Table S1 ALV-J strains used for analyzing NGSs

Isolate	Accession no.	Isolate	Accession no.	Isolate	Accession no.
HPRS103	Z46390	**SDAU1102**	KU159178	**GX20YL05**	MW491266
NX0101	AY897227	**SD1109**	KF768000	**HN1001-2**	HQ260975
Js-nt	HM235667	**WB1106j**	JX570795	**GX12NN20**	KT598483
JS09GY3	GU982308	**WB11058J**	JX570793	**NHH**	HM235668
SCAU-HN06	KQ900844	**WB11098(J)**	JX848322	**PK19SA01**	MN956380
TBC-J6	MT409625	**SD100502J**	HQ270188	**10022-16**	GU222400
TBC-J4	MT409624	**HLJ09SH02**	HQ634807	**LN08SY10**	HQ634802
GD1407	KU500034	**SDAU1704**	KY980660	**SCAU11-XG**	KC149971
GX14HG01	KU997685	**DBYJ1102**	KC875858	**GD1109**	JX254901
GD18QY22	MN262620	**GX20YL09**	MW491270	**JL1801**	MN419348
GD14J2	KU500032	**WSC112**	KJ631322	**YZ9902**	HM235670
GD17FS01	MN262599	**HAY013**	HM235665	**Hc1**	AF247391
JX19ND03	MN262539	**NM2002-1**	HM235669	**SDAU1702**	KY980658
JX19TH01	MN262528	**IMC10200**	AY234051	**FJ201306**	KM655820
JL1802	MN419349	**SDC2000**	AY234052	**SCMZ92**	KF796647
GD13GZ	KU500030	**GD17ZQ06**	MN262604	**HuB09JY04**	JN378888
WGZ13	KJ631313	**SD9901**	AY897220	**ZB110604-6**	KC841157
JL1803	MN419350	**4817**	AF247385	**ZB110604-5**	KC841156
XX2-09	HM775331	**SD0002**	AY897224	**ZB110604-3**	KC841154
SD1804	MN419338	**SD9902**	AY897221	**GX14HG03**	KY983569
GM209-4	MH379645	**JS1807**	MN419341	**CAHHM01**	HM640944
GM209-5	MH379646	**SDMG1801**	MN413674	**JS09GY6**	GU982310
HB1801	MN419352	**TJ1801**	MN419353	**HLJ13SH01**	KM376510
LH20180301	MK944404	**GD18JM01**	MT538241	**HB2010001**	MZ197985
SD1810	MN419347	**JS14NT02**	MN735302	**JL093-1**	JN624878
JS1808	MN419342	**CAUSY01**	JF932001	**JL08CH3-1**	HQ634809
JS1806	MN419340	**sdau1002**	JN389518		

Table S2 Primers used for constructing mutant infectious clones of ALV-J

Primer	Sequence
N17	TGGGTCACCTGGGCATATAAGACGGGCCAAAC
	GTTTGGCCCGTCTTATATGCCCAGGTGACCCA
N62	GCTACTGCTTGCGAATATGACACCGATTTAGC
	GCTAAATCGGTGTCATATTCGCAAGCAGTAGC
N78	ATGTTTAATACAGACTCTATATACGACCCTCCCTTG
	CAAGGGAGGGTCGTATATAGAGTCTGTATTAAACAT
N98	GGTCCCAAATGATCAAGTATGGAACAAAACGTACGTG
	CACGTACGTTTTGTTCCATACTTGATCATTTGGGACC
N116	TGTGCTATAAAGAGAACTATCGCAGTAGCAGTAG
	CTACTGCTACTGCGATAGTTCTCTTTATAGCACA
N131	CATTTTTGATGGGAATTTTTATGGGACTGGTGGGG
	CCCCACCAGTCCCATAAAAATTCCCATCAAAAATG
N159	CTTATAAGACCCTATGTCTATCAATCATGGACGATGGT
	ACCATCGTCCATGATTGATAGACATAGGGTCTTATAAG
N185	TTGTGGATTCACCAGCTATGAGACTCGTTATTATAGC
	GCTATAATAACGAGTCTCATAGCTGGTGAATCCACAA
N193	CTCGTTATTATAGCGGGTATTATTCCGATTGGTGTAG
	CTACACCAATCGGAATAATACCCGCTATAATAACGAG
N209	GAATGGTCAGGTGGTTATTGCACGGCGGAAT
	ATTCCGCCGTGCAATAACCACCTGACCATTC
N226	GTTTACCTTCAGGACGTATGAGTCAGAGGTGTT
	AACACCTCTGACTCATACGTCCTGAAGGTAAAC
N234	CAGAGGTGTTGTGGAATTATGGGACTGCTAAGGC
	GCCTTAGCAGTCCCATAATTCCACAACACCTCTG
N284	ATGACGTATGGGCCGTATATTACGGGTCACCGC
	GCGGTGACCCGTAATATACGGCCCATACGTCAT