TABLE S1. Location of hot springs surveyed in Yellowstone National Park, USA.

Sample Name	**Lat**	**Long**	**Date**	**pH**	**Temperature (°C)**
Amp-21	N44 48.06666	W110 43.72332	Aug-09	2.0	76
Amp-22	N44 47.82834	W110 43.46664	Aug-09	2.0	90
Mon-1	N44 41.09832	W110 45.24498	Aug-09	1.5	86
Mon-2	N44 41.09502	W110 45.22998	Aug-09	1.5	75
Mon-3	N44 42.755	W110 45.22998	Aug-09	1.5	70
Mon-4	N44 42.74833	W110 45.23334	Aug-09	1.5	87
Mon-5	N44 41.79498	W110 45.22998	Aug-09	1.5	79
Mon-6	N44 41.07666	W110 45.23502	Aug-09	1.5	79
Mon-7	N44 41.055	W110 45.22002	Aug-09	1.5	69
NL-10	N44 45.214	W110 43.432	Aug-09	4.5	93
NL-17	N44 45.11832	W110 43.70832	Aug-09	2.0	81
NL-18	N44 45.12666	W110 43.71336	Aug-09	2.0	83
NL-19	N44 45.12168	W110 43.71834	Aug-09	2.0	78
NL-20	N44 45.12834	W110 43.72164	Aug-09	3.0	85
SL-1	N44 21.45167	W110 47.61333	Aug-09	6.0	83
SL-2	N44 21.38	W110 47.77666	Aug-09	3.0	89
SL-3	N44 21.225	W110 47.84	Aug-09	2.5	83
SL-4	N44 21.01	W110 47.35016	Aug-09	5.0	80
SL-5	N44 21.1	W110 47.99833	Aug-09	4.0	81
SL-6	N44 21.1	W110 47.98	Aug-09	5.0	85

Syl-8	N44 41.99502	W110 45.91998	Aug-09	3.5	77
Syl-9	N44 41.95836	W110 46.03836	Aug-09	5.0	82
Syl-10	N44 41.96832	W110 46.07832	Aug-09	2.0	86
Syl-11	N44 43.63666	W110 46.09002	Aug-09	2.0	87
Syl-12	N44 41.95836	W110 46.11666	Aug-09	1.5	80
Syl-13	N44 41.93334	W110 46.10832	Aug-09	5.0	81
Syl-14	N44 42	W110 46.24002	Aug-09	2.0	73
Syl-15	N44 42.03498	W110 45.96666	Aug-09	4.5	85

TABLE S2. PCR primers used to confirm selected contigs from the RNA virus metagenomes.

Name	Sequence	Start	End	Length
Contig00002 2192F	TTTAGCGGTCACGCCGGCTG	2192	2211	20
Contig00002 2756R	CGCTCCAGCTCACGTCGTGG	2737	2756	20
Contig00009 702F	ATTGTGAGCTACGCGCGGGG	702	721	20
Contig00009 1337R	GGCGAGGAAACCCGTGTGCT	1318	1337	20

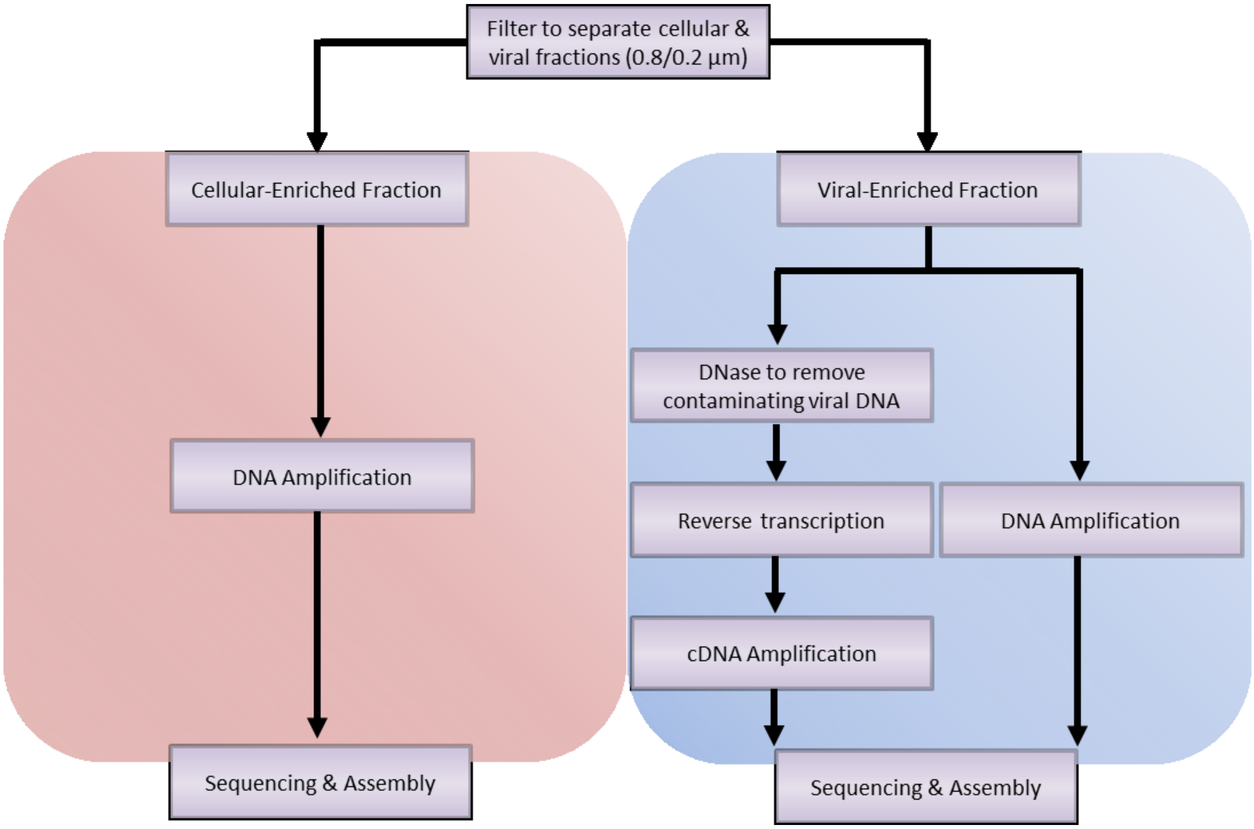

FIG. S1. Overview of the experimental flow to produce viral RNA enriched, viral DNA enriched, and cellular enriched metagenomes.

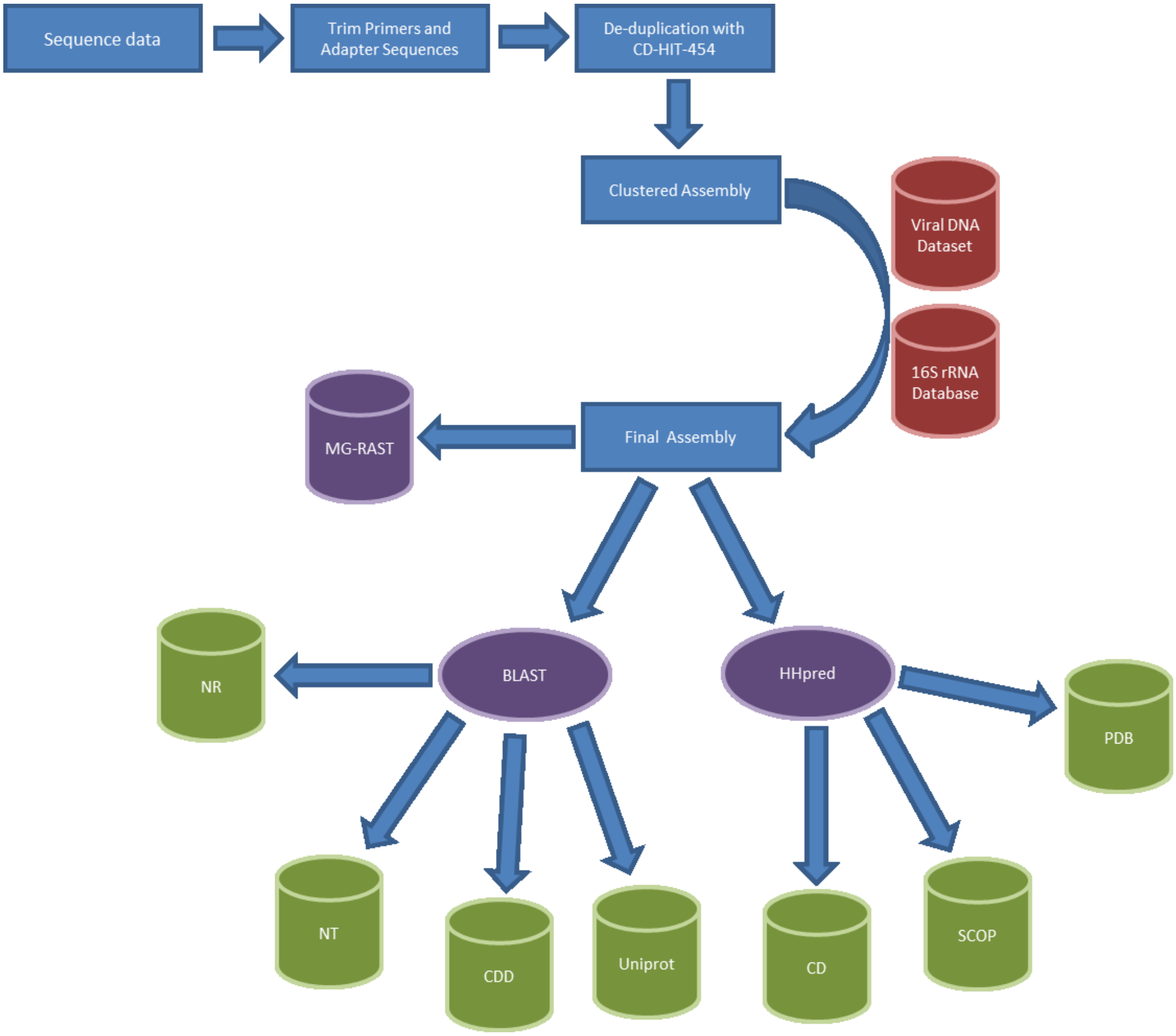

FIG. S2. Metagenomic viral RNA assembly outline. Raw sequence data was processed through a series of quality checks and redundant sequences are removed. Assembled contigs were compared against the paired viral DNA metagenomes and 16S rRNA databases. Matching contigs were removed from further analysis. Contigs are compared against a number of databases using a NCBI BLAST, MG-RAST and selected contigs against HHpred.

Statistical tests on constrained tree topologies with different positions of the putative archaeal virus RdRp. Likelihood and p-values for constrained trees (see Methods).

Tree #	LL	ΔLL	p
Unconstrained	-67716.4	n/a	>0.05
1	-67733.8	-17.5□16.2	>0.05
2	-67717.8	-1.5□13.9	>0.05
3	-67732.1	-15.7□18.6	>0.05
4	-67742.6	-26.3□20.4	>0.05
5	-67731.2	-14.8□19.3	>0.05
6	-67728.9	-12.5□14.0	>0.05
7	-67735.7	-19.3□20.5	>0.05
8	-67739.2	-22.8□20.0	>0.05
9	-67731.3	-14.9□18.7	>0.05
10	-67718.9	-2.6□11.5	>0.05

LL – Log Likelihood

ΔLL – Log Likelihood difference compared to the unconstrained tree p – p-value

Tree topologies in Newick format