Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:19:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013278.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_SRR6013278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013278.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:19:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,401,280
Mapped reads	3,085,750 / 90.72%
Unmapped reads	315,530 / 9.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,011 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	96,720 / 2.84%
Duplication rate	1.9%
Clipped reads	1,577,183 / 46.37%

2.2. ACGT Content

Number/percentage of A's	56,064,070 / 27.87%
Number/percentage of C's	39,074,594 / 19.42%
Number/percentage of T's	60,210,894 / 29.93%
Number/percentage of G's	45,782,891 / 22.76%
Number/percentage of N's	43,364 / 0.02%
GC Percentage	42.18%

2.3. Coverage

Mean	0.065

Standard Deviation	0.6062

2.4. Mapping Quality

Mean Mapping Quality	43.08

2.5. Mismatches and indels

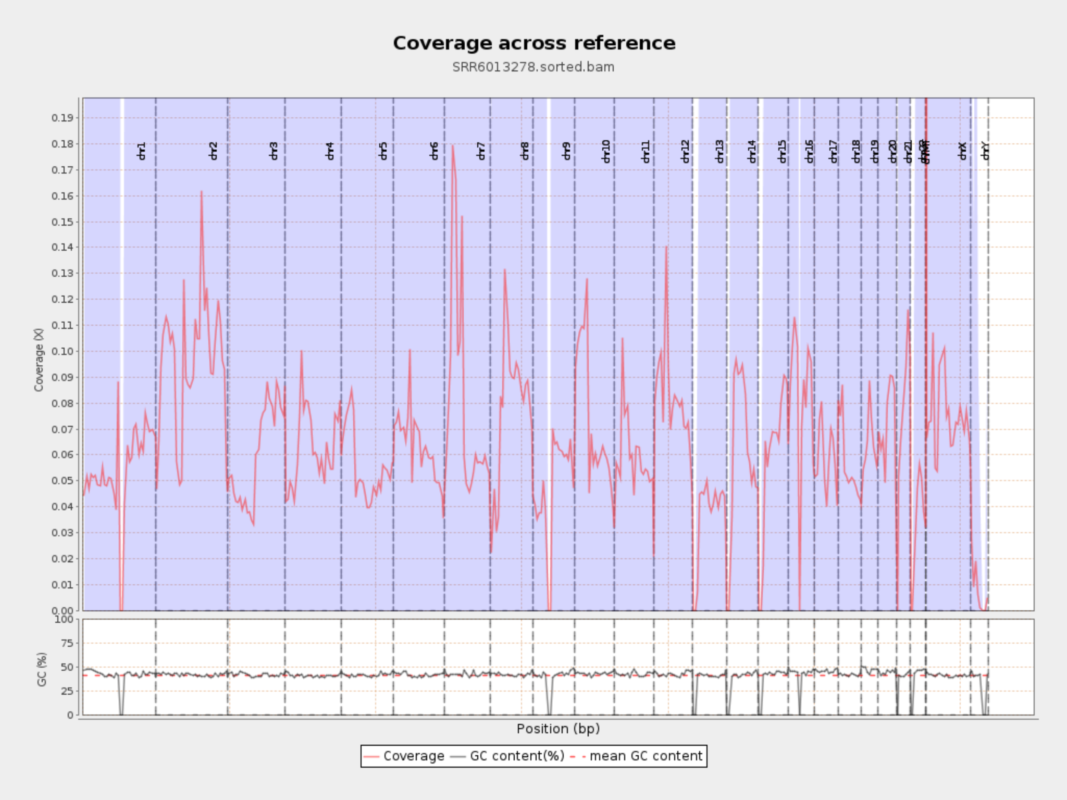
General error rate	0.83%
Mismatches	1,644,135
Insertions	14,534
Mapped reads with at least one insertion	0.47%
Deletions	47,298
Mapped reads with at least one deletion	1.52%
Homopolymer indels	43.44%

2.6. Chromosome stats

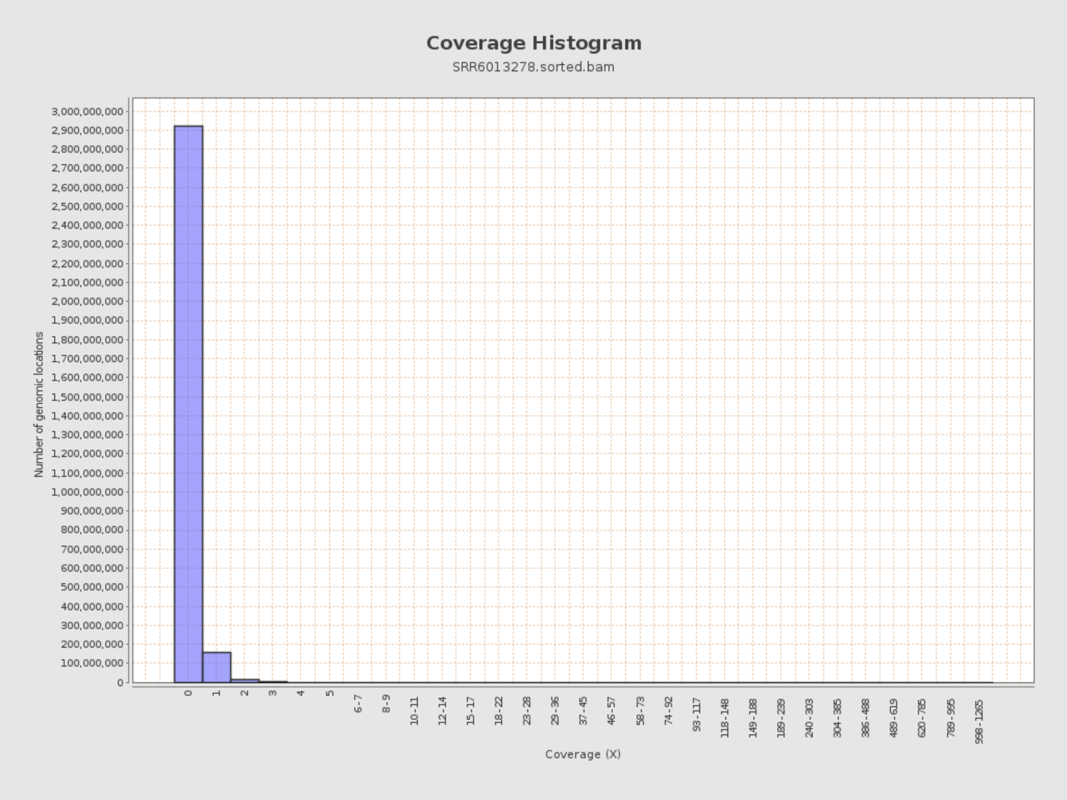
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13474489	0.0541	1.0638
chr2	243199373	23554317	0.0969	0.697
chr3	198022430	11866541	0.0599	0.2712
chr4	191154276	12032160	0.0629	0.2916
chr5	180915260	10019917	0.0554	0.264
chr6	171115067	10895854	0.0637	0.4515
chr7	159138663	12516928	0.0787	1.3555

chr8	146364022	11495198	0.0785	0.4893
chr9	141213431	6718445	0.0476	0.4763
chr10	135534747	10031807	0.074	0.6796
chr11	135006516	8050835	0.0596	0.4328
chr12	133851895	11048584	0.0825	0.3263
chr13	115169878	4192926	0.0364	0.2142
chr14	107349540	6660740	0.062	0.3339
chr15	102531392	5920189	0.0577	0.2675
chr16	90354753	7266385	0.0804	0.3546
chr17	81195210	4783269	0.0589	0.347
chr18	78077248	4443865	0.0569	0.9129
chr19	59128983	3790658	0.0641	0.8124
chr20	63025520	4610815	0.0732	0.3112
chr21	48129895	3657824	0.076	0.3363
chr22	51304566	1706994	0.0333	0.1975
chrMT	16571	361177	21.7957	14.439
chrX	155270560	11705286	0.0754	0.3666
chrY	59373566	451996	0.0076	0.136

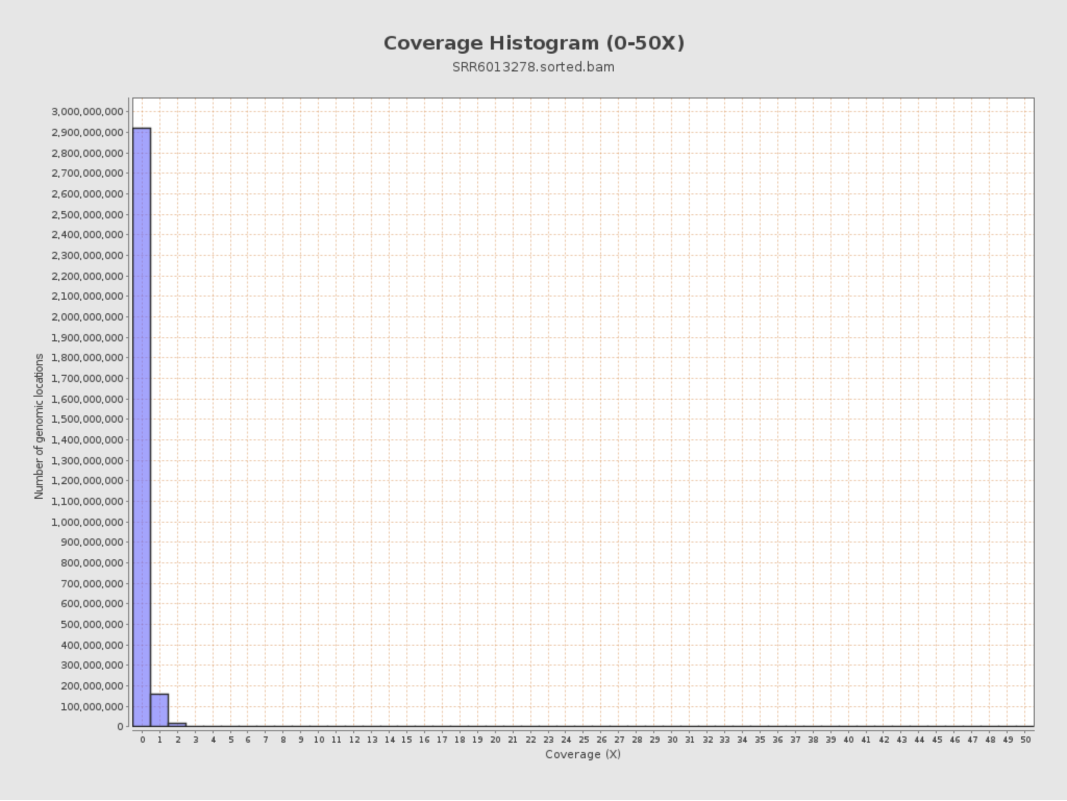
3. Results : Coverage across reference



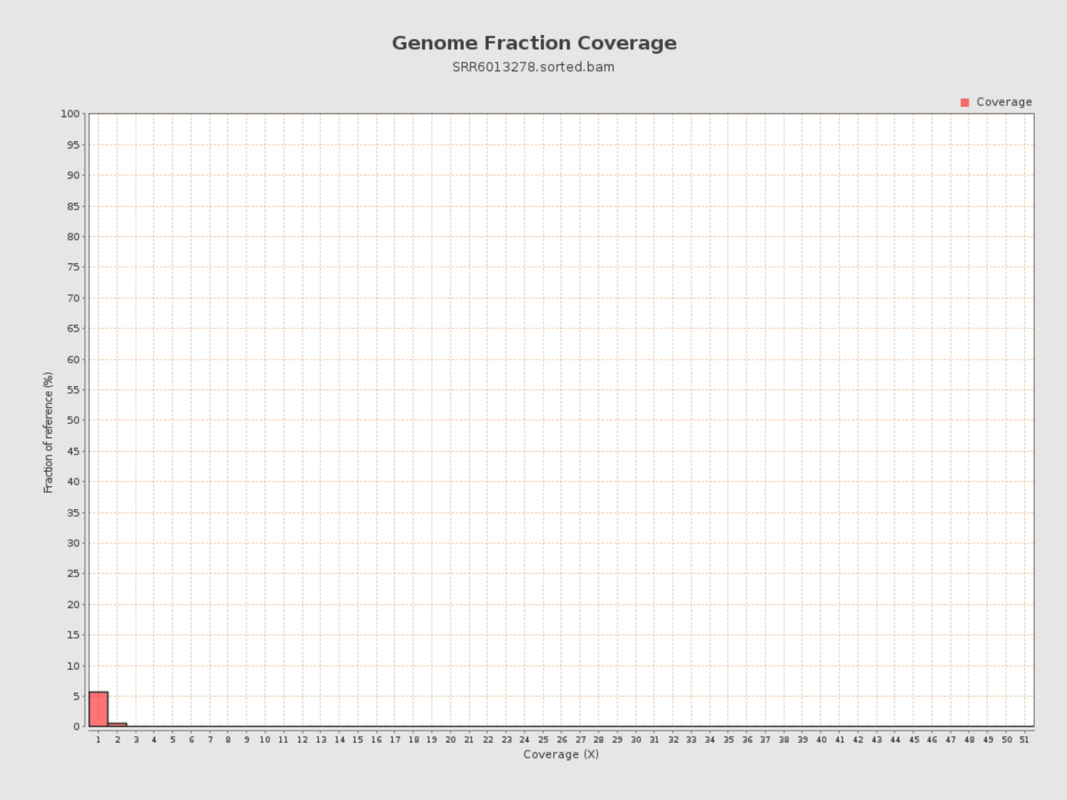
4. Results : Coverage Histogram



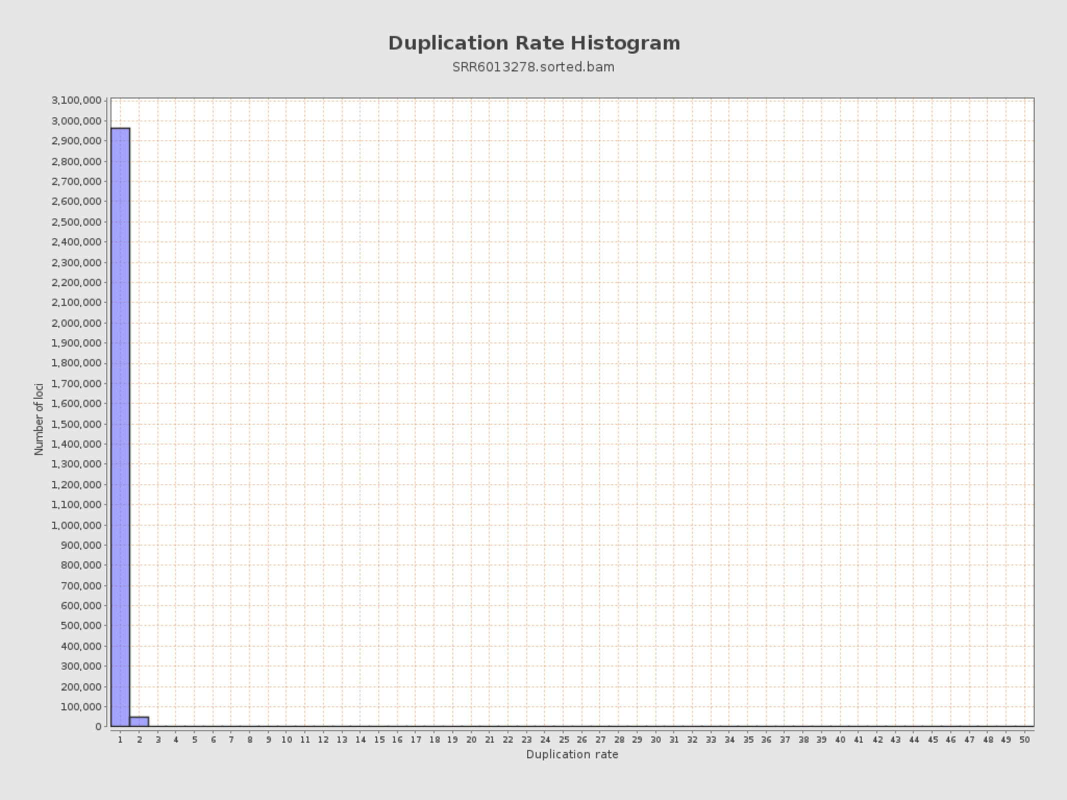
5. Results : Coverage Histogram (0-50X)



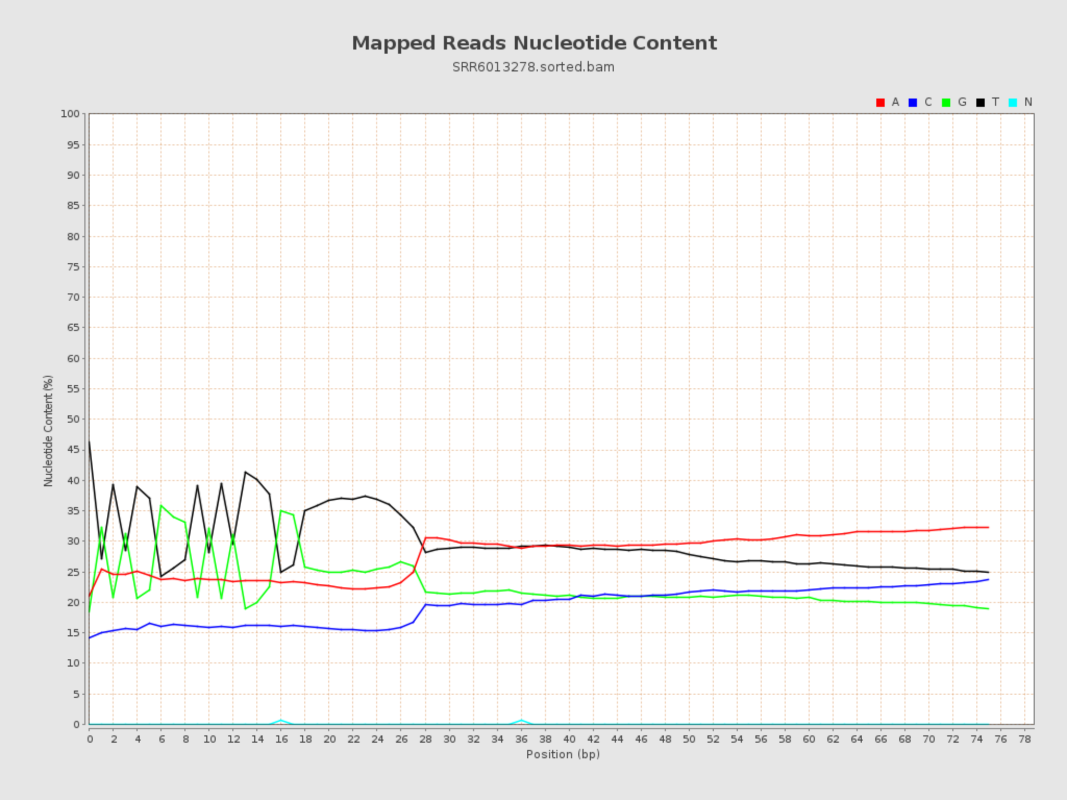
6. Results : Genome Fraction Coverage



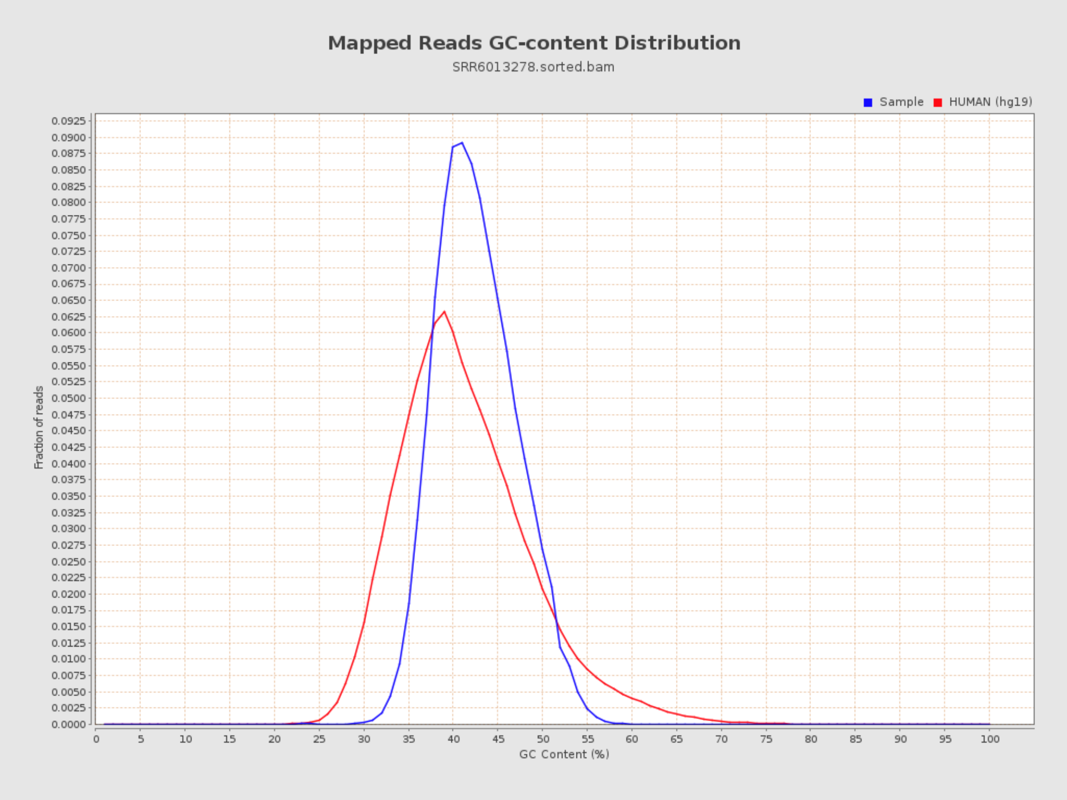
7. Results : Duplication Rate Histogram



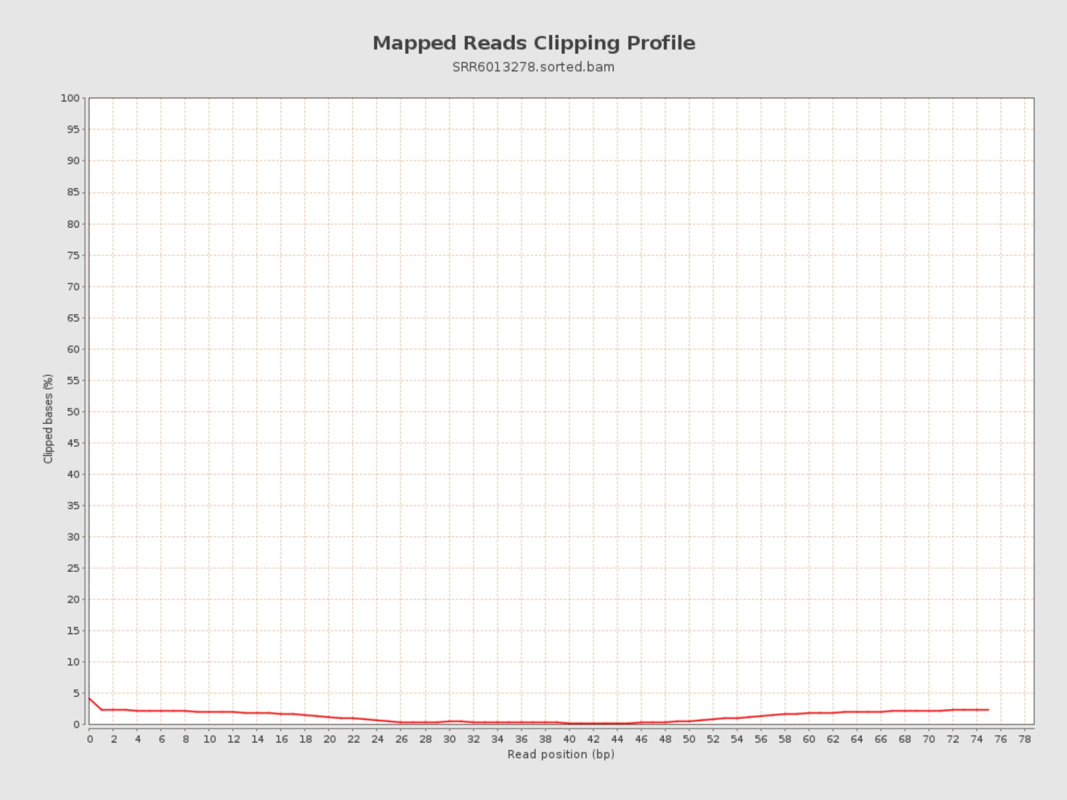
8. Results : Mapped Reads Nucleotide Content



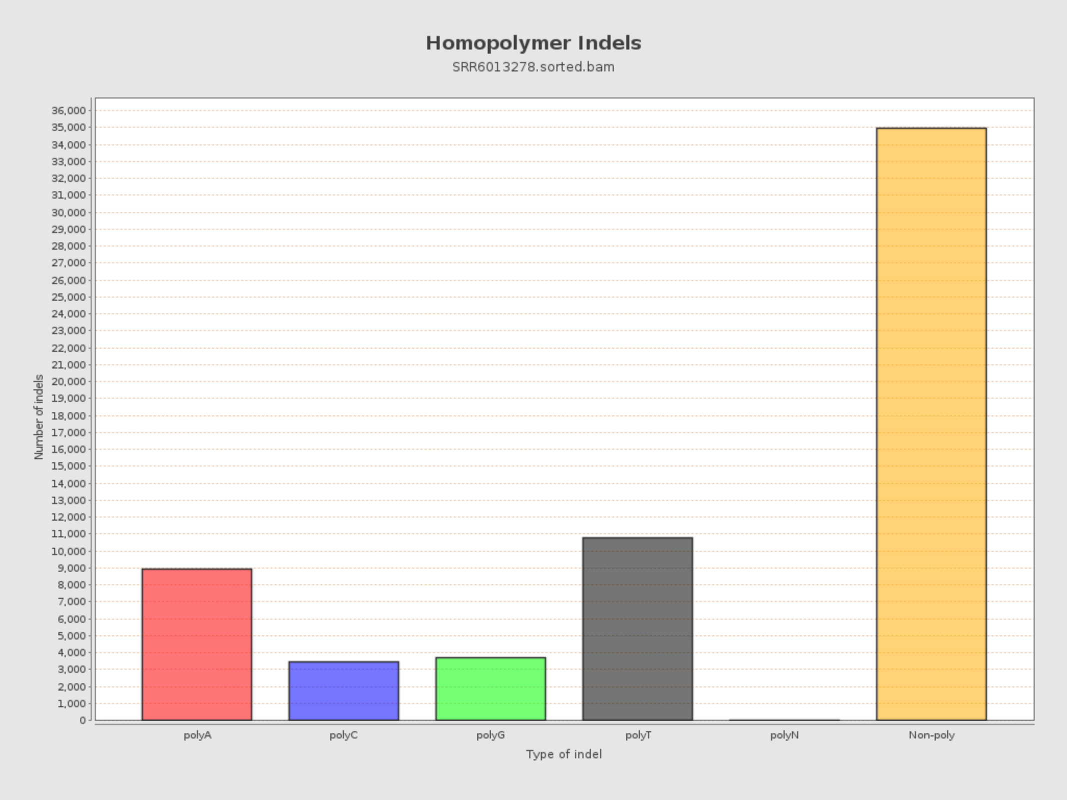
9. Results : Mapped Reads GC-content Distribution



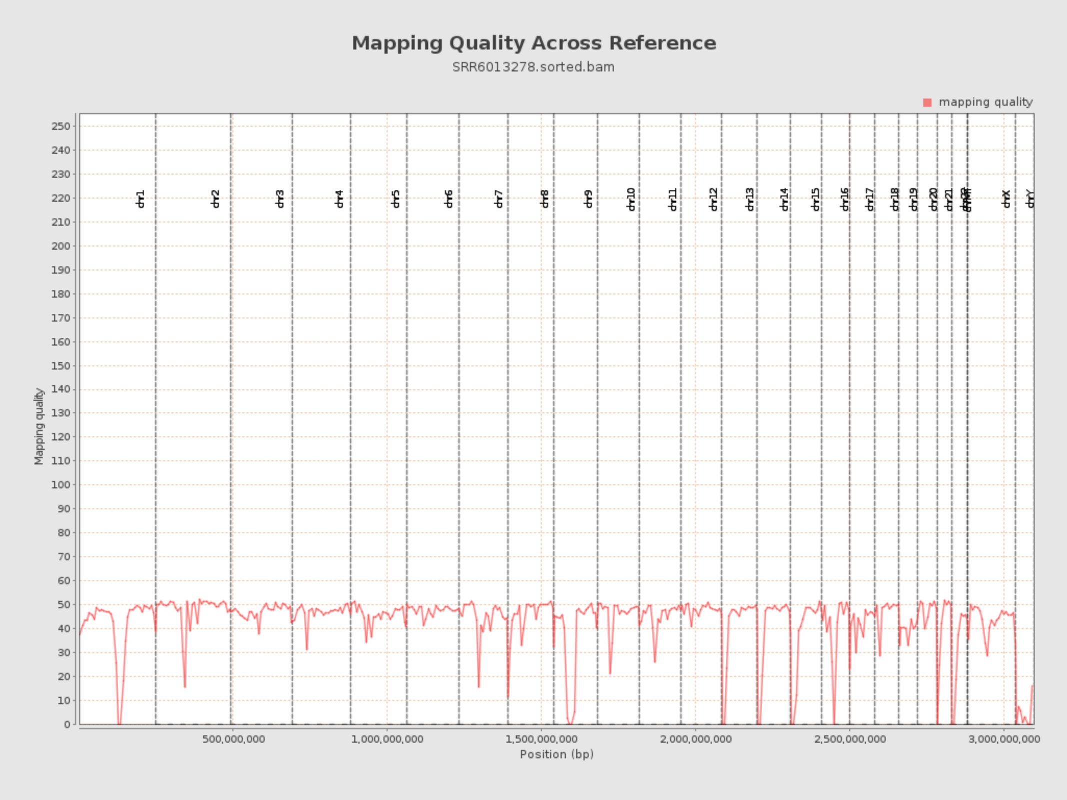
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram