

**Table S3.** Amino acid changes identified in the Sicilian dataset of hRSV-B protein G gene sequences and relative frequency. AA substitution and position are defined in comparison with the BA9 prototype strain BA4128/99B (GenBank accession number: AY333364).

Position	Substitution	Frequency (%)	Position	Substitution	Frequency (%)
<b>5</b>	K --> R	1.0	<b>135</b>	G --> D/S	2.8
<b>6</b>	N --> S	1.0	<b>136</b>	R --> I/T	99.4
<b>18</b>	D --> N	2.0	<b>137</b>	T --> I	22.2
<b>57</b>	A --> T	1.2	<b>138</b>	T --> S	100.0
<b>69</b>	V --> I	0.6	<b>140</b>	P --> L/S	7.9
<b>74</b>	V --> I	0.6	<b>142</b>	Q --> H/K	2.8
<b>76</b>	V --> I	4.0	<b>143</b>	N --> K/S	1.1
<b>87</b>	I --> M/T	3.5	<b>144</b>	N --> H	0.6
<b>90</b>	Y --> H	0.6	<b>149</b>	K --> E	0.6
<b>91</b>	L --> P	8.6	<b>152</b>	P --> S	0.6
<b>94</b>	V --> I	0.6	<b>154</b>	N --> K	4.5
<b>97</b>	E --> D	0.6	<b>156</b>	P --> S	1.1
<b>98</b>	R --> K	1.1	<b>157</b>	K --> *	100.0
<b>99</b>	V --> A	0.6	<b>159</b>	K --> *	100.0
<b>100</b>	S --> G/N	10.3	<b>171</b>	V --> I	0.5
<b>102</b>	S --> P	0.6	<b>174</b>	S --> G	0.5
<b>105</b>	L --> P	100.0	<b>175</b>	I --> V	1.1
<b>106</b>	T --> I	0.5	<b>177</b>	G --> S	0.5
<b>107</b>	T --> A/D	99.4	<b>192</b>	N --> S	0.5
<b>108</b>	T --> A/P	2.3	<b>194</b>	P --> Q	2.2
<b>109</b>	P --> Q/S	2.3	<b>199</b>	T --> A	0.5
<b>110</b>	P --> L/S	2.3	<b>200</b>	I --> T	100.0
<b>112</b>	Y --> H/Q	99.4	<b>204</b>	N --> K/T	1.7
<b>113</b>	T --> I/M	1.0	<b>205</b>	K --> Q	0.5
<b>115</b>	S --> L/P	4.0	<b>206</b>	P --> S	1.1
<b>116</b>	A --> T	2.3	<b>207</b>	P --> T	0.5
<b>117</b>	T --> A	1.1	<b>209</b>	K --> E	0.5
<b>118</b>	I --> T	3.4	<b>211</b>	T --> K	3.9
<b>120</b>	P --> T	2.3	<b>212</b>	N --> T	0.5
<b>121</b>	N --> T	1.4	<b>213</b>	K --> E	0.5
<b>122</b>	T --> A	0.6	<b>214</b>	R --> K	1.1
<b>124</b>	S --> L	2.3	<b>215</b>	D --> H/Y	3.3
<b>126</b>	T --> A	1.4	<b>216</b>	P --> L/S	12.1
<b>128</b>	H --> Y	0.6	<b>217</b>	K --> I	0.5
<b>129</b>	T --> K	0.6	<b>218</b>	K --> P/T	100.0
<b>130</b>	T --> I	17.6	<b>219</b>	L --> P	100.0
<b>131</b>	A --> T	23.3	<b>220</b>	A --> S	0.5
<b>133</b>	T --> A	1.1	<b>222</b>	T --> P	0.5

Position	Substitution	Frequency (%)
223	L --> M/P/S/T	89.5
224	K --> E	0.5
225	K --> E	1.1
227	T --> A/N	19.3
228	T --> A	1.7
229	I --> T	7.7
231	P --> L/S	5.5
232	T --> A	0.5
233	K --> R	0.5
234	K --> N	0.5
236	T --> I	0.5
237	P --> L/S	2.2
239	T --> I	0.5
240	T --> K	1.7
243	D --> G/N	3.9
244	T --> S	0.5
245	S --> N	1.7
247	S --> P	98.3
249	S --> P	2.2
251	V --> A/M	2.2
252	L --> F/P	2.2
254	T --> I	73.5
255	T --> N	0.5
256	T --> I/S	2.2
257	S --> P	2.8
258	K --> N/R	9.4
259	H --> Q	0.5
260	T --> K	0.5
261	E --> K	1.1
263	D --> E/N/Y	2.2
267	S --> L/P	12.7
269	S --> F	1.7
270	T --> A/I	79.0
271	V --> A	91.7
272	L --> F/P	9.4
277	S --> P	8.3
281	I --> T	99.4
282	Q --> L	1.1
284	Q --> L	2.2
285	S --> F/P	1.7
286	L --> P	5.0
287	H --> Y	76.8

Position	Substitution	Frequency (%)
290	T --> I	39.2
291	P --> S	1.7
292	E --> K/Q	1.1
296	N --> S/F	1.1
297	S --> M	0.5
302	T --> A/I	1.1
303	A --> P/T	10.5
304	S --> F	2.2
305	E --> D/K	3.9
306	P --> S	0.5
307	S --> P/Y	1.1
308	T --> I	0.5
309	S --> P	0.5
312	T --> A/F/I/N	32.6
313	Q --> *	84.0
314	K --> R	87.3
316	* --> Q	92.8
317	S --> P	1.1
318	Y --> C	0.5
322	F --> I/S	1.1