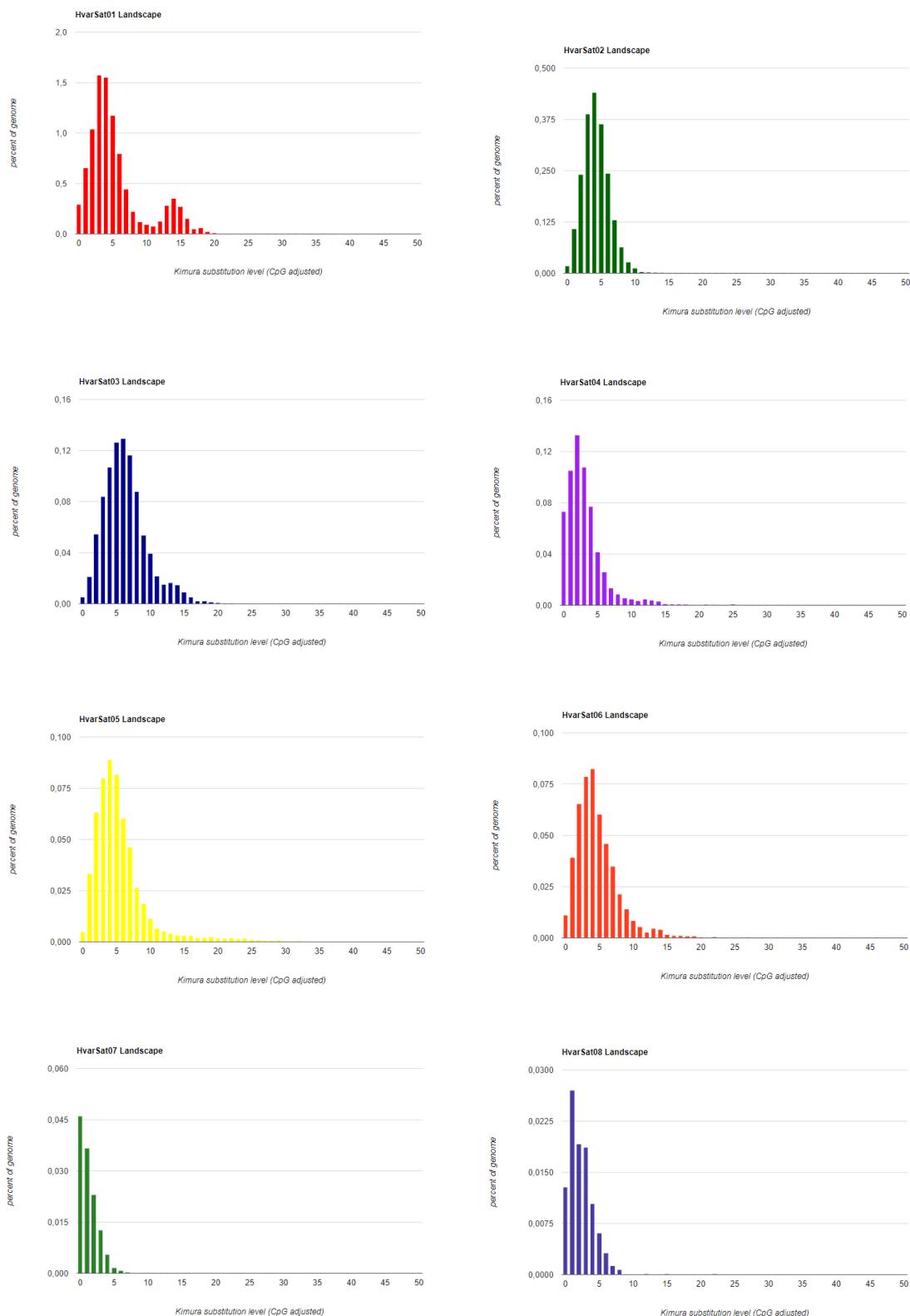
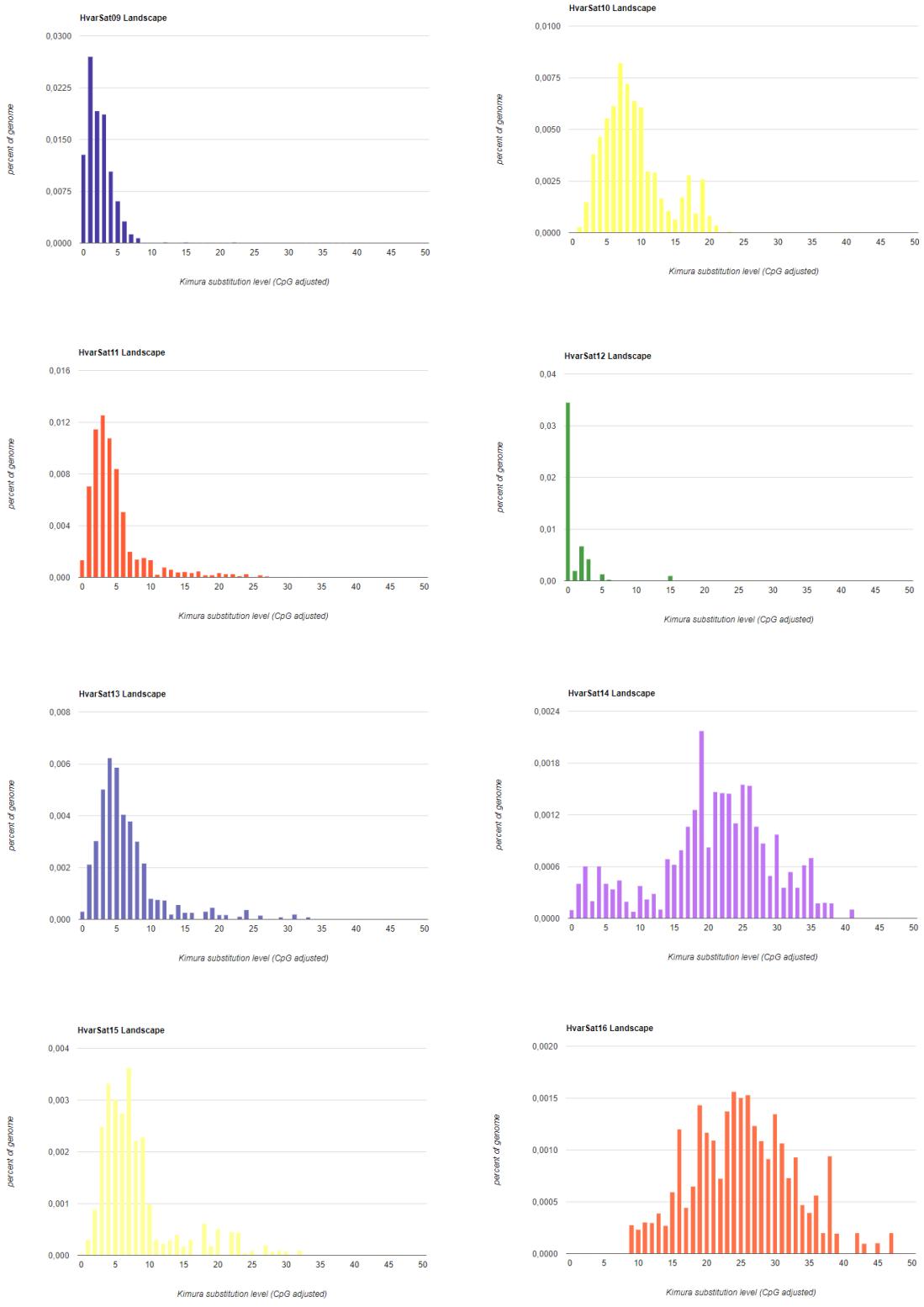


Supplementary Material

Supplementary Figure S1. Separate repeat landscape of each satDNA family in *Hippodamia variegata* satellitome.



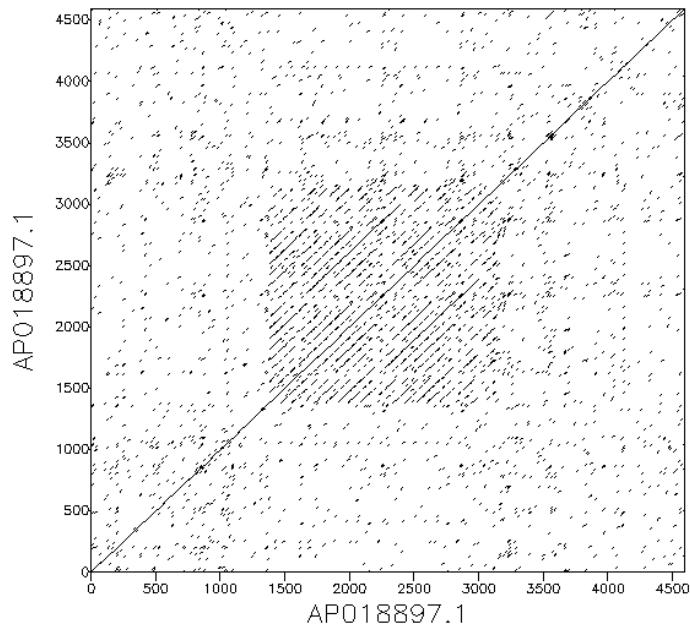




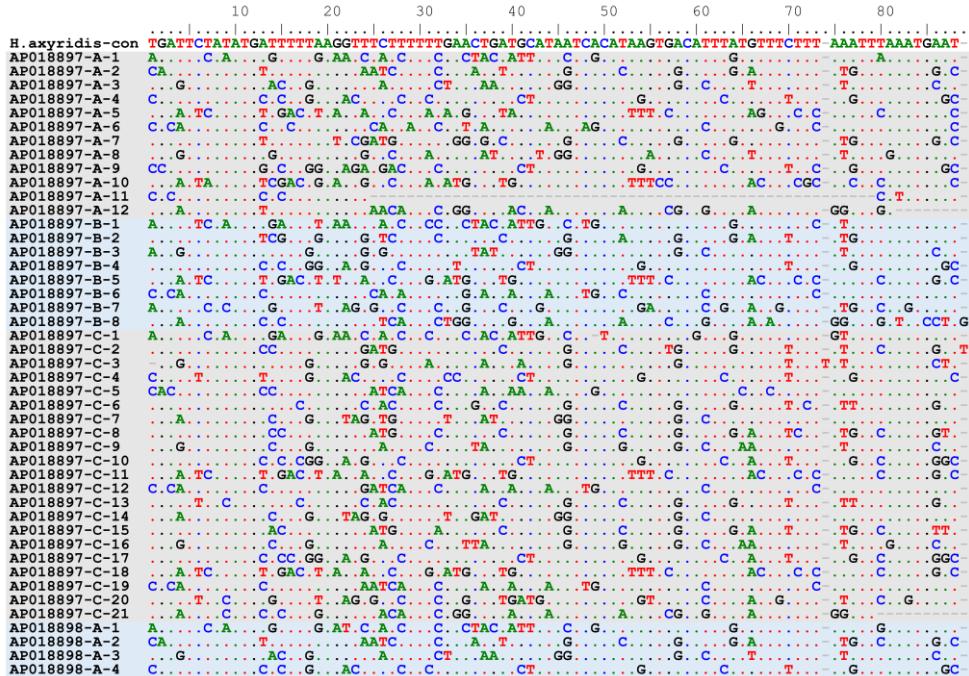


Supplementary Figure S2. (A) Dotplot of an internal region of one of the scaffolds of *Harmonia axyridis* with the presence of a tandem array of repeat sequences with similarity with the HvarSat16-87 satDNA family of *H. variegata*. (B) Alignment and consensus sequence of repeat sequences found in two scaffolds of *Harmonia axyridis* (accession number AP018897 and AP018898). (C) Alignment of HvarSat16-87 and the consensus sequence of the repeat sequences found in *Harmonia axyridis*.

A



B



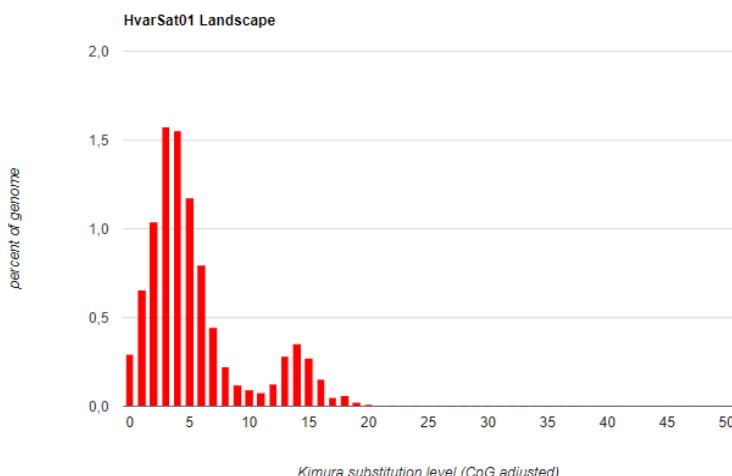
AP018898-A-5 . A.TC . T.GAC.T.A.A.C. A.A.G..TA. TTT.C . AG . C.C . C . G.C
AP018898-A-6 C.CA . C.C . CA . A.C. G.AA . A. AG . C . G . C . G . C . G.C
AP018898-A-7 . T . T.CGATG . GG . C . G . C . G . C . G . TG . G.C
AP018898-A-8 . G . G . C . A . AT . T.GG . A . C . T . C . T . G . G.C
AP018898-A-9 CC . G.C . GG . AGA.GAC . C . CT . G . C . T . C . G . GC
AP018898-A-10 . A.TA . TCGAC . G.A . G.C . A.ATG . TG . TTTCC . AC . CGC . C.C
AP018898-A-11 C.C . C.C . CAA . T . G . C . G . C . G . C . C . G.C
AP018898-A-12 . A . T . AACCA . C.GG . AC . A . A . CG . G . A . GG . G . TC . CCT . C
AP018898-B-1 A . T . TCA . GA . TAA . A.C . CC . CTAC.ATG . C . G . A . AT . A . CT . CCG . C
AP018898-B-2 TCG . G . TCA . C . C . C . G . A . G . A . G . A . C . T . G . C . T
AP018898-B-3 G . TCG . G . TCA . C . C . C . G . A . G . A . G . A . T . G . C . TG
AP018898-B-4 A . G . G . G . G . G . TAT . CT . GG . G . C . G . A . T . G . C . T
AP018898-B-5 C . C . GG . A.G . C . T . CT . G . G . C . G . A . T . G . C . GC
AP018898-B-6 . A.TC . T.GAC.T.T.A.C . G.ATG . TG . TTT.C . AC . C.C . C . C . G.C
AP018898-B-7 C.CA . C . CAA . G.A . A . A . TG . C . C . G . C . G . A . T . G . C . G.C
AP018898-B-8 A . C.C . G . T . AG . G . C . C . G . C . G . A . C . G . A . G . T . C . G . G.C
AP018898-B-9 . A . C.C . C . TCA . CTGG . G . A . A . C . G . A . A . GG . G . T . C . G.C

C

HvarSat16-87 AGAAATTATAGTTTTTGAGATCTCCTTAAATATGGAAAGAATACTCACACAAATGACATTATGTTCTCAAATTCAAATGAAC
H. axyridis T...T.C.....A....A..G.T...T...TTG.ACT...T.C...A....T.G.....T.....T.....T.....T.....T

Supplementary Figure S3. (A) Repeat landscape of the Hvar-Sat01-277 satellite DNA showing the existence of two types of repeats. (B) Alignment of the consensus sequence of the Hvar-Sat01-277 with the most abundant repeats (type I) and with the less abundant (type II).

A



B

Supplementary Table S1. Consensus sequence and accession numbers of the satDNA families found in *Hippodamia variegata*.

Accession number	Consensus sequences
MT613047	>HvarSat01-277 CTCGATTATCAAATCTCAACTCTCATCCCTACCGAAGTCGAGATAATCA TGTCAATCATGAATGCACGAAATCATCAAGAACGAAGCATTATGGTTCA GTTCTCGATTCACCCATTGACCAATAACATAGTGTATAAATGCATTGA ATGTGTTAACAGATTCAAAATCGGAGAAAAGTGTCTGTCATAGGAAATGT CAAGTTGACAAGATGGGAGTATAGGAATGACTGAAATTCTATAATTCTCA GACTCAACTGATTCTCA
MT613048	>HvarSat02-127 TTTTGTTATTCGAAAACCTCTGATTCTGATTACAAAACAGTAACATT CATCTCATTCTGACGCTGACGAAACGAGATATTAGGTTGAAGGTTCTTGA ATTCCACTCGGATTCTGGTT
MT613049	>HvarSat03-217 TTATAAAAGGAGGCCACTCGATCGATAGATGATCATTCAAATCGGAATAGC GTCGTGAATACATCGTAGGTAGAGTTGAAAATTAAATAAAACTTCAATAAA ATTTCAGGTGATAGACCAGTCCTGCAAATGCAAGACTTCATTGTAGTTG CGTCACTCTACTCGAAAATACTACTCGGTCGCGTTACGTACAGTTACG TCGGGGTAGC
MT613050	>HvarSat04-487 TTATGGAGGTCTAAAAACCGGTCGAGGTGCTCCAGAAAAAAATACCAACTT GAATTATTTACCCATATTGTGGTCGGTAGAGCGTCTCAAAGTCAACTCGAA AATGAAAAATGGAAAAACAACTTTATTTCGCGAAAACTAGGACAG ATAATTCCGGGGTTGTAATTGAAATTGTATATTACTCGATTGCTTCATCTGAT GAAGGCAAATAATTGCACATTCTCGATTAAAATTTCACCTTCAAAA TGAAAATTTCAAATTCAAACCTGTATATTTCGGCGCCATCGCGCAGATC GATGCGAGGTTTCGAAAGGTCTCAGTGGATCAGATCTCAATCCAAG CACAAAAAATCGAAAAAAAAATTGAAATTGACCGAAAAATCGTAA GGGGTTGACCCCCCTAAACGCTATATTCCATTCTCAGAGGCAATCTAG GAGAGCTATCGTAATTGTTG
MT613051	>HvarSat05-324 GATCGGATTCAAAACACAGGAGCTAGAGCAGATTATAGATTTCCTACGC GAACCATCGTTAGGTAAATTCTGATTTCAGTCTGGTTGATATTCA GGGTGAAAATGATATTATTGAAATCTGCACCCGAATTGACCTGAAAC GATACCCCACATCCCCCAGAAGGATTAGAAATTTCGAAAATCCCTATC TTACATAGGTCGGTACCCAAAAGTGCCTTAAAATTTCGGAATAT CGGGCTGAAAATCAGAACATAGGTAGAAGAGGCCGTGGTTCATATGCG ACTAGATCAGCTC
MT613052	>HvarSat06-175 ATATTCTGAAAATATTCACTCCGATAGGCCCGTCTTCATAGAAAAAATC GAGAAAAACACTAAATTTCACTCAAAATTCACTAAAATTCAATTAAATT GAAAAAAAAGGCCCTACACCGTATGTAGGGCATTATTGTACCTTCAAAA GATGGAAGACACCGAGGCAGC
MT613053	>HvarSat07-2000 CAGAATATAAAATAATTCAACAGTCAAGTTAACAGAAAAACACATATTCA CATATCTACAATAATTACAAATGATCGATAGAAAAAAAAGCATAATTCTA ACCCATCAATATTTCACATGGGGCGTCAGAAATTGAATAATGTAAAAAAT

AATTCAAAATATGAAAATTGATGAATAATCAGTCAGGTATATAACAAAAAG
AAACATATTCATATATCTACAAAAACTACGAACGATCAATAGGAAATAAAA
CATATCGTGAATTCTAACCTATGCCATTTCAGTTCAATACG
ACAAGACCAATTAAGCCTAGGCATGGAATTCACATGATTCCGCCTCATAT
GCTTGATGGTATTTCAATAAAATTATCATTCTCAATCTGCACATTGGGT
ATTCCTGACTTTTTGTGTTCTGTGGTATTCTGAGCACTTCATTT
CTAGAAAGCGTTTCCAGTCATTGGGCTTATATCATAATCACTGATGTAT
AATTCAAATTACTATGAAGCAATGATTCAATTGCCTGATTTCATAGGA
TCGTTTCTGCACTGATTCAACAATTCAAAATTTCGAACACTCAACTT
GTCGTTACTCTGTTATTTCAGTCATATCACAGGATTGTCATTGTT
TTTCACAAGAACGTTGAAGTCTATTTCAGTCAGTCGGATCTGGAAA
TTTAGGGGCTTGAGAATTGAGCTTCAAGGCTTCAACCCAGTGGCTG
CGGGTGCAGCATTTCAGTTGCTGAGCCTCGAAAAATTCAAACGTG
ACGCTGTTGGTATGAAACGGTTGCTCGTTCTGCTGACCCCAATCT
GTCTGAAATAATTCCCTTCTCGTCATATCATTCTACTCAATATAGA
AATTATGTCAGTCATGAAGTTCACCTATATTCAAGATGAATTGTCGAAT
CAACCATTGGTATTCAATTGCTGCATCTCCATCTGCCACATAGACT
TGTATTGGGCTTCCTCAAAATTCAATGGGATTCACTTCTGTAGGCAGA
AGCATCGTCCCTGACCATTGATCAATTCTCGTGTGAAGTATTCAATTG
TGATACCGTCCAATCTGAATTAGAATTAACTTAATTGATATCTTAGTT
AACGAACACTGAGGAAAAATTCAATTAAAGGATTGAAATGG
AAAAGATATTGAAAATTATTCACAACAATTGAGATATTCAACATAA
AAATGGATGATTGGATTCAATCCACGAAATGGAAATAATTGACAAAAAA
GACGATTTCAAATTATATCGATGATAATTGAACTGTCGAAACTCAAT
TCATGTATCATCAAAATTATTGATATGATGAAAATCAAGAGATGAAA
ATAAAACAAATATCATAACGAAATTGTGCAATTGAACTCACCCACGTA
TATTCAACCACACTTATTCAAAACTACAATTTCGTTCCGTTCACTTAGAA
ATATAGATAGCACTAAATGTGACACCTTATAGCGCTCTATTAAAGTACTT
CGCTTCAGGATTCTCGGAACTATTATGACAAAGGGTAGTTCTGAGAAGGTA
CATTATCTCGTCTTAATCTTGTGTTGATCTAATCGTATCATGACTCGG
TAATTCGAAATATCTACTACAAAGGGTAGTTCTGAGAAGGTAATTATCTC
GGTCTTAATCTTGTAGGTATCTAATCGTATCATGACTCAGTAATTG
AAATTTCATCACAAAGGATAATTCTGGAGAGATATTATCTTCACAGAA
ATATCGGTACCAAGAACATTGTTGGCATCCGATTATCTGGTATCAGTAAA
ACAATCTTATATTAAGTAATTATGAAAAGTATTATCTGACTGGAAAT
CTCAGTAC

MT613054

>HvarSat08-972
TGAATTACTGAGTGACGGCATAATTATATGGTCGATTATAGAATATAAGAT
TTGTTTCAAATCTGTATGACTCAAGAATGGTCCAGAGGGAAACCATT
CTTGAGGTATTAATTACTGATCAAATTTCAGAAAATGAGACAAAT
TCTAGGAAATACTTTGTTCCGCTAGGATAAACACTACTGCTACAATA
GATATAGCTGATCAAGTGAAAGGACACCGACATTGAGAACTGAATT
TAACCTACGTTAATGGAATCTGGATGAATGTTATCAATATCCGACAATCAA
CCTTCAGGCAGGAAGTGACTTGTGTTCAACACTGTATGATAAACAAACCT
TTGGAACCATTCTCAAGGTCTACATTAAGTATTGAGATAAGAAACCGTCT
CTAACAAAAGAGGAGATAATCATTCTAGGAAAATAATTATTCGGAATGA
AAACATCTCTAATAAGCACAATCTGAAACAAGAAGTAGAAGTCAGTGC
GTTGGTTGGTAGAATCATACGTTGTACATCAGTTGCGATGATGAAAGTTCA
AGCAGGTGAGGACAAACATAACATTGACTACTTCATGAGAAAGGAATT
AATTATGAAATCTCGAGCAGGGTAATTGAGTGTGAGTGTGAGAATAATTTCAT
TCCAATCTTTATTGATTCAATCGAATCAATTCTGGTTCCGGCGAAA

	TATCAGAAATTATCTATCAAAGATCCAGAACAGTATCTATCGACCCACA ATATAACATTGTGACTGGAGAAATTAAATCAGAAATTATCGAGTCITGAGTT TTCATTCGACTATCTTGCAGAATTTCGGTTCATATTGACAAAATTCAA ATTCCGTATGTTAAATCTACTGAATGACGGCATAATTATATCGTTGATTATA GAATACAAGATTGTTCAAATCTGTATGATAAAC
MT613055	>HvarSat09-292 AATTCGGGGTCGTAGATTCAAAAAACTGGTTATTGGGCTTAGAGGGTGA ACCAAGTGGATTTCTCTAAAAACATGGGTTCCAAGGACTCCTGACACTT TGGAGCGGAAAGGACCTGATTTCTGAATCTACGACCCAGATTCCATGAA ATGACACCCAACATCGCCTATGTATGATGAAAAATTTCGACTCGGTTCCAAC CTTCGTAAGAGAAAAATCAAATTGTGAAAAACGTCAAAACTACTCATC GTAGGTGGTCATGTTGGTATCAATTCTACT
MT613056	>HvarSat10-91 TTCATTGTTGGCACAGGAAGTGAGGAATGCAAAAATTCTACTGGCTCTACT CAACTGCCTAGCTCAAATATCCACCATTATTTTATTAA
MT613057	>HvarSat11-141 CAACCATATTTCGTATGTGGATCCTTATATCAATGTGATTAACGTATAAAA AAATCATCGACTCGCAAAGGGTTCAAGGGGTGAAAAATCAACCCTAAAC TGCAAAATTCTATATCTCGAAACAATTGGAGTATCA
MT613058	>HvarSat12-150 ACTAGTATGCCCGGGGATCCTACGTTCAAATGCAGCGAGCTCGTATAA CCCTTAAGAGTTGCTTTGTTGTAAGTTGCAAATCGAAGTTAGAT TGAGTTCTACGTCGAGCGGCCGATATCCTGCAGATGCACTCCAGT
MT613059	>HvarSat13-148 TCTATTTCAAAAACCTCTCGAGTCGTAAGTCGAATTCTGAAATT TTTTCGGTGAATATATCCCTCTGAACGCCCTAGAAGATCCACATATCCA CATATTGTCGGCAAAACTCACCACACCCCCCTCC
MT613060	>HvarSat14-309 GGATGAAAAGTTGACAACGTGCGATATATTCAAGAGTTAGAGTATTCCCTT CAATATAATTCAAGAAATGTTGATTCACTGGATGTTTTATGTCAATTTC AATATCTATCAATTCAAGTGAGTAAATATTGTTACATCCGAAAAGTTGT TTTCGAATAGAAATAAGACGATTCGTATTACAATATTATTCTGAAA AGAAAGACTCATAACTCTGGTTTAGAATGAAACTCATTGCGAT GCATATTGAAAATGGCTCGAAATGAGATTCCAAAACAAAATTCA
MT613061	>HvarSat15-158 TAATTAACACCAAAACCTAATCAAGATATGCGACAACGTCTTTTGATT TTAGAGAACTTGAATGTTCGAAGAACAGAAATCTTCGAAGTCCCCCGTAT CTCTCCTACGGCGCGACAATCAATTGTCGACTAGAAATGATTATTCAAA CA
MT613062	>HvarSat16-87 AGAATTATATGTTTTGAGATCTCCTTAATATTGGAAGAATACTCACACA AATGACATTATGTTCTCAAATTCAAATGAAC
MT613063	>HvarSat17-176 CACTCTCGACTGATCGCATAATAATTGTTGTAGGTTGTGATGTCGG CCAAGAACCTTGAGTGTGTTCGAAAGATCATTATTATGTACTTTTA AAACTTCGTTCATCTATGAACCCCTAGACCCCCAGCTCCAAGAGTCGAAA AATGCCGTCTTGGCGT
MT613064	>HvarSat18-191 AGCGAGGTACCGCTCTGTACAACCCCTAATCTTGTGCAACGTCTACACCC CGAGGGTGGAGCTATCATTGAGTTGATACTCCATCGTCCCTCAAGTGGAAATC AGTCGTGGAGTTCTAATTGCGAGCAACTCTTATTAGGAGCAACCAGGCC

	AGGTTCCATCTTGAGGAAAAGGGTAACCTTCCG
MT613065	>HvarSat19-143 TCGAAAATCGAGCGTGAATATTAAGGGTGAAATTCAACCCCTGAACCCC ATCGCAAGTCAAATTTTTTCGATATCGAATAATTATGTCACGAAGAATA TTCTGCCAAGTTATGATGCAGGTATTACGTTCCCT
MT613066	>HvarSat20-141 TTTTTCAACCCCTAACTTGAAAAATTCAATCTCGGAAACTATTCTCCGGA GCACATACAGACTCGTATGTTGTTCATTATGAGGAAACCAATGATCCCTG AAAATATGATCGACTTCCGAAGGAGTACGGGGGTG
MT613067	>HvarSat21-152 TGGTCGCGCATTGAAACCGAGATATAAGCAAAAAATGTCAAAATGACA GTTTTTCAATTCTGTCTCAAATAACGTGCCCAAATTGATTGAAAGAAG AAATCAATTACCAAAGAGCGATGCCACTCTCGTAAAAGATTTCG
MT613068	>HvarSat22-145 TATAGATTGGAAAAATTGAAATTCAATTCCGGCCAACTTATGTCAG CCCGGAAACCCAGCATTTCATCGATATTGAAAATTGAAATGCTAGC GAAATGCTGGGAATGCTGAAGAAAAACTGAAAATCTCT
MT613069	>HvarSat23-378 GAGATGAAAGATGAGAAGAAACGAAAACGCCCTCATCTGATAAAACGCC AGAACTTTGAAAAAGTGAAGAAATCACCTCAGTCTCCAGCTGATCGAGT ACCGGGAGTAAGTAAAAAGTACCCAGTTCTGAGACGCCAAATCGGT TTCACCTGTAGATGTTCTGAACACAAAGTAATTACCGAGTCAGTAGAAATG AAAGAAACAATTATCAAAAATCACCAGACTCTATCGAGAAACCTAGTCA CGACATTCTCTCCAAAACTGAACATATTGTTGATTCAACTGAAAAGAAG AAGGAACCCATGACTCGACAAAGGATCATGTTGAAAACCTACCATTGAAA CCGGTTGATCATGTCAGAA
MT613070	>HvarSat24-105 GATACTCGTGAGGCAGTCGACCCAATGCTAGATGTTACAGTTGTCTGCT TCAGATGTGCTACTTCAGTAGTTGGTCAGATGGTTCTGTTGATCTGGTGC
MT613071	>HvarSat25-150 ATGAAATATCGTAAAATACGTATCGAAGAATAGGAAAAATCATATTCA CTTGACAGTCATTGCGAAATAGTTGAGAAAAATTTCATTTGAAAATTTCATT AGGGGTAATTCACTAAGAAGCAGGGGTGCAAGAAATTTC
MT613072	>HvarSat26-164 CCACTGAAAAATCGTTCACAAAAAGTAATATTATAGGGAAAAAAA TTTTCTATTGCGAAACCGTGGCTGGCTCGAAATTGATTTCCGATT CCAACCAGGGTCAACTCTGTTGAAAATTTCATGTTAGAGTCATCAATA CCAACAAT
MT613073	>HvarSat27-41 AGATGAAGATTCAACAATAGCCAAGCAGAACAAATAGAAAT
MT613074	>HvarSat28-57 GAGAGTTGAAACCAAGAGGGTTCTCGGCTGCTCGAGGAAGTAGTGTCC GGGGAC
MT613075	>HvarSat29-169 TTTCATTACAATTCAATTGTTAGCGTTCCAGCAGGAGAATCTATGCAA TATAAAAACATATAACGTTATTGATTTCATCTACATTGTTAGACTGCTTCAATAGGAGAATCTA TGCAATATGGA