

Table S1. Amino acid changes identified in the Sicilian dataset of hRSV-A protein G gene sequences and relative frequency. AA substitution and position are defined in comparison with the ON1 prototype strain ON67-1210A (GenBank accession number: JN257693).

Position	Substitution	Frequency (%)	Position	Substitution	Frequency (%)
7	Q --> L/R	2.7	147	T --> I	0.8
9	T --> A	2.7	149	K --> R	0.8
26	I --> T	0.9	151	R --> H	7.0
57	A --> V	5.4	152	Q --> K	0.8
67	H --> N/Q	3.1	154	K --> R	0.8
69	V --> F	0.8	161	N --> D	0.8
71	L --> P	2.3	163	F --> L	0.8
78	D --> N	0.8	173	C --> W	0.8
80	T --> A/M	7.0	178	N --> D/G	8.5
82	Q --> R	0.8	193	K --> R	0.8
86	T --> I	0.8	200	T --> I/P	2.3
93	Q --> L/R	1.6	206	P --> Q	20.2
98	G --> E	0.8	209	K --> R	7.0
99	I --> T	1.6	210	T --> I/S	2.3
100	S --> N	1.6	214	D --> E	1.6
101	F --> L/S	5.4	215	P --> L/S	3.1
102	S --> F/T	5.4	216	K --> N/R	5.4
106	G --> E	4.6	222	P --> L	2.3
107	T --> A	0.8	224	E --> G/K/V	13.9
108	T --> I	0.8	225	V --> A	9.3
111	S --> F/P	13.2	226	L --> F/P	2.3
113	T --> I	7.7	227	T --> I	2.3
114	I --> T	0.8	230	P --> T	5.4
115	L --> P	3.1	231	T --> A	0.8
120	P --> L	0.8	232	G --> R	5.4
128	S --> P/T	9.3	234	P --> L	7.0
130	T --> I	1.6	235	T --> A	0.8
131	V --> I/D	8.5	239	T --> A	0.8
132	K --> E	0.8	240	K --> R/E	0.8
133	I --> V/T	4.6	241	T --> P	0.8
134	K --> I	34.1	243	I --> S	33.3
135	N --> K/T	3.1	245	T --> A	0.8
137	T --> A	1.6	247	L --> P/Q	8.5
140	Q --> R	0.8	248	L --> I	20.9
142	L --> S	13.2	249	T --> N	0.8
144	S --> I	0.8	250	S --> F	4.6
146	P --> L/S/T	22.5	253	K --> R	8.5
			254	G --> E/R	1.6

Position	Substitution	Frequency (%)
255	N --> D/S	3.1
256	P --> S	3.1
257	E --> K	3.1
258	H --> Q/Y	20.9
262	E --> K	34.1
263	E --> G/K	8.5
265	L --> F/I	6.2
266	H --> L	7.7
267	S --> L	3.1
270	S --> F/P/Y	3.9
271	E --> D/K	7.0
272	G --> S	2.3
273	Y --> H/S	7.7
274	L --> P	58.1
275	S --> G/N	3.1
276	P --> Q/S	2.3
278	Q --> L	2.3
279	V --> I	1.6
280	Y --> H	3.1
284	G--> D/S	10.1
285	Q --> R	4.6
287	E --> D/G/K	2.3
289	L --> P	5.5
291	S --> L	11.7
294	S --> P/Y	2.3
295	E --> G/K/V	3.9
296	G --> S	6.2
298	L --> P/S	77.3
299	S --> I	0.8
300	P --> S	3.1
303	V --> A/I	21.9
304	Y --> H	57.0
306	T --> I	1.6
308	E --> K	2.3
310	L --> P	29.5
311	S --> P	7.0
313	S --> F	3.9
314	L --> P	25.6
317	S --> F	6.2
319	T --> A/I/S	13.2
320	T --> A/I/K	34.1