Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:54:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013270.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_SRR6013270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013270.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:54:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,535,144
Mapped reads	2,928,952 / 64.58%
Unmapped reads	1,606,192 / 35.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,886 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	278,325 / 6.14%
Duplication rate	6.89%
Clipped reads	1,879,986 / 41.45%

2.2. ACGT Content

Number/percentage of A's	51,253,010 / 28.46%
Number/percentage of C's	38,943,014 / 21.63%
Number/percentage of T's	49,725,446 / 27.61%
Number/percentage of G's	40,140,477 / 22.29%
Number/percentage of N's	18,904 / 0.01%
GC Percentage	43.92%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.5626

2.4. Mapping Quality

Mean Mapping Quality	40.98

2.5. Mismatches and indels

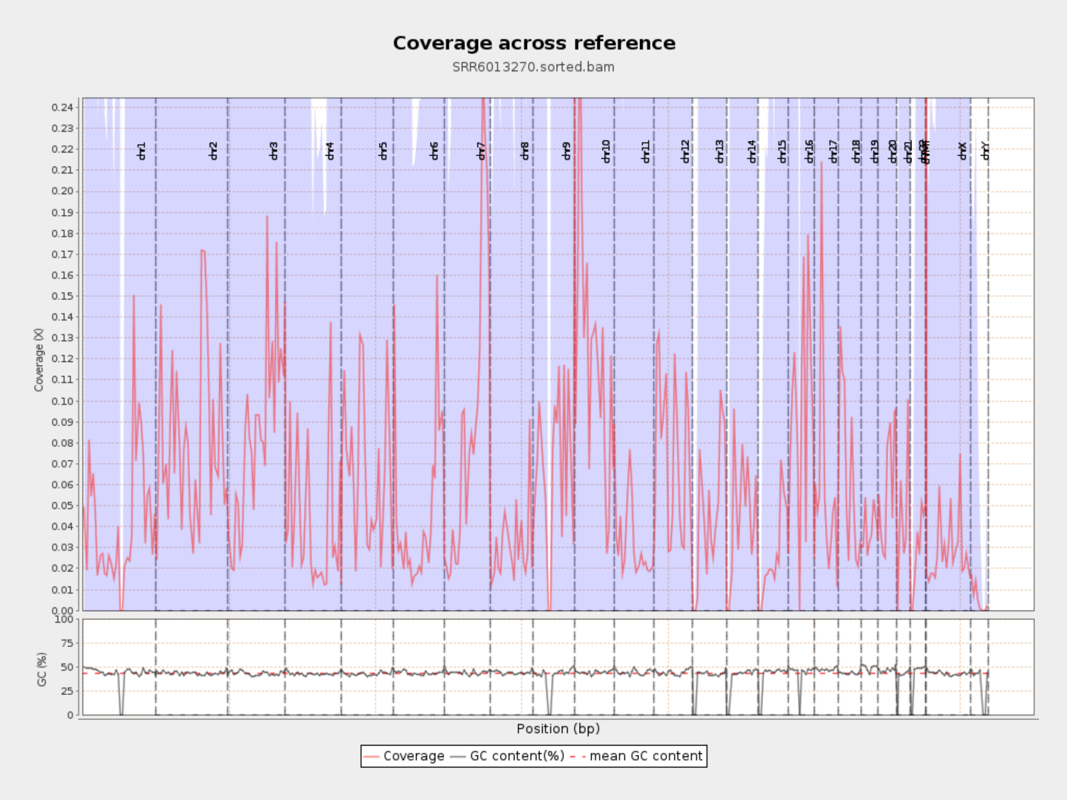
General error rate	0.76%
Mismatches	1,354,930
Insertions	11,464
Mapped reads with at least one insertion	0.39%
Deletions	34,153
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.15%

2.6. Chromosome stats

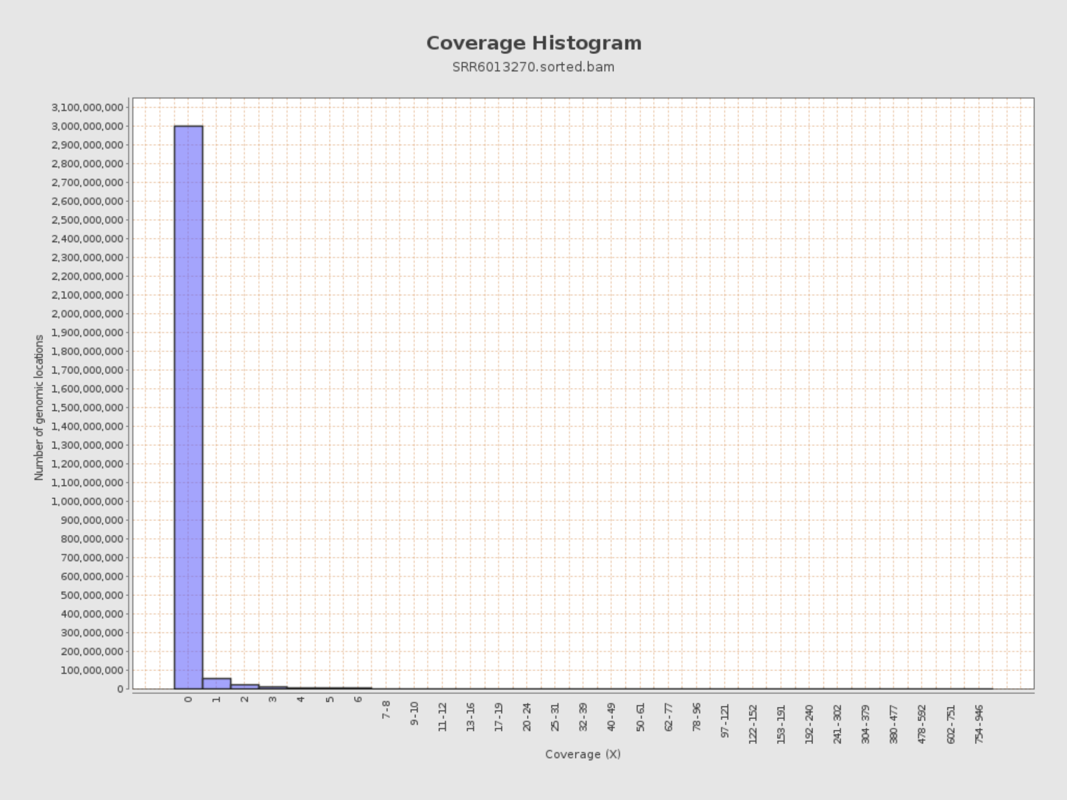
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10563056	0.0424	0.4917
chr2	243199373	19881118	0.0817	0.8237
chr3	198022430	16466100	0.0832	0.492
chr4	191154276	8227690	0.043	0.3679
chr5	180915260	11729588	0.0648	0.4402
chr6	171115067	8017444	0.0469	0.4324
chr7	159138663	14060553	0.0884	0.792

chr8	146364022	4587022	0.0313	0.4309
chr9	141213431	9831923	0.0696	0.6147
chr10	135534747	16545738	0.1221	0.859
chr11	135006516	4433258	0.0328	0.4767
chr12	133851895	9901635	0.074	0.4778
chr13	115169878	5585985	0.0485	0.4008
chr14	107349540	4950071	0.0461	0.6035
chr15	102531392	2646299	0.0258	0.6069
chr16	90354753	8499602	0.0941	0.5526
chr17	81195210	4796905	0.0591	0.5684
chr18	78077248	5154265	0.066	0.8402
chr19	59128983	2273983	0.0385	0.5674
chr20	63025520	3690051	0.0585	0.4167
chr21	48129895	2031669	0.0422	0.3869
chr22	51304566	1452249	0.0283	0.2868
chrMT	16571	72673	4.3856	3.9706
chrX	155270560	4423173	0.0285	0.3847
chrY	59373566	316287	0.0053	0.1217

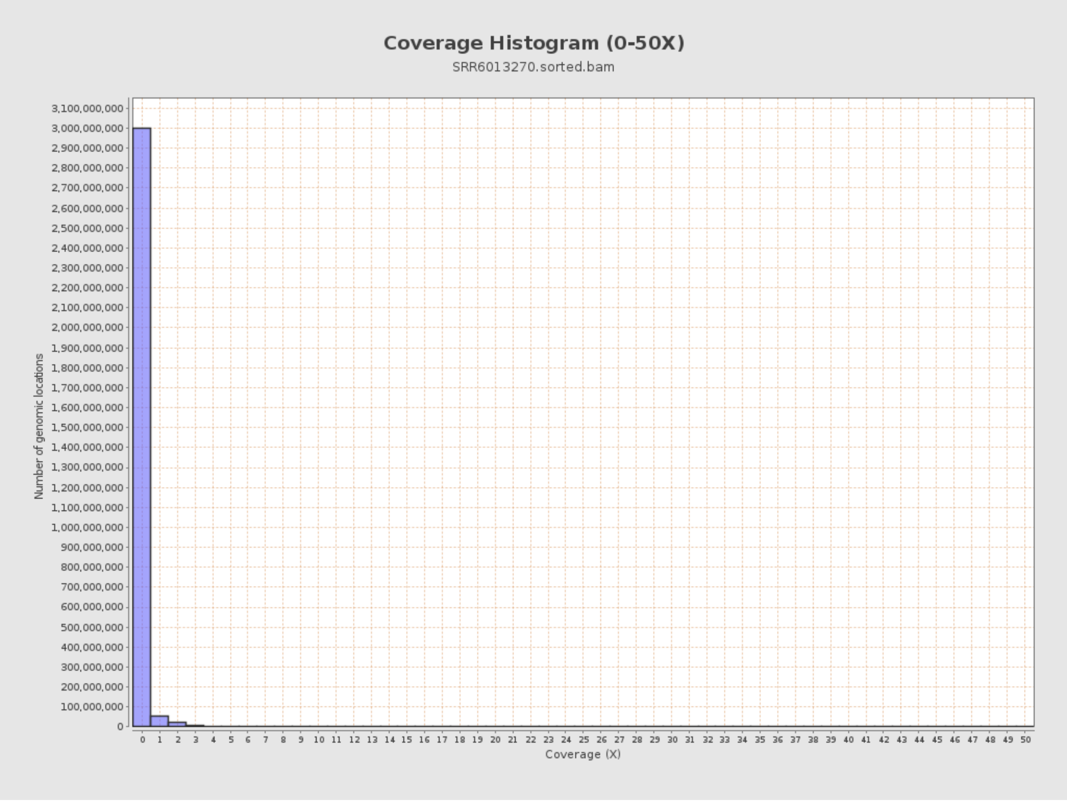
3. Results : Coverage across reference



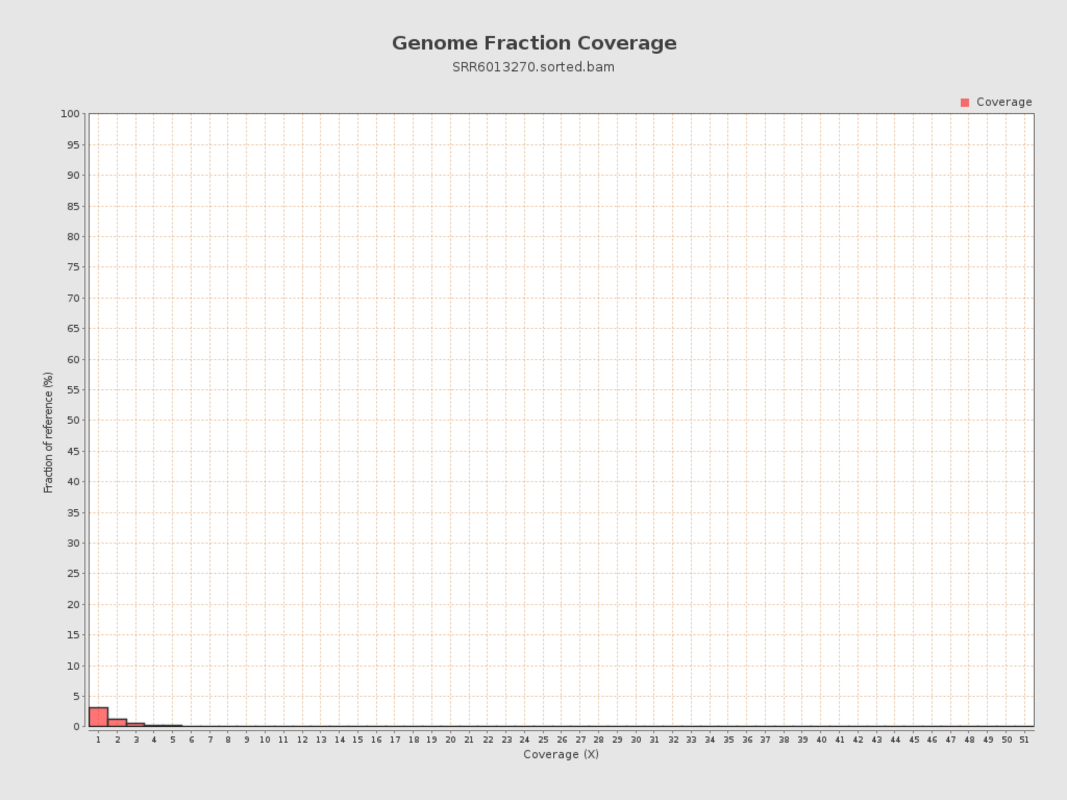
4. Results : Coverage Histogram



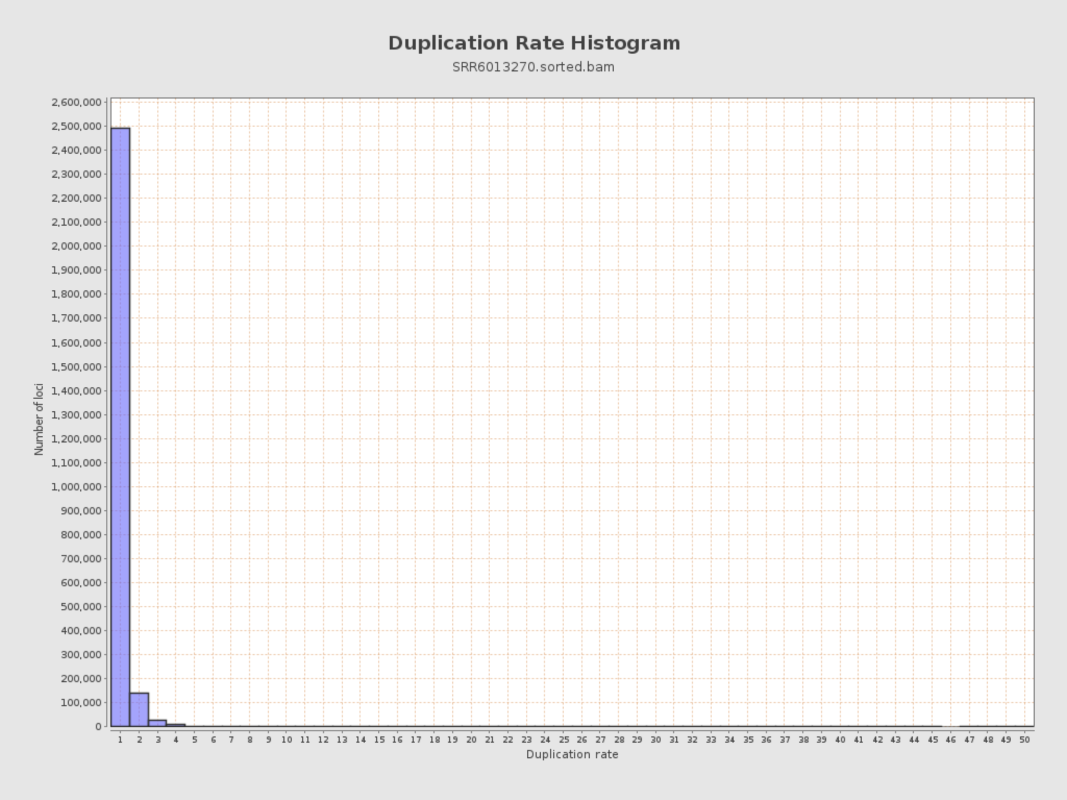
5. Results : Coverage Histogram (0-50X)



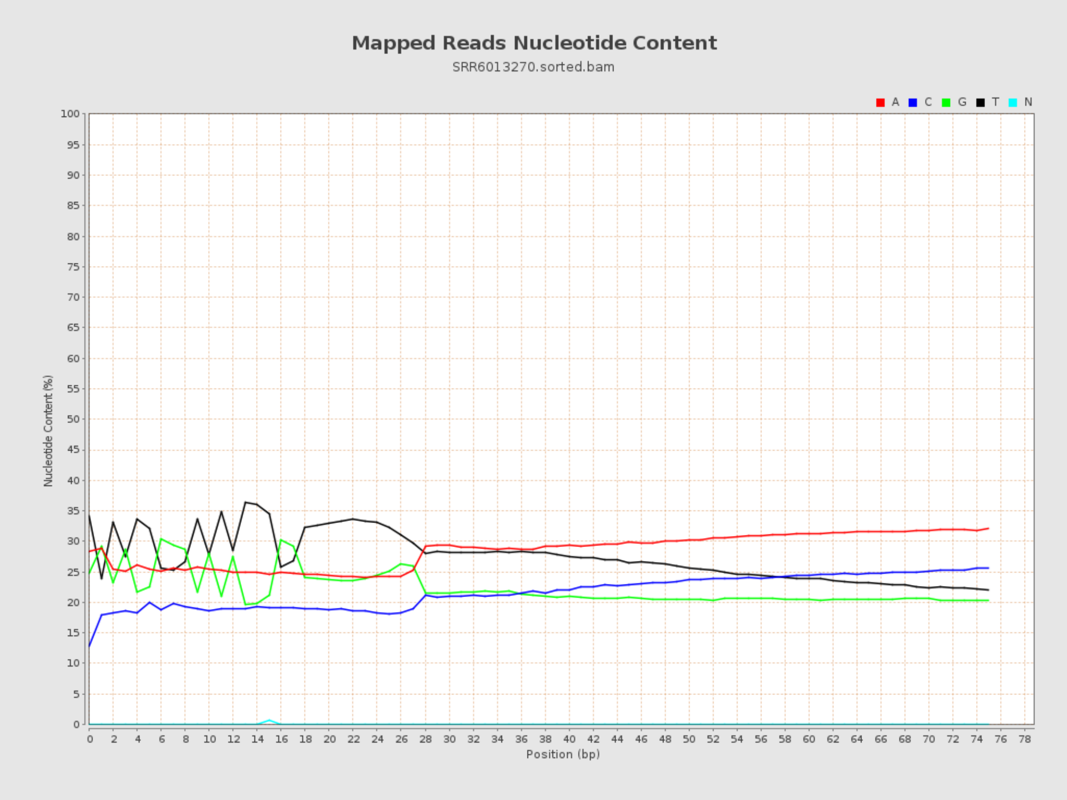
6. Results : Genome Fraction Coverage



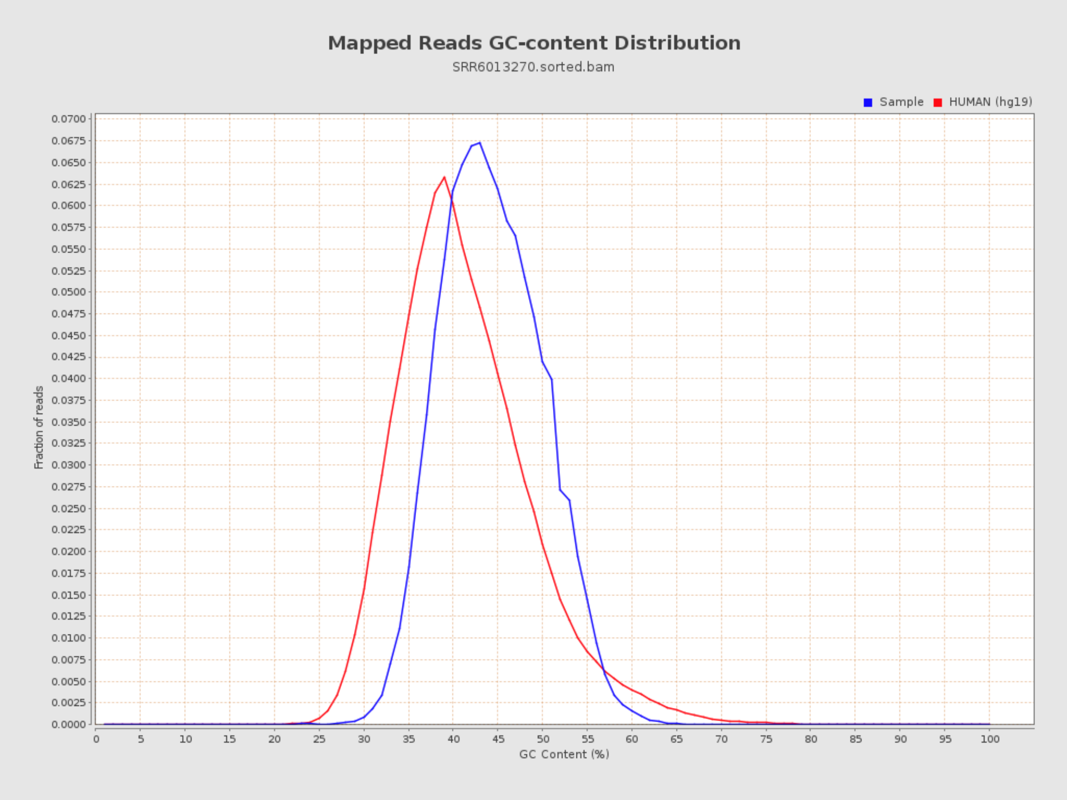
7. Results : Duplication Rate Histogram



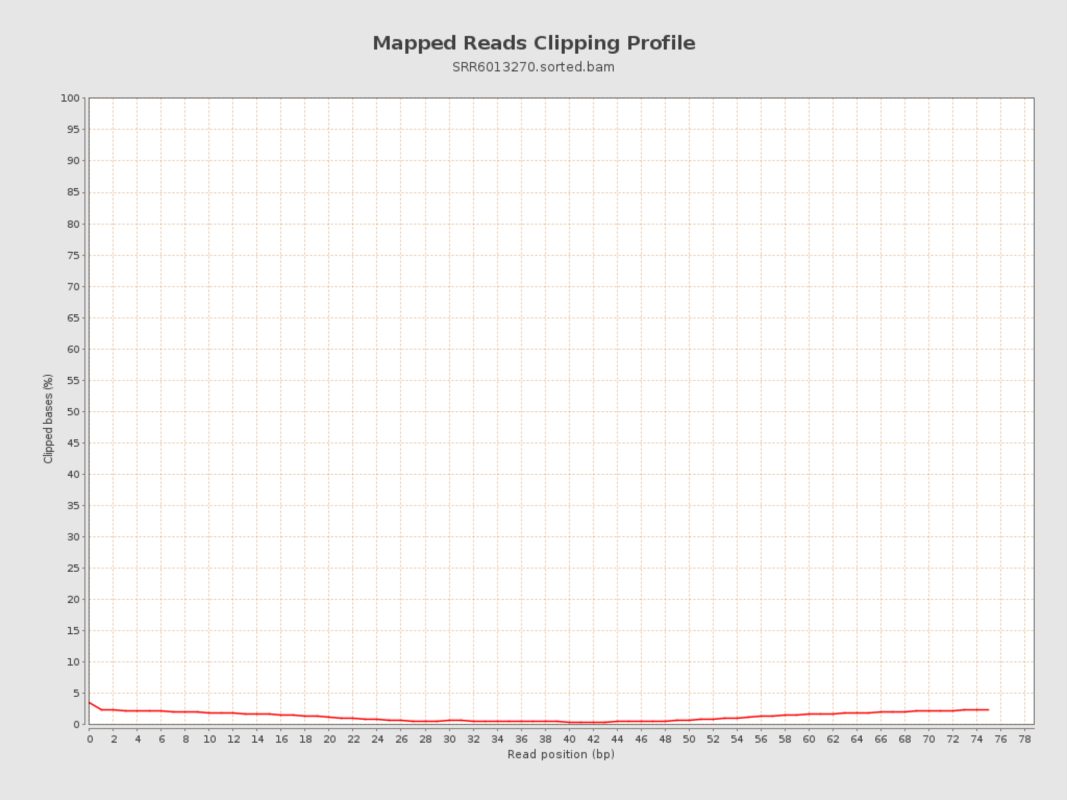
8. Results : Mapped Reads Nucleotide Content



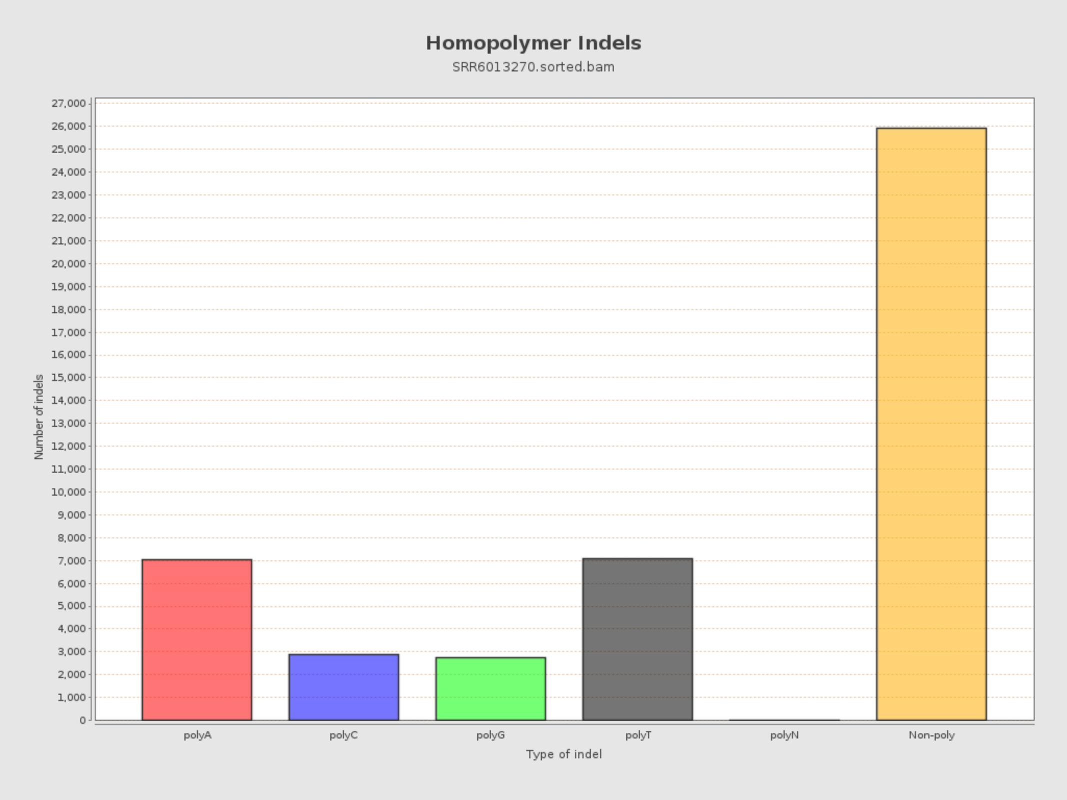
9. Results : Mapped Reads GC-content Distribution



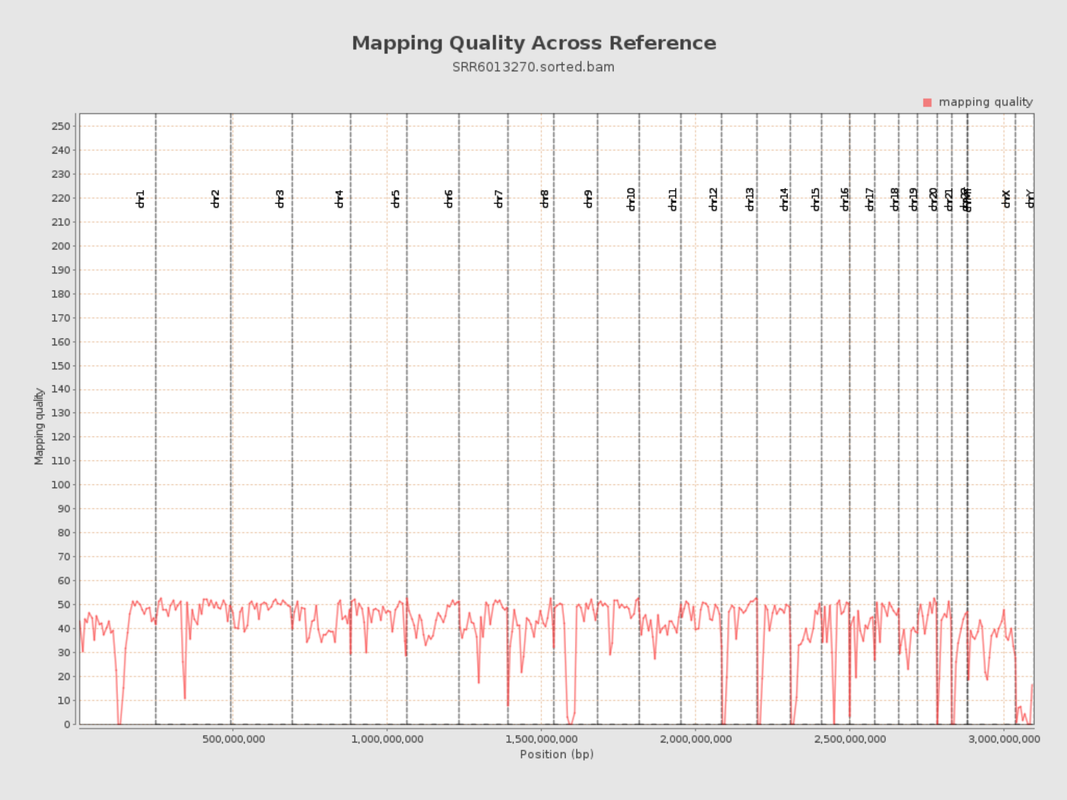
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram