

Gene	<i>Vg-like A</i> dsiRNA fragment	Proportion of correctly aligned nucleotides	Alignment of the longest aligned fragment
<i>Vg1</i>	1	68%	accatgaacacacaacagctgactgaa -CCATCAACAGGCTACAGCATACTAT- **** * * * * * * * * * *
<i>Vg1</i>	2	64%	cgcaagaattaaatccgcgaggtgttc -CCATGAATTGCGTCCGTGAGACTTT- ** * * * * * * * * * *
<i>Vg1</i>	3	60%	gagtgtcagtcgaggtcccttagcggc -CGAGTACGTTCAAGTTCCTTTCAG- * * * * * * * * * * *
<i>Vg2</i>	1	48%	CGTCCC GATGGTAACTCATAGCATT -ATCAACAGGCTACAGCATACTAT- * * * * * * * * * *
<i>Vg2</i>	2	52%	TCATAGCATTGGGCTTGTTTCAGCTTTC -CCATGAATTGCGTCCGTGAGACTTT- * * * * * * * * * *
<i>Vg2</i>	3	60%	TCGACTGTCTTCCCTGCTTCTTTGTCGC -CGAGTACGTTCAAGTTCCTTTCAG- *** * * * * * * * * * *
<i>Vg3</i>	1	28%	GGAACCACATGGTGTT -CTACAGCATACTAT- * * * * * * * * *
<i>Vg3</i>	2	60%	gtaatgtattgtgtat atgagaact -CCATGAATTGCGTCCGTGAGACTTT- *** * * * * * * * * * *
<i>Vg3</i>	3	32%	atgtcccttttccc -AGTTCCTTTCAG- ** * * * * * *
<i>Vg-like A</i>	1	100%	ACCATCAACAGGCTACAGCATACTATG -CCATCAACAGGCTACAGCATACTAT- *****
<i>Vg-like A</i>	2	100%	ACCATGAATTGCGTCCGTGAGACTTTA -CCATGAATTGCGTCCGTGAGACTTT- *****
<i>Vg-like A</i>	3	100%	ACGAGTACGTTCAAGTTCCTTTCAGC -CGAGTACGTTCAAGTTCCTTTCAG- *****
<i>Vg-like B</i>	1	68%	gcgttctatagacttcagcatcgtata -CCATCAACAGGCTACAGCATACTAT- * * * * * * * * * *
<i>Vg-like B</i>	2	64%	accaggatttttcgagcctgtggcttaa -CCATGAATTGCGTCCGTGAGACTTT- *** * * * * * * * * *
<i>Vg-like B</i>	3	44%	gcgagttcattagactt -CGAGTACGTTCAAGT ***** * * * * *
<i>Vg-like C</i>	1	44%	gcctacattatattatc -GCTACAGCATACTAT-- ***** * * * *

<i>Vg-like C</i>	2	44%	atcacgtacgttataattatc -TIGCGTCCGTGAGACTTT-- * *** ** * * *
<i>Vg-like C</i>	3	36%	caaattcgtgggcagtc --AGTTCCTTTGCAG-- * *** * ****