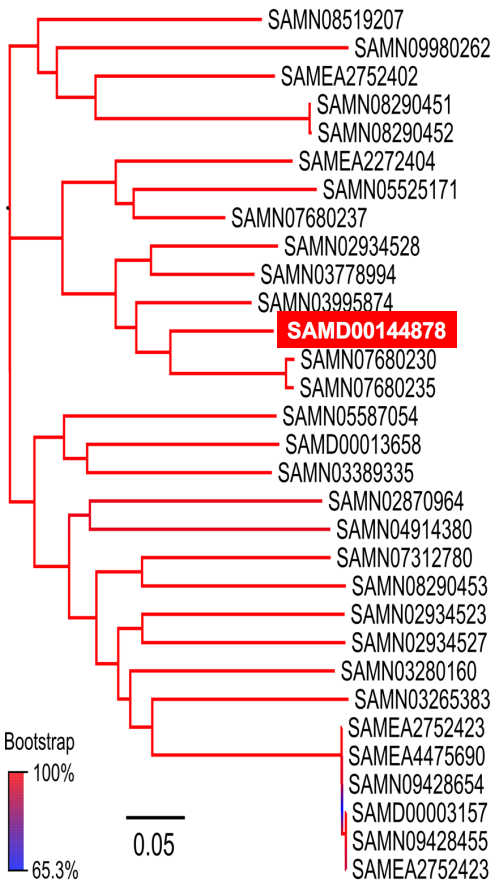

Strain	Country	Collection Date (yyyy/mm/dd)	Material	Antimicrobial Resistance Gene
AFG_SD01_1510_Aca_091	Afghanistan	2015/10/00	Stray dog fecal sample	blaMOX-12, blaOXA-504, blaPAC-1, dfrA1, qacEdelta1, sul1
OLC2686_Aeromonas	Canada	2017/00/00	Wastewater influent	aph(3")-Ib, aph(3')-Ia, aph(6)-Id, blaGES-5, blaMOX-12, blaOXA-504, mph(F), qacEdelta1, sul1, tet(A)
CECT 4221	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504
R25-2	China	2016/11/01	Wastewater sludge from bioreactor	aph(3")-Ib, aph(6)-Id, blaMOX-12, blaOXA-504, floR, tet(31)
T25-39	China	2016/11/01	Wastewater sludge from bioreactor	aph(3")-Ib, aph(6)-Id, blaMOX-12, blaOXA-504, floR, tet(31)
Ae398	N/A	0000/00/00	N/A	blaMOX-8, blaOXA-504
CHZ306	Brazil	2007/03/27	Zooplankton from seawater	blaMOX-8, blaOXA-504, tet(E)
ZJ66-1	China	2017/04/00	River	blaMOX-8, blaOXA-504, mcr-3.3, tet(E)
FDAARGOS_76	United States	2013/06/21	Human stool	blaMOX-12, blaOXA-2, blaOXA-504, qacEdelta1, sul1
A23	China	2013/08/14	Supermarket	ant(3")-Ih-aac(6')-IId, blaMOX-12, blaOXA-2, blaOXA-504, blaPER-3, catB3, mph(A), qacEdelta1, sul1
429865	Mexico	2013/00/00	Human urine	ant(3")-Ia, blaMOX-12, blaOXA-504, catA, catA2, qacEdelta1, sul1, tet(C)
GSH8M-1	**Japan**	**2018/08/06**	**Sewage effluent**	**aac(6')-Ia, aadA2, blaKPC-2, blaMOX-12, blaOXA-504, mcr-3.3, mph(A), qacEdelta1, sul1**
ZJ33-3	China	2017/04/00	Human rectal swab	blaMOX-12, blaOXA-504, catA, mcr-3.3, qacEdelta1, sul1, tet(A)
ZJ17-2	China	2017/04/00	River	blaMOX-12, blaOXA-504, catA, mcr-3.3, qacEdelta1, sul1, tet(A)
CH129	Brazil	2006/02/17	Seawater	blaMOX-12, blaOXA-504
N/A	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504
8LM	Brazil	2010/12/17	Human stool	blaMOX-12, blaOXA-504
YL12	Malaysia	2014/01/10	Compost	blaMOX-12, blaOXA-504
VBF856	India	2015/04/13	Human stool	ARR-3, aac(6')-Ib, aadA16, aph(3")-Ib, aph(6)-Id, blaMOX-12, blaOXA-181, blaOXA-504, catB3, dfrA1, floR, mph(A), qacEdelta1, qnrS2, tet(A)
TCO22	N/A	0000/00/00	Danio rerio gut	aph(3')-Ia, blaMOX-12, blaOXA-504, mph(A), tet(E)
R25-6	China	2016/11/01	Wastewater sludge from bioreactor	aadA2, aph(3")-Ib, aph(3')-Ia, aph(6)-Id, blaMOX-12, blaOXA-504, dfrA12, floR, mph(A), qacEdelta1, sul1, tet(E)
FDAARGOS_72	United States	2013/09/16	Human stool	blaMOX-12, blaOXA-504
FDAARGOS_75	United States	2013/06/28	Human stool	blaMOX-12, blaOXA-504
BWH65	United States	2014/00/00	N/A	blaMOX-3, blaOXA-504
L12	Malaysia	2014/04/00	Lake water	blaMOX-12, blaOXA-504, mcr-3.6
CECT 838	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504
NCTC12244	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504
HAMBI_1972	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504
N/A	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504
HAMBI_1972	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504
CECT 838	N/A	0000/00/00	N/A	blaMOX-12, blaOXA-504

Fig. S2 Coregenome phylogeny of *Aeromonas caviae* GSH8M-1 among publicly available 30 strains (updated at 2018/10/29).
Using the complete genome sequence of GSH8M-1 (4,611,279 bp), bwa-read mapping analysis identified 70.53% of the full genome as core-genome sequence and a total of 229,493 single nucleotide variations (SNVs) were identified, excluding prophages and repeated regions.