Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:38:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004084.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_SRR6004084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:38:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,263,413
Mapped reads	3,884,074 / 91.1%
Unmapped reads	379,339 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,356 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	519,354 / 12.18%
Duplication rate	9.89%
Clipped reads	1,804,947 / 42.34%

2.2. ACGT Content

Number/percentage of A's	72,378,016 / 27.97%
Number/percentage of C's	48,513,261 / 18.74%
Number/percentage of T's	81,035,696 / 31.31%
Number/percentage of G's	56,615,913 / 21.88%
Number/percentage of N's	270,274 / 0.1%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0836

Standard Deviation	0.6577

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Mismatches and indels

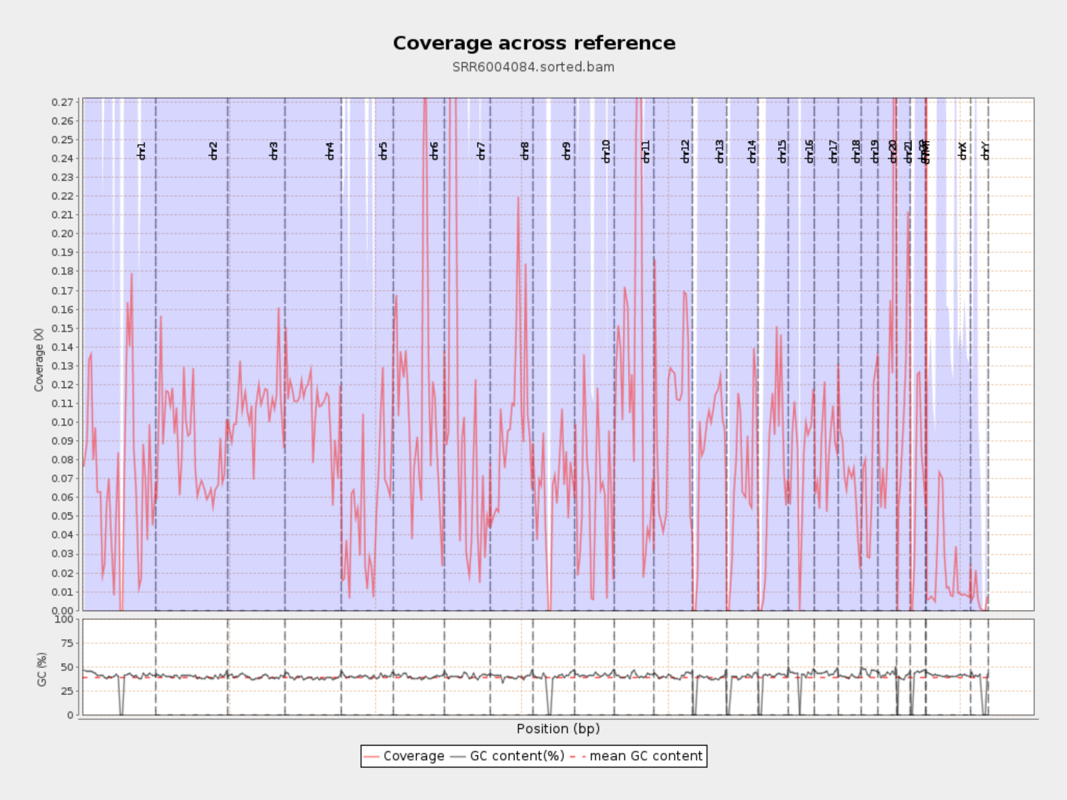
General error rate	0.81%
Mismatches	2,068,019
Insertions	17,930
Mapped reads with at least one insertion	0.46%
Deletions	63,429
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.41%

2.6. Chromosome stats

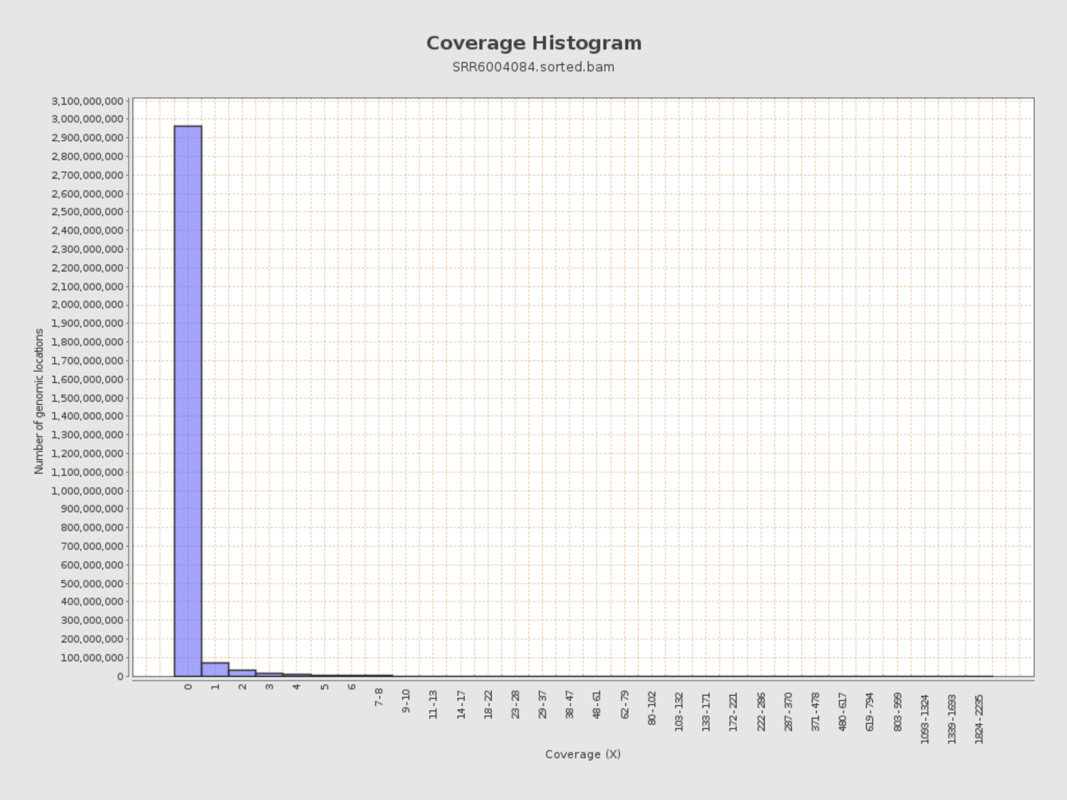
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17403180	0.0698	0.6361
chr2	243199373	21256509	0.0874	0.7638
chr3	198022430	21496356	0.1086	0.5596
chr4	191154276	20716435	0.1084	0.5773
chr5	180915260	9598203	0.0531	0.3869
chr6	171115067	19367636	0.1132	0.6149
chr7	159138663	16776055	0.1054	0.7743

chr8	146364022	14652384	0.1001	1.404
chr9	141213431	8635466	0.0612	0.5234
chr10	135534747	7925632	0.0585	0.4991
chr11	135006516	17406432	0.1289	0.8671
chr12	133851895	14275954	0.1067	0.5627
chr13	115169878	9842710	0.0855	0.5008
chr14	107349540	7636855	0.0711	0.4855
chr15	102531392	7224991	0.0705	0.4503
chr16	90354753	7211484	0.0798	0.4943
chr17	81195210	6726081	0.0828	0.5506
chr18	78077248	5523754	0.0707	0.9307
chr19	59128983	4440281	0.0751	0.5793
chr20	63025520	8892890	0.1411	0.6793
chr21	48129895	5229954	0.1087	0.5762
chr22	51304566	3428244	0.0668	0.4251
chrMT	16571	34880	2.1049	2.673
chrX	155270560	2849550	0.0184	0.2692
chrY	59373566	372347	0.0063	0.1502

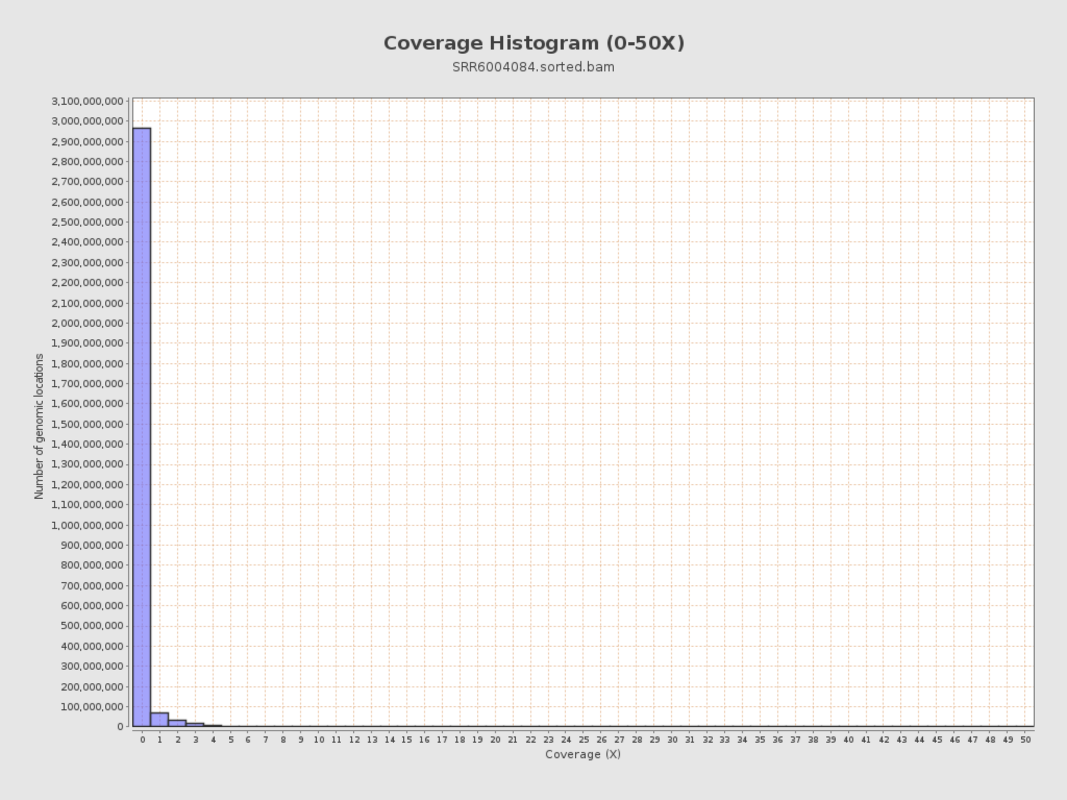
3. Results : Coverage across reference



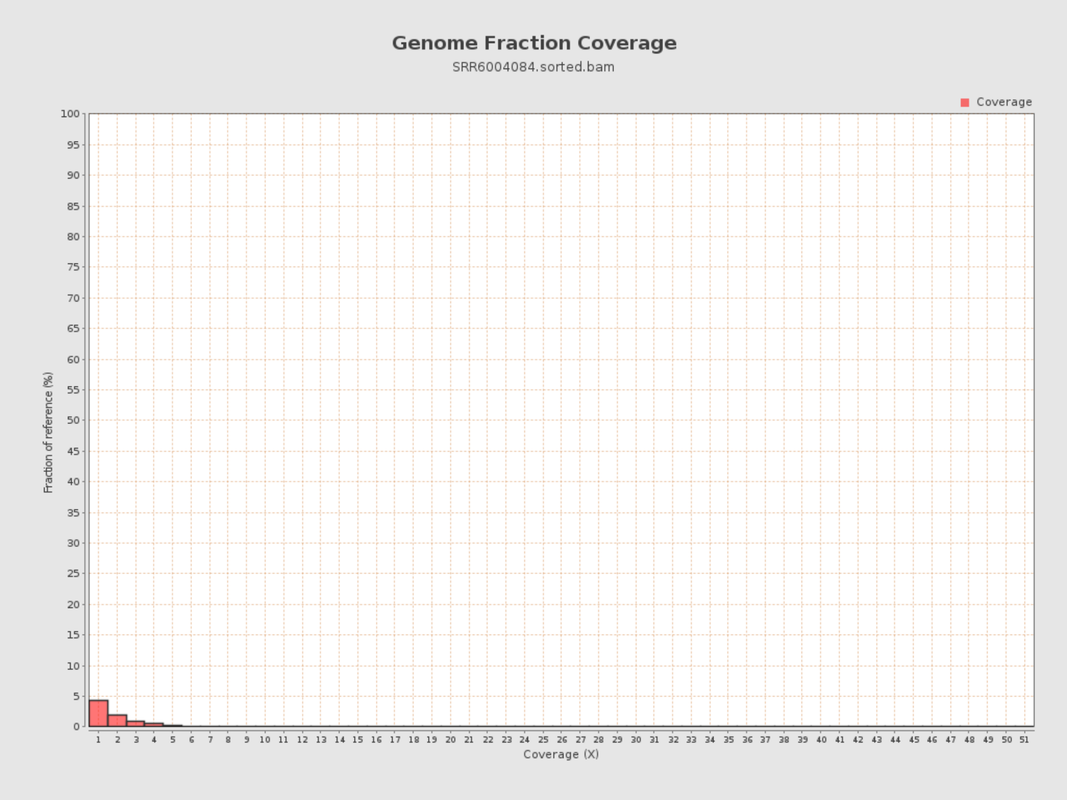
4. Results : Coverage Histogram



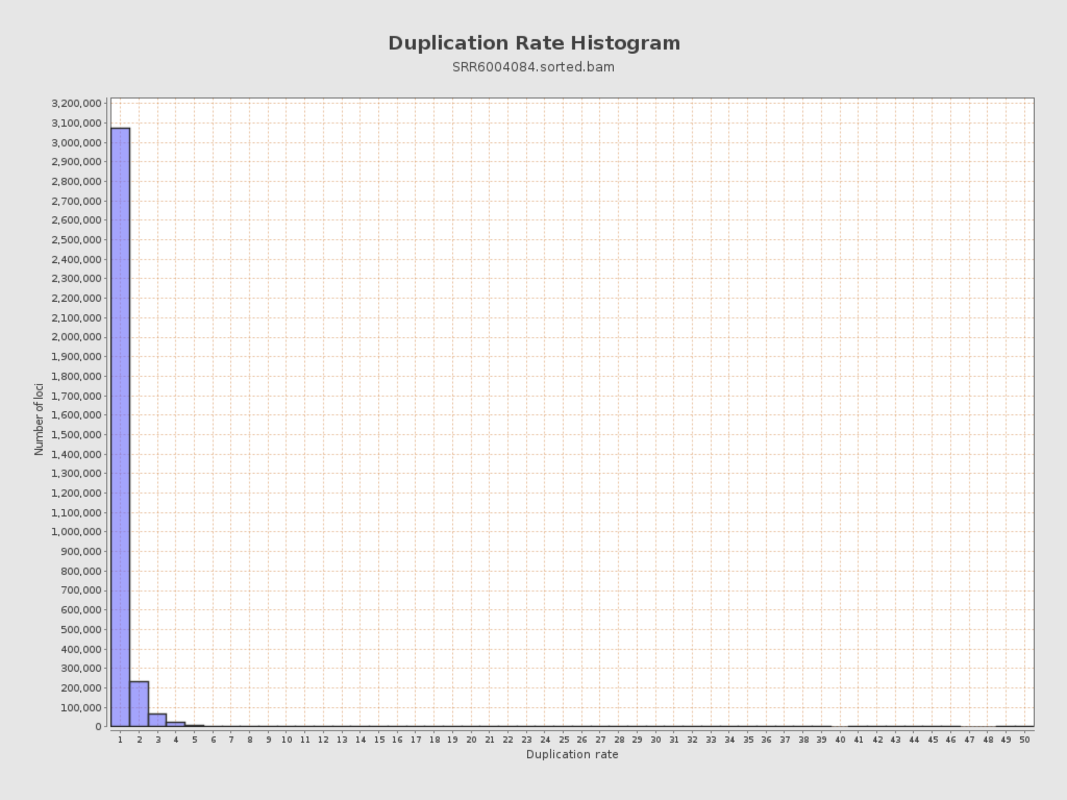
5. Results : Coverage Histogram (0-50X)



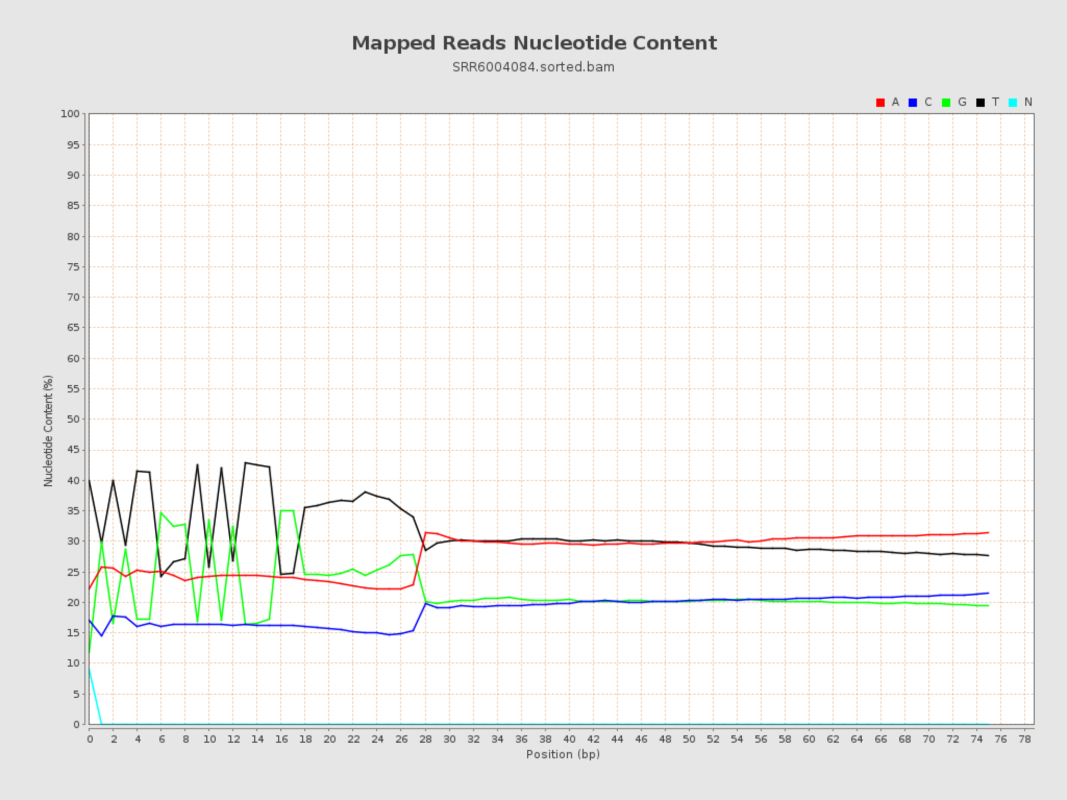
6. Results : Genome Fraction Coverage



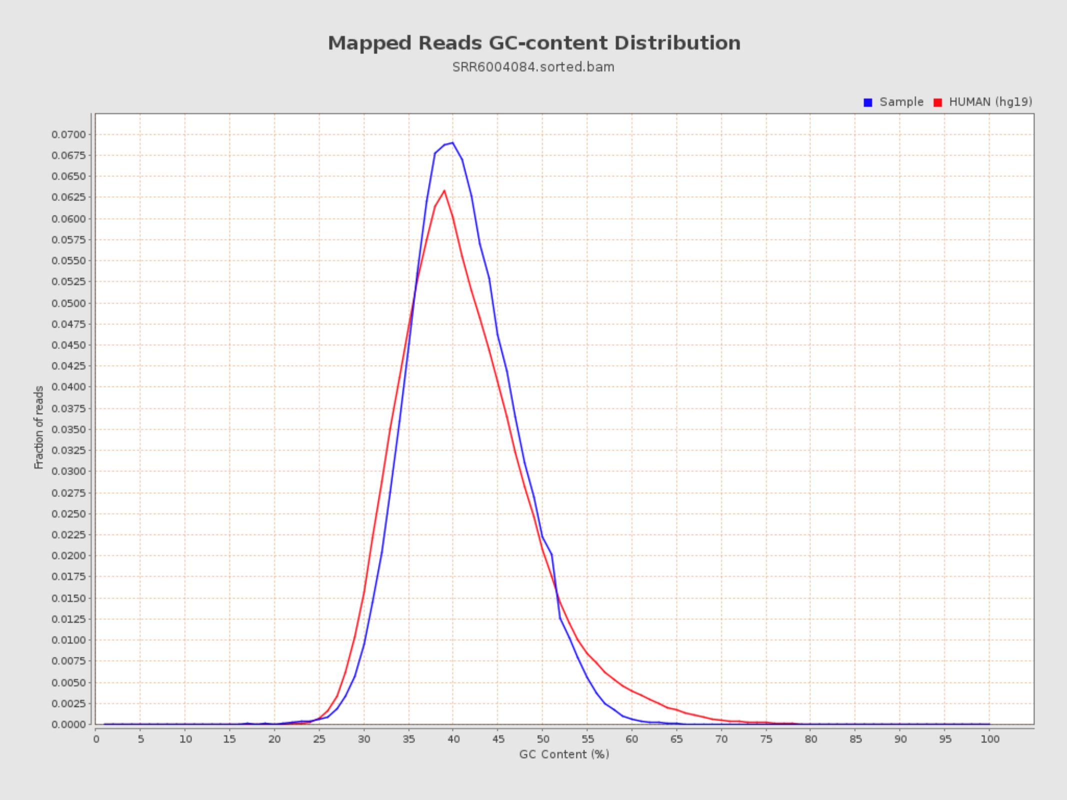
7. Results : Duplication Rate Histogram



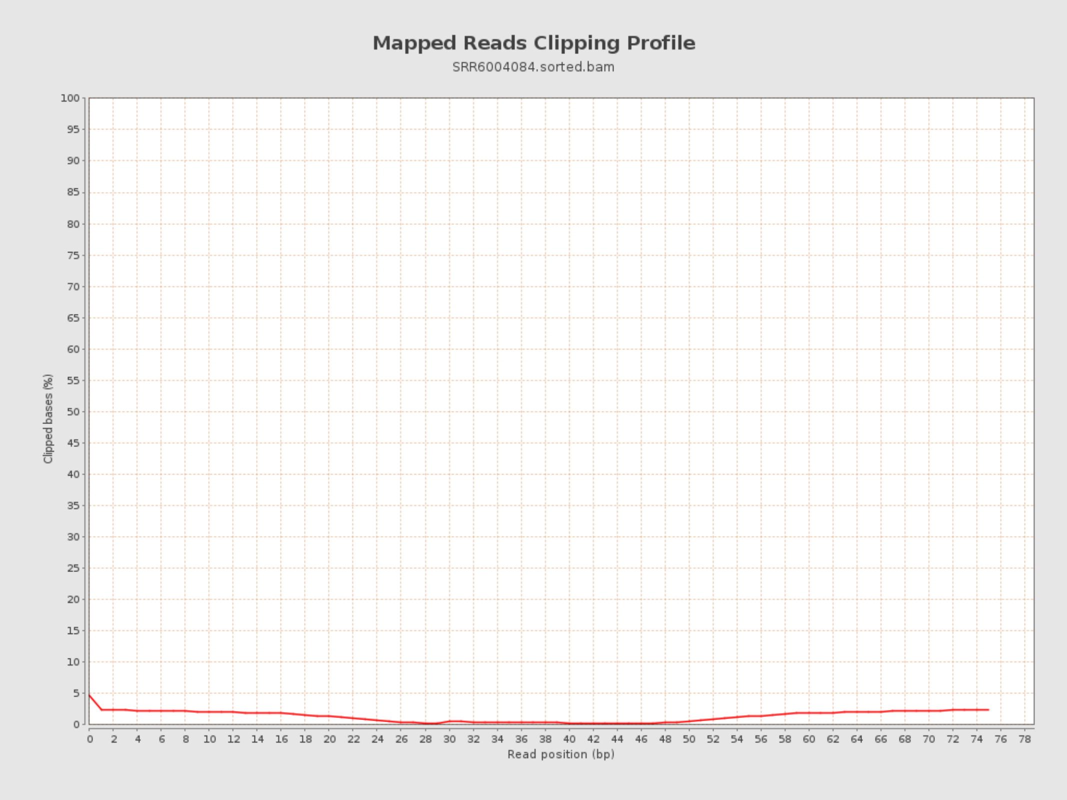
8. Results : Mapped Reads Nucleotide Content



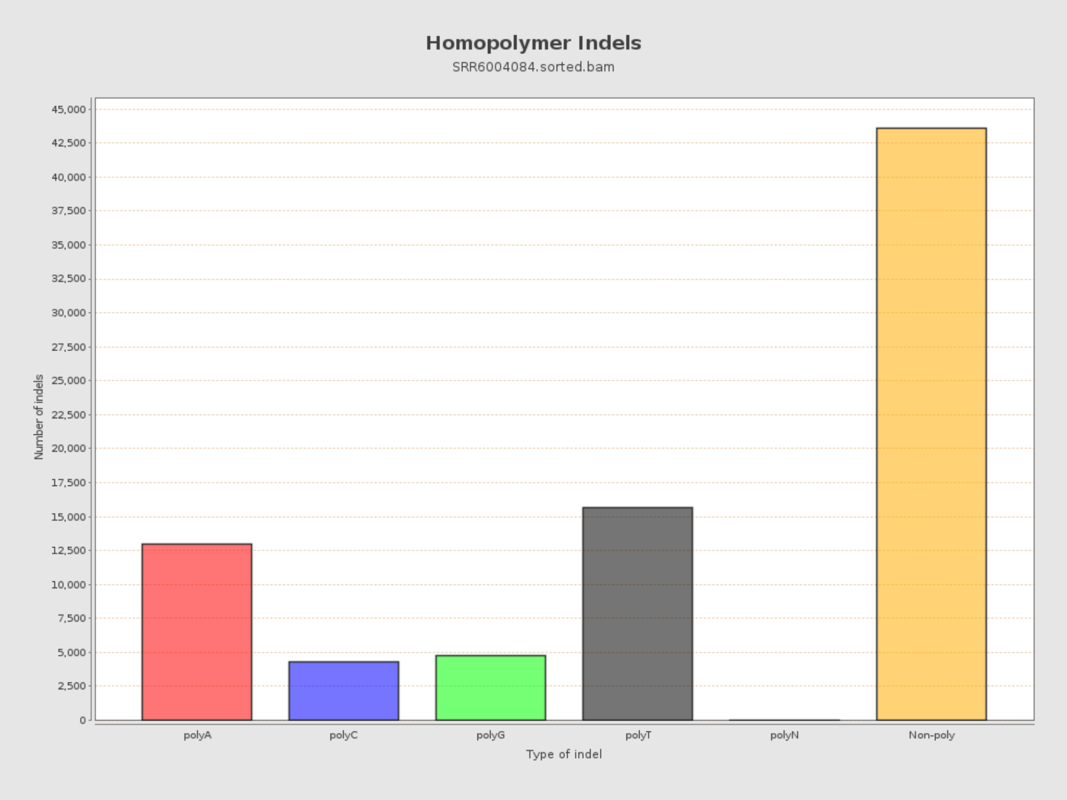
9. Results : Mapped Reads GC-content Distribution



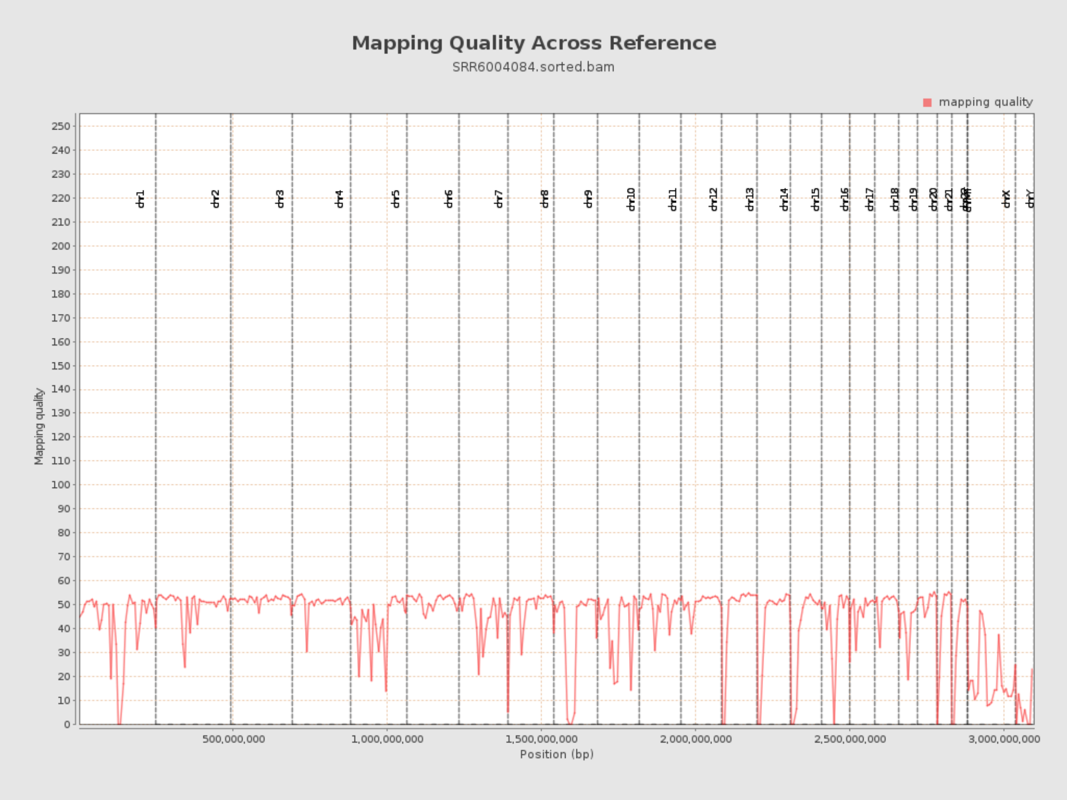
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram