

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:02:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063606.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_SRR6063606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:02:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,343,246
Mapped reads	2,977,070 / 89.05%
Unmapped reads	366,176 / 10.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,257 / 0.88%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	1,074,924 / 32.15%
Duplication rate	19.16%
Clipped reads	1,779,568 / 53.23%

2.2. ACGT Content

Number/percentage of A's	46,695,607 / 24.91%
Number/percentage of C's	34,075,202 / 18.18%
Number/percentage of T's	61,246,882 / 32.67%
Number/percentage of G's	45,419,291 / 24.23%
Number/percentage of N's	20,146 / 0.01%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0606

Standard Deviation	0.8718
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2.4. Mapping Quality

Mean Mapping Quality	43.48
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2.5. Mismatches and indels

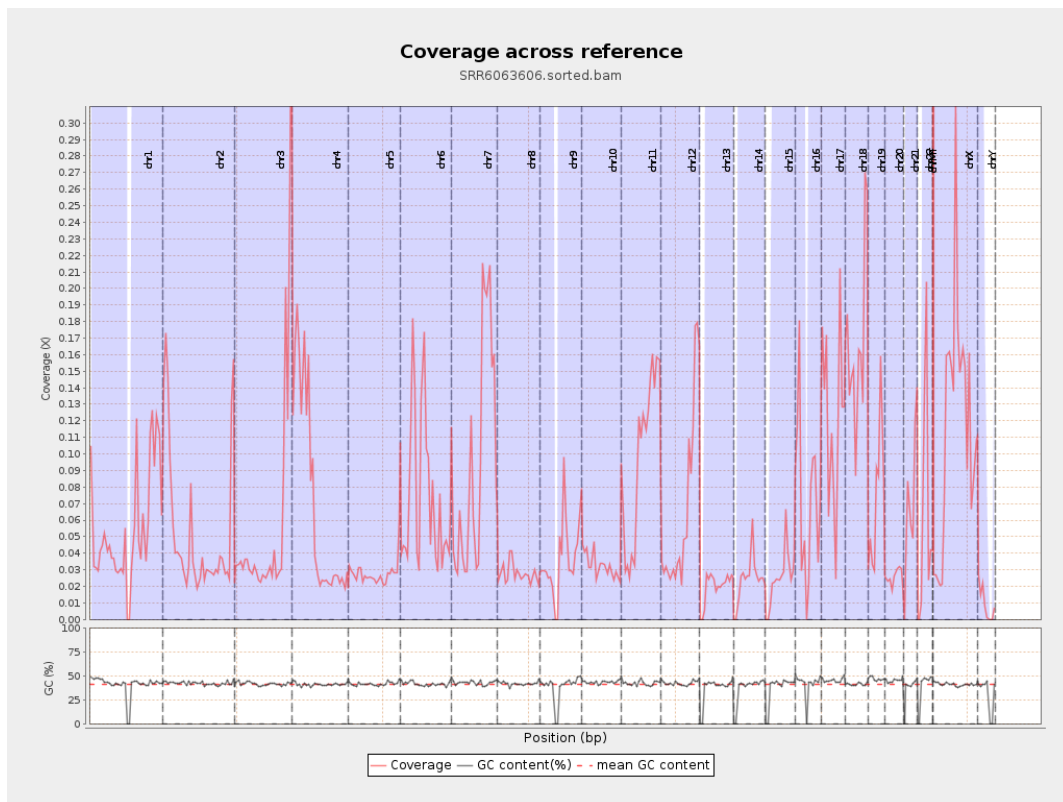
General error rate	0.6%
Mismatches	1,108,987
Insertions	11,050
Mapped reads with at least one insertion	0.37%
Deletions	44,774
Mapped reads with at least one deletion	1.49%
Homopolymer indels	43.37%

2.6. Chromosome stats

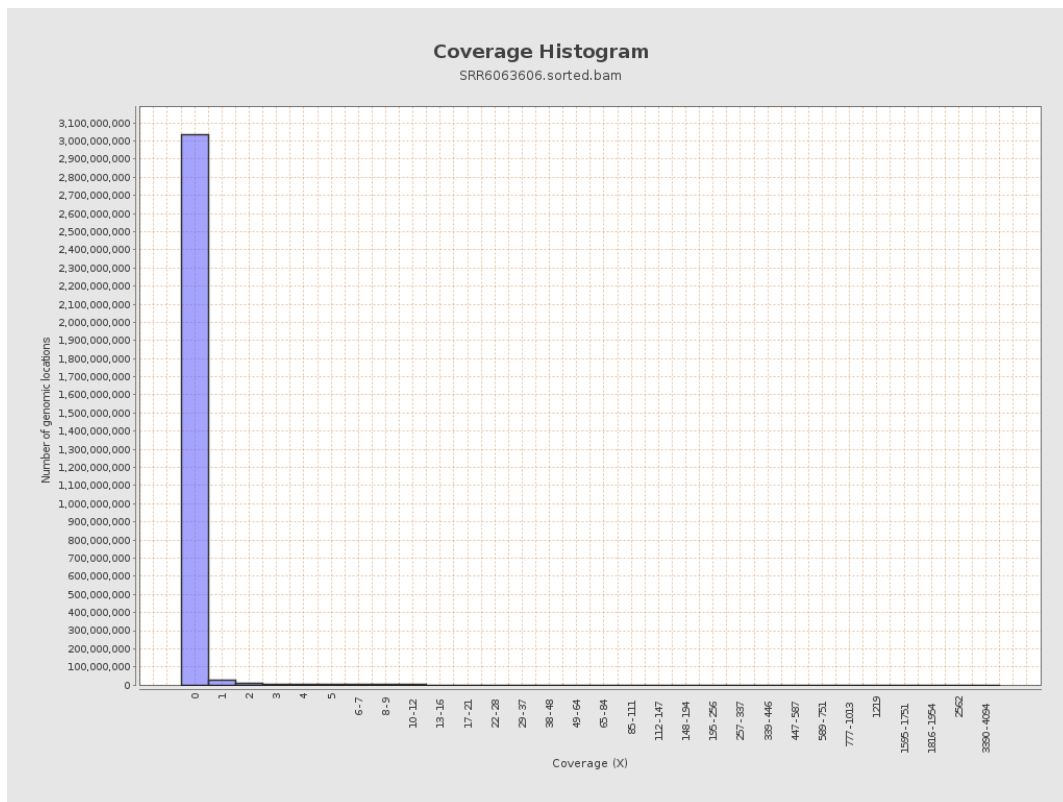
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13678365	0.0549	0.7304
chr2	243199373	12641190	0.052	1.9791
chr3	198022430	11292955	0.057	0.5968
chr4	191154276	13537966	0.0708	0.665
chr5	180915260	5216472	0.0288	0.409
chr6	171115067	12596048	0.0736	0.8612
chr7	159138663	15181376	0.0954	0.837

chr8	146364022	4033686	0.0276	0.7306
chr9	141213431	5133102	0.0363	0.6128
chr10	135534747	4398202	0.0325	0.4556
chr11	135006516	13157841	0.0975	0.8322
chr12	133851895	8684059	0.0649	0.6512
chr13	115169878	2261500	0.0196	0.4323
chr14	107349540	2630666	0.0245	0.3913
chr15	102531392	2563413	0.025	0.4531
chr16	90354753	6552215	0.0725	0.6769
chr17	81195210	9872159	0.1216	0.9139
chr18	78077248	12922808	0.1655	1.3203
chr19	59128983	4262101	0.0721	0.8096
chr20	63025520	1641879	0.0261	0.4016
chr21	48129895	3334587	0.0693	0.6655
chr22	51304566	3301441	0.0643	0.6436
chrMT	16571	303068	18.2891	14.1291
chrX	155270560	17794929	0.1146	0.8903
chrY	59373566	542379	0.0091	0.2161

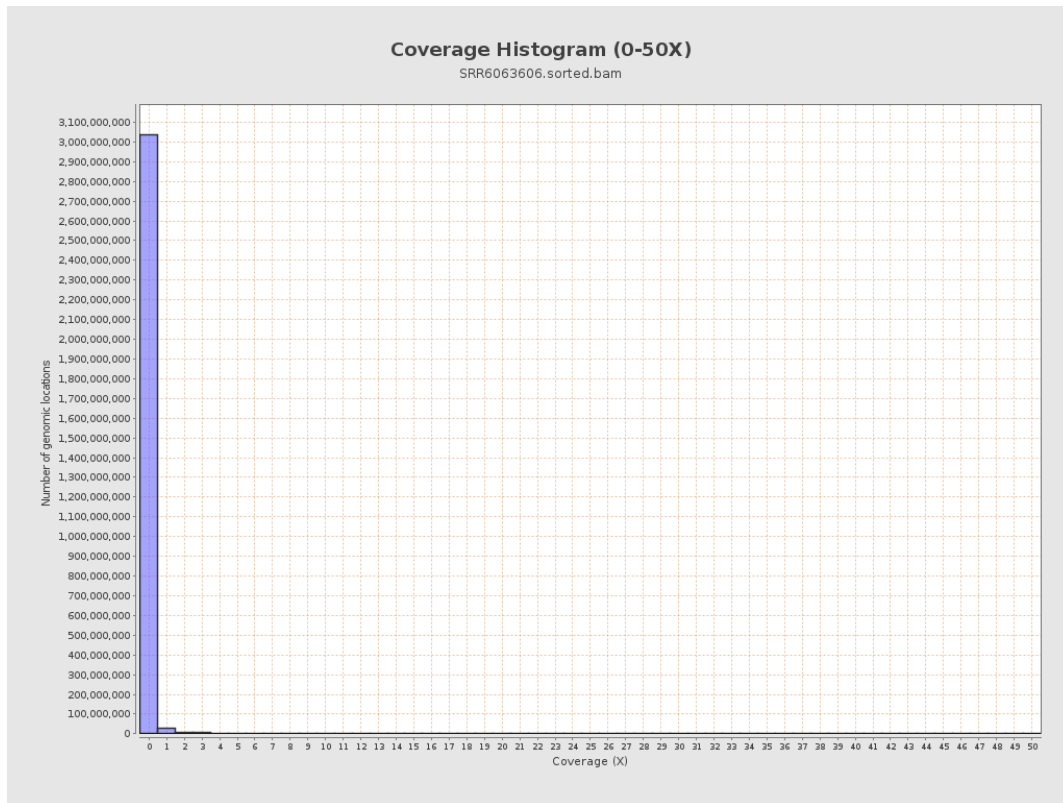
3. Results : Coverage across reference



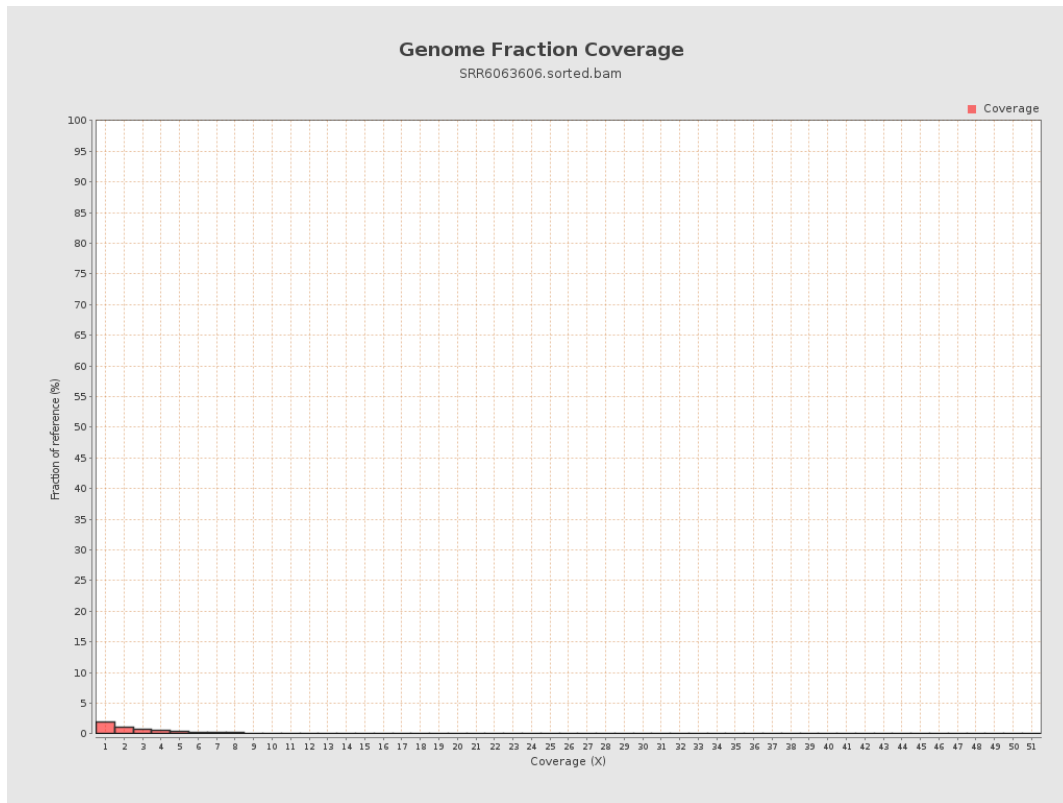
4. Results : Coverage Histogram



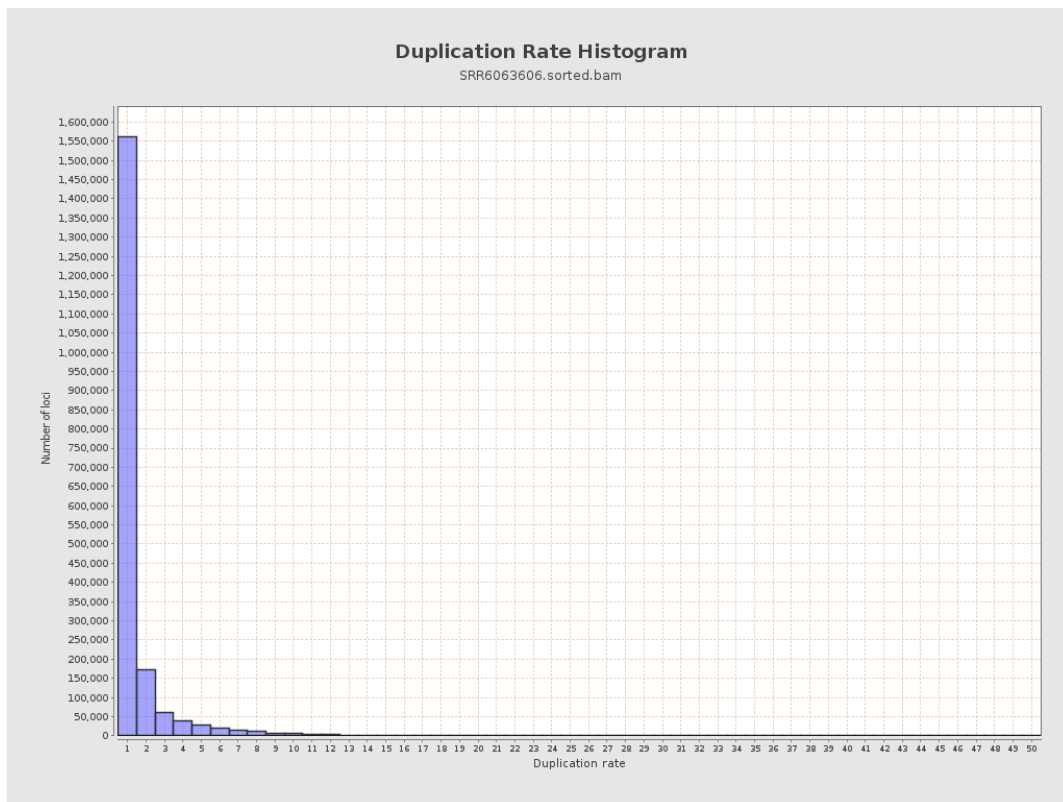
5. Results : Coverage Histogram (0-50X)



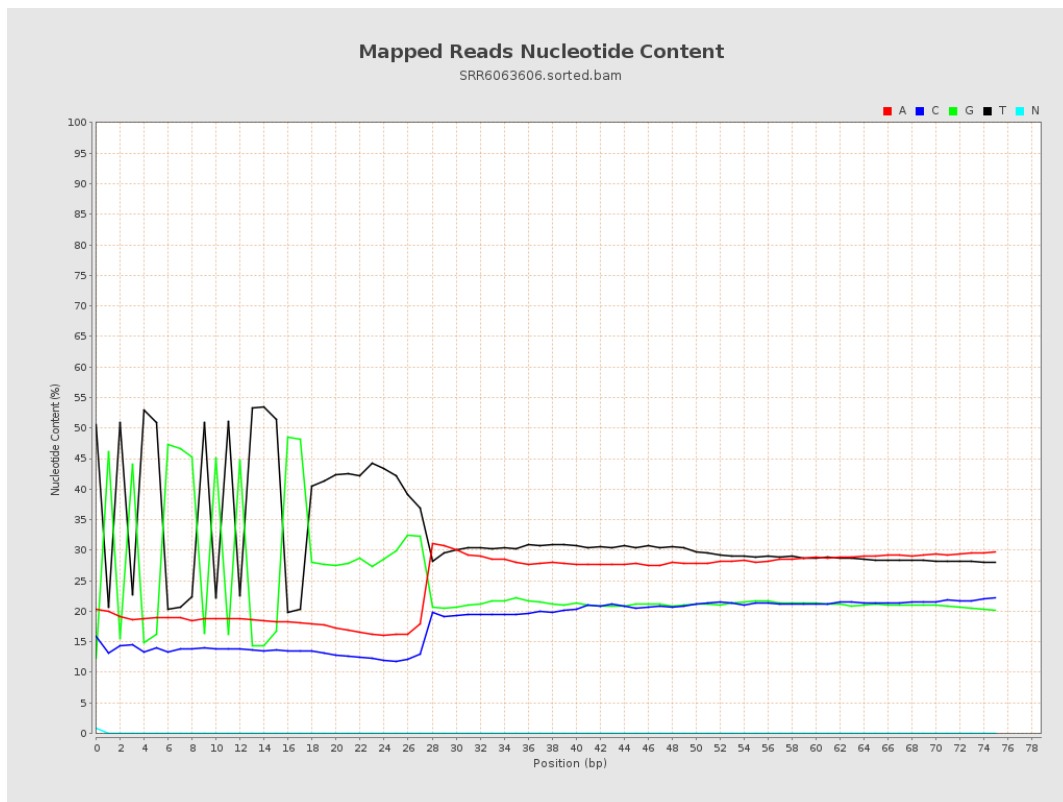
6. Results : Genome Fraction Coverage



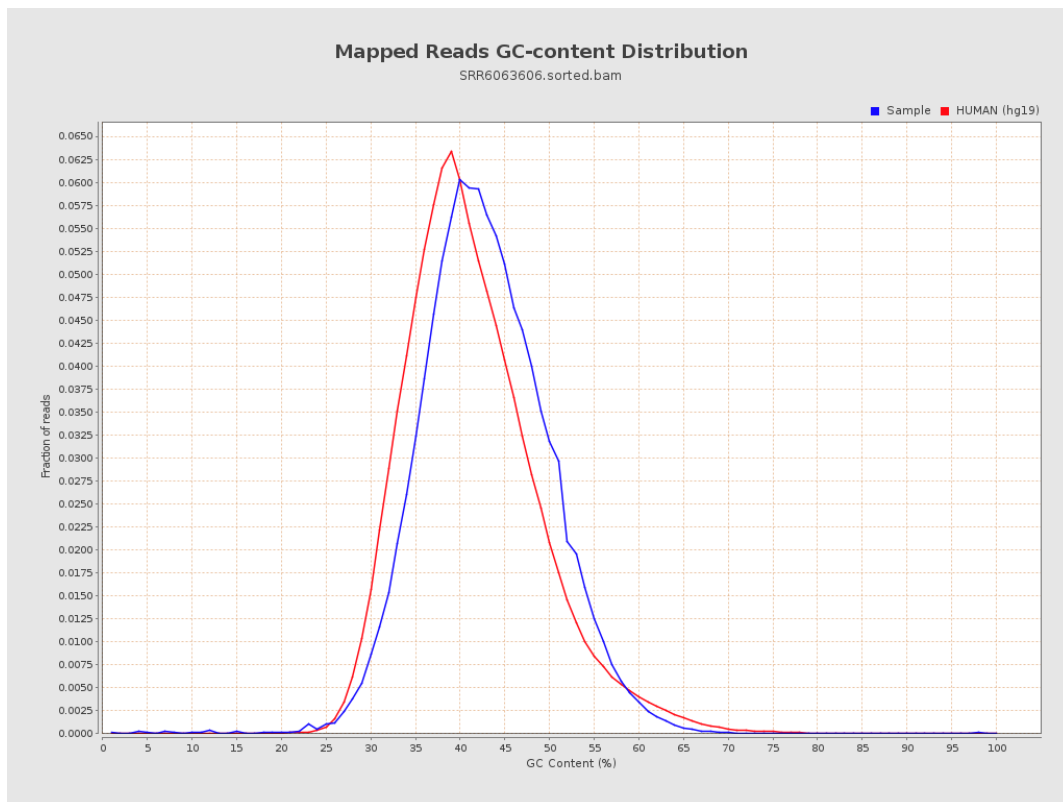
7. Results : Duplication Rate Histogram



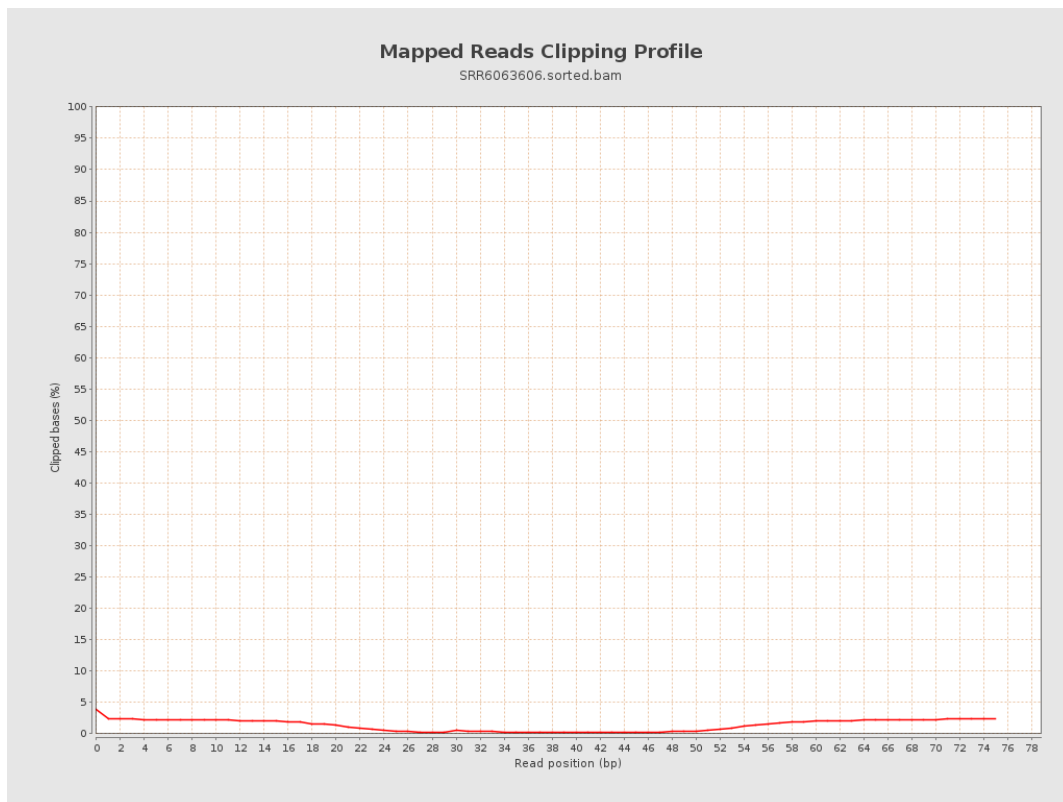
8. Results : Mapped Reads Nucleotide Content



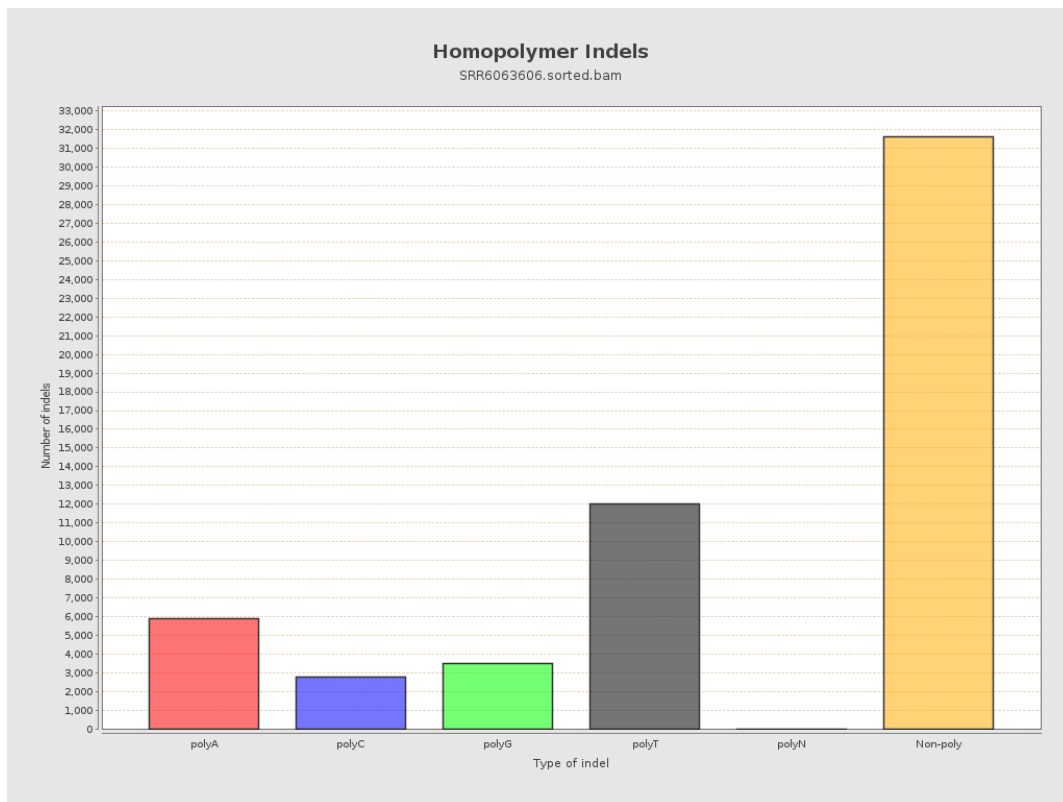
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

