**Mapping:** BSMAP version 2.73

./bsmap -a //input.fastq.gz -d /genome.v9.fa -o output.sam -p 16

Output: [http://eagle.fish.washington.edu/cnidarian/BiGill\_BSMAP\_GiIlMBD\_genome\_v9\_v1.sam](http://eagle.fish.washington.edu/cnidarian/BiGill_BSMAP_GiIlMBD_genome_v9_v1.sam" \t "_blank) (supplementary file S1)

**Extracting methylation ratios:** methratio.py version x.x

python [methratio.py](http://methratio.py/" \t "_blank) -d /genome.v9.fa -u -z -g -o  /output.txt -s /output.sam

Output:   
http://eagle.fish.washington.edu/cnidarian/BiGill\_methratio\_v9\_A.txt

(supplementary file S2)

**Filtering and formatting methylation data as GFF:** SQLShare

Methratio output to GFF (filtering for: *only CG context with 5x coverage*)

SELECT    
  chr as seqname,    
'methratio' as source,    
'CpG' as feature,   
pos as start,  
pos + 1 as [end],  
cast(ratio as float) as score,    
strand,    
'.' as frame,    
'.' as attribute  
    
  FROM [sr320@washington.edu].       
[BiGill\_methratio\_v9\_A.txt]   
where context like '\_\_CG\_'and CT\_Count >= 5 and ratio <> 'NA'

Output

[https://sqlshare.escience.washington.edu/sqlshare - s=query/mgavery%40washington.edu/BiGill\_methratio\_v9\_filtered\_asgff](https://sqlshare.escience.washington.edu/sqlshare#s=query/mgavery%40washington.edu/BiGill_methratio_v9_filtered_asgff)

(supplementary file S3)

**Filtering for only methylated CpG:** SQLShare

filtering for: *only loci with meth ratio ≥0.5*

SELECT \* FROM [mgavery@washington.edu].[CGbigill5x\_gt25\_gff]  
  WHERE score >= 0.500  
  ORDER BY score

Output

[https://sqlshare.escience.washington.edu/sqlshare - s=query/mgavery%40washington.edu/BiGill\_methratio\_v9\_filtered\_MethylatedOnly\_asgff](https://sqlshare.escience.washington.edu/sqlshare#s=query/mgavery%40washington.edu/BiGill_methratio_v9_filtered_MethylatedOnly_asgff)

(supplementary file S4)