Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:56:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004072.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_SRR6004072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:56:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,206,891
Mapped reads	1,993,233 / 90.32%
Unmapped reads	213,658 / 9.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,498 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	105,751 / 4.79%
Duplication rate	4.24%
Clipped reads	828,308 / 37.53%

2.2. ACGT Content

Number/percentage of A's	37,311,402 / 27.82%
Number/percentage of C's	24,750,030 / 18.46%
Number/percentage of T's	42,675,967 / 31.82%
Number/percentage of G's	29,356,421 / 21.89%
Number/percentage of N's	9,926 / 0.01%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.3994

2.4. Mapping Quality

Mean Mapping Quality	46.78

2.5. Mismatches and indels

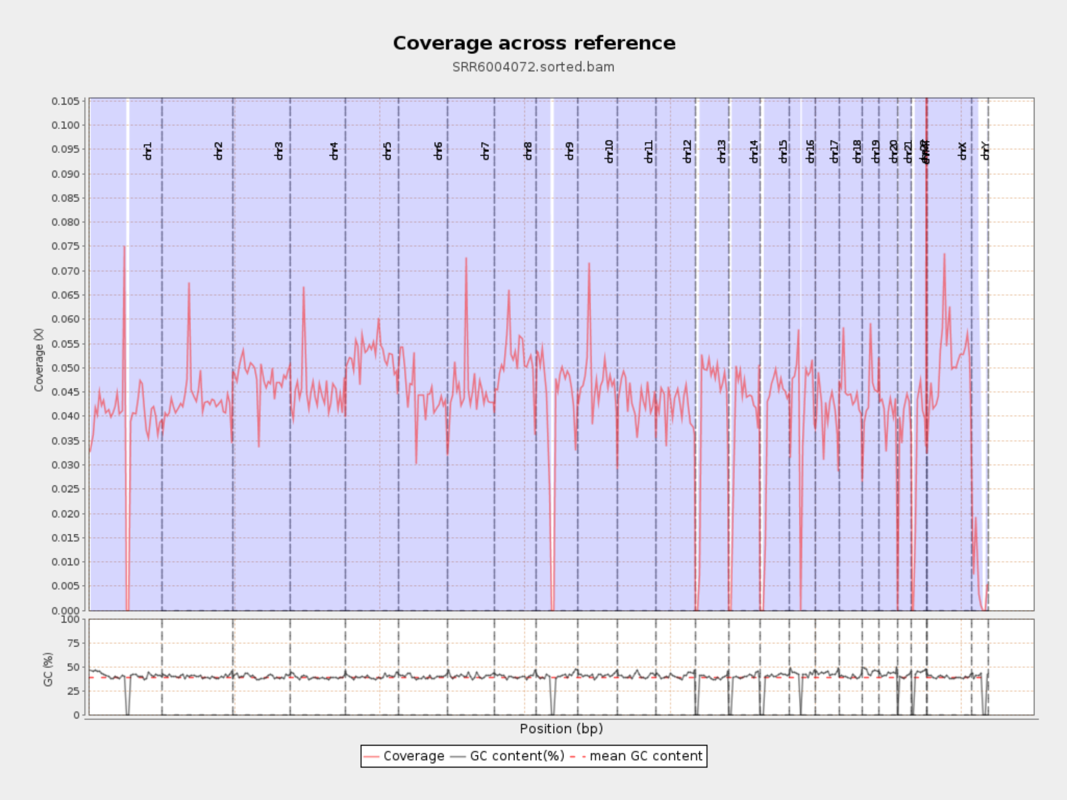
General error rate	0.86%
Mismatches	1,140,469
Insertions	9,746
Mapped reads with at least one insertion	0.48%
Deletions	33,368
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.37%

2.6. Chromosome stats

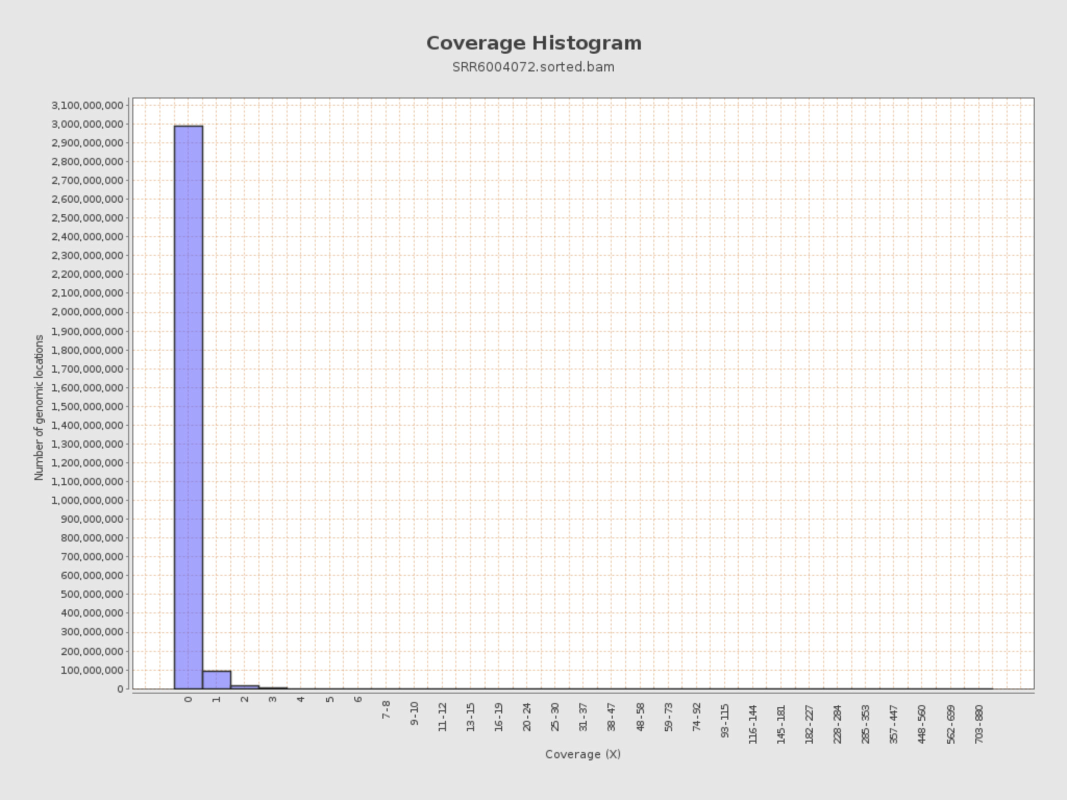
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9809367	0.0394	0.7812
chr2	243199373	10572674	0.0435	0.4142
chr3	198022430	9521063	0.0481	0.2588
chr4	191154276	8614606	0.0451	0.2728
chr5	180915260	9532657	0.0527	0.2732
chr6	171115067	7641409	0.0447	0.2766
chr7	159138663	7284802	0.0458	0.4902

chr8	146364022	7512578	0.0513	0.513
chr9	141213431	5790418	0.041	0.3529
chr10	135534747	6462848	0.0477	0.3557
chr11	135006516	5841276	0.0433	0.3375
chr12	133851895	5641836	0.0421	0.2473
chr13	115169878	4670906	0.0406	0.2428
chr14	107349540	4026945	0.0375	0.2527
chr15	102531392	3790988	0.037	0.2277
chr16	90354753	3850313	0.0426	0.2698
chr17	81195210	3275109	0.0403	0.2589
chr18	78077248	3537187	0.0453	0.729
chr19	59128983	2652937	0.0449	0.4986
chr20	63025520	2549896	0.0405	0.2455
chr21	48129895	1752869	0.0364	0.2486
chr22	51304566	1519993	0.0296	0.2012
chrMT	16571	3513	0.212	0.5246
chrX	155270560	7945904	0.0512	0.2933
chrY	59373566	360104	0.0061	0.1442

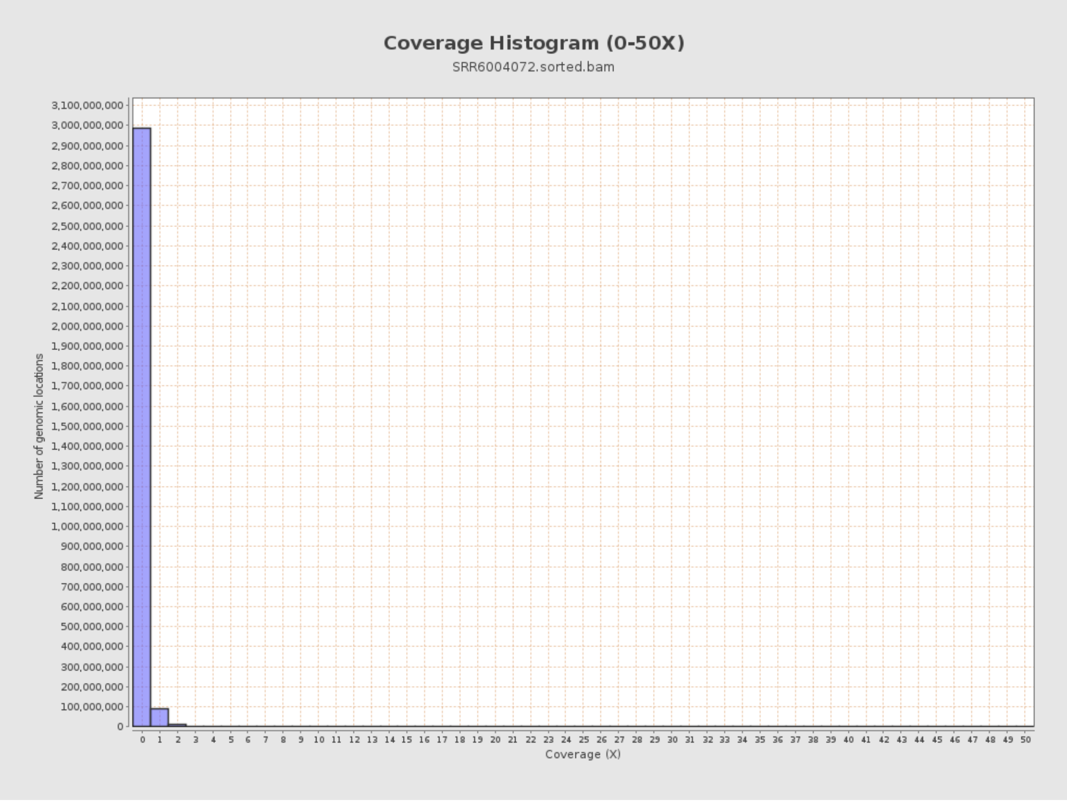
3. Results : Coverage across reference



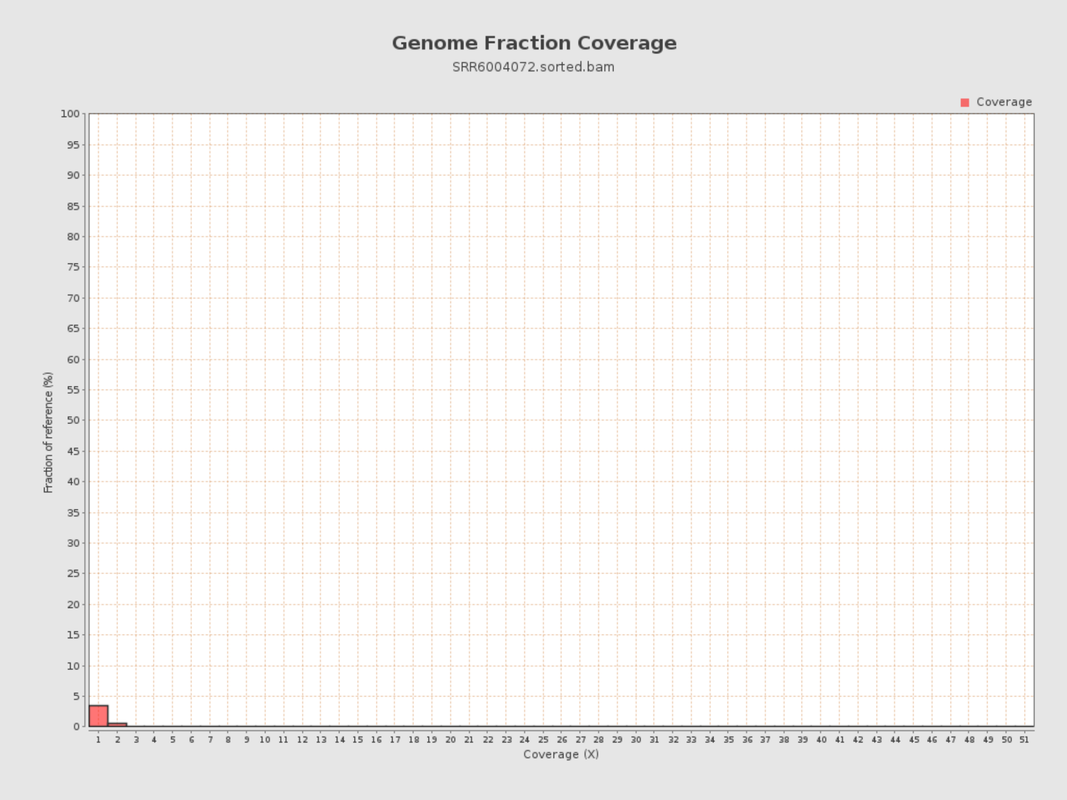
4. Results : Coverage Histogram



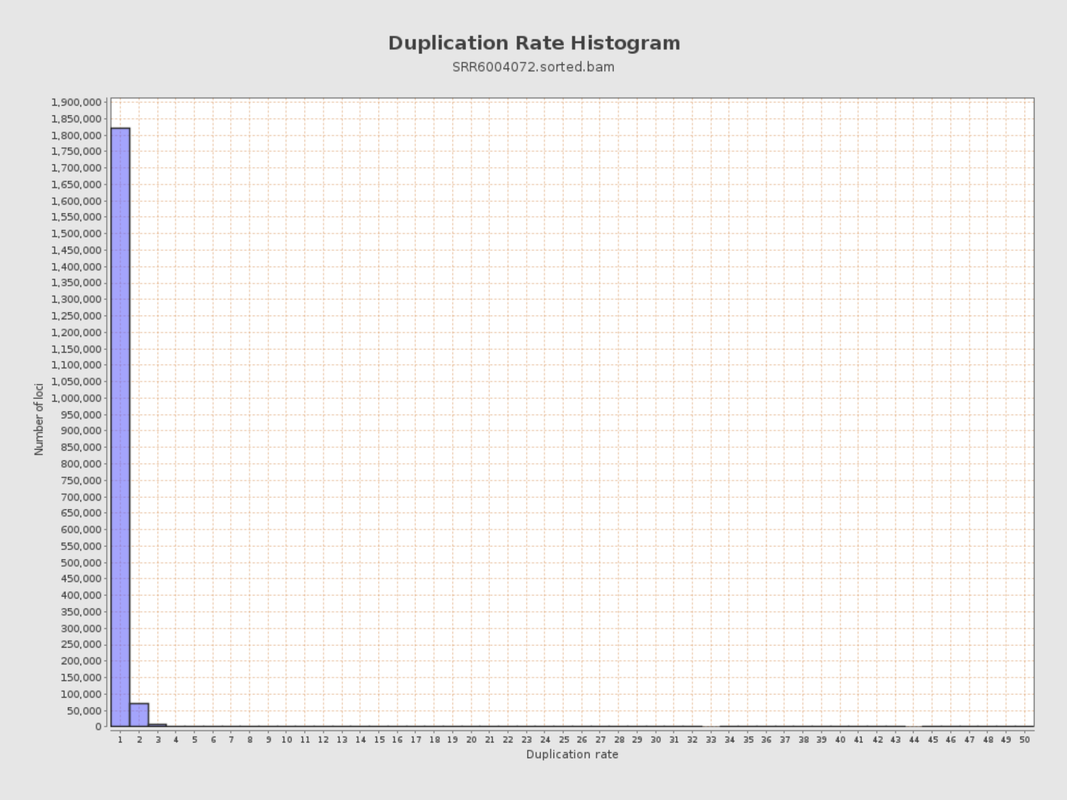
5. Results : Coverage Histogram (0-50X)



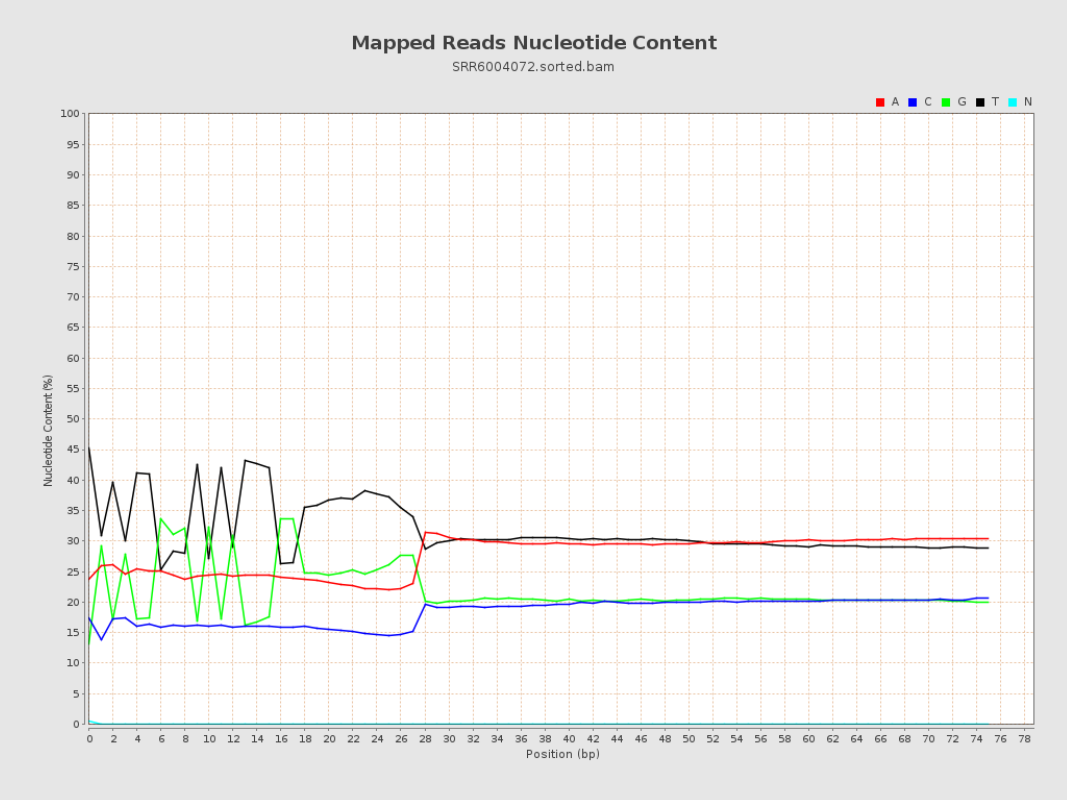
6. Results : Genome Fraction Coverage



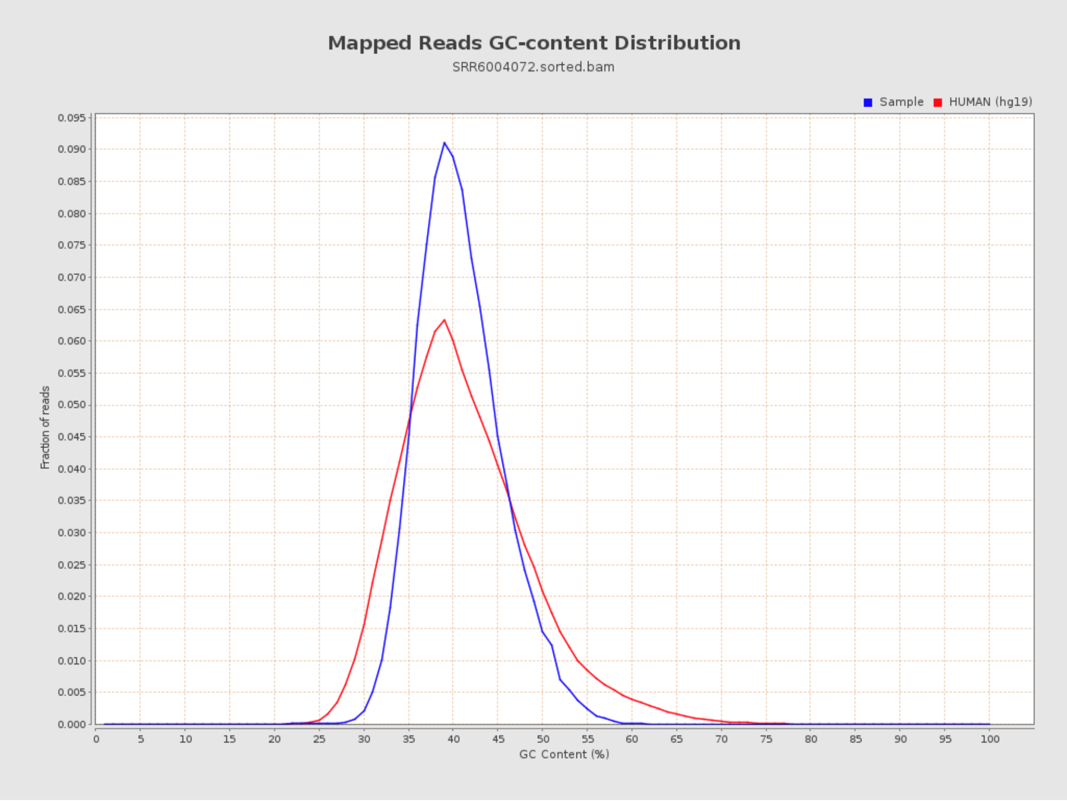
7. Results : Duplication Rate Histogram



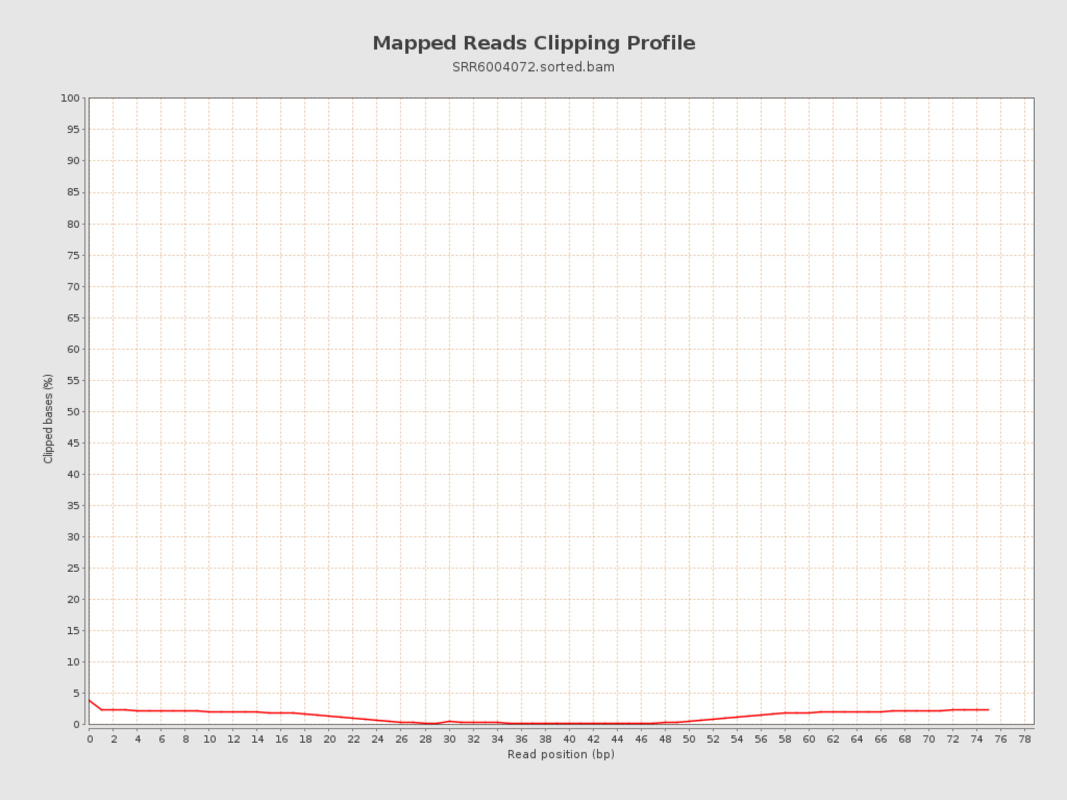
8. Results : Mapped Reads Nucleotide Content



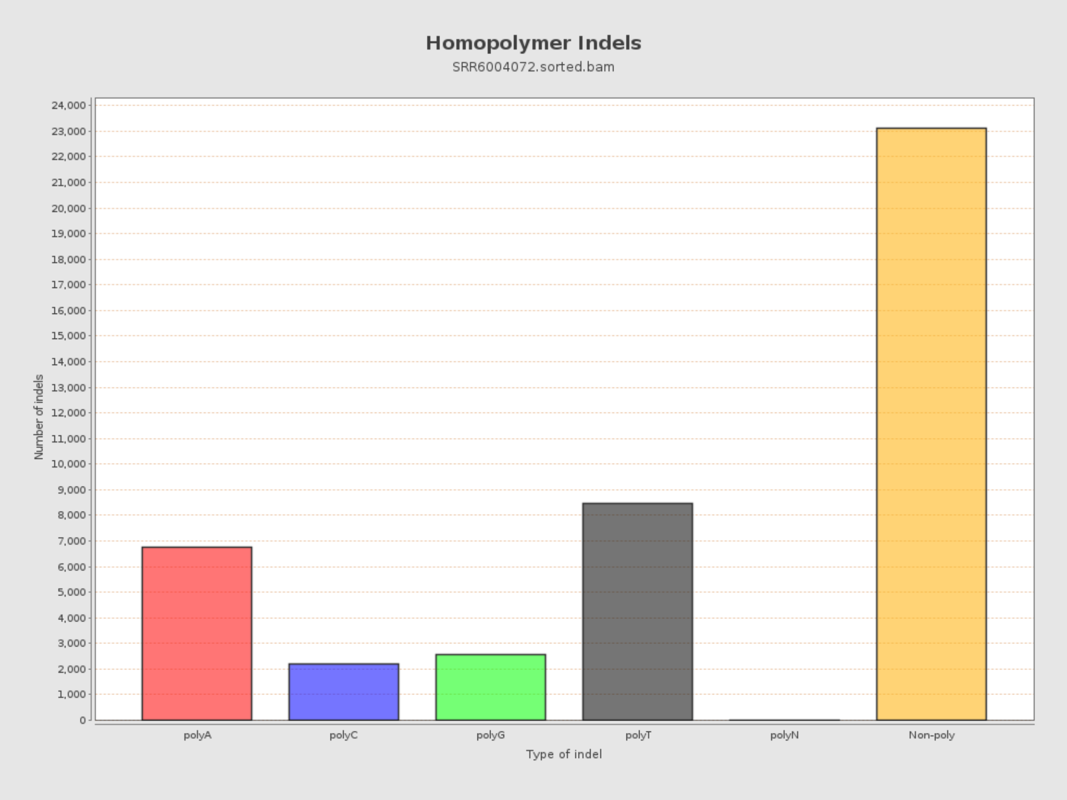
9. Results : Mapped Reads GC-content Distribution



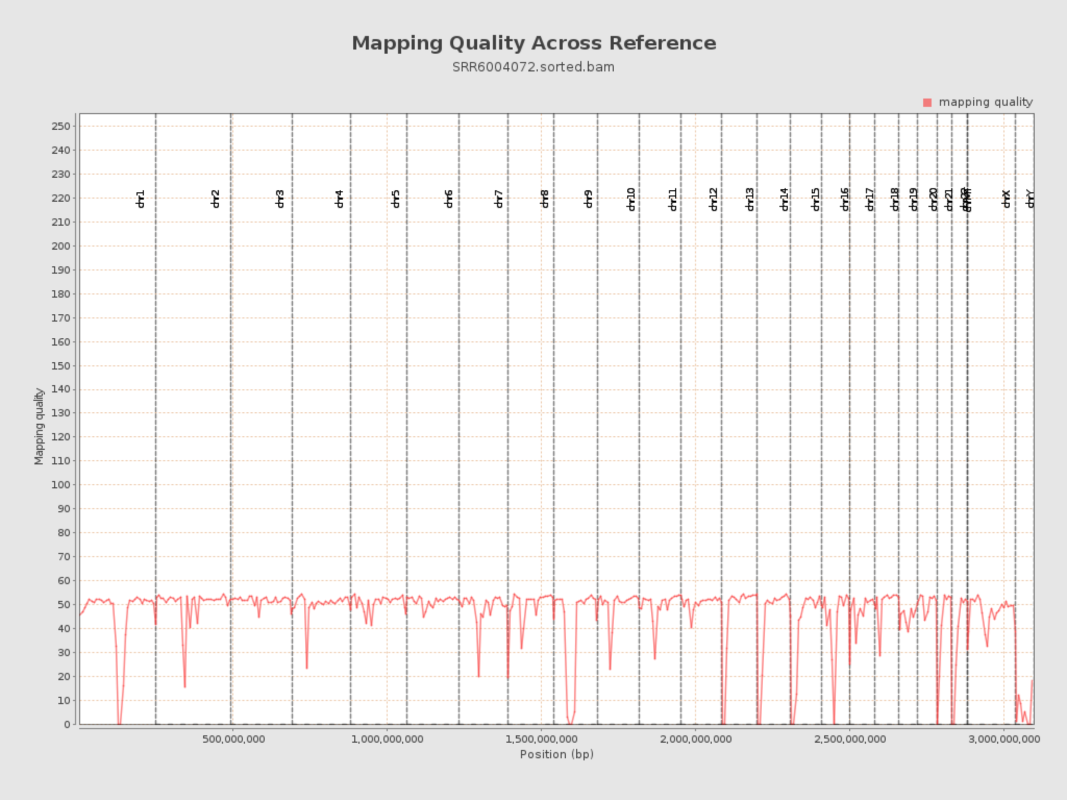
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram