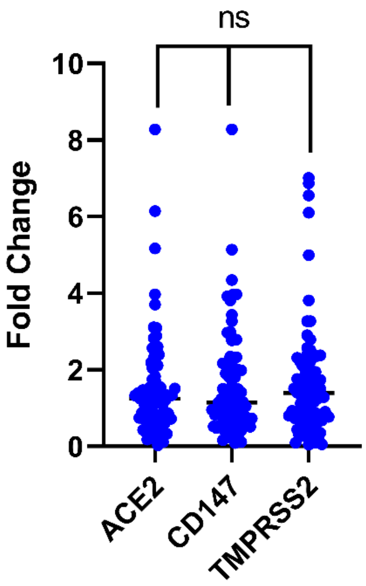
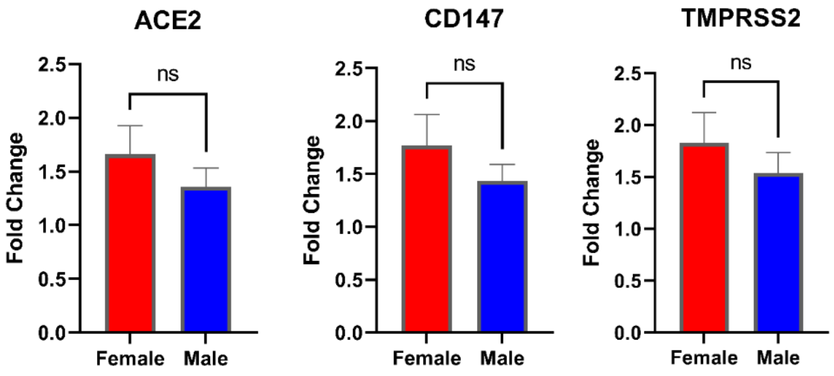
Supplementary Table 1. Primer Sequences used in the study

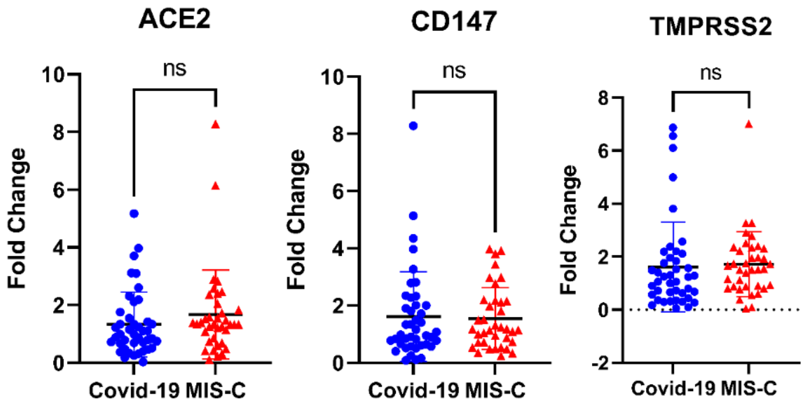
Target Gene	**Forward Primer**	**Reverse Primer**
ACE2	5’-TCCATTGGTCTTCTGTCACCCG-3’	5’-AGACCATCCACCTCCACTTCTC-3’
CD147	5’-GGCTGTGAAGTCGTCAGAACAC-3’	5’-ACCTGCTCTCGGAGCCGTTCA -3’
TMPRSS2	5’-CCTCTAACTGGTGTGATGGCGT-3’	5’-TGCCAGGACTTCCTCTGAGATG-3’
GAPDH	5’-GTCTCCTCTGACTTCAACAGCG-3’	5’-ACCACCCTGTTGCTGTAGCCAA-3’



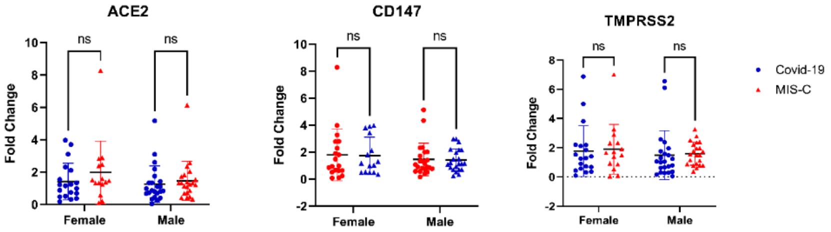
Supplementary Figure 1. Fold change of *ACE2*, *CD147*, and *TMPRSS2* in Nasopharyngeal Samples of Children. Fold changes were calculated from ΔΔCt values. Analysis was done by using the Kruskal-Wallis test. p=0.7576.



Supplementary Figure 2. Comparison of *ACE2*, *CD147*, and *TMPRSS2* Expression. Fold changes were calculated from ΔΔCt values. Analysis was done by using the Mann-Whitney two-tailed test. Error bars represent the standard error of the mean. P values for gender comparison of *ACE2, CD14,* and *TMPRSS2* genes are 0.3502, 0.9118, and 0.6666 respectively.



Supplementary Figure 3. Fold Change Differences of *ACE2*, *CD147*, and *TMPRSS2* in Covid-19 and MIS-C Groups. Analysis was done by using the nonparametric Mann-Whitney two-tailed test. Error bars represent the standard deviation of the mean. *P* values for *ACE2*, *CD147*, and *TMPRSS2* are 0.1327, 0.7159, and 0.1135 respectively.



Supplementary Figure 4. Comparison of the target genes in Covid-19 and MIS-C groups. Analysis was done by using multiple nonparametric Mann-Whitney two-tailed tests. Error bars represent the standard deviation of the mean.