

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:17:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080814.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR3080814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:17:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,987,234
Mapped reads	2,454,272 / 82.16%
Unmapped reads	532,962 / 17.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,288 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	183,069 / 6.13%
Duplication rate	6.22%
Clipped reads	971,656 / 32.53%

2.2. ACGT Content

Number/percentage of A's	49,338,110 / 29.47%
Number/percentage of C's	31,172,759 / 18.62%
Number/percentage of T's	51,713,652 / 30.89%
Number/percentage of G's	35,159,210 / 21%
Number/percentage of N's	22,852 / 0.01%
GC Percentage	39.62%

2.3. Coverage

Mean	0.0541

Standard Deviation	0.4343
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.97
----------------------	-------

2.5. Mismatches and indels

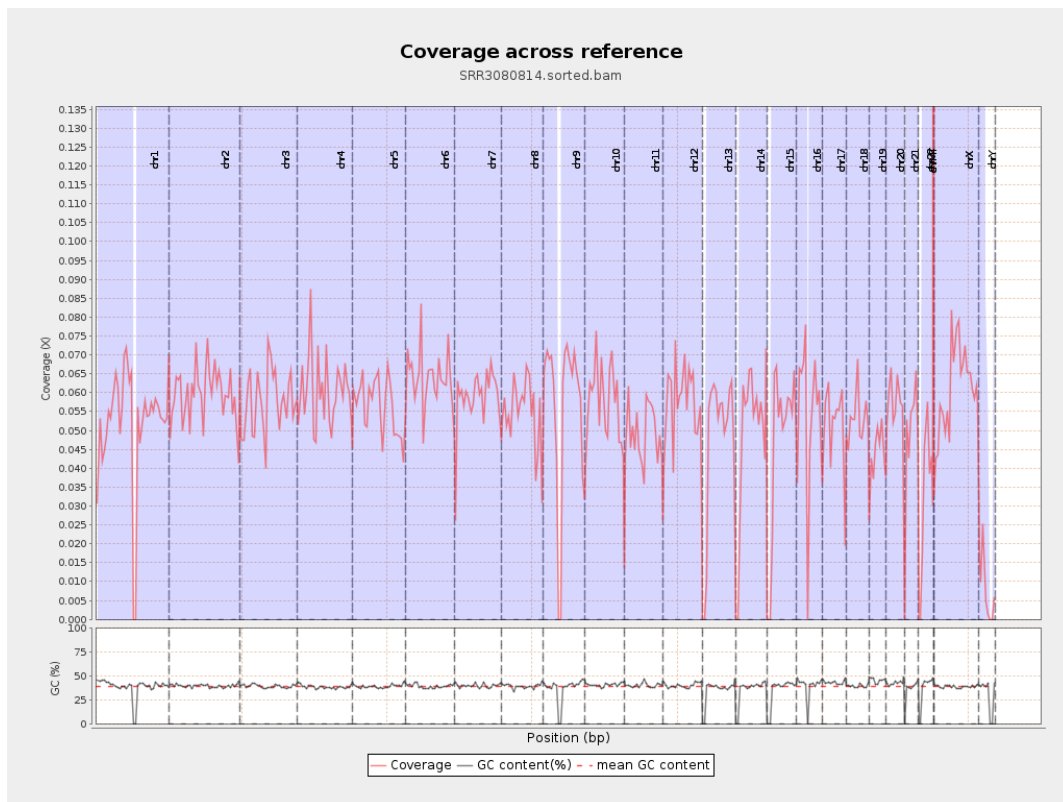
General error rate	0.83%
Mismatches	1,357,776
Insertions	13,427
Mapped reads with at least one insertion	0.54%
Deletions	34,821
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.31%

2.6. Chromosome stats

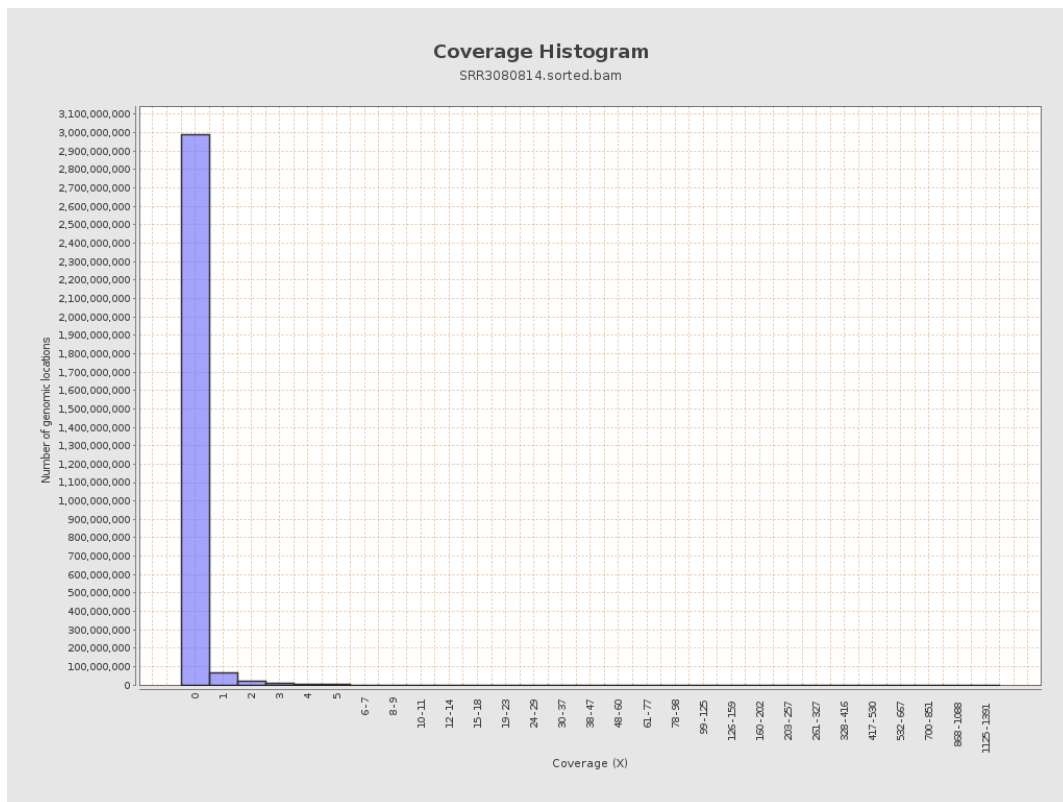
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12865403	0.0516	0.4772
chr2	243199373	14512515	0.0597	0.4708
chr3	198022430	11416559	0.0577	0.3518
chr4	191154276	11549079	0.0604	0.3871
chr5	180915260	10237686	0.0566	0.3479
chr6	171115067	10893040	0.0637	0.4185
chr7	159138663	9457161	0.0594	0.4112

chr8	146364022	7988202	0.0546	0.9163
chr9	141213431	7992018	0.0566	0.4102
chr10	135534747	7824449	0.0577	0.4325
chr11	135006516	6563696	0.0486	0.3571
chr12	133851895	7686866	0.0574	0.3539
chr13	115169878	5388415	0.0468	0.3178
chr14	107349540	5122814	0.0477	0.332
chr15	102531392	4836582	0.0472	0.3161
chr16	90354753	4921250	0.0545	0.3562
chr17	81195210	4075851	0.0502	0.3363
chr18	78077248	4136301	0.053	0.6092
chr19	59128983	2607787	0.0441	0.4432
chr20	63025520	3578989	0.0568	0.3522
chr21	48129895	2332303	0.0485	0.3429
chr22	51304566	1628567	0.0317	0.2548
chrMT	16571	12511	0.755	1.4175
chrX	155270560	9395080	0.0605	0.37
chrY	59373566	444991	0.0075	0.1921

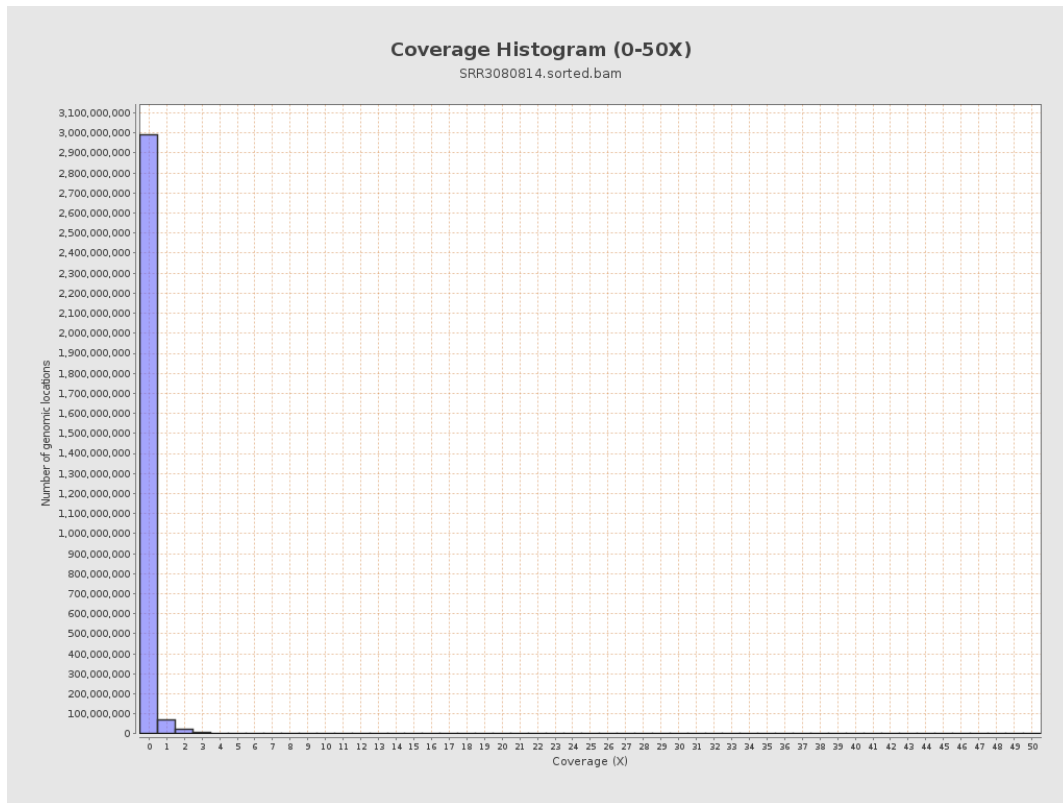
3. Results : Coverage across reference



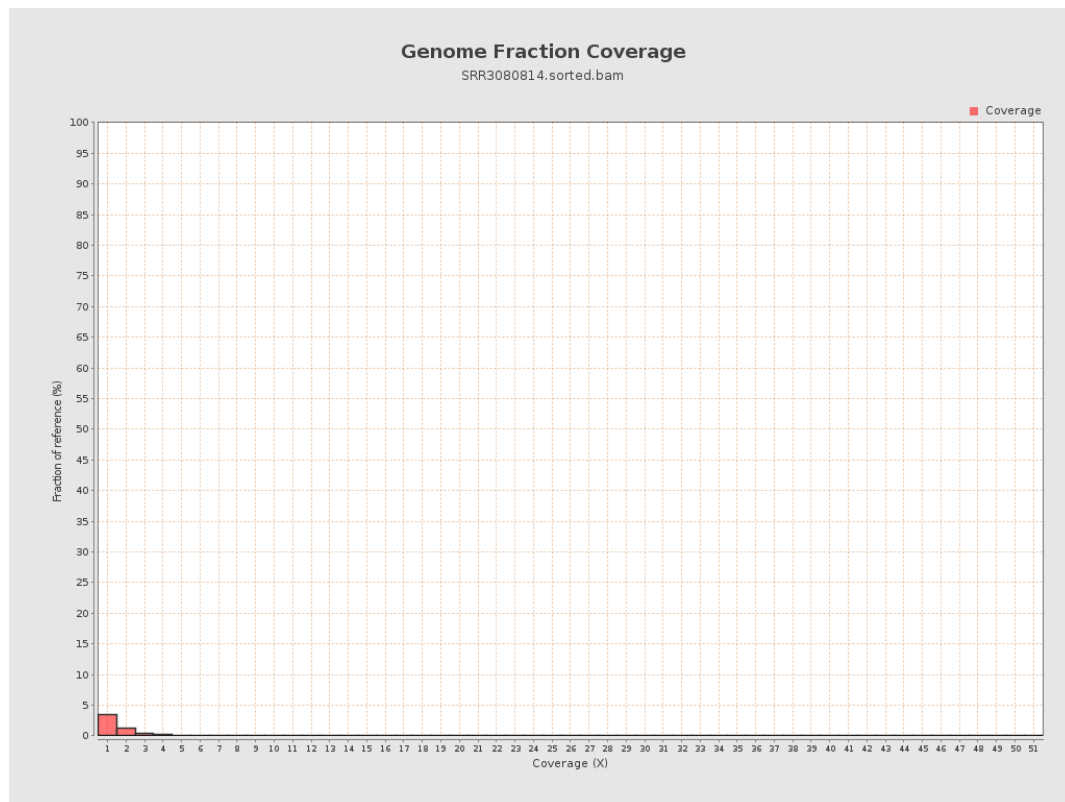
4. Results : Coverage Histogram



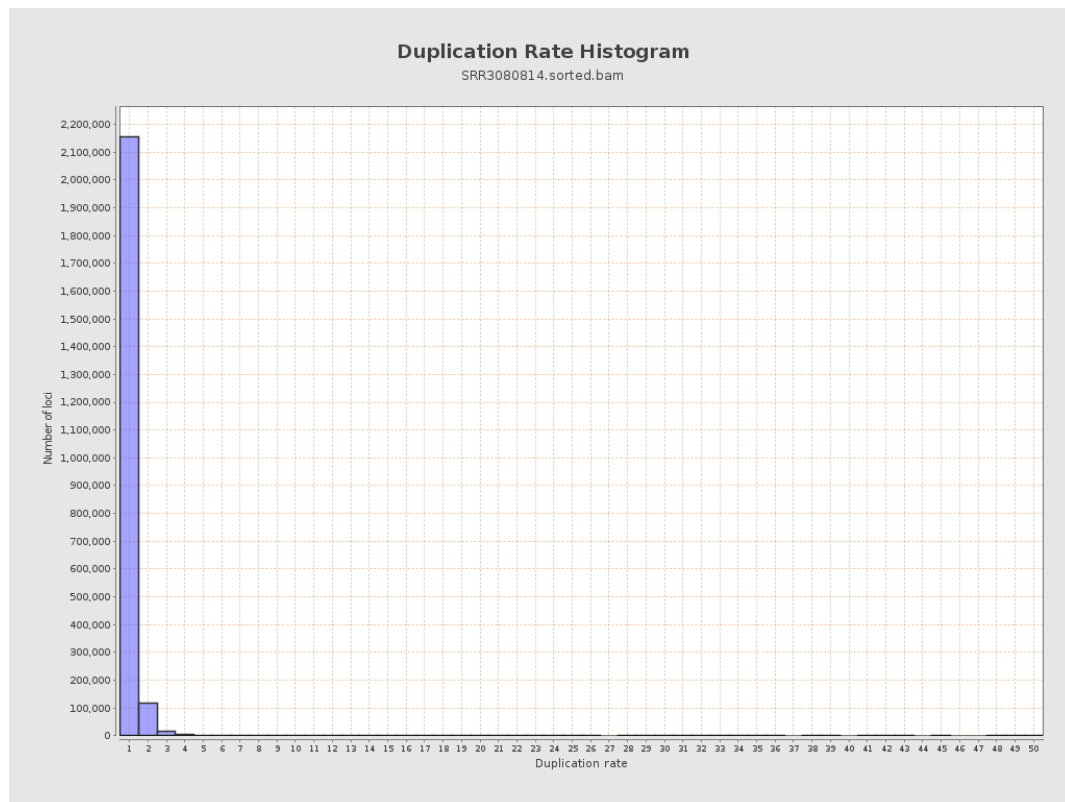
5. Results : Coverage Histogram (0-50X)



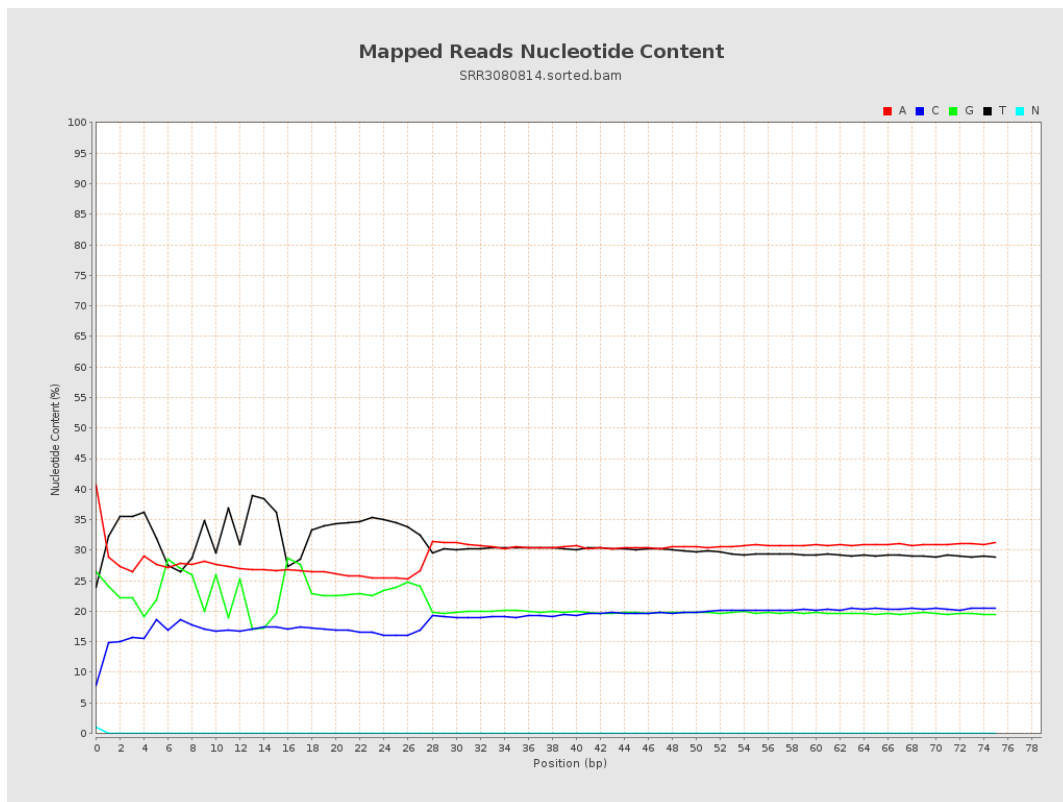
6. Results : Genome Fraction Coverage



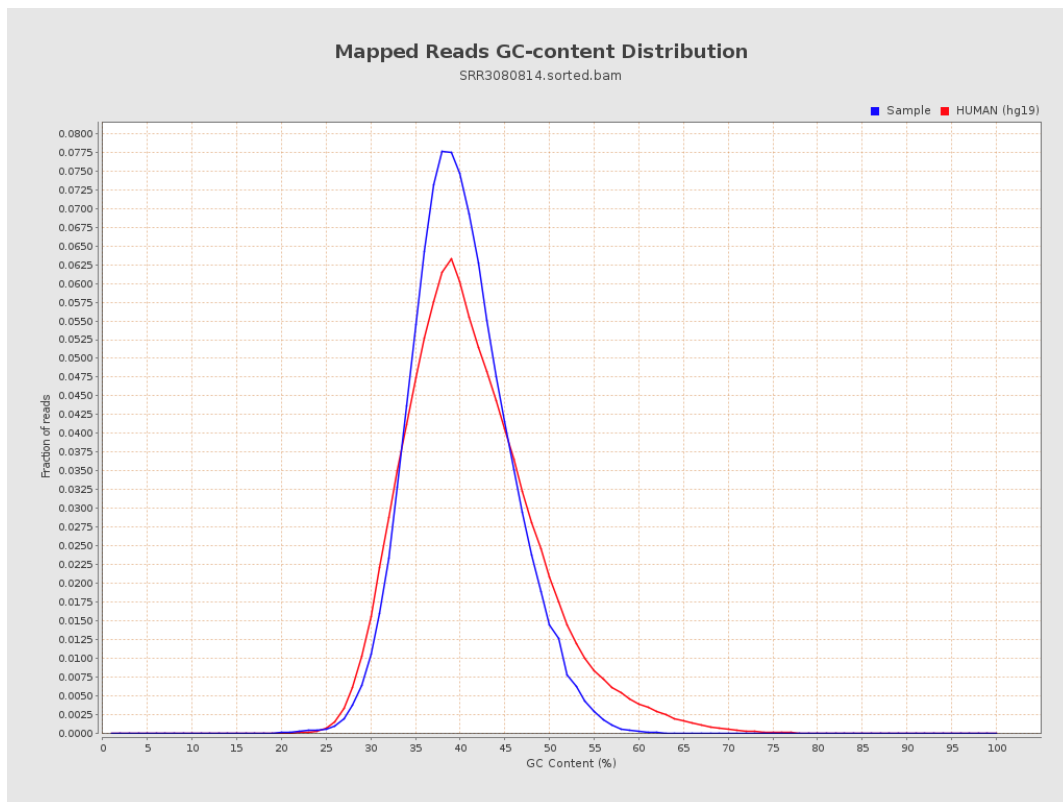
7. Results : Duplication Rate Histogram



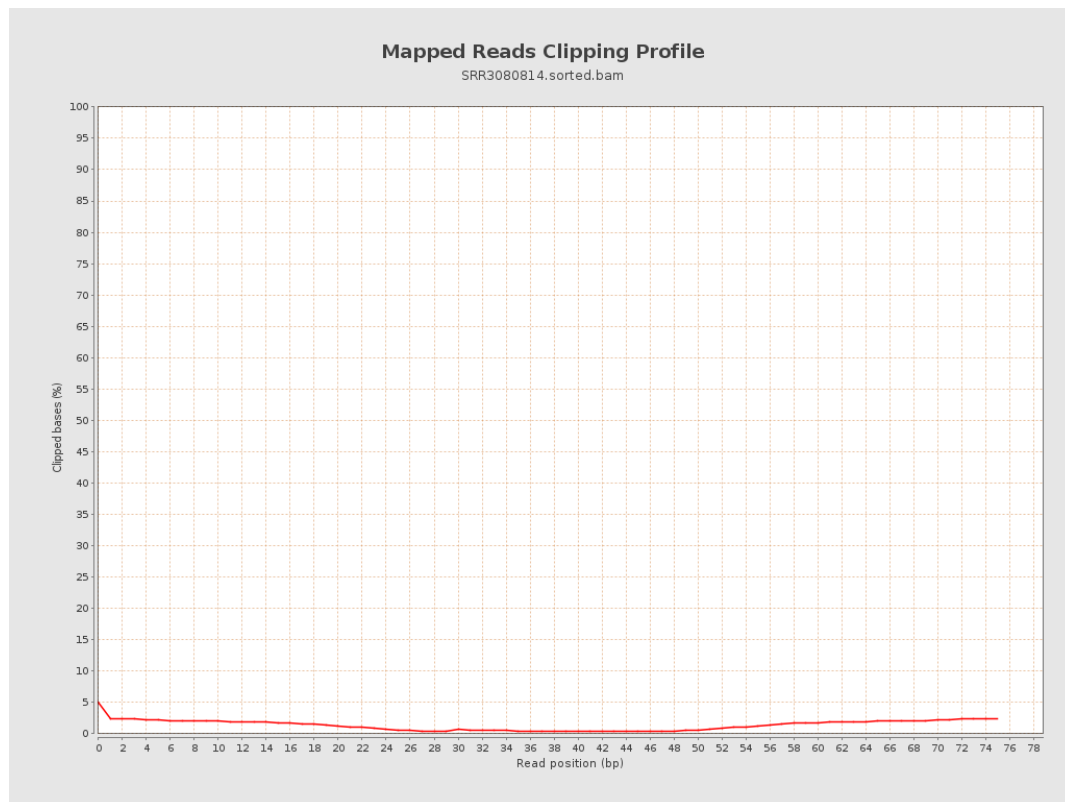
8. Results : Mapped Reads Nucleotide Content



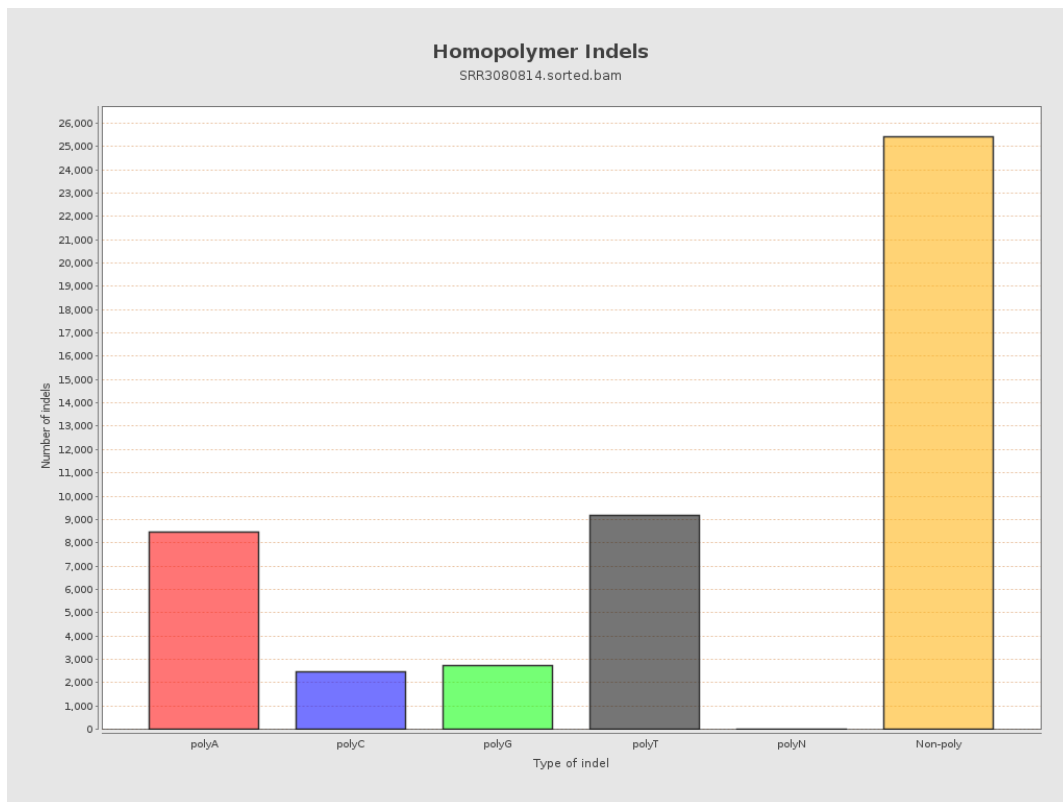
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

