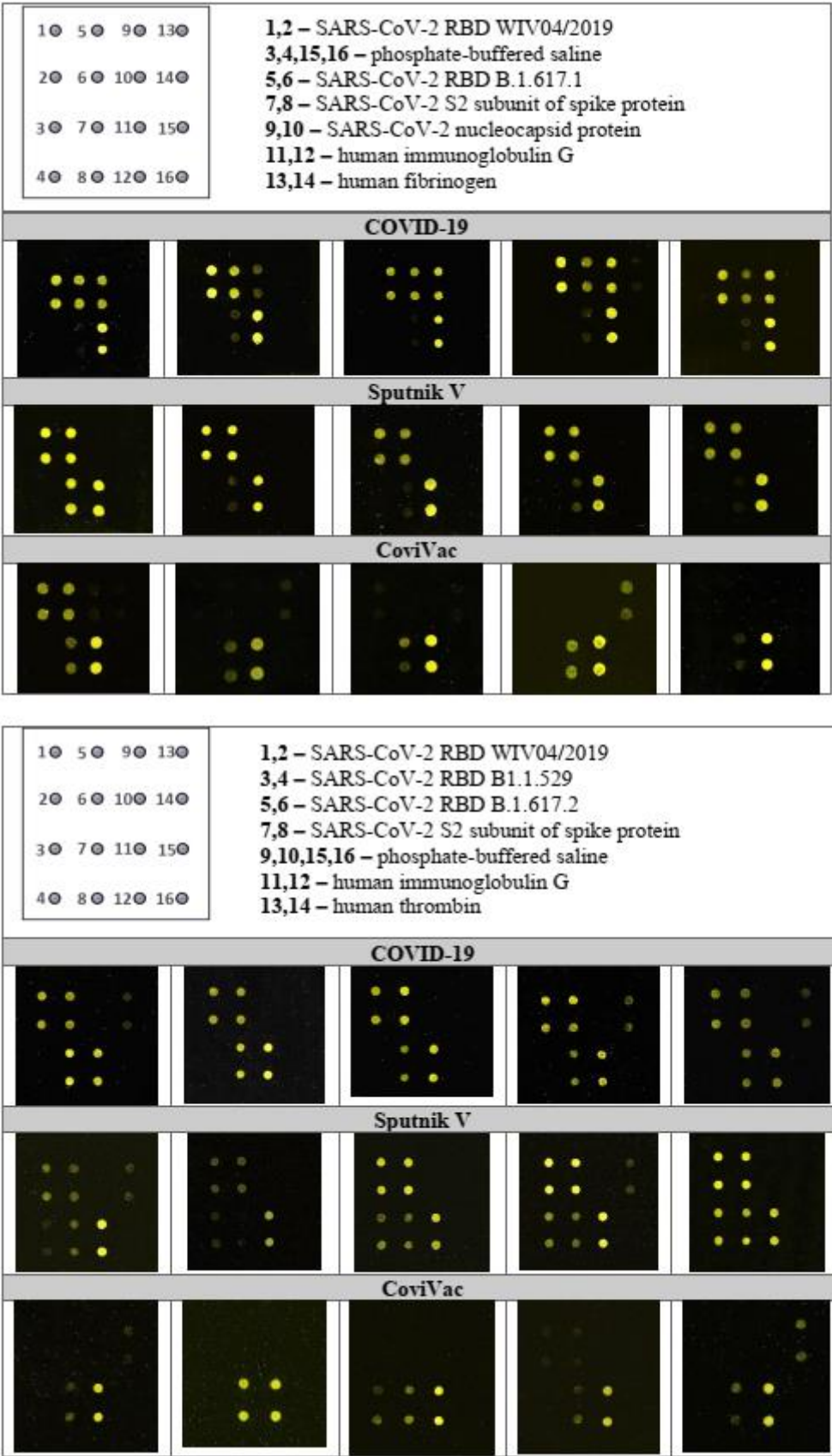


**Table S1.** Detailed information on serum samples tested in this study.

<b>Patient group</b>		
		<b>n=22</b>
Gender	Male	12
	Female	10
Median age (years)		59.0
Severity	Mild cases	14
	Moderate cases	6
	Hard cases	2
<b>Sputnik V group</b>		
		<b>n=31</b>
Gender	Male	16
	Female	15
Median age (years)		38.4
<b>CoviVac group</b>		
		<b>n=30</b>
Gender	Male	5
	Female	25
Age (years)		
<b>Control group</b>		
		<b>n=31</b>
Sample collection data (year)		2018

**Figure S1.** Examples of the array scans

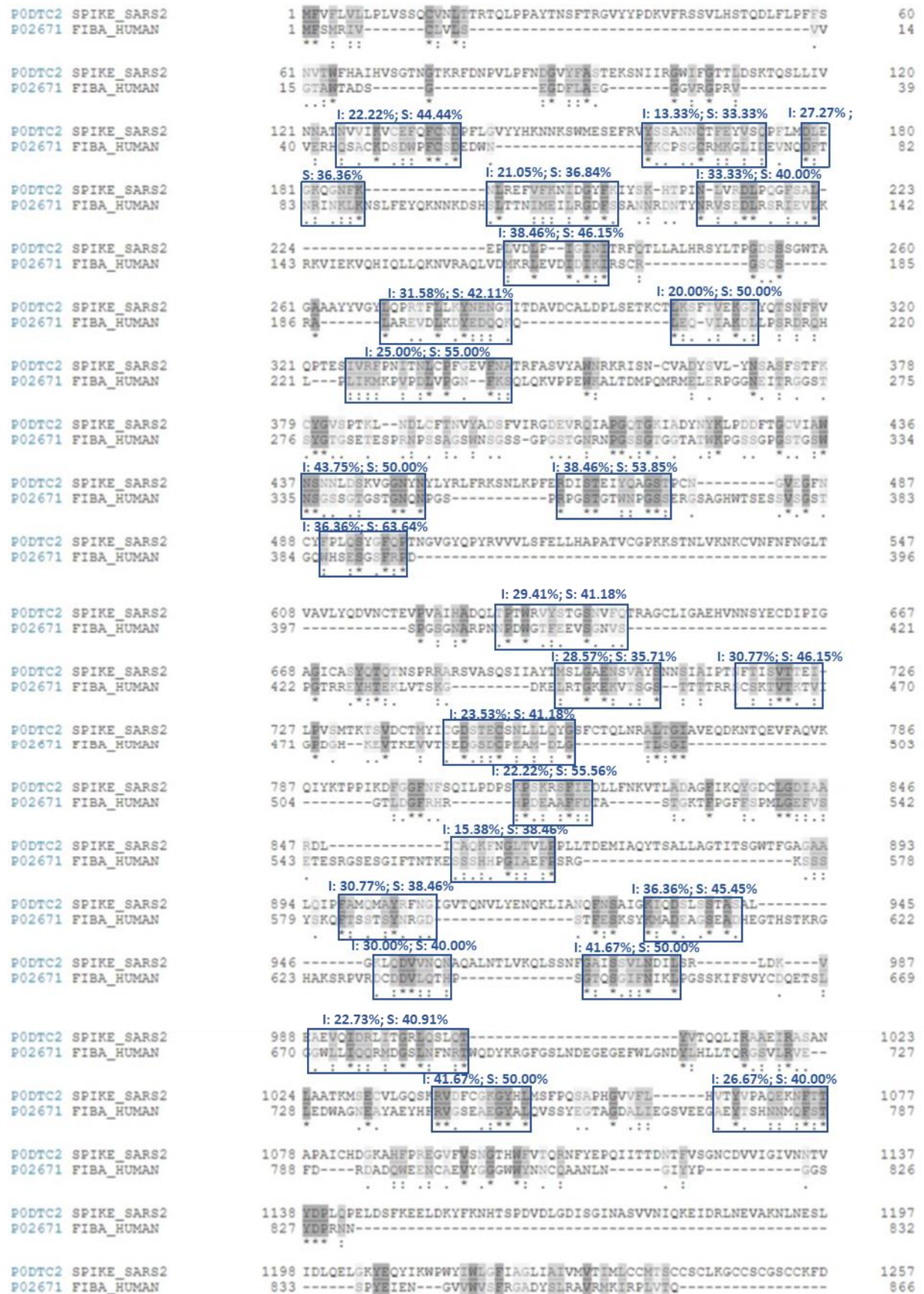


**Table S2.** Sensitivity, selectivity and accuracy for microarray method

	<b>RBD</b>	<b>S2</b>	<b>N</b>
<b>COVID-19 (n=60)</b>			
<b>True Positives</b>	29	29	30
<b>False Positives</b>	1	1	2
<b>True Negatives</b>	26	27	25
<b>False Negatives</b>	4	3	3
<b>Sensitivity</b>	0.89	0.84	0.90
<b>Specificity</b>	0.95	0.98	0.98
<b>AUC</b>	0.96	0.93	0.97

**Figure S2.** The sequence alignment of the SARS-Cov-2 S protein and human fibrinogen (Chain A)

I – Identity; S - Similarity

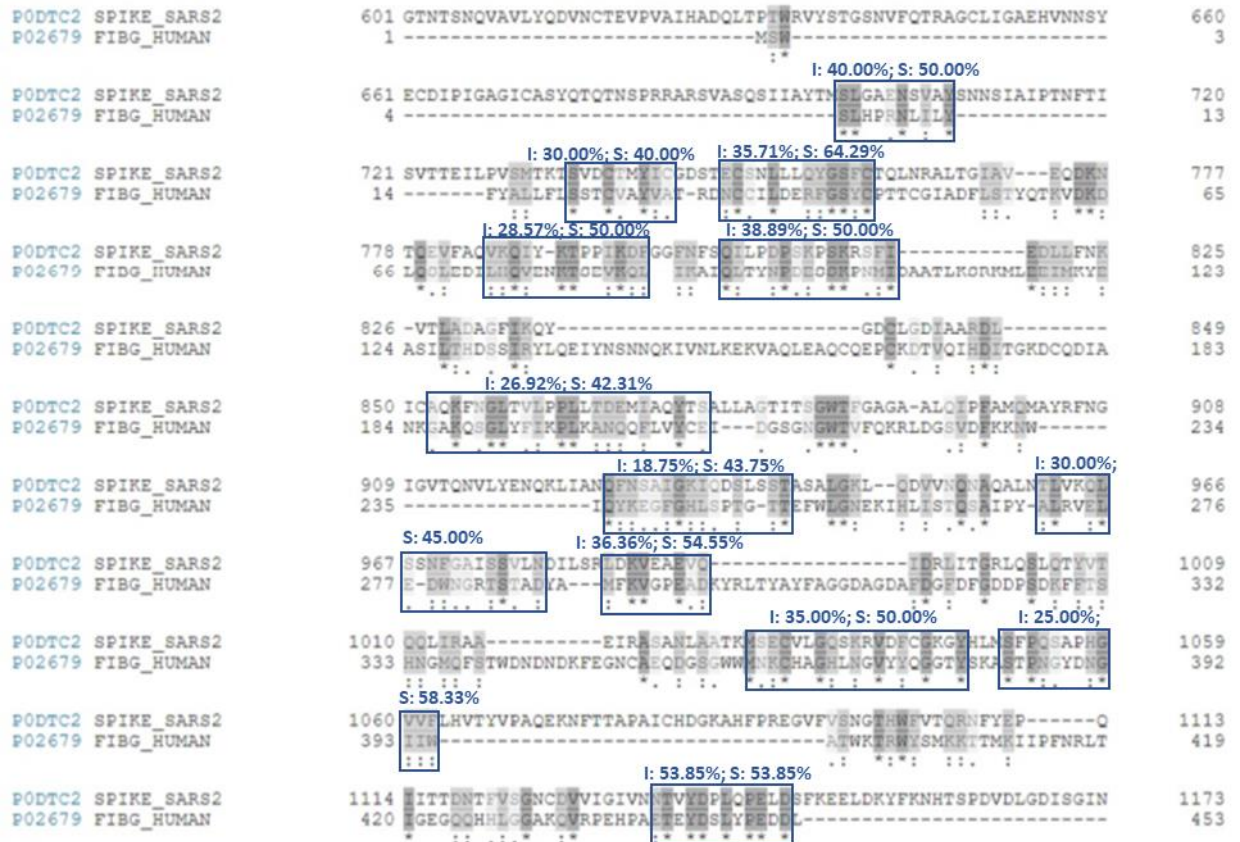






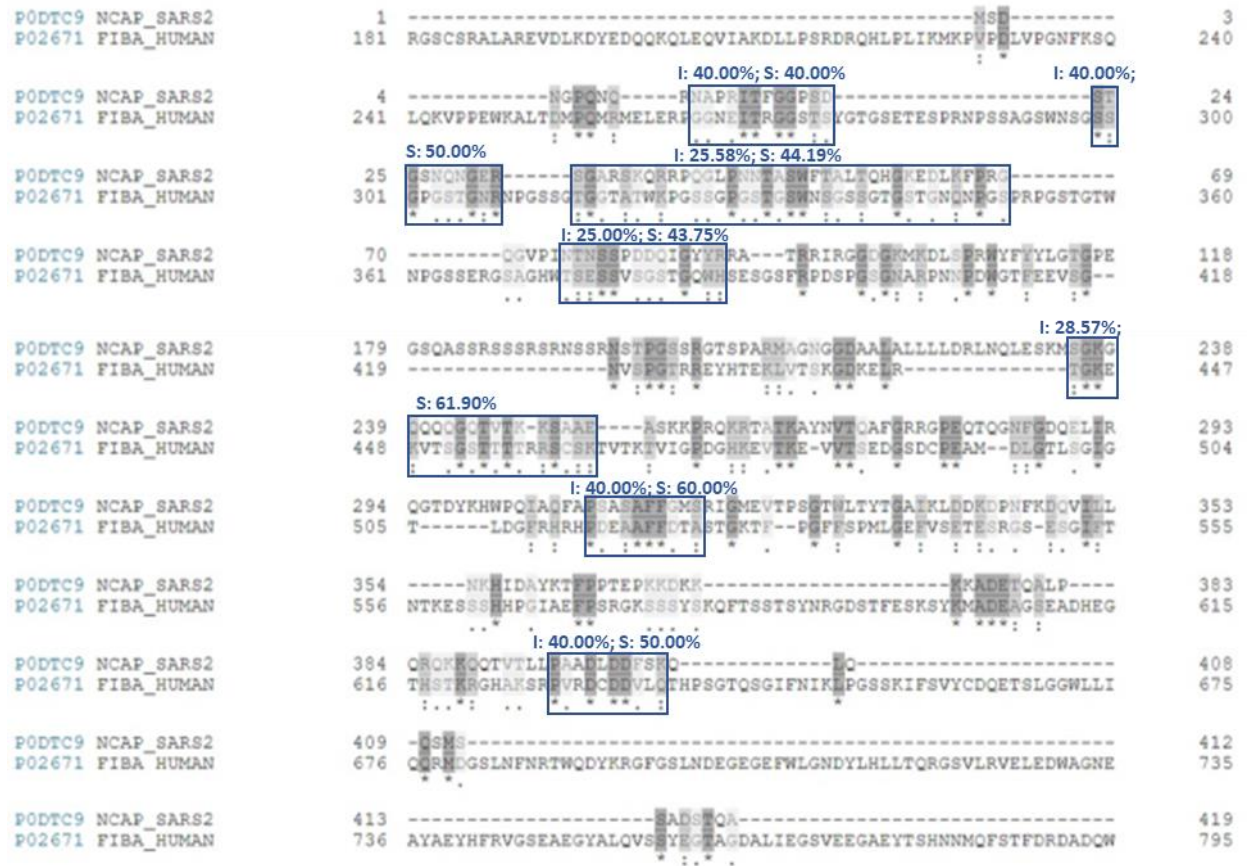
**Figure S4.** The sequence alignment of the SARS-Cov-2 S protein and human fibrinogen (Chain G)

I – Identity; S - Similarity



**Figure S5.** The sequence alignment of the SARS-Cov-2 N protein and human fibrinogen (Chain A)

I – Identity; S - Similarity



**Figure S6.** The sequence alignment of the SARS-Cov-2 N protein and human fibrinogen (Chain B)

I – Identity; S - Similarity

P0DTC9 NCAP_SARS2	1	-----MSDNGPQNG	9
P02675 FIBB_HUMAN	1	MKRMVSWSFHKLKTMKHLHLLLCVFLVKSQGVNDNEEGFFSARGHRPLDKKREEAPSLR	60
		:::*.:	
P0DTC9 NCAP_SARS2	10	RNAPRITFGGPSDSTGSNQNGERSGARSQRRPQGLPNNTASWFTALTQHGKEDLK--FP	67
P02675 FIBB_HUMAN	61	PAPPPISGGGYRARPAK-----AAATQKKVERKAPDAGG-C-----LHADFDLGVLCP	107
		* *: ** .. * : : : : * : . *.. ** *	
P0DTC9 NCAP_SARS2	68	RGQ-----GVPINTN-----	77
P02675 FIBB_HUMAN	108	TGCQLQEALLQQERPIRNSVDELNNNVEAVSQTSSTSSSQYMYLLKDLWQKQKQKQVDNEN	167
		* **..	
P0DTC9 NCAP_SARS2	78	-----SPDDQIGYYFRAT-----RRIRGGDG	99
P02675 FIBB_HUMAN	228	TVSCNIPFVVGKECEEIIRKGGTSEMYLIQPDSSVKPYFVYCDMNTENGWTVIQNRQD	287
		.....*	
P0DTC9 NCAP_SARS2	100	KMKDLSFRWYFYLLGTGPEAGLPYGANK---DGIWVATEGALNTPKDHIGTRNPANNAA	156
P02675 FIBB_HUMAN	288	GSVDFGRKWDPFYKQGFENVATNTDGKNYCGLPGEYWLGNDK-----ISQLTRMGPT	339
		*.: * * * * * * * * * * * * : : * . . :	
P0DTC9 NCAP_SARS2	157	IVLQLP--QGTTLPKGFYAEGSRGGSQASSRSSRSRNSRSTPGSSRGTSFARMAGNG	214
P02675 FIBB_HUMAN	340	LLIEMEDWKGDKV-----KAHYGGFTVQNEANK-----YQISVNKYRGTA	379
		: : : : * : . : . * * . . . . . *	
P0DTC9 NCAP_SARS2	215	GDAALALLLLDRLNQLESKMSGKGQ---QQGQTV---TKKSAAEA	268
P02675 FIBB_HUMAN	380	GNA-----LMDGASQL---MGENRTMTIHNGMFFSTYDRDNDGWLTS	425
		*:* *:* .** *: : : * : . : . . . . .	
P0DTC9 NCAP_SARS2	269	NVTQAFGRRGPEQTQGNFGDQELIRQGTDYKHWPQIAQ-FAPSASAFFG-----MSRIG	321
P02675 FIBB_HUMAN	426	-----KEDGGGWYNRCHAANPNRGYYWGGQYTWDMAKHG	460
		: . * : : * . . : * * : *	
P0DTC9 NCAP_SARS2	322	MEVTHSGTWLTYTGR	381
P02675 FIBB_HUMAN	461	--TDIGVVWMNWKGSWYSMR-----KMSMKIRPFFFPQQ-----	491
		. . . * : : : *	

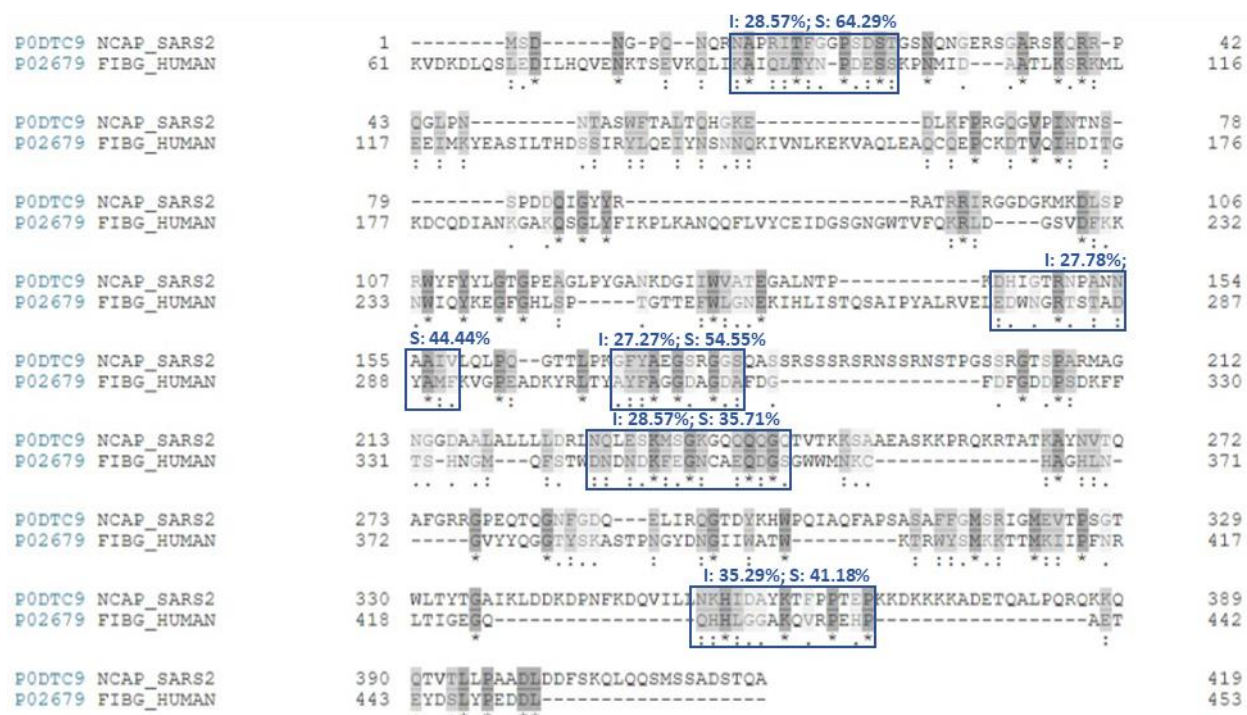
I: 40.00%; S: 50.00%

I: 36.36%; S: 54.55%

I: 27.27%; S: 54.55%

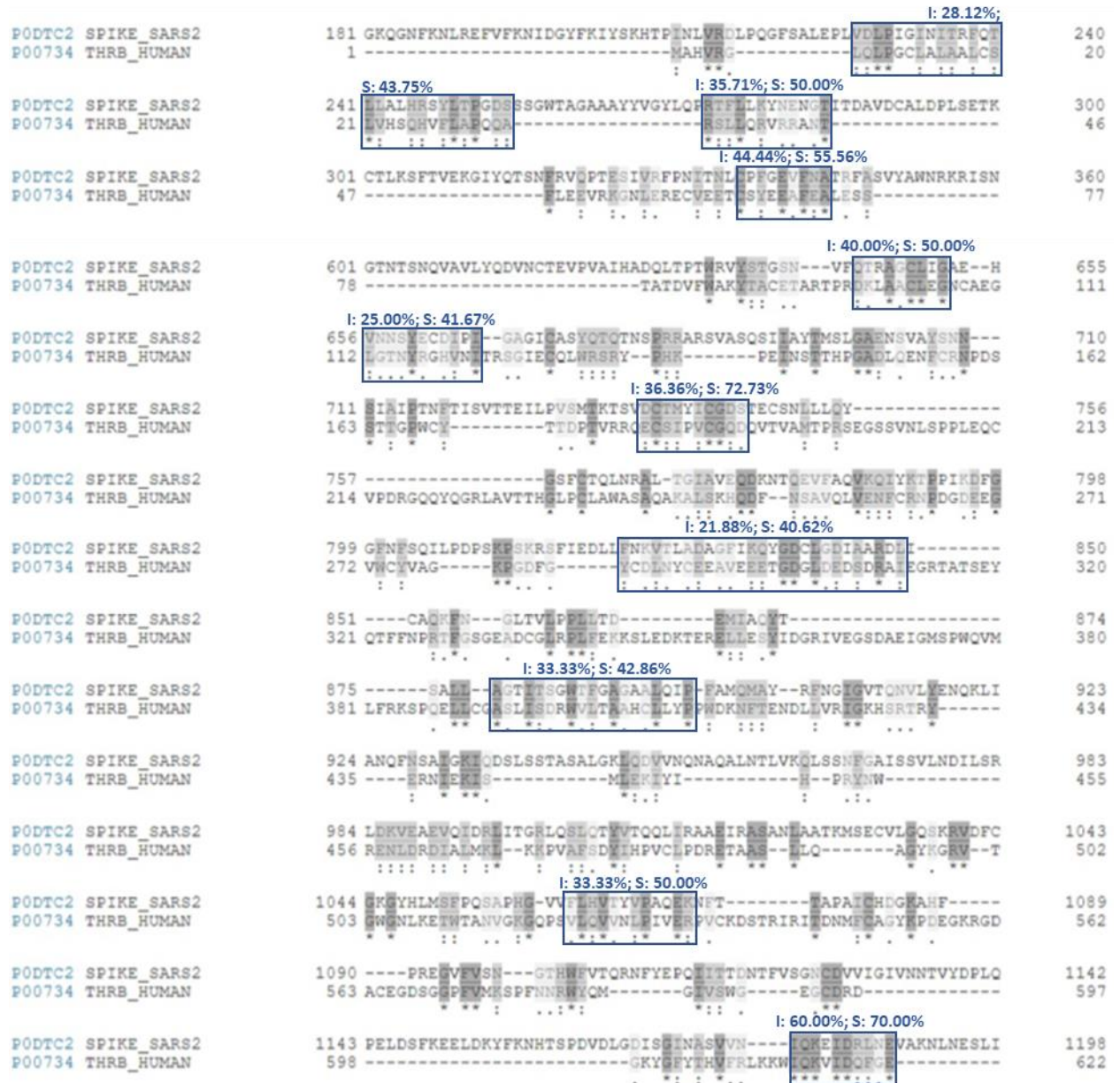


I – Identity; S - Similarity



**Figure S8.** The sequence alignment of the SARS-Cov-2 S protein and human prothrombin

I – Identity; S - Similarity



**Figure S9.** The sequence alignment of the SARS-Cov-2 N protein and human prothrombin

I – Identity; S - Similarity

