CLUSTAL 2.1 multiple sequence alignment

1Vg270421 ATATATATATATATATATATATATATATATAATATATATATATAATACAATATATGTATA

1Vg294361 -------TACTTGTATAGATATAATTATG-----TGTCTGTATATAACAGTATATCTATC

LVAN2Vgcpromoter ------------ATAAACATAGGGTGGCTGCAAATTTATGCGGCCAGCTATACTGCTACT

LVAN2Vgbpromoter -----TGAAATTCTATGTATTTTTTGATGATGGGTCGGTTAGCGTAGCAAAACCCCCCCG

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1Vg270421 TACACACATACATATCTATCTATCTATCTATCTATCTATCTATCTATCATCTATATATCT

1Vg294361 TATACACGTAAGTACATACAAATATGTATAGG-------CATATATTCATATAAATAGAT

LVAN2Vgcpromoter AGTAAAAGAACTCAATATATGAAGTAGTAAAAGAAAGAAAAATTACTAAGATATAGAGAC

LVAN2Vgbpromoter GCGCGCTATACATGTGTGAGGAACCATTAGAATGTGTCCCGTTGAAGAGGGGGAGAGAGA

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1Vg270421 ATCTATCTATATATATATGTATGTATGTATATATATACATATTTATACAAACACACACAC

1Vg294361 ATATATGTACACACACAGACACACACACACACACACACACACACACACACACACACACAC

LVAN2Vgcpromoter AAAAAATATTGCACAAAAATCACATCATCTTATGACACAGATAAGGGATGAGATATTCGA

LVAN2Vgbpromoter GAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGAAGAGAGGAGGAAGGAGGGAAAG

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1Vg270421 ACACATATATATACATATATATATTCATATATT-TTATACATATACATATAAACATTCAT

1Vg294361 ACATATATATATATATATATATATATATATATATATATATATATATATATATATGTGAAC

LVAN2Vgcpromoter GATATGAAGTAGATAGCATAAAATGCAGATAAG--------GTCAGCTTGGTACAGGCGG

LVAN2Vgbpromoter AGGAGGAAGGAAGGGAGGAGGGATTGAGGAGGG-AGAGGGAGAGGAGAGGGAGGGTGAGG

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1Vg270421 CATATATACATATATATATATATATATTATATATATATATATATAATATATATATATATA

1Vg294361 AATAGAGAGAGAGAGAGAGACAGAGGAGAGAGAGAGAGAGACAGAGTATATATATATATA

LVAN2Vgcpromoter AGTGAAATGCGGTGACGTCATGCATATTCGAAATACCGTGCTAGATAATGCATATTTTAA

LVAN2Vgbpromoter GGAGAGGGAGAGGGAGAGGGAGAGGGAGGGAGAGGGAGAGGGAGAGGAAGAGGAGGAAGA

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1Vg270421 TATATATATATATATATACAGACAGAGAGAGATACAGAGAGAGAAGAGAGAGAGAGAAGA

1Vg294361 TATATATATATATATATATATATATATATATATATATATATATATATATATATATATATA

LVAN2Vgcpromoter TTTCATCATTATCATTTTCATTTATTAATTTAAATTTGATTCAATGTATGGTATTTTTTA

LVAN2Vgbpromoter GGAAGAGGAAGAGGAAGAGGGAGAGGGAGAGGGTAGAGGGAGGGAGGGAGGGAGGGGAGA

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1Vg270421 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAAT

1Vg294361 TATATAGATGGATAGATAGATATAGATATATATATATAGA-----------------TAT

LVAN2Vgcpromoter TGTAATACTG-AGAGATAATGTAAATGTCTCTTTTCTGGT-----------------ACC

LVAN2Vgbpromoter AGAAAAAGAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG------------AGA

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1Vg270421 ATATGCATTCATATATATATACATATATATATATATATTATATATACATATACATACATA

1Vg294361 ATTTGTTTTCATGGGTATCTATCTATCTATCTATCTAT---ATATCTATATCTATATATA

LVAN2Vgcpromoter TATTTTCTCCTTTTTGGTCTCATATTGCATATATTTTTTTCATTTTCGCATAGATATATA

LVAN2Vgbpromoter GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA

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1Vg270421 TGTATACATATATACATATACATATATTAATATATGTTTTATATATATATACATATACAT

1Vg294361 TATATATATATATATATATACATATAT---------------ATATACATACATATATGT

LVAN2Vgcpromoter AGACTGCTTTGGAATTGAATGTTTTCAG-----TTTTATTTACAGTTTTGCTCTTTACTT

LVAN2Vgbpromoter GAGGGGCGGGGGGGGAGGAAAAAGTAGAAAG----------GAAGAGAAAGGGATAGTTA

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1Vg270421 ATATATATATGTATATATATATATATATATATAT-ATATATATATATATATATATATATA

1Vg294361 AAATATATATGTATATATATATATATATATATATTATATATATATATATATATATATATA

LVAN2Vgcpromoter ATATCTTAATGTAATTATTCATTTATTCATATGGTAATTCAGAATACCTTCGCGGGGCCG

LVAN2Vgbpromoter TACATAGAGAGAAATAAATAAAATGAAAAAATGAGAAATCGATACACATGTACACACAAA

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1Vg270421 TATATATATATATATATATATATATATATAAATGCACAAACATATATACATATATATATG

1Vg294361 TATATATATATATATGTATATATATATATATATATATATATATATATATATATATATATA

LVAN2Vgcpromoter ATTACAATGATACTGGTAACGGTGAGCTCCCCTAAGCCTATACTACCCATAGATGTAGGA

LVAN2Vgbpromoter TATATATATATATATATATATATATATATATATATATATATATATATATATATATATATA

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1Vg270421 TATATATATGTATATATATATTATATATATATATATATATATATAATATATATATATATA

1Vg294361 TAATATATATATATATATGTTTATGTGTGTATATATATGTATACAGAGAGAGAGAAAGAG

LVAN2Vgcpromoter CGTACCCTGTGGTAGCCCGATCGTAGGGGAAGTACCAGGGACATTGAGGGGTAAAATGTG

LVAN2Vgbpromoter TATATATATATATATCACGCACACACCCATATATATATATATATATATATATTATATATA

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1Vg270421 TATTATATATATTTATCTATACACACACACACACACACACACACACACACACACACACCA

1Vg294361 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

LVAN2Vgcpromoter AAATATTTATACAGAAAATATCACCCCCCCCCAACCCCTGTCCTGGAAG-----ACAAAG

LVAN2Vgbpromoter TATTATATATATATATATATAATATATATATATATATATATATATATATATATGTATGTG

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1Vg270421 CACACACAACATATATATATATATATATATATATATATATATATACATATACATATACAT

1Vg294361 AGAGAGAGAGAGATACATATATATATATATATATATATATATATATATATATGTGTGTGT

LVAN2Vgcpromoter AATCCTCCACGTATTCACGGCAGGATAGTGCTTAGAATGGGTGGTGGATGTGTGGTGTGG

LVAN2Vgbpromoter TGTGTGTGTG-TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTACATTGTGATAAATAGAT

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1Vg270421 ATACATATACATATACATATAGATACATGCATACATACATACATACATACACACACACAC

1Vg294361 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

LVAN2Vgcpromoter GTGGCTGAAGCTCTTAGTCTGGAGGATAGGGTGACGCCGCGGTGCACAGTGTAACCTTAC

LVAN2Vgbpromoter AAAACAAAAAAATAGAGAGATAGAGAGAGAGATAGAGAGAGAGAATCAGAAAGAAATAGA

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1Vg270421 ACACACACACACCACACACACACATACACAC-ATATATATATATATATATATATATATAT

1Vg294361 GTGTGTGTGTG---TGTGTAAATATATATAT-ATATATATATATATATATATATATATAT

LVAN2Vgcpromoter ATTTAGGTCCTGGGTTTATGAAGTGATGGGA-ATG-GTCGACAACCGGGTGTGTGCATGC

LVAN2Vgbpromoter GGAAGATAGAGGGAGAGGTAAACTACTGAAAGATAGATGCAATACAGACAGAGTAGATAA

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1Vg270421 ATATATATATATATATATATATATATATATATATAT-TATATATATATGTCAGTGTGTTT

1Vg294361 ATATATATATATATATATATATATGTATATGTATATGTATATGTATATATATATATATAT

LVAN2Vgcpromoter ATCGGAGAGAATGTTGCAGTCCTTCCAGTAATCGGGGATCATGATCGGTCAAGGGACGAC

LVAN2Vgbpromoter TGAGTAAGAGACAAAAGACACACAAAAAAAGAAGAAAAAAAAGTAAAAATAAAGATAAAA

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1Vg270421 GTGTGTGCATCCATCTATCTATATATGTGTATATACATACATATAATATATATATATAAT

1Vg294361 ATATATATATATATATATATATATATATATATATATATGCATATAAATGTACAAATATGT

LVAN2Vgcpromoter TCGTTTCTTAACATCTGCAAGTAGG-GTCTAGCTGGTTCAGTCCTCGACCGCGACGAGGG

LVAN2Vgbpromoter AAGTAAAAAGGGCAATTTAAAGCGAGATCCAGAATTTAGAGAAAAATAGACCTTTACGCC

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1Vg270421 ATATATATATTATATATATTATATATATATATATATATATATATATATATATATATATAT

1Vg294361 GTATATATATTTATATATACGGATATATATACATATGCACACACACACACACACACACAC

LVAN2Vgcpromoter AAAGATCGCGTGTCTCCCCCAGAACTTCCCGTCAGTAACTCCACCCACGTTGTATTTGTG

LVAN2Vgbpromoter TCATTTCCATAATCTTCTGCCTCCAATCTTTCAAGAAAAACGACGACCGCCCAATCGCGT

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1Vg270421 ACATAGA--CACATACACACACACTCACACACACACACAGACACACACACACACACACAC

1Vg294361 ACACACA--CACACACACACACACACACACACACACACACACACACACACCAGCATACTC

LVAN2Vgcpromoter GCGGTCG--AACTTGCACTCTTCTACTTGTACTTCGACG-ACTTTTTCTTAGCCCTAATC

LVAN2Vgbpromoter CTTATCAGCCAAATTAATCCAAAATTTCATCCGCCAGCTGATTAGAATCGAGCTGATTAG

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1Vg270421 ACACACACACACA-------------------CACACACACACACACACACACACATATG

1Vg294361 ACGGACACATACAGAAAGGGAAAAAGAAA-TGCGCACACAGACACACACACACATACACA

LVAN2Vgcpromoter ACATGCTGCTGATCCATGGCCCAGGGAATGCTTACCCCTTGGCAGAAACTCGACCTGTTG

LVAN2Vgbpromoter GCTAACACGGATGATAGTCATAAGGGGGAAAAAAGTACTGTAAACACTGAACACTTTGTA

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1Vg270421 TATATATATATGTATACATATATATGT---------------------TATATATATATA

1Vg294361 TATATGTATGTGTATACATGTGTATATATGTGTGTGTCTTTGTGTGTGATTGTGTGTCTC

LVAN2Vgcpromoter GAGATGCTCGCAAAGCCCAGTGCAAGCTCTCGCCACATGGGCTGGACCGTGAATGCCTCA

LVAN2Vgbpromoter CCCTGAGGTGTGTACACGGCAGGTTGCACGGGTGATGTACACTCTTTAACCGACCCCCGC

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1Vg270421 TATATATATATATATATATATATATATATATATATATATATATATATATATATAGTATAT

1Vg294361 AGTCCGTTTATATATATATATATATATATATATATATATATATATATATATATA-TATAT

LVAN2Vgcpromoter GGATCAACAGGATATTCATATCGAGGTGAGCCCACTAATAGAAGGATCTCATTGATATCG

LVAN2Vgbpromoter GGTAGTACATAATGCAGTAATGATAGTGATGACGTCTGGCTTTCAGGCTTCAGAATCACC

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1Vg270421 AT---------------------GTATATACATATATATATGAATATATATGTATATGTA

1Vg294361 AT---------------------ATATATATATATATATATATATATATATATATATATA

LVAN2Vgcpromoter AGGCGGACCAGCGACACAGCCGCCTCTCCTGCTTCGCGCCGCAAACTTGTTGCCCGTCTG

LVAN2Vgbpromoter AGTTG------------------CTATTCACCTGCGAACACCTGACTCTGGACAGGAGGT

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1Vg270421 TATATATATATATATATATATATATATATATATATATATATATATATATTATATATATAA

1Vg294361 TATATATATATATATATATATTATATATTATATATATGTATGTATGTATTATATACATAA

LVAN2Vgcpromoter AGCAGGATTTGCCCGCACTTTCCGCAGCCCATCCCTGAGCAGTACTTGGAAAGTGTACAG

LVAN2Vgbpromoter GGGGGAGGTGGGGGAGGTGGGGGAGGTGGGGAGGTGGGGAGGTGGGGGAGGTGGAGGAGG

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1Vg270421 TG-----CACACACACACACACT-ACATACACACATATATATATATAT-----ATATACA

1Vg294361 ATGCACACACACACACACACACACACACACACACACACATACATATAT-----ATATATA

LVAN2Vgcpromoter TATTATGCTGAAGCACTGACGACACAGCACACGTAATGCTTCATCTAAGACCAATCTACA

LVAN2Vgbpromoter TAGGNTATATATATATATATATATATATATATATTATAATATATATAT-----ATATATA

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1Vg270421 TATATATATATTATATATATATAATGTAATATATATATATATATATATATATATATATAT

1Vg294361 TATATATATATATATATATATATATATATATATAATATATATATATATATATATATATAT

LVAN2Vgcpromoter TGGTTTTGTACACTGATATTGTGGTGCCATACACATTTTATAACAATTTAGTGCGTTATG

LVAN2Vgbpromoter TATATATATATATATATATATATATATATATATATATATATATATATATATAATATATAT

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1Vg270421 ATATATATATATAATATATATAATATCTGTATATACATATAAATAATATATATATGAATA

1Vg294361 ATAAGTATATATATCTATATATATACATATATATACACACATATGTTTAAACACACACGC

LVAN2Vgcpromoter ATAGCCTGGAACACCTGTAATGAAAAGCATG-GTAGTTACCTGCAATGGAACACTATTGA

LVAN2Vgbpromoter ATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT

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1Vg270421 TATAATATATA-TATATATATACACATATATATAT--------------------AATAT

1Vg294361 ACATGTGTGTG-TGTCTGTGTGTGCATGTGTGTGTGTGTGGGGGGTGAGTGTGCGTATGT

LVAN2Vgcpromoter TCAAGTGGATGGTTGCTGTGAGTAGTTGTTTACTGAGAG-------------TTTGTTTA

LVAN2Vgbpromoter ATATATATATA-TATATATATATATATATATATAT-------------------ATATAT

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1Vg270421 ATATATATATATATATATATATATATATATTATATACATATACACATATATATATATATA

1Vg294361 GTGTGGGTATGTATATGTATATATATAACATATGGACATCTATATCTATACATTTATTCA

LVAN2Vgcpromoter TTGGGAGTGTTTTGTTATAAGTGATTGTCGTTGTGAATGGTTGTACTTTGTGAGTGGCTG

LVAN2Vgbpromoter ATATATATATATAATATATATATATATATATATATATATATATATATATATATATATATA

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1Vg270421 TACATA-----TCATATATATATATATATATATATATGTATATGTGTGTGTGTATGCTTG

1Vg294361 TTAATAGATAGATATACATACATACATCATGTATCATATATATGTGTGTGTGTATGCTTG

LVAN2Vgcpromoter TTCGCTGTGAGCGATGGTTCGGTGTGAGCGGTTGTTCGCTGTGAGCGNTATATATATATA

LVAN2Vgbpromoter TATATATATATATATATATATATATATATATATATATATATATATATATATATATATATA

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1Vg270421 TTCTTTTTTCTGTACCTTCCATTTACCGTTGATTTATCGCGTACTTG--GATAAGCTTCA

1Vg294361 TTCTTTTTTCTGTACCTTCCATTTACCGTTGATTTATCGCGTACTTG--GATAAGCTTCA

LVAN2Vgcpromoter TATATATATATATATATGTAAGGGTATATGAATGATTCATATTATTGACGAGAATTCCCT

LVAN2Vgbpromoter TATATATATATATATATAGTAGGGTATATGAATGATTCATATTATTGACGAGAATTCCCT

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1Vg270421 GAAAAGAGCTCGGTGATTCACGGCGACATGCAAACGTCACTTAAAACTCTCGAGGAGGTG

1Vg294361 GAAAAGAGCTCGGTGATTCACGGCGACATGCAAACGTCACTTAAAACTCTCGAGGAGGTG

LVAN2Vgcpromoter GCAGAAAGAACTTTGTCAAAAACTGAATTGCTTACAG-ACTGTCTAGTCCAGATTAGAT-

LVAN2Vgbpromoter TCAGAAAGAACTTTGTCAAAAACTGAATTGCTTACAG-ACTGTCTAGTCCAGATTAGATA

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1Vg270421 ACGCTGCGATCCCGGTCAGCTGGAGATGGCGACGGGTATATAAGGCCGAGGCGCAGGGGG

1Vg294361 ACGCTGCGATCCCGGTCAGCTGGAGATGGCGACGGGTATATAAGGCCGAGGCGCAGGGGG

LVAN2Vgcpromoter ---ATGCAATTCG--TGTGACTCATGTCATGTCGGGTATAAAAGGCAGAGACTCAGCAGG

LVAN2Vgbpromoter TGACGGGCAATTCG-TGTGACTCATGTCATGTCGGGTATAAAAGGCAGAGACTCAGCAGG

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1Vg270421 TCGGGCAGTAGTCTTGGTGATCGCTCAGAACCACCATG

1Vg294361 TCGGGCAGTAGTCTTGGTGATCGCTCAGAACCACCATG

LVAN2Vgcpromoter TCGTCCAGTAGTCGTGGTGACCGGGTAGAGCCACCATG

LVAN2Vgbpromoter TCGTCCAGTAGTCGTGGTGACCGGGTAGAGCCACCATG

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Supplement File 2: Comparison of the promoter region of LvVg1 (i.e. 1Vg27042 and 1Vg294361) and LvVg2 (i.e. LVAN2Vgcpromoter, LVAN2Vgbpromoter). The 200-300 bp upstream promoter region of LvVg1 and LvVg2 genes are highly homologous. The homologies decrease at the more distal region (i.e. >350 bp onward). The ATG indicates the first codon of all Vg gene and the potential TATA factor binding site is shown by the red boxes.