Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:03:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524988.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_SRR10524988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524988.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:02:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,008,634
Mapped reads	3,697,230 / 92.23%
Unmapped reads	311,404 / 7.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,589 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	261,273 / 6.52%
Duplication rate	5.29%
Clipped reads	3,696,013 / 92.2%

2.2. ACGT Content

Number/percentage of A's	56,683,451 / 26.44%
Number/percentage of C's	37,574,300 / 17.52%
Number/percentage of T's	67,317,094 / 31.4%
Number/percentage of G's	52,837,720 / 24.64%
Number/percentage of N's	2,282 / 0%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0693

Standard Deviation	0.5293

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

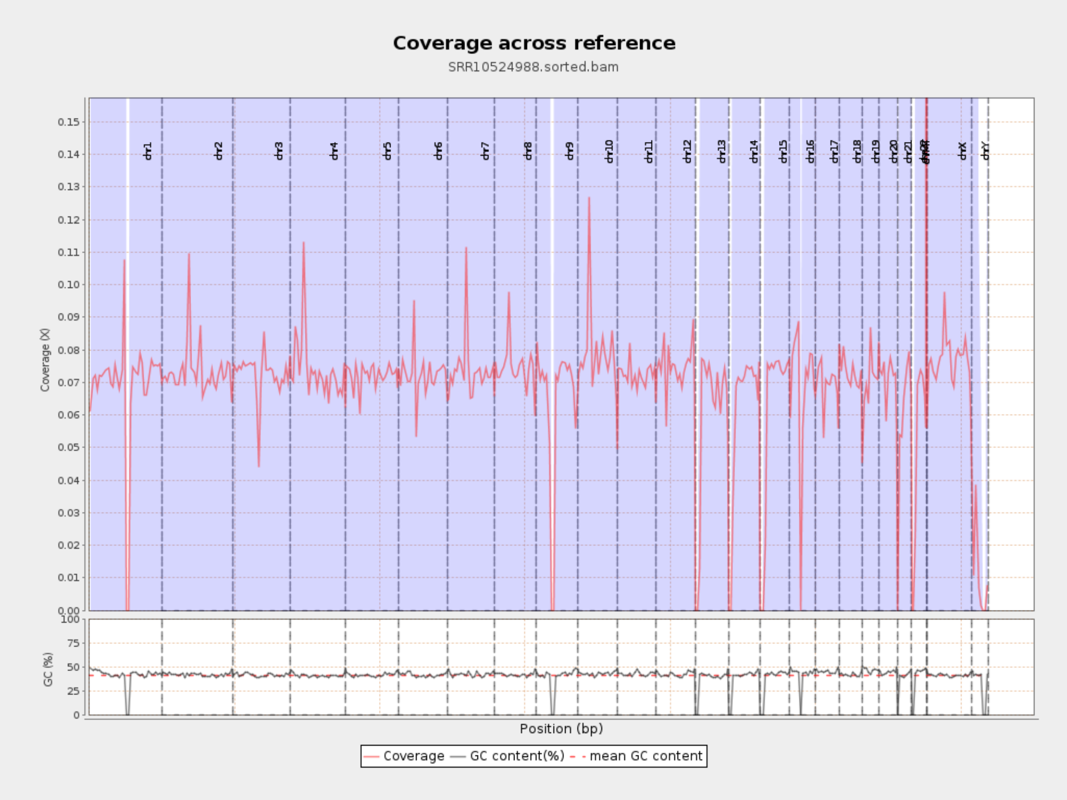
General error rate	0.5%
Mismatches	1,045,388
Insertions	13,877
Mapped reads with at least one insertion	0.37%
Deletions	39,351
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.66%

2.6. Chromosome stats

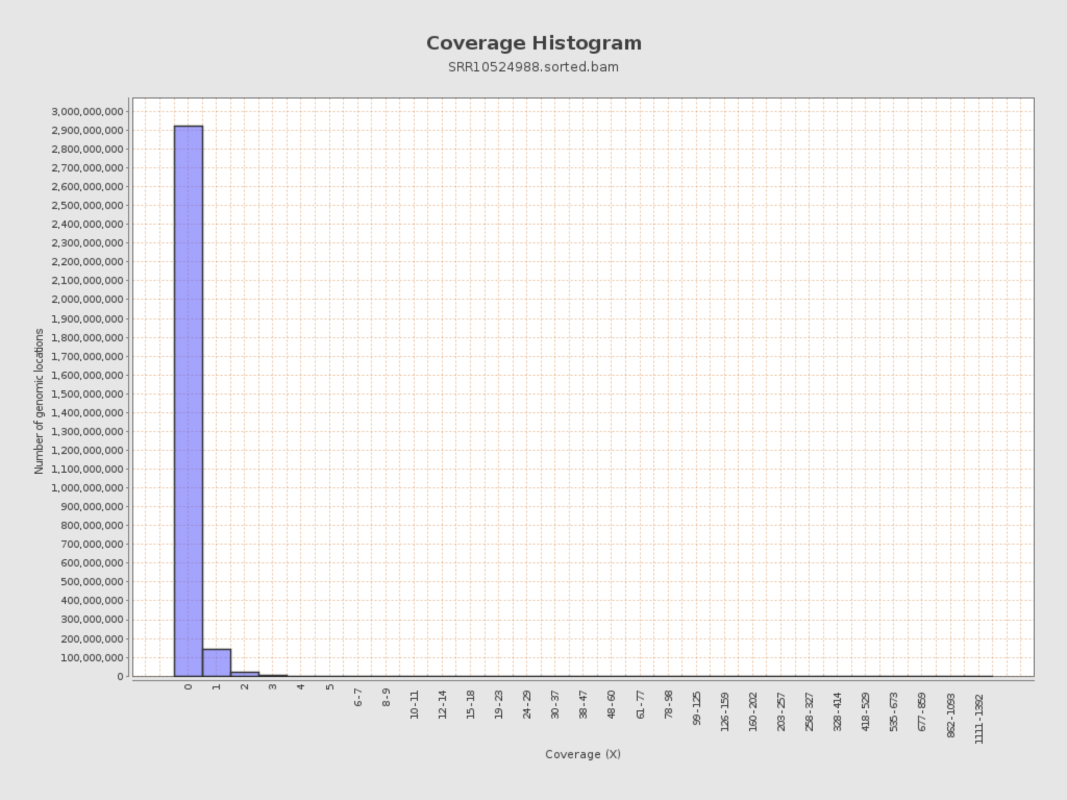
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17077705	0.0685	1.004
chr2	243199373	17933555	0.0737	0.62
chr3	198022430	14322628	0.0723	0.3287
chr4	191154276	14130603	0.0739	0.4041
chr5	180915260	13049886	0.0721	0.3296
chr6	171115067	12408232	0.0725	0.4535
chr7	159138663	11782547	0.074	0.6665

chr8	146364022	10914786	0.0746	0.5606
chr9	141213431	8898384	0.063	0.4497
chr10	135534747	10795211	0.0796	0.5546
chr11	135006516	9719666	0.072	0.4972
chr12	133851895	10011917	0.0748	0.3418
chr13	115169878	6750424	0.0586	0.2993
chr14	107349540	6421220	0.0598	0.3173
chr15	102531392	6171380	0.0602	0.3376
chr16	90354753	6210169	0.0687	0.355
chr17	81195210	5582931	0.0688	0.3752
chr18	78077248	5718116	0.0732	0.8
chr19	59128983	4170169	0.0705	0.6681
chr20	63025520	4481178	0.0711	0.3379
chr21	48129895	2860939	0.0594	0.3615
chr22	51304566	2474778	0.0482	0.2632
chrMT	16571	13482	0.8136	1.0782
chrX	155270560	11929081	0.0768	0.3987
chrY	59373566	652869	0.011	0.2873

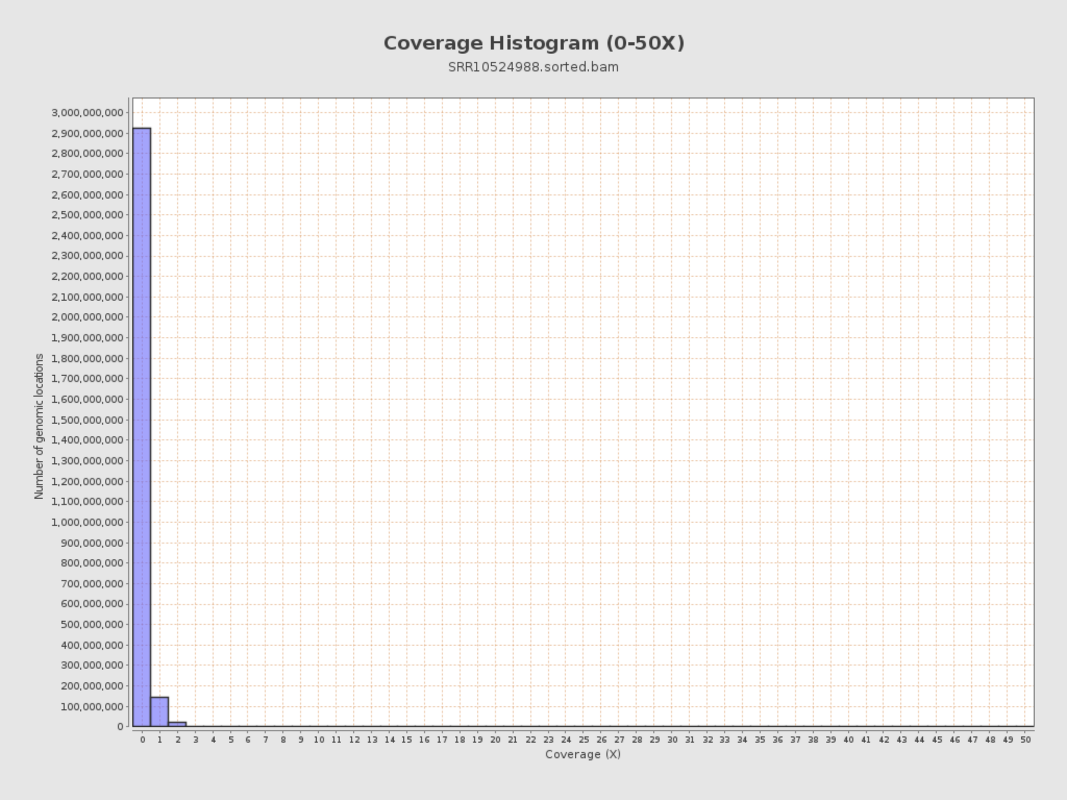
3. Results : Coverage across reference



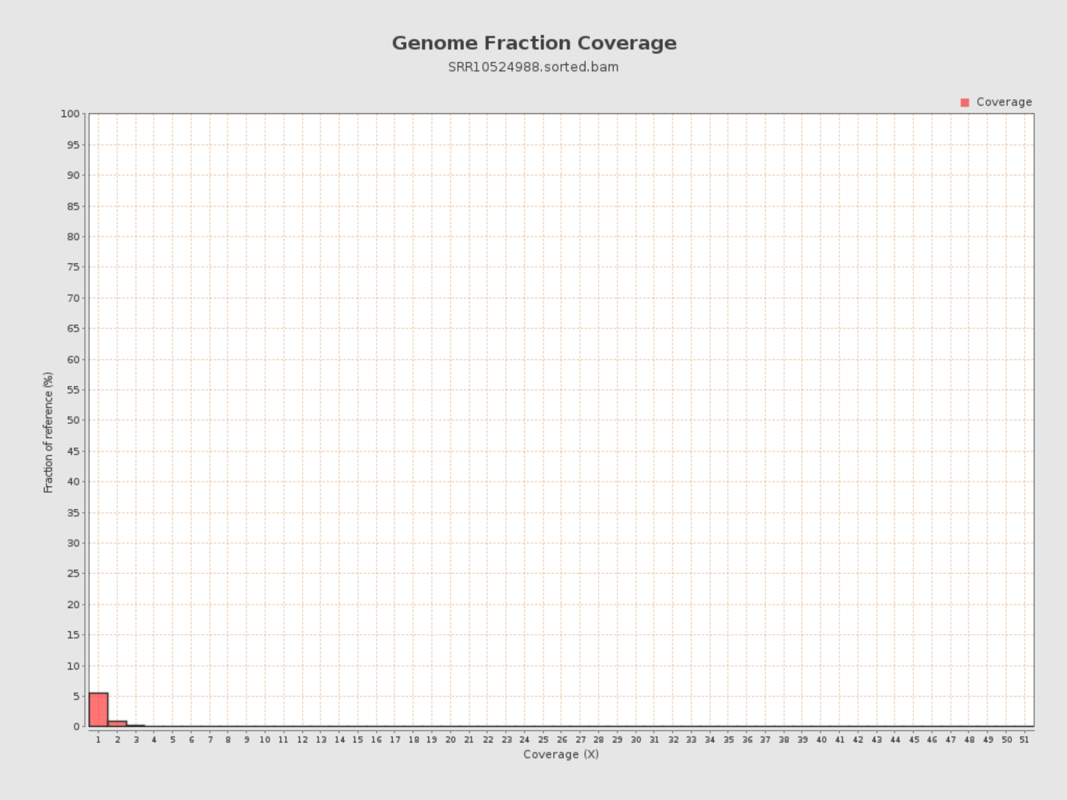
4. Results : Coverage Histogram



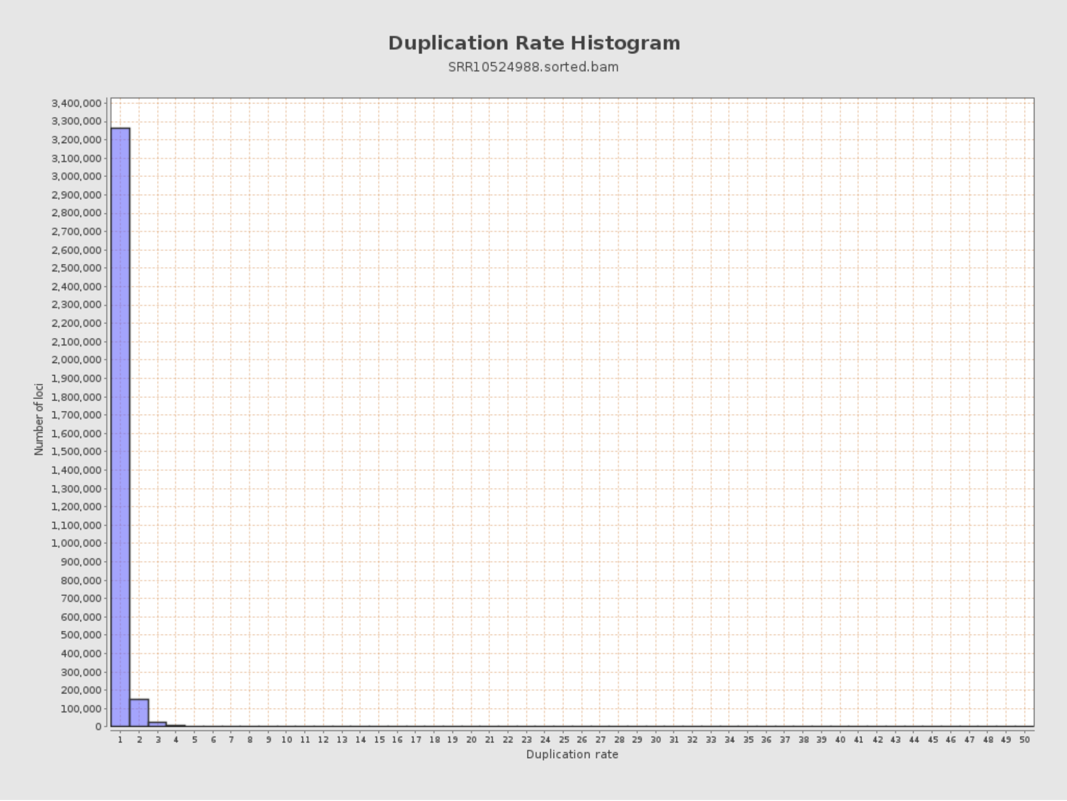
5. Results : Coverage Histogram (0-50X)



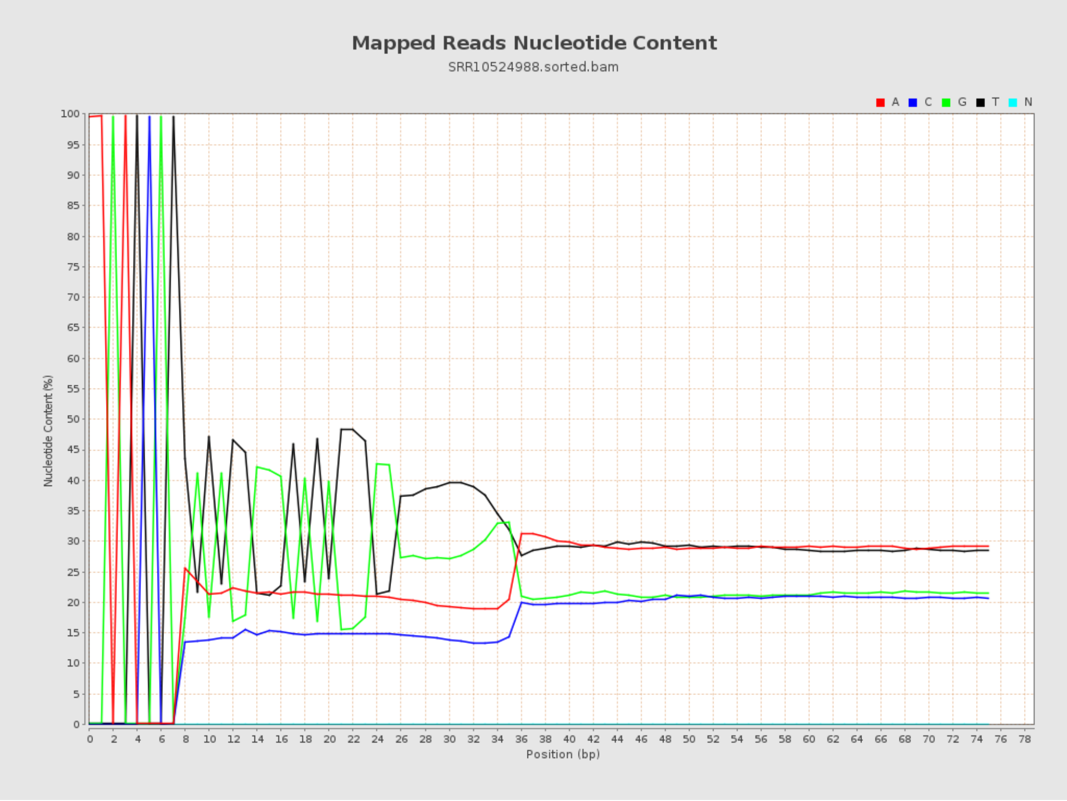
6. Results : Genome Fraction Coverage



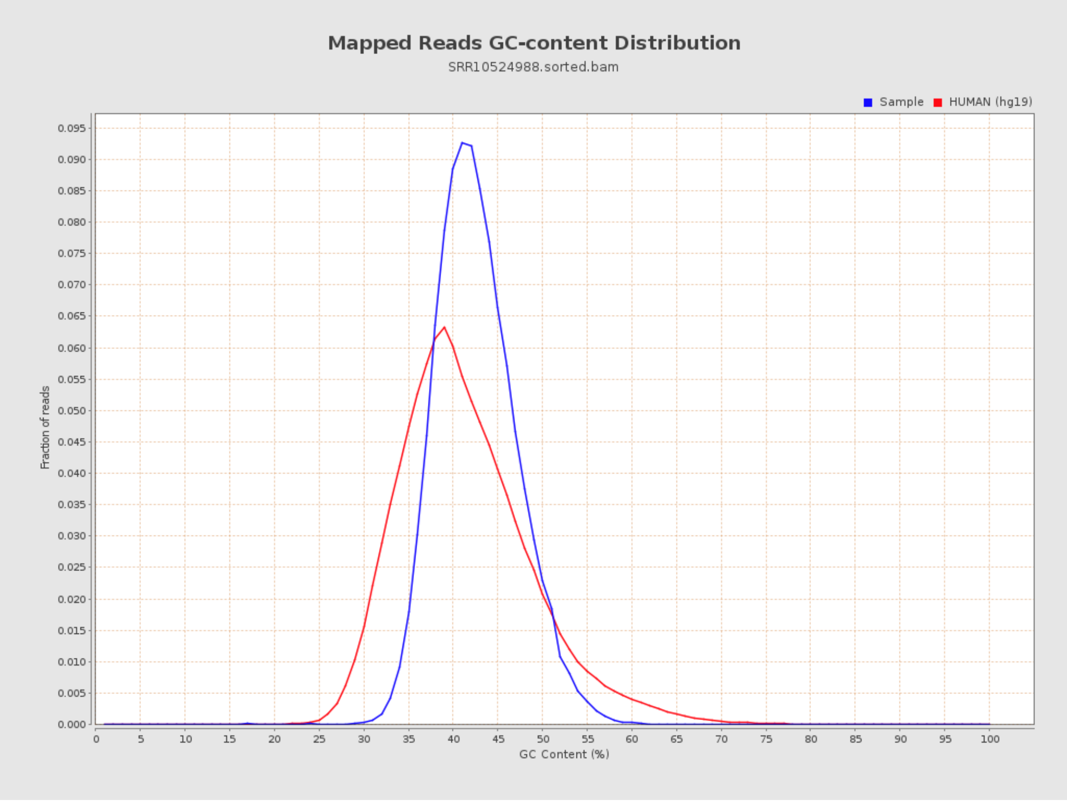
7. Results : Duplication Rate Histogram



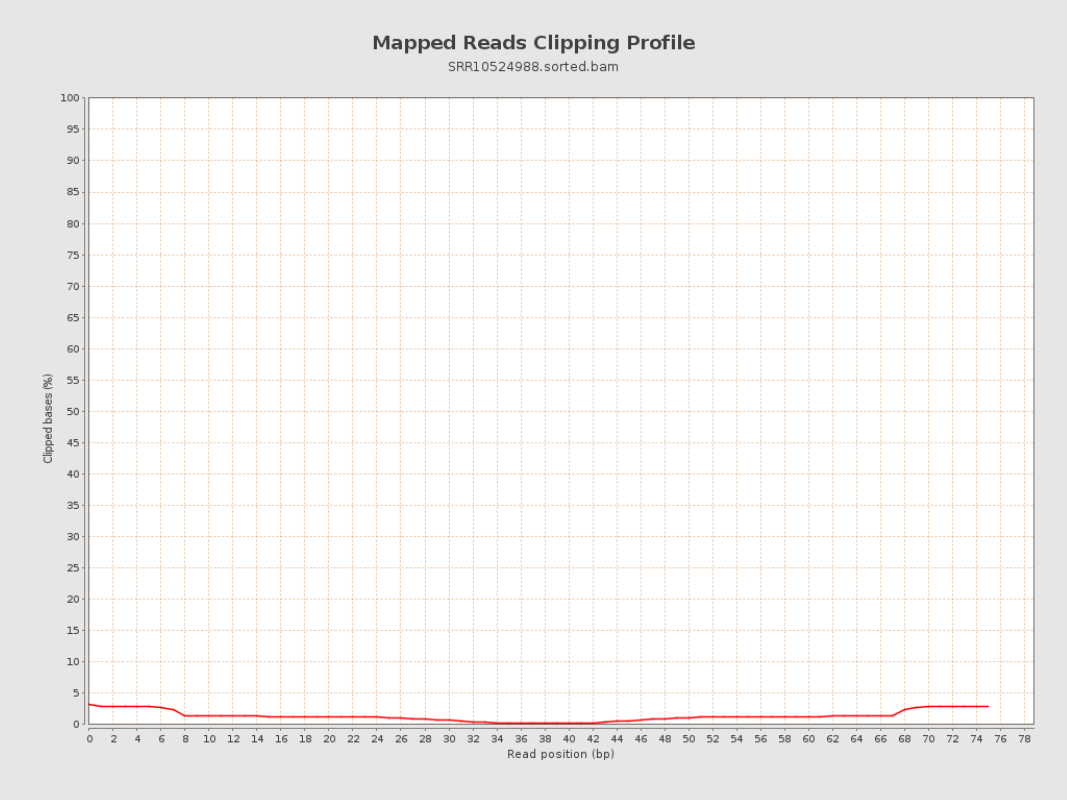
8. Results : Mapped Reads Nucleotide Content



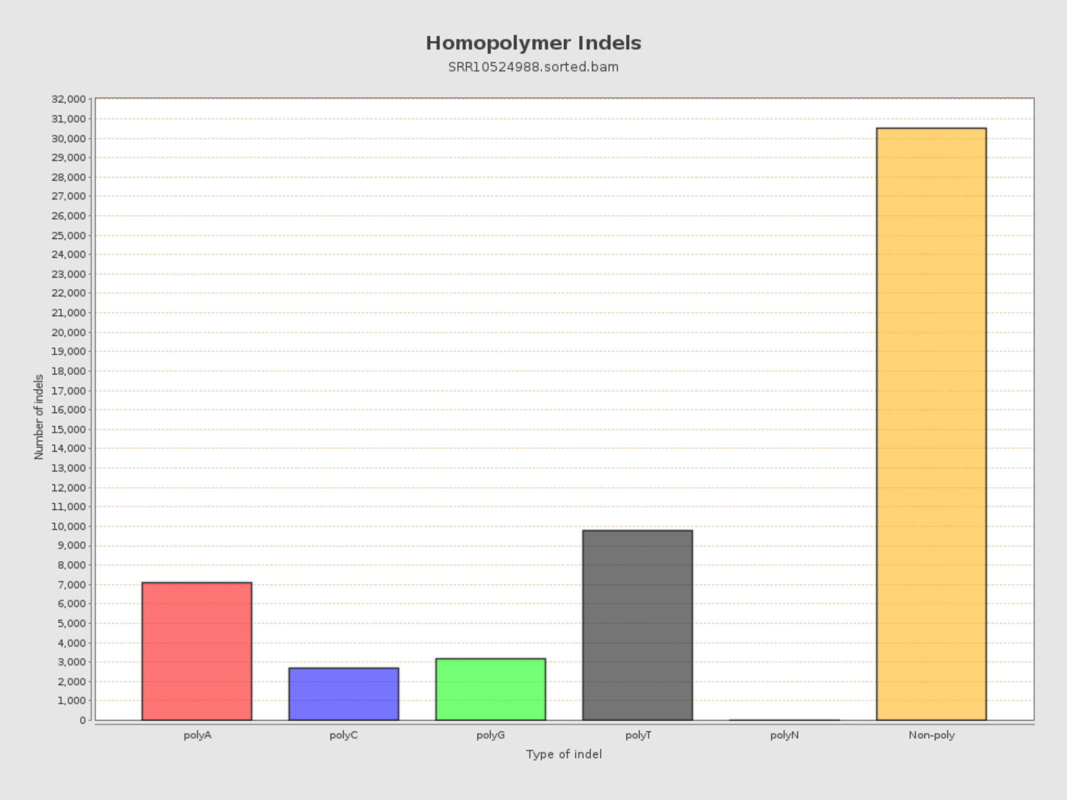
9. Results : Mapped Reads GC-content Distribution



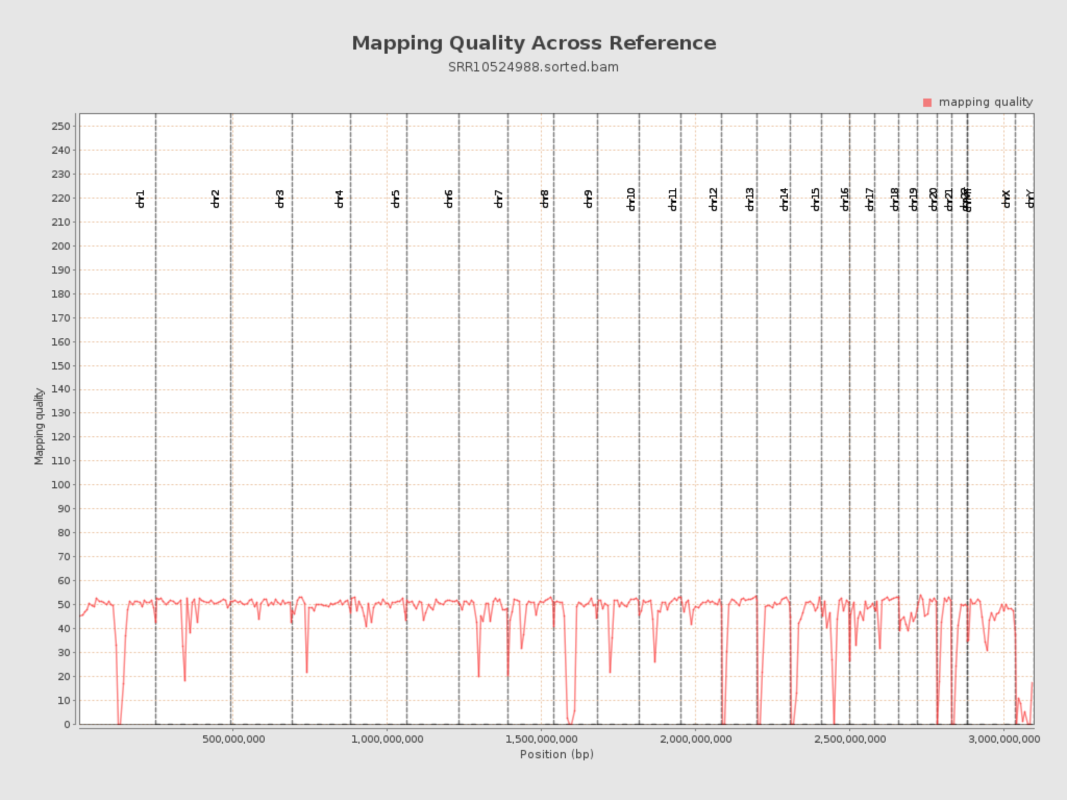
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram