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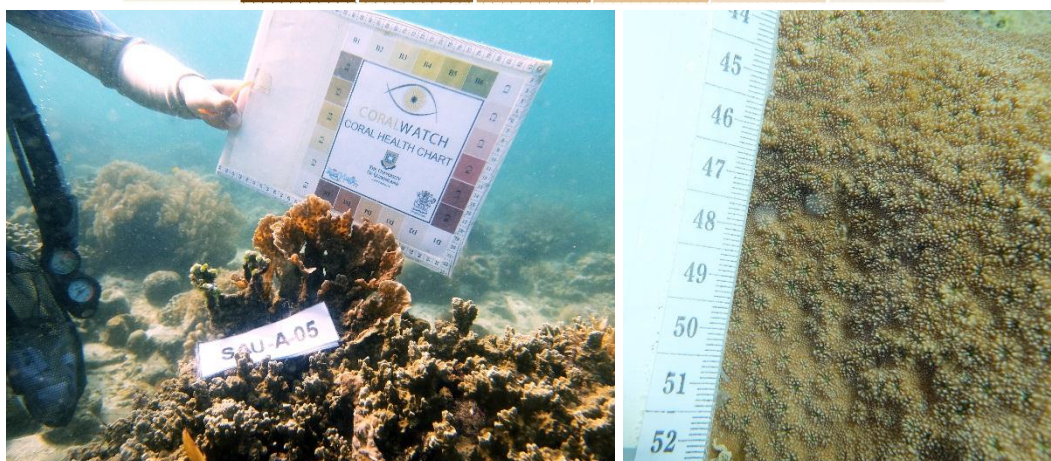
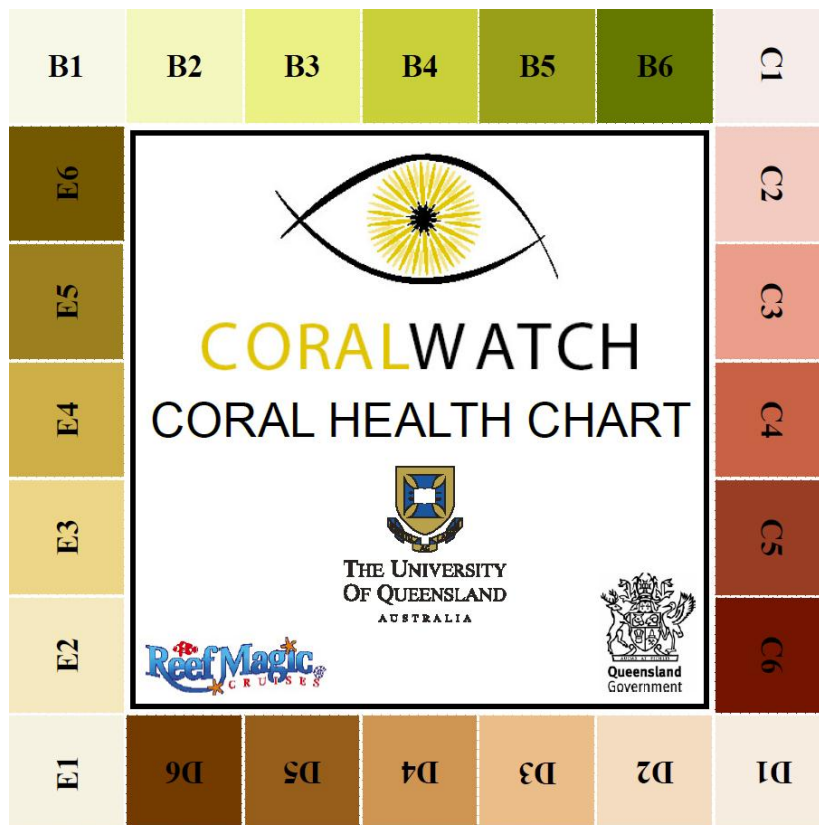
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## **LAMPIRAN-LAMPIRAN**



Lampiran 2. Tampilan kartu charta warna CoralWatch dan instrument charta warna





## Lampiran 3. Kolom hasil pengamatan fitur morfologi

| No  | Aspek   | Detail Aspek  |
|---|---|---|
| 1   | Lokasi (kode sampel)                                  | : _____ (_____)   |
|   | Identitas foto  | : _____ .jpeg   |
|   | Kedalaman ditemukan                                   | : -_____ m  |
|   | Karakteristik koloni                                  |   |
|   | A. Bentuk koloni                                      | : encrusting (Enc) / foliaceous (Fol) / laminar tier (Tie) / laminar tube (Tub) |
|   | B. Pertumbuhan polip                                  | : unifasial (Uni) / bifasial (Bi)   |
|   | C. Warna jaringan pada rangka <sup>a</sup>            | : kode warna (B / C / D / E)  |
| Karakteristik koralit   |   |   |
| A. Tipe koralit   | : menonjol (Bul) / rata (Im)                          |   |
| B. Rerata diameter dalam ( <i>mouth disk/MD</i> )   | : (____+____+____+____ mm) / 5 = _____ mm             |   |
| C. Rerata diameter koralit ( <i>corallite diameter/CD</i> )   | : (____+____+____+____ mm) / 5 = _____ mm             |   |
| D. Rerata jarak antar koralit ( <i>inter-corallite distance/ICD</i> )   | : (____+____+____+____ mm) / 5 = _____ mm             |   |
| E. Densitas polip ( <i>polyp density/PD</i> )   | : >4 polip/cm <sup>2</sup> ; ≤4 polip/cm <sup>2</sup> |   |
| F. Warna kolumela <sup>b</sup>  | : kode warna (B / C / D / E)                          |   |
| Catatan:<br>Sampel _____ ditemukan pada kedalaman _____ m, memiliki bentuk koloni _____, dengan pertumbuhan polip tipe _____ dan tipe koralit _____. Sampel menunjukkan rerata jarak antar koralit _____ mm, dengan rerata diameter koralit sebesar _____ mm dan diameter cakram mulut _____ mm, serta densitas polip _____ polip/cm <sup>2</sup> . Sampel memiliki warna kolumela tipe _____ dengan warna jaringan tipe _____ berdasarkan kartu charta CoralWatch. |   |   |

<sup>a, b</sup> Penilaian warna berpatokan pada 4 (empat) blok warna pada charta warna CoralWatch

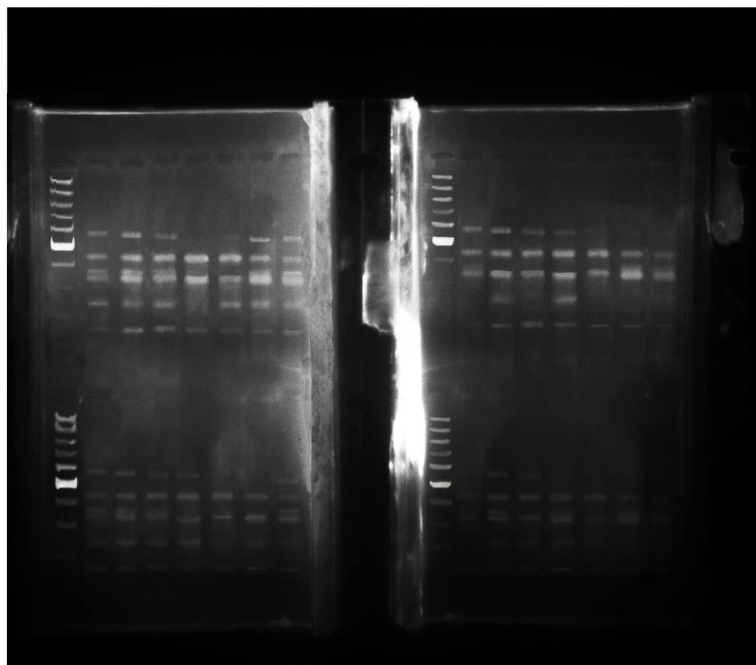


Lampiran 5. Hasil tabulasi data biner karakterisasi fitur morfologi

| Kelompok Karakter    | Bentuk Koloni |     |     |     | Tipe polip |    | Warna jaringan |   |   | Warna kolumella |    |    |    | Tipe koralit |     | MD (cm) |      | CD (cm) |      | ICD (cm) |      | Densitas Polip (polip/cm <sup>2</sup> ) |    |
|----------------------|---------------|-----|-----|-----|------------|----|----------------|---|---|-----------------|----|----|----|--------------|-----|---------|------|---------|------|----------|------|---|----|
|                      | Enc           | Fol | Tub | Tie | Uni        | Bi | C              | D | E | B               | C  | D  | E  | Im           | Bul | ≤0.1    | >0.1 | ≤0.3    | >0.3 | ≤0.2     | >0.2 | ≤4                                      | >4 |
| Detail Karakter      | 1             | 2   | 3   | 4   | 5          | 6  | 7              | 8 | 9 | 10              | 11 | 12 | 13 | 14           | 15  | 16      | 17   | 18      | 19   | 20       | 21   | 22                                      | 23 |
| <b>Kode Karakter</b> |               |     |     |     |            |    |                |   |   |                 |    |    |    |              |     |         |      |         |      |          |      |   |    |
| <b>Sampel</b>        |               |     |     |     |            |    |                |   |   |                 |    |    |    |              |     |         |      |         |      |          |      |   |    |
| SAU-A-01             | 1             | 0   | 0   | 0   | 1          | 0  | 0              | 0 | 1 | 0               | 0  | 0  | 1  | 0            | 1   | 0       | 1    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAU-A-02             | 1             | 0   | 0   | 0   | 1          | 0  | 0              | 0 | 1 | 1               | 0  | 0  | 0  | 0            | 1   | 0       | 1    | 0       | 1    | 1        | 0    | 1                                       | 0  |
| SAU-A-03             | 0             | 0   | 1   | 0   | 1          | 0  | 0              | 0 | 1 | 1               | 0  | 0  | 0  | 0            | 1   | 0       | 1    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAU-A-04             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAU-A-05             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 1            | 0   | 0       | 1    | 1       | 0    | 1        | 0    | 1                                       | 0  |
| SAU-B-01             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 1               | 0  | 0  | 0  | 0            | 1   | 1       | 0    | 0       | 1    | 1        | 0    | 1                                       | 0  |
| SAU-B-02             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 0            | 1   | 0       | 1    | 0       | 1    | 0        | 1    | 1                                       | 0  |
| SAU-B-03             | 0             | 0   | 1   | 0   | 0          | 1  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 0            | 1   | 0       | 1    | 0       | 1    | 1        | 0    | 1                                       | 0  |
| SAU-B-04             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 1               | 0  | 0  | 0  | 0            | 1   | 0       | 1    | 0       | 1    | 1        | 0    | 1                                       | 0  |
| SAU-B-05             | 0             | 0   | 0   | 1   | 1          | 0  | 0              | 1 | 0 | 1               | 0  | 0  | 0  | 0            | 1   | 1       | 0    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAU-C-01             | 0             | 0   | 0   | 1   | 1          | 0  | 1              | 0 | 0 | 0               | 1  | 0  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAU-C-02             | 0             | 1   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 0            | 1   | 0       | 1    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAU-C-03             | 0             | 1   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 0       | 1    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAU-C-04             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 0            | 1   | 0       | 1    | 0       | 1    | 1        | 0    | 1                                       | 0  |
| SAU-C-05             | 0             | 1   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 0               | 1  | 0  | 0  | 1            | 0   | 0       | 1    | 1       | 0    | 1        | 0    | 1                                       | 0  |
| SAS-A-01             | 1             | 0   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 1       | 0    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAS-A-02             | 1             | 0   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 0       | 1    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAS-A-03             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 1                                       | 0  |
| SAS-A-04             | 1             | 0   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 1       | 0    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAS-A-05             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAS-B-01             | 1             | 0   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAS-B-02             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAS-B-03             | 1             | 0   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 1               | 0  | 0  | 0  | 0            | 1   | 0       | 1    | 0       | 1    | 1        | 0    | 0                                       | 1  |
| SAS-B-04             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAS-B-05             | 0             | 0   | 1   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 0            | 1   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAS-C-01             | 1             | 0   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAS-C-02             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 1            | 0   | 1       | 0    | 1       | 0    | 1        | 0    | 1                                       | 0  |
| SAS-C-03             | 1             | 0   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 0       | 1    | 0       | 1    | 1        | 0    | 1                                       | 0  |
| SAS-C-04             | 1             | 0   | 0   | 0   | 1          | 0  | 1              | 0 | 0 | 1               | 0  | 0  | 0  | 1            | 0   | 0       | 1    | 1       | 0    | 1        | 0    | 0                                       | 1  |
| SAS-C-05             | 0             | 1   | 0   | 0   | 1          | 0  | 0              | 1 | 0 | 0               | 0  | 1  | 0  | 1            | 0   | 0       | 1    | 1       | 0    | 1        | 0    | 1                                       | 0  |

### Lampiran 6. Hasil dokumentasi elektroforesis PCR-RAPD

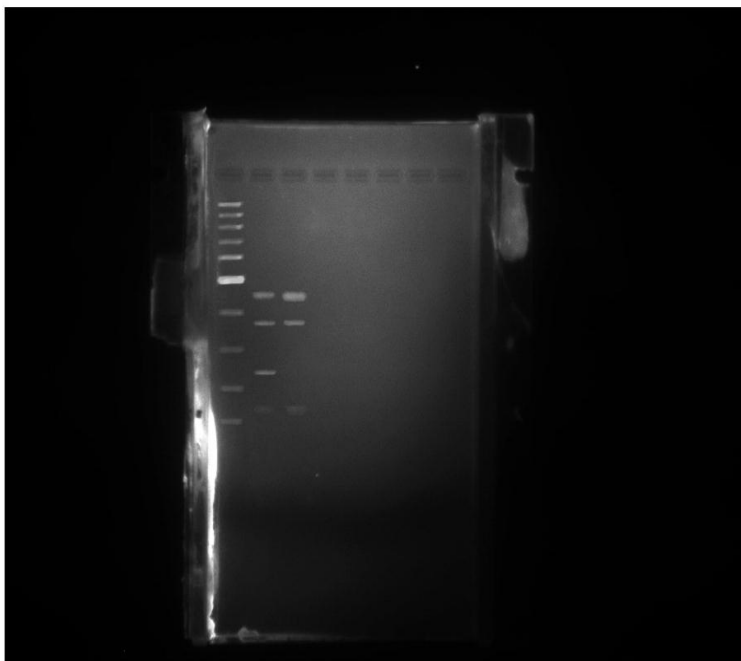
All sample RAPD 1-28



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Page 1 of 1

All sample RAPD 29-30



G:/AL IRSYAD/Scholarship/S2 DALAM NEGERI-Non beasiswa/UNHAS PASCA SARJ...Lab/Elektroforesis/RAPD karang FIX/FIX  
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Page 1 of 1

Lampiran 7. Profil sekuens beberapa sampel terpilih *Echinopora lamellosa*

| Kode Sampel | Sekuens  |
|-------------|--|
| SAU-A-01    | NNNNNNNNCTTGCNGATCTGAGGTCAGGTAGATACCTTCGTTGCGCTCGGGCAGACAGACGCGGGCG<br>GGAACCCACCAGCGCGCGAAGGACTGCCCGTACTTTTTAGCCTCCGCTGGTGCCTGCGGGATG<br>GACCACAACCGCGGGCAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAAACGGAGTGCAGCGCGGC<br>CGTGACGCCTCAACGCCGCAGGCAGAAAAGCGCGACAAGCGCGCCCCTGCCTGCGATGGATGATT<br>TCCGACACTCAGACAGACATGCTCCTGGGAGAACCCAAGAGCGCCATTTGCGTTCAAAGATTCGAT<br>GATTCACTGAATTCTGCAATTCACACTACTTATCGCAGCTGGCTGCGTTCTTCATCGATGCGTGAGC<br>CAAGAGATCCACCGTCAAAGTTGTCTCTGGCATTTTTTTTTTCTTCCGACTTTGGCGCTGAGCGCC<br>GCCGCATATCAGACGACAGACACGTACATGGTAAAACACGAGGCGGGGCTGGCGAGGCGGCCCG<br>GCGTCGCCGCGCGTCCGGTCGCCATTTAACGGCCAGGCCGACCCCTAATGGTTAGGTACGGTTCA<br>CAGAGCAAGACAACGGATGTTGTTCTTGGATGGCATCGGTAATGATCCTTCCGCAGGTTACCTACG<br>GAAACCTTGTTACGACTTTTACTTCTCTAAAGGAACCAAGAAAA      |
| SAU-C-02    | NNNTNGNNNCTTNTGATCTGAGGTCAGGTAGATACCTTCGTTGCGCTCGGGCAGACAGACGCGGGCG<br>GAACCCACCAGCGCGCGAAGGACTGCCCGTACTTTTTAGCCTCCGCTGGTGCCTGCGGGATGG<br>ACCACAACCGCGGGCAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAAACGGAGTGCAGCGCGGCC<br>GTGACGCCTCAACGCCGCAGGCAGAAAAGCGCGACAAGCGCGCCCCTGCCTGCGATGGATGATTT<br>CCGACACTCAGACAGACATGCTCCTGGGAGAACCCAAGAGCGCCATTTGCGTTCAAAGATTCGATG<br>ATTCACTGAATTCTGCAATTCACACTACTTATCGCAGCTGGCTGCGTTCTTCATCGATGCGTGAGCCA<br>AGAGATCCACCGTCAAAGTTGTCTCTGGCATTTTTTTTTTCTTCCCAACTTGGGCGTTAACGCCACC<br>GNNNNNNAACAACAACCCNGNCNAAGGCGAAAACACAAGCCGGGGTGGGGAAGGGGGCGGGCGG<br>GCGCCCGCCGGCCCGGCCCTTTAACCGCCAAGGCCAACCCCAAAGTTAAGNACCGGTTACCA<br>AACAAAAACAACGAAGGTGGTTCTTATGATGGGAATNGGAATGGATCTTCCCCCAGGTCCACTTACGAA<br>AACTTGGTTCCAACCTTTATACTTCTCTACAGTACAAAAAAGAAAAA |
| SAU-C-04    | NNNNNNGNNNCNTGCCTGATCTGAGGTCAGGTAGATACCTTCGTTGCGCTCGGGCAGACAGACGCGG<br>CGGGAACCCACCAGCGCGCGAAGGACTGCCCGTACTTTTTAGCCTCCGCTGGTGCCTGCGGGGA<br>TGGACCACAACCGCGGGCAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAAACGGAGTGCAGCGCG  |

| Kode Sampel | Sekuens  |
|-------------|--|
|             | <p>GCCGTGACGCCTCAACGCCGCAGGCAGAAAAGCGCGACAAGCGCGCCCCTGCCTGCGATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCCAAGAGCGCCATTTGCGTTCAAAGATTGATGATTCACTGAATTCTGCAATTCACACTACTTATCGCAGCTGGCTGCGTTCTTCATCGATGCGTGAGC<br/> CAAGAGATCCACCGTCAAAAGTTGTCTCTGGCATTCTTTTCTTCCGACTTTGGCGCTGAGCGCCGCCGCATATCAGACGACAGACACGTACATGGTGAAAACACGAGGCGGGGCTGGCGAGGCGGCCGCGCTCGCCGCGCGTCCGGTCCGATTTAACGGCCAGGCCGACCCCTAATGGTTAGGTACGGTTCA<br/> CAGAGCAAGACAACGGATGTTGTTCTTGGATGGCATCGGTAATGATCCTTCCGCAGGTTACCTACGGAAACCTTGTTACGACTTTTACTTCTCTAAATGAACAAGAA</p>  |
| SAS-A-02    | <p>NNNNNNNNNCTTGCCTGATCTGAGGTCAGGTAGATACGTACCTCCGTTGCCTCGGCGACAGGCGCGCGGGAACCCACCAGCGCGCGAAGGACTGCCCGTACTTTTTAGCCTCCGCTGGTGCCTGTGGGATGGACCACAACCGCGGGCAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAACGGAGTGCGCGCGGCCGTGACGCCTCAACGCCGCAGGCAGTAGAGCGCGACAAGCGCGCCCCTGCCTGCGATGATGATTGCCGACACTCAGACAGACATGCTCCTGGGAGAACCCAAGAGCGCCATTTGCGTTCAAAGATT<br/> CGATGATTCACTGAATTCTGCAATTCACACTACTTATCGCAGCTGGCTGCGTTCTTCATCGATGCGTGAGCCAAGAGATCCACCGTCAAAAGTTGTCTCTGGCATTCTTTTCTTCCCTTCGACTTTGGCGCCAA<br/> GCGCCGCCGCGCCACAGATCAGACAGACACGTATGTGAAAACACGAGGCGGGGCTGGCGAGGCGGCCGCGCGTCCGCGCGGTCCGGTCCGATTTAACGGCCAGGCCGACCCCTAATGGTTAGGTACGGTTACAGAGCAAGACAACGGATGTTGTTCTTGGATGGCATCGGTAATGATCCTTCCGCAGGTTCA<br/> CCTACGGAAACCTTGTTACGACTTTTACTTCTCTAATTGAACAAGACATATCAATGAACGGAGGAAT<br/> T</p> |
| SAS-B-04    | <p>NNNNNNNNNCTTGCNTGATCTGAGGTCAGGTAGATACCTTCGTTGCCTCGGCGACAGGCGCGGGCGGGAACCCACCAGCGCGCGAAGGACTGCCCGTACTTTTTAGCCTCCGCTGGTGCCTGCGGGATGGACCACAACCGCGCCGAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAACGGAGTGCGCGCGGCCGTGACGCCTCAACGCCGCAGGTGAGCGCGCAAGCGCGCCCCTGCGATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCCAAGAGCGCCATTTGCGTTCAAAGATTGATGATTCACT<br/> GAATTCTGCAATTCACACTACTTATCGCAGCTGGCTGCGTTCTTCATCGATGCGTGAGCCAAGAGAT</p>   |

| Kode Sampel | Sekuens  |
|-------------|--|
|             | CCACCGTCAAAGTTGTCTCTGGCATTTCCTTCCGACTTTGGCGCTGAGCGCCGCCGCATA<br>TCAGACGACAGACACGTACATGGTGAAAACACGAGGCCGGGGCTGGCGAGGCCGCCGCGCGTCGC<br>CGCGCGTCCGGTCGCCATTTAACGGCCAGGCCGACCCCTAATGGTTAGGTACGGTTCACAGAGCAA<br>GACAACGGATGTTGTTCTTGGATGGCATCGGTAATGATCCTTCCGCAGGTTACCTACGGAAACCTT<br>GTTACGACTTTTACTTCCTCTAAATGAACAAGACATATCAGTACAACGAAGGAAC   |
| SAS-C-01    | ANNNNGNNNCTTGCCTGATCTGAGGTCAGGTAGATACCTTCGTTGCCTCGGCGACAGACGCGGC<br>GGGAACCCCNCCAGCGCGCGAAGGACTGCCCGTACTTTTTATCCTCCGCTGGTGCCTGCGGGAT<br>GGACCACAACCGCGGCGAGTCTCTGCCCCTTCAAGGGACACGGCCGCAAACGGAGTGCAGCGCGG<br>CCGTGACGCCTCAACGCCGCAGGCAGAAAAGCGCGACAAGCGCGCCCCTGCCTGCGATGGATGAT<br>TTCCGACACTCAGACAGACATGCTCCTGGGAGAACCCAAGAGCGCCATTTGCGTTCAAAGATTCGAT<br>GATTCACTGAATTCTGCAATTCACACTACTTATCGCAGCTGGCTGCGTTCTTCATCGATGCGTGAGC<br>CAAGAGATCCACCGTCAAAGTTGTCTCTGGCATTTCCTTCCGACTTTGGCGCTGAGCGCC<br>GCCGCATATCAGACGACAGACACATACATGGTGAAAACACAAGGCCGGGGCTGGCGAGGCCGCCGC<br>GCGTCGCCGCGCGTCCGGTCGCCATTTAACGGCCAGGCCGACCCCTAATGGTTAGGTACGGTTCA<br>CAGAACAAGACAACAGATGTTGTTCTTGGATGGCATCGGTAATGATCCTTCCGCAGGTTACCTACG<br>GAAACCTTGTTACGACTTTTACTTCCTCTAATTGAACAAGAAA |

Lampiran 8. Detail BLAST dari hasil sekuensi sampel terpilih *Echinopora lamellosa*

| Sekuen Sample | Panjang Sekuens (bp) | Hasil BLAST  |            |             |            |        |                       | Kode Akses Referensi |
|---------------|----------------------|--|------------|-------------|------------|--------|-----------------------|----------------------|
|               |                      | Deskripsi Kecocokan  | Skor Total | Query Cover | Nilai Eror | %ID    | Panjang Sekuens Akses |                      |
| SAS-A-02      | 728                  | <i>Echinopora lamellosa</i> isolate S109   | 1120       | 95%         | 0.0        | 95.98% | 743                   | HQ203318.1           |
|               |                      | Query 14 CCTGATCTGAGGTCAGGTAGATACGTACCTCCGTTTCGCCCTCGGCGACAGGCGCGCGGGA 73<br>       <br>Sbjct 743 CCTGATCTGAGGTCAGGTAGATACGTACCTCCGTTTCGCCCTCGGCGACAGGCGCGCGGGA 684<br><br>Query 74 ACCCCACCAGCGCGGAAGGACTGCCCGTACTTTTAGCCTCCGCTGGTGGCTGTGGGG 133<br>       <br>Sbjct 683 ACCCCACCAGCGCGGAAGGACTGCCCGTACTTTTAGCCTCCGCTGGTGGCTG-CGGG 625<br><br>Query 134 ATGGACCACAACCGCGCGAGTCTCTCGCCCTCAAGGGACACGGCCGCAA-CGGAGTG 192<br>       <br>Sbjct 624 ATGGACCACAACCGCGCGAGTCTCTCGCCCTCAAGGGACACGGCCGCAAACGGAGTG 565<br><br>Query 193 CGCGCGCGCTGACGCCTCAACGCCGAGGCACTAGAGCGGACAAGCGCCCTGCCT 252<br>       <br>Sbjct 564 CGCGCGCGCTGACGCCTCAACGCCGAGGCAAAAAGCGGACAAGCGCCCTGCCT 505<br><br>Query 253 GCGATGGATGATGCGGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCAT 312<br>       <br>Sbjct 504 GCGATGGATGATTCGGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCAT 445<br><br>Query 313 TTGCGTTCAAAGATTCGATGATTCAGTGAATTCGCAATTCACACTACTTATCGCAGCTG 372<br>       <br>Sbjct 444 TTGCGTTCAAAGATTCGATGATTCAGTGAATTCGCAATTCACACTACTTATCGCAGCTG 385<br><br>Query 373 GCTGCGTTCATCGATGCGTGAGCCAAGAGATCCACCGTCAAAAAGTTGTCTCTGGCA 432<br>       <br>Sbjct 384 GCTGCGTTCATCGATGCGTGAGCCAAGAGATCCACCGTCAAAAAGTTGTCTCTGGCAT 325<br><br>Query 433 ttttttttCCTTCCTTCGACTTTGGCGCCAAGCGCGCGCCGCGCACAGATCAGACAGAC 492<br>       <br>Sbjct 324 TTTTTTT-CCTTCC---GACTTTGGCGCTGAGCGCGCGCGC-ATATCAGA-C-GACAGAC 272<br><br>Query 493 ACGT--AT-GTAAAACACGAGCGGGGCTGGCGAGGCGCGCGCTCGCCGCGCTCC 549<br>     <br>Sbjct 271 ACGTACATGTTGAAAACACGAGCGGGGCTGGCGAGGCGCGCGCTCGCCGCGCTCC 212<br><br>Query 550 GGTCCGCAATTAACGGCCAGGCCACCCCTAATGGTTAGGTACGGTTACAGAGCAAGAC 609<br>       <br>Sbjct 211 GGTCCGCAATTAACGGCCAGGCCACCCCTAATGGTTAGGTACGGTTACAGAGCAAGAC 152<br><br>Query 610 AACGGATGTTGTTCTTGGATGGCATCGGTAATGATCCTTCCGCAAGTTACCTACGGAAA 669<br>       <br>Sbjct 151 AACGGATGTTGTTCTTGGATGGCATCGGTAATGATCCTTCCGCAAGTTACCTACGGAAA 92<br><br>Query 670 CCTTGTTACGACTTTTACTTCCTCTAATGAACAAG 705<br>       <br>Sbjct 91 CCTTGTTACGACTTTTACTTCCTCTAATGATCAAG 56 |            |             |            |        |                       |                      |



| Sekuen Sample   | Panjang Sekuens (bp) | Hasil BLAST                              |            |             |            |        |                       | Kode Akses Referensi |
|---|----------------------|--|------------|-------------|------------|--------|-----------------------|----------------------|
|   |                      | Deskripsi Kecocokan                      | Skor Total | Query Cover | Nilai Eror | %ID    | Panjang Sekuens Akses |                      |
| SAU-C-01  | 708                  | <i>Echinopora lamellosa</i> isolate S109 | 809        | 95%         | 0.0        | 87.92% | 743                   | HQ203318.1           |
| <p>Query 14 CTGATCTGAGGTGAGGTAGATAC---CTTC-GTTTCGCTCGGGCAGACAGCGGGGGAA 69<br/>                 Sbjct 742 CTGATCTGAGGTGAGGTAGATACGTACCTCGGTTCGCTCGGGCAGACAGCGGGGGAA 683</p> <p>Query 70 CCCCACCAGCGCGGAAGGACTGCCGACTTTTTAGCCTCCGCTGGTGCCTGCGGAT 129<br/>                 Sbjct 682 CCCCACCAGCGCGGAAGGACTGCCGACTTTTTAGCCTCCGCTGGTGCCTGCGGAT 623</p> <p>Query 130 GGACCACAACCGCGGAGTCTCTGCCCCAAGGGACACGGCCGAAACGGAGTGGC 189<br/>                 Sbjct 622 GGACCACAACCGCGGAGTCTCTGCCCCAAGGGACACGGCCGAAACGGAGTGGC 563</p> <p>Query 190 CGCGCCGTGACGCTCAACGCCGAGGCAAGCAAGCGCCCGCCCTGCCTGC 249<br/>                 Sbjct 562 CGCGCCGTGACGCTCAACGCCGAGGCAAGCAAGCGCCCGCCCTGCCTGC 503</p> <p>Query 250 GATGGATGATTCCGACTCAGACAGACATGCTCCTGGGAGAACCAGAGCGCCATT 309<br/>                 Sbjct 502 GATGGATGATTCCGACTCAGACAGACATGCTCCTGGGAGAACCAGAGCGCCATT 443</p> <p>Query 310 GCGTTCAAAGATTCGATGATTCAGTGAATTCTGCAATTCACACTACTTATCGCAGTGGC 369<br/>                 Sbjct 442 GCGTTCAAAGATTCGATGATTCAGTGAATTCTGCAATTCACACTACTTATCGCAGTGGC 383</p> <p>Query 370 TGCGTCTTCATCGATGCGTGAGCCAAAGATCCACCGTCAAAGTTGCTCTGGCAtt 429<br/>                 Sbjct 382 TGCGTCTTCATCGATGCGTGAGCCAAAGATCCACCGTCAAAGTTGCTCTGGCAtt 323</p> <p>Query 430 ttttttCTCCCAACTTGGGGTTAA-CGCCCCACGNNNNNNAACAACAACNGNCNA 488<br/>                 Sbjct 322 TTTTTCCTCCGA-CTTTGGCGCTGAGCGCCG-CCGCATATCAGACGACAGACAGTACA 265</p> <p>Query 489 AGCGGAAAACACAAGCCGGGG-TGGGGAAGGGGGCGGGG-CGCC-CGCCGGCCCGCC 545<br/>                 Sbjct 264 TGGTGAAAACACAGCGGGGGCTGGCG-AGGCGGCCGCGCTCGCCGCGC-GTCCGGTCG 207</p> <p>Query 546 CCCTTTAACCGCCAAGGCCAACCCAAA-GGTAAAGNACGGTTACCAACAAAACAAC 604<br/>                 Sbjct 206 CCATTTAACGGCC-AGGCGGACCCCTAATGGTTAGGTAC-GGTTACAGAGCAAGACAAC 149</p> <p>Query 605 GAAGGTGGTTCTTG-ATGGGAATNGG-AATGGATCTTCCCCAGGTCCACTTACGAAAAC 662<br/>                 Sbjct 148 GGATGTTGTCTTGATGGCA-TCGGTAATG-ATCCTTCGCGAGGTTACCTACGGAAAAC 91</p> <p>Query 663 TTGGTTCCAACTTTATACTTCTCTCTA 689<br/>                 Sbjct 90 CTGTGTACGACTT-TACTTC-CTCTA 66</p> |                      |  |            |             |            |        |                       |                      |

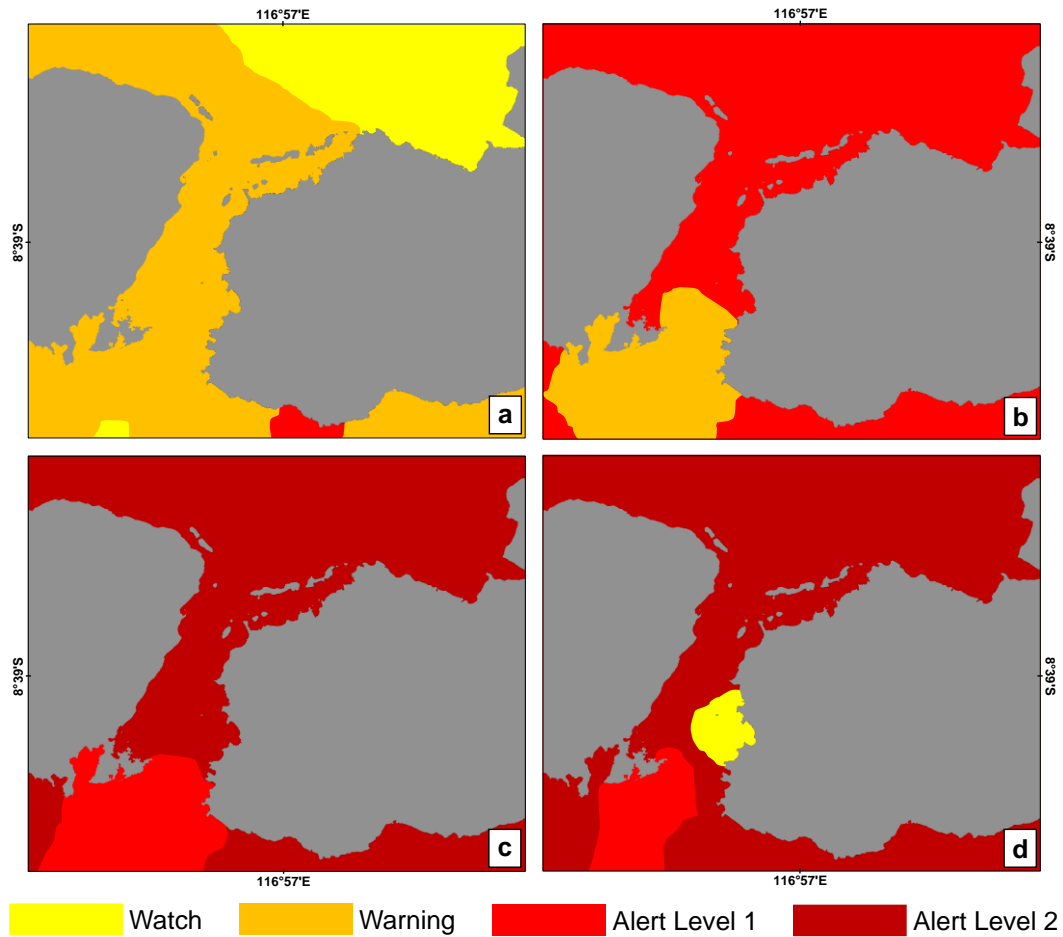
| Sekuen Sample | Panjang Sekuens (bp) | Hasil BLAST   |            |             |            |        |                       | Kode Akses Referensi |
|---------------|----------------------|---|------------|-------------|------------|--------|-----------------------|----------------------|
|               |                      | Deskripsi Kecocokan   | Skor Total | Query Cover | Nilai Eror | %ID    | Panjang Sekuens Akses |                      |
| SAU-A-01      | 702                  | <i>Echinopora lamellosa</i> isolate S109  | 1203       | 96%         | 0.0        | 98.68% | 743                   | HQ203318.1           |
|               |                      | Query 16 GATCTGAGGT CAGGTAGATAC--CTTC-GTTCGCCTCGGCGACAGACGCGCGGGAACC 71<br>     <br>Sbjct 740 GATCTGAGGT CAGGTAGATACGTACCTCGGTCGCCTCGGCGACAGACGCGCGGGAACC 681     |            |             |            |        |                       |                      |
|               |                      | Query 72 CCACCAGCGCGGAAGGACTGCCCTACTTTTAGCCTCCGCTGGTGCCTGCGGGATGG 131<br>     <br>Sbjct 680 CCACCAGCGCGGAAGGACTGCCCTACTCTTAGCCTCCGCTGGTGCCTGCGGGATGG 621          |            |             |            |        |                       |                      |
|               |                      | Query 132 ACCACAACCGCGCGAGTCTCTCTGCCCTCAAGGGACACGGCCGCAAACGGAGTGC GCG 191<br>     <br>Sbjct 620 ACCACAACCGCGCGAGTCTCTCTGCCCTCAAGGGACACGGCCGCAAACGGAGTGC GCG 561   |            |             |            |        |                       |                      |
|               |                      | Query 192 CGGCCGTGACGCCTCAACGCCGAGGACAGAAAAGCGCGACAAGCGCGCCCTGCCTGCGA 251<br>     <br>Sbjct 560 CGGCCGTGACGCCTCAACGCCGAGGACAGAAAAGCGCGACAAGCGCGCCCTGCCTGCGA 501   |            |             |            |        |                       |                      |
|               |                      | Query 252 TGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATTTGC 311<br>     <br>Sbjct 500 TGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATTTGC 441   |            |             |            |        |                       |                      |
|               |                      | Query 312 GTTCAAAGATTTCGATGATTCACTGAATTCGCAATTCACACTACTTATCGCAGCTGGCTG 371<br>     <br>Sbjct 440 GTTCAAAGATTTCGATGATTCACTGAATTCGCAATTCACACTACTTATCGCAGCTGGCTG 381 |            |             |            |        |                       |                      |
|               |                      | Query 372 CGTTCCTCATCGATGCGTGAGCCAAGAGATCCACCGTCAAAGTTGTCTCTGGCAttttt 431<br>     <br>Sbjct 380 CGTTCCTCATCGATGCGTGAGCCAAGAGATCCACCGTCAAAGTTGTCTCTGGCATTTTT 321   |            |             |            |        |                       |                      |
|               |                      | Query 432 ttttCCTTCGGACTTTGGCGCTGAGCGCCGCGCATATCAGACGACAGACACGTACATGG 491<br>     <br>Sbjct 320 TTT-CCTTCGGACTTTGGCGCTGAGCGCCGCGCATATCAGACGACAGACACGTACATGG 262   |            |             |            |        |                       |                      |
|               |                      | Query 492 TGA AAACACGAGCGGGGCTGGCGAGGCGCGCGCTCGCCGCGCTCCGGTCCGCCATT 551<br>     <br>Sbjct 261 TGA AAACACGAGCGGGGCTGGCGAGGCGCGCGCTCGCCGCGCTCCGGTCCGCCATT 202       |            |             |            |        |                       |                      |
|               |                      | Query 552 TAACGGCCAGGCGACCCCTAATGGTTAGGTACGGTTACAGAGCAAGACAACGGATGTT 611<br>     <br>Sbjct 201 TAACGGCCAGGCGACCCCTAATGGTTAGGTACGGTTACAGAGCAAGACAACGGATGTT 142     |            |             |            |        |                       |                      |
|               |                      | Query 612 GTTCTTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGAAAACCTTGTACG 671<br>     <br>Sbjct 141 GTTCTTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGAAAACCTTGTACG 82        |            |             |            |        |                       |                      |
|               |                      | Query 672 ACTTTTACTTCCCTAAAGGA 692<br>     <br>Sbjct 81 ACTTTTACTTCCCTAAATGA 61   |            |             |            |        |                       |                      |

| Sekuen Sample | Panjang Sekuens (bp) | Hasil BLAST   |            |             |            |        |                       | Kode Akses Referensi |
|---------------|----------------------|---|------------|-------------|------------|--------|-----------------------|----------------------|
|               |                      | Deskripsi Kecocokan   | Skor Total | Query Cover | Nilai Eror | %ID    | Panjang Sekuens Akses |                      |
| SAU-C-04      | 701                  | <i>Echinopora lamellosa</i> isolate S109  | 1218       | 97%         | 0.0        | 98.69% | 743                   | HQ203318.1           |
|               |                      | Query 15 CCTGATCTGAGGTCAGGTAGATAC---CTTC-GTTCGCCTCGGCGACAGACGCGGGGA 70<br>     <br>Sbjct 743 CCTGATCTGAGGTCAGGTAGATACGTACCTCGGTTCCGCTCGGCGACAGACGCGGGGA 684         |            |             |            |        |                       |                      |
|               |                      | Query 71 ACCCCACCAGCGCGGAAGGACTGCCGTACTTTTGTAGCCTCCGCTGGTGGCTGCGGGA 130<br>     <br>Sbjct 683 ACCCCACCAGCGCGGAAGGACTGCCGTACTCTTTAGCCTCCGCTGGTGGCTGCGGGA 624         |            |             |            |        |                       |                      |
|               |                      | Query 131 TGGACCACAACCGCGGAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAACGGAGTGC 190<br>     <br>Sbjct 623 TGGACCACAACCGCGGAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAACGGAGTGC 564         |            |             |            |        |                       |                      |
|               |                      | Query 191 GCGCGCCGCTGACGCTCAACGCCGAGGACAGAAAAGCGCGACAAGCGCCCTGCCTG 250<br>     <br>Sbjct 563 GCGCGCCGCTGACGCTCAACGCCGAGGACAGAAAAGCGCGACAAGCGCCCTGCCTG 504           |            |             |            |        |                       |                      |
|               |                      | Query 251 CGATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATT 310<br>     <br>Sbjct 503 CGATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATT 444     |            |             |            |        |                       |                      |
|               |                      | Query 311 TCGGTTCAAAGATTCGATGATTCACCTGAATTCGCAATTCACACTACTTATCGCAGCTGG 370<br>     <br>Sbjct 443 TCGGTTCAAAGATTCGATGATTCACCTGAATTCGCAATTCACACTACTTATCGCAGCTGG 384   |            |             |            |        |                       |                      |
|               |                      | Query 371 CTGCGTTCTTCATCGATGCGTGAGCCAAAGAGATCCACCGTCAAAAAGTTGTCTTGGCAtt 430<br>     <br>Sbjct 383 CTGCGTTCTTCATCGATGCGTGAGCCAAAGAGATCCACCGTCAAAAAGTTGTCTTGGCATT 324 |            |             |            |        |                       |                      |
|               |                      | Query 431 ttttttCCTTCGACTTTGGCGCTGAGCGCCCGCATATCAGACGACAGACAGTACA 490<br>     <br>Sbjct 323 TTTTTT-CCTTCGACTTTGGCGCTGAGCGCCCGCATATCAGACGACAGACAGTACA 265            |            |             |            |        |                       |                      |
|               |                      | Query 491 TGGTGAAAACACGAGCGGGGCTGGCGAGGCGCCGCGCTCGCCGCGGTCGCGGTCGCC 550<br>     <br>Sbjct 264 TGGTGAAAACACGAGCGGGGCTGGCGAGGCGCCGCGCTCGCCGCGGTCGCGGTCGCC 205         |            |             |            |        |                       |                      |
|               |                      | Query 551 ATTTAACGGCCAGGCCACCCCTAATGGTTAGGTACGGTTCCACAGACAAGACAACGGAT 610<br>     <br>Sbjct 204 ATTTAACGGCCAGGCCACCCCTAATGGTTAGGTACGGTTCCACAGACAAGACAACGGAT 145     |            |             |            |        |                       |                      |
|               |                      | Query 611 GTTGTCTTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGGAAACCTTGT 670<br>     <br>Sbjct 144 GTTGTCTTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGGAAACCTTGT 85            |            |             |            |        |                       |                      |
|               |                      | Query 671 ACGACTTTTACTTCCTCTAAATGAACAAG 699<br>     <br>Sbjct 84 ACGACTTTTACTTCCTCTAAATGATCAAG 56   |            |             |            |        |                       |                      |

| Sekuen Sample | Panjang Sekuens (bp) | Hasil BLAST   |            |             |            |        |                       | Kode Akses Referensi |
|---------------|----------------------|---|------------|-------------|------------|--------|-----------------------|----------------------|
|               |                      | Deskripsi Kecocokan   | Skor Total | Query Cover | Nilai Eror | %ID    | Panjang Sekuens Akses |                      |
| SAS-B-04      | 713                  | <i>Echinopora lamellosa</i> isolate S109  | 1140       | 94%         | 0.0        | 96.94% | 743                   | HQ203318.1           |
|               |                      | Query 16 TGATCTGAGGTCAGGTAGATAC---CTTC-GTTCGCCTCGGCGACAGGCGCGGGGAAC 71<br>     <br>Sbjct 741 TGATCTGAGGTCAGGTAGATACGTACCTCGGTTTCGCCTCGGCGACAGACGCGGGGAAC 682<br>     <br>Query 72 CCCACCAGCGCGGAAGGACTGCCCGTACTTTTTCAGCCTCCGCTGGTGCCTGCGGGATG 131<br>     <br>Sbjct 681 CCCACCAGCGCGGAAGGACTGCCCGTACTCTTTAGCCTCCGCTGGTGCCTGCGGGATG 622<br>     <br>Query 132 GACCACAACCGCGCGAGTCTCTGCCCCTCAAGGGACACGGCGCAAACGGAGTGC 191<br>     <br>Sbjct 621 GACCACAACCGCGCGAGTCTCTGCCCCTCAAGGGACACGGCGCAAACGGAGTGC 562<br>     <br>Query 192 GCGGCCGTGACGCTCAACGCCGAGG---TGAGCGCGGCAAGCGCCCTGC---G 243<br>     <br>Sbjct 561 GCGGCCGTGACGCTCAACGCCGAGGCAAAAAGCGCGACAAGCGCCCTGCCTGC 502<br>     <br>Query 244 ATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATTTG 303<br>     <br>Sbjct 501 ATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATTTG 442<br>     <br>Query 304 CGTTCAAAGATTCGATGATTCACTGAATTCGCAATTCACACTACTTATCGCAGCTGGCT 363<br>     <br>Sbjct 441 CGTTCAAAGATTCGATGATTCACTGAATTCGCAATTCACACTACTTATCGCAGCTGGCT 382<br>     <br>Query 364 GCGTTCCTCATCGATGCGTGAGCCAAAGATCCACCGTCAAAGTTGTCTTGCCAtttt 423<br>     <br>Sbjct 381 GCGTTCCTCATCGATGCGTGAGCCAAAGATCCACCGTCAAAGTTGTCTTGCCATTTT 322<br>     <br>Query 424 tttttCCTCCGACTTTGGCGCTGAGCGCCCGCCATATCAGACGACAGACACGTACATG 483<br>     <br>Sbjct 321 TTTT-CCTCCGACTTTGGCGCTGAGCGCCCGCCATATCAGACGACAGACACGTACATG 263<br>     <br>Query 484 GTGAAAACACGAGCGGGGCTGGCGAGGCGCGCGCTCGCCGCGCTCCGGTCCGCCAT 543<br>     <br>Sbjct 262 GTGAAAACACGAGCGGGGCTGGCGAGGCGCGCGCTCGCCGCGCTCCGGTCCGCCAT 203<br>     <br>Query 544 TTAACGGCCAGGCCGACCCCTAATGGTTAGTACGGTTCACAGAGCAAGACAACGGATGT 603<br>     <br>Sbjct 202 TTAACGGCCAGGCCGACCCCTAATGGTTAGTACGGTTCACAGAGCAAGACAACGGATGT 143<br>     <br>Query 604 TGTTCCTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGGAAACCTTGTGTAC 663<br>     <br>Sbjct 142 TGTTCCTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGGAAACCTTGTGTAC 83<br>     <br>Query 664 GACTTTTACTTCTCTAAATGAACAAG 690<br>     <br>Sbjct 82 GACTTTTACTTCTCTAAATGATCAAG 56<br> |            |             |            |        |                       |                      |

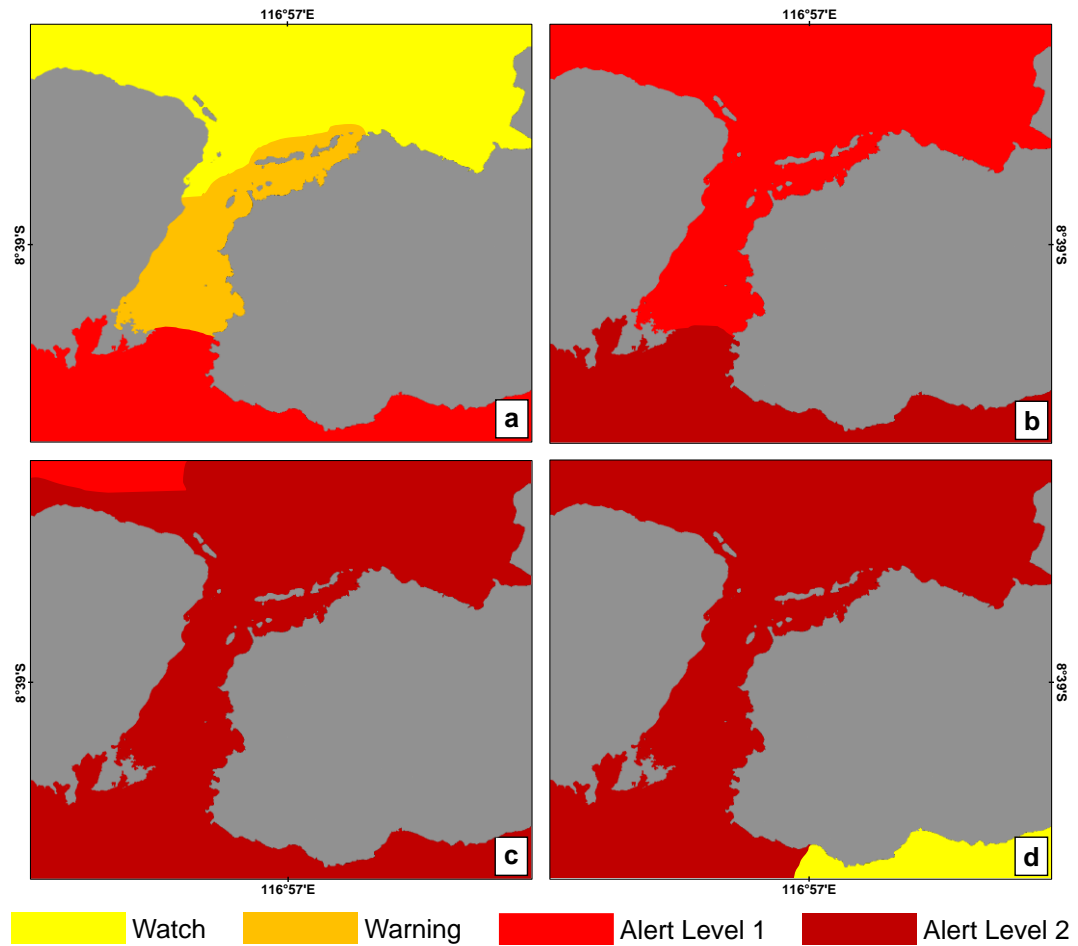
| Sekuen Sample | Panjang Sekuens (bp) | Hasil BLAST   |            |             |            |        |                       | Kode Akses Referensi |
|---------------|----------------------|---|------------|-------------|------------|--------|-----------------------|----------------------|
|               |                      | Deskripsi Kecocokan   | Skor Total | Query Cover | Nilai Eror | %ID    | Panjang Sekuens Akses |                      |
| SAS-C-01      | 701                  | <i>Echinopora lamellosa</i> isolate S109  | 1181       | 97%         | 0.0        | 97.68% | 743                   | HQ203318.1           |
|               |                      | Query 14 CCTGATCTGAGGT CAGGTAGATAC---CTTC-GTTCGCCTCGGCGACAGACGCGGGGA 69<br>     <br>Sbjct 743 CCTGATCTGAGGT CAGGTAGATACGTACCTCGGTCGCCTCGGCGACAGACGCGGGGA 684      |            |             |            |        |                       |                      |
|               |                      | Query 70 ACCCNCCAGCGCGGAAGGACTGCCCGTACTTTTTATCCTCCGCTGGTGCCTGCGGGA 129<br>     <br>Sbjct 683 ACCCCACCAGCGCGGAAGGACTGCCCGTACTCTTTAGCCTCCGCTGGTGCCTGCGGGA 624       |            |             |            |        |                       |                      |
|               |                      | Query 130 TGGACCACAACCGCGGAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAACGGAGTGC 189<br>     <br>Sbjct 623 TGGACCACAACCGCGGAGTCTCTCTGCCCTTCAAGGGACACGGCCGCAACGGAGTGC 564       |            |             |            |        |                       |                      |
|               |                      | Query 190 GCGCGCCCGTGACGCCTCAACGCCGCGAGGCAGAAAAGCGGACAAGCGGCCCTGCCTG 249<br>     <br>Sbjct 563 GCGCGCCCGTGACGCCTCAACGCCGCGAGGCAGAAAAGCGGACAAGCGGCCCTGCCTG 504     |            |             |            |        |                       |                      |
|               |                      | Query 250 CGATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATT 309<br>     <br>Sbjct 503 CGATGGATGATTTCCGACACTCAGACAGACATGCTCCTGGGAGAACCAAGAGCGCCATT 444   |            |             |            |        |                       |                      |
|               |                      | Query 310 TCGGTTCAAAGATTGATGATTCACTGAATTCTGCAATTCACACTACTTATCGCAGCTGG 369<br>     <br>Sbjct 443 TCGGTTCAAAGATTGATGATTCACTGAATTCTGCAATTCACACTACTTATCGCAGCTGG 384   |            |             |            |        |                       |                      |
|               |                      | Query 370 CTGCGTTCTTCATCGATGCGTGAGCCAAAGAGATCCACCGTCAAAGTTGTCTCTGGCAtt 429<br>     <br>Sbjct 383 CTGCGTTCTTCATCGATGCGTGAGCCAAAGAGATCCACCGTCAAAGTTGTCTCTGGCATT 324 |            |             |            |        |                       |                      |
|               |                      | Query 430 ttttttCCTTCCGACTTTGGCGCTGAGCGCCGCGCATATCAGACGACAGACACATACA 489<br>     <br>Sbjct 323 TTTTTT-CCTTCCGACTTTGGCGCTGAGCGCCGCGCATATCAGACGACAGACACGTACA 265    |            |             |            |        |                       |                      |
|               |                      | Query 490 TGGTGAAAACACAAGCGGGGCTGGCGAGGCGGCGCGCTCGCCGCGCTCCGGTCCGCC 549<br>     <br>Sbjct 264 TGGTGAAAACACAGGCGGGGCTGGCGAGGCGGCGCGCTCGCCGCGCTCCGGTCCGCC 205       |            |             |            |        |                       |                      |
|               |                      | Query 550 ATTTAACGGCCAGGCCGACCCCTAATGGTTAGGTACGGTTCACAGAACAAGACAACAGAT 609<br>     <br>Sbjct 204 ATTTAACGGCCAGGCCGACCCCTAATGGTTAGGTACGGTTCACAGAGCAAGACAACGGAT 145 |            |             |            |        |                       |                      |
|               |                      | Query 610 GTTGTCTTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGGAAACCTTGTT 669<br>     <br>Sbjct 144 GTTGTCTTGGATGGCATCGGTAATGATCCTTCCGAGGTTACCTACGGAAACCTTGTT 85        |            |             |            |        |                       |                      |
|               |                      | Query 670 ACGACTTTTACTTCCTCTAATTGAACAAG 698<br>     <br>Sbjct 84 ACGACTTTTACTTCCTCTAATGATCAAG 56  |            |             |            |        |                       |                      |

Lampiran 9. Peta prediksi wilayah terdampak pemutihan berdasarkan sebaran SPL pada tahun 2010



**Catatan:** wilayah resiko terdampak pemutihan karang pada bulan a) Februari, b) Maret, c) April, dan d) Mei tahun 2010

Lampiran 10. Peta prediksi wilayah terdampak pemutihan berdasarkan sebaran SPL pada tahun 2016



**Catatan:** wilayah resiko terdampak pemutihan karang pada bulan a) Februari, b) Maret, c) April, dan d) Mei tahun 2016

Lampiran 11. Beberapa koloni muda karang *Echinopora lamellosa* yang berhasil didokumentasikan selama pengambilan sampel

