

Supplementary Table 1: Primers used for qPCR analyses.

gene	forward	reverse
ACE2	GGGATCAGAGATCGGAAGAAGAAA	AGGAGGTCTGAACATCATCAGTG
HLA-ABC	GCCTACCACGGCAAGGATTAC	GGTGGCCTCATGGTCAGAGA
CD274	AAGGGAGAATGATGGATG	ATTCTCCTCCTCTGCTTT
TAP1	GGAATCTCTGGCAAAGTCCA	TGGGTGAACTGCATCTGGTA
TAP2	CCAAGACGTCTCCTTTGCAT	TTCATCCAGCAGCACCTGTC
TAPBP	TGGGTAAGGGACATCTGCTC	ACCTGTCCTTGCAGGTATGG
PSMB9	TGCTGCATCCACATAACCAT	TGTGCACTCTCTGGTTCAGC
PSMB8	TCTGCGTCATCAGCAAGAAC	GCCATTCAGGAAGTGTCCAT
PSMB10	GGGCTTCTCCTTCGAGAACT	CAGCCCCACAGCAGTAGATT
B2M	CTCGCGCTACTCTCTCTT	AAGACCAGTCCTTGCTGA
ERAP1	TCATCCTCCCAGAAGAGGTG	AACCTTGAAACACGGGCATA
CANX	TGTGAGTCAGCTCCTGGATG	GACCACAGCTCCAAACCAAT
CALR	TGGACCCGATATTTGTGGA	TCCCCAATCCTTCGATTCTG
IRF1	GCAGCTACACAGTTCCAGG	GTCCTCAGGTAATTTCCCTTCCT
IRF2	TGCGGTCCTTGACTTCAACTA	ATATTCCTCTTCCGCCAGTG
IRF9	GTCCAGCTGTCTGGAAGACT	TCCTCTTCCTCCTTCCTCTC
JAK1	CCACTACCGGATGAGGTTCTA	GGGTCTCGAATAGGAGCCAG
JAK2	TCTGGGGAGTATGTTGCAGAA	AGACATGGTTGGGTGGATACC
TYK2	GAGATGCAAGCCTGATGCTAT	GGTCCCGAGGATTCATGCC
STAT1	CAGCTTGACTCAAAATTCCTGGA	TGAAGATTACGCTTGCTTTTCCT
STAT2	GAGCCAGCAACATGAGATTGA	GCCTGGATCTTATATCGGAAGCA
STAT3	ATCACGCCTTCTACAGACTGC	CATCCTGGAGATTCTCTACCACT
STAT6	CGAGTAGGGGAGATCCACCTT	GCAGGAGTTTCTATCAAGCTGTG
STING	GTCTCCAAGCCTCTGGACTG	TGTCAAGTCCTGGACCCTTC
IFI6	GGTCTGCGATCCTGAATGGG	TCACTATCGAGATACTTGTGGGT
IFIT1	TTGATGACGATGAAATGCCTGA	CAGGTCACCAGACTCCTCAC
IFIT2	AAGCACCTCAAAGGGCAAAAC	TCGGCCCATGTGATAGTAGAC
IFIT3	AACAGATGTCCTCCGCAGTG	TTCCGTCTCCAGGAACCTCAG
OAS2	GACACTGCAGAAGGTTTCCG	CTGCATTGTCGGCACTTTCC
OASL	CCATTGTGCCTGCCTACAGAG	CTTCAGCTTAGTTGGCCGATG
HLA-B	CAGTTCGTGAGGTTTCGACAG	CAGCCGTACATGCTCTGGA
OAS1	GGGATTTTCGGACGGTCTTGG	TCGTCCGTCTCATCGTCTGC
DDX60	GACAGGTCCAGGTGTCAGTTT	TTGGTCTCGTGTGCCTTTTTG
CMPK2	CCAGGTTGTTGCCATCGAAG	CAAGAGGGTGGTGACTTTAAGAG
SCD	TCTAGCTCCTATACCACCACCA	TCGTCTCCAACCTATCTCCTCC
ABCG1	ATTCAGGGACCTTTTCTATTCCG	CTCACCACTATTGAACTTCCCG
SREBF1	GCCCCTGTAACGACCACTG	CAGCGAGTCTGCCTTGATG
FGFR4	CGACACAAGAACATCATCAACC	CATCACATTGTCTCAGTCACC
PHGDH	CTGCGGAAAGTGCTCATCAGT	TGGCAGAGCGAACAATAAGGC
FBXO27	ACAGACTCCTCGTCCAACCTTC	GGCAGGCATTGTTGTTCCAC
PREX1	GGCATTCTGCATCGCATC	CGGGTGTAACAATACTCCAAGG
CRAT	GTGGCTCAAGACCGCCTAC	GCAGCAAATCGGAGCTGAC
AIF1L	GGTGCTTCCTGCACAGAGAT	GACCGTTTCCCAGCATCAT
PXMP4	CCCCCATCACGCCTTCTAAA	GGAGGGCACAGGGAGTTTTTC
ACTB	ACTCTTCAGCCTTCCTTCC	AGCACTGTGTTGGCGTACAG
GAPDH	CTGGTAAAGTGGATATTGTTGCCAT	TGGAATCATATTGGAACATGTAAACC

Supplementary Table 2: DEGs linked to different types of diseases. Top DEGs annotated to each of these diseases are presented.

gene_name	disease_id
IFI6	C0000786,C0011311,C0019196,C0021400,C0023903,C0024623,C0026764,C0033860,C0042769,C0596263,C0699791,C1140680,C2239176
IFIT1	C0004114,C0014175,C0019196,C0021400,C0024141,C0024623,C0027092,C0030389,C0036421,C0042769,C0206633,C0282687,C0699791,C1140680,C3463824,C3714514
IFIT2	C0007137,C0021400,C0025202,C0035235,C0043124,C1096184,C1319315,C1621958,C3714514
IFIT3	C0002395,C0004364,C0008497,C0013080,C0021400,C0022104,C0023418,C0023530,C0024141,C0027627,C0235974,C0346647,C0524851,C1458155
OAS2	C0007682,C0008055,C0011311,C0011570,C0011581,C0011615,C0011854,C0013595,C0014061,C0019163,C0019196,C0021400,C0025289,C0033860,C0036421,C0041696,C0042769,C0153381,C0220641,C0282687,C0338715,C0376358,C0524909,C0600139,C0936250,C1269683
OASL	C0014061,C0019196,C0021400,C0024141,C0036421,C0040336,C0375023,C0524909,C0524910,C1096184
HLA-B	C0000737,C0000809,C0000832,C0000887,C0001175,C0001403,C0001418,C0001627,C0001824,C0001973,C0002171,C0002390,C0002395,C0002736,C0002871,C0002874,C0002902,C0002940,C0003123,C0003493,C0003838,C0003862,C0003864,C0003872,C0003873,C0004096,C0004352,C0004364,C0004565,C0004623,C0004763,C0004943,C0005411,C0005586,C0006118,C0006142,C0006267,C0006309,C0006413,C0007102,C0007130,C0007131,C0007134,C0007137,C0007194,C0007222,C0007570,C0007847,C0007873,C0007930,C0008031,C0008313,C0008533,C0008728,C0009324,C0009402,C0009447,C0009676,C0009763,C0010051,C0010346,C0010418,C0010823,C0011168,C0011311,C0011334,C0011603,C0011609,C0011615,C0011633,C0011644,C0011847,C0011849,C0011854,C0011860,C0011991,C0013080,C0013132,C0013182,C0013221,C0013264,C0013295,C0013421,C0014070,C0014175,C0014457,C0014518,C0014544,C0014661,C0014743,C0014859,C0015230,C0015397,C0015405,C0015672,C0015696,C0015967,C0016059,C0016382,C0017086,C0017152,C0017160,C0017168,C0017178,C0017181,C0017636,C0017638,C0017661,C0017677,C0017980,C0018099,C0018133,C0018213,C0018522,C0018621,C0018790,C0018801,C0018939,C0018989,C0018995,C0019050,C0019069,C0019100,C0019101,C0019114,C0019163,C0019187,C0019196,C0019360,C0019655,C0019693,C0020097,C0020456,C0020458,C0020517,C0020538,C0020

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ABC G1	C0002395,C0002726,C0003850,C0004153,C0005586,C0006142,C0007131,C0007222,C0009402,C0009404,C0010054,C0010068,C0011847,C0011849,C0011860,C0013080,C0013537,C0020443,C0020473,C0022661,C0023794,C0023893,C0024115,C0025500,C0027022,C0027051,C0027404,C0028754,C0031117,C0034050,C0034069,C0041107,C0042373,C0043094,C0151744,C0242383,C0376358,C0524620,C0525045,C0600139,C0678222,C0745103,C0856169,C1292778,C1335302,C1527249,C1709246,C1839839,C1852197,C1863340,C1956346,C1970943,C1970945,C2613439,C2700438,C2700439,C2700440,C3658248
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PRE X1	C0004352,C0006142,C0011860,C0022660,C0025202,C0027627,C0040336,C0162429,C0178874,C0376358,C0596263,C0600139,C0678222,C0854917,C0936223,C1282496,C1458155,C1512981
CRA T	C0006142,C0007102,C0007873,C0009402,C0017921,C0018802,C0027404,C0029925,C0041327,C0085580,C0271650,C0376358,C0524620,C0600139,C0678222,C0699790,C1458155,C1527249,C3463824
PXM P4	C0178874,C0376358,C0600139

Supplementary Table 3: Correlation of ACE2 expression with HLA class I and APM components and IFN pathway components were performed using R2 Genomics (<http://r2.amc.nl>) and two different cancer datasets, Tumor Breast Invasive Carcinoma - TCGA – 1097 and Mixed Cancer GDC - TCGA – 11003.

	Tumor Breast Invasive Carcinoma - TCGA - 1097		Mixed Cancer GDC - TCGA - 11003	
	r-value	p-value	r-value	p-value
HLA-A	0.198	3.93e-11	0.278	1.26E-194
HLA-B	0.214	7.79e-13	0.249	9.35E-156
HLA-C	0.136	5.85e-06	0.227	6.8E-129
HLA-E	0.276	1.30e-20	0.256	3.95E-164
HLA-G	0.128	2.23e-05	0.296	4.85E-222
TAP1	0.246	1.47e-16	0.19	2.51E-90
TAP2	0.290	1.20e-22	0.092	4.87E-22
TAPBP	0.144	1.80e-06	0.217	4.79E-117
CALR	0.252	2.66e-17	0.006	0.546
CANX	-0.063	0.036	0.107	2.82E-29
ERAP1	0	1	0.244	1.3E-148
ERAP2	0.045	0.136	0.111	1.46E-31
PSMB9	0.207	4.71e-12	0.232	1.25E-134
PSMB8	0.128	2.26e-05	0.281	1.71E-198
PSMB10	0.136	6.06e-06	0.254	2.55E-161
CD274	0.169	1.96e-08	0.084	7.97E-19
B2M	0.152	4.03e-07	0.206	1.56E-105
IFNG	0.185	7.12e-10	0.036	0.00017
IFNGR1	0.376	4.36e-38	0.187	8.63E-87
IFNGR2	0.250	4.96e-17	0.076	1.16E-15
JAK1	0.114	1.61e-04	0.247	2.38E-152
JAK2	0.158	1.45e-07	0.045	0.00000205
STAT1	0.141	2.87e-06	0.076	1.17E-15
IRF1	0.206	6.32e-12	0.186	1.71E-86

Supplementary Table 4:

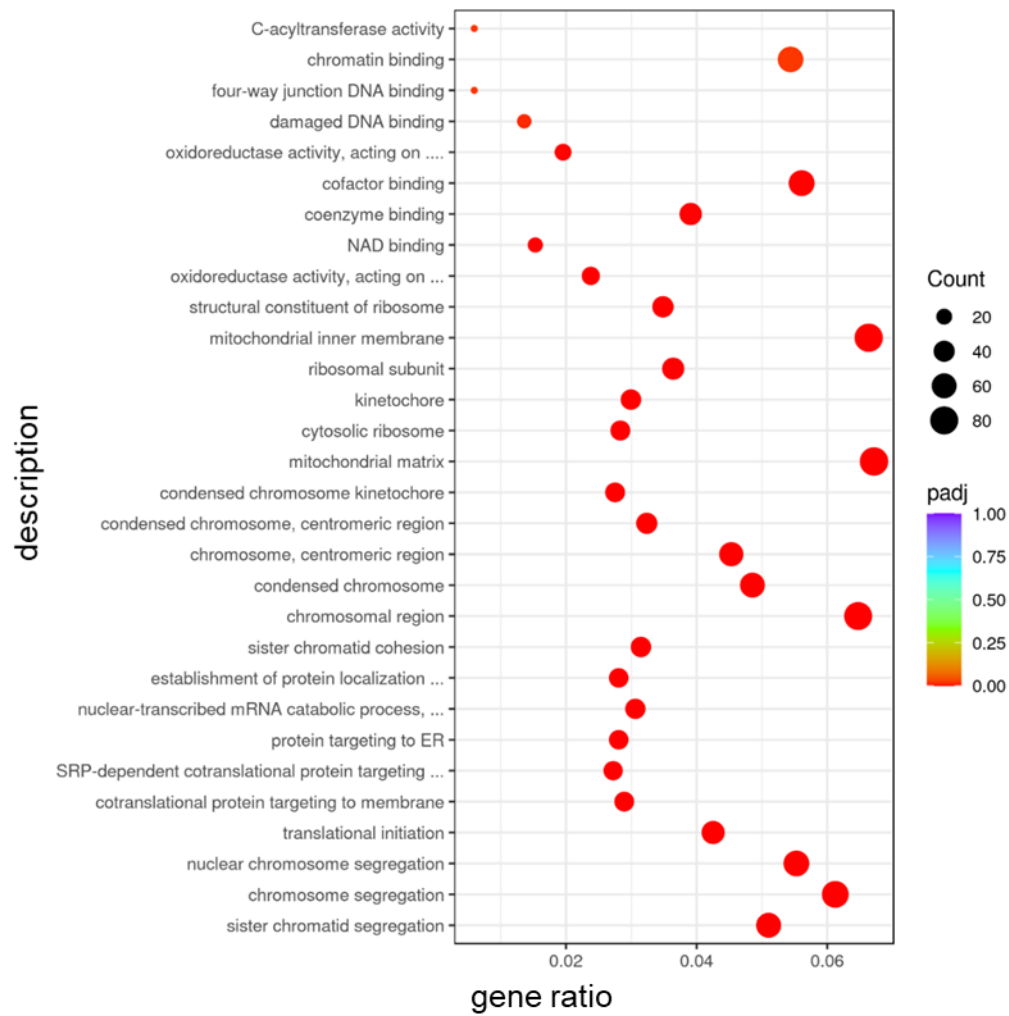
A: Analysis of cytokine release with ACE2^{high/low} cells upon nivolumab treatment and altered cytokine expression profile in PBMCs upon SARS-CoV-2 infection.

cytokines	ACE2 ^{low}	ACE2 ^{high}	ACE2 ^{high} vs. low
	mean		p value
CSF2	4.18	4.09	0.47
IFNG	6.62	9.37	0.10
IL1B	6.90	1.86	0.12
IL2	323.83	758.20	0.01
IL4	0.67	0.21	0.06
IL5	0.43	0.32	0.38
IL6	57.13	12.62	0.18
CXCL8	3216.50	2969.48	0.30
IL9	1.10	↓ SC	n/a
IL10	5.15	1.80	0.02
IL12A	1.24	↓ SC	n/a
IL13	5.34	↓ SC	n/a
IL17A	0.47	↓ SC	n/a
CCL2	377.78	93.76	0.04
CCL3	7.48	13.33	0.24
CCL4	65.34	87.89	0.24
TNF	10.28	10.98	0.44

B: Transcriptional response of different cytokine levels to SARS-CoV-2 infection in lung biopsies (n=2) compared to their healthy counterparts (GEO accession: GSE147507).

Gene_Symbol	healthy	COVID-19
CSF2	1017.2458	171.7929
IL2	3.036295	1
IL4	2.431805	1
IL5	3.420165	1
IL6	25225.35	19153.55
IL1B	5637.209	71878.2
IL9	1	1
IL10	121.2407	342.545
IL12A	57.1823	1
IL13	10.06294	1
IL17A	3.733445	1
IFNG	12.45225	1
CCL2	18723.99	182502
CCL3	1736.7923	97884.55
CCL4	707.44	238525.5
TNF	75.6832	2916.045

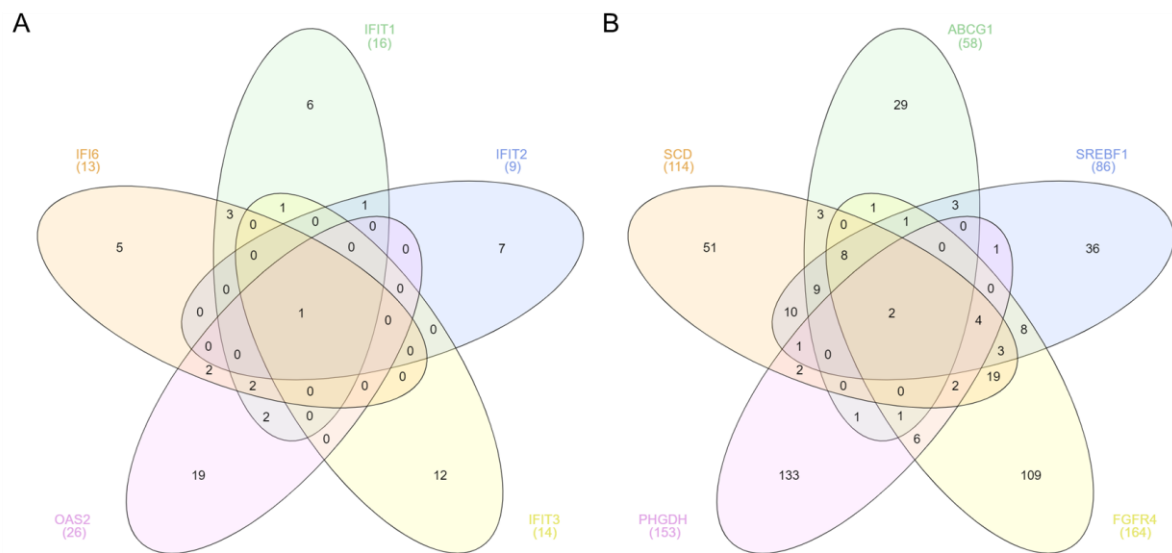
Supplementary Figure 1: The top 20 enriched GO terms from downregulated genes of ACE2^{high} vs. ACE2^{low} MCF-7 cells.



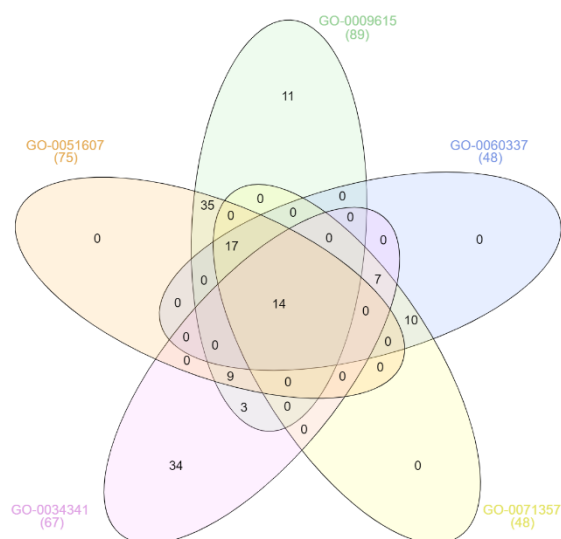
Supplementary Figure 2: Common disease annotations pattern of DEGs of ACE2^{high} vs. ACE2^{low} MCF-7 cells.

A: Disease annotations of the top 5 upregulated genes demonstrated a link to viral infections, most commonly to one disease term, influenza (disease id: C0021400)

B: the downregulated genes were annotated to two disease terms of BC (malignant tumor of breast (disease id: C0006142) and breast carcinoma (disease id: C0678222). The Venn diagram was made using InteractiVenn.

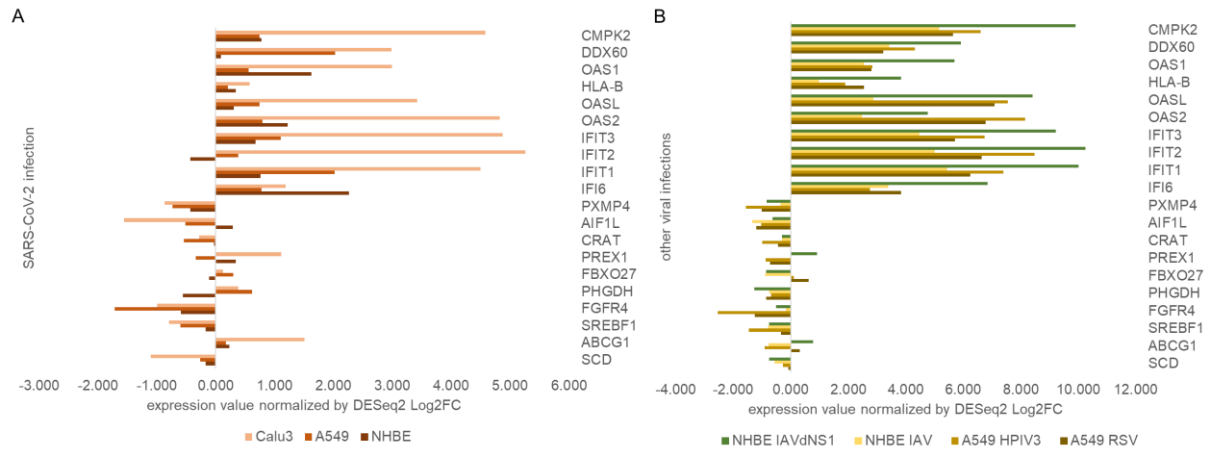


Supplementary Figure 3: Commonly enriched upregulated genes of DEGs of ACE2^{high} vs. ACE2^{low} MCF-7 cells. A Venn diagram was made to the top five GO terms, namely 'defense response to other organism', 'response to type I IFN', 'defense response to virus', 'response to virus', and 'type I IFN signaling pathway'. The 14 genes include OAS1, OAS2, OAS3, OASL, STAT1, IFITM3, IRF1, IRF2, IRF7, IRF9, BST2, IFITM1, IFITM2 and NLRC5.

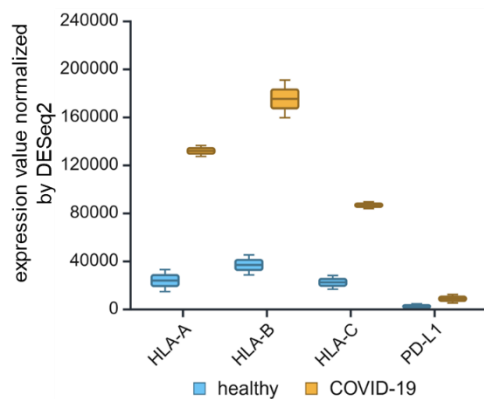


Supplementary Figure 4: Comparison of the upregulated gene profile of ACE2^{high} cells with the SARS-CoV-2 and other respiratory viruses infected cells (GEO accession: GSE147507).

A, B: top 10 up- and downregulated genes of ACE2^{high} MCF-7 cells with the SARS-CoV-2 infections (A) and other respiratory viruses such as IAV, IAVdNS1, HPIV3 and RSV (B).



Supplementary Figure 5: Transcriptional response of HLA-A, -B and -C and PD-L1 levels to SARS-CoV-2 infection in lung biopsies (n=2) compared to their healthy counterparts (GEO accession: GSE147507).



Supplementary Figure 6: Transcriptomic expressions of HLA-A, -B and -C in cell lines after infection with other respiratory viruses, such as IAV and IAVdNS1 on cell line NHBE, HPIV3 and RSV on cell line A549 (GEO accession: GSE147507).

