Interspecific analysis for SNPs in EST libraries of oil palm, Elaeis *guineensis* and *E. oleifera*

Cluster 1

Size of Consensus sequence = 319

Number of sequences = 2

Minimum redundancy = 1

A gi|112819439|gb|EE593315.1|EE593315 EgTEST0029 Elaeis guineensis Lambda ZAP-II Express Library Elaeis guineensis cDNA clone TE-86 5', mRNA sequence
B gi|93154510|gb|EB643580.1|EB643580 EoEST062 Oil palm Lambda ZAP-II Express Library Elaeis oleifera cDNA clone OE-62 5' similar to Ribosomal protein (Ribosomal L28e), mRNA sequence

SNP fond = 1 transition

| Position | Site | cosegregation | weighted |
|---|---|---|---|
| 303 | A G | 1/1 | 100.00 |

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GTTGCCAAGTCTGGGGTGAAGAAGAGGAACCGGCAGGCTGTTCAAGTAAAATACTAGGTTTCTGGATGGT
GTTCCAGCTGGCCTGATTGGCTGTTCTTCAACTATTTCTTTTTCTTCAAAGTTTAGTTGAAGGCTTCTCA
AGTAGAATCATGAAACTATTTCCCTCATTTTCTTTTTTTCCGTTTTACCTTTAAGTTTTCTGGGAGATTA
GTTTAATTTGAGATGCTTTATTTGCTTTGGCCGGTTATGAGTTTGAAACAATGTGATGGTTTAGATGATT
TTAAGCCCTCCACATTTTTATA[A/G]AAAAAAAAAAAAAAAA
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Cluster 2

Size of Consensus sequence = 708

Number of sequences = 3

Minimum redundancy = 1

A gi|93154458|gb|EB643528.1|EB643528 EoEST010 Oil palm Lambda ZAP-II Express Library Elaeis oleifera cDNA clone OE-10 5' similar to Ribosomal protein S10p/S20e, mRNA sequence
B gi|112819436|gb|EE593337.1|EE593337 EgTEST0051 Elaeis guineensis Lambda ZAP-II Express Library Elaeis guineensis cDNA clone TE-149 5' similar to 40S subunit ribosomal protein, mRNA sequence
C gi|112819435|gb|EE593336.1|EE593336 EgTEST0050 Elaeis guineensis Lambda ZAP-II Express Library Elaeis guineensis cDNA clone TE-148 5' similar to 40S subunit ribosomal protein, mRNA sequence

SNP fond = 2 (1 transition and 1 Transversion)

| Position | Site | cosegregation | weighted |
|---|---|---|---|
| 478 | G A A | 1/2 | 50.00 |
| 512 | G T G | 1/2 | 50.00 |

GTCGCAGCAGCGCCGCACCTCGAAACCCTTGGTGAGTGTCAGCGGAATCGTCGTAGTTGGTGGTGTTGGT
GAAGGGAAAAGAGGCATGGCGGCGGTGTATGCTCCACCTCCGATGAAGGCGGCCGGAAAGCTGGGGATGG
AGGAGTCCCCGGAGAATCTCCACCGCATCCGGATCACCCTCTCCTCCAAGAACGTCAAGAATCTCGAGAA
AGTTTGTTCGGATCTGGTGAGGGGAGCCAAGGACAAGAGGCTGAAGGTCAAGGGACCGGTGAGGATGCCC
ACTAAGGTCCTCCACATCACCACCCGCAAATCCCCCTGCGGCGAAGGGACCAACACATGGGATCGGTTTG
AGCTTCGTGTACACAAGAGGGTGATCGATCTTATTAGCTCACCTGAAGTGGTGAAGCAGATTACCTCAAT
CACCATTGAACCTGGTGTGGAGGTTGAAGTGACAATTGCAGATCCATGATTCAGCTG[A/G]AAACTTTG
ATGCAATTATATAGACAGTTGTTTT[G/T]TCCGCCATCTGGAATGAGCGCAACCAGTATGTAGTCTAAA
AGATAATAACACTCGTTTTTTCATTATATTTTTCTTAAGGAAATCTTAATCCTTGGTTTCTATTAATATG
AGATTTTTGCTTAAACATCCAGTTTTGTGCCCGTCGAAGGAATCCTAGTGTNCCTTTCAGTTATTTCCAA
AAAAAAAAAAAAAAAA

Cluster 3

Size of Consensus sequence = 723

Number of sequences = 2

Minimum redundancy = 1

A gi|93154463|gb|EB643533.1|EB643533 EoEST015 Oil palm Lambda ZAP-II Express Library Elaeis oleifera cDNA clone OE-15 5' similar to Brassica napus BURP domain containing protein mRNA, mRNA sequence

B gi|112819404|gb|EE593301.1|EE593301 EgTEST0015 Elaeis guineensis Lambda ZAP-II Express Library Elaeis guineensis cDNA clone TE-54 5' similar to dehydration-induced protein, mRNA sequence

SNP fond = 55 (32 transition and 23 Transversion)

| Position | Site | cosegregation | weighted |
|---|---|---|---|
| 47 | G A | 55/55 | 100.00 |
| 52 | C T | 55/55 | 100.00 |
| 53 | G A | 55/55 | 100.00 |
| 59 | G A | 55/55 | 100.00 |
| 62 | C G | 55/55 | 100.00 |
| 68 | G A | 55/55 | 100.00 |
| 71 | A G | 55/55 | 100.00 |
| 81 | A T | 55/55 | 100.00 |
| 84 | T C | 55/55 | 100.00 |
| 90 | T A | 55/55 | 100.00 |
| 91 | G A | 55/55 | 100.00 |
| 94 | G C | 55/55 | 100.00 |
| 112 | T C | 55/55 | 100.00 |
| 115 | C G | 55/55 | 100.00 |
| 123 | T C | 55/55 | 100.00 |
| 126 | G A | 55/55 | 100.00 |
| 149 | T G | 55/55 | 100.00 |
| 173 | T A | 55/55 | 100.00 |
| 181 | G T | 55/55 | 100.00 |
| 188 | A G | 55/55 | 100.00 |

| | | | |
|---|---|---|---|
| 194 | G C | 55/55 | 100.00 |
| 202 | G C | 55/55 | 100.00 |
| 209 | A G | 55/55 | 100.00 |
| 217 | C T | 55/55 | 100.00 |
| 221 | A G | 55/55 | 100.00 |
| 225 | C G | 55/55 | 100.00 |
| 227 | C A | 55/55 | 100.00 |
| 241 | C T | 55/55 | 100.00 |
| 246 | C G | 55/55 | 100.00 |
| 253 | T C | 55/55 | 100.00 |
| 256 | A G | 55/55 | 100.00 |
| 267 | T A | 55/55 | 100.00 |
| 268 | T A | 55/55 | 100.00 |
| 273 | C G | 55/55 | 100.00 |
| 281 | T G | 55/55 | 100.00 |
| 287 | G T | 55/55 | 100.00 |
| 296 | A G | 55/55 | 100.00 |
| 304 | T C | 55/55 | 100.00 |
| 307 | T C | 55/55 | 100.00 |
| 313 | C T | 55/55 | 100.00 |
| 323 | C T | 55/55 | 100.00 |
| 335 | G T | 55/55 | 100.00 |
| 336 | C T | 55/55 | 100.00 |
| 337 | G A | 55/55 | 100.00 |
| 338 | T A | 55/55 | 100.00 |
| 343 | G A | 55/55 | 100.00 |
| 344 | A G | 55/55 | 100.00 |
| 347 | G A | 55/55 | 100.00 |
| 392 | A G | 55/55 | 100.00 |
| 394 | G A | 55/55 | 100.00 |
| 400 | C T | 55/55 | 100.00 |
| 419 | G T | 55/55 | 100.00 |
| 429 | G A | 55/55 | 100.00 |
| 472 | T G | 55/55 | 100.00 |
| 490 | G C | 55/55 | 100.00 |

CTTCTCCTCCGCGAAGCTCCCGGAGATCCTTTCCCGCCTCTCCATC[A/G]CGCC[TA/CG]ACTCC[A/G]
TC[G/C]AAGCC[A/G]AG[G/A]CCATGAAGA[T/A]GA[C/T]CCTTC[AA/TG]GA[C/G]TGCGAGG
AGCCGGCGAT[C/T]GA[G/C]GGAGAGA[C/T]CA[A/G]ATACTGCGCCACCTCGGTCGAG[G/T]CCA
TGGTGGATTTCAGCACGTCC[A/T]GCCTTGG[T/G]ACTCGT[G/A]ACGTC[C/G]AAGCCCT[C/G]T
CGACG[G/A]CGGTCGA[T/C]AGG[G/A]AGG[G/C]T[A/C]CACCGAAACAAGT[T/C]TACA[G/C]
CATATC[C/T]AA[G/A]GTGCAGAAGC[AA/TT]CCTA[G/C]CTCTAAG[G/T]TGGTG[T/G]TTTGC
CAC[G/A]GTGAGAA[C/T]TA[C/T]GCATA[T/C]GCTGTGTTC[T/C]ACTGCCACACG[TTAA/GCGT]
GCGC[AG/GA]AG[A/G]CGTACAAGGTGTCGATGGTCGGGAAGGATGGGACCAAGGTGGAG[G/A]C[A/G]
GTGGC[T/C]GCATGCCACACCGACACG[T/G]CCGGATTCA[A/G]CCCCGAGCACGTCGCCTTCAAGGTGC
TCAACGTCAAGCCCGG[G/T]ACGGTGCCCATCTGCCA[C/G]TCCCTACCGCAGAGCGATATTGTTTGGACT
CCCAAAAAATAGAGCATCTCATCGTTGGAGATGAAGGTGCGATTGCCCTAGAAAGCTTCTACAGAAGATTTCT
TTGGCTAGGCTATCCTATTGTACTGTTTCCTTTGTCATGGCGCCTGTCAGATGTTATGGGTGATGTATATGTA

TTCCTGGTTGCATAAGTAAAAGTAGAATTATGTTATGTAAAAAAAAAAAAAAAAAA

Cluster 4

Size of Consensus sequence = 490

Number of sequences = 4

Minimum redundancy = 1

A gi|112819407|gb|EE593304.1|EE593304 EgTEST0018 Elaeis guineensis Lambda ZAP-II Express Library Elaeis guineensis cDNA clone TE-62 5' similar to metallothionein-like protein, mRNA sequence
B gi|93154533|gb|EB643603.1|EB643603 EoEST085 Oil palm Lambda ZAP-II Express Library Elaeis oleifera cDNA clone OE-85 5' similar to Metallothionein-like protein, mRNA sequence
C gi|112819397|gb|EE593294.1|EE593294 EgTEST0008 Elaeis guineensis Lambda ZAP-II Express Library Elaeis guineensis cDNA clone TE-37 5' similar to Metallothionein-like protein, mRNA sequence
D gi|93154497|gb|EB643567.1|EB643567 EoEST049 Oil palm Lambda ZAP-II Express Library Elaeis oleifera cDNA clone OE-49 5' similar to Metallothionein protein,

2 SNPs detected (1 transition 1 transversion)

| Position | Site | cosegregation | weighted |
|---|---|---|---|
| 13 | T . C C | 2/2 | 75.00 |
| 455 | A A T T | 2/2 | 100.00 |

CAAACATTGTCT[C/T]TGGTTTCCTGCTTCGAAACTCAAAACATGTCGACCTGCGGCAACTGCGATTGT
GCTGACAAGAGCCAGTGTGTGAAGAAGGGAAACAGCTACGGCATCGAGATCATCGAGACCGAAAAGAGCA
ACTTCAACAATGTCATCGATGCCCCGGCTGCTGCTGAGCACGAGGGCAACTGCAAGTGTGGTGCTAGCTG
TGCTTGTGTGGATTGCAAGTGTGGCCAATGAGCAACATCTATGAGCACTATAGCAAACAAGAAAAGAAAG
AGATATGTGTGATATGGGTATGTTGGACTAAATAATTTGGATATGTTTCTGTCATGGTGTGTTATTGTAG
CAAGGATGTGTGTCTGTCATGGTGTGTTATTGTTGTAAGGTTGGAGGAAGACAATATCTGGCTTCCTTAT
CCAGTTTCGCACTAATTTCTATTACCTGTTCTAATTAA[T/A]GGATTGCTATTGGTAGAAAAAAAAAAA
AAAAAAAA