

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:22:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063596.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_SRR6063596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063596.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:22:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,945,202
Mapped reads	1,614,992 / 83.02%
Unmapped reads	330,210 / 16.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,916 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	243,905 / 12.54%
Duplication rate	11.9%
Clipped reads	1,050,847 / 54.02%

2.2. ACGT Content

Number/percentage of A's	26,819,458 / 26.68%
Number/percentage of C's	17,897,172 / 17.8%
Number/percentage of T's	32,987,962 / 32.82%
Number/percentage of G's	22,816,455 / 22.7%
Number/percentage of N's	2,097 / 0%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0325

Standard Deviation	0.3883
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2.4. Mapping Quality

Mean Mapping Quality	44.96
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2.5. Mismatches and indels

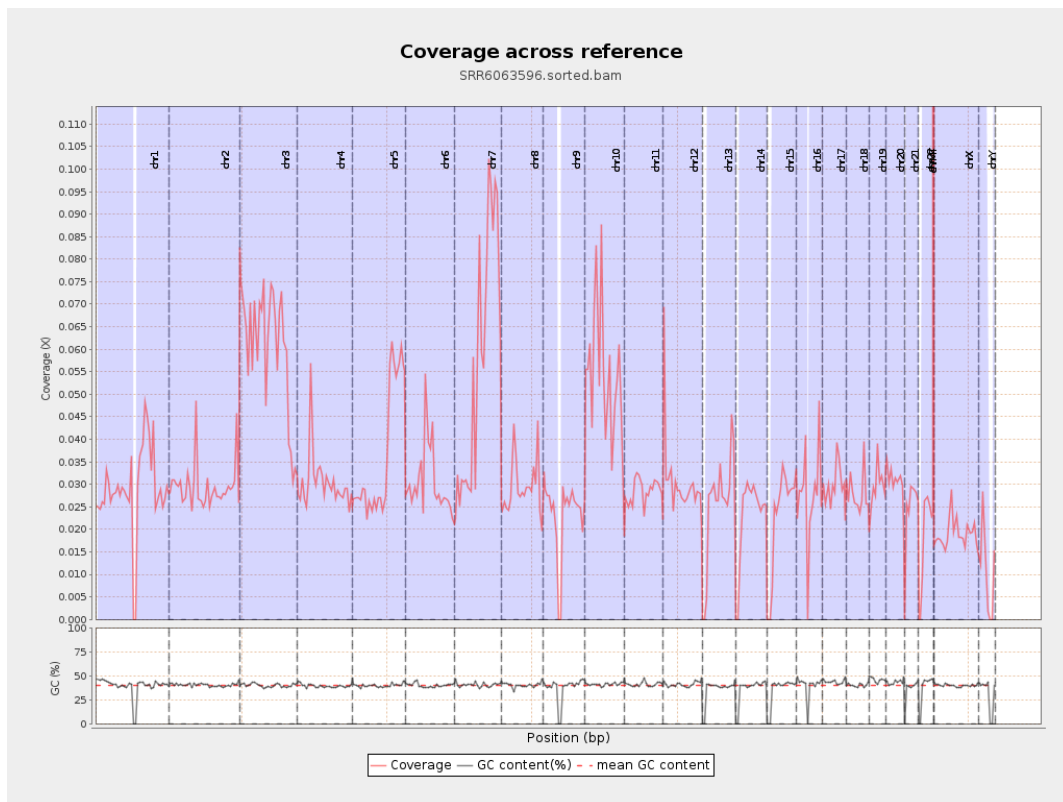
General error rate	0.94%
Mismatches	927,378
Insertions	8,078
Mapped reads with at least one insertion	0.5%
Deletions	26,823
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.59%

2.6. Chromosome stats

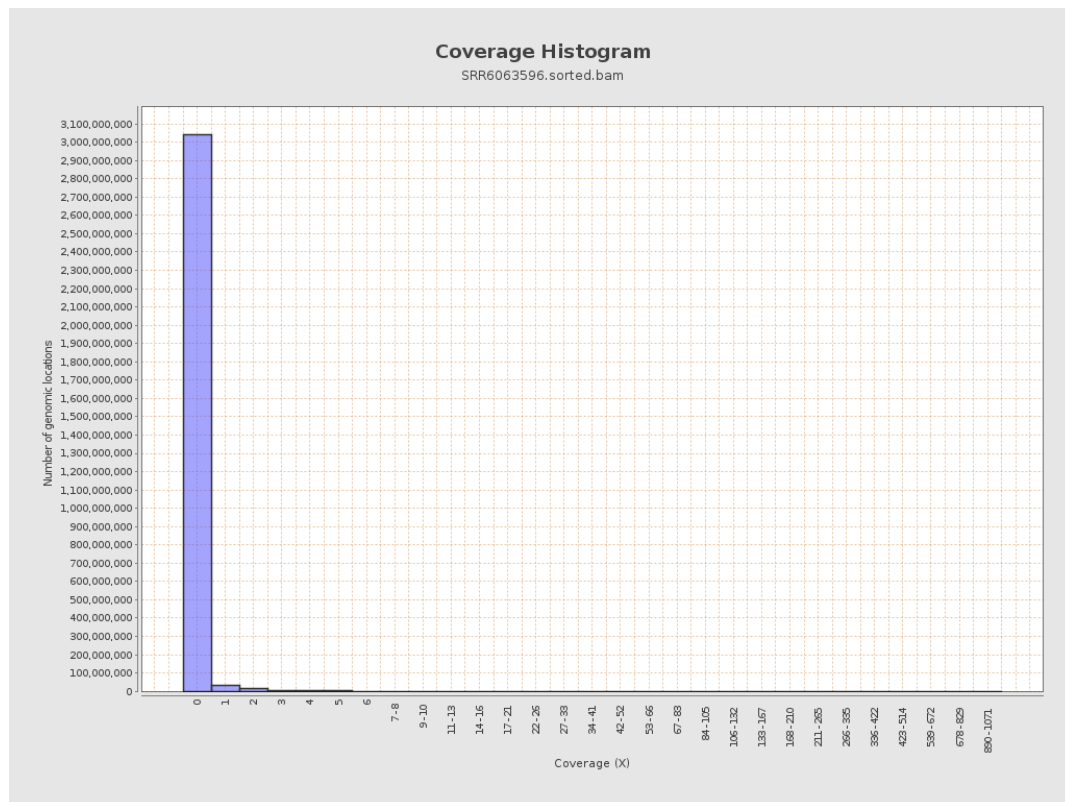
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7261456	0.0291	0.3895
chr2	243199373	7183033	0.0295	0.5033
chr3	198022430	12013433	0.0607	0.4038
chr4	191154276	5792706	0.0303	0.3065
chr5	180915260	6626171	0.0366	0.3108
chr6	171115067	5200214	0.0304	0.3042
chr7	159138663	9155605	0.0575	0.5643

chr8	146364022	4292606	0.0293	0.7103
chr9	141213431	3226849	0.0229	0.2935
chr10	135534747	7445042	0.0549	0.4768
chr11	135006516	3820568	0.0283	0.3975
chr12	133851895	4102249	0.0306	0.2863
chr13	115169878	2927640	0.0254	0.26
chr14	107349540	2462325	0.0229	0.2537
chr15	102531392	2351865	0.0229	0.2431
chr16	90354753	2494337	0.0276	0.2725
chr17	81195210	2423436	0.0298	0.2973
chr18	78077248	2202217	0.0282	0.4198
chr19	59128983	1763999	0.0298	0.3727
chr20	63025520	1949065	0.0309	0.292
chr21	48129895	1181104	0.0245	0.2609
chr22	51304566	911357	0.0178	0.2049
chrMT	16571	207089	12.4971	12.6557
chrX	155270560	2962492	0.0191	0.2358
chrY	59373566	611734	0.0103	0.1899

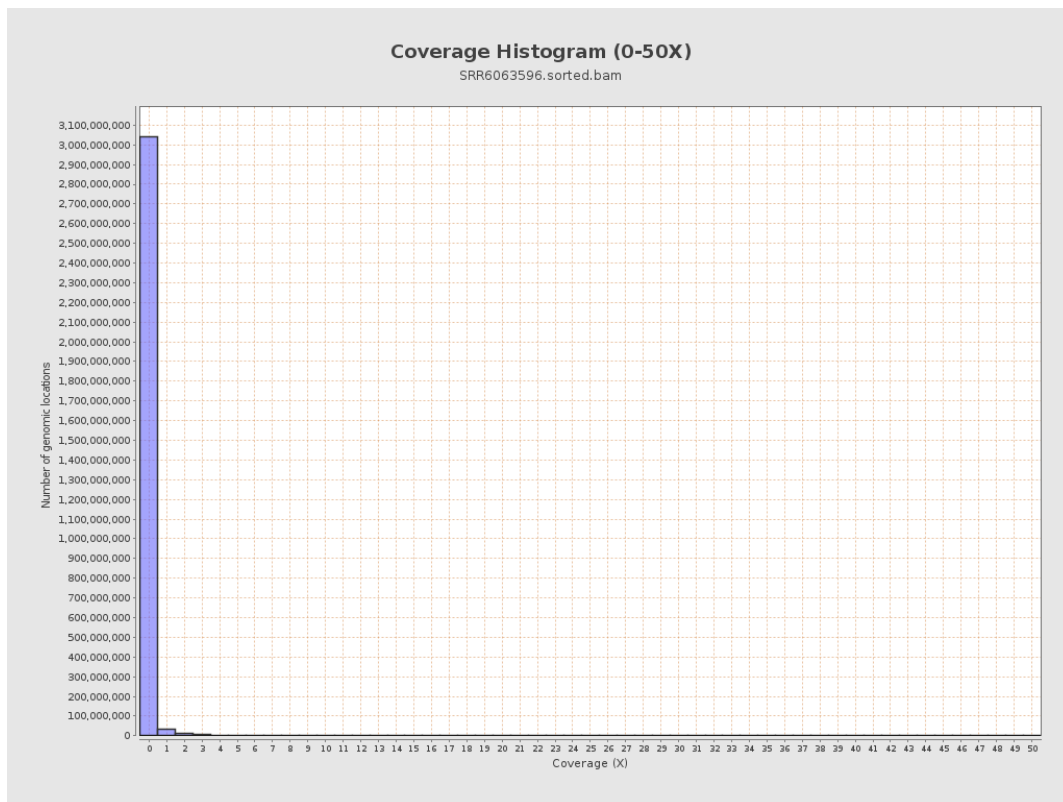
3. Results : Coverage across reference



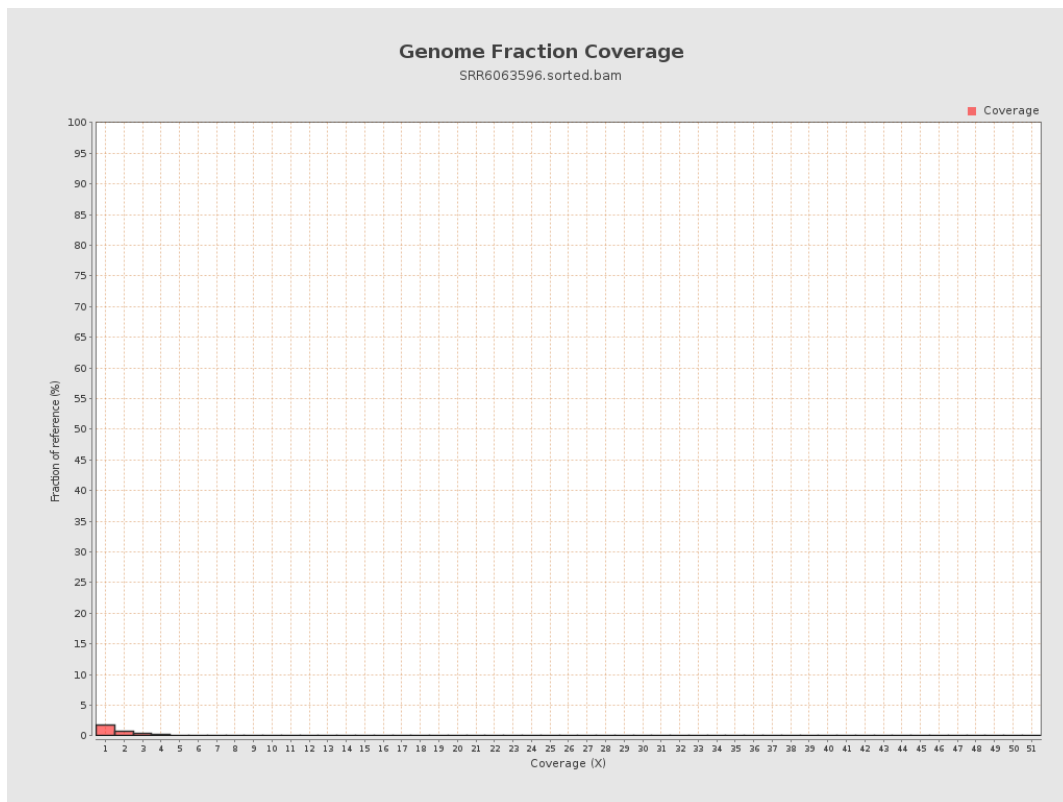
4. Results : Coverage Histogram



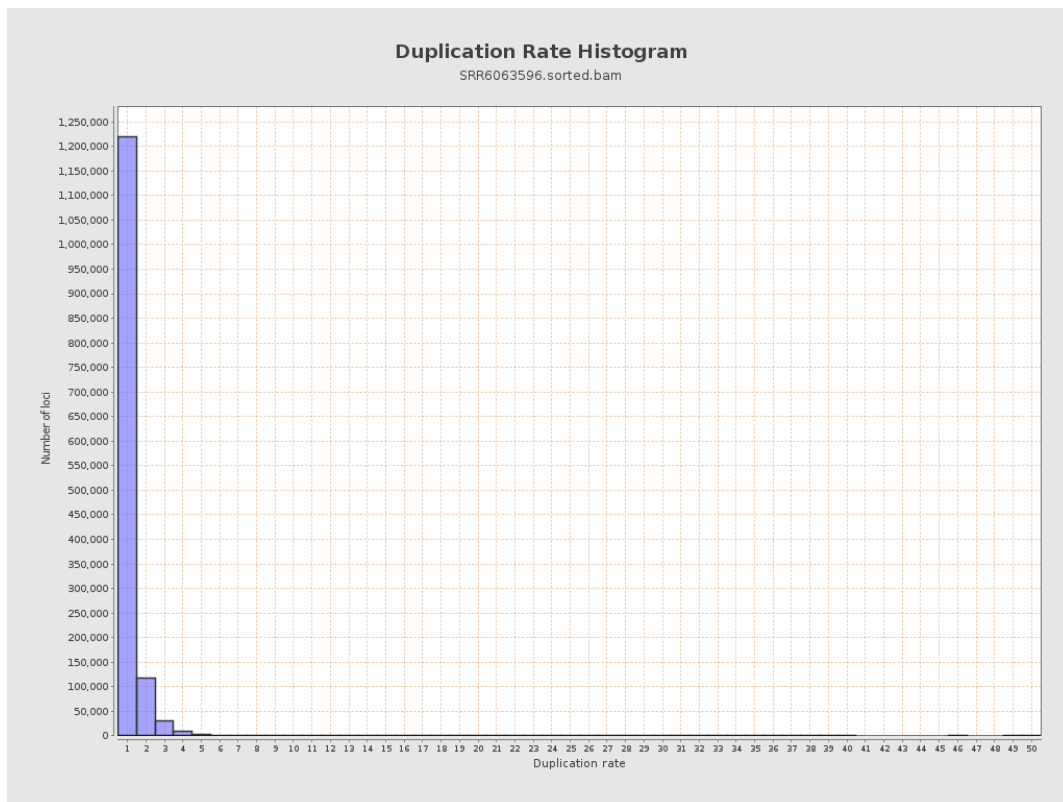
5. Results : Coverage Histogram (0-50X)



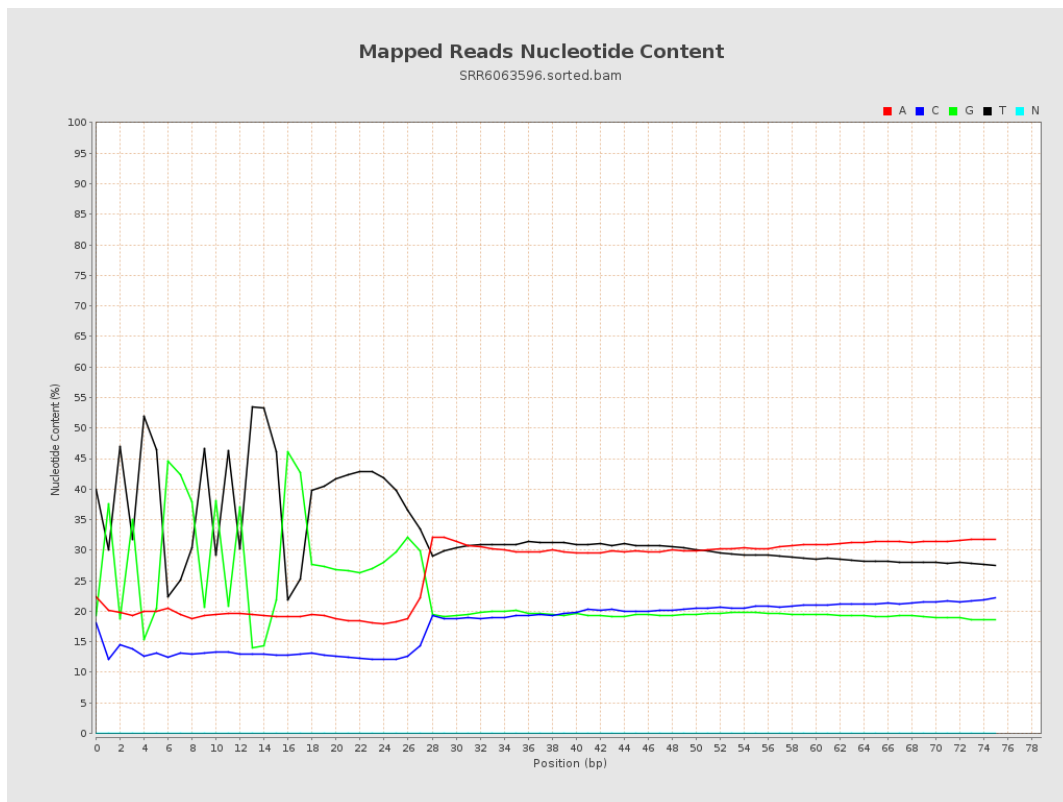
6. Results : Genome Fraction Coverage



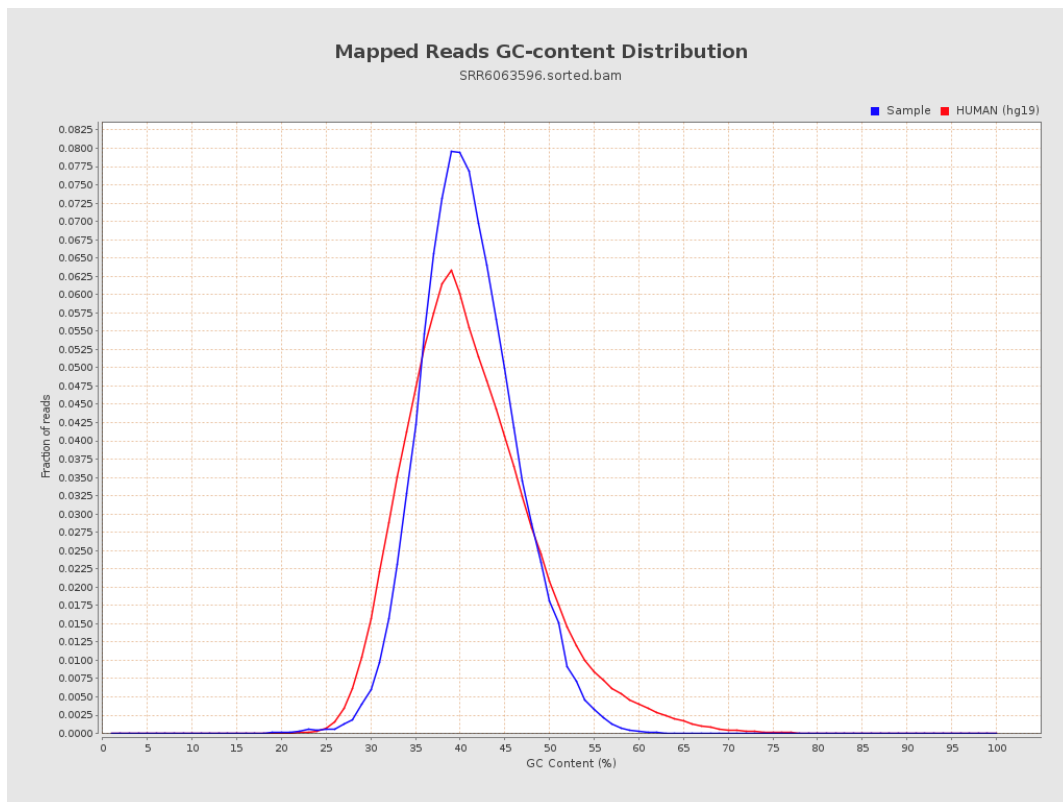
7. Results : Duplication Rate Histogram



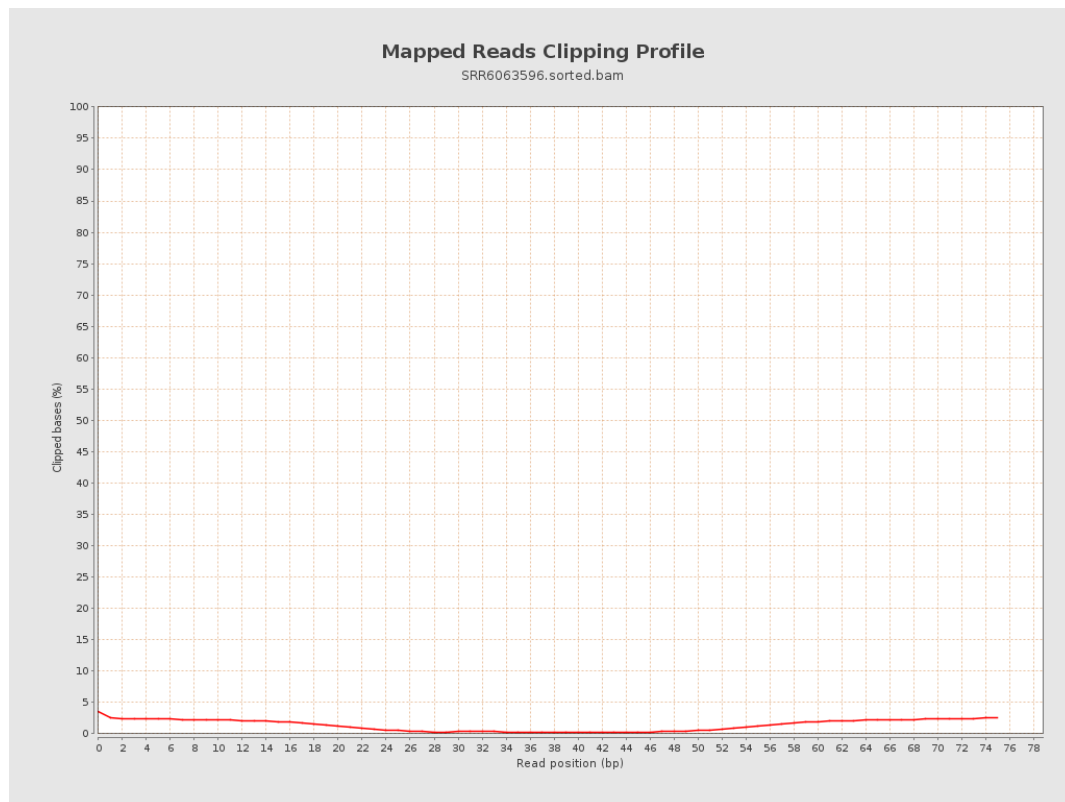
8. Results : Mapped Reads Nucleotide Content



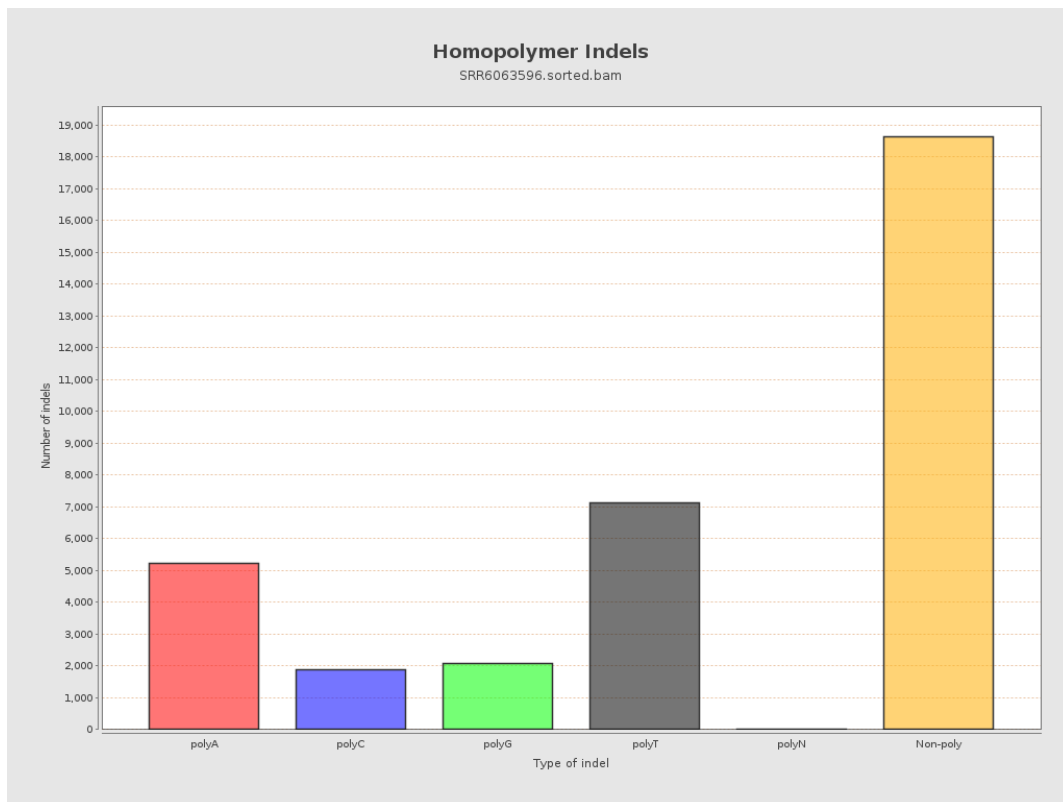
9. Results : Mapped Reads GC-content Distribution



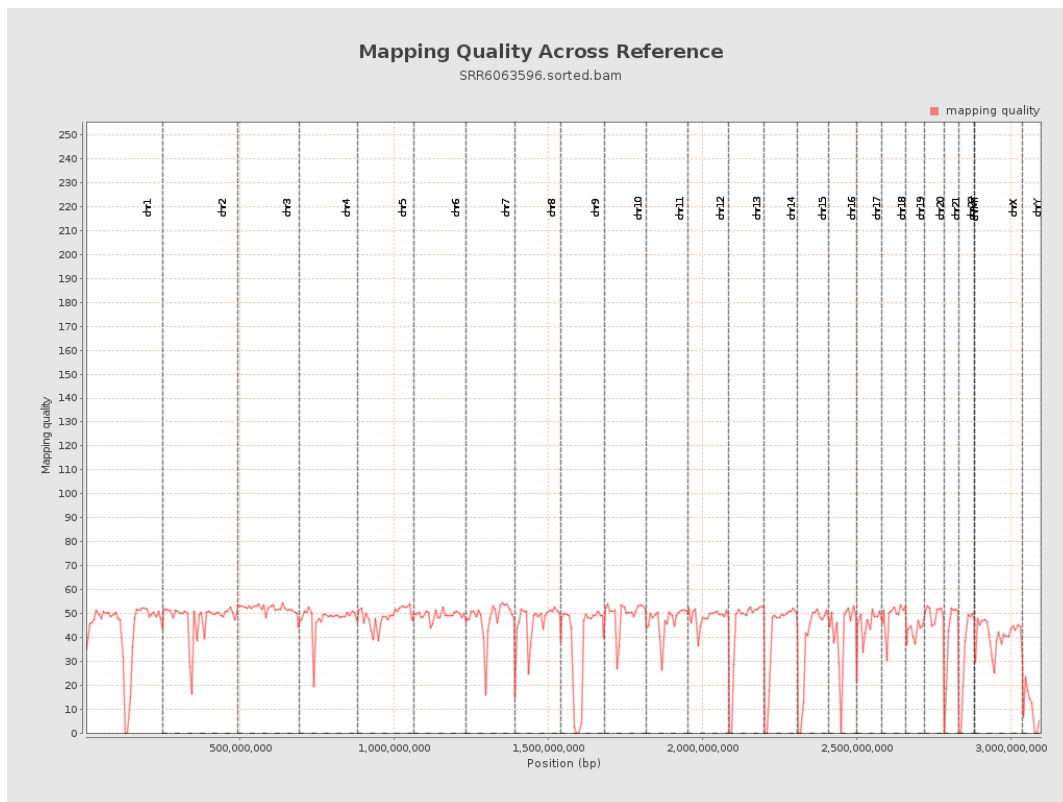
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

