

Supplemental information

**SARS-CoV-2 Nsp13 encodes
for an HLA-E-stabilizing peptide that abrogates
inhibition of NKG2A-expressing NK cells**

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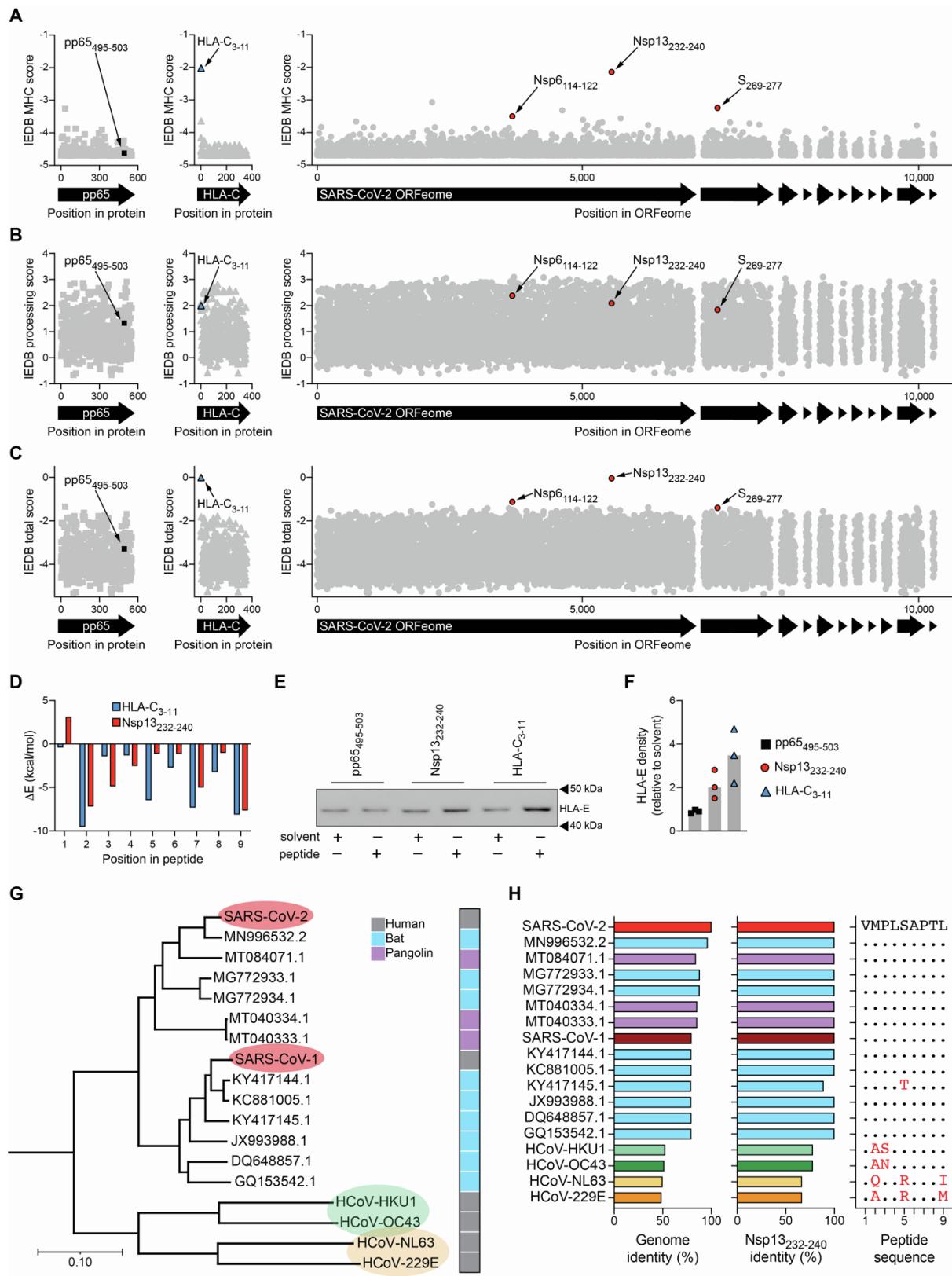


Figure S1. SARS-CoV-2 Nsp13 encodes for an HLA-E-stabilizing peptide. Related to Figure 1.

(A-C) *In silico* epitope predictions using the IEDB analysis resource. Left: pp65 protein. Middle: HLA-C*01:02 protein. Right: SARS-CoV-2 ORFeome (isolate Wuhan-Hu-1).

(A) Predicted HLA-E*01:01 binding scores. (B) Predicted proteasomal cleavage and transport scores. (C) Total scores combining HLA-E binding and processing. (D) Decomposed contributions of single amino acids to delta energy of binding as indicator of theoretical affinity determined by MD simulations (n=3 independent simulations). (E-F) Stability of HLA-E/peptide complexes as determined by cellular thermal shift assays using protein isolates from K562/HLA-E cells. (E) Cellular thermal shift assay and western blot analysis on HLA-E protein isolated form K562/HLA-E cells after incubation with the indicated peptides or corresponding solvent controls. Protein stability was assessed at 65 °C and detected by an anti-HLA-E antibody. (F) Densitometry of HLA-E signal ratio between indicated peptides and corresponding solvent controls. (n=3 independent experiments). (G) Phylogenetic relationships between the genomes of SARS-CoV-2, SARS-CoV-1, common cold-causing HCoVs, and sarbecovirus isolates from bats and pangolins as determined by Clustal ω . Scale bar indicating nucleotide substitution per site. (H) Sequence identities relative to SARS-CoV-2. Left: genome identity as determined by Clustal ω . Middle: Nsp13₂₃₂₋₂₄₀ peptide sequence identity. Right: Nsp13₂₃₂₋₂₄₀ amino acid sequence comparison between viruses. Sequence alterations relative to SARS-CoV-2 are highlighted in red. Data are mean (D) or mean and individual datapoints (F).

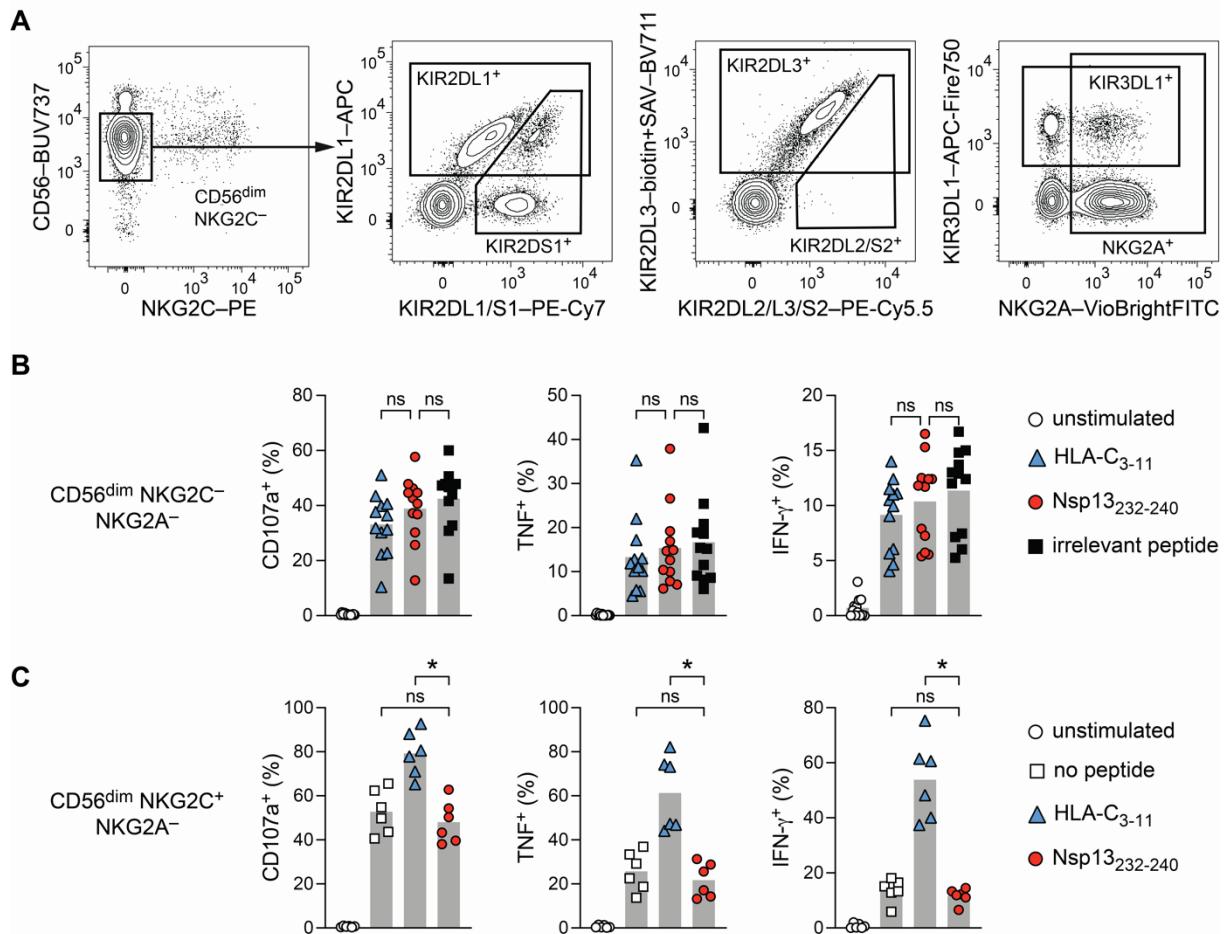


Figure S2. Nsp13₂₃₂₋₂₄₀ presented by HLA-E does not affect NKG2A⁻ nor NKG2C⁺ NK cells. Related to Figure 3.

(A) Gating strategy for flow cytometric analyses of NK cell subsets. After gating on viable CD14⁻ CD19⁻ CD3⁻ events, CD56^{dim} NKG2C⁻ NK cells were selected, and Boolean gating was performed on KIR2DS1⁻ KIR2DL2/S2⁻ subsets. (B) Summaries of activation of CD56^{dim} NKG2C⁻ NKG2A⁻ NK cells upon co-culture with peptide-pulsed K562/HLA-E target cells. Left: degranulation. Middle: TNF expression. Right: IFN- γ expression (n=12 donors in 5 independent experiments). (C) Summaries of activation of adaptive CD56^{dim} NKG2C⁺ NKG2A⁻ NK cells upon co-culture with peptide-pulsed K562/HLA-E target cells. Left: degranulation. Middle: TNF expression. Right: IFN- γ expression (n=6 donors in 5 independent experiments). Data are mean and individual datapoints (B and C). Statistical significance was tested using Friedman test with Dunn's multiple comparison test (B and C). *P < 0.05.

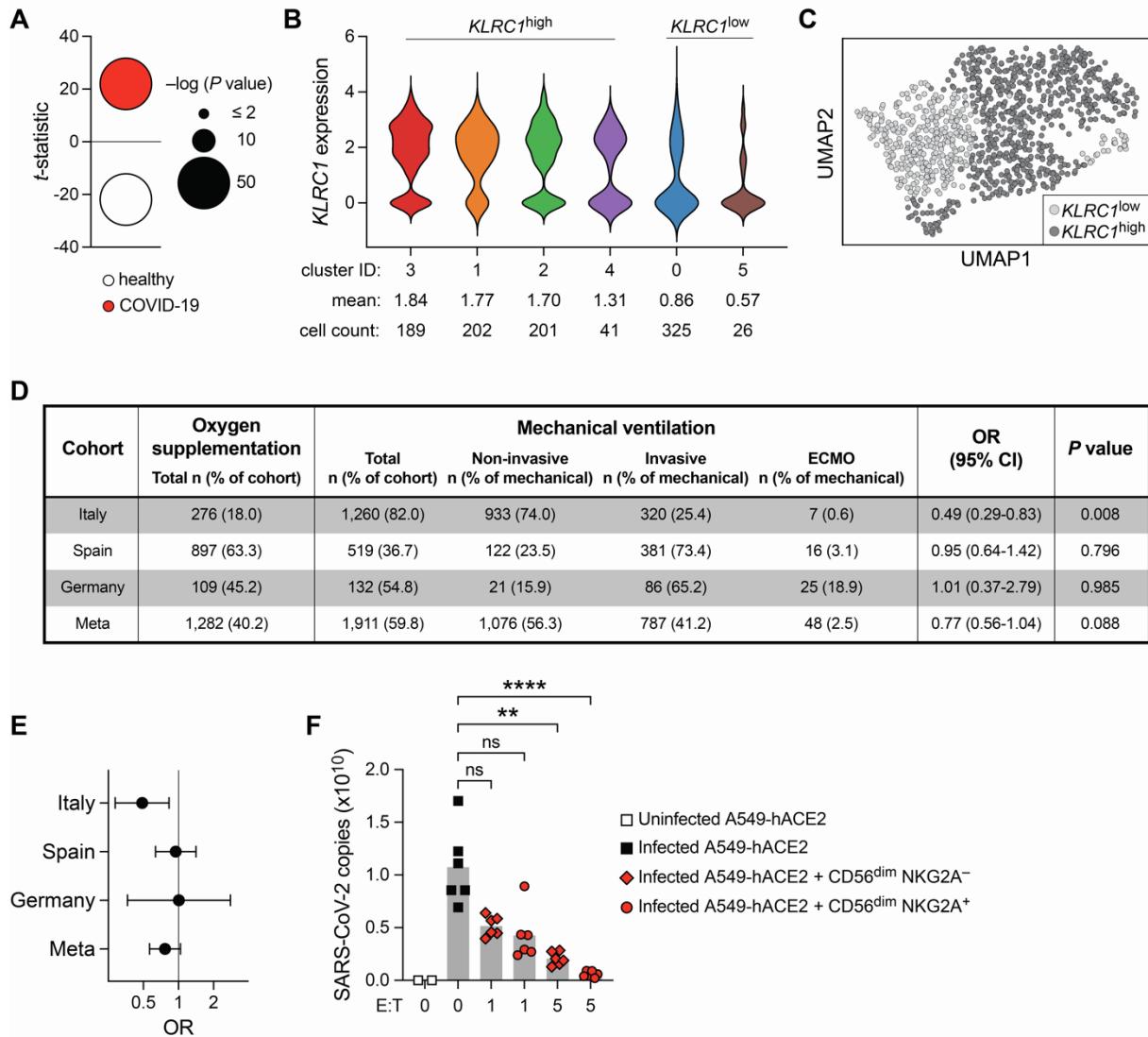


Figure S3. NKG2A-expressing NK cells are activated in patients with COVID-19 and proficiently suppress SARS-CoV-2 replication *in vitro*. Related to Figure 4.

(A-C) Single cell-RNA-sequencing analysis of NK cells from BALF (Liao et al., 2020). (A) *t*-statistic characterizing the separation of NK cells from BALF of healthy donors and patients with COVID-19 using a previously described signature of inflammatory NK cell responses (Yang et al., 2019). (B) Leiden clusters sorted according to mean *KLRC1* expression and grouped into *KLRC1*^{high} (clusters 3, 1, 2, and 4) and *KLRC1*^{low} (clusters 0 and 5) bins. (C) UMAP plot as in **Figure 4E** overlaid with *KLRC1* bins. (D-E) Genetic Association Analysis of *HLA-B* –21 in patients with COVID-19 with respiratory failure. (D) Summary table of genetic association of the –21M/M genotype with COVID-19 respiratory severity in three distinct cohorts and a meta-analysis (Severe Covid-19 GWAS Group et al., 2020). ECMO (Extracorporeal membrane oxygenation). (E) Forest plot depicting the odds ratio (OR) of –21M/M carriership with

the requirement for mechanical ventilation in the indicated cohorts. Meta (meta-analysis). (F) A549-hACE2 were infected with SARS-CoV-2 (isolate SARS-CoV-2/human/SWE/01/2020) and co-cultured with sorted CD56^{dim} NKG2A⁻ or CD56^{dim} NKG2A⁺ NK cells at 1 h post-infection as in **Figure 4G**. Absolute virus copies in adherent A549-hACE2 were quantified at 24 h post-infection by RNA extraction and RT-qPCR using the CDC nCoV-2019 N1 assay (n=6 NK cell donors in 2 independent experiments). Data are either distributions (B), OR and 95% CI (E), or mean and individual datapoints (F). Statistical significance was tested using student's t-test (A), logistic regression (D and E), or Friedman test with Dunn's multiple comparison test (F). ** $P < 0.01$ and **** $P < 0.0001$.

Table S1. Characteristics of patients with COVID-19 from the Karolinska COVID-19 Immune Atlas. Related to Figure 4.

Re-analysis of NK cell activation was performed on a previously described cohort of patients (Maucourant et al., 2020). Moderate and severe groups were combined and two patients excluded due low cell counts. Further details can be found at <https://covid19cellatlas.com/#/project/cohort>.

Clinical characteristics		Patients with moderate COVID-19	Patients with severe COVID-19
Group size	n	10	17
Risk factors			
Age, median (range)	56.5 (18-76)	58 (40-78)	
Sex, n female/male	3/7	3/14	
BMI, median (range)	27.63 (23-35.06)	29 (23-55)	
Smoking – current, n (%)	1 (10)	2 (12)	
Smoking – prior, n (%)	2 (20)	5 (29)	
Smoking – non-smoker, n (%)	2 (20)	9 (53)	
Smoking – unknown, n (%)	5 (50)	1 (6)	
Preexisting conditions			
None, n (%)	4 (40)	5 (29)	
Diabetes mellitus, n (%)	3 (30)	5 (29)	
Hypertension, n (%)	2 (20)	6 (35)	
Coronary heart disease, n (%)	– (–)	2 (12)	
Asthma, n (%)	1 (10)	2 (12)	
Viremia at sampling	n (%)	4 (40)	8 (47)
Symptoms on admission			
Fever, n (%)	10 (100)	17 (100)	
Cough, n (%)	9 (90)	14 (82)	
Dyspnea, n (%)	10 (100)	17 (100)	
Body ache, n (%)	3 (30)	9 (53)	
Gastrointestinal, n (%)	1 (10)	3 (18)	
Days from symptom onset	To admission, median (range)	8.5 (4-14)	9 (3-14)
	To sampling, median (range)	13.5 (6-19)	14 (5-24)
Peak oxygen therapy			
None, n (%)	2 (20)	0 (0)	
Low flow <10 L/min, n (%)	6 (60)	0 (0)	
Low flow 10-15 L/min, n (%)	1 (10)	3 (18)	
High flow, n (%)	1 (10)	1 (6)	
Ventilator, n (%)	0 (0)	12 (71)	
ECMO, n (%)	0 (0)	1 (6)	
Treatment prior to sampling			
Anticoagulant	10 (100)	15 (88)	
Corticosteroids	2 (20)	12 (71)	
Antibiotics	3 (30)	12 (71)	
Antivirals	0 (0)	1 (6) Remdesivir	
Cytokine inhibitors	0 (0)	2 (12) Anakinra, Tocilizumab	
Clinical course			
Days on ICU, median (range)	0 (0)	14 (0-45)	
Days intubated, median (range)	0 (0)	11 (0-45)	
Days hospitalized, median (range)	8 (5-39)	21 (10-57)	
SOFA score at sampling, median (range)	1 (0-2)	6 (2-12)	
Outcome			
Discharged, n (%)	10 (100)	12 (71)	
Death, n (%)	0 (0)	4 (24)	
Unknown, n (%)	0 (0)	1 (6)	

Table S2. Gene set of inflammatory NK cell responses. Related to Figure 4.

List of genes indicative of inflammatory responses of NK cells (“inflamed” cluster) obtained from Yang et al., 2019. Genes integrated into an inflammatory score are marked with *.

Genes		
<i>PMAIP1</i> *	<i>EHD4</i> *	<i>GZMK</i> *
<i>IFIT3</i> *	<i>PTGER4</i>	<i>FCER1G</i> *
<i>IFIT2</i> *	<i>APOL6</i> *	<i>EFHD2</i> *
<i>CCL3</i> *	<i>KLRB1</i> *	<i>ZBTB20</i> *
<i>CCL3L1</i>	<i>FTH1</i> *	<i>RAC2</i> *
<i>CCL3L3</i>	<i>XIST</i>	<i>SBF2</i>
<i>TNF</i>	<i>NANS</i> *	<i>CTSW</i> *
<i>NFKBIZ</i> *	<i>ZEB2-AS1</i> *	<i>CORO1A</i> *
<i>CCL4</i> *	<i>TMSB4X</i> *	<i>GZMA</i> *
<i>OASL</i> *	<i>CD7</i> *	<i>CLIC1</i> *
<i>ISG15</i> *	<i>CDKN1A</i> *	<i>BTG1</i> *
<i>GCA</i>	<i>DDX3Y</i> *	<i>IGFBP7</i> *
<i>PPP1R15A</i>	<i>ARHGAP11B</i>	<i>SFT2D2</i> *
<i>CCL4L2</i>	<i>ZBP1</i> *	<i>CLEC2B</i> *
<i>IFIT1</i> *	<i>NR4A2</i> *	<i>CMC1</i> *
<i>RPS4Y1</i> *	<i>MT2A</i> *	<i>ARPC5</i> *
<i>LTA</i>	<i>TTTY15</i>	<i>CLIC3</i> *
<i>TNFAIP3</i> *	<i>ACTB</i> *	<i>CFL1</i> *
<i>FOS</i> *	<i>HERC5</i> *	<i>CTD-2037K23.2</i>
<i>CCL4L1</i>	<i>PRF1</i> *	<i>CD160</i> *
<i>ZC3HAV1</i> *	<i>C20orf24</i>	<i>KLF9</i>
<i>CD69</i> *	<i>DDIT4</i> *	<i>BTG2</i> *
<i>AC069363.1</i>	<i>LINC-PINT</i>	<i>ZEB2</i>
<i>LAX1</i> *	<i>ANKRD28</i> *	<i>RHOB</i> *
<i>HELB</i> *	<i>FGR</i> *	<i>PPP2R5C</i> *
<i>YBX1</i> *	<i>TNIP1</i> *	<i>MIA3</i> *
<i>ETV3</i> *	<i>MYL12B</i> *	<i>ANXA2</i> *
<i>CCL5</i> *	<i>RBM39</i> *	<i>ELF1</i> *
<i>RP1-40E16.12</i>	<i>RGS1</i>	<i>C1orf162</i> *
<i>MYL12A</i> *	<i>TXNIP</i> *	<i>PRDM1</i>

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