqc to ensure that the raw data were of high quality. The sequencing reads of each FASTQ file were then aligned with the GENCODE human reference genome GRCh37.p13 with STAR aligner v2.6 and the alignment quality of each BAM file was evaluated with RSeQC. Reads were quantified with featureCounts v1.6.0 to generate gene-level feature counts from the read alignment, based on GENCODE GRCh37.p13 gene annotation. The gene-level feature counts were then normalized and $\log_2$-transformed with DESeq2, to obtain gene expression values for all genes and all samples. Differential gene expression analyses were conducted by contrasting the intracellular poly(I:C)-stimulated samples or the SARS-CoV-2–infected samples with the non-stimulated samples. For each gene expression analysis, we performed TMM normalization and gene-wise generalized linear model regression by edgeR, and the genes displaying significant differential expression were selected according to the following criteria: FDR ≤ 0.05 and |log2(FoldChange)| ≥ 1. Differential gene expression was plotted as a heatmap with ComplexHeatmap, and genes and samples were clustered based on complete linkage and the Euclidean distances of gene expression values. Geneset enrichment analysis (GSEA) was conducted with the fgsea package, by projecting the ranking of fold-change in expression onto the Hallmark gene sets (*71*).

Single-cell RNA sequencing of PBMCs

We performed single-cell RNA-seq (scRNA-seq) on SARS-CoV-2– and mock-stimulated PBMCs sampled from four individuals with inborn errors of the OAS–RNaseL pathway (P1 with OAS1 deficiency, P2 and P3 with OAS2 deficiency, P5 with RNase L deficiency), three individuals with inborn errors of type I IFN immunity, and eight healthy donors—one pediatric control and one adult control with a history of past asymptomatic SARS-CoV-2 infection, two pediatric controls and four adult controls with no history of prior SARS-CoV-2 infection. The cryopreserved PBMCs were thawed, stimulated and processed for scRNA-seq. Across all samples, we captured 46,157 high-quality single-cell transcriptomes that were classified into five major immune cell lineages: myeloid, B, $CD4^+$ T, $CD8^+$ T, and natural killer (NK) cells. The data were then analyzed as described in detail in the supplementary materials.

We also performed scRNA-seq on cryopreserved PBMCs from P5 (RNase L-deficient, aged 4 years) sampled during the acute (9 days after MIS-C onset) and convalescent (~1 month after onset) phases, together with cells from one healthy adult and two pediatric controls. We compared the data obtained with a previously published dataset for patients with pediatric acute SARS-CoV-2 infection or MIS-C (*33*). Clustering analysis showed lower levels of monocytes and type 1 and type 2 conventional dendritic cells (cDCs) in these patients and an expansion of the activated T cell population strongly expressing *MKI67* (Fig. 5F and fig. S8, A and B). Other subsets were largely unaffected. Pseudobulk differential expression analysis were performed at the single-cell level for monocytes, myeloid dendritic cells (mDCs), B lymphocytes, plasmacytoid dendritic cells (pDCs), and activated T cells. Bulk RNA-seq was performed on sorted non-classical monocytes and pDCs to further confirm the scRNA-seq findings. We also quantitatively inferred cell–cell communications with CellChat (*74*) to identify the signal-outgoing and the signal-receiving cell subsets. The data generated during this study were analyzed in an integrative manner with historical controls from the laboratory (one pediatric and seven adult controls), publicly available control PBMC datasets downloaded from the 10X Genomics web portal (https://support.10xgenomics.com/single-cell-gene-expression/datasets), and a previously published dataset for patients with acute SARS-CoV-2 infection and MIS-C (GEO accession: GSE167029), as described in detail in the supplementary materials. In addition, two other previously published sets of scRNA-seq data for pediatric healthy controls

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and children with acute SARS-CoV-2 infection or MIS-C (GSE166489; Zenodo DOI: https://doi.org/10.5281/zenodo.5524378) were used for an independent cohort analysis.

Statistical analysis

For experiments performed in vitro, quantitative data were obtained for cells carrying the different mutations and control cells, or cells treated with different stimuli, from at least three biological replicates. For each biological replicate, up to six technical replicates were performed and averaged for downstream analysis. Cytokine determinations were log-transformed after subtracting the limit of detection for the experiment concerned. Mean quantitative values were compared between cells carrying the various mutations and control cells or cells treated with different stimuli in unequal-variance *t* tests. Where relevant, statistical test results are indicated in the corresponding figures. ns: not significant, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$, $****P < 0.0001$.

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ACKNOWLEDGMENTS

We thank the patients and their families for participating in our research. We thank all members of both branches of the Laboratory of Human Genetics of Infectious Diseases for discussions and technical and administrative support. We thank A. W. Ashbrook for managing the Rice laboratory BSL3 facility. We thank the Memorial Sloan Kettering Cancer Center for help isolating and sequencing the NY SARS-CoV-2 isolate. We thank R. Padgett and G. Stark at the Cleveland Clinic for discussions. We also thank A. Codina and C. Jou from the Biobanc de l'Hospital Infantil Sant Joan de Déu per a la Investigació, which is integrated into the Spanish Biobank Network of ISCIII, for sample and data procurement. **Funding:** The Laboratory of Human Genetics of Infectious Diseases is supported by the Howard Hughes Medical Institute, the Rockefeller University, the St. Giles Foundation, the National Institutes of Health (NIH) (R01AI088364 and R21AI160576), the National Center for Advancing Translational Sciences (NCATS), NIH Clinical and Translational Science Award (CTSA) program (UL1TR001866), the Yale Center for Mendelian Genomics and the GSP Coordinating Center funded by the National Human Genome Research Institute (NHGRI) (UM1HG006504 and U24HG008956), the Yale High-Performance Computing Center (S10OD018521), the Fisher Center for Alzheimer's Research Foundation, the Meyer Foundation, the JBP Foundation, the French National Research Agency (ANR) under the "Investments for the Future" program (ANR-10-IAHU-01), the Integrative Biology of Emerging Infectious Diseases Laboratory of Excellence (ANR-10-LABX-62-IBEID), the French Foundation for Medical Research (FRM) (EQU201903007798), the ANR GenMISC (ANR-21-COVR-039), the ANRS-COV05, ANR GENVIR (ANR-20-CE93-003) and ANR AABIFNCOV (ANR-20-CO11-0001) projects, the ANR-RHU program (ANR-21-RHUS-08), the European Union's Horizon 2020 research and innovation program under grant agreement No. 824110 (EASI-genomics), the HORIZON-HLTH-2021-DISEASE-04 program under grant agreement 01057100 (UNDINE), the ANR-RHU Program ANR-21-RHUS-08 (COVIFERON), the Square Foundation, Grandir - Fonds de solidarité pour l'enfance, the Fondation du Souffle, the SCOR Corporate Foundation for Science, the French Ministry of Higher Education, Research, and Innovation (MESRI-COVID-19), Institut National de la Santé et de la Recherche Médicale (INSERM) and Paris Cité University. We acknowledge support from the National Institute of Allergy and Infectious Diseases (NIAID) of the National Institutes of Health under award R01AI104887 to R.H.S. and S.R.W. The Laboratory of Human Evolutionary Genetics (Institut Pasteur) is supported by the Institut Pasteur, the Collège de France, the French Government's Investissement d'Avenir program, Laboratoires d'Excellence "Integrative Biology of Emerging Infectious Diseases" (ANR-10-LABX-62-IBEID) and "Milieu Intérieur" (ANR-10-LABX-69-01), the Fondation de France (no. 00106080), the Fondation pour la Recherche Médicale (Equipe FRM DEQ20180339214 team), and the ANR COVID-19-POPCELL (ANR-21-CO14-0003-01). A.Puj. is supported by the ACCI20-759 CIBERER, the EasiGenomics H2020 Marató TV3 COVID 2021-31-33, the HORIZON-HLTH-2021-ID: 101057100 (UNDINE), the Horizon 2020 program under grant no. 824110 (EasiGenomics grant no. COVID-19/PID12342), and the CERCA Program/Generalitat de Catalunya. The Canarian Health System sequencing hub was funded by the Instituto de Salud Carlos III (COV20_01333 and COV20_01334), the Spanish Ministry of Science and Innovation (RTC-2017-6471-1; AEI/FEDER, UE), Fundación MAPFRE Guanarteme (OA21/131), and Cabildo Insular de Tenerife (CGIEU0000219140 and "Apuestas científicas del ITER para colaborar en la lucha contra la COVID-19"). The CoV-Contact Cohort was funded by the French Ministry of Health and the European Commission (RECOVER project). Our studies are also funded by the Ministry of Health of the Czech Republic Conceptual Development of Research Organization (FNBr, 65269705), and the ANID COVID0999 funding in Chile. G.N. and A.N. are supported by Regione Lazio (Research Group Projects 2020) No. A0375-2020-36663, GecoBiomark. A.M.P, M.L.D. and J.P.T are supported by the Inmungen-CoV2 project of CSIC. This work was supported in part by the Intramural Research Program of the NIAID, NIH. The research work of A.M.P, M.L.D, and J.M.P.T. was funded by the European Commission –NextGenerationEU (Regulation EU 2020/2094), through CSIC's Global Health Platform (PTI Salud Global). IM is a senior clinical investigator at FWO Vlaanderen supported by a VIB GC PID Grant, by FWO Grants G0B5120N (DADA2) and G0E8420N and by the Jeffrey Modell Foundation. IM holds an ERC-StG MORE2ADA2 grant. Her work is also supported by ERN-RITA. A.Y. is supported by fellowships from the European Academy of Dermatology and Venereology and the Swiss National Science Foundation, and an Early Career Award from the Thrasher Research Fund. Y.-H.C. is supported by an A*STAR International Fellowship (AIF). M.O. was supported by the David Rockefeller Graduate Program, the New York Hideyo Noguchi Memorial Society (HNMS), the Funai Foundation for Information Technology (FFIT), and the Honjo International Scholarship Foundation (HISF), and the National Cancer Institute (NCI) F99 Award (F99CA274708). A.A.A. was supported by Ministerio de Ciencia Tecnología e Innovación MINCIENCIAS, Colombia (111584467551/CT 415-2020). D.L. is supported by a French Medical Research Foundation (FRM) fellowship for medical residents and fellows. E.H. received funding from the Bank of Montreal Chair of Pediatric immunology, Foundation of CHU Sainte-Justine, CIHR grants #PCC-466901 and # MM1-181123, and Canadian Pediatric Society IMPACT study. Q.P.H. received funding from the European Union's Horizon 2020 research and innovation program (ATAC, 101003650), the Swedish Research Council, and the Knut and Alice Wallenberg Foundation. Work in the Laboratory of Virology and Infectious Disease was supported by NIH grants P01AI138398-S1, 2U19AI111825, R01AI091707-10S1, and R01AI161444; a George Mason University Fast Grant; the G. Harold and Leila Y. Mathers Charitable Foundation; the Meyer Foundation; and the Bawd Foundation. R.P.L. is on the Board of Directors of both Roche and the Roche subsidiary, Genentech. J.L.P. was supported by the Francois Wallace Monahan Postdoctoral Fellowship at The Rockefeller University and the European Molecular Biology Organization Long-Term Fellowship (ALTF 380-2018). **Author contributions:** D.L., J.L.P., A.Y., B.D., Y.A., M.O., R.P., M.P., Z.L., L.B., A.Bis., W.L., M.H., J.C., C.G., A.A., V.L., J.M.L., F.J., H.-H.H., E.M., M.Mor., K.B., S.M., C.F., Y.Z., A.A.A., R.B., A.S., T.L.V., M.Mat., A.G., M.M.-V., F.P., T.L., R.Lev., A.-L.N., J.R., J.P., Y.-H.C., M.-P.M., R.M.P.-R., S.B., L.L., M.L.D., N.F., F.R., J.P.-T., S.C., T.E., F.G., P.L., S.R.W., A.M.P., C.D., J.B., A.Pue., S.B.-D., B.Boi., T.M., Q.Z., L.N., V.B., R.P.L., E.J., A.Bel., L.Q.-M., C.M.R., R.H.S., S.-Y.Z., and J.-L.C. performed or supervised experiments, generated and analyzed data, and contributed to the manuscript by providing figures and tables. 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agreement (MTA) with the Rockefeller University. The cell lines generated from this study are available from S.-Y.Z. and J.-L.C upon request under MTAs from the Rockefeller University and the Imagine Institute. Patient-specific cellular materials from patients enrolled at the NIAID are available from H.C.S. under a MTA with the NIH, provided that the request fulfills all articles listed in a MTA with the originating institute where the materials were collected. WGS data for patients sequenced by NIAID through TAGC were deposited under dbGaP accession number phs002245. Other genomic sequences of the patients reported in this paper are available from the authors upon request under a data transfer agreement. The raw RNA-seq data generated from this study are deposited in the NCBI database under the NCBI-SRA project PRJNA898284.

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SUPPLEMENTARY MATERIALS

science.org/doi/10.1126/science.abo3627
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Submitted 29 January 2022; resubmitted 16 August 2022
Accepted 14 December 2022
Published online 20 December 2022
10.1126/science.abo3627

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Table 1. Homozygous or potentially compound-heterozygous rare non-synonymous variants of the *OAS* and *RNASEL* genes in MIS-C patients. Homozygous or potentially compound-heterozygous non-synonymous variants with a minor allele frequency (MAF) < 0.01 (gnomAD) and found in our cohort of MIS-C patients are shown. Exp function, experimental function of each variant as tested in the RNase L–dependent rRNA degradation assay (OAS1, OAS2, RNase L) and FRET assay (OAS1, OAS2).

Gene	Nucleotide change	Amino acid change	Zygosity	MAF (gonad)	CADD_Phred	Exp function
OAS1	c.139C>T	p.Arg47* (R47*)	hom	0.00017327	36	LOF
OAS2	c.1604G>A	p.Arg535Gln (R535Q)	hom	0.00028695	13.58	Hypomorph
OAS2	c.773A>T	p.Gln258Leu (Q258L)	het		3.888	Hypomorph
OAS2	c.868G>A	p.Val290Ile (V290I)	het	0.0005153	5.585	Hypomorph
OAS3	c.145G>A	p.Ala49Thr (A49T)	het	0.00243639	9.48	Isomorph
OAS3	c.1475G>A	p.Arg492His (R492H)	het	0.0054987	9.95	Isomorph
OAS3	c.1703G>A	p.Arg568Lys (R568K)	het	0.00104951	0.472	Isomorph
OAS3	c.2795G>A	p.Arg932Gln (R932Q)	het	0.0094	23.2	LOF
OAS3	c.3089A>G	p.Gln1030Arg (Q1030R)	het		23.9	Isomorph
OAS3	c.1586A>G	p.Gln529Arg (Q529R)	het	0.00000401	5.85	Isomorph
OAS3	c.792C>A	p.His264Gln (H264Q)	het	0.001001261	0.924	Isomorph
OAS3	c.442C>T	p.Pro148Ser (P148S)	het	0.000036	22.9	Isomorph
OAS3	c.3259G>A	p.Val1087Met (V1087M)	het	0.003936537	22.5	Isomorph
RNASEL	c.790A>G	p.Ile264Val (I264V)	hom		6.597	Isomorph
RNASEL	c.793G>T	p.Glu265* (E265*)†	hom	0.0031	33	LOF
RNASEL	c.175G>A	p.Gly59Ser (G59S)†	hom	0.0031	22.9	Isomorph

†RNASEL variants p.E265* and p.G59S were in complete linkage disequilibrium (https://www.internationalgenome.org), forming a haplotype.

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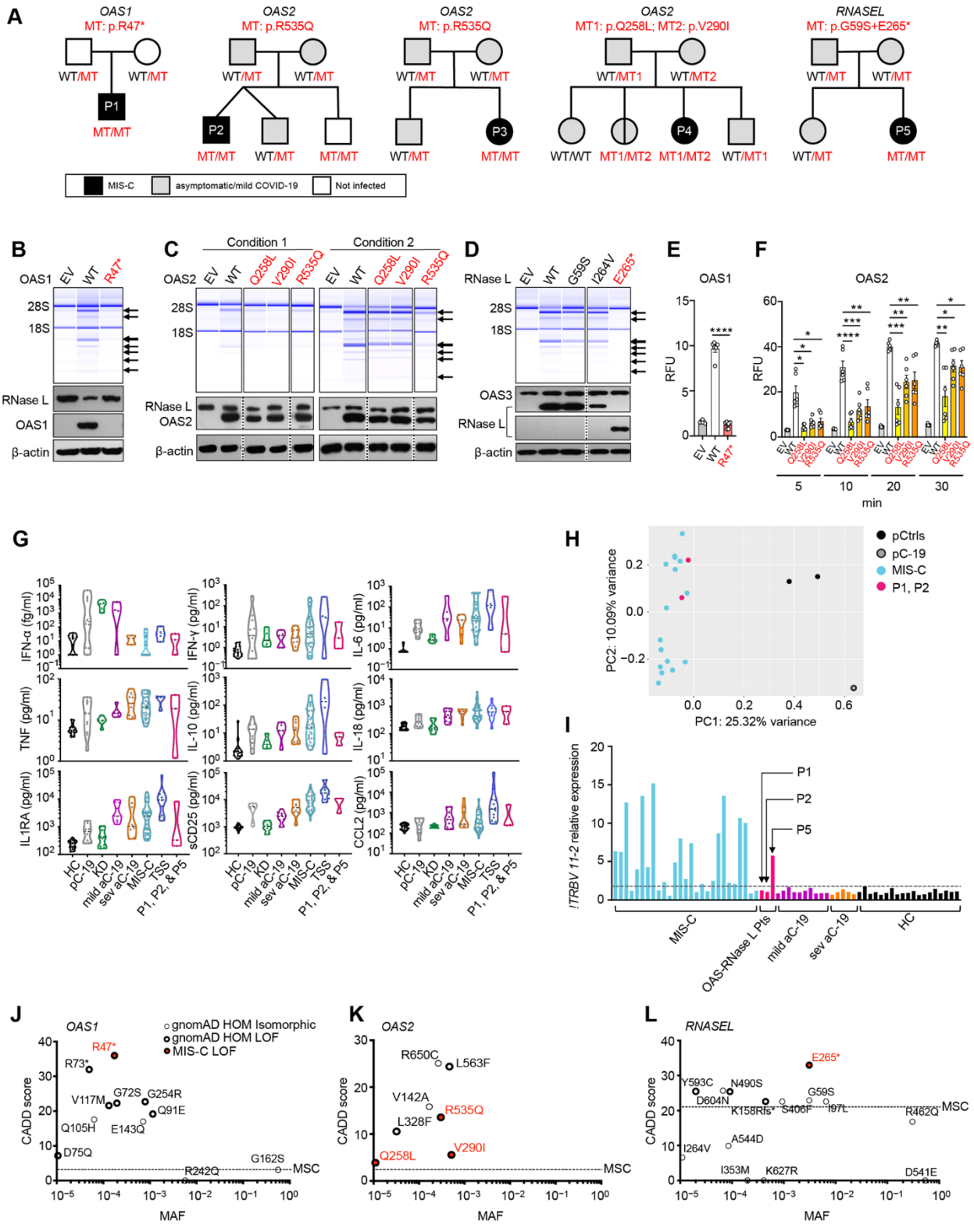
Table 2. Demographic and clinical information for MIS-C patients biallelic for deleterious variants of the OAS–RNase L pathway.
IEI, inborn error of immunity; SCV2, SARS-CoV-2; IVIG, Intravenous immunoglobulins; ND, not determined.

Patient	P1	P2	P3	P4	P5
IEI (inheritance mode)	*OAS1* (AR)	*OAS2* (AR)	*OAS2* (AR)	*OAS2* (AR)	*RNASEL* (AR)
Age of MIS-C	3 mo	3 yo	14 yo	9 yo	4 yo
Sex	M	M	F	F	F
Ethnicity	Filipino	Spanish	Turkish	Turkish	French Canadian
Resident country	Spain	Spain	Turkey	Turkey	Canada
SCV2 virology	Nasal swab PCR (−); Blood PCR (−); blood anti-SCV2 IgG (+); blood antigen-N (−)	Nasal swab PCR (−); Blood PCR (−); blood anti-SCV2 IgG (+); blood antigen-N (−)	Nasal swab PCR (−); Blood PCR (ND); blood total anti-SCV2 (+); blood antigen-N (ND)	Nasal swab PCR (−); Blood PCR (ND); blood anti-SCV2 IgM, IgG (+); blood antigen-N (ND)	Nasal swab PCR (−); Blood PCR (−); blood anti-SCV2 IgG (+); blood antigen-N (−)
Hemogram	Normal	Normal	Normal	Normal	Normal
Increased markers of multiorgan inflammation	CRP, ferritin, pro-BNP, GM-CSF, IL1RA, MCP1, sCD25, IL18, TNF	CRP, Ferritin, Pro-BNP, MCP1, sCD25, IL1RA, IL18, TNF	CRP, ferritin, troponin	Ferritin, troponin, pro-BNP	sCD25
TRBV 11-2 expansion	(−)	(−)	ND	ND	(+)
Clinical presentation	Kawasaki-like disease: Fever, gastrointestinal symptoms, hepatosplenomegaly, aseptic meningitis with neurological symptoms (irritability), peripheral edema, lymphadenopathy, bilateral coronary aneurysm (Z score +8, +8.7), possible cerebral arterial aneurysm	Kawasaki disease: Fever, rash, bilateral eyelid edema and erythema, conjunctival hyperemia	Kawasaki-like disease: Fever, rash, bilateral non-purulent conjunctivitis, strawberry tongue, abdominal pain, vomiting, dyspnea, mild mitral insufficiency. 1.5 months prior, the patient had fever, headache and sore throat when her mother had COVID-19. Developed Oligoarthicular juvenile idiopathic arthritis (JIA) 5 mo after MIS-C.	Fever, vomiting, coughing, myocarditis, left ventricular failure, pulmonary edema with paracardiac infiltration, polyneuropathy	Kawasaki disease: Fever, rash, erythema and edema of the feet, anterior uveitis, cervical lymphadenopathy

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Treatment	IVIG, aspirin, corticosteroids, anticoagulation therapy	IVIG, aspirin	IVIG, Methylprednisolone, heparin	IVIG, pulse steroid, anakinra, mechanical ventilation	IVIG
Outcome	Recovery	Recovery	Recovery, persistent arthralgias in both knees 1.5 years after MIS-C	Recovery	Recovery

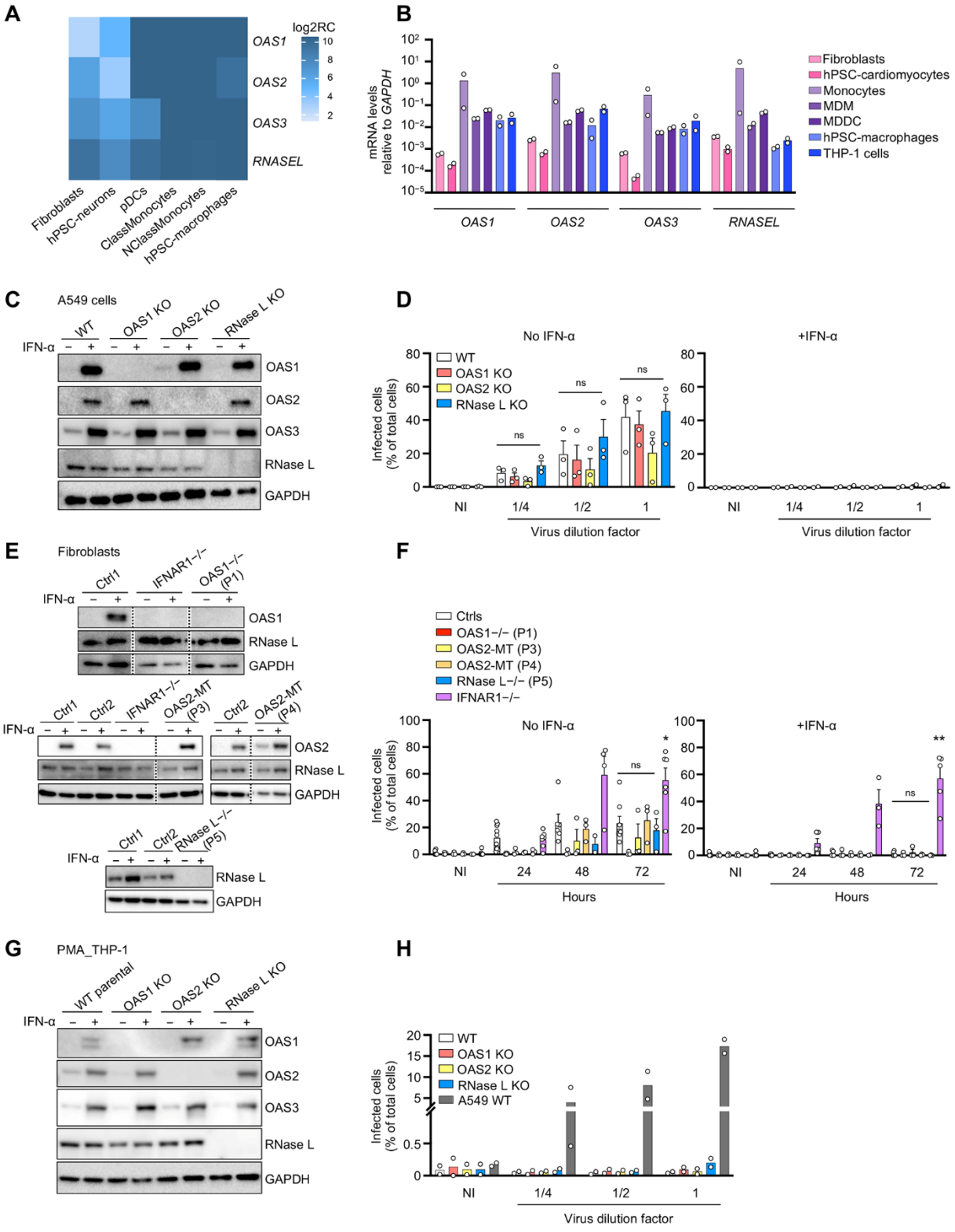
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Fig. 1. Biallelic *OAS1*, *OAS2*, and *RNASEL* variants in patients with MIS-C. (**A**) Family pedigrees with allele segregation. Mutant: "MT" in red. Wild-type: "WT" in black. (**B** to **D**) Functional assays for WT and mutant OAS1 (B), OAS2 (C), and RNase L (D). Variants for which homozygotes or compound heterozygotes were present in our MIS-C cohort were tested. Upper panels: RNase L-mediated cleavage of rRNA in a cell-free system based on transfected HeLa M cells. Lower panels: immunoblots of the indicated proteins. EV: empty vector. Arrows indicate degraded rRNA species. OAS2 variants (C) were tested under two different sets of conditions (see Methods). The results shown in (B) to (D) are representative of three independent experiments. (**E** and **F**) FRET assay of 2-5A synthesized in response to poly(I:C) stimulation by WT and MT OAS1 (E) or OAS2 (F). RFU: relative fluorescence units. The data shown are the means ± SEM of six biological replicates. Statistical analysis was performed as described in the Methods. **P* < 0.05, ***P* < 0.01, ****P* < 0.001, *****P* < 0.0001. (**G**) Concentrations of various cytokines in plasma samples from OAS–RNase L–deficient patients during MIS-C (P1, P2, and P5); comparison with those of healthy controls (HC), pediatric (pC-19) or adult COVID-19 pneumonia (aC-19) patients, typical Kawasaki disease patients (KD), other MIS-C patients with no known genetic etiology (MIS-C), and patients with toxic shock syndrome (TSS). (**H**) Principal component analysis (PCA) of gene expression quantified by whole-blood bulk RNA-seq for P1 and P2 during MIS-C relative to pediatric controls (pCtrls), previously published MIS-C patients, and a pediatric patient with mild COVID-19 (pC-19). (**I**) Relative levels of *TRBV 11-2* (encoding Vβ21.3) RNA in blood samples from P1, P2, and P5 during MIS-C, relative to other MIS-C patients, adults with mild or severe COVID-19 (mild aC-19, sev aC-19), and healthy controls. (**J** to **L**) CADD-MAF graph of *OAS1* (J), *OAS2* (K) and *RNASEL* (L) variants for which homozygotes are reported in gnomAD and/or found in our MIS-C cohort.

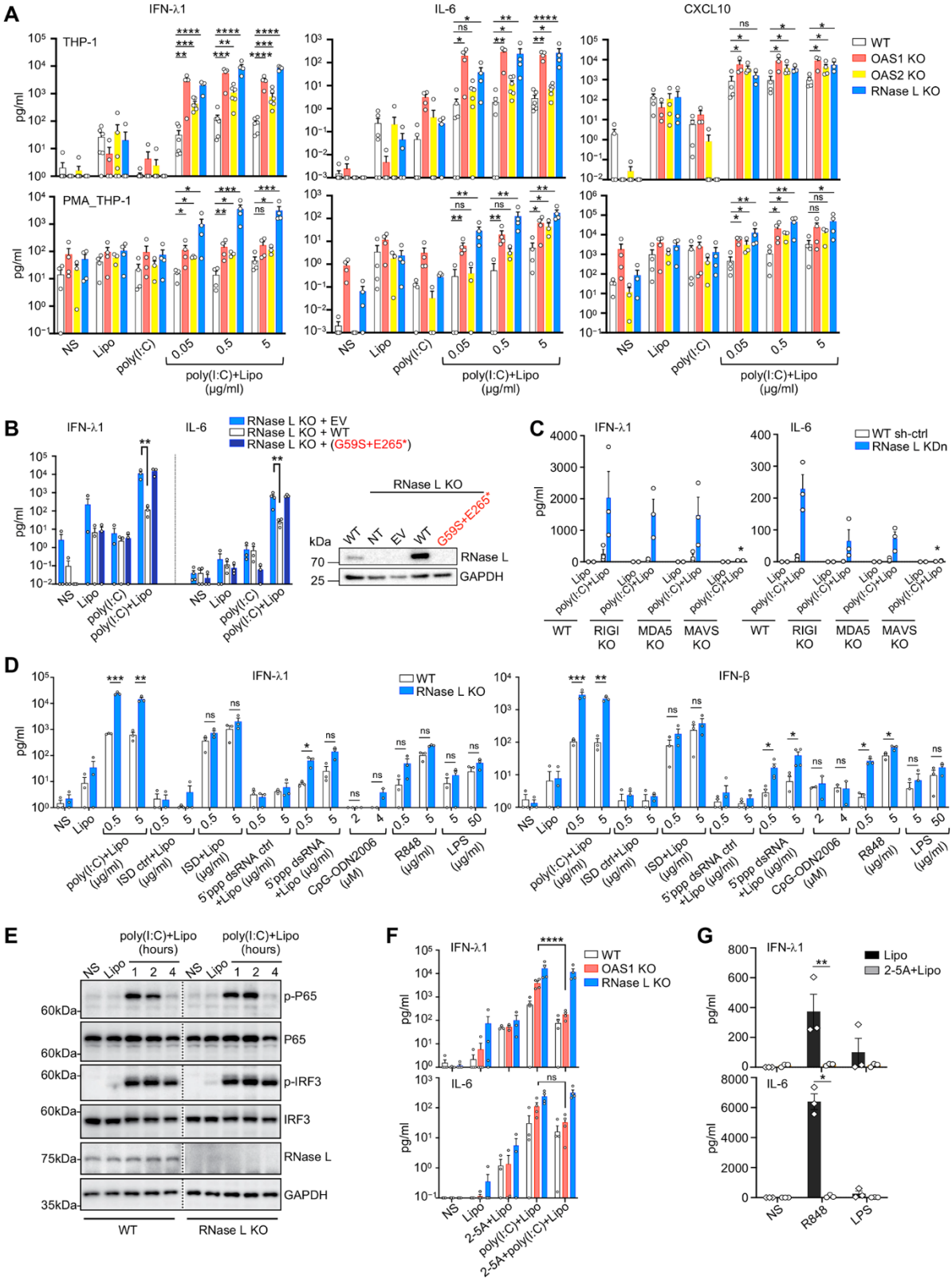
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Fig. 2. Expression pattern of the OAS–RNase L pathway genes and their role in SARS-CoV-2 restriction. (**A** and **B**) Relative *OAS1*, *OAS2*, *OAS3*, and *RNASEL* mRNA levels measured by bulk RNA-seq (A) or RT-qPCR (B), in various cell types. hPSC: human pluripotent stem cell; ClassMonocytes: classical monocytes; NClassMonocytes: non-classical monocytes; MDM: monocyte-derived macrophages; MDDC: monocyte-derived dendritic cells. Log2RC: $\log_2$ read count. (**C** and **D**) Immunoblot of the indicated proteins (C) and immunofluorescence (IF) of SARS-CoV-2 N-protein (D), in A549+ACE2/TMPRSS2 cells with and without knockout (KO) of OAS1, OAS2, OAS3, or RNase L. IF analysis for N-protein were performed 24 hours after infection with various dilutions of SARS-CoV-2. Dilution factors of 1/4, 1/2, and 1 correspond to MOI values of 0.0002, 0.0005 and 0.001, respectively. (**E** and **F**) Immunoblot of the indicated proteins (E) and IF analysis for the SARS-CoV-2 N-protein (F), in SV40-fibroblasts+ACE2 from healthy controls (Ctrl1 and Ctrl2), patients with *OAS-RNASEL* mutations (P1, P3, P4, and P5), and a previously reported patient with complete IFNAR1 deficiency (*IFNAR1*$^{-/-}$). IF analysis for N-protein was performed at various time points after infection at a MOI of 0.08. (**G** and **H**) Immunoblot of the indicated proteins (G) and IF analysis for the SARS-CoV-2 N-protein (H), in THP-1 cells with and without KO of OAS1, OAS2 or RNase L. IF analyses for N-protein were performed in PMA-primed THP-1 cells 24 hours after infection with various dilutions of SARS-CoV-2. Dilution factors of 1/4, 1/2 and 1 correspond to MOI of 0.012, 0.025 and 0.05, respectively. WT A549+ACE2/TMPRSS2 cells were included as a positive control for SARS-CoV-2 infection. The data points are means ± SEM from three [(D) and (F)] or means from two [(B) and (H)] independent experiments with three to six technical replicates per experiment. Statistical analyses were performed as described in the Methods. ns: not significant. *$P < 0.05$, **$P < 0.01$.

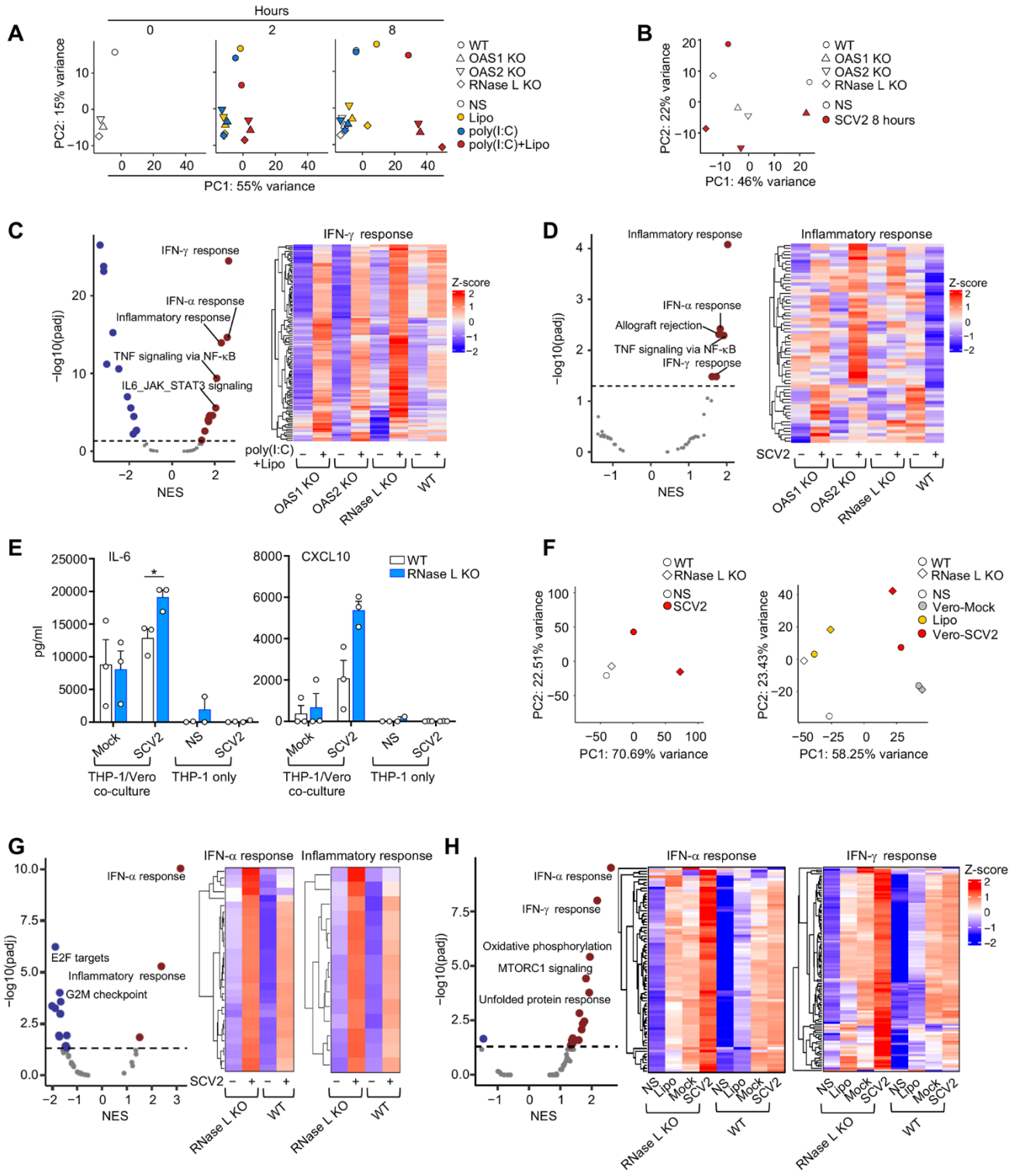
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Fig. 3. Exaggerated inflammatory responses of OAS–RNase L-deficient THP-1 cells. (**A**) Concentrations of various cytokines in the supernatant of OAS1 KO, OAS2 KO, RNase L KO, or parental THP-1 cells (upper panels) or PMA-primed THP-1 cells (lower panels) treated as indicated for 24 hours. (**B**) IFN-λ1 and IL-6 concentrations in the supernatant of RNase L KO THP-1 cells transduced with the WT or P5's variant *RNASEL* cDNA, or EV, and treated as indicated for 24 hours. On the right, RNase L protein levels, as assessed by immunoblotting. (**C**) IFN-λ1 and IL-6 concentrations in the supernatant of parental, RIG-I KO, MDA5 KO, or MAVS KO THP-1 cells with or without (WT sh-ctrl) RNase L knockdown (KDn), treated as indicated for 24 hours. (**D**) IFN-λ1 and IFN-β concentrations in the supernatant of parental or RNase L KO THP-1 cells, treated as indicated for 24 hours. (**E**) Immunoblot of phosphorylated P65 and IRF3 in parental and RNase L KO THP-1 cells treated as indicated. The results shown are representative of two independent experiments. (**F**) IFN-λ1 and IL-6 concentrations in the supernatant of parental, OAS1 KO, or RNase L KO THP-1 cells treated as indicated for 24 hours. (**G**) IFN-λ1 and IL-6 concentrations in WT THP-1 cells treated as indicated for 24 hours. In (A) to (D), (F), and (G), the data points are means ± SEM from three to five independent experiments with one to two technical replicates per experiment. Statistical analysis was performed as described in the Methods. ns: not significant. **P* < 0.05, ***P* < 0.01, ****P* < 0.001, *****P* < 0.0001. NS: non-stimulated; Lipo: lipofectamine only; poly(I:C): extracellularly added poly(I:C); poly(I:C)+Lipo: intracellular poly(I:C) in the presence of lipofectamine; 2-5A+Lipo: intracellular 2-5A in the presence of lipofectamine; 2-5A+poly(I:C)+Lipo: intracellular poly(I:C) in addition to intracellular 2-5A. EV: Empty vector. NT: not transfected.

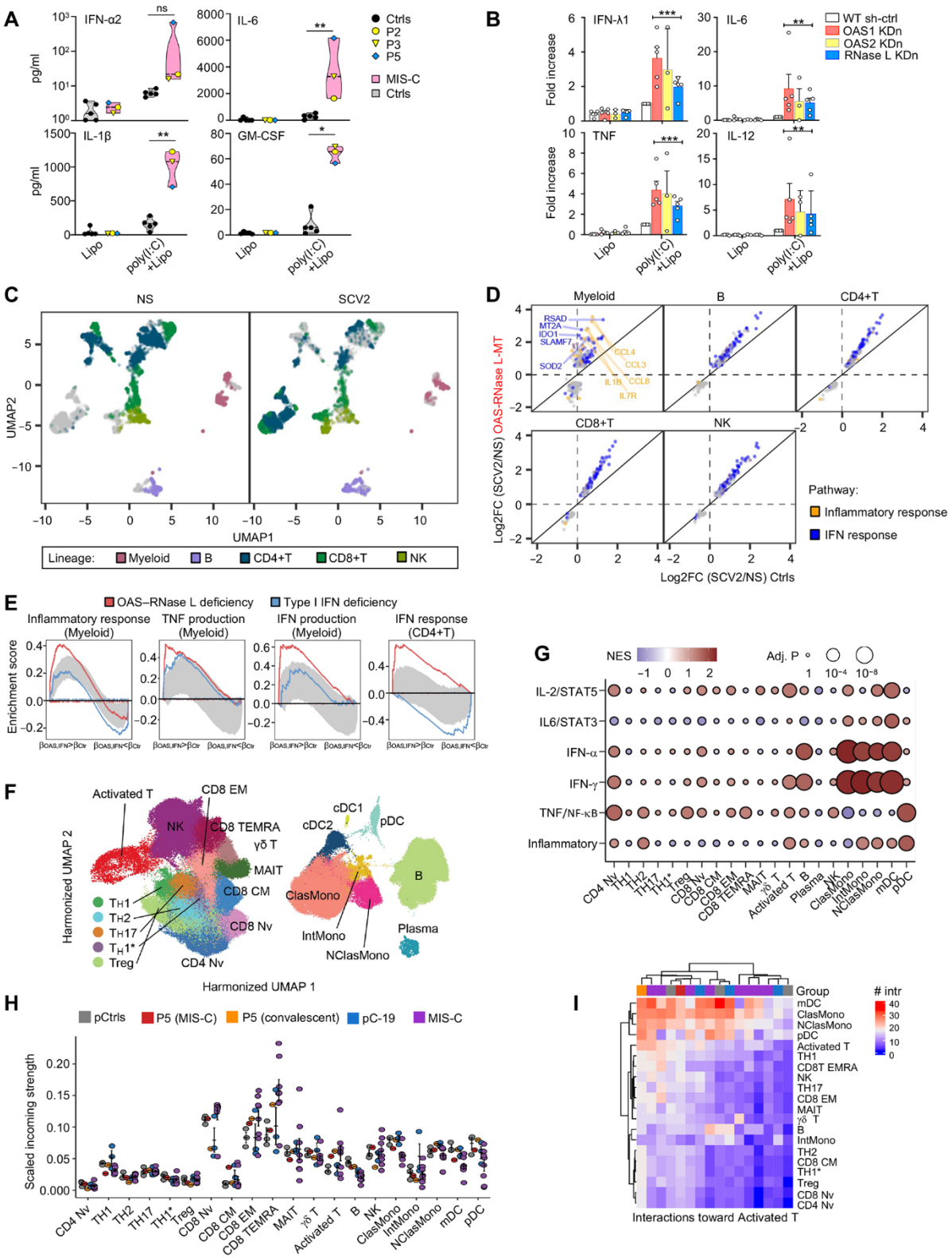
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Fig. 4. Exaggerated inflammatory responses to SARS-CoV-2 of OAS–RNase L-deficient THP-1 cells. (**A** and **B**) Principal component analysis (PCA) of RNA-seq–quantified gene expression for OAS1 KO, OAS2 KO, RNase L KO and parental (WT) THP-1 cells left non-stimulated (NS), treated as indicated for 2 or 8 hours (A), or stimulated with SARS-CoV-2 (SCV2) at a MOI of 0.01 for 8 hours (B). (**C** and **D**) Differential expression analysis (DEA) and gene set enrichment analysis (GSEA) for genes induced by 8 hours of intracellular poly(I:C) stimulation (C) or by 8 hours of SCV2 stimulation (D). The OAS1 KO, OAS2 KO and RNase L KO THP-1 cells were compared to parental (WT) THP-1 cells. Volcano plot: immune system-related pathways. NES: normalized enrichment score. Heatmaps: gene expression for the "IFN-γ response" (C) or "inflammatory response" (D) Hallmark gene sets. (**E**) IL-6 and CXCL10 concentrations in the supernatant of parental or RNase L KO THP-1 cells treated as indicated for 24 hours. The data points are means ± SEM from three independent experiments with three technical replicates per experiment. Statistical analysis was performed as described in the Methods. $*P < 0.05$. (**F**) PCA of RNA-seq–quantified gene expression, for RNase L KO and parental THP-1 cells cocultured with Vero cells with or without SCV2 infection for 24 hours (left) or transfected for 8 hours with RNA from Vero cells with or without SCV2-infection (right). (**G** and **H**) DEA and GSEA for genes induced in RNase L KO THP-1 cells, with comparison to parental THP-1 cells after 24 hours of coculture with SCV2-infected or mock-infected Vero cells (G), or after 8 hours of transfection with RNA from SCV2-infected or mock-infected Vero cells (H). Volcano plots: immune system-related pathways. Heatmaps: gene expression for the indicated Hallmark gene sets. Heatmaps represent Z-score-scaled $\log_2$ read counts per million. NS: non-stimulated; Lipo: lipofectamine; SCV2: SARS-CoV-2.

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Fig. 5. Exaggerated myeloid cell activation in response to SARS-CoV-2 underlies MIS-C. (**A**) Concentrations of cytokines in the supernatant of PBMCs from OAS–RNase L-deficient patients (grouped in pink violin-zone), and three healthy pediatric and two healthy adult controls (Ctrls) (gray violin-zone). The data points are means of biological duplicates. (**B**) Fold-increase in the concentrations of cytokines in the supernatant of MDDCs with KDn of OAS1, OAS2, or RNase L, or transduced with control shRNA (WT sh-ctrl). The fold-change is expressed relative to the values for poly(I:C)+lipo-stimulated WT sh-ctrl cells. Data shown are means ± SEM from three independent experiments, with one to two technical replicates per experiment. For (A) and (B), statistical analysis was performed as described in the Methods. NS: non-stimulated, ns: not significant, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$. (**C** to **E**) scRNA-seq of PBMCs from OAS–RNase L-deficient patients (OAS–RNase L-MT) or healthy controls after 6 hours of incubation with SARS-CoV-2 (SCV2) or mock infection (NS). (C) Uniform manifold approximation and projection (UMAP) of single PBMC transcriptomes. (D) Cell type-specific transcriptional responses. Genes passing the FDR<0.01 and |log2FC|>0.5 thresholds are shown. (E) GSEA of SCV2-induced genes across immune-related Hallmark gene sets. PBMCs from three patients with type I IFN pathway deficiency are controls for defective type I IFN responses. Gray zone: expected enrichment scores under the null hypothesis (95%CI calculated over 100 randomized genes). (**F** to **I**) scRNA-seq of PBMCs from P5 and from healthy controls. A published dataset for pediatric patients with acute SARS-CoV-2 infection (pC-19) and MIS-C was also integrated. (F) UMAP of clustering analysis. (G) Pseudobulk differential expression analysis with GSEA. P5 (convalescent phase) was compared to local pediatric controls (pCtrls). Immune-related pathways are shown. [(H) and (I)] Intercellular communication analysis with CellChat. (H) Incoming signal strength and (I) the number of interactions for representative cell subsets.

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Inborn errors of OAS–RNase L in SARS-CoV-2–related multisystem inflammatory syndrome in children

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Science, **Ahead of Print** • DOI: 10.1126/science.abo3627

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