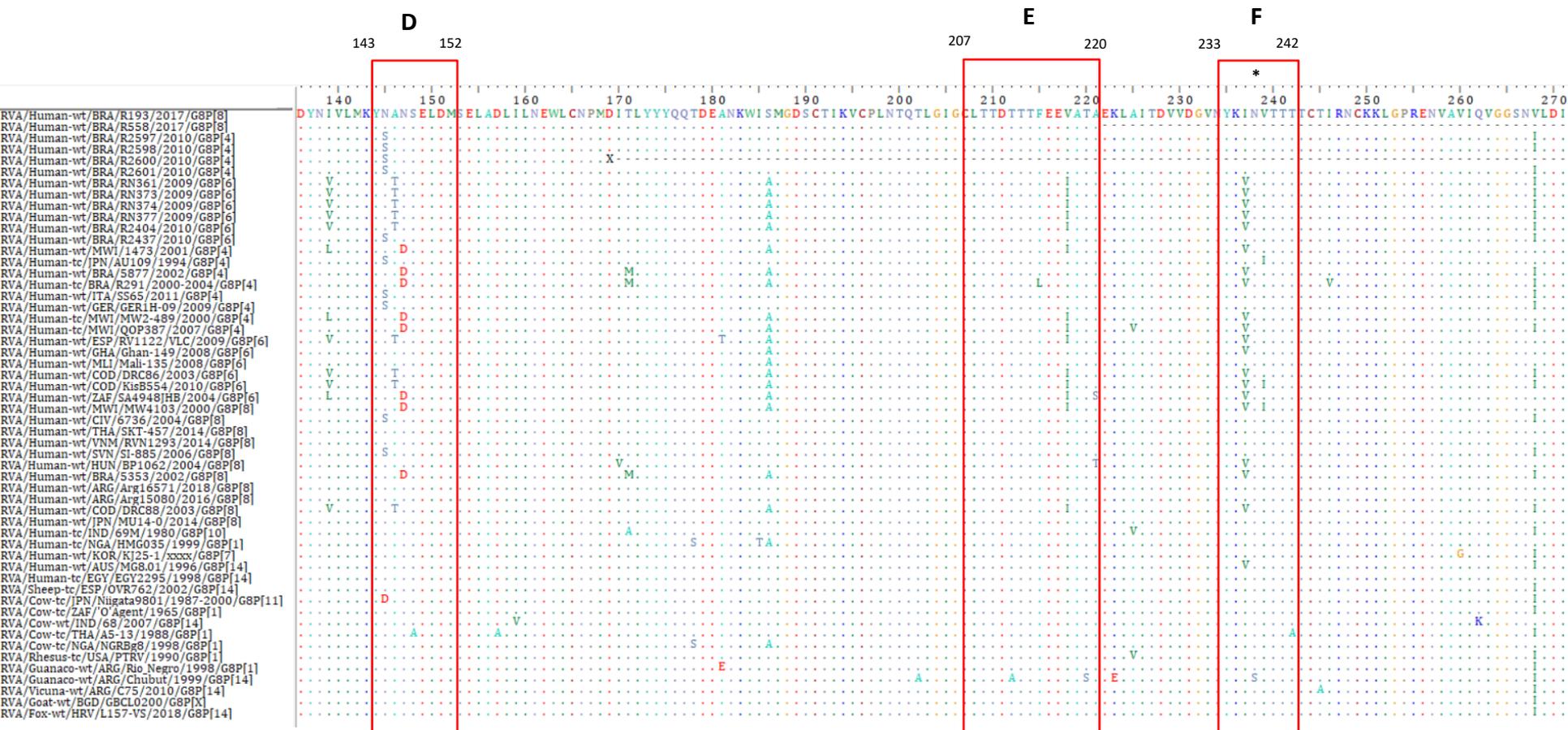
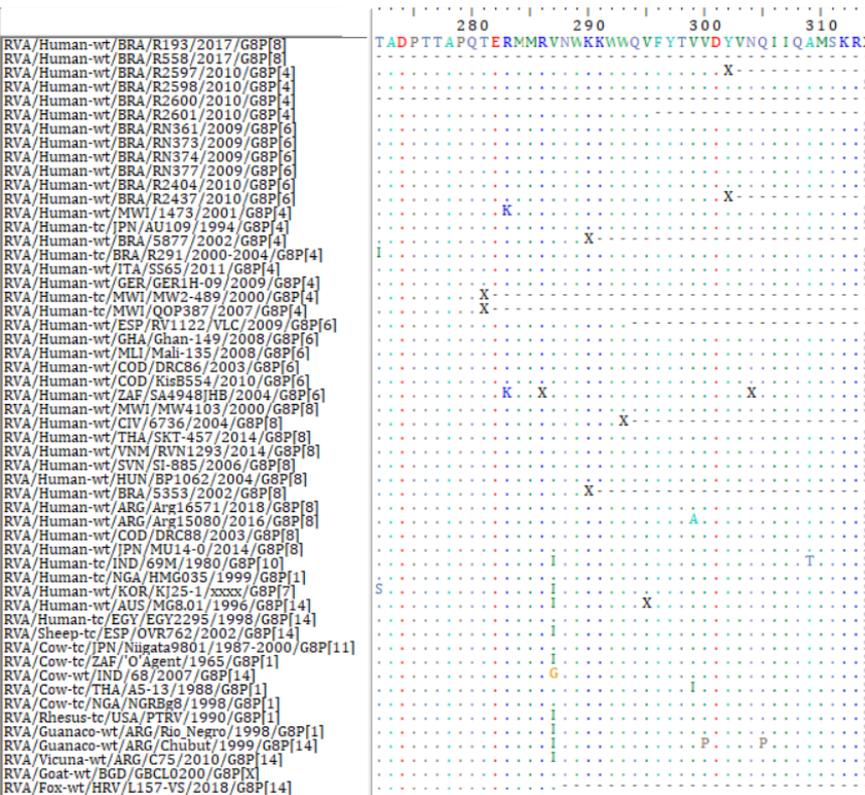


Supplement S1. Length and nucleotide position of each gene segment of the human rotavirus G8 strains detected in Brazil, 2007-2020.

Gene segment	Size (nt)	Encoded protein	ORF position (nt)	IAL-R193 G8P[8]		IAL-R558 G8P[8]		IAL-R2601 G8P[4]		IAL-R2600 G8P[4]		IAL-R2598 G8P[4]		IAL-R2597 G8P[4]		IAL-R2437 G8P[6]		IAL-R2404 G8P[6]		IAL-RN377 G8P[6]		IAL-RN374 G8P[6]		IAL-RN373 G8P[6]		IAL-RN361 G8P[6]	
				Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)	Size (nt)	Position (nt)
1	3,302	VP1	19-3,285	677	1-676	648	1-645	663	16-678	606	16-621	598	16-613	620	16-635	604	8-611	606	8-613	606	8-613	605	8-612	671	8-678	606	8-613
2	2,690	VP2	17-2,656	648	2-649	653	1-653	610	51-660	608	53-660	595	66-660	600	61-660	649	12-660	649	12-660	649	12-660	648	13-660	648	13-660	648	13-660
3	2,591	VP3	50-2,557	697	6-702	652	2-653	629	50-678	629	50-678	612	50-661	629	50-678	643	45-687	609	45-653	639	45-683	634	45-678	634	45-678	524	456-979
4	2,362	VP4	10-2,337	771	64-834	767	73-839	756	73-828	781	56-836	747	77-823	750	75-824	753	78-830	763	73-835	766	77-842	731	104-834	766	78-843	759	71-829
5	1,611	NSP1	11-1,492	770	612-1381	1451	62-1512	1512	10-1521	956	573-1528	928	582-1509	811	586-1396	947	575-1521	797	576-1372	994	573-1566	794	576-1369	770	572-1341	881	636-1516
6	1,356	VP6	24-1,217	1270	15-1284	1306	35-1340	1250	35-1284	1292	35-1326	1203	90-1292	1241	60-1300	1297	35-1328	1281	42-1322	1290	38-1327	1294	35-1328	1285	36-1320	1094	119-1212
7	1,104	NSP3	16-948	472	144-615	886	125-110	804	202-1005	765	221-985	804	202-1005	962	43-1004	938	40-977	918	60-977	960	47-1006	966	43-1008	967	40-1006	914	68-979
8	1,059	NSP2	30-983	429	257-685	683	328-1010	779	83-861	940	57-996	782	66-847	954	62-1015	923	79-1001	916	83-998	837	53-889	588	415-1002	930	61-988	863	124-986
9	1,062	VP7	49-1,029	914	75-988	711	1-711	879	55-933	449	106-554	930	65-994	925	29-953	925	29-953	801	194-994	944	58-1001	773	226-998	937	58-994	725	279-1003
10	751	NSP4	42-569	663	49-711	666	47-712	613	59-671	664	45-708	663	46-708	661	42-702	706	2-707	666	46-711	630	47-676	602	45-646	637	38-674	582	59-640
11	667	NSP5/6	5-598	612	1-612	667	1-667	667	1-667	667	1-667	667	1-667	667	1-667	667	1-667	667	1-667	667	1-667	667	1-667	667	1-667	667	1-667
Total genome	18,474	-	-	7,923	-	9,090	-	9,192	-	8,357	-	8,529	-	8,820	-	9,052	-	8,673	-	8,982	-	8,302	-	8,912	-	8,263	-

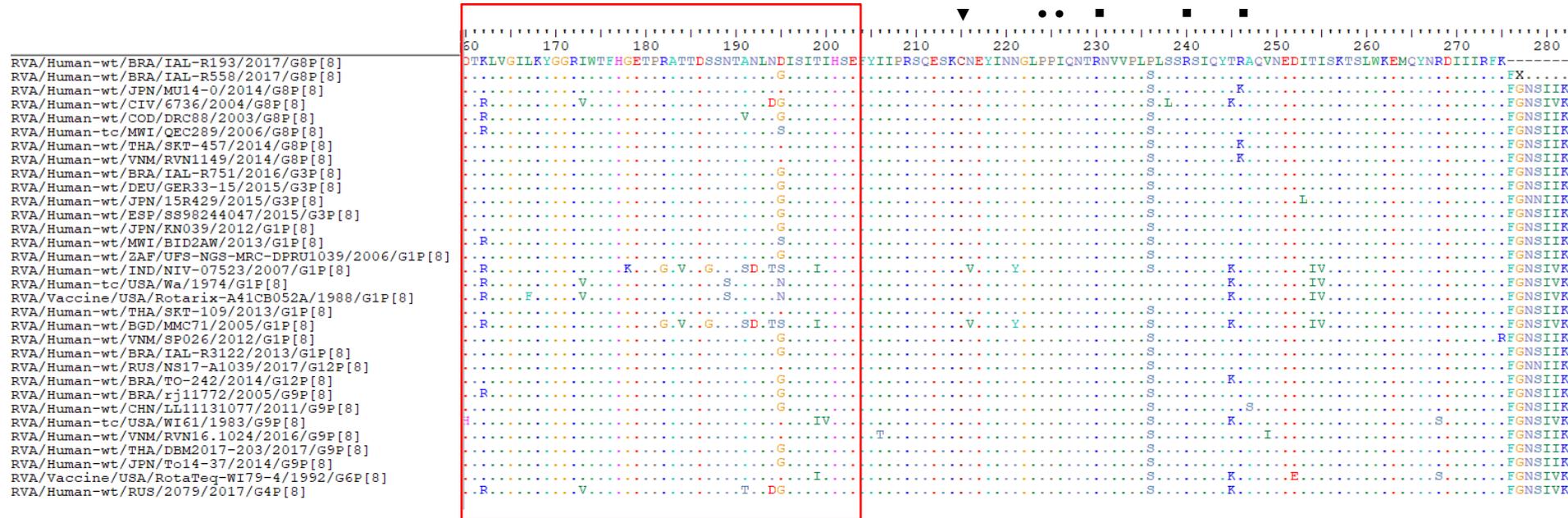




Supplement S2. Deduced amino acid sequence of the VP7 protein of human G8 RVA strains detected in Brazil from 2007-2020. The VP7 antigenic regions A–F are indicated. The N-linked glycosylation sites at positions 69-72 and 238-241 are indicated by asterisks.

Hypervariable region

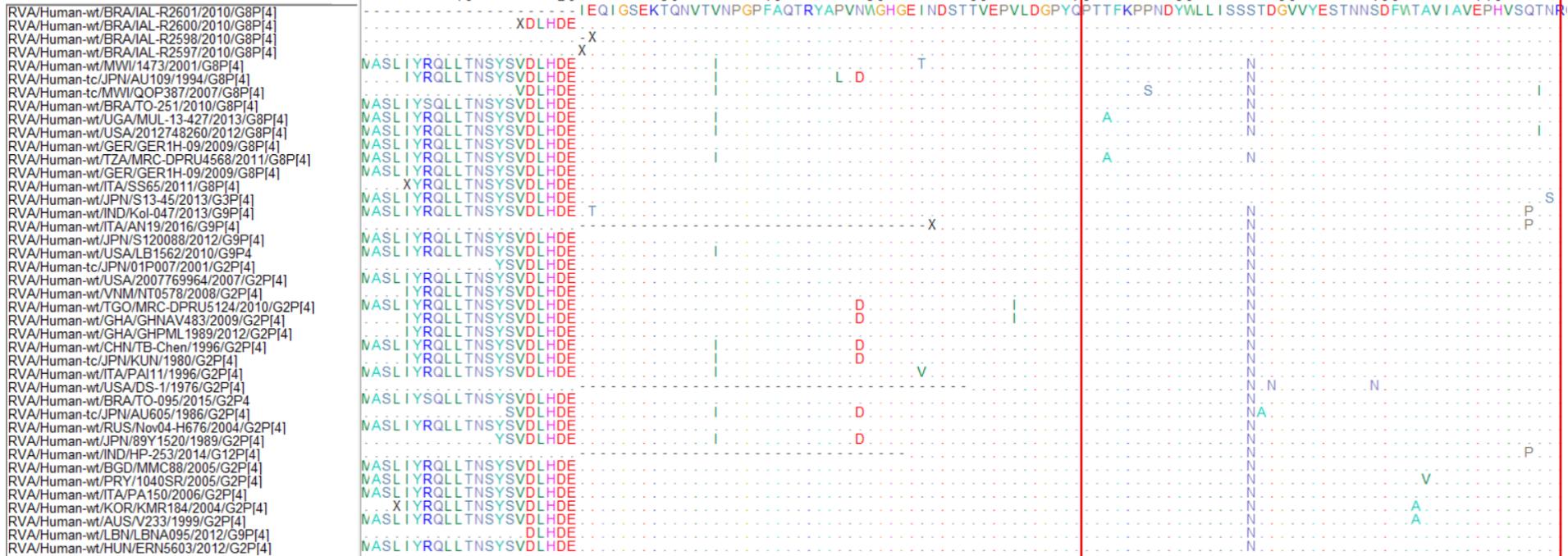
204



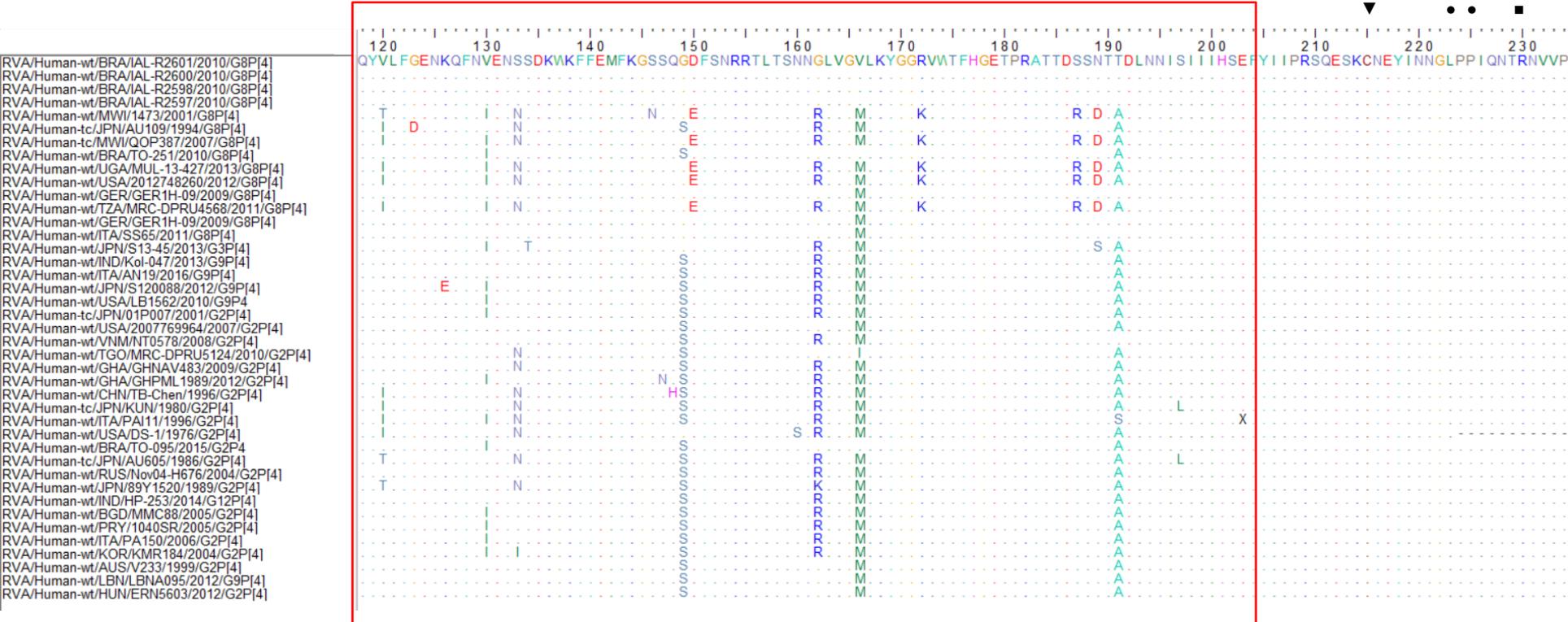
Supplement S3. Deduced amino acid sequence of the VP8* trypsin cleavage product of the VP4 protein of the human rotavirus G8P[8] strains detected in Brazil, 2007-2020, and of a selection of P[8] rotaviruses. The hypervariable region (aa 71–204), and the highly conserved cysteine (▼), proline (●) and arginine (■) are indicated.

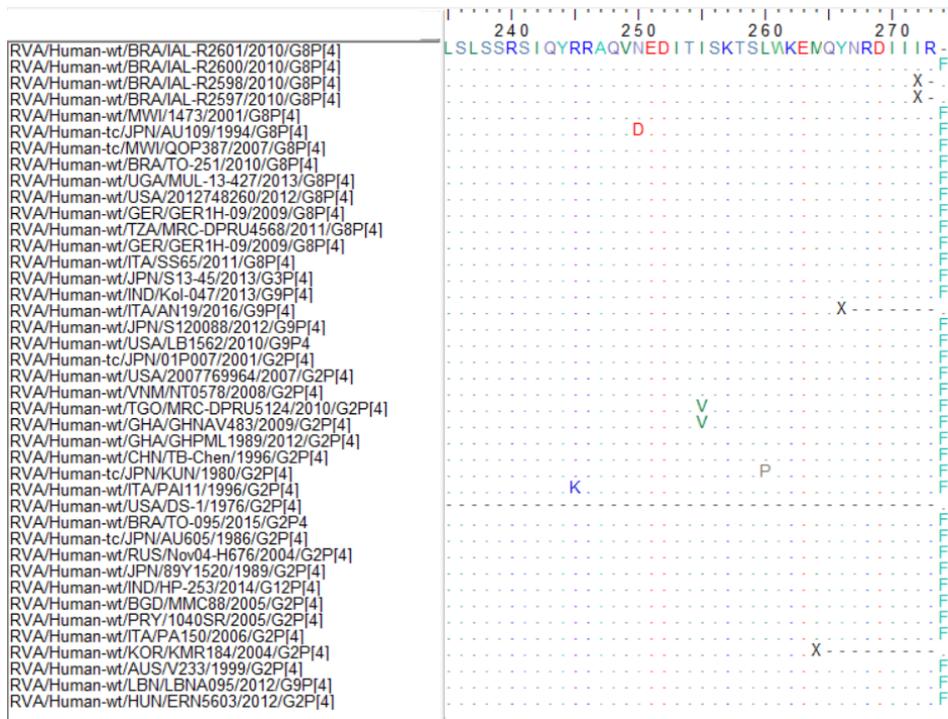
Hypervariable region

71



Hypervariable region





Supplement S4. Deduced amino acid sequence of the VP8* trypsin cleavage product of the VP4 protein of the human rotavirus G8P[4] strains detected in Brazil, 2007-2020, and of a selection of P[4] rotaviruses. The hypervariable region (aa 71–204), and the highly conserved cysteine (▼), proline (●) and arginine (■) are indicated.

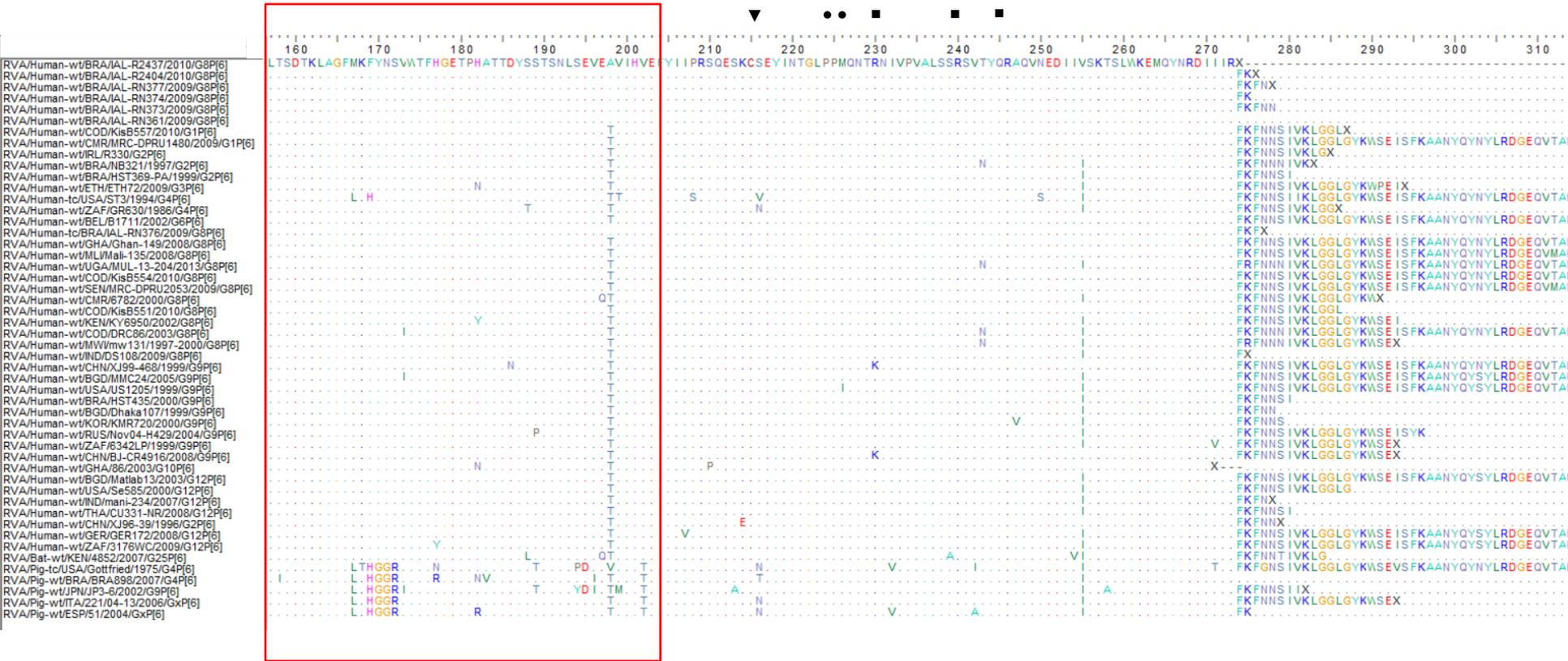
Hypervariable region

71

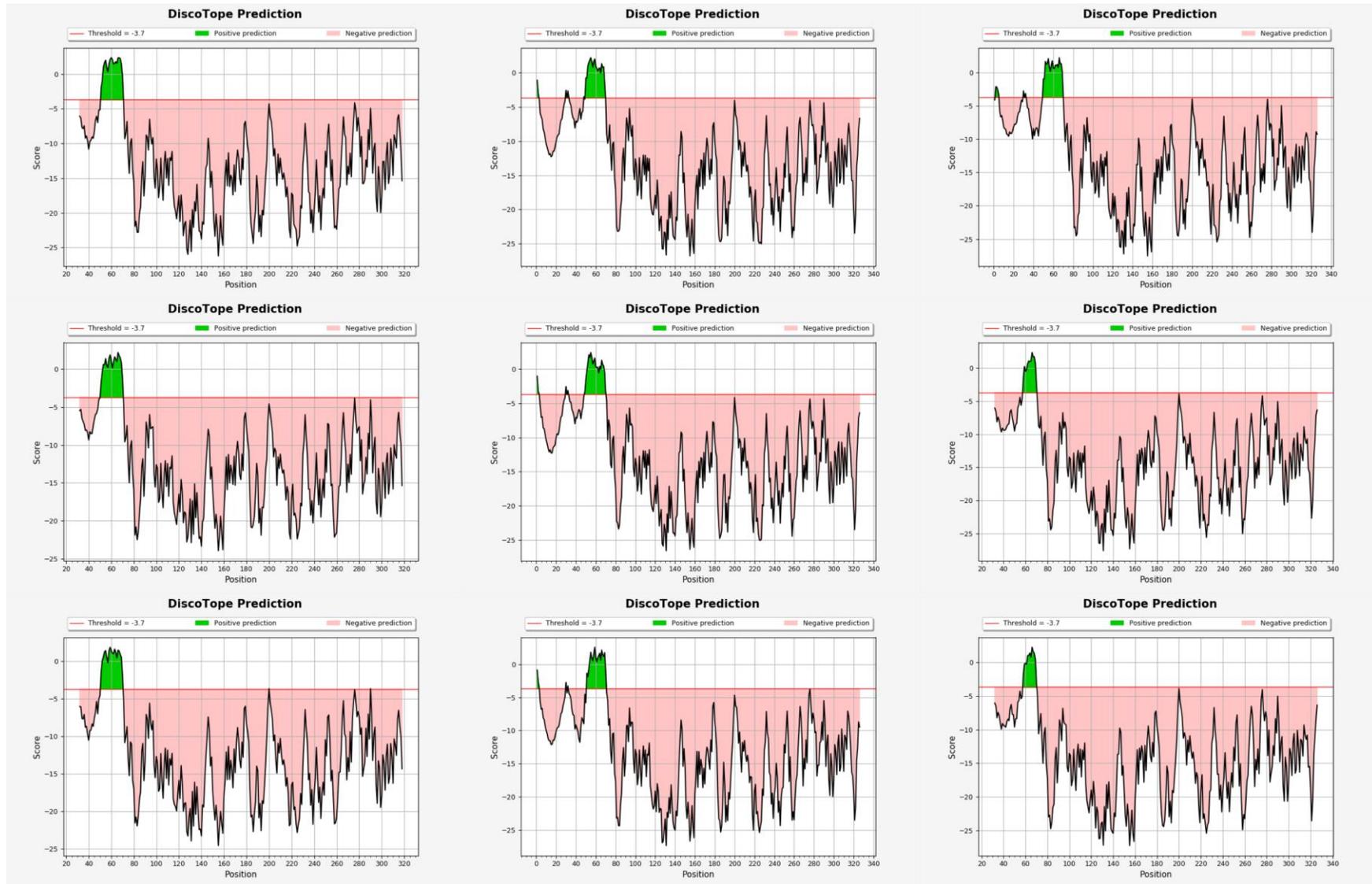


Hypervariable region

204



Supplement S5. Deduced amino acid sequence of the VP8* trypsin cleavage product of the VP4 protein of the human rotavirus G8P[6] strains detected in Brazil, 2007-2020, and of a selection of P[6] rotaviruses. The hypervariable region (aa 71–204), and the highly conserved cysteine (▼), proline (●) and arginine (■) are indicated.



Supplement S6. Conformational B Cell Epitope predictions. Modeled structures were inspected individually for elucidation of potential discontinuous epitopes using IEDB website (<https://www.iedb.org/>).