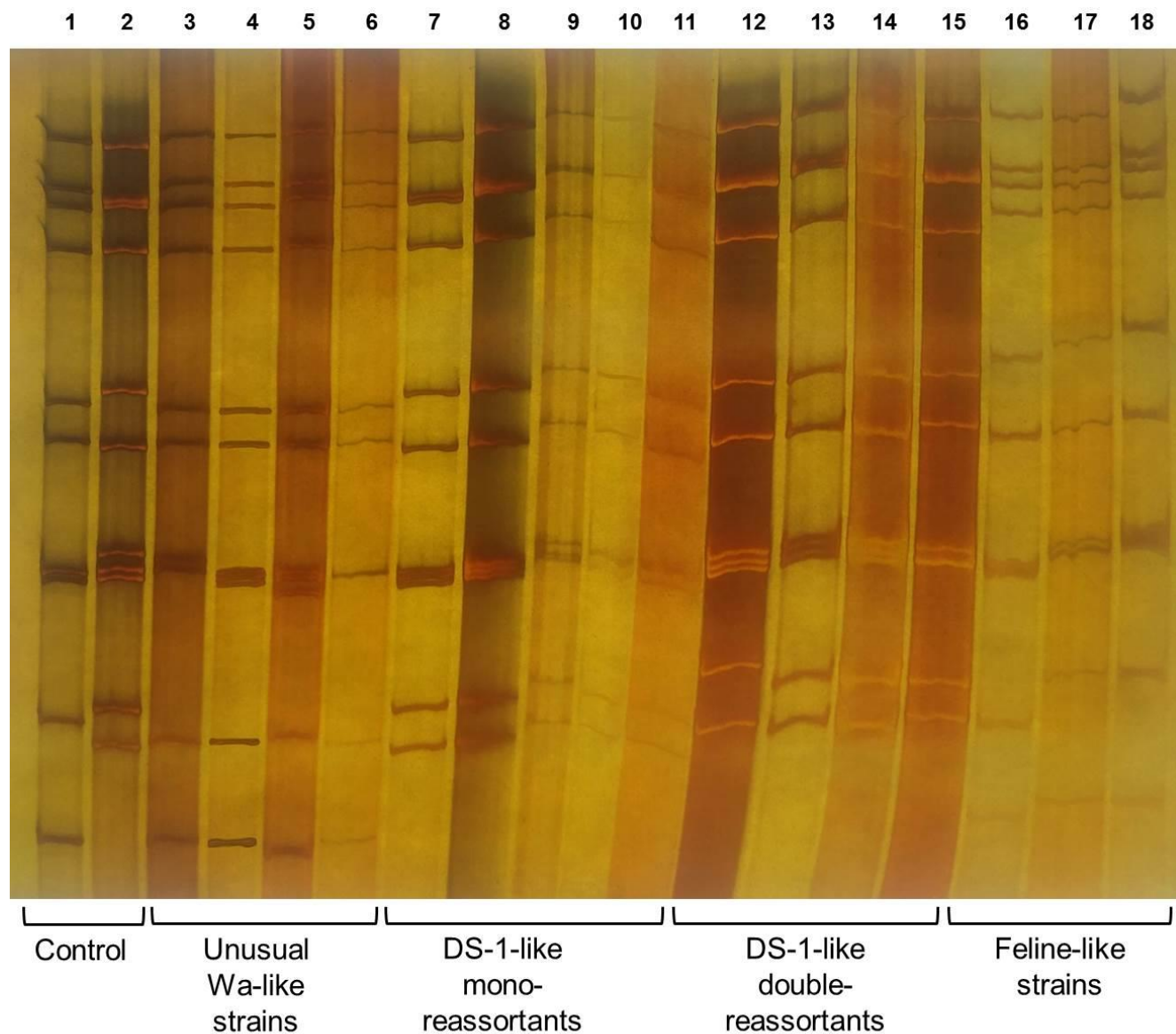


Supplement Figure S1

RNA patterns in PAGE of the 16 Nizhny Novgorod rotaviruses included in the study



- 1 - Control Wa-like strain (385/18);
- 2 - Control DS-1-like strain (437/18);
- 3 - 3150/16;
- 4 - 734/17;
- 5 - 2745/18;
- 6 - 2866/17;
- 7 - 735/17;
- 8 - 85/19;
- 9 - 403/19;

- 10 - 387/19;
- 11 - 684/19;
- 12 - 2578/17;
- 13 - 1013/18;
- 14 - 1019/18;
- 15 - 2785/18;
- 16 - 1061/17;
- 17 - 148/17;
- 18 - 2748/18.

Supplement Table S2**Rotavirus infection cases included in the study**

N	Strain	Disease onset date	Gender	Age	Diagnosis	Intensive care unit
1	RVA/Human-wt/RUS/NN1061-16/2016/G6P[9]	June 2016	Male	1 year	Acute intestinal infection	No
2	RVA/Human-wt/RUS/NN3150-16/2016/G12P[8]	November 2016	Male	14 years	Acute intestinal infection	No
3	RVA/Human-wt/RUS/NN148-17/2017/G3P[9]	January 2017	Female	1 year and 1 month	Acute intestinal infection	No
4	RVA/Human-wt/RUS/NN734-17/2017/G9P[8]	May 2017	Female	1 year and 4 months	Acute intestinal infection	No
5	RVA/Human-wt/RUS/NN735-17/2017/G9P[4]	May 2017	Female	3 years	Acute intestinal infection	No
6	RVA/Human-wt/RUS/NN2578-17/2017/G3P[8]	October 2017	Male	2 years	Acute intestinal infection	No
7	RVA/Human-wt/RUS/NN2866-17/2017/G3P[8]	October 2017	Male	9 months	Acute intestinal infection	No
8	RVA/Human-wt/RUS/NN1013-18/2018/G3P[8]	June 2018	Female	9 months	Acute intestinal infection	No
9	RVA/Human-wt/RUS/NN1019-18/2018/G3P[8]	June 2018	Male	9 months	Acute intestinal infection	No
10	RVA/Human-wt/RUS/NN2745-18/2018/G9P[8]	November 2018	Female	6 years	Acute intestinal infection	No
11	RVA/Human-wt/RUS/NN2748-18/2018/G3P[9]	November 2018	Female	1 year and 6 months	Acute intestinal infection	No
12	RVA/Human-wt/RUS/NN2785-18/2018/G8P[8]	November 2018	Male	4 years	Acute intestinal infection	No
13	RVA/Human-wt/RUS/NN85-19/2019/G4P[4]	January 2019	Male	1 year and 2 months	Acute intestinal infection	No
14	RVA/Human-wt/RUS/NN387-19/2019/G2P[8]	March 2019	Male	4 years	Acute intestinal infection	No
15	RVA/Human-wt/RUS/NN403-19/2019/G4P[4]	March 2019	Male	1 year and 2 months	Acute intestinal infection	No
16	RVA/Human-wt/RUS/NN684-19/2019/G2P[8]	May 2019	Female	4 years	Acute intestinal infection	No

Supplement Table S3**Lengths of the partial nucleotide sequences obtained in this study**

Strain	Segments										
	VP7	VP4	VP1	VP2	VP3	VP6	NSP1	NSP2	NSP3	NSP4	NSP5/6
RVA/Human-wt/RUS/NN1061-16/2016/G6P[9]	795	707	613	584	575	643	609	560	644	632	564
RVA/Human-wt/RUS/NN3150-16/2016/G12P[8]	781	654	599	619	595	665	605	507	654	633	557
RVA/Human-wt/RUS/NN148-17/2017/G3P[9]	815	785	515	564	543	568	555	528	644	568	640
RVA/Human-wt/RUS/NN734-17/2017/G9P[8]	811	813	511	618	546	573	501	582	516	593	636
RVA/Human-wt/RUS/NN735-17/2017/G9P[4]	841	819	567	617	509	565	563	572	637	636	567
RVA/Human-wt/RUS/NN2578-17/2017/G3P[8]	821	803	623	591	520	525	554	602	605	503	787
RVA/Human-wt/RUS/NN2866-17/2017/G3P[8]	810	794	609	591	567	635	517	608	647	633	570
RVA/Human-wt/RUS/NN1013-18/2018/G3P[8]	533	790	539	607	593	623	620	533	640	635	567
RVA/Human-wt/RUS/NN1019-18/2018/G3P[8]	544	801	543	509	583	524	611	571	615	642	531
RVA/Human-wt/RUS/NN2745-18/2018/G9P[8]	564	814	503	642	502	655	595	582	607	641	555
RVA/Human-wt/RUS/NN2748-18/2018/G3P[9]	554	799	515	597	576	557	596	635	606	604	540
RVA/Human-wt/RUS/NN2785-18/2018/G8P[8]	762	802	606	564	584	583	620	565	640	636	515
RVA/Human-wt/RUS/NN85-19/2019/G4P[4]	514	805	555	519	604	638	608	632	544	545	501
RVA/Human-wt/RUS/NN387-19/2019/G2P[8]	518	816	553	622	562	511	533	614	636	635	567
RVA/Human-wt/RUS/NN403-19/2019/G4P[4]	540	817	554	543	561	649	610	505	636	635	567
RVA/Human-wt/RUS/NN684-19/2019/G2P[8]	534	654	551	633	577	502	607	510	599	560	761

Supplement Table S4

The closest relatives of Nizhniy Novgorod mono-reassortant strains

Genes	Strains				
	<i>RUS/NN735-17/G9P[4]</i>	<i>RUS/NN85-19/G4P[4]</i>	<i>RUS/NN403-19/G4P[4]</i>	<i>RUS/NN387-19/G2P[8]</i>	<i>RUS/NN684-19 G2P[8]</i>
VP7	MT223970 RUS/NN568-18, 99.8%	MW132532 RUS/NN69-19, 99.3%	MW132532 RUS/NN69-19, 99.3%	MT149303 RUS/NN75-19, 99.0% LC477376 JPN/Tokyo18-42, 99.0%	MT149303 RUS/NN75-19 99.1% LC477376 JPN/Tokyo18-42 99.1%
VP4	MT223988 RUS/NN861-18, 99.8% MT053447 GER/FB041, 99.3%	MT149304 RUS/NN167-19, 99.6% MT053447 GER/FB041, 99.4%	MT149304 RUS/NN167-19, 99.6% MT053447 GER/FB041 99.4%	LC066664 THA/SSKT-41, 99.4% KX758598 RUS/NN1091-14, 99.3%	LC066664 THA/SSKT-41, 99.5% KX758598 RUS/NN1091-14, 99.4%
VP1	MT224003 RUS/NN861-18, 99.6%	MT224003 RUS/NN861-18, 99.6%	KJ919391 HUN/ERN5644, 99,8% MT224003 RUS/NN861-18, 99.6%	KJ919391 HUN/ERN5644, 99,8% MT224003 RUS/NN861-18, 99.6%	KJ919391 HUN/ERN5644, 99,8% MT224003 RUS/NN861-18, 99.6%
VP2	KR705444 BEL/BE98, 99.6% KJ919447 HUN/ERN5174, 99.6% MT223976 RUS/NN861-18, 99.5%	KR705444 BEL/BE98, 99.6% KJ919447 HUN/ERN5174, 99.6% MT223976 RUS/NN861-18, 99.5%	MT223976 RUS/NN861-18, 99.5% KR705444 BEL/BE98, 99.3% KJ919447 HUN/ERN5174, 99.3%	MT223976 RUS/NN861-18, 99.8% KR705444 BEL/BE98, 99.4% KJ919447 HUN/ERN5174, 99.4%	MT223976 RUS/NN861-18, 99.8% KR705444 BEL/BE98, 99.4% KJ919447 HUN/ERN5174, 99.4%
VP3	MT224033 RUS/NN861-18, 99.3% KR705445 BEL/BE98, 99.2% KC443213 AUS/CK20040, 99.2%	KR705445 BEL/BE98, 99.8% KC443213 AUS/CK20040, 99.8% MT224033 RUS/NN861-18, 99.5%	KR705445 BEL/BE98, 99.8% KC443213 AUS/CK20040, 99.8% MT224033 RUS/NN861-18, 99.5%	KR705445 BEL/BE98, 99.6% KC443213 AUS/CK20040, 99.6% MT224033 RUS/NN861-18, 99.5%	KR705445 BEL/BE98, 99.6% KC443213 AUS/CK20040, 99.6% MT224033 RUS/NN861-18, 99.5%
VP6	HM467951 USA/LB2772, 99.8% KY271808 RUS/NN262-16, 99.6%	KY271807 RUS/NN156-16, 99.8% MN552129 RUS/ NS17-A1047, 99.8%	KY271807 RUS/NN156-16, 99.9% MN552129 RUS NS17-A1047, 99.9%	MT224046 RUS/NN861-18 99.6%	LC514474 THA/DBM2017-016, 99.8% LC477416 JPN/Tokyo17-09, 99.6%
NSP1	MT224061 RUS/NN861-18, 99.6% KR705438 BEL/BE98, 99.3%	MT224061 RUS/NN861-18, 99.8% KR705438 BEL/BE98, 99.6%	MT224061 RUS/NN861-18, 99.8% KR705438 BEL/BE98, 99.8%	MT224061 RUS/NN861-18, 99.8% KR705438 BEL/BE98, 99.6%	MT224061 RUS/NN861-18, 99.6% KR705438 BEL/BE98, 99.4%
NSP2	MN552047 RUS/NS16-A415, 99.4% LC477570 JPN/Tokyo17-16, 99.4% MT224076 RUS/NN861-18, 99.2%	MN552047 RUS/NS16-A415, 99.9% LC477570 JPN/Tokyo17-16, 99.9% MT224076 RUS/NN861-18, 99.8%	MN552047 RUS/NS16-A415, 99.8% LC477570 JPN/Tokyo17-16, 99.8% MT224076 RUS/NN861-18, 99.6%	MN552047 RUS/NS16-A415, 99.9% LC477570 JPN/Tokyo17-16, 99.9% MT224076 RUS/NN861-18, 99.8%	MN552047 RUS/NS16-A415, 99.9% LC477570 JPN/Tokyo17-16, 99.9% MT224076 RUS/NN861-18, 99.8%
NSP3	MT224091 RUS/NN861-18, 99.9%	MT224091 RUS/NN861-18, 99.8%	MT224091 RUS/NN861-18, 99.9%	MT224088 RUS/NN560-18, 99.4% LC477616 JPN/Tokyo18-42, 99.4%	MT224088 RUS/NN560-18, 99.4% LC477616 JPN/Tokyo18-42, 99.4%
NSP4	MT224106 RUS/NN861-18, 99.6%	MT224106 RUS/NN861-18, 99.4%	MT224106 RUS/NN861-18, 99.6%	MT224102 RUS/NN425-18, 99.6% MN206138_RUS/NN557-17, 99.6%	MT224103 RUS/NN560-18, 99.5%
NSP5/6	KR705442 BEL/BE98, 99.6% LC477660 JPN/Tokyo17-16, 99.6% MT224120 RUS/NN478-18, 99.0%	KR705442 BEL/BE98, 99.6% LC477660 JPN/Tokyo17-16, 99.6% MT224120 RUS/NN478-18, 99.1%	KR705442 BEL/BE98, 99.5% LC477660 JPN/Tokyo17-16, 99.5% MT224120 RUS/NN478-18, 98.8%	KR705442 BEL/BE98, 99.5% LC477660 JPN/Tokyo17-16, 99.5% MT224120 RUS/NN478-18, 99.0%	KR705442 BEL/BE98, 99.5% LC477660 JPN/Tokyo17-16, 99.5% MT224120 RUS/NN478-18, 98.8%

Strains with the highest nucleotide identity with rotaviruses under investigation are at the top of cells.

Relative strains from Nizhniy Novgorod are blue.

Supplement Table S5

DS-1-like strains from other countries included as references in present study

No	Strain	Genotype	Reference
1	RVA/Human-wt/THA/SSKT-41/2013/G1P[8]	G1-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2	[1]
2	RVA/Human-wt/THA/SKT-289/2013/G3P[8]	G3-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2	[2]
3	RVA/Human-wt/THA/KKL-17/2013/G8P[8]	G8-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2	[3]
4	RVA/Human-wt/AUS/WAPC2016/2014/G3P[8]	G3P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2	[4]
5	RVA/Human-wt/VNM/RVN1149/2014/G8P[8]	G8-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2	[5]
6	RVA/Human-wt/THA/NP-130/2014/G8P[8]	G8-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2	[3]
7	RVA/Human-wt/ESP/SanSebastian98244047_DS-1/2015/G3P[8]	G3-P[8]-I2-R2-C2-M2-Ax-N2-T2-E2-H2	[6]
8	RVA/Human-wt/JPN/SO1162/2017/G8P[8]	G8-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2	[7]

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Supplement Table 6

The closest relatives of Nizhniy Novgorod DS-1-like double reassortant strains

Genes	Strains			
	<i>RUS/NN2578-17/G3P[8]</i>	<i>RUS/NN1013-18/G3P[8]</i>	<i>RUS/NN1019-18/G3P[8]</i>	<i>RUS/NN2785-18/G8P[8]</i>
VP7	KU550297_ESP/SS98244047, 99.4% LC086730_THA/SKT-289, 99.2% ON565650_RUS/NN2866-17/G3P[8], 97.5%	LC086730_THA/SKT-289, 99.8% KU550297_ESP/SS98244047, 99.4% ON565650_RUS/NN2866-17/G3P[8], 97.4%	LC086730_THA/SKT-289, 99.8% KU550297_ESP/SS98244047, 99.4% ON565650_RUS/NN2866-17/G3P[8], 97.4%	LC074731_VNM/RVN1149, 99.4% LC386070_JPN/SO1162, 99.4%
VP4	KU550285_ESP/SS98244047, 99.9% ON565661_RUS/NN3150-16/G12P8, 98.8%	KU059791_AUS/WAPC2016, 99.9% LC086728_THA/SKT-289, 99.9% ON565661_RUS/NN3150-16/G12P8, 99.0%	KU059791_AUS/WAPC2016, 99.9% LC086728_THA/SKT-289, 99.9% ON565661_RUS/NN3150-16/G12P8, 99.0%	KU059791_AUS/WAPC2016, 99.7% LC086728_THA/SKT-289, 99.7% ON565661_RUS/NN3150-16/G12P8, 98.1%
VP1	KU550285_ESP/SS98244047, 99.7% MT224003_RUS/NN861-18/G2P4, 98.5%	LC086725_THA/SKT-289, 99.5% KU059788_AUS/WAPC2016, 99.3% MT224003_RUS/NN861-18/G2P4, 98.1%	LC086725_THA/SKT-289, 99.8% KU059788_AUS/WAPC2016, 99.6% MT224003_RUS/NN861-18/G2P4, 98.3%	KU550285_ESP/SS98244047, 99.1% MT224003_RUS/NN861-18/G2P4, 97.8%
VP2	KU059789_AUS/WAPC2016, 99.6% MT224015_RUS/NN560-18/G2P4, 96.2% MN206129_RUS/NN557-17/G2P4, 96.2%	KU059789_AUS/WAPC2016, 99.6% MT224015_RUS/NN560-18/G2P4, 96.2% MN206129_RUS/NN557-17/G2P4, 96.2%	KU059789_AUS/WAPC2016, 99.6% MT224015_RUS/NN560-18/G2P4, 96.2% MN206129_RUS/NN557-17/G2P4, 96.2%	KU550273_ESP/SS98244047, 99.4% MT224015_RUS/NN560-18/G2P4, 95.7% MN206129_RUS/NN557-17/G2P4, 95.7%
VP3	KU550279_ESP/SS98244047, 99.2% MT224033_RUS/NN861-18/G2P4, 96.2%	LC086727_THA/SKT-289, 99.6% MT224033_RUS/NN861-18/G2P4, 96.7%	LC086727_THA/SKT-289, 99.6% MT224033_RUS/NN861-18/G2P4, 96.7%	LC086727_THA/SKT-289, 99.0% MT224033_RUS/NN861-18/G2P4, 96.4%
VP6	KT006918_ESP/SS98244047, 99.8% LC086729_THA/SKT-289, 99.8% MT224043_RUS/NN560-18/G2P4, 97.2%	KT006918_ESP/SS98244047, 99.2% LC086729_THA/SKT-289, 99.2% MT224043_RUS/NN560-18/G2P4, 96.7%	KT006918_ESP/SS98244047, 99.2% LC086729_THA/SKT-289, 99.2% MT224043_RUS/NN560-18/G2P4, 96.6%	ON565561_RUS/NN387-19/G2P8, 99.2% KY271808_RUS/NN262-16/G2P4, 99.1% KT006918_ESP/SS98244047, 95.0% LC086729_THA/SKT-289, 95.0%
NSP1	KU550303_ESP/SS98244047, 98.3% MT224058_RUS/NN560-18/G2P4, 96.0% MN206134_RUS/NN557-17/G2P4, 96.0%	KU059794_AUS/WAPC2016, 99.3% LC086731_THA/SKT-289, 99.3% MN206134_RUS/NN557-17/G2P4, 97.1% MT224058_RUS/NN560-18/G2P4, 96.3%	KU059794_AUS/WAPC2016, 99.8% LC086731_THA/SKT-289, 99.8% MN206134_RUS/NN557-17/G2P4, 97.6% MT224058_RUS/NN560-18/G2P4, 97.3%	KU550303_ESP/SS98244047, 98.9% MN206134_RUS/NN557-17/G2P4, 96.3% MT224058_RUS/NN560-18/G2P4, 96.1%
NSP2	KT006915_ESP/SS98244047, 99.1% MT224073_RUS/NN560-18/G2P4, 97.2% MN206135_RUS/NN557/G2P4, 97.0%	LC086732_THA/SKT-289, 99.1% MT224073_RUS/NN560-18/G2P4, 96.7% MN206135_RUS/NN557/G2P4, 96.5%	LC086732_THA/SKT-289, 99.9% MT224073_RUS/NN560-18/G2P4, 97.8% MN206135_RUS/NN557/G2P4, 97.6%	KT006915_ESP/SS98244047, 99.5% MT224073_RUS/NN560-18/G2P4, 96.9% MN206135_RUS/NN557/G2P4, 96.5%
NSP3	KU550315_ESP/SS98244047, 99.6% MT224088_RUS/NN560-18/G2P4, 95.5% MN206136_RUS/NN557-17/G2P4, 94.9%	LC086733_THA/SKT-289, 99.1% MT224088_RUS/NN560-18/G2P4, 95.2% MN206136_RUS/NN557-17/G2P4, 94.5%	LC086733_THA/SKT-289, 98.8% MT224088_RUS/NN560-18/G2P4, 95.2% MN206136_RUS/NN557-17/G2P4, 94.3%	KU550315_ESP/SS98244047, 99.5% MT224088_RUS/NN560-18/G2P4, 95.0% MN206136_RUS/NN557-17/G2P4, 94.7%
NSP4	KT006916_ESP/SS98244047, 99.0% MT224103_RUS/NN560-18/G2P4, 98.3% MN206138_RUS/NN557-17/G2P4, 98.0%	KU059797_AUS/WAPC2016, 99.6% MT224106_RUS/NN861-18/G2P4, 98.9%	KU059797_AUS/WAPC2016, 99.6% MT224106_RUS/NN861-18/G2P4, 98.9%	KT006916_ESP/SS98244047, 98.7%, MN206138_RUS/NN557-17/G2P4, 97.6% MT224103_RUS/NN560-18/G2P4, 97.5%
NSP5/6	KU059798_AUS/WAPC2016, 99.8% LC169851_THA/KKL-17, 99.8% LC066671_THA/SSKT-41, 99.8% LC086735_THA/SKT-289, 99.8% MT224121_RUS/NN861-18/G2P4, 99.1% MN206137_RUS/NN557-17/G2P4, 98.8%	KU059798_AUS/WAPC2016, 99.8% LC169851_THA/KKL-17, 99.8% LC066671_THA/SSKT-41, 99.8% LC086735_THA/SKT-289, 99.8% MT224121_RUS/NN861-18/G2P4, 99.1% MN206137_RUS/NN557-17/G2P4, 98.7%	KU059798_AUS/WAPC2016, 99.8% LC169851_THA/KKL-17, 99.8% LC066671_THA/SSKT-41, 99.8% LC086735_THA/SKT-289, 99.8% MT224121_RUS/NN861-18/G2P4, 99.1% MN206137_RUS/NN557-17/G2P4, 98.7%	KU059798_AUS/WAPC2016, 99.8% LC169851_THA/KKL-17, 99.8% LC066671_THA/SSKT-41, 99.8% LC086735_THA/SKT-289, 99.8% MT224121_RUS/NN861-18/G2P4, 99.1% MN206137_RUS/NN557-17/G2P4, 98.7%

Strains with the highest nucleotide identity with rotaviruses under investigation are at the top of cells.

Relative strains from Nizhniy Novgorod are blue.