Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:19:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004060.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_SRR6004060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:19:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,052,550
Mapped reads	2,750,879 / 90.12%
Unmapped reads	301,671 / 9.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,490 / 1.23%
Read min/max/mean length	30 / 76 / 76.43
Duplicated reads (estimated)	182,158 / 5.97%
Duplication rate	5.33%
Clipped reads	1,377,956 / 45.14%

2.2. ACGT Content

Number/percentage of A's	50,832,819 / 28.16%
Number/percentage of C's	33,095,625 / 18.34%
Number/percentage of T's	57,283,766 / 31.74%
Number/percentage of G's	39,148,167 / 21.69%
Number/percentage of N's	137,846 / 0.08%
GC Percentage	40.02%

2.3. Coverage

Mean	0.0583

Standard Deviation	0.5021

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

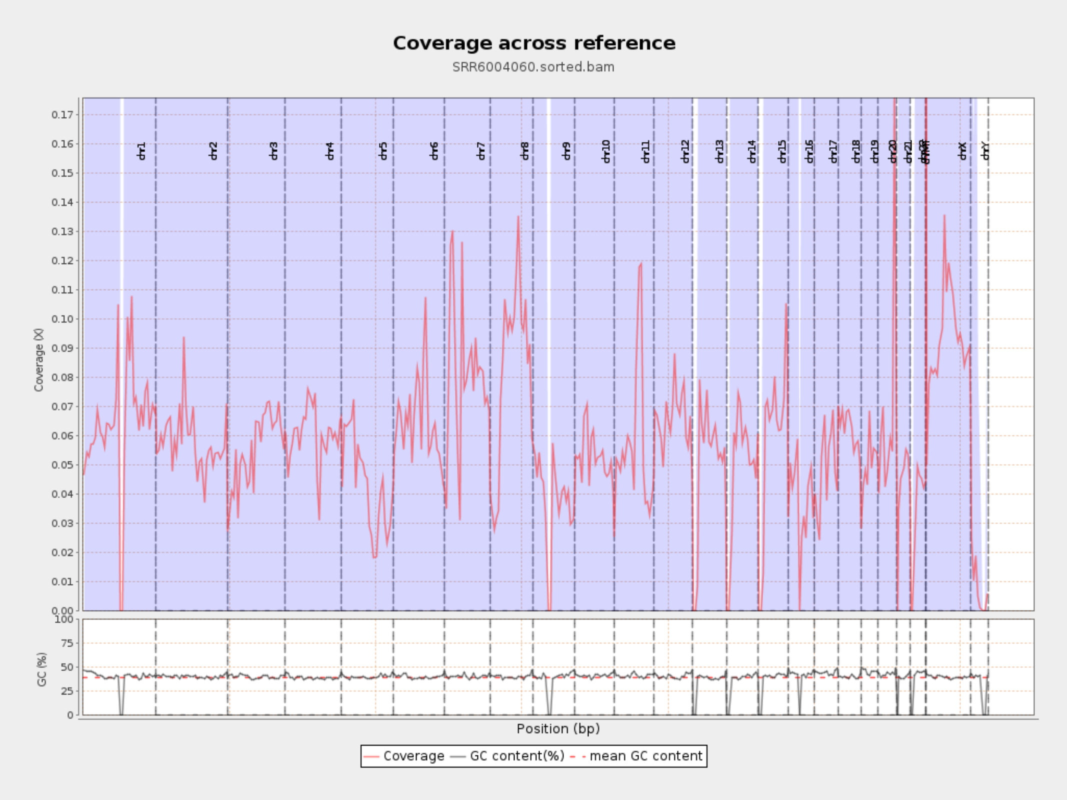
General error rate	0.89%
Mismatches	1,584,626
Insertions	12,792
Mapped reads with at least one insertion	0.46%
Deletions	60,812
Mapped reads with at least one deletion	2.18%
Homopolymer indels	44.67%

2.6. Chromosome stats

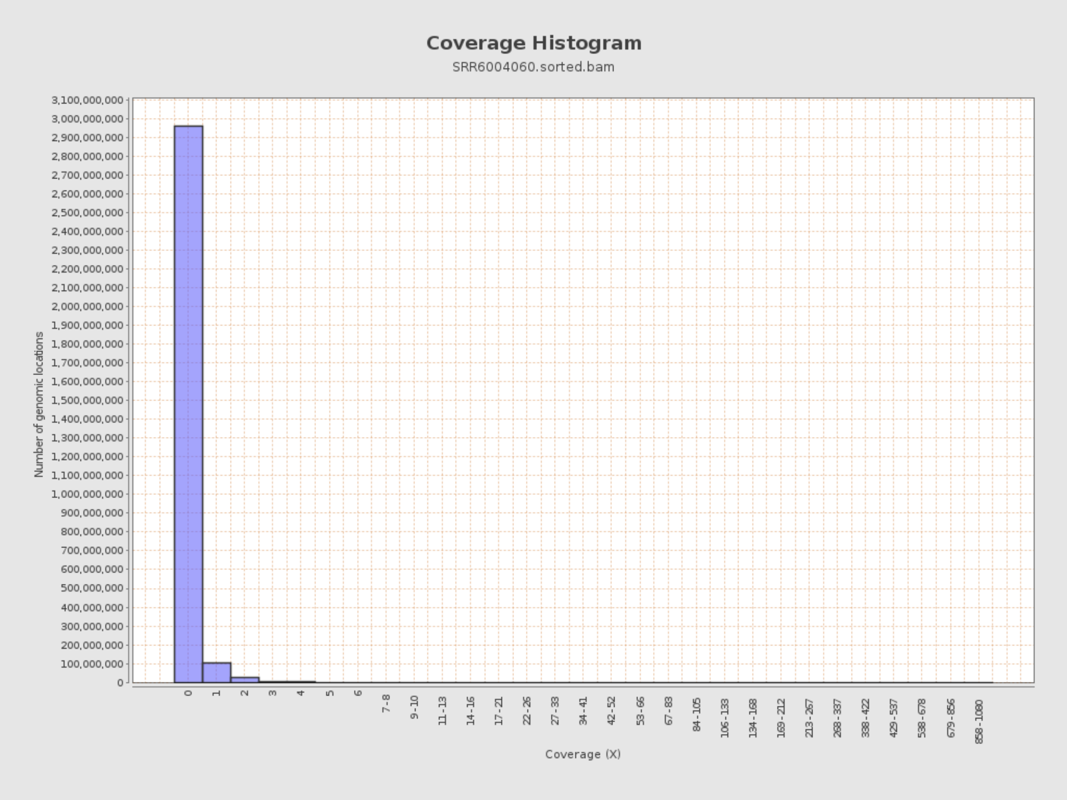
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15963897	0.064	0.934
chr2	243199373	14068928	0.0578	0.4859
chr3	198022430	10887905	0.055	0.2925
chr4	191154276	11437142	0.0598	0.3107
chr5	180915260	7865314	0.0435	0.2642
chr6	171115067	11156364	0.0652	0.3695
chr7	159138663	12673033	0.0796	0.8407

chr8	146364022	12147055	0.083	0.7155
chr9	141213431	5343762	0.0378	0.4207
chr10	135534747	7164598	0.0529	0.3848
chr11	135006516	7720847	0.0572	0.4275
chr12	133851895	8867246	0.0662	0.3338
chr13	115169878	5770549	0.0501	0.2802
chr14	107349540	5219459	0.0486	0.3146
chr15	102531392	5967831	0.0582	0.3022
chr16	90354753	3305899	0.0366	0.273
chr17	81195210	3914058	0.0482	0.2965
chr18	78077248	4851793	0.0621	0.8173
chr19	59128983	2984507	0.0505	0.6105
chr20	63025520	4602561	0.073	0.3532
chr21	48129895	2047471	0.0425	0.2761
chr22	51304566	1651209	0.0322	0.2194
chrMT	16571	8250	0.4979	0.9089
chrX	155270560	14535780	0.0936	0.4354
chrY	59373566	444656	0.0075	0.1289

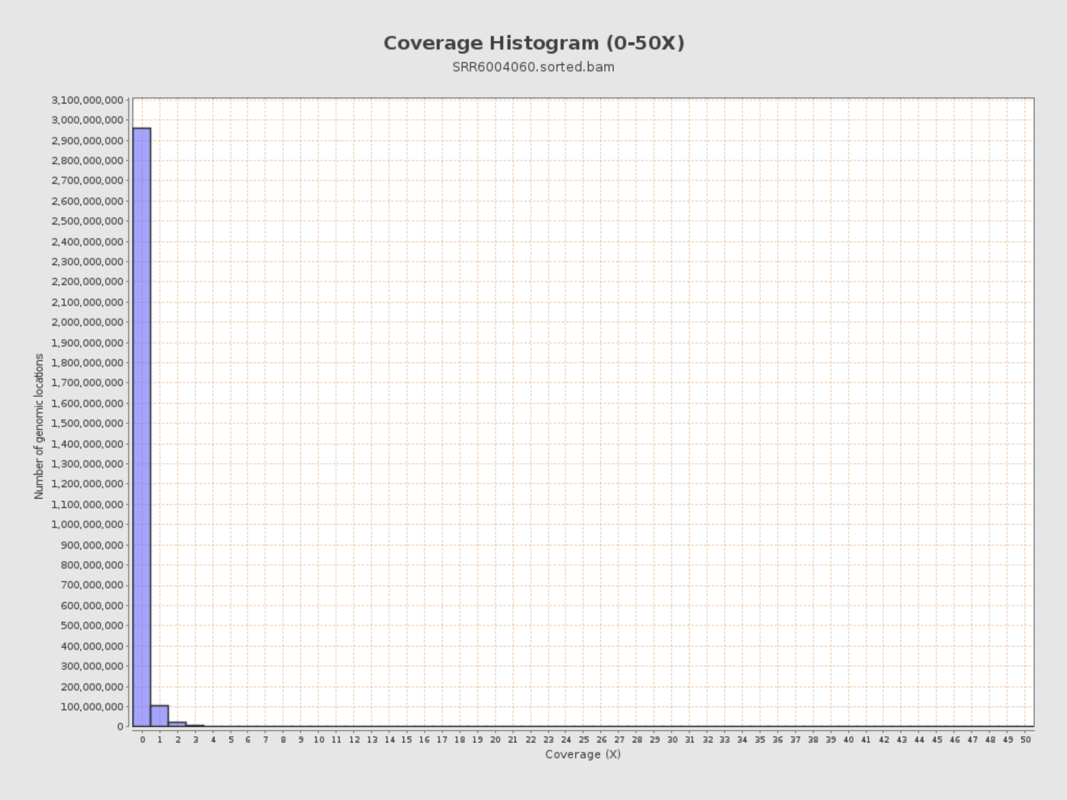
3. Results : Coverage across reference



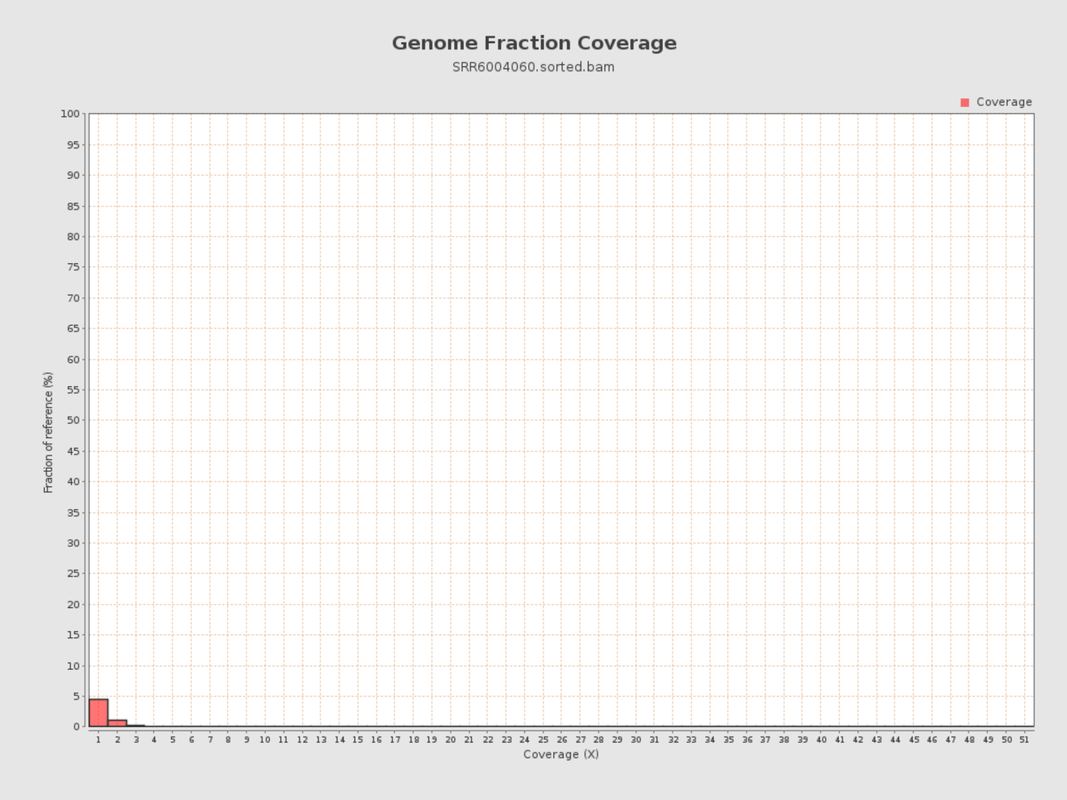
4. Results : Coverage Histogram



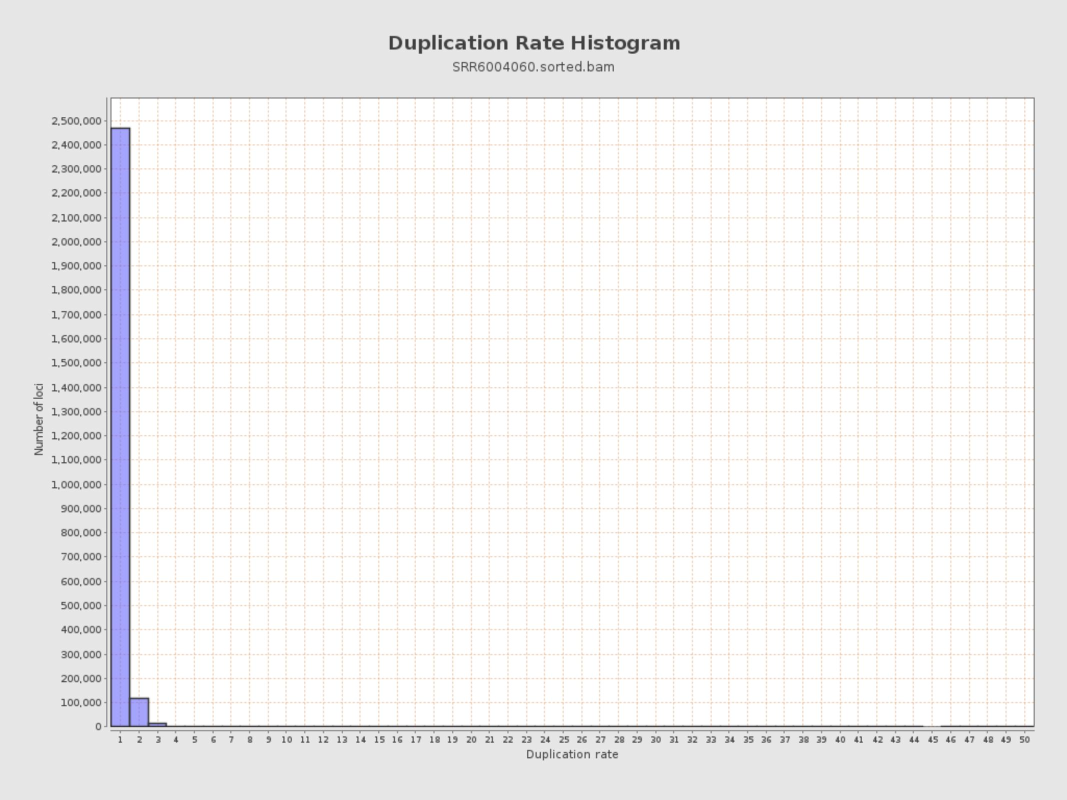
5. Results : Coverage Histogram (0-50X)



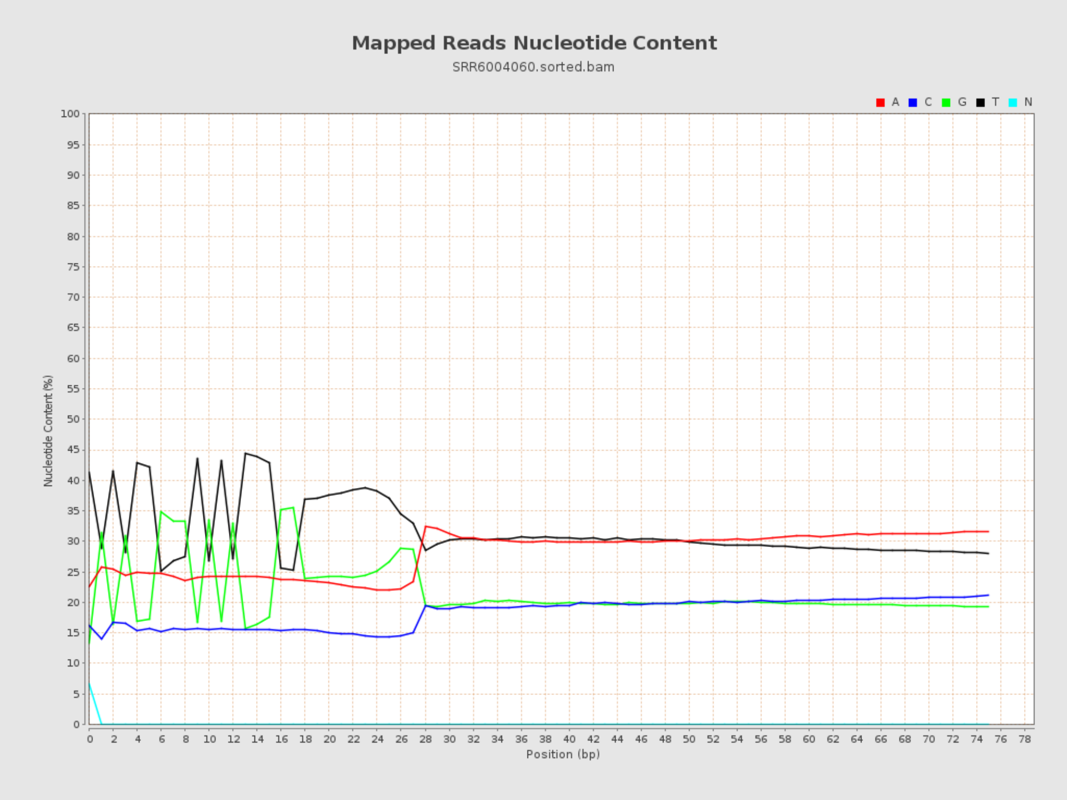
6. Results : Genome Fraction Coverage



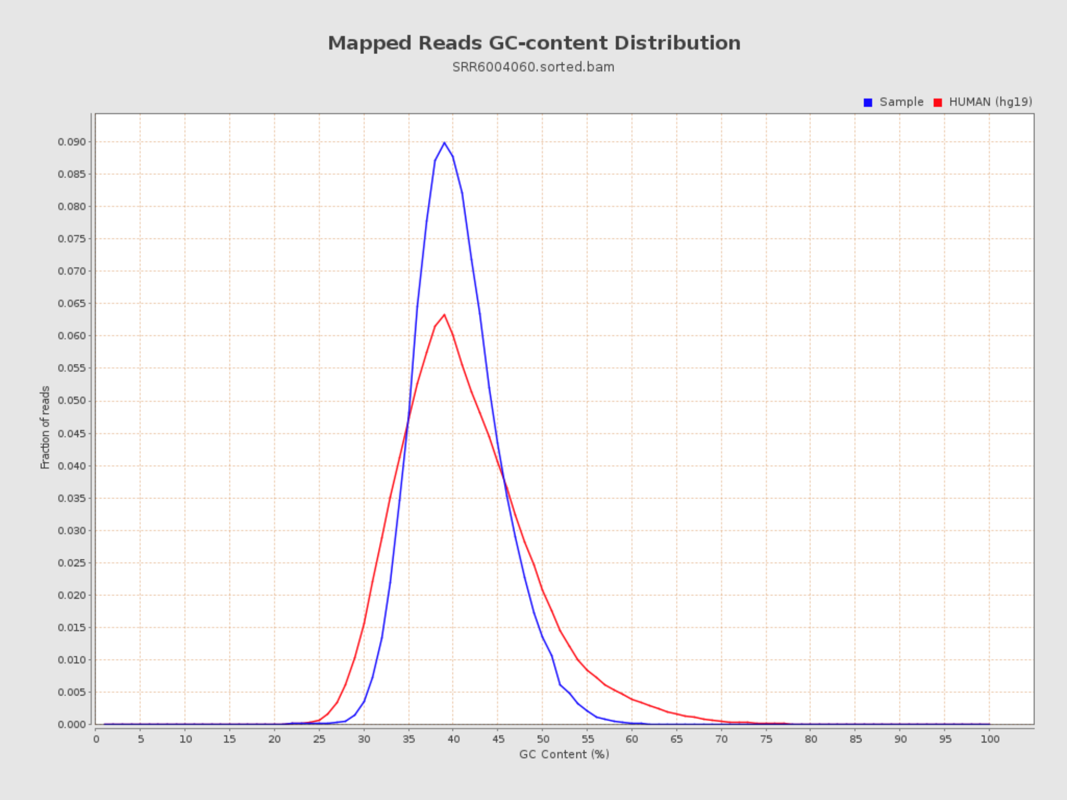
7. Results : Duplication Rate Histogram



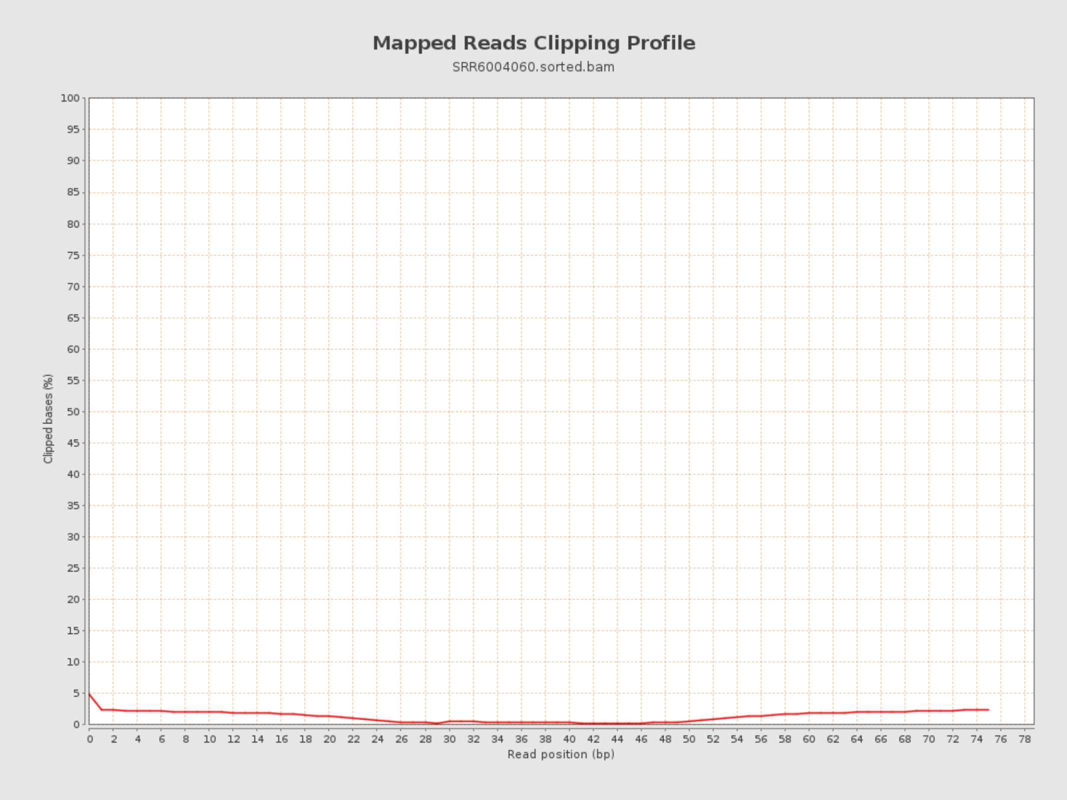
8. Results : Mapped Reads Nucleotide Content



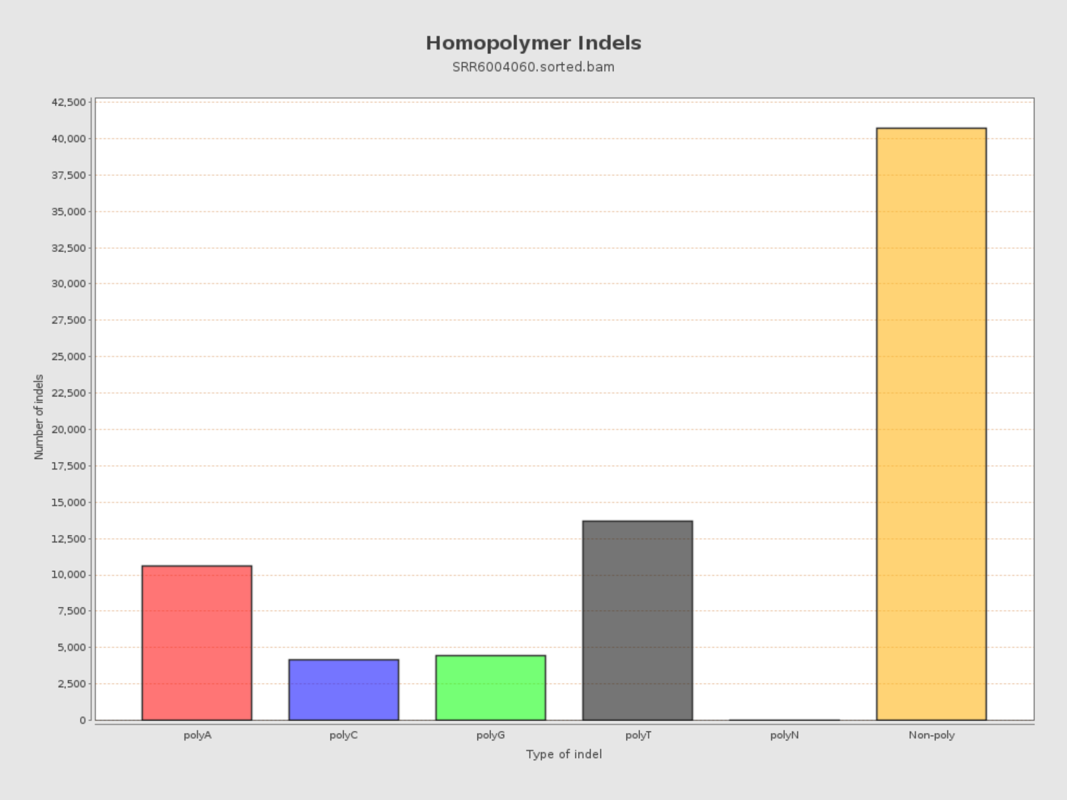
9. Results : Mapped Reads GC-content Distribution



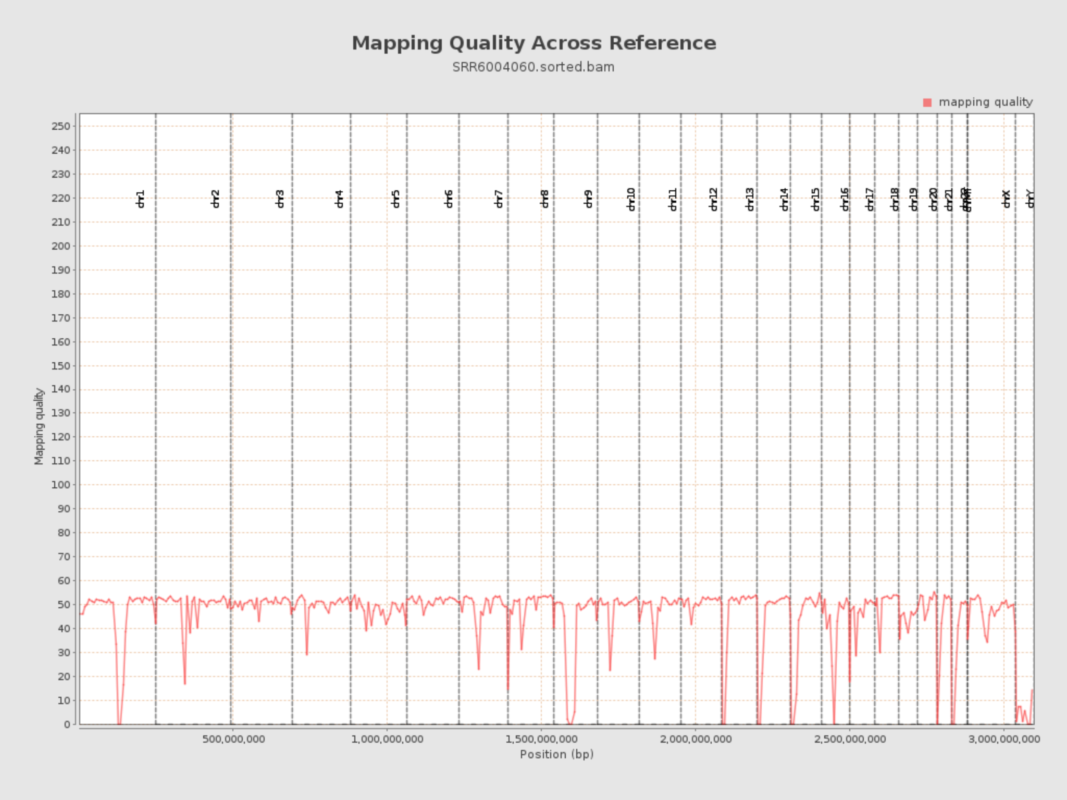
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram