

Assembly: GCA_930367235.1_idSarRose1.1_genomic

[illegible]

GGCGGGCTTGAATTCCTTGTTTCAAGGGTTGTTCAATCCCTTGATTGTGAAATTTTACGAATGCAAAAAAAGGATTAAAAATTAATGCTCAAAGTCATCTGAAAGGAAAGTTTGTTAAATAAAAAACAAAAACACAACACAACATACTCAG
GAAATTTGAAGCTTTGGTACTTGAGTGTGTAATAATACAAAGCTTAAGAGGAAAGACCGTTAAGGGTGACCGCCAAATTTTTTTTTTTTTTTT

	Sar_ros1	Sar_ros2
Sar_ros1	-	34
Sar_ros2		-

Pairwise sequence identity matrix (%) showing similarity between lncRNA sequences.

[illegible]

Upstream promoter alignment showing conserved regions. Sequences include Pol III promoters (noeCR34335, Arthropod_7SK, 7SL, RNase_MRP, RNaseP_nuc, U6, U6atac, tRNAsec, snoRNAme18SA1806) and Pol II promoters (U1, U2, U3, U4, U4atac, U5, U7, U8, U11, U12, OrCD1). Conserved positions are highlighted in the alignment.