Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:02:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004074.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_SRR6004074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:02:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,459,549
Mapped reads	2,254,146 / 91.65%
Unmapped reads	205,403 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,641 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	105,528 / 4.29%
Duplication rate	3.81%
Clipped reads	942,428 / 38.32%

2.2. ACGT Content

Number/percentage of A's	43,686,051 / 28.67%
Number/percentage of C's	28,308,406 / 18.58%
Number/percentage of T's	48,183,458 / 31.62%
Number/percentage of G's	32,164,509 / 21.11%
Number/percentage of N's	27,101 / 0.02%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0492

Standard Deviation	0.3893

2.4. Mapping Quality

Mean Mapping Quality	46.94

2.5. Mismatches and indels

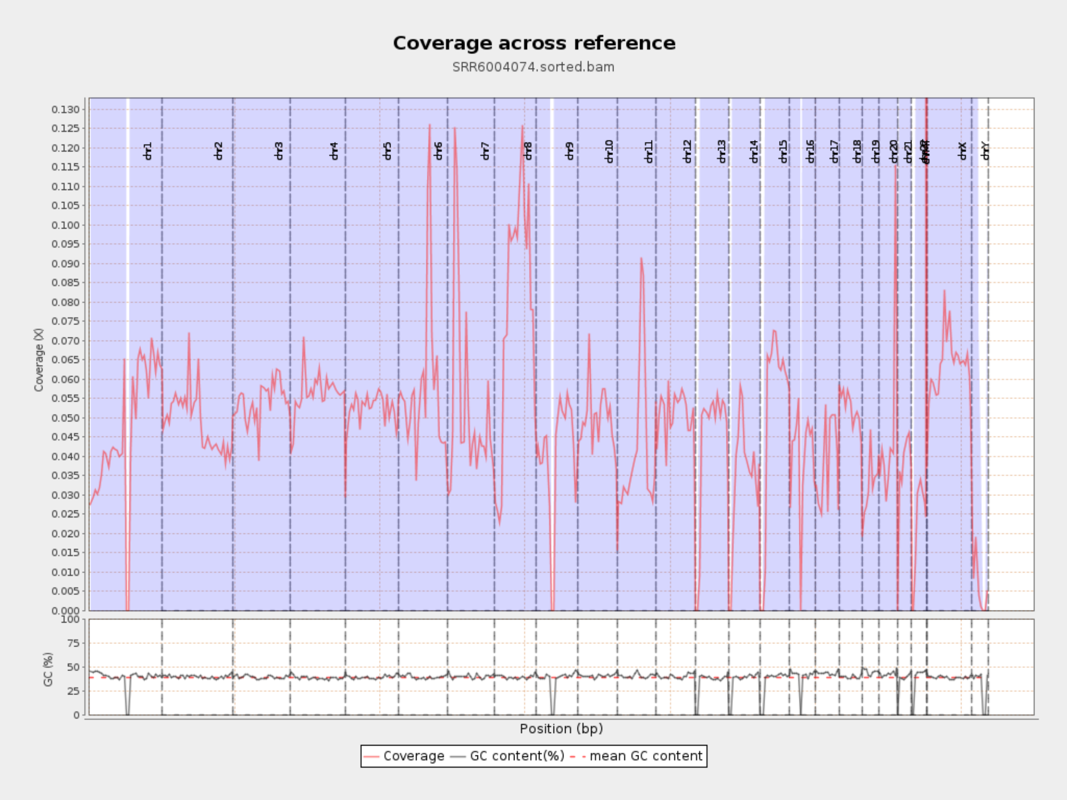
General error rate	0.87%
Mismatches	1,301,169
Insertions	10,886
Mapped reads with at least one insertion	0.48%
Deletions	36,841
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.59%

2.6. Chromosome stats

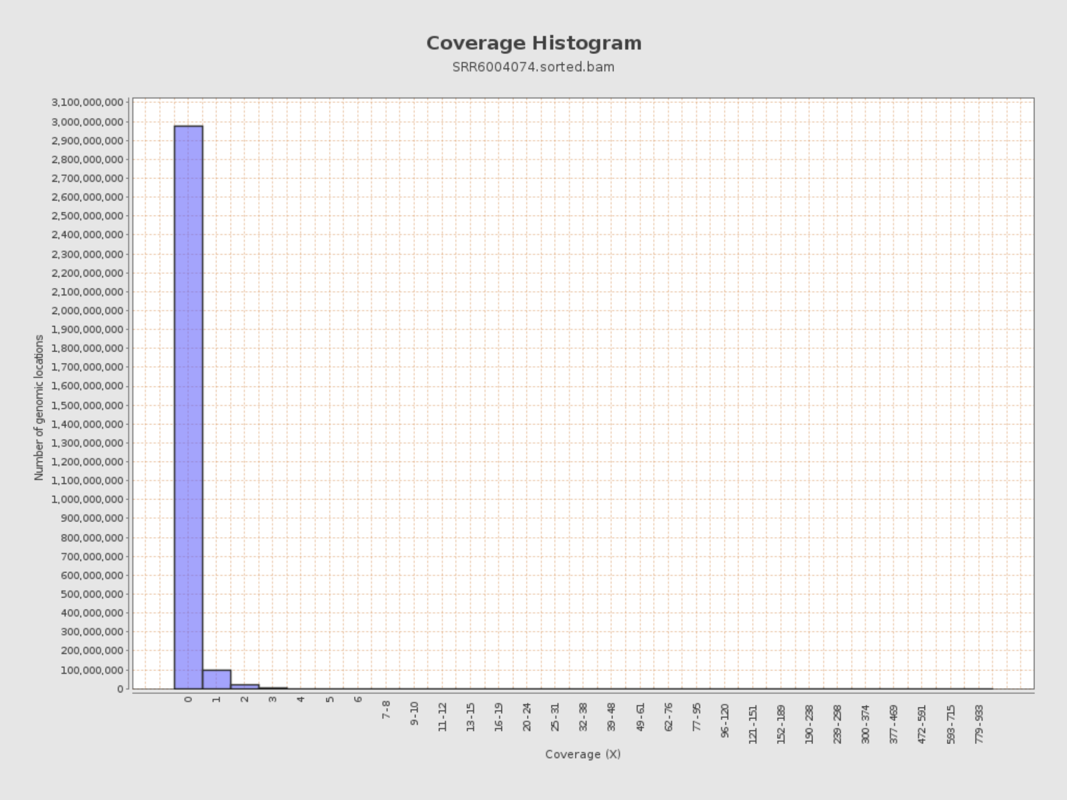
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11576177	0.0464	0.623
chr2	243199373	11913426	0.049	0.4074
chr3	198022430	10751689	0.0543	0.2788
chr4	191154276	10761216	0.0563	0.3024
chr5	180915260	9502900	0.0525	0.2757
chr6	171115067	9950192	0.0581	0.3143
chr7	159138663	8609227	0.0541	0.5452

chr8	146364022	11439009	0.0782	0.6574
chr9	141213431	5673969	0.0402	0.341
chr10	135534747	6758093	0.0499	0.3626
chr11	135006516	5703102	0.0422	0.308
chr12	133851895	6828422	0.051	0.2776
chr13	115169878	4976590	0.0432	0.255
chr14	107349540	3678981	0.0343	0.2423
chr15	102531392	5319477	0.0519	0.273
chr16	90354753	3591374	0.0397	0.2636
chr17	81195210	3160711	0.0389	0.2508
chr18	78077248	4109882	0.0526	0.6076
chr19	59128983	1936018	0.0327	0.4452
chr20	63025520	3079875	0.0489	0.2723
chr21	48129895	1744856	0.0363	0.2453
chr22	51304566	1099665	0.0214	0.1711
chrMT	16571	30361	1.8322	1.9293
chrX	155270560	9857847	0.0635	0.3258
chrY	59373566	380954	0.0064	0.1364

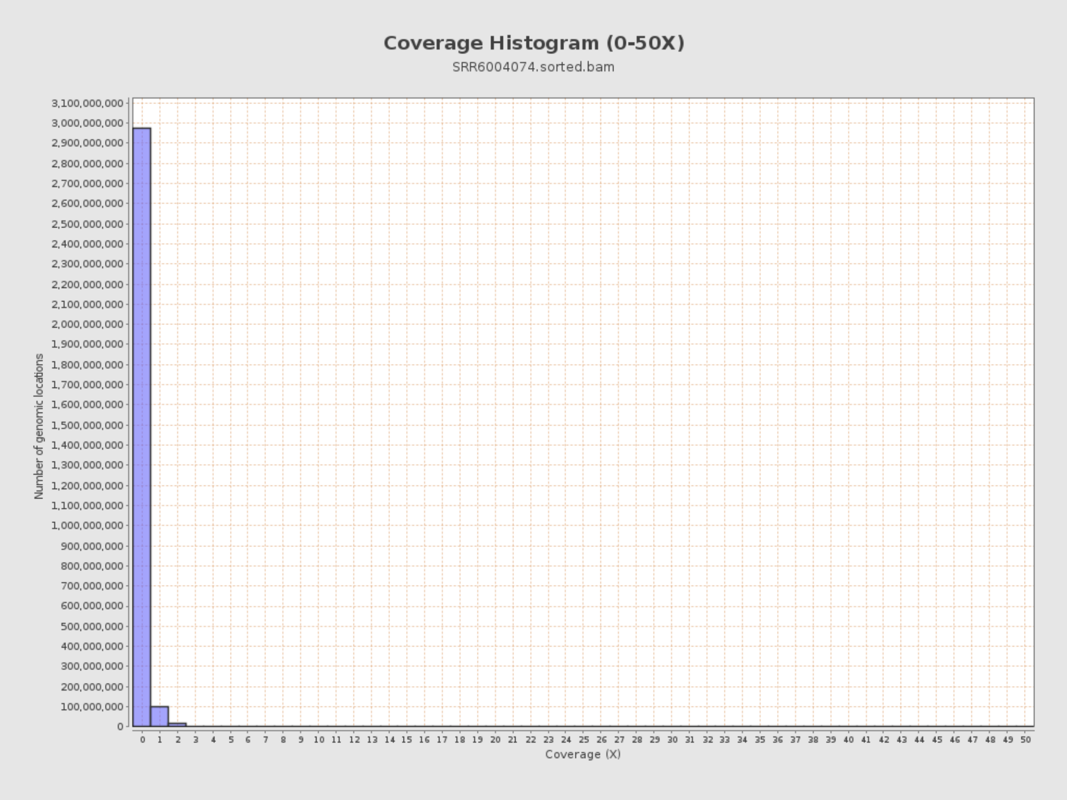
3. Results : Coverage across reference



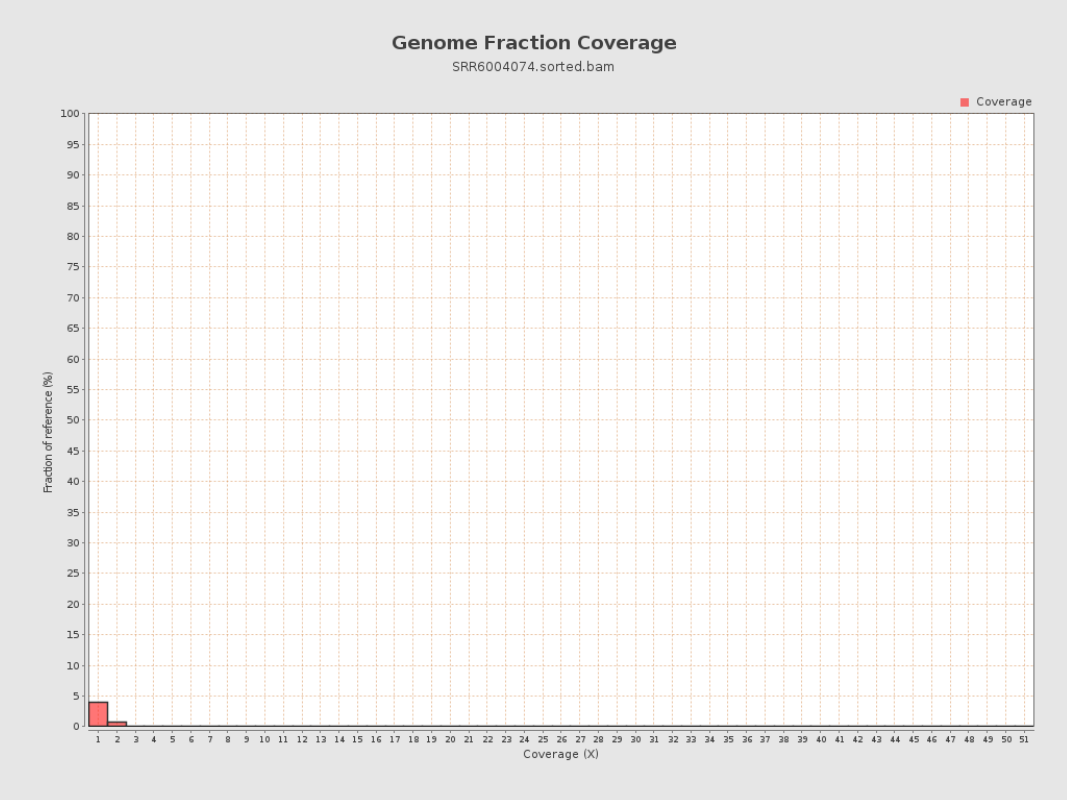
4. Results : Coverage Histogram



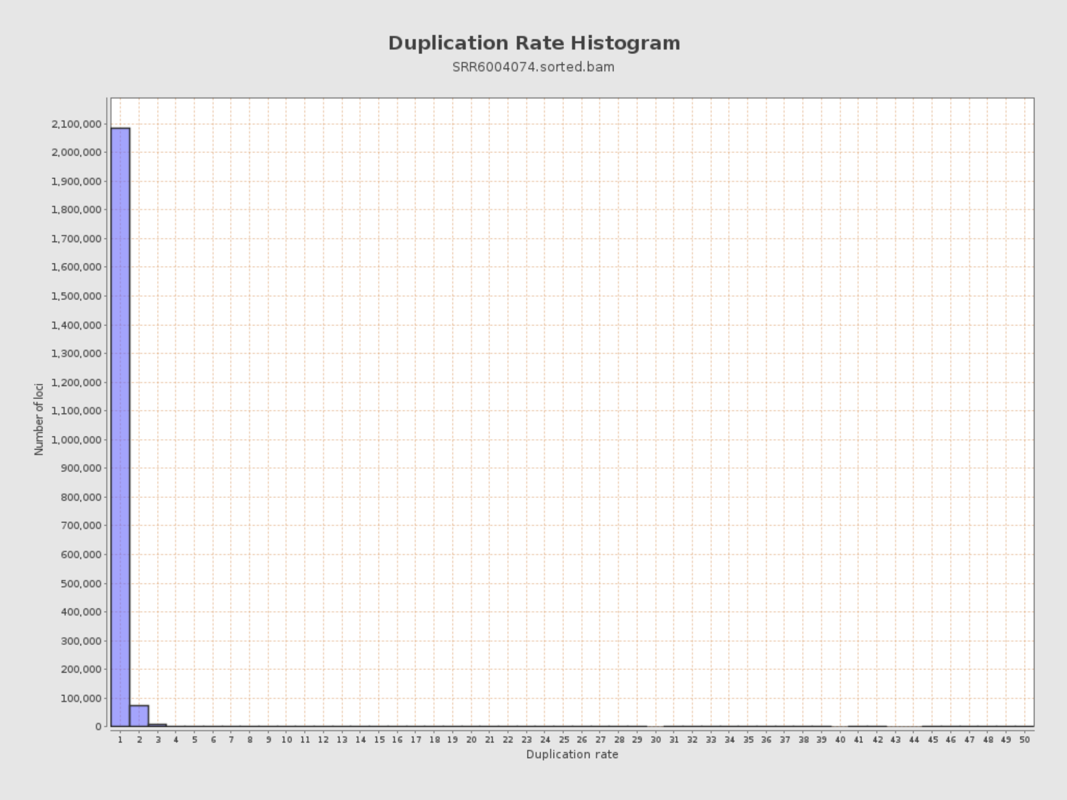
5. Results : Coverage Histogram (0-50X)



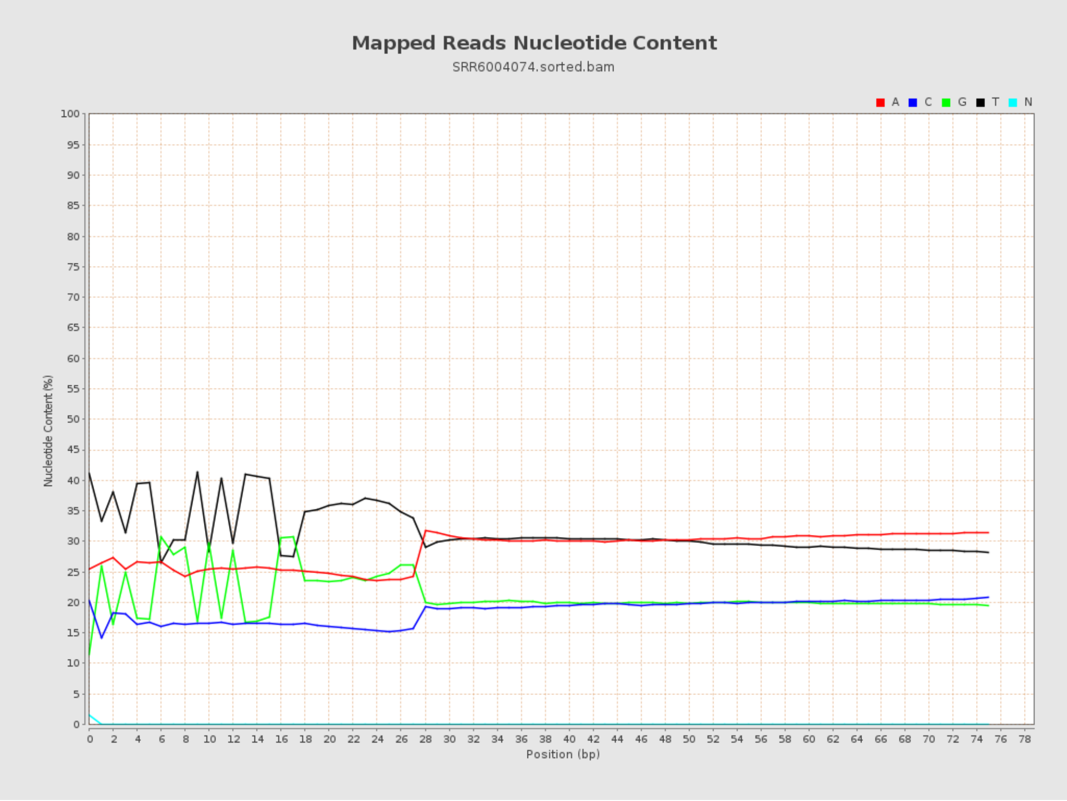
6. Results : Genome Fraction Coverage



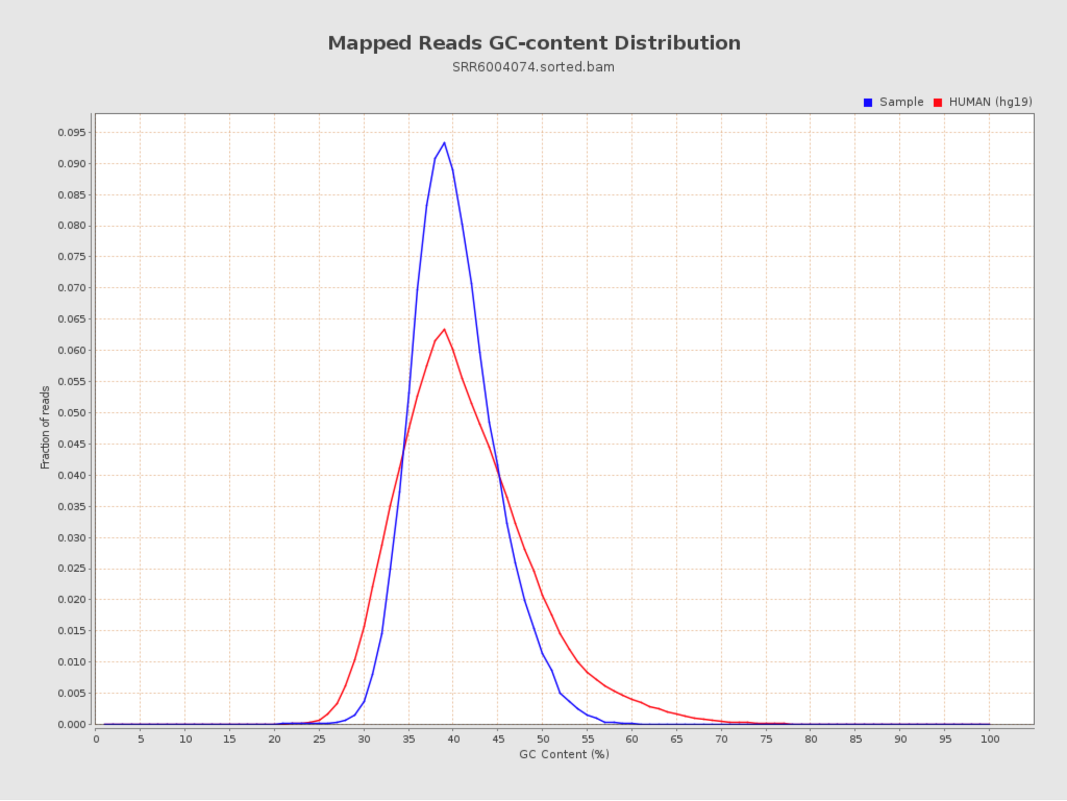
7. Results : Duplication Rate Histogram



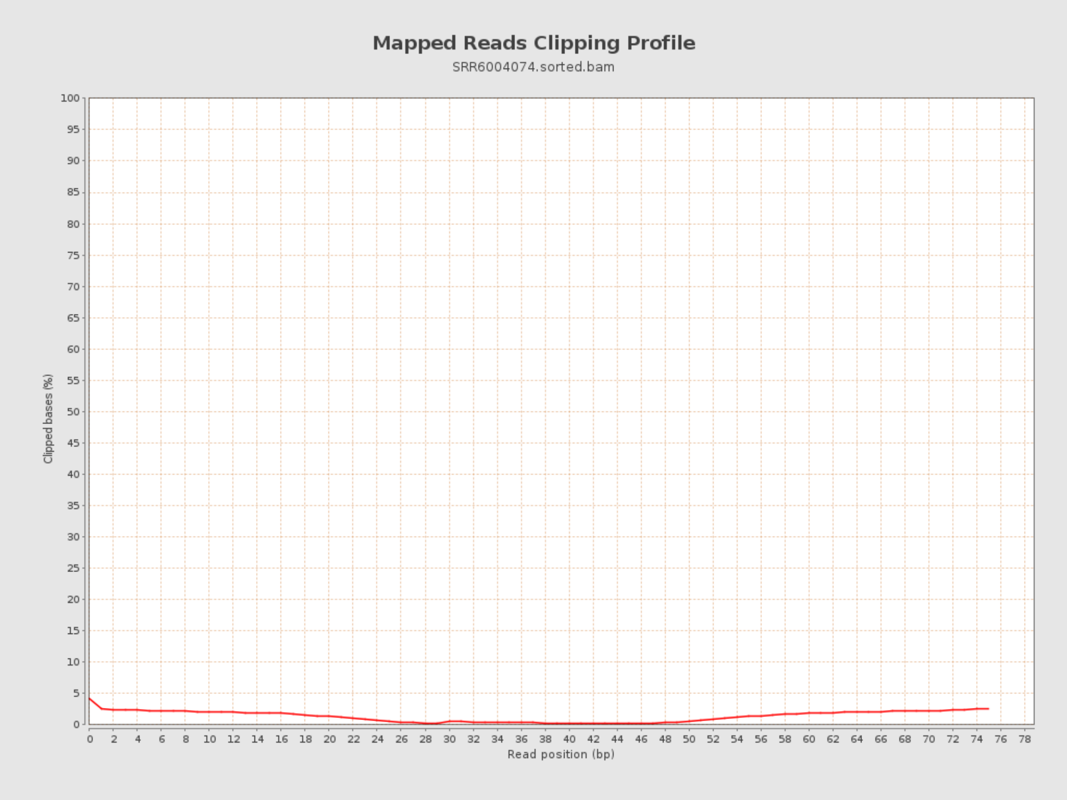
8. Results : Mapped Reads Nucleotide Content



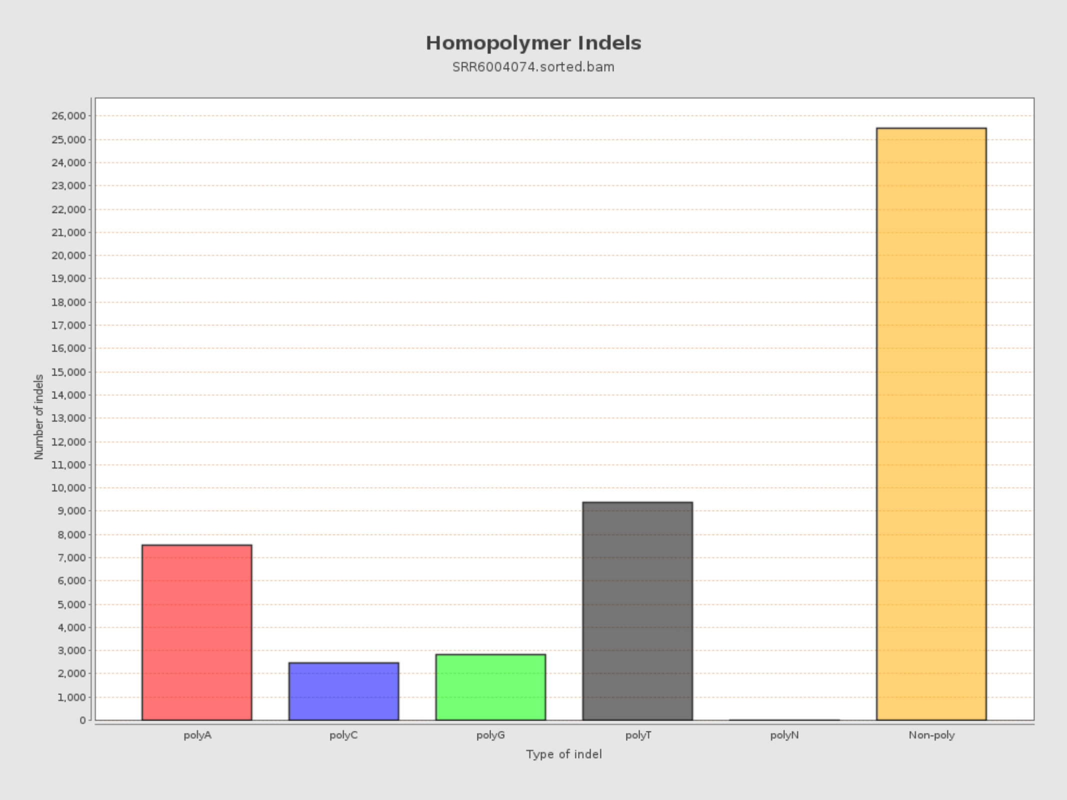
9. Results : Mapped Reads GC-content Distribution



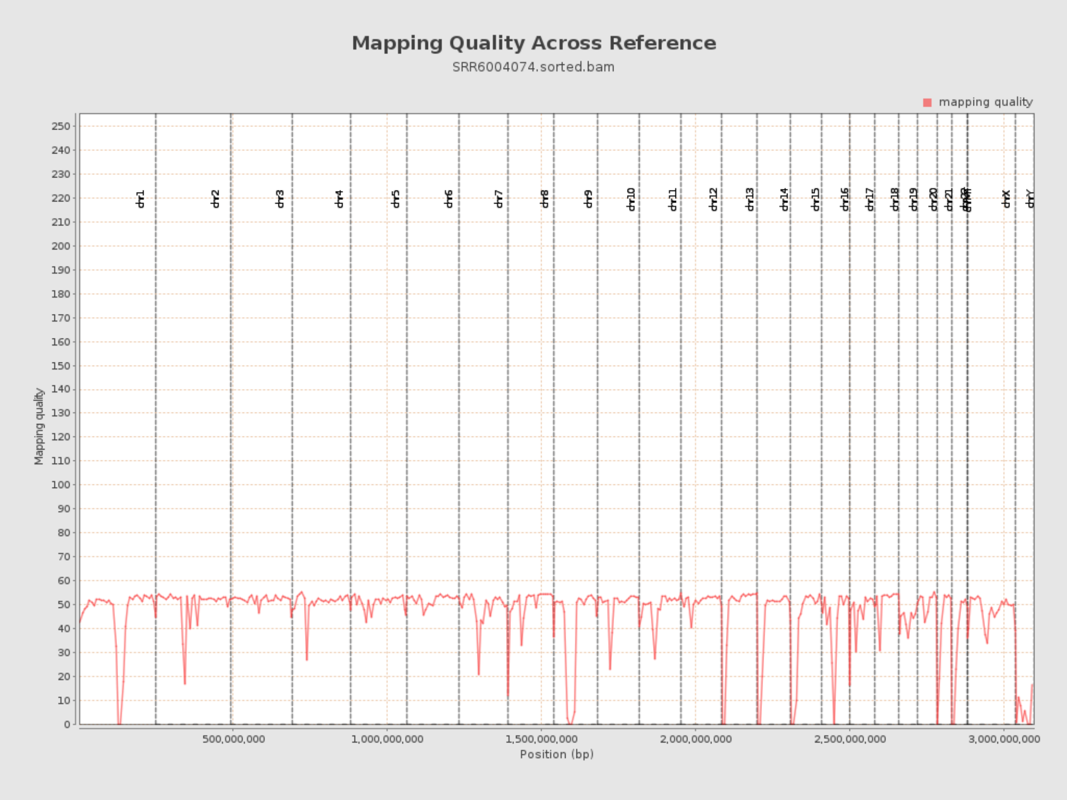
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram