

Table 1. Summary of the SARS-specific proteomic features identified by SELDI ProteinChip technology (Online Data Supplement)

| Mass, m/z (min – max) | Normalized Peak Intensities (Percentage of total peak intensity) in Pediatric Patients with SARS, mean (SD) | | Normalized Peak Intensity in Control Patients ^b , mean (SD) | Correlation with SARS-CoV RNA, r [P value] ^c | ROC curve area (SE), [P value] ^d |
|-----------------------------|---|---|--|---|---|
| | Earliest available plasma samples | Plasma samples at recovery [P value] ^a | | | |
| 11,710 (11,685 – 11,735) | 0.269 (0.277) | 0.024 (0.008), [0.008] | 0.041 (0.028) | 0.237 [0.037] | 0.952 (0.042), [0.001] |
| 78,300 (78,100 – 78,500) | 0.149 (0.083) | 0.079 (0.017), [0.008] | 0.093 (0.029) | 0.232 [0.041] | 0.800 (0.095), [0.026] |
| 84,700 (84,500 – 84,900) | 0.122 (0.033) | 0.049 (0.028), [0.008] | 0.052 (0.052) | 0.483 [< 0.0005] | 0.876 (0.076), [0.005] |
| 89,450 (89,250 – 89,650) | 0.111 (0.040) | 0.061 (0.021), [0.016] | 0.070 (0.032) | 0.341 [0.005] | 0.867 (0.077), [0.007] |
| 91,750 (91,550 – 91,950) | 0.098 (0.043) | 0.033 (0.028), [0.016] | 0.036 (0.031) | 0.431 [< 0.0005] | 0.886 (0.071), [0.004] |
| 94,650 (94,450 – 94,850) | 0.108 (0.044) | 0.051 (0.034), [0.039] | 0.039 (0.033) | 0.329 [0.006] | 0.924 (0.059), [0.002] |
| 98,250 (98,000 – 98,500) | 0.103 (0.032) | 0.022 (0.019), [0.008] | 0.022 (0.030) | 0.303 [0.011] | 0.981 (0.024), [< 0.0005] |
| 100,400 (100,150 – 100,650) | 0.112 (0.052) | 0.028 (0.013), [0.008] | 0.049 (0.040) | 0.434 [< 0.005] | 0.905 (0.065), [0.003] |
| 103,150 (102,900 – 103,400) | 0.060 (0.036) | 0.015 (0.013), [0.016] | 0.021 (0.022) | 0.408 [0.001] | 0.895 (0.069), [0.003] |
| 106,050 (105,800 – 106,300) | 0.055 (0.034) | 0.008 (0.008), [0.008] | 0.014 (0.020) | 0.353 [0.004] | 0.933 (0.052), [0.001] |
| 107,800 (107,550 – 108,050) | 0.056 (0.034) | 0.010 (0.009), [0.008] | 0.013 (0.018) | 0.371 [0.002] | 0.924 (0.056), [0.002] |
| 110,800 (110,550 – 111,050) | 0.050 (0.032) | 0.016 (0.007), [0.008] | 0.018 (0.018) | 0.275 [0.019] | 0.886 (0.076), [0.004] |
| 112,650 (112,350 – 112,950) | 0.041 (0.028) | 0.008 (0.004), [0.008] | 0.012 (0.015) | 0.259 [0.026] | 0.905 (0.065), [0.003] |
| 117,150 (116,850 – 117,450) | 0.036 (0.030) | 0.006 (0.003), [0.008] | 0.012 (0.015) | 0.251 [0.030] | 0.905 (0.064), [0.003] |
| 165,600 (165,100 – 166,100) | 0.015 (0.008) | 0.003 (0.001), [0.008] | 0.005 (0.004) | 0.353 [0.004] | 0.952 (0.044), [0.001] |

^a Compared with the paired earliest available SARS samples, Wilcoxon Signed Rank test;

^b Significantly different from the earliest available SARS samples (two-class unpaired test at a median false discovery rate of zero, SAM algorithm);

^c Correlation relationship between proteomic features and SARS-CoV RNA in the serial plasma samples of the 8 pediatric SARS patients (Spearman Rank Correlation test);

^d ROC curve analysis in differentiating 7 SARS samples (6 collected within the first week and 1 collected on the 8th day of admission) from the 15 control samples.