**Electronic Supplementary Material**

**Supplemental Methods**:

*ddRAD Library Methods*

DNA was extracted using Mag-Bind Tissue DNA kits (Omega Bio-Tek) and digested with *Eco*RI and *Msp*I. A barcoded adapter was ligated to *Eco*RI restriction sites and a common adapter was ligated to *Msp*I restriction sites, using equimolar quantities of each digested sample. Samples were then pooled into four ‘index’ libraries consisting of ~34 individuals each and size selected using a Pippin Prep DNA size selection system (Sage Science Inc.). Fragments were selected using a mean size of 375 bp, with a ‘tight’ selection window (± 37 bp). Illumina flow-cell adapter sequences and index-specific identifiers were added to each index library, using 12 cycles of PCR.

*mtDNA Sequencing*

Thirty-microlitre PCR reactions contained 1X reaction buffer (pH 8.5), 2 mM MgCl2, 0.25 mM of each dNTP, 250 pmol of each primer, 0.05 U/μL *Taq* polymerase and 1.0 μL of template. Reaction conditions consisted of initial denaturation at 95°C for 2 min followed by 35 cycles at 94°C for 30 s, 54° for 60 s, and 72°C for 65 s, and a final extension at 72°C for 10 min. Amplified products were sent to Beckman Coulter to be cleaned and sequenced bi-directionally.

*Bioinformatic Analysis*

The combination of paired-end (PE) and single-end (SE) libraries called for customization to the default *dDocent* pipeline (Puritz *et al*. 2014). PE read files were placed in a working directory and a modified version of *dDocent* (version 1.0) was run with a cutoff value of 2 and a clustering % of 0.95. There were three modifications for reference contig assembly to help deal with a large repetitive genome.

1. During the clustering command of *Rainbow* ([Chong *et al*. 2012](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbts482)), the mismatch parameter was changed to 2 and the –L command was implemented.
2. During the div command of *Rainbow* ([Chong *et al*. 2012](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbts482)), the minimum frequency for a new variant was changed from 0.2 to 0.05.
3. During the merge command of *Rainbow* ([Chong *et al*. 2012](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbts482)), the minimum number of reads to assemble was lowered from 5 to 3 and the maximum number of divided clusters to merge and the maximum number of reads to assemble was raised from 300 to 500.

After reference assembly was completed, SE reads were returned to the working directory. The read mapping portion of *dDocent* (version 1.0) was modified again to help deal with a large repetitive genome. The default clipping penalties were changed to (20,5), the mismatch parameter was lowered from 4 to 3, and the gap opening penalty was lowered from 6 to 5. Additionally, reads with more than 20% clipping were removed with AWK after mapping. These settings would enhance the ability for highly polymorphic reads to map to the reference, but also remove reads that have only have a small matching portion. Afterwards, default values of *dDocent* (version 1.0) were used to call to call variants. Raw variant calls were subjected to several filtering steps to reduce false positives. A script to reproduce the filtering steps is available at Dryad (doi:10.5061/dryad.7k4c1). Raw variants were filtered sequentially via VCFtools ([Danecek](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbtr330) *[et al.](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbtr330)* [2011](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbtr330)) or custom bash scripts, using the following steps:

1. Loci were removed that had a minor allele count of less than 2, a PHRED quality score of less than 20, and a call rate of less than 50%.
2. All genotypes with less than 5 reads were changed to missing.
3. Loci were removed that now had less than a 75% call rate, and a minor allele frequency of less than 0.01.
4. 13 individuals (out of 134) were removed for having more than 40% missing data, using the script filter\_missing\_ind.sh (<https://github.com/jpuritz/dDocent/blob/master/scripts/filter_missing_ind.sh>).
5. The highly related individual (as described in main text; LK\_007) was removed. Loci called in less than 97.5% of individuals and with a minor allele frequency of less than 5% were removed.

After this point, variant calls were filtered using a custom script (FB\_filters\_Bhead.sh; Dryad: doi:10.5061/dryad.7k4c1) that utilizes vcflib (<https://github.com/ekg/vcflib>) and VCFtools ([Danecek](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbtr330) *[et a](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbtr330)*[l. 2011](https://dx.doi.org/10.1093%2Fbioinformatics%2Fbtr330)) to filter loci based on FreeBayes INFO criteria and depth:

1. Loci were removed if the average allele balance at heterozygous genotypes was less than 28% (i.e., if a genotype had 100X coverage, there would have to be an average of 28 or more reads from the alternate allele across all heterozygous genotypes). Additionally, if the quality sum of the reference or alternate allele was 0, the locus was removed. This removes sites that have a large portion of spurious heterozygous genotype calls.
2. Loci were then removed if the quality score was less than half of the total depth. With FreeBayes, excessive depth can give inflated quality scores.
3. Loci were removed if the ratio between the mean mapping quality of the alternate and reference allele was less than 0.9 or more than 1.05.
4. Loci were then removed if the majority of reads did not come from only one read orientation. Our insert size was much larger than our PE read lengths, so true RAD loci should not have forward and reverse reads that overlap.
5. Loci also were removed based on the status of properly paired reads. True variants should have reads coming from all properly paired reads, or only from reads that are not properly paired (some RAD loci do not assemble well for the PE read, leaving only forward reads). However, false variants tend to have properly paired reference reads and not properly paired alternate reads. Loci were retained if more than 0.05% of reference reads were properly paired and less than 0.05% of alternate reads were properly paired and vice versa.
6. Of the remaining loci, the average depth (and standard deviation) across all individuals was calculated. Loci that have a depth greater than the average depth plus on SD are removed if the quality score is less than 2 times the depth. This filter is based off results reported in ([arXiv:1404.0929v1](http://arxiv.org/abs/1404.0929v1)) by Li (2014).
7. Only loci that were in the bottom 90% of mean depth (less than 79.94) were kept to remove any possible paralogs or repetitive genomic regions.

After these two filter steps, loci were filtered based on locality-based tests of Hardy Weinberg equilibrium. Loci were removed that had a *P* value of less than 0.001 in at least 25% of the populations, using the script filter\_hwe\_by\_pop.pl (<https://github.com/jpuritz/dDocent/blob/master/scripts/filter_hwe_by_pop.pl>). Variant calls were then decomposed into SNP and INDEL calls, using vcflib; INDELS were then removed with VCFtools to produce a VCF file of SNP only calls. SNPs were then filtered again for paralogs by removing loci that had more than 3 SNPs within 5 bp and loci that had had more than 4 SNPs within 17 bp. This final set of SNP calls was used for all subsequent analyses.

**Supplemental References**

1. Chong Z, Ruan J, Wu CI (2012) Rainbow: an integrated tool for efficient clustering and assembling RAD-seq reads. *Bioinformatics*, **28**, 2732-2737.

2. Danecek P, Auton A, Abecasis G, *et al.* (2011) The variant call format and VCFtools. *Bioinformatics*, **27**, 2156-2158.

3. Li H (2014) Towards better understanding of artifacts in variant calling from high-coverage samples. *Bioinformatics*, **30**, 2843-2851.

4. Puritz JB, Hollenbeck CM, Gold JR (2014) dDocent: a RADseq, variant-calling pipeline designed for population genomics of non-model organisms. *PeerJ*, **2**, e431.

**Table S1.** Summary of diversity statistics for 5,914 SNPs and sequences (1,064 base pairs) of the mitochondrial control region for samples of bonnetheads from North Carolina (NC) and three localities along the Gulf Coast of Florida: Florida Bay (FB), Tampa Bay (TB), and Panama City (PC). *n* - sample size; *π* - nucleotide diversity; *H* – number of haplotypes; *h* – nucleon diversity.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| ***SNPs*** | **NC** | **FB** | **TB** | | **PC** |
| *n* | 22 | 32 | | 31 | 36 |
| *π* | 0.2996 | 0.3189 | | 0.3163 | 0.3168 |
| ***mtDNA*** |  |  | |  |  |
| *n* | 23 | 24 | | 27 | 25 |
| *H* | 7 | 17 | | 17 | 16 |
| *h* | 0.719 ± 0.077 | 0.938 ± 0.039 | | 0.940 ± 0.031 | 0.947 ± 0.029 |
| *π* | 0.0010 ±0.0008 | 0.0025 ±0.0015 | | 0.0022 ±0.0014 | 0.0026±0.0016 |

**Table S2.** Distribution of haplotypes and GenBank Accession numbers for mitochondrial control region sequences from samples of bonnetheads off North Carolina (NC) and three locations along the Gulf Coast of Florida: Florida Bay (FB), Tampa Bay (TB) and Panama City (PC).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **NC** | **FB** | **TB** | **PC** | **Genbank Accession #** |
| H1 | 6 | 1 | 2 | 2 | KT031755 |
| H2 | 11 | 1 | 6 | 3 | KT031756 |
| H3 | 1 | - | - | - | KT031757 |
| H4 | 1 | - | - | - | KT031758 |
| H5 | 1 | - | - | - | KT031759 |
| H6 | 2 | 6 | 2 | 5 | KT031760 |
| H7 | 1 | - | - | - | KT031761 |
| H8 | - | - | - | 1 | KT031762 |
| H9 | - | - | - | 2 | KT031763 |
| H10 | - | - | - | 1 | KT031764 |
| H11 | - | - | - | 1 | KT031765 |
| H12 | - | - | - | 2 | KT031766 |
| H13 | - | - | - | 1 | KT031767 |
| H14 | - | - | 1 | 1 | KT031768 |
| H15 | - | - | - | 1 | KT031769 |
| H16 | - | - | - | 1 | KT031770 |
| H17 | - | 2 | 3 | 1 | KT031771 |
| H18 | - | 1 | 1 | 1 | KT031772 |
| H19 | - | - | - | 1 | KT031773 |
| H20 | - | - | - | 1 | KT031774 |
| H21 | - | - | 1 | - | KT031775 |
| H22 | - | - | 2 | - | KT031776 |
| H23 | - | - | 1 | - | KT031777 |
| H24 | - | 1 | - | - | KT031778 |
| H25 | - | - | 1 | - | KT031779 |
| H26 | - | 1 | - | - | KT031780 |
| H27 | - | 1 | - | - | KT031781 |
| H28 | - | 1 | - | - | KT031782 |
| H29 | - | 1 | - | - | KT031783 |
| H30 | - | - | 1 | - | KT031784 |
| H31 | - | - | 1 | - | KT031785 |
| H32 | - | 1 | - | - | KT031786 |
| H33 | - | 1 | - | - | KT031787 |
| H34 | - | 1 | - | - | KT031788 |
| H35 | - | - | 1 | - | KT031789 |
| H36 | - | - | 1 | - | KT031790 |
| H37 | - | 1 | - | - | KT031791 |
| H38 | - | 1 | - | - | KT031792 |
| H39 | - | 2 | - | - | KT031793 |
| H40 | - | - | 1 | - | KT031794 |
| H41 | - | - | 1 | - | KT031795 |
| H42 | - | 1 | - | - | KT031796 |
| H43 | - | - | 1 | - | KT031797 |
| H44 | - | 1 | - | - | KT031798 |
| Total | 23 | 25 | 27 | 25 |  |

**Table S3.** Results of standard least squares regression of allele frequencies at outlier loci by latitude: loci are organized as bi-allelic and multi-allelic. Values of *r*2 > 0.90 and *P* < 0.05 are italicized and bolded. %X and %Y are percentage contribution to abscissa and ordinate from DAPC analysis, using k-means clustering.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Haplotype** | ***r2*** | ***P*-value** | % X | %Y |
| ***Bi-allelic*** |  |  |  |  |
| E28275:1/2 | ***0.93*** | ***0.037*** | 7.54 | 0.08 |
| E29236:1/2 | ***0.92*** | ***0.042*** | 0.42 | 0.62 |
| E43805:1/2 | ***0.90*** | ***0.050*** | 6.22 | 0.08 |
| E53310:1/2 | 0.85 | 0.075 | 2.56 | 1.10 |
| E61036:1/2 | 0.49 | 0.299 | 0.02 | 0.16 |
| E64126:1/2 | ***0.91*** | ***0.048*** | 0.56 | 0.02 |
| E65274:1/2 | 0.76 | 0.130 | 0.54 | 1.80 |
| E66074:1/2 | ***0.92*** | ***0.043*** | 8.94 | 0.04 |
| E68107:1/2 | 0.76 | 0.127 | 2.64 | 3.56 |
| E82240:1/2 | ***0.90*** | 0.053 | 7.50 | 0.70 |
| E87901:1/2 | 0.83 | 0.089 | 0.46 | 4.36 |
| E92875:1/2 | ***0.93*** | ***0.035*** | 2.68 | 0.00 |
| E94551:1/2 | ***0.92*** | ***0.041*** | 8.28 | 0.02 |
| E95266:1/2 | ***0.90*** | ***0.049*** | 0.90 | 0.14 |
| E102269:1/2 | 0.84 | 0.084 | 0.02 | 10.58 |
| E106435:1/2 | ***0.92*** | ***0.041*** | 8.28 | 0.02 |
| E107376:1/2 | 0.61 | 0.222 | 0.18 | 1.28 |
| E113131:1/2 | 0.86 | 0.073 | 2.10 | 1.24 |
| E117105:1/2 | 0.86 | 0.071 | 3.52 | 0.38 |
| E167424:1/2 | 0.87 | 0.069 | 2.04 | 1.76 |
| E195370:1/2 | 0.83 | 0.089 | 3.54 | 1.12 |
|  |  |  |  |  |
| ***Multi-allelic*** |  |  |  |  |
| E52101:1/… | 0.67 | 0.179 | 0.22 | 0.26 |
| :2/… | 0.29 | 0.457 | 0.07 | 13.98 |
| :3/… | 0.06 | 0.763 | 0.55 | 10.46 |
| E69589:1/… | 0.76 | 0.126 | 0.36 | 2.44 |
| :2/… | 0.87 | 0.070 | 0.32 | 3.18 |
| :3/… | ***0.92*** | ***0.042*** | 0.00 | 0.05 |
| E73988:1/… | ***0.92*** | ***0.038*** | 2.81 | 0.09 |
| :2/… | ***0.92*** | ***0.043*** | 3.48 | 0.07 |
| :3/… | 0.84 | 0.085 | 0.04 | 0.31 |
| E75833:1/… | 0.17 | 0.593 | 0.05 | 4.02 |
| :2/… | **0.90** | 0.054 | 1.05 | 1.14 |
| :3/… | **0.94** | ***0.029*** | 0.62 | 0.88 |
| E94553:1/… | 0.87 | 0.069 | 2.31 | 0.21 |
| :2/… | 0.79 | 0.112 | 0.58 | 0.07 |
| :3/… | ***0.92*** | ***0.042*** | 0.57 | 0.53 |
| E110379:1/… | 0.35 | 0.405 | 0.24 | 18.46 |
| :2/… | 0.89 | 0.057 | 0.86 | 7.43 |
| :3/… | ***0.93*** | ***0.034*** | 2.08 | 2.92 |
| E71001:1/… | ***0.92*** | ***0.039*** | 1.09 | 0.07 |
| :2/… | 0.73 | 0.146 | 0.05 | 1.18 |
| :3/… | 0.79 | 0.109 | 0.63 | 1.07 |
| :4/… | 0.67 | 0.182 | 0.00 | 0.04 |
|  |  |  |  |  |
| E109425:1/… | ***0.95*** | ***0.028*** | 2.35 | 1.15 |
| :2/… | ***0.92*** | ***0.038*** | 4.37 | 0.11 |
| :3/… | 0.45 | 0.331 | 0.34 | 0.48 |
| :4/… | 0.02 | 0.862 | 0.00 | 0.00 |
| E131866:1/… | ***0.90*** | 0.052 | 3.91 | 0.01 |
| :2/… | 0.89 | 0.055 | 0.04 | 0.06 |
| :3/… | ***0.93*** | ***0.037*** | 1.92 | 0.24 |
| :4/… | 0.72 | 0.150 | 0.15 | 0.03 |

**Table S4.** Results of analysis of molecular variance (Amova) for all three data sets. Data include % of variation (%), degrees of freedom (df), and sum of squares (SS).

AMOVA using Outlier Loci (O-SNPs):

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **Nested in** | **%** | **df** | **SS** | ***FST*** | ***P*-value** |
| Among Individuals | Population | 72.93 | 236 | 1245.48 | -- | -- |
| Among Population | -- | 27.07 | 3 | 365.10 | 0.271 | <0.00001 |

AMOVA using Neutral Loci (N-SNPs):

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **Nested in** | **%** | **df** | **SS** | ***FST*** | ***P*-value** |
| Among Individuals | Population | 99.21 | 236 | 163871.48 | -- | -- |
| Among Population | -- | 0.79 | 3 | 3068.96 | 0.008 | <0.00001 |

AMOVA using mtDNA haplotypes:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Source of Variation** | **Nested in** | **%** | **df** | **SS** | ***ΦST*** | ***P*-value** |
| Among Individuals | Population | 92.23 | 95 | 74.52 |  | -- |
| Among Populations | -- | 7.77 | 3 | 7.26 | 0.078 | <0.00001 |

**Table S5.** Results of Blast search for sequence similarity of SNP containing loci: E-value, expected number of hits at random; PI. Percent identity.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Locus** | **Description** | **E-value** | **PI** | **Accession #** | **Hit start** | **Hit end** |
| ***Di-Allelic*** |  |  |  |  |  |  |
| E28275\_L100 | zebrafish DNA clone CH211-168G2 in linkage group 9 | 1.06E-03 | 83.7 | BX005152 | 12226 | 12274 |
|  | zebrafish DNA clone DKEY-159B16 in linkage group 9 | 1.06E-03 | 83.7 | CR407600 | 70212 | 70164 |
|  | *Mustelus manazo* DNA, HE1 SINE clone: Mm 3 | 3.72E-03 | 70.8 | AB027718 | 181 | 86 |
| E29236\_L100 | *Triakis scyllium* TNFRSF6B gene for tumor necrosis factor | 9.96E-17 | 83.5 | AB282596 | 1771 | 1681 |
|  | *Carcharhinus leucas* microsatellite C105 | 3.48E-16 | 83.0 | KJ916108 | 55 | 147 |
|  | *Triakis scyllium* MIP3 gene for macrophage inflammatory protein-3α | 1.21E-15 | 82.4 | AB174766 | 2935 | 3025 |
| E43805\_L100 | *Ginglymostoma cirratum* clone GC\_BA-557 | 1.69E-07 | 84.7 | AC164927 | 65082 | 65024 |
|  | *Ginglymostoma cirratum* clone GC\_BA-557B6 | 1.69E-07 | 84.7 | AC164927 | 83026 | 82978 |
|  | *Carcharhinus plumbeus* RAG1 (partial) and RAG2 (complete) | 1.69E-07 | 84.7 | AY172838 | 8908 | 8966 |
| E53310\_L100 | *Carcharhinus isodon* clone *Cis*172 microsatellite | 1.06E-03 | 89.7 | JQ365996 | 56 | 94 |
|  | Predicted: *Equus caballus* Zinc finger protein 226 (ZNF226) | 1.3E-02 | 87.5 | XM\_005596327 | 2151 | 2112 |
|  | Predicted: *Equus caballus* Zinc finger protein 226 (ZNF226) | 1.3E-02 | 87.5 | XM\_005596328 | 1916 | 1877 |
| E61036\_L100 | None |  |  |  |  |  |
| E64126\_L100 | None |  |  |  |  |  |
| E65274\_L142 | *Mustelus manazo* DNA, HE1 SINE, clone:Mm 2 | 6.29E-13 | 85.9 | AB027717 | 38 | 108 |
|  | *Triakis scyllium* IL-1 gene for interleukin-1β | 7.66E-12 | 86.6 | AB074142 | 3145 | 3211 |
|  | *Triakis scyllium* MIP3 gene for macrophage inflammatory protein-3α | 2.67E-11 | 84.5 | AB174766 | 3231 | 3161 |
| E66074\_L100 | None |  |  |  |  |  |
| E68107\_L100 | Predicted*: Latimeria chalumnae* Zinc finger protein 850-like (LOC1 02360397) | 2.67E-11 | 80.7 | XM\_005995770 | 1396 | 1314 |
|  | Predicted: *Colius striatus* Zinc finger protein 501-like (LOC10455 9532) | 1.14E-09 | 80.0 | XM\_010204559 | 482 | 403 |
|  | Predicted: *Xenopu*s (*silurana) tropicalis* Zinc finger protein 84-like (LOC101730679) | 3.97E-09 | 76.6 | XM\_004919267 | 571 | 478 |
| E87901\_L109 | *Carcharhinus sorrah* microsatellite *Cs*08 | 5.88E-26 | 87.4 | AY545211 | 752 | 643 |
|  | *Carcharhinus plumbeus* T cell receptor gamma (TCRG) | 2.05E-25 | 86.4 | FJ854492 | 17993 | 18102 |
| E92875\_L100 | *Stegastes partitus* Zinc finger and scan domain-protein 2-like (LOC103371773) | 3.72E-03 | 86.0 | XM\_008301224 | 1162 | 1120 |
|  | *Stegastes partitus* Zinc finger and scan domain-protein 2-like (LOC103371773) | 3.72E-03 | 86.0 | XM\_008301232 | 782 | 740 |
| E94551\_L100 | *Mustelus manazo* DNA, HE1 SINE clone:Mm2 | 7.66E-12 | 92.6 | AB027717 | 65 | 12 |
|  | *Triakis scyllium* MIP3 gene for macrophage inflammatory protein-3α | 7.66E-12 | 92.6 | AB174766 | 3204 | 3257 |
|  | *Mustelus manazo* DNA, HE1 SINE clone:Mm 3 | 3.26E-10 | 90.7 | AB027718 | 65 | 12 |
| E95266\_L148 | *Callorhinchus milii* clone P02H01.kidney.K065 | 1.3E-02 | 91.4 | JX052830 | 4 | 38 |
|  | *Callorhinchus milii* clone, NADH dehydrogenase (Ubiquinone) 1 beta subcomplex | 1.3E-02 | 91.4 | JX209076 | 25 | 59 |
|  | *Callorhinchus milii* NADH Dehydrogenase (Ubiquinone) 1 beta subcomplex | 1.3E-02 | 91.4 | NM\_001292677 | 1 | 35 |
| E102269\_L100 | None |  |  |  |  |  |
| E106435\_L100 | *Mustelus manazo* DNA, HE1 SINE, clone:Mm 2 | 3.71E-22 | 86.9 | AB027717 | 239 | 144 |
|  | *Mustelus manazo* DNA, HE1 SINE, clone:Mm 4 | 3.71E-22 | 88.9 | AB027719 | 231 | 143 |
|  | *Triakis scyllium* MIP3 gene for macrophage inflammatory protein-3α | 3.71E-22 | 87.9 | AB174766 | 3030 | 3125 |
| E107376\_L100 | *Carcharhinus plumbeus* T cell receptor gamma (TCRG) | 1.06E-03 | 72.3 | FJ854492 | 25169 | 25069 |
| E113131\_L101 | *Ginglymostoma cirratum* Zinc finger protein 112, β2m , βrd2 genes | 3.72E-03 | 84.8 | AB571627 | 68553 | 68598 |
| E117105\_L100 | None |  |  |  |  |  |
| E195370\_L100 | *Brugia pahangi* genome assembly B | 3.72E-03 | 93.9 | LK964241 | 31402 | 31434 |
|  |  |  |  |  |  |  |
| ***Multi-allelic*** |  |  |  |  |  |  |
| E52101\_L100 | *Scyliorhinus canicula* Cluster\_HOXD sequence | 5.00E-15 | 83.0 | FQ032660 | 58525 | 58612 |
|  | *Mustelus manazo* DNA, HE1 SINE, clone:Mm 2 | 2.00E-12 | 81.0 | AB027717 | 52 | 136 |
|  | *Carcharhinus plumbeus* RAG1 (partial) and RAG2 (complete) | 1.0E-10 | 80.0 | AY172838 | 3341 | 3425 |
| E69589\_L100 | *Carcharhinus plumbeus* T cell receptor gamma (TCRG) | 4.0E-09 | 83.0 | FJ854492 | 18165 | 18105 |
|  | *Carcharhinus* *sorrah* microsatellite CS08 sequence | 6.00E-07 | 90.0 | AY545211 | 601 | 648 |
|  | *Carcharhinus plumbeus* Ig lambda light chain gene, COMPLETE CDS | 6.00E-07 | 90.0 | U34992 | 6243 | 6290 |
| E75833\_L160 | *Sphyrna lewin* GRLN Gene for preproghrelin, COMPLETE CDS | 3.26E-10 | 79.5 | AB254130 | 3838 | 3925 |
|  | *Mustelus manazo* DNA, HE1 SINE, clone:Mm 2 | 3.97E-09 | 78.7 | AB027717 | 57 | 145 |
|  | *Triakis scyllium* MIP3 gene for macrophage inflammatory protein-3α | 4.83E-08 | 77.5 | AB174766 | 3212 | 3124 |
| E82240\_L100 | *Homo sapiens* BAC clone RP11-334C6 from chromosome 7 | 1.3E-02 | 84.4 | AC073418 | 55859 | 55815 |
|  | *Pan troglodytes* BAC clone CH251-734F1 from chromosome 7 | 1.3E-02 | 84.4 | AC190230 | 179380 | 179336 |
|  | *Pan troglodytes* BAC clone CH251-541E24 from chromosome 7 | 1.3E-02 | 84.4 | AC192728 | 31156 | 31112 |
| E94553\_L100 | *Botryotinia fuckeliana* T4 supercontig\_34\_1 genomic supercontig | 1.3E-02 | 84.0 | FQ790278 | 92859 | 92814 |
|  | *Botryotinia fuckeliana* B05.10 hypothetical protein (BC1G\_13291) | 1.3E-02 | 84.0 | XM\_001548305 | 1089 | 1044 |
|  | *Torpedo marmorata* mRNA fragment for acetylcholinesterase c-term | 4.53E-02 | 96.6 | X13173 | 1745 | 1773 |
| E71001\_L100 | None |  |  |  |  |  |
| E73988\_L143 | *Scyliorhinus canicula* cluster\_HOXBS | 2.00E-14 | 79.0 | FQ032659 | 65153 | 65252 |
|  | *Triakis scyllium* IL-1 gene for interleukin-1β | 2.00E-13 | 79.0 | AB074142 | 899 | 1002 |
|  | *Scyliorhinus canicula* cluster\_HOXD sequence | 1.00E-10 | 78.0 | FQ032660 | 15011 | 15107 |
| E109425\_L100 | None |  |  |  |  |  |
| E110379\_L124 | None |  |  |  |  |  |
| E131866\_L100 | *Triakis scyllium* IL-1 gene for interleukin-1β | 2.34E-18 | 81.7 | AB074142 | 1087 | 984 |
|  | *Triakis scyllium* MIP3 gene for macrophage inflammatory protein-3α | 9.96E-17 | 81.6 | AB174766 | 3443 | 3540 |
|  | *Ginglymostoma cirratum* clone GC\_Ba-678C3 | 4.24E-15 | 80.6 | AC165195 | 14263 | 14360 |
| E167414\_L100 | *Callorhinchus milii* gamma-aminobutyric acid type B receptor | 3.05E-04 | 83.0 | XM\_007884901 | 1038 | 1090 |