

Assembly: GCA\_037042425.1\_ASM3704242v1\_genomic

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.94

GGGGCGGTGATGACATTCCGCAGTAACGACGGTTGGGCAGATCCCGTCTCCACCCCATACTCTCGAATTGTGCCCGTTGGTAGCTAAAGTTACGATTGGAATTGAAAACAGCAAAAGCAAACTTTCTCATCTCTCTCTGAAACAAAACTAA



5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.87

GGCGGTTCATGCGTCTCCGAGTTGTTGGGTTGGTCACATCCCCGACTATGAGTCAATTGTGACAAATATATGAATTTCTTGCTTGTAACCAACCGAATCCATTTCATTATTCTTAAACCAACCAACAC

Age Group	Very satisfied	Satisfied	Dissatisfied	Very dissatisfied	No answer
18-24	10%	20%	30%	20%	10%
25-34	15%	25%	25%	20%	10%
35-44	10%	20%	30%	20%	10%
45-54	10%	20%	30%	20%	10%
55-64	10%	20%	30%	20%	10%
65+	10%	20%	30%	20%	10%

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.81

GGCGGTCATGC6TCTCAGAGCT6TTT6TTTGGGTTGGTCACATCCCCGACTATGAGTCAATT6TGACAAATATATGAATTTTCTTGCTCT6TAAAAAAACCGAATTCACATTTTATTTATTCCTAAAAAACCATTTGCAATCAATCCCCT



5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.81

GGCGGTCATGCGTCTCCTAGCTGCTGTTGGGTTGGTCACATCCCCGACTATGAGTCAATTGTGACAAATATATGAATTTTCTGTCTCTGTAAAAACCGAATCCACATTTCAATTTATTCTAAAAAACCATTGCAATCAGTCCCCTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.96

GGCGGGTCATGCGTCTCCGAGCTGTGGGTTTTGGGTGGTGCACATCCCCGACTATGAGTCAATTGTGACAGATATATGAATTTCTTGTCTTGTAAAAAACCGAATCCACATTCATTATTAACAAAAAATCCATTACATTGCTATAAT



5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.86

GGCGGTCATGCGTCTCCGAGCTGCTGTTTGGGTTGGTCACATCCCCGACTATGAGTCAATTGTGACAAATATATGAATTTTCTTGCTTGTAAAAAAGCGAATTCACATTTCAATTATTACTAAAAACCATTCGAATAATCACTTTAA

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5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.88

GGCGGTCATGCCCTCTCCGAGCTGTATGCTTTGGGTTGGTCACATCCCCGACTATAAGTCAATTGTGACAAATTTTATATGCTTGTTTTCATTTATGAATTCATTATTATTATTATTATAATATCATTATTATTCATTATTAAAT

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.87

GGCGGTCATGCCTCTCCGAGCTGTTGTTGGGTTGGTCACAGCCCCGACTATGAGTCAATTGTGACAAATATATGAATTTTCTTGTCTGTAAAAAACCGAATTCCACATTTATTATGAACAAAAACCAATACATATGCCCGACAAT

ATTATCGGCGGCTCATGCTCTGACCTCTTCTCTCTGCTGCTTTT

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.89

GGCGGTCATGCGCTCCGAGCTGTGTGTTTTGGGTGGTACATCCCCGACTGTGAGTCAATTGTGACAGATATGAAATTTCTTGCTTGTAACCAACCGAATCCACATTTCATTTATGAACAAAAACCGATACATGTCCCACCAC



5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.80

GGCGGTCATGCGTCTCCGTGCTGTGGTTTGGGTTGGTCACATCCCCACTATGAGTCAATTGTTACAAATATATGAATTTTCTTGCCCTGTATAAAACCGAATTCACATTTCAATTATTGATATAAAAAACCAATTGCTATTCTTAGAAA

Age Group	Very satisfied	Satisfied	Dissatisfied	Very dissatisfied	No answer
18-24	10%	10%	10%	10%	60%
25-34	10%	10%	10%	10%	60%
35-44	10%	10%	10%	10%	60%
45-54	10%	10%	10%	10%	60%
55-64	10%	10%	10%	10%	60%
65+	10%	10%	10%	10%	60%

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.81

GGCGGTCATGCGTCTCCGAGCTGCGTGTTTCAGGTTGGCCACATCCCGGACTATAAGTCGATTCCGACTATAAGTCAATTGTGGCAATGTTGCTTGTTGATGTCCTTCAGGCTTACACCTACGATAAGTCGCATCAACAATATGAAATG



5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 6nt PSE: 0.85

GGCGGTCATGGTCCTCCGAGCTGTTGTTGGGTTGGTCACATCCCCGACTATGAGTCAATTGTGACAAATATATAAATTTCTTGATGCGTTGTATAAAACCGAATCCACATTTCAATTAATCCTAAAAAACCATTCGAATGACACTAA

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.96

GGCGGTCATGCGTCTCCGAGCTGTGTGTTTGGGTTGGTCACATCCCCGACTATATGAGTCAATTGTGATAAATATATAAAATTTTCTTGATGCGTCCACATTTCATTTATTAAACAAAAACCATTGCTATATTGTGGATTGTTTTATT



5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.80

GGCGGTCATGCGTCTCCGAGCTGCAATGATTCAGGTTGGCCACATCCGAGACTACAAGTCAATTGTGGCAAATGTTGTTTGTGATGTCCC TCACACTTACACCTACGATAAGTCGCATCAACAATATAAAATGATATATAAGCTAGCTCG



5' motif: GCGGT 3' motif: ACCGC Internal max. Poly-T: 4nt Trailing-T: 5nt PSE: 0.88

Hir\_dun16 | JBAMBM010000133.1:1248857-1249001 (+) | 145 nt | lncRNA: noe consensus e-value: 1.2e-06

5' motif: GCGGT 3' motif: ATCGC Internal max. Poly-T: 3nt Trailing-T: 5nt PSE: 0.80

GGCGGTCATGCGTCTCCGAGCTGCGTGTTCAGGTTGGCCACATCCCCGACTATAAGTTCGATTCCGACTACAAGTCAATTGTGGTAGATATAAAATGATATAGCTAGCTCGTGGGACGCCCTTGGTCTGATCGCCACTTTT

## Pairwise Identity Summary

Sequences: 16

**Comparisons: 120**

**Identity range: 8.7% - 97.8% (avg: 61.6%)**

**Distribution:** Low (<30%): 15 | Medium (30-60%): 27 | High (≥60%): 78

[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.