

S1. List of Genomes (GenBank Accession numbers) used for Multiple Sequence Alignment (MSA) for primer development for sanger based whole genome sequencing of dengue virus serotypes.

S1.1 List of Genomes(GenBank Accession numbers) used for MSA based primer development for DENV1

- gi|395394295|gb|JN903579| /1/India/Dengue virus 1 isolate D1/IN/RGCB419/2008, complete genome
- gi|395394297|gb|JN903580| /1/India/Dengue virus 1 isolate D1/IN/RGCB585/2009, complete genome
- gi|395394299|gb|JN903581| /1/India/Dengue virus 1 isolate D1/IN/RGCB592/2009, complete genome
- gi|428624553|gb|JQ922548| /1/India/Dengue virus 1 isolate DENV-1/IND/55290/2005, complete genome
- gi|344165818|gb|JF459993| /1/Myanmar/Dengue virus 1 strain 49440 from Myanmar, complete genome
- gi|56698941|gb|AY713476| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.305/01 polyprotein gene, complete cds
- gi|56718853|gb|AY726549| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.37726/01 polyprotein gene, complete cds
- gi|56718857|gb|AY726551| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.44168/01 polyprotein gene, complete cds
- gi|56718861|gb|AY726553| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.49440/02 polyprotein gene, complete cds
- gi|56698937|gb|AY713474| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.194/01 polyprotein gene, complete cds
- gi|56718859|gb|AY726552| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.44988/02 polyprotein gene, complete cds
- gi|56698939|gb|AY713475| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.206/01 polyprotein gene, complete cds
- gi|395394293|gb|JN903578| /1/India/Dengue virus 1 isolate D1/IN/RGCB294/2007, complete genome
- gi|56718855|gb|AY726550| /1/Myanmar/Dengue virus type 1 strain D1.Myanmar.38862/01 polyprotein gene, complete cds

S1.2 List of Genomes(GenBank Accession numbers) used for MSA based primer development for DENV2

- gi|428621862|gb|JX475906| /2/India/Dengue virus 2 isolate 1392, complete genome
- gi|567319891|gb|KF041232| /2/Pakistan/Dengue virus 2 isolate D2/Pakistan/2011-23/2011, complete genome
- gi|567319895|gb|KF041234| /2/Pakistan/Dengue virus 2 isolate D2/Pakistan/2011-4/2011, complete genome
- gi|567319893|gb|KF041233| /2/Pakistan/Dengue virus 2 isolate D2/Pakistan/2011-3/2011, complete genome
- gi|567319897|gb|KF041235| /2/Pakistan/Dengue virus 2 isolate D2/Pakistan/209/2009, complete genome
- gi|567319901|gb|KF041237| /2/Pakistan/Dengue virus 2 isolate D2/Pakistan/78/2009, complete genome
- gi|595077843|gb|KJ010186| /2/Pakistan/Dengue virus 2 isolate DENV-2/PK/2013, complete genome
- gi|558611823|gb|KF360005| /2/Pakistan/Dengue virus 2 isolate DENV-2/PK, complete genome
- gi|595077841|gb|KJ010185| /2/Pakistan/Dengue virus 2 isolate DENV-2/PK/2011, complete genome
- gi|661903101|gb|KJ701507| /2/Pakistan/Dengue virus 2 isolate DENV-2/Pk/Swat-02, complete genome
- gi|228541894|gb|FJ898454| /2/India/Dengue virus 2 isolate DENV-2/IN/BID-V2961/2006, complete genome
- gi|187479897|gb|DQ448231| /2/India/Dengue virus 2 isolate GWL18 INDI-01, complete genome
- gi|513046351|gb|JQ955624| /2/India/Dengue virus 2 isolate Od2112, complete genome
- gi|428621831|gb|JQ955623| /2/India/Dengue virus 2 isolate RR44, complete genome
- gi|567319899|gb|KF041236| /2/Pakistan/Dengue virus 2 isolate D2/Pakistan/51/2008, complete genome
- gi|428625064|gb|JQ922551| /2/India/Dengue virus 2 isolate DENV-2/IND/053598/2005, complete genome
- gi|671760834|gb|KJ918750| /2/India/Dengue virus 2 isolate P23085 INDI-60, complete genome

S1.3 List of Genomes(GenBank Accession numbers) used for MSA based primer development for DENV3

- gi|305672623|gb|GQ466079| /3/India/Dengue virus 3 isolate DEL-72, complete genome
- gi|256600129|gb|FJ644564| /3/India/Dengue virus 3 isolate ND143 from India, complete genome
- gi|428625095|gb|JQ922556| /3/India/Dengue virus 3 isolate DENV-3/IND/58760/2005, complete genome
- gi|428625097|gb|JQ922557| /3/India/Dengue virus 3 isolate DENV-3/IND/59826/2005, complete genome
- gi|89242727|gb|AY496871| /3/Bangladesh/Dengue virus type 3 isolate BDH02-1, complete genome
- gi|89242729|gb|AY496873| /3/Bangladesh/Dengue virus type 3 isolate BDH02-3, complete genome
- gi|89242731|gb|AY496874| /3/Bangladesh/Dengue virus type 3 isolate BDH02-4, complete genome
- gi|89242733|gb|AY496877| /3/Bangladesh/Dengue virus type 3 isolate BDH02-7, complete genome

S1.4 List of Genomes(GenBank Accession numbers) used for MSA based primer development for DENV4

- gi|891070675|gb|KP723482| /4/China/Dengue virus 4 isolate DENV4/CN/GZ29/2010, complete genome
- gi|380307325|gb|JF741967| /4/China/Dengue virus 4 isolate GZ1D4, complete genome
- gi|389092828|gb|JQ822247| /4/China/Dengue virus 4 isolate GZ30, complete genome
- gi|428625153|gb|JQ922560| /4/India/Dengue virus 4 isolate DENV-4/IND/0952326/2009, complete genome
- gi|478248149|gb|KC333651| /4/China/Dengue virus 4 strain GZ/9809/2012, complete genome

S2. List of designed primers for DENV1 to 4 serotypes details:

S2.1 List of primers (all in 5' to 3' direction) for **Dengue virus type 1** genome sequencing developed on genome **JN903578.1**(Genbank)

:

S.No	Primer Nucleotide Sequence	Type	locus	Length	GC	Tm	Start	Stop
1	TACGTGGACCGACAAGAACAGTTTCG	fr	1	26	50	66.2	1	26
2	TGCACATATTGACACCTACAGAGGTC	rr	503	26	46	64.6	503	528
3	AACATAATGAACAGGAGGAAAAGATCCGTGAC	fr	360	32	41	65.9	360	391
4	TGAGTGATGGATGTTCTATGGCATGTG	rr	847	28	47	66.1	847	874
5	AGACTTGGGCTTTGCGACACCCAG	fr	796	24	58	68	796	819
6	TCTTGTTCTCCACCAGTGTAGCTTCTC	rr	1156	28	47	66.1	1156	1183
7	ATTGAACTCTTGA AACCGGAGGTCACGAAC	fr	1050	30	44	66	1050	1079
8	CTTTGTCAGTAACTATAGGATTGGCTG	rr	1981	27	41	63.1	1981	2007
9	GTGGCTGAGACCCAGCATGGAAC	fr	1857	23	61	68.1	1857	1879
10	GCATCTCCTACAACCACTGTGAATTTTCATGTC	rr	2655	32	44	67.2	2655	2686
11	TTCTGCTGACATGGTTGGGATTA AATTCAAGG	fr	2305	32	41	65.9	2305	2336
12	GTACCTCACACACATCAAAAATCCAATTCC	rr	3227	30	40	64.6	3227	3256
13	GCTGAAATTGCGTGACTCCTACACCC	fr	2912	26	54	67.7	2912	2937
14	CTGAGACATTGGCTCCAACCATGATGC	rr	3634	27	52	67.6	3634	3660
15	GAGAATCTAGTCAGGTCAATGGTCTCTGC	fr	3435	29	49	67.5	3435	3463
16	TGGACCTCCACTAGTATGTTGTGTGAGG	rr	4327	28	50	67.5	4327	4354
17	CCTTTGGATGCAAACCACTAACCATGTTTC	fr	4057	30	43	66	4057	4086
18	CCCTTCTTGATGCTTTGGCTTG	rr	5007	24	50	64.6	5007	5030
19	AGGCGAAGTTGGAGCCATAGCTCTAG	fr	4868	26	54	67.7	4868	4893
20	CGCTCTGGACCATCCTTAGTATTACC	rr	5804	27	48	66.1	5804	5830
21	GGCTACGACTGGATCACTGATTTTCC	fr	5550	26	50	66.2	5550	5575
22	GTTTTCTATTTC AATATTAGGTCACCTG	rr	6373	30	37	63.3	6373	6402
23	GGAAAGGAACAACCAAGGTGTTGGAGGAG	fr	6209	28	54	69	6209	6236
24	TAACATCAACACCGCCGCTGTCAGTGTC	rr	7133	28	54	69	7133	7160
25	GAAAACCACCACCATGCTACAATGC	fr	6876	25	48	64.6	6876	6900
26	TAGGTGTTAAATTCTGACTTGCTCAGTTGG	rr	7616	30	40	64.6	7616	7645

27	GTTACTGATACTTTGTACATCACAGATTCTC	fr	7334	31	36	63.3	7334	7364
28	TCCACTGCCACATGTCTTGTTCC	rr	8340	23	52	64.6	8340	8362
29	GGTTTCATGTGGAACAGGAAACATTGTGTC	fr	8219	30	43	66	8219	8248
30	CTCCCTCTCTGTGCACGAGATC	rr	8856	24	58	68	8856	8879
31	ACACCAAGAGCAAAACGAGGCACAGC	fr	8646	26	53	67.7	8646	8671
32	GATTGGGAGTTTCCAATTCGCTAGTAAAAAG	rr	9443	32	40	65.9	9443	9474
33	GATACATACTCAGAGACATATCAAAGATTCCG	fr	9106	32	38	64.7	9106	9137
34	GGCATGGCACCCTATTTCCCTC	rr	9722	23	56	66.3	9722	9744
35	CGAATTGGAACTCCCAATCTAGCTAAGAG	fr	9455	30	43	66	9455	9484
36	CTATTTTCTTTATTTTCATGAGTGTGTTGGC	rr	10263	31	36	63.3	10263	10293
37	GAGAAGGCTCATCGGGAATGAGAATTATCTAG	fr	10169	32	44	67.2	10169	10200
38	TGATTCAACGGCACCATTCCATTTCTGGC	rr	10686	30	47	67.4	10686	10715

S2.2 List of primers (all in 5' to 3' direction) for **Dengue virus type 2** genome sequencing developed on genome **JX475906.1** (Genbank)

:

S. No	Primer Nucleotide Sequence	Type	Locus	Length	GC	TM	Start	Stop
1	AGTTGTTAGTCTACGTGGACCGACAAAG	fr	1	28	46	66	1	28
2	CCTTCCAATCTTTTCTAAAGCCTCTC	rr	339	28	46	66	339	366
3	GTTTCCTAACAATCCCACCAACAGC	fr	260	25	48	65	260	284
4	CCATGTTCTAAGACTATGTCAACCCAGC	rr	992	28	47	66	992	1019
5	CCATAGGAACAACATATTTCCAAAGAGTCCTG	fr	866	32	41	66	866	897
6	GATCCTAAAACAACAACATCCTGTTTCTTCG	rr	1670	31	39	65	1670	1700
7	TCAGGGGAAGAGAATGCAGTTGGAAATG	fr	1369	28	47	66	1369	1396
8	TCGAACATTTGGCCGATTGAGCTTC	rr	2120	25	48	65	2120	2144
9	CAACATGGAACAATAGTTATCAGAGTACAATATG	fr	1882	34	33	63	1882	1915
10	CCTGCCTGCATGATTCTTTGATGTC	rr	2695	26	50	66	2695	2720
11	ACCGGGACAACCTGAAGCTCAGC	fr	2085	22	59	66	2085	2106
12	CATCCTGCCTTTCTTTCAACTTCAGC	rr	2925	26	46	65	2925	2950

13	CAACACAAACAGAGCTTGGAACTCACTAG	fr	2853	29	45	66	2853	2881
14	CTTTCCATGCATTTTGTAGTATCACTGCATTTGG	rr	3943	34	43	66	3943	3976
15	GACCTCCAAGGAATTGATGATGACC	fr	3765	25	48	65	3765	3789
16	GCCCATGATGGTTCAATCCTCTTCC	rr	4705	25	52	65	4705	4728
17	CAAGCAGAAAGGGATTCTTGGATACTC	fr	4596	27	45	65	4596	4622
18	ACCCATTCATGTCCAGAATCCACG	rr	5549	25	48	65	5549	5573
19	AGAACATTAATCCTGGCCCCTACTAGAG	fr	5170	28	47	66	5170	5197
20	TTCACGCTCTGGTTCAAACATGCTGGG	rr	6037	27	52	68	6037	6063
21	AGCAATGCACCAATCATGGATGAGGAAAG	fr	5503	29	45	66	5503	5531
22	AAGCGTCAGCAAAGCAATGTCTCCAG	rr	6529	27	48	66	6529	6555
23	GAAAATCCCTGACCCTGAATCTAATCAC	fr	6371	28	43	65	6371	6398
24	TTCTTCATGATGGAAAAGAGAAGTCCAGC	rr	7522	29	42	65	7522	7550
25	CACAGCAGCCCTTCTTTTATTGGTAGCAC	fr	7146	29	48	67	7146	7174
26	CAAGTTTAGGACTCTGAGTGTCGTCCTGC	rr	8041	30	50	69	8041	8070
27	TGGACTTCTCTTTCCATCATGAAGAACAC	fr	7524	30	40	65	7524	7553
28	GATGCTGATCCAGTCTGTTTTGTTTCG	rr	8496	27	45	65	8496	8522
29	CACCAAACCTAGACATAATTGGAAAAAGAATAG	fr	8381	33	34	63	8381	8413
30	GTCACCATTCTTCATTTTTAAGTCCTCTAG	rr	9199	32	35	63	9199	9230
31	GGCACGAAGAACTAATGAAAATCACGG	fr	8674	28	43	65	8674	8701
32	TGAAGGTTCCCATGTTGTATGTCTTTCC	rr	9632	29	42	65	9632	9660
33	GGCGTGAGAGTTATCAAGAATGGC	fr	9521	25	52	66	9521	9545
34	TTAATTCTGCCTTCTACCACAAGACCC	rr	10259	27	45	65	10259	10285
35	ATCAAACAGCAATAAACCAAGTCAGATCC	fr	10156	30	40	65	10156	10186
36	ATGATGCTGAGGAGACAGCAGG	rr	10649	22	54	65	10649	10670

S2.3 List of primers (all in 5' to 3' direction) for **Dengue virus type 3** genome sequencing developed on genome **GQ466079.1** :

S.No	Primer Sequence	Type	locus	Length	GC	Tm	Start	Stop
1	AGTTGTTAGTCTACGTGGACCGACAAG	fr	1	27	48	66.1	1	27
2	CTCGTGAAGTCAAGTGGAAAGCAAGTG	rr	429	27	48	66.1	429	455
3	GCCAGATGGGGAACCTTCAAGAAGTC	fr	293	26	53	67.7	293	318
4	CTTCCTTAGGGTCGCCAGTTGGGTG	rr	1084	25	60	69.5	1084	1108
5	AAGTCGAGAAGGTAGAGACATGGGC	fr	792	25	52	66.2	792	816
6	CCCAAGGGTTCATATTCAGGCAAG	rr	1450	25	52	66.2	1450	1474
7	GAACCGATAGAGGGAAAAGTGGTGC	fr	1301	25	52	66.2	1301	1325
8	TCCTATCGCAATGCATGAAAATGACATGG	rr	2349	29	41	64.6	2349	2377
9	CAAATATTCGGAAGTGCTTACACAGCCC	fr	2240	28	46	66.1	2240	2267
10	CTGTGATGACAACTGTTGTTCCCTTACAATAG	rr	3247	32	40	65.9	3247	3278
11	CGGTGTGCTAGAGAGTGACATGATC	fr	3115	25	52	66.2	3115	3139
12	ATGCTCGAAGACTGGCACACTGG	rr	4004	23	57	66.3	4004	4026
13	GTTACAACGCGCAGAGGACATTGAACAAATG	fr	3808	31	41	66	3808	3838
14	CCCTTCTCCAGTTCTGCTTTCTGTG	rr	4551	26	50	66.2	4551	4576
15	GAAGAGGCTGAGCAAACAGGAGTGTC	fr	4310	26	54	67.7	4310	4335
16	TCTCTCTTCTGTGTGTTTCTGTTGTC	rr	5252	31	42	66	5252	5282
17	GCCATTGTTAGAGAGGCAATCAAGAGACG	fr	5132	29	48	67.5	5132	5160
18	CCTATCTGTATATTTGATCCCTTCTGATGCTAC	rr	6164	33	40	65.9	6164	6196
19	GATAGAGTGATCGACCCAAGAAGATGTC	fr	5774	28	46	66.1	5774	5801
20	GACTATAGCCGACGCGATCCATTG	rr	6677	24	53	67.7	6677	6700
21	ACACGTCAGAACATGGCGGTAG	fr	6465	22	55	64.5	6465	6486
22	GAATCGTATATTACAGGATCTAGGTCTATCG	rr	7275	31	39	64.6	7275	7305
23	AACCAGGCAGTGGTCTGATGG	fr	7028	22	60	66.4	7028	7049
24	CTATGACTCTTCCTTCGGGAATGACCATG	rr	7771	29	48	67.5	7771	7799
25	CAATTATCCCGAAAGAGTTGACCTTACAAG	fr	7619	33	40	65.9	7619	7651
26	CTGTGATCTCCATAACCTTTCTTGTCCCTGGC	rr	8662	32	47	66.1	8662	8693
27	GTCTCTCAGTCAACATGGTATCCAGATTG	fr	8246	30	44	66	8246	8275
28	CTGTGTTTCCAGGGTCCATTTGCTGTG	rr	9222	25	52	66.2	9222	9246
29	GAAACTTGTGGACAGAGAACGTGAACTC	fr	8857	28	47	66.1	8857	8884
30	CTTTGATGGCTGCCATTGAGGTATGTC	rr	9632	27	48	66.1	9632	9658

31	CAGACCTCGAGAACCCTCATCTG	fr	9456	23	56	66.3	9456	9478
32	CACAGCTTCTCCGTA CTGTGGC	rr	10310	23	56	66.3	10310	10332
33	GGAGTCGGAGGGAGCCATTTGGTAAAC	fr	10243	27	55	69.2	10243	10269
34	CCATTTTCTGGCGTTCTGTGCCTGGAATG	rr	10652	29	51	68.9	10652	10680

S2.4 List of primers (all in 5' to 3' direction) for **Dengue virus type 4** genome sequencing developed on genome **JQ922560.1** (Genbank)

:

S.No	Primer sequence	Type	Locus	Length	GC	TM	Start Position	Stop Position
1	TTAGTCTGTGTGGACCGACAAGGACAG	fr	1	27	52	68	1	27
2	AATCCTGGGTTTCTGAGTATCCAACCTCTC	rr	806	29	45	66	806	834
3	AGTGGGGAACGGAGACGAGAGAAG	fr	683	24	59	68	683	706
4	GGGTTATCGTAGCTGTCACTCCGTG	rr	1406	25	56	68	1406	1430
5	GAAGTGGCTCTGTTAAGAACCTATTGCATCGAAGC	fr	1088	31	45	67	1088	1118
6	CATCTCTTATCTCTATGGGAACTTTGCATGG	rr	1928	31	42	66	1928	1958
7	AATGGTGACGTTTAAGGTCCCTCATGC	fr	1642	27	48	66	1642	1668
8	AGAAACAAAGTAATCCCTCCAACAGCTATGC	rr	2370	31	42	66	2370	2400
9	GATTTTGGCTCTGTTGGTGGACTGCTC	fr	2195	27	52	68	2195	2221
10	ATGTGTGGGTCTTGGGCCATAGACATG	rr	3084	27	52	68	3084	3110
11	GTGAAAGGGGTGTTATCCAAAGGCAAGAG	fr	2696	29	48	67	2696	2724
12	GCACAAAGGGTGGTCAACCAACCAATATC	rr	3571	30	50	69	3571	3600
13	GAACAACAGTCACCATTCAAGAGGATTGTGACC	fr	3264	33	46	68	3264	3296
14	CATTCTTTAGAAGGGCGCTTCCAAG	rr	4177	26	50	66	4177	4202
15	GCCCTTTCCTTGACTTTCATAAAATCAACAATGC	fr	3917	34	38	66	3917	3950
16	GCTAGAACTTGAACGTCTTCTTTATCCC	rr	4785	31	42	66	4785	4815
17	TGGCAATTCCAGTCACAATGACCCTATGG	fr	4464	29	49	67	4464	4492
18	GAACCTGTTGATGATAAAAGTCTTGTGTG	rr	5314	32	38	65	5314	5345
19	GAATTGGCGAACAGATTATGAAGTGGATG	fr	5028	30	44	66	5028	5057
20	TTGCTGGAGTCACTGGAATAGGACC	rr	5852	25	52	66	5852	5878
21	CAGAGCAATAGCCCAATAGAAGATATCGAGAG	fr	5498	32	44	67	5498	5529

22	GAAGATGCCTGCTGTCATAGCTCCTAG	rr	6554	27	52	68	6554	6580
23	AATTGCCAGTTTGCCAACGTACCTTTCCTC	fr	6400	30	47	67	6400	6429
24	ATGTTAGCTGTGGACACGGCTATAGTCG	rr	7458	28	50	68	7458	7485
25	CTTGGTGTGCCGCTATTAGCAATGGGATGC	fr	7079	28	54	70	7079	7108
26	CATAGGAATCGGTTCTTCATGTCCTGGACC	rr	7877	30	50	69	7877	7906
27	GGATCTAAAATCAAGTATGCAGTGTCCAGAG	fr	7700	31	42	66	7700	7730
28	ACAGTCTGGGATTTTTCTTCTCCCGAGGAG	rr	8708	31	49	69	8708	8738
29	TCCTTCGACAGGCTCGGCATCCTC	fr	8486	24	63	70	8486	8514
30	AGGGGCCATCTGTTCTGTGATCAGCTCTTC	rr	9206	30	53	70	9206	9235
31	GATACATCCTGGAGGACATAGATAAGAAAGATG	fr	9105	33	40	66	9105	9137
32	AGGCTAAGCGCAGGTCCTTCTATG	rr	9863	25	56	68	9863	9887
33	GAAAGAGTTGAGAAATGGCTGAAAGAGTGTG	fr	9482	31	42	66	9482	9512
34	GCCTCCCTGGGATTTTTACGCCTCCCG	rr	10353	24	58	68	10353	10376
35	GAAGGAGTTCTGTAATTACCAACAACAAACACC	fr	10247	33	40	66	10247	10279
36	CACGAGGAAGCTGTACTCCTGGTG	rr	10716	24	58	68	10716	10740

ABBREVIATIONS DETAILS :

Type-> Orientation **fr** -> Forward; **rr** -> Reverse;

GC-> GC content in percent;

TM-> Melting Temperature of primer in degree celsius calculated by MWG Operon (Eurofins) tool;

Length -> Number of nucleotide bases in primer;

Locus -> Reference Genome start position;

Start-> Genome start position;

Stop-> Genome stop position

S3. To assess impact of variations (mismatches/ Indels) in designed primers to their sequencing output. Mapping of primer sequence to available genome sequence of dengue virus type in CDC positive control mix, particularly their 3 prime end (Here 3 prime end of primer is last five nucleotide bases with their numbering starting last base of primer as first of 3 prime end). Variations between primer sequence and corresponding genome sequence also 3 prime region were computed. For mapping to sequencing output purpose, sequenced read quality were also compared.

S3.1 Mapping results of primers designed for dengue virus type 1 to genome of **DENV1 strain (Haw, GenBank Id: EU848545)** present in CDC positive control mix.

DENV4 Primers		Primer Mapping to DENV4 strain DENV1 strain (Haw, GenBank Id: EU848545)genome sequence by BLAST tool				Sequenced Result Output			Read Mapping to reference
S.No	Primer No.	Mapping (Start)	Mapping (End)	Number of Mismatch of primer sequence to genome sequence	If mismatch in 3 prime end of primer sequence(Last 5 nucleotide bases) to genome sequence; mismatch base details	Total Nucleotide Bases in read	High Quality bases (number)	Quality Percentage	Assemble to reference
1	1F	12	37	0	NO variation	415	124	29.87951807	Yes
2	1R	515	540	2	NO variation				
3	2F	372	403	5	NO variation	408	361	88.48039216	Yes
4	2R	859	886	1	NO variation				
5	3F	808	831	2	NO variation	365	320	87.67123288	Yes
6	3R	1168	1195	2	YES; 1 mismatch at 2nd base				
7	4F	1062	1091	3	YES; 1 mismatch at 3rd base	427	148	34.66042155	Yes
8	4R	1993	2019	3	NO variation				
9	5F	1869	1891	0	NO variation	380	349	91.84210526	Yes

10	5R	2667	2698	2	NO variation				
11	6F	2317	2348	2	NO variation	381	258	67.71653543	Yes
12	6R	3238	3268	4	YES; 1 mismatch at 5th base				
13	7F	2924	2948	2	NO variation	413	372	90.07263923	Yes
14	7R	3646	3672	2	NO variation				
15	8F	3447	3475	4	NO variation	404	330	81.68316832	Yes
16	8R	4339	4366	1	NO variation				
17	9F	4069	4098	3	NO variation	407	372	91.4004914	Yes
18	9R	5018	5042	1	NO variation				
19	10F	4880	4905	1	NO variation	431	303	70.30162413	Yes
20	10R	5816	5842	1	NO variation				
21	11F	5562	5587	2	YES; 1 mismatch at 3rd base	406	360	88.66995074	Yes
22	11R	6385	6414	3	NO variation				
23	12F	6221	6248	1	NO variation	0	0	0	No Data
24	12R	7145	7172	4	YES; 1 mismatch at 4th base				
25	13F	6888	6912	1	NO variation	420	304	72.38095238	Yes
26	13R	7628	7657	2	NO variation				
27	14F	7346	7376	3	NO variation	389	303	77.89203085	Yes
28	14R	8374	8352	0	NO variation				
29	15F	8231	8260	0	NO variation	427	386	90.39812646	Yes

30	15R	8868	8891	2	YES; 1 mismatch at 3rd base				
31	16F	8658	8683	1	NO variation	420	366	87.14285714	Yes
32	16R	9455	9485	6	NO variation				
33	17F	9118	9149	2	YES; 1 mismatch at 1st base	378	338	89.41798942	Yes
34	17R	9734	9756	1	NO variation				
35	18F	9467	9496	7	YES; 2 mismatch at 3rd,5th base	378	266	70.37037037	No
36	18R	10275	10305	6	YES; 1 mismatch at 2nd base				
37	19F	10181	10212	1	NO variation	0	0	0	No Data
38	19R	10696	10725	1	NO variation				

S3.2 Mapping results of primers designed for dengue virus type 2 to genome of DENV2 strain (NGC, GenBank Id: AF038403) present in CDC positive control mix.

DENV2 Primers	Primer Mapping to DENV2 strain (NGC, GenBank Id: AF038403) genome sequence by BLAST tool	Sequenced Result Output	Read Mapping to reference
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S.No	Primer No.	Mapping (Start)	Mapping (End)	Number of Mismatch of primer sequence to genome sequence	If mismatch in 3 prime end of primer sequence(Last 5 nucleotide bases) to genome sequence; mismatch base details	Total Nucleotide Bases in read	High Quality bases (number)	Quality Percentage	Assemble to reference
1	1F	1	28	0	NO variation	383	320	83.55091384	Yes
2	1R	338	366	2	NO variation				
3	2F	260	284	0	NO variation	385	334	86.75324675	Yes
4	2R	992	1049	0	NO variation				
5	3F	866	897	3	YES; 1 mismatch at 5th base	406	360	88.66995074	Yes
6	3R	1670	1700	0	NO variation				
7	4F	1369	1396	2	NO variation	390	359	92.05128205	Yes
8	4R	2120	2144	4	YES; 1 mismatch at 5th base				
9	5F	1882	1915	0	NO variation	366	330	90.16393443	Yes
10	5R	2685	2720	0	NO variation				
11	6F	2085	2106	3	YES; 1 mismatch at 1st base	368	292	79.34782609	Yes
12	6R	2925	2950	3	YES; 1 mismatch at 4th base				
13	7F	2853	2879	3	YES; 1 mismatch at 2nd base	390	333	85.38461538	Yes
14	7R	3943	3976	2	NO variation				
15	8F	3765	3785	1	YES; 1 mismatch at 1st base	377	333	88.32891247	Yes
16	8R	4706	4730	2	YES; 2 mismatch at 1st ,2nd base				

17	9F	4586	4622	2	YES; 1 mismatch at 3rd base	379	323	85.22427441	Yes
18	9R	5549	5573	2	NO variation				
19	10F	5170	5190	2	NO variation	389	347	89.20308483	Yes
20	10R	6037	6063	2	YES; 1 mismatch at 3rd base				
21	11F	5503	5531	1	NO variation	377	294	77.98408488	Yes
22	11R	6528	6555	2	NO variation				
23	12F	6371	6398	2	NO variation	377	314	83.28912467	Yes
24	12R	7522	7550	0	NO variation				
25	13F	7146	7174	4	NO variation	384	350	91.14583333	Yes
26	13R	8041	8070	2	NO variation				
27	14F	7524	7533	0	NO variation	372	335	90.05376344	Yes
28	14R	8497	8522	1	NO variation				
29	15F	8381	8413	3	NO variation	386	339	87.8238342	Yes
30	15R	9199	9230	3	NO variation				
31	16F	8674	8701	1	NO variation	386	322	83.41968912	Yes
32	16R	9632	9660	0	NO variation				
33	17F	9521	9545	2	NO variation	388	314	80.92783505	Yes
34	17R	10261	10285	4	YES; 2 mismatch at 2nd,5th base				
35	18F	10156	10185	2	NO variation	365	281	76.98630137	Yes
36	18R	10650	10671	0	NO variation				

S3.3 Mapping results of primers designed for dengue virus type 4 to genome of DENV4 strain (H241, GenBank Id: AY947539) present in CDC positive control mix.

DENV4 Primers		Primer Mapping to DENV4 strain (H241, GenBank Id: AY947539) genome sequence by BLAST tool				Sequenced Result Output			Read Mapping to reference
S.No	Primer No.	Mapping (Start)	Mapping (End)	Number of Mismatch of primer sequence to genome sequence	If mismatch in 3 prime end of primer sequence (Last 5 nucleotide bases) to genome sequence; mismatch base details	Total Nucleotide Bases in read	High Quality bases (number)	Quality Percentage	Assemble to reference
1	1F	12	37	0	NO variation	415	124	29.87951807	Yes
2	1R	515	540	2	NO variation				
3	2F	372	403	5	NO variation	408	361	88.48039216	Yes
4	2R	859	886	1	NO variation				
5	3F	808	831	2	NO variation	365	320	87.67123288	Yes
6	3R	1168	1195	2	YES;; 1 mismatch at 2nd base				
7	4F	1062	1091	3	YES;; 1 mismatch at 3rd base	427	148	34.66042155	Yes
8	4R	1993	2019	3	NO variation				
9	5F	1869	1891	0	NO variation	380	349	91.84210526	Yes
10	5R	2667	2698	2	NO variation				
11	6F	2317	2348	2	NO variation	381	258	67.71653543	Yes
12	6R	3238	3268	4	YES;; 1 mismatch at 5th base				

13	7F	2924	2948	2	NO variation	413	372	90.07263923	Yes
14	7R	3646	3672	2	NO variation				
15	8F	3447	3475	4	NO variation	404	330	81.68316832	Yes
16	8R	4339	4366	1	NO variation				
17	9F	4069	4098	3	NO variation	407	372	91.4004914	Yes
18	9R	5018	5042	1	NO variation				
19	10F	4880	4905	1	NO variation	431	303	70.30162413	Yes
20	10R	5816	5842	1	NO variation				
21	11F	5562	5587	2	YES;; 1 mismatch at 3rd base	406	360	88.66995074	Yes
22	11R	6385	6414	3	NO variation				
23	12F	6221	6248	1	NO variation	0	0	0	No Data
24	12R	7145	7172	4	YES; 1 mismatch at 4th base				
25	13F	6888	6912	1	NO variation	420	304	72.38095238	Yes
26	13R	7628	7657	2	NO variation				
27	14F	7346	7376	3	NO variation	389	303	77.89203085	Yes
28	14R	8374	8352	0	NO variation				
29	15F	8231	8260	0	NO variation	427	386	90.39812646	Yes
30	15R	8868	8891	2	YES; 1 mismatch at 3rd base				
31	16F	8658	8683	1	NO variation	420	366	87.14285714	Yes
32	16R	9455	9485	6	NO variation				

33	17F	9118	9149	2	YES; 1 mismatch at 1st base	378	338	89.41798942	Yes
34	17R	9734	9756	1	NO variation				
35	18F	9467	9496	7	YES; 2 mismatch at 3rd,5th base	378	266	70.37037037	No
36	18R	10275	10305	6	YES; 1 mismatch at 2nd base				
37	19F	10181	10212	1	NO variation	0	0	0	No Data
38	19R	10696	10725	1	NO variation				

S4. Whole Genomes (UTR5-> UTR3)sets from Asian Region and South Asian region insilico testing analysis using e-PCR tool and genomes which were predicted to have 15 or more primers amplifying as output by e-PCR tool using designed primer sets as query.

S4.1.1 List of Whole genomes of **Dengue Virus type 1** from **Asian region** (till July 2015 from NCBI Virus variation database).

FJ461330	GQ199847	EU249491	EU081238	FJ898429	EU081278	JQ045638	JQ045637	FJ432725
JQ045649	EU482810	EU482505	EU081228	JQ045634	EU677176	KC762640	KC762645	FJ547065
EU280167	EU482814	EU482511	FJ882525	JQ048541	FJ182024	JQ922545	FJ182035	GQ868632
EU660412	JQ045664	FJ024451	FJ898374	LC011948	FJ182028	FJ639689	FJ898371	JQ287661
FJ410218	FJ196847	GQ199772	HM181943	EU677171	EU249492	EU677167	AB608789	FJ898392
EU482823	FJ024432	EU726780	FJ410247	FJ882516	EU482480	FJ410211	EU677155	FJ182021
FJ176779	FJ562101	FJ410270	JQ045654	EU482534	EU482516	FJ898427	EU677178	EU482519
HG316482	FJ547063	GQ199810	KC762633	FJ461318	JQ045631	EU482507	JQ045647	JQ045628
JN903578	FJ898430	FJ882552	EU677174	JQ045659	GQ199852	EU081258	FJ410220	HQ891314
FJ639673	GQ868636	JQ045653	AY732477	HG316481	EU677159	EU677156	FJ461327	EU081227
FJ410235	FJ461341	JQ045661	GQ868630	FJ461340	JQ922548	EU081230	FJ882563	GQ868635
FJ024457	FJ882534	JN638341	FJ410257	FJ882520	FJ410262	FJ687430	EU482825	FJ882560
FJ410194	FJ882539	GU131921	GQ199785	GQ868606	FJ410268	FJ390383	EU660393	EU482820
EU482539	GQ199803	GQ199784	FJ898394	FJ882540	FJ898422	JQ045642	FJ373296	EU482502
KC762625	FJ898390	FJ882559	FJ410230	GQ199799	FJ898428	FJ882546	EU081237	KC762638
EU677153	FJ373305	EU482716	GQ199796	GU131782	GQ868619	GQ868614	EU081260	EU482520

GQ199791	FJ432748	EU482540	GQ868609	EU249495	EU660395	GU131739	AB189121	JN903579
FJ882565	GQ199841	EU081252	EU660396	EU482527	FJ898375	KC762646	FJ410260	FJ024446
FJ639684	EU482713	FJ024427	HQ891315	FJ687427	FJ898377	GQ199822	FJ882544	FJ898401
JQ045629	HM181949	FJ882531	KP772252	FJ182027	HQ624983	GQ199828	FJ898402	AB204803
FJ182033	FJ882553	GQ199774	FJ410273	FJ898399	EU081264	EU482538	FJ898414	EU677170
FJ882568	GQ199845	GQ199806	JQ045662	GQ199854	FJ898408	FJ639672	FJ882549	FJ410234
EU482806	FJ196841	GQ199838	FJ639680	JN697058	JQ045643	FJ639678	HM469966	GQ199792
EU482484	KC762626	HM181954	FJ882532	HM181952	KC172834	EU660392	FJ410222	EU482811
FJ390381	FJ469907	JN638343	GQ199777	FJ410274	FJ639677	FJ898378	FJ639675	KP398852
FJ461336	GQ868618	AY732482	GQ199807	FJ898387	FJ373298	HQ624984	EU677162	FJ461324
FJ687431	FJ024448	FJ410205	JF937612	AF309641	FJ182036	EU081265	FJ182026	HM631852
EU660418	GQ199837	FJ410207	EU482812	AY726554	FJ410285	FJ024443	FJ410242	KJ726662
FJ205881	KC762642	GQ199842	AY713474	FJ024463	EU482797	GQ199780	FJ410248	FJ024450
FJ898424	AY732475	EU482792	FJ410196	FJ410201	FJ469908	FJ898419	FJ882521	FJ182032
JN638336	FJ639685	EU482815	FJ906965	FJ898417	EU081235	FJ410227	EU482508	FJ410199
EU677168	FJ182018	KC762639	HM181959	GU131683	EU482492	FJ898389	JQ045633	EU482807
FJ410258	FJ432745	FJ182003	FJ410192	GU131888	FJ196843	GQ199856	GU131732	FJ639676
EU249494	FJ410232	KC762649	FJ432744	FJ639670	LC011945	EU482709	JQ917404	FJ410243
EU482506	FJ410280	GQ868639	FJ432746	FJ882522	HM181945	EU482800	FJ461332	EU249493
EU081231	GQ199817	FJ432738	JF937598	FJ196844	GQ199843	AY726550	EU482799	JQ045630
FJ205876	EU482500	FJ882536	EU482715	EU081247	EU482486	DQ193572	JQ922546	JN638339
FJ882542	JN903580	KC762652	KJ438293	EU081272	EU081271	FJ024455	EU726778	FJ687432
FJ898404	JQ045648	AY726549	FJ432737	FJ410254	FJ687428	FJ390386	FJ410210	FJ882526
LC011949	FJ182030	EU677151	GQ199779	EU081259	FJ461319	JQ045657	GQ199829	GQ199824

FJ898385	EU482712	FJ410281	GQ199801	EU660403	FJ024428	EU081229	FJ898426	FJ882566
EU482795	EU482803	FJ882561	FJ882558	FJ410209	FJ024464	EU677173	FJ432740	EU677175
FJ410287	EU482809	KR052012	EU482789	JQ287660	FJ882517	EU482532	FJ410253	FJ461335
FJ410289	EU482481	EF025110	EU482791	GQ199814	FJ898384	EU482495	GQ868605	GQ868612
FJ639691	EU482483	FJ639686	FJ024430	KC762623	EU482526	FJ196846	GQ199773	AY726555
EU660391	EU677165	EU081248	FJ432723	FJ176780	AY726553	FJ024439	JQ045636	AY732476
FJ182019	FJ850068	FJ182020	KC762648	AB178040	EU081242	FJ882524	FJ898416	FJ410269
FJ410244	EU677152	FJ024459	EU482805	GQ199804	GQ199798	GQ199834	JQ045656	GQ868610
JQ045635	FJ205882	FJ432735	EU482485	GQ199848	FJ898412	EU482529	AB608787	EU482710
KF971871	FJ410213	GQ199836	EU482522	FJ410191	FJ410251	KC762636	LC011947	FJ639692
FJ410225	GQ199794	EU482794	JN054255	GQ199786	GQ868607	KF289072	FJ024462	GQ868602
FJ410264	FJ882562	JN638342	EU359008	EU482718	GQ868613	EU081245	FJ461313	EU660390
FJ898379	KF887994	EU081233	FJ639669	GQ868633	EU482512	AY732478	FJ882519	EU677160
FJ898406	EU482798	FJ410198	GQ199790	FJ882554	AY835999	EU687247	GU131778	FJ898372
EU482537	FJ898409	FJ410212	KC762644	JQ045665	JN638340	EU081274	KC762631	EU081232
FJ687426	GQ199851	FJ882547	EU081257	FJ024435	GQ398255	FJ024441	FJ882543	EU081234
FJ410239	FJ639694	EU482808	FJ410238	FJ461312	FJ461308	GU131721	EU482528	EU081261
FJ882541	FJ182029	FJ687433	EU677158	GQ199820	FJ898386	FJ024425	EU081246	EU660419
AY732479	FJ410245	GQ199793	FJ410282	FJ898411	HM181939	FJ024429	EU081273	FJ898425
FJ024442	FJ898421	JQ045639	FJ898381	KC762630	GQ199775	GQ199840	KJ649286	JQ045644
FJ898398	EU081277	KC762641	FJ882564	EF457905	EU482498	AY713475	FJ410277	GU131828
GQ199855	FJ410249	KC762628	FJ882567	FJ432732	GQ199813	EU081250	EU482490	EU482796
EU482510	FJ882528	GQ199850	KJ726664	FJ882515	FJ859029	FJ461306	KC172829	EU482802
EU081244	FJ687429	GQ868615	AB189120	FJ882535	GQ199811	FJ410272	FJ461315	EU482488

HM469967	FJ461333	EU482535	FJ205884	GQ199830	EU482816	GQ199816	FJ898388	EU677150
EU677172	EU081267	KF971869	FJ461320	EU482817	JQ045652	EU482476	KC762637	FJ410263
EU482533	FJ410261	EU677166	FJ639681	KC762654	FJ882530	JQ045663	AY708047	FJ898407
FJ024438	KC172835	FJ390382	EU482824	EU081281	GQ199833	AY732480	FJ024440	EU482708
FJ024460	EU660394	FJ410246	JN697056	LC016760	KR071622	FJ432747	GQ199781	EU482536
FJ461317	FJ373297	FJ898420	EU677177	FJ024447	EU081255	GQ199778	KC762629	JQ045645
KC762635	GQ199826	EU482504	FJ882548	FJ410240	AY722803	GQ199802	FJ432742	GQ199844
FJ639671	JQ045632	FJ461323	EU482706	EU249490	EU726781	FJ898391	GQ199805	EU081243
GQ199771	EU081236	FJ882527	EU482494	KC762643	EU482793	FJ898397	EU482717	EU081270
FJ882523	EU081263	GQ199825	KF971870	JQ692085	HM181957	EU482499	EU482514	HM181956
GQ199809	EU726777	EU482711	EU081269	EU081256	FJ024436	AB195673	EU081253	FJ882538
FJ410255	EU482828	JN638338	EU081279	FJ024433	JQ045658	FJ432734	EU081280	FJ024437
GQ199783	JQ045646	EU081262	GU131894	EU482821	JF459993	FJ432736	FJ432719	FJ461316
FJ898396	FJ461307	JN903581	KF955406	EU482503	EU081249	FJ882518	FJ410206	FJ461328
EU081251	FJ461310	FJ898400	EU687251	FJ410283	FJ432739	GQ199788	FJ906963	FJ898383
EU081275	EU482489	EU482707	FJ182025	FJ882529	KC762651	EU482524	GQ199821	EU482487
JN819423	KC762632	EU482531	FJ882545	EU482521	FJ639683	KC762650	JQ045650	KC762634
FJ744702	EU726782	FJ639693	FJ898403	HQ891313	EU677169	FJ024431	AY722801	FJ024472
FJ882570	FJ410276	JQ045641	EU482515	FJ639688	FJ410265	FJ461339	FJ432727	FJ898405
FJ898418	EU482827	JQ922544	FJ639687	KJ933413	EU677154	JF937651	GQ199815	EU482491
EU482496	JQ045667	FJ639679	FJ639696	FJ410231	FJ410204	FJ898431	KC762622	GU131923
FJ196845	EU677163	FJ898373	EU677161	KJ726663	FJ410286	EU081266	AY732483	FJ906728
FJ432729	FJ898393	GU131759	EU482509	FJ182031	GQ199819	FJ410266	GQ199787	FJ410250
EU482477	EU081241	EU081268	JQ045640	FJ461325	GU131750	EU482804	GQ199853	FJ410256

KC762620	EU677140	EU677139	FJ410284	JQ045651	FJ182023	EU482482	EU482501	GQ868608
AY732481	FJ024453	FJ410226	GQ199800	FJ850069	FJ024456	GQ199818	FJ432733	GQ199776
GQ199831	FJ898423	FJ410279	FJ410267	EU677157	FJ410197	EU482523	FJ410236	GQ199808
GQ199835	EU482525	FJ882537	JQ045626	FJ205883	EU482517	JN054256	GQ199839	FJ898395
AY713476	AY726552	FJ898382	FJ469909	FJ410214	KC762624	KC762627	GQ199849	KC759167
FJ024426	AB608786	FJ882555	FJ639674	EU081226	FJ432749	KJ726665	KC762653	FJ196848
GQ199789	FJ390388	EU482801	EU726779	FJ639695	EU482479	FJ410216	EU081240	FJ432730
FJ898410	KJ438296	KP723473	FJ898376	EU660397	JQ045660	FJ898380	FJ024434	GQ199782
KP686070	GQ199797	JQ045668	EU482826	GQ199795	FJ182034	GQ199823	FJ882551	EU081239
JN205310	FJ898415	AY726551	JN638337	GQ868611	EU482822	FJ639682	EU482818	LC011946
EU660402	FJ024445	EU677164	FJ639690	GQ199827	FJ882569	FJ182022	JQ045666	GQ199812
FJ410275	FJ410252	FJ024444	FJ461331	JN697057	EU482513	EU482518	JN638344	KC762621
FJ410278	HM469968	GQ199846	HM181958	EU482813	FJ196842	JQ287664	FJ547060	EU482790
FJ898413	KR028435	HQ891316	EU482478	JQ045655	KC762647	FJ024449	FJ410203	EU482819
EU482493	HM181948	EU081276	EU660401	FJ882557	AY713473	FJ882533	FJ906964	EU482497
EU482530	GQ199832	GQ868637	FJ882550	EU482714	EU081254	AY732474	FJ882556	AY722802

S4.1.2 List of genomes from DENV1 Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

- gb|AB189120
- gb|AB189121
- gb|AB195673
- gb|HM469967
- gb|JN903578

- gb|JQ922548
- gb|JQ922544

S4.2.1 List of Whole genomes of **Dengue Virus type 2** from **Asian region** (till July 2015 from NCBI Virus variation database)

KM279591	KM279594	GQ868624	GQ398263	EU687249	KF041233	KM279599	EU482669
EU482666	KM279579	EU482451	KM279524	KC762680	KF041235	KC762670	FJ196853
KC762665	AJ968413	FJ859028	KM279587	KM279555	KM279575	FJ410237	KC762666
FJ410259	EU482787	EU482474	KM279566	KM279529	GQ868544	JX649148	DQ645552
EU482543	FJ410208	KM279563	GQ868542	KM279601	KM279562	KM279542	KM279525
KM279522	JX649147	EU482786	KM279558	KM279549	EU482475	EU482463	KF360005
DQ645546	FJ205879	DQ181798	FJ410202	KC762672	KM279598	FM210220	FJ744713
AB189123	KF041232	KC762674	EU482668	KM279584	KC762675	DQ645544	FJ410219
KM279556	KM279541	KM279595	KF041237	KM279569	KM279528	DQ645541	EU482671

FJ810410	KM279547	KM279519	KC131142	KJ701507	KM279548	DQ448231	KC762669
FJ461321	KC762667	EU482700	KM279568	GQ868545	FJ639704	KM279572	FJ810411
EU482647	KM279521	EU482542	EU677148	EU482702	FM210231	FM210209	EU482698
KJ918750	GU131886	FM210202	EU660415	KM279597	KM279567	EU482703	FJ687440
FJ410233	FJ196851	AF204177	FJ410195	FJ639705	EU482673	EU482657	FM210227
EU482672	FM210241	KM279540	FJ410217	FM210204	KC762660	DQ181802	DQ645547
GQ868623	DQ645549	EU482670	EU482650	GU131929	FJ906958	FJ687437	FJ410288
KM279570	DQ645550	EU482541	FJ432724	EU482465	KM279523	EU482776	FJ390385
FJ639697	FJ687442	KM279520	GQ398258	FM210215	EU482667	FJ687447	EU482779
FJ687441	EU179857	EU482645	DQ645543	EU081178	FJ639698	FM210224	DQ645556
FJ744710	DQ645542	FJ906957	EU081180	KC762668	EU482646	FJ744724	JN819418
FM210211	EU482656	KM279577	FJ639832	GQ398259	AB189124	EU482651	FJ744721
FJ639829	DQ181803	DQ645553	EU482464	KC762663	GQ868622	EU660414	FJ373299
EU482653	KM279534	FJ639699	KP723479	AB479041	KR779782	EU482676	FM210208
FJ639831	GQ868620	GQ868625	KM279543	EU482674	EU179859	KM279516	FJ639830
FM210242	FJ810409	JQ045678	KC762662	FJ744722	AB479042	FM210239	EU660413
DQ181806	FJ744723	EU482697	AB189122	FJ196852	FJ639702	GQ398257	FM210245
FJ410228	KM279552	JF327392	GU131900	FJ390384	FJ744711	KM279539	DQ181805
KM279551	EU482780	EU179858	EU482648	EU482699	FM210233	FJ687434	FJ687439
EU482781	FJ410223	FJ744720	FM210221	DQ645551	KM279571	FJ410200	FJ562098
FJ873811	KM279590	FJ410224	EU081177	EU482641	FJ687446	KM279533	EF051521
FM210228	KC762664	FJ744712	EU482675	KP012546	EU482654	EU482446	GQ868631
GQ398268	GU289914	JQ045676	FJ639711	KC762661	KM279550	KC762673	EU482777

EU482705	JQ922549	EU482655	EU482652	FJ687443	KJ734727	AF276619	KC964094
FM210217	HQ891024	EU482466	JQ955624	FM210246	FJ205880	FJ024452	KC762657
KM279531	EU482704	KM279553	FJ744717	DQ181804	JX475906	EU482467	JQ922552
EU482448	FM210225	FM210213	EU482658	GQ868591	FJ410241	EU687250	FJ744718
FJ390387	EU660417	FM210219	FM210210	JQ955623	FM210243	EU726767	EU677138
KC762658	EU482679	FJ687438	DQ181801	FJ744716	EU482784	EU569721	FM210234
FJ810412	FJ639828	FM210226	FJ205877	EU660416	KM279532	GQ398267	GQ398264
KM279518	FJ744725	EU359009	FJ410221	EU482678	FJ687445	AY858036	GQ398262
JQ922551	EU482665	EU482662	GU131902	FJ205878	EU482445	DQ645555	KM279530
EU677137	KM279513	EU482469	EU482782	JQ045670	FJ687435	FJ639706	EU482447
EU482701	FJ744715	EU482471	FM210223	GQ868621	FJ461309	FJ461305	FJ024461
KC762678	FM210222	FJ744714	KM279592	EU726776	EU482663	KM279526	KM279536
KM279560	FM210238	KM279582	FJ882602	FM210207	JQ922550	KM279573	FJ898454
FJ687436	GQ252677	FJ687444	EU482783	FJ547067	KC762677	EU687248	DQ645540
KC964095	KJ010185	JQ045684	FM210216	KC964093	EU482644	KM279554	KM279565
EU482659	EU482640	FM210205	KR779786	EU482778	JX470186	EU482785	AY858035
KF479233	EU482775	KC762655	FJ547064	KJ010186	GQ398260	FJ467493	KM279586
DQ181800	EU482468	FJ461311	EU482677	KM279514	EU482661	DQ181797	KM279545
GQ252676	EU482449	FJ196854	FM210236	EU482664	KF041236	KM279564	FJ410193
FJ024454	KC762659	KM279535	FM210244	GQ398265	FJ639707	FJ024458	KM279593
GQ398261	DQ645554	EU482643	JN368476	GQ868638	FJ432726	EU482649	GQ868543
GU131924	AF119661	FJ639700	EF105379	EU482774	KM279527	FM210203	EU482472
FM210237	FJ639701	FM210235	KM279515	AF204178	EU482788	FJ639717	KM279578

KM279537	FM210232	FJ410215	KC762679	DQ181799	KM279557	KM279583	KM279517
EU687246	EU482642	EU482660	FJ639710	KM279589	FM210206	KC762671	FJ639703
DQ645548	GQ398266	EU482473	FJ898452	KM279600	KC762656	DQ645545	FJ639709
KM279544	KM279588	KM279596	FJ461314	KM279546	KM279559	EU081179	EU677149
FJ639708	KM279561	EU482450	KM279538	JQ045686	EU482470	FM210214	FM210230
KM279581	KC762676	KF041234					

S4.2.2 List of genomes from DENV2 Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

gb AB189122	gb KM279584	gb KM279571	gb KM279593	gb KJ701507	gb KC762670	gb KR779782	gb DQ645546
gb AB189123	gb KM279524	gb KM279544	gb KM279562	gb EU482640	gb KC762676	gb EU359009	gb DQ645547
gb AB189124	gb KM279586	gb KM279545	gb KM279563	gb EU482672	gb KC762662	gb KC131142	gb DQ645548
gb JX475906	gb KM279525	gb KM279546	gb KM279594	gb KP012546	gb KC762661	gb AY858035	gb DQ645549
gb KF041232	gb KM279526	gb KM279547	gb KM279564	gb KP723479	gb KC762655	gb GQ398258	gb DQ645550
gb KF041233	gb KM279527	gb KM279548	gb KM279565	gb KM279598	gb KC762656	gb GQ398259	gb DQ645551
gb KF041234	gb KM279528	gb KM279549	gb KM279595	gb KM279599	gb KC762673	gb GQ398268	gb DQ645552
gb KF041235	gb KM279529	gb KM279550	gb KM279566	gb KM279600	gb KC762663	gb GQ398263	gb DQ645553
gb KF041236	gb KM279587	gb KM279589	gb KM279572	gb KM279576	gb KC762675	gb GQ398264	gb DQ645554
gb KF041237	gb KM279530	gb KM279551	gb KM279573	gb KM279577	gb KC762671	gb GQ398260	gb DQ645555

gb KM279513	gb KM279531	gb KM279552	gb KM279567	gb KM279578	gb KC762664	gb GQ398262	gb DQ645556
gb KM279514	gb KM279532	gb KM279553	gb KM279568	gb KM279601	gb KC762674	gb GQ398261	gb AF204178
gb KM279515	gb KM279533	gb KM279554	gb KM279569	gb KM279579	gb KC762672	gb GQ398267	gb AF204177
gb KM279516	gb KM279534	gb KM279590	gb KM279575	gb FJ196852	gb KC762667	gb GQ398266	gb DQ645540
gb KM279517	gb KM279535	gb KM279555	gb KM279570	gb FJ196853	gb KC762659	gb GQ398265	gb DQ645541
gb KM279518	gb KM279536	gb KM279556	gb KM279596	gb FJ196854	gb KC762657	gb JF327392	gb EU081177
gb KM279519	gb KM279537	gb KM279557	gb FJ898454	gb KC964094	gb KC762666	gb KF479233	gb EU081178
gb KM279520	gb KM279588	gb KM279591	gb JQ922549	gb KC964093	gb KC762677	gb AY858036	gb EU081179
gb KM279581	gb KM279538	gb KM279597	gb FJ882602	gb DQ448231	gb KC762668	gb EU179858	gb EU081180
gb KM279582	gb KM279539	gb KM279592	gb GQ252676	gb JX470186	gb KC762678	gb EU179859	gb AF276619
gb KM279521	gb KM279540	gb KM279558	gb GQ252677	gb KC762665	gb KC762679	gb EU179857	gb DQ181798
gb KM279522	gb KM279541	gb KM279559	gb KF360005	gb KC762669	gb KC762680	gb DQ645543	gb DQ181800
gb KM279523	gb KM279542	gb KM279560	gb KJ010185	gb KC762658	gb JQ955624	gb DQ645544	gb EF051521
gb KM279583	gb KM279543	gb KM279561	gb KJ010186	gb KC762660	gb JQ955623	gb DQ645545	

S4.3.1 List of Whole genomes of **Dengue Virus type 3** from **Asian region** (till July 2015 from NCBI Virus variation database)

DQ401689	DQ401694	DQ401695	KF955332	EU081198	JQ045688	GQ868629	AY496874
EU081208	KC762691	FJ432743	EU081206	FJ639726	EU367962	EU482454	AY858044
GU131938	GQ868626	AB214879	KJ622199	GU131914	FJ639729	GU131946	DQ675520
EU482452	KF955457	JQ045689	KC261634	KF041258	DQ675522	DQ675529	FJ562097
EU081181	AY858046	DQ675523	FJ639713	FJ744739	EU482462	FJ744728	AY676352
EU482461	KF041257	GQ868627	FJ562103	DQ675519	EU081199	EU081220	AY876494
AY496879	GU131913	AY858045	EU081197	EU081185	EU081225	AY858041	GU131917
EU081224	GU131943	HG316484	GU131937	FJ744732	FJ744731	FJ744730	FJ639721
KF824903	GU131906	AF317645	FJ461338	KC762688	KJ622198	EU081189	AY676349
GU131942	FJ639725	GU131910	EU482455	DQ675527	AY858042	AY496871	DQ863638
GQ868593	FJ744729	GQ199888	AY858048	EU081187	GU131904	GU131940	FJ639720
KC762681	EU081221	KF041256	JN662391	EU482457	FJ461337	AY676353	FJ547066
GU363549	GQ199887	KF041254	FJ639723	EU081201	EU081214	FJ410229	KC762684
AY496877	FJ461326	KJ622197	KC762689	FJ639728	EU081182	EU081191	EU081196
EU081222	AB189128	FJ744740	EU081223	KF955458	GQ466079	EU482456	KJ737430
FJ744726	KC762687	EU081211	GQ868628	FJ461334	GU131935	FJ882572	EU081190
EU081213	EU081188	EU081183	JQ045690	DQ675525	AY770511	FJ882574	FJ639712
AB189125	EU660411	AB189127	GU131939	AY676351	FJ810413	DQ675531	EU660407

GU131905	EU081210	GU131936	HM631854	FJ687448	EU660409	KC762692	EU081218
AY858043	KJ737429	GU131944	FJ744733	AY496873	EU081204	DQ675533	FJ562102
GU131916	AY858040	KC762686	DQ675528	EU482458	FJ744737	KF954949	AY099336
FJ744736	FJ644564	DQ675521	FJ744727	FJ461329	KC762682	JQ922555	EU482460
FJ562099	EU081216	FJ639722	HG316483	KF954947	EU081194	DQ401692	AB214880
KC762683	EU482459	FJ810414	KF955459	DQ401690	DQ675532	KF955461	JQ045687
AY858038	EU081202	EU660410	JQ045692	AY676350	EU081209	DQ675524	EU081207
EU081193	KJ622194	JF504679	AY858037	KF955507	FJ882571	FJ639727	FJ432728
JN368477	EU081192	EU081195	FJ639730	JQ045691	AY858039	FJ461322	FJ639716
FJ639719	AB214882	GU131934	EU081186	KJ622193	EU482453	KJ622196	KF955474
EU081219	EU081212	JQ045695	KJ622192	EU081215	DQ675530	GQ199889	DQ401693
FJ744738	AY648961	FJ432731	FJ882573	FJ639731	FJ639714	KF824902	
EU660408	EU081200	EU081203	KF954948	FJ639715	KF955460	EU081184	
EU081217	KC762693	FJ744734	JQ922556	KF041255	DQ401691	DQ675526	
KJ622191	JQ045694	KC762685	FJ432741	FJ547061	FJ562100	KF041259	
GQ868634	EU081205	JQ411814	AY676348	AY923865	FJ547062	GU131941	
GQ252674	KF954946	JQ045693	AY662691	KF954945	AY858047	AB189126	
JQ922557	FJ432722	AB214881	KJ622195	KC762690	FJ639724	FJ744735	

S4.3.2 List of genomes from DENV3 Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

gb AB189125	gb GU131937	gb GQ199887	gb EU482460	gb JQ045690	gb KJ737429	gb AY496873	gb EU081214
gb AB189126	gb GU131938	gb GQ199888	gb EU482461	gb JQ045691	gb DQ863638	gb AY496874	gb EU081215
gb AB189127	gb GU131939	gb GQ252674	gb EU482462	gb JQ045692	gb KJ737430	gb AY496877	gb EU081216
gb AB189128	gb GU131941	gb GQ199889	gb EU660407	gb JQ045693	gb AY858040	gb AY099336	gb EU081217
gb AB214879	gb GU131942	gb FJ882571	gb EU660408	gb JQ045694	gb AY858041	gb DQ401690	gb EU081218
gb AB214880	gb GU131943	gb FJ882572	gb EU660409	gb JQ045695	gb AY770511	gb AY496879	gb EU081219
gb AB214881	gb GU131944	gb FJ882573	gb EU660410	gb GU363549	gb JN662391	gb DQ401689	gb EU081220
gb AB214882	gb GU131946	gb FJ882574	gb EU660411	gb KJ622197	gb AY858042	gb DQ401691	gb EU081221
gb EU367962	gb FJ639712	gb FJ744726	gb FJ432722	gb KJ622198	gb AY858043	gb DQ401692	gb EU081222
gb KF954946	gb FJ639713	gb FJ744727	gb FJ432728	gb KJ622191	gb AY858044	gb DQ401693	gb EU081223
gb KF954947	gb FJ639714	gb FJ744728	gb FJ432731	gb KJ622199	gb AY858046	gb DQ401694	gb EU081224
gb KF954948	gb FJ639715	gb FJ744729	gb FJ562097	gb KJ622192	gb AY858047	gb DQ401695	gb EU081225
gb KF954949	gb FJ639716	gb FJ744730	gb FJ432741	gb KJ622193	gb AY858048	gb AY876494	gb EU081182
gb KF954945	gb KF955461	gb FJ744731	gb FJ562099	gb KJ622194	gb AY858038	gb AY923865	gb EU081183
gb KF041259	gb FJ639719	gb FJ687448	gb FJ432743	gb KJ622195	gb AY858039	gb EU081193	gb EU081184
gb KF041258	gb KF955332	gb FJ810413	gb KF955457	gb KJ622196	gb JN368477	gb EU081194	gb EU081185
gb KF041257	gb FJ639720	gb FJ744732	gb FJ562100	gb KC762681	gb HG316483	gb EU081195	gb EU081186
gb KF041255	gb GQ868626	gb FJ744733	gb FJ547061	gb KC762682	gb HG316484	gb EU081196	gb EU081187
gb KF041256	gb GQ868627	gb FJ810414	gb FJ547062	gb KC762683	gb AY662691	gb EU081197	gb EU081188
gb KF041254	gb FJ639721	gb FJ744734	gb FJ461322	gb KC762684	gb DQ675519	gb EU081198	gb EU081189
gb GQ466079	gb FJ639722	gb FJ744735	gb KF955458	gb KC762686	gb DQ675520	gb EU081199	gb EU081190
gb JQ922556	gb FJ639723	gb FJ744736	gb FJ562102	gb KC762685	gb DQ675521	gb EU081200	gb EU081191
gb JQ922557	gb FJ639724	gb FJ744737	gb FJ410229	gb KC762687	gb DQ675522	gb EU081201	gb EU081192

gb JQ922555	gb FJ639725	gb FJ744738	gb FJ461326	gb KC762688	gb DQ675523	gb EU081202	gb EU081181
gb GU131905	gb FJ639726	gb FJ744739	gb FJ461329	gb KC762689	gb DQ675524	gb EU081203	gb AY648961
gb GU131906	gb GQ868628	gb FJ744740	gb KF955459	gb KC762690	gb DQ675525	gb EU081204	gb AY676353
gb GQ868634	gb FJ639727	gb GQ868593	gb FJ547066	gb KC762691	gb DQ675526	gb EU081205	gb AY676352
gb GU131910	gb GQ868629	gb EU482452	gb KF955460	gb KC762692	gb DQ675527	gb EU081206	gb AY676351
gb GU131913	gb FJ639728	gb EU482453	gb FJ461334	gb KC762693	gb DQ675528	gb EU081207	gb AY676350
gb GU131914	gb FJ639729	gb EU482454	gb FJ461337	gb FJ644564	gb DQ675529	gb EU081208	gb AY676349
gb GU131916	gb FJ639730	gb EU482455	gb FJ461338	gb JQ411814	gb DQ675530	gb EU081209	gb AY676348
gb GU131917	gb FJ639731	gb EU482456	gb FJ562103	gb KF824902	gb DQ675531	gb EU081210	
gb GU131934	gb KF955507	gb EU482457	gb JQ045687	gb KF824903	gb DQ675532	gb EU081211	
gb GU131935	gb HM631854	gb EU482458	gb JQ045688	gb JF504679	gb DQ675533	gb EU081212	
gb GU131936	gb KF955474	gb EU482459	gb JQ045689	gb AY858037	gb AY496871	gb EU081213	

S4.4.1 List of Whole genomes of **Dengue Virus type 4** from **Asian region** (till July 2015 from NCBI Virus variation database)

KM190936
 AY618988
 JX024758
 KC762699
 AY618993
 FJ196849
 JF262779
 AY618991
 JQ922559
 JQ922560
 KC333651
 KC762696
 KC762695
 KF041260
 EF457906

GQ398256
KC762698
KP792537
AF289029
FJ196850
JF262783
KC762697
GQ868594
JQ822247
AY618989
JX024757
AY618992
JQ922558

S4.4.2 List of genomes from DENV4 Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

gb|KF041260|
gb|JQ922560|
gb|GQ868594|
gb|KP723482|
gb|JF741967|
gb|JQ822247|
gb|JF262783|
gb|KC762694|
gb|KC762696|
gb|KC762698|
gb|KJ160504|
gb|AY618991|
gb|AY618990|
gb|AY618992|
gb|AF289029|

S4.5.1 List of Whole genomes of **Dengue Virus type 1** from South **Asian region** (till July 2015 from NCBI Virus variation database).

JN903578
JN903580
JN903581
JQ922544
HQ891315
JN054255
KJ726664
JQ692085
HQ891313
KJ726663
JQ922548
JQ922545
KF289072
JN054256
KJ726665
JQ917404
JQ922546
HQ891314
JN903579
KP398852
KJ726662
HQ891316

S4.5.2 List of genomes from DENV1 South Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

gb|JN903578|
gb|JQ922548|
gb|JQ922544|

S4.6.1 List of Whole genomes of **Dengue Virus type 2** from South **Asian region** (till July 2015 from NCBI Virus variation database).

KJ918750
JQ922551

GQ252676
KF041232
JQ922549
GQ252677
KJ010185
KF041237
JQ955624
FJ882602
KJ701507
JQ955623
KJ010186
KF041233
KF041235
JX475906
JQ922550
KF041236
DQ448231
KF360005
JQ922552
FJ898454
KF041234

S4.6.2 List of genomes from DENV2 South Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

gb|JX475906|
gb|KF041232|
gb|KF041233|
gb|KF041234|
gb|KF041235|
gb|KF041236|
gb|KF041237|
gb|FJ898454|
gb|JQ922549|
gb|FJ882602|

gb|GQ252676|
gb|GQ252677|
gb|KF360005|
gb|KJ010185|
gb|KJ010186|
gb|KJ701507|
gb|DQ448231|
gb|JQ955624|
gb|JQ955623|

S4.7.1 List of Whole genomes of **Dengue Virus type 3** from South **Asian region** (till July 2015 from NCBI Virus variation database).

DQ401689
AY496877
GQ252674
JQ922557
KF041257
GQ199887
FJ644564
GQ199888
KF041256
KF041254
JQ411814
FJ882573
JQ922556
KF041258
AY496873
KF041255

GQ466079
AY770511
FJ882571
DQ401691
AY496871
FJ882572
FJ882574
JQ922555
DQ401692
GQ199889
KF041259
AY496874
AY099336
KF955474
DQ401693

S4.7.2 List of genomes from DENV3 South Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

gb|KF041259|
gb|KF041258|
gb|KF041257|
gb|KF041255|
gb|KF041256|
gb|KF041254|
gb|GQ466079|
gb|JQ922556|
gb|JQ922557|
gb|JQ922555|
gb|KF955474|
gb|GQ199887|
gb|GQ199888|
gb|GQ252674|
gb|GQ199889|
gb|FJ882571|
gb|FJ882572|
gb|FJ882573|
gb|FJ882574|
gb|FJ644564|
gb|JQ411814|
gb|AY770511|
gb|AY496871|
gb|AY496873|

gb|AY496874|
gb|AY496877|
gb|AY099336|
gb|DQ401689|
gb|DQ401691|
gb|DQ401692|
gb|DQ401693|

S4.8.1 List of Whole genomes of **Dengue Virus type 4** from South **Asian region** (till July 2015 from NCBI Virus variation database).

KJ160504
JQ922559
JQ922560
KF041260
JF262783
JQ922558

S4.8.2 List of genomes from DENV3 South Asian whole genomes set for which 15 or more primers predicted to amplify as per e-PCR tool output result.

gb|KF041260|
gb|JQ922560|
gb|JF262783|
gb|KJ160504|