Leatherback SNP analysis

Raw data files were generated during 2 MiSeq runs, MS57 and MS61, they are SE 150bp reads. The panel includes 205 snp loci and 31 msat loci

Misc files Included

* Dc\_pac\_sample\_info.xlsx: the first sheet in this file has a list of LabID, Location, RunID, and PlateID for all the pacific leatherbacks that we have run GTseq on. The second tab has all of our database information for each of those labID, the 3rd tab is the genotype data from genescans that has been generated, and the last tab is a list of msat loci that have been used on leatherbacks in various projects, it is really just a note to myself about where I may be able to find genescan data for loci that we are now using with GTseq.
* Map2ref.sh: A bash script that I run on the raw data, which trims adapters/low quality from raw reads, maps the trimmed reads using BWA to DcGTseqPanel\_205\_112122.fasta, generates SAM and BAM files, then extracts the msat reads using the fwd primer to find the reads. I have included the raw files, the samfiles, the sorted bam and bam.bai, as well as the msat.fastq files. The script also counts raw reads, trimmed reads, mapped reads, msat reads, unmapped reads, and a coverage file for each sample which counts the read depth for each snp locus at bp76. I didn’t include all of those files, but I am happy to round them up if you would like. I primarily use them to assess the run and to remove “failed” samples from the freebayes run. If a sample has an average read depth of <10, I do not include it in my freebayes analysis.
* Dcor\_DcPanel\_205\_maf.targetsnps\_012224.recode.vcf: This is the vcf file generated by freebayes, you may notice there are some samples in there from Mexico, St. Criox(STX), and S.Africa. I included those in the freebayes analysis to look for variability across ocean basins.
* dc\_msat\_primerF.txt: this is the file that I use in the Map2ref.sh script to extract the msat reads from the trimmed fastq
* Dc\_primer-input\_120222.txt: this is for MEGASAT it is the input file.