Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 07:15:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1298936.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_SRR1298936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1298936.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 07:15:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1298936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	168,345,296
Mapped reads	162,309,245 / 96.41%
Unmapped reads	6,036,051 / 3.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	64,535 / 0.04%
Read min/max/mean length	30 / 100 / 100.01
Duplicated reads (estimated)	103,102,765 / 61.24%
Duplication rate	56.85%
Clipped reads	4,346,758 / 2.58%

2.2. ACGT Content

Number/percentage of A's	3,947,460,573 / 24.45%
Number/percentage of C's	4,123,449,124 / 25.54%
Number/percentage of T's	4,023,998,664 / 24.93%
Number/percentage of G's	4,044,492,328 / 25.05%
Number/percentage of N's	3,690,641 / 0.02%
GC Percentage	50.6%

2.3. Coverage

Mean	5.2155

Standard Deviation	47.8758

2.4. Mapping Quality

Mean Mapping Quality	49.02

2.5. Mismatches and indels

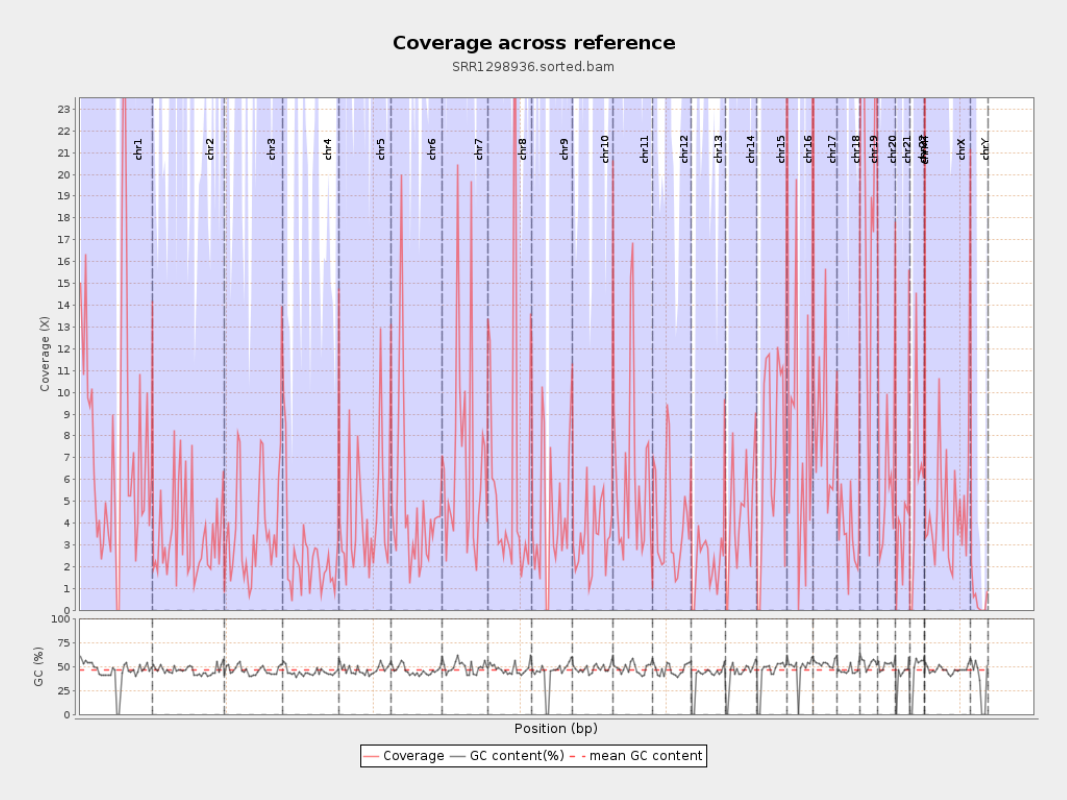
General error rate	0.7%
Mismatches	111,523,395
Insertions	729,285
Mapped reads with at least one insertion	0.44%
Deletions	1,217,504
Mapped reads with at least one deletion	0.74%
Homopolymer indels	46.59%

2.6. Chromosome stats

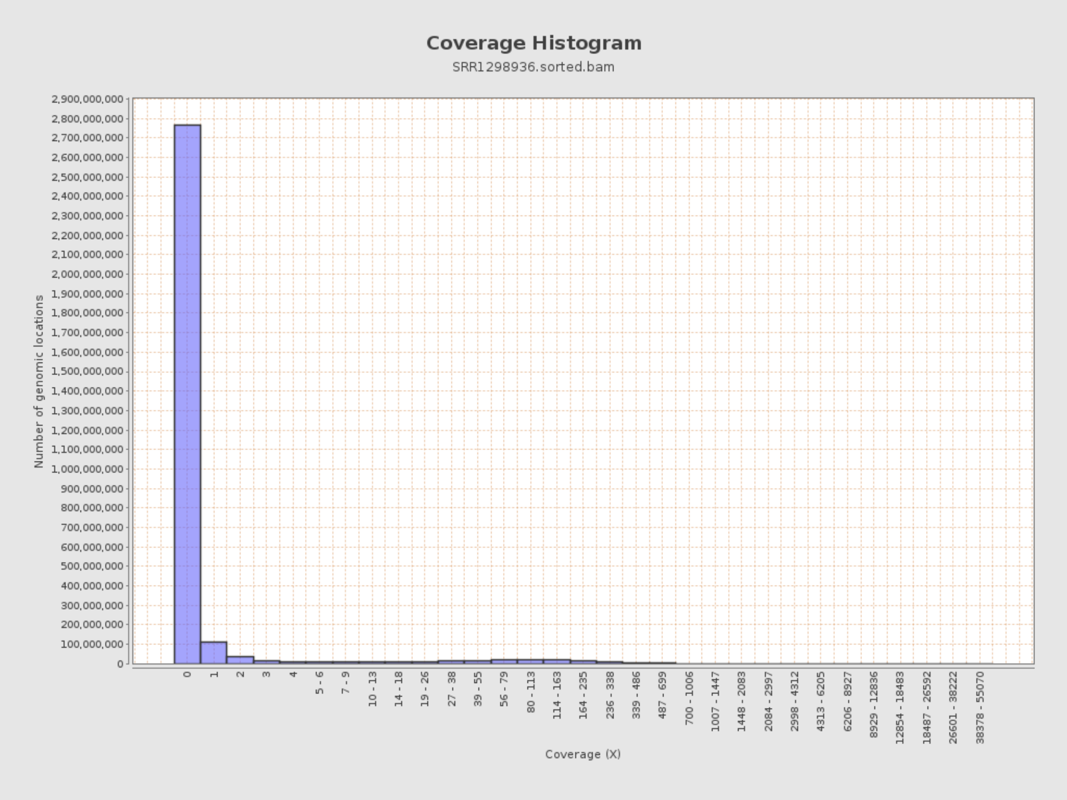
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1926189706	7.7279	52.1474
chr2	243199373	840816871	3.4573	27.5025
chr3	198022430	761345728	3.8447	30.079
chr4	191154276	476809049	2.4944	26.2608
chr5	180915260	831694690	4.5972	53.1528
chr6	171115067	803669072	4.6967	33.0466
chr7	159138663	1109877110	6.9743	109.6168

chr8	146364022	852336780	5.8234	90.7436
chr9	141213431	629840676	4.4602	31.9115
chr10	135534747	462691594	3.4138	22.9757
chr11	135006516	870094107	6.4448	36.6465
chr12	133851895	543152704	4.0579	23.5405
chr13	115169878	259759468	2.2554	19.1827
chr14	107349540	471796221	4.395	30.5708
chr15	102531392	728837309	7.1084	44.1964
chr16	90354753	779709045	8.6294	47.6846
chr17	81195210	688068315	8.4742	43.9531
chr18	78077248	267009693	3.4198	32.5811
chr19	59128983	1186661035	20.069	81.8457
chr20	63025520	386162512	6.1271	36.7897
chr21	48129895	221336575	4.5987	41.5472
chr22	51304566	307077393	5.9854	36.0826
chrMT	16571	803471	48.4866	15.4767
chrX	155270560	709974914	4.5725	32.1013
chrY	59373566	29937964	0.5042	23.6957

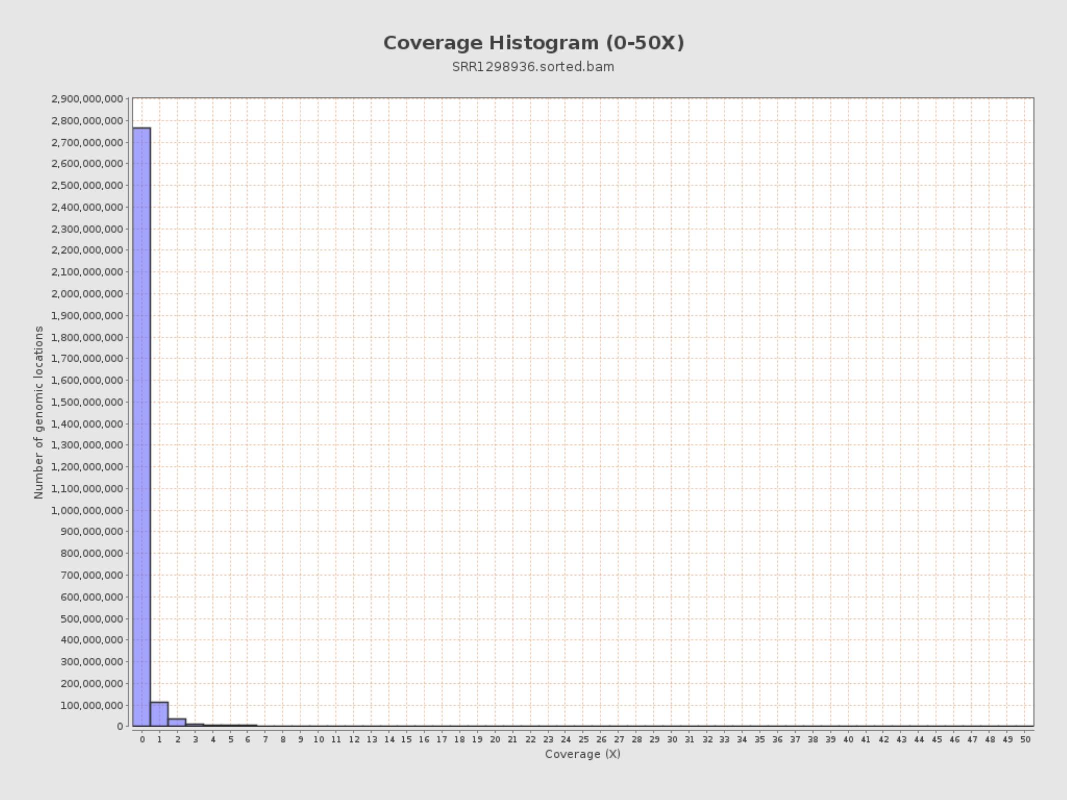
3. Results : Coverage across reference



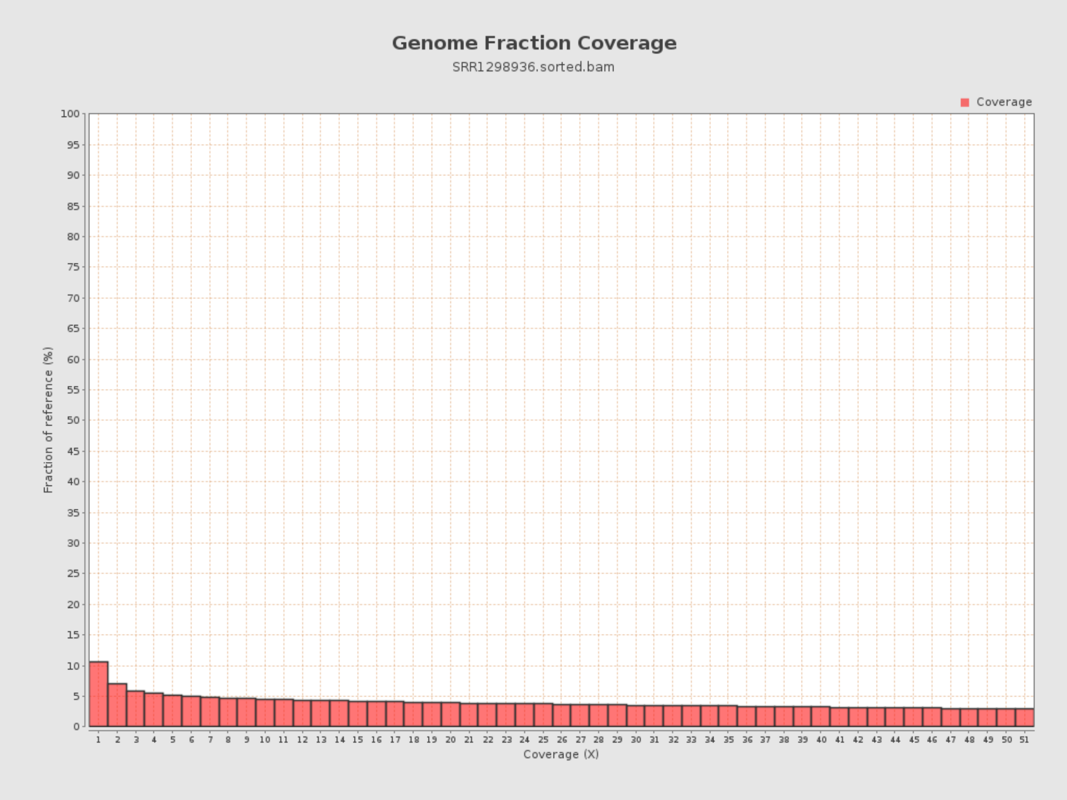
4. Results : Coverage Histogram



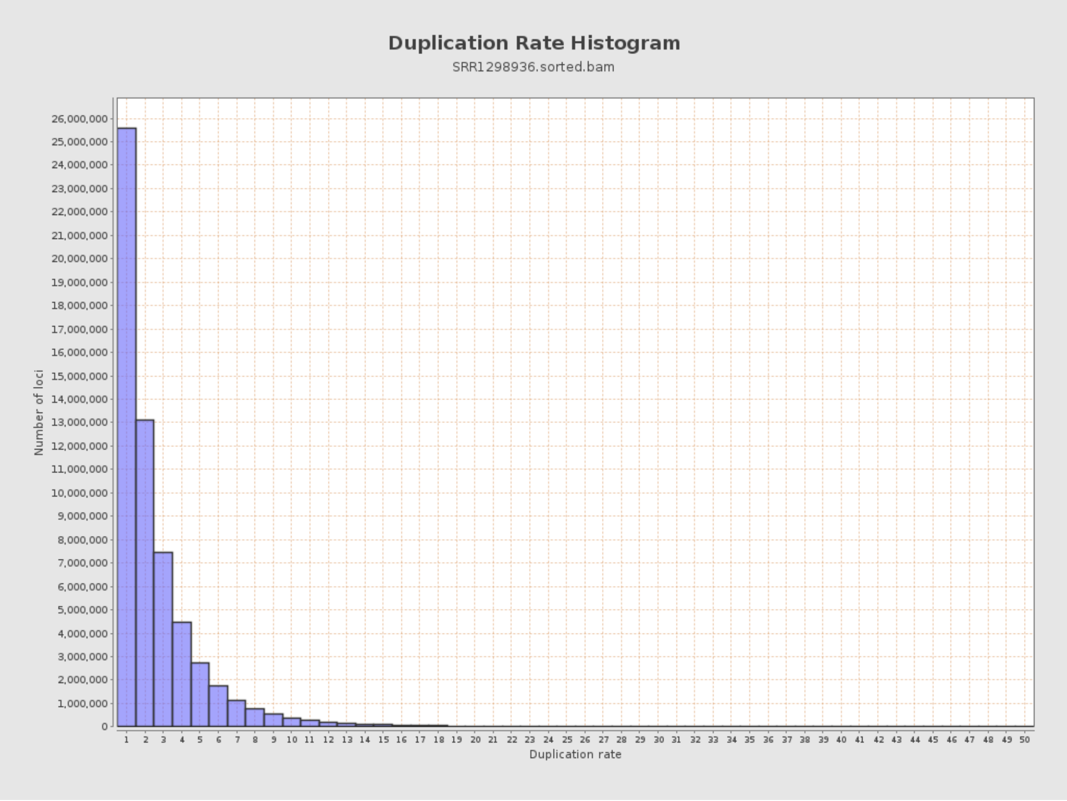
5. Results : Coverage Histogram (0-50X)



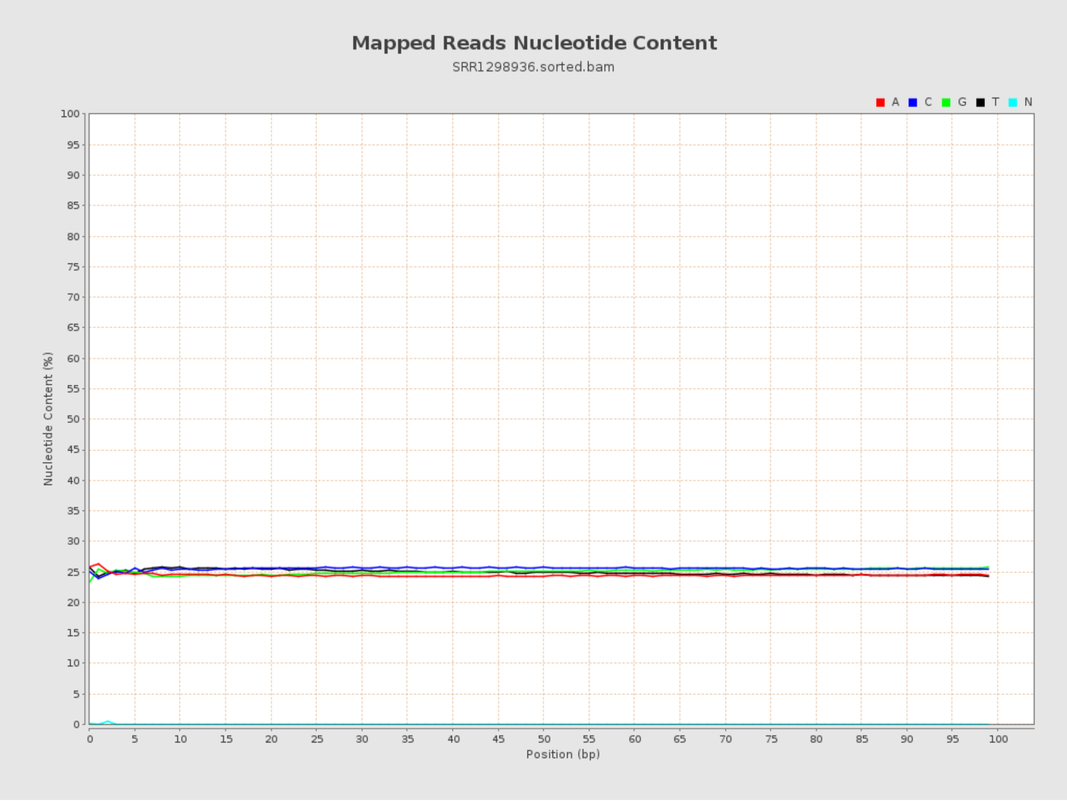
6. Results : Genome Fraction Coverage



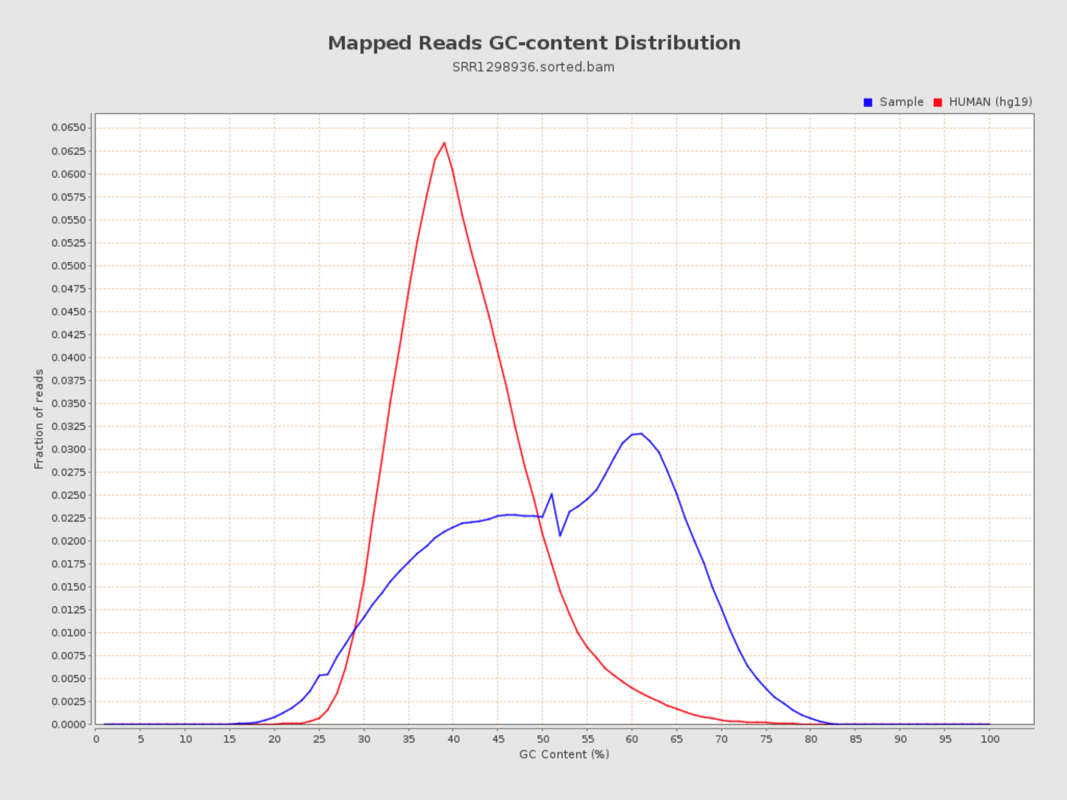
7. Results : Duplication Rate Histogram



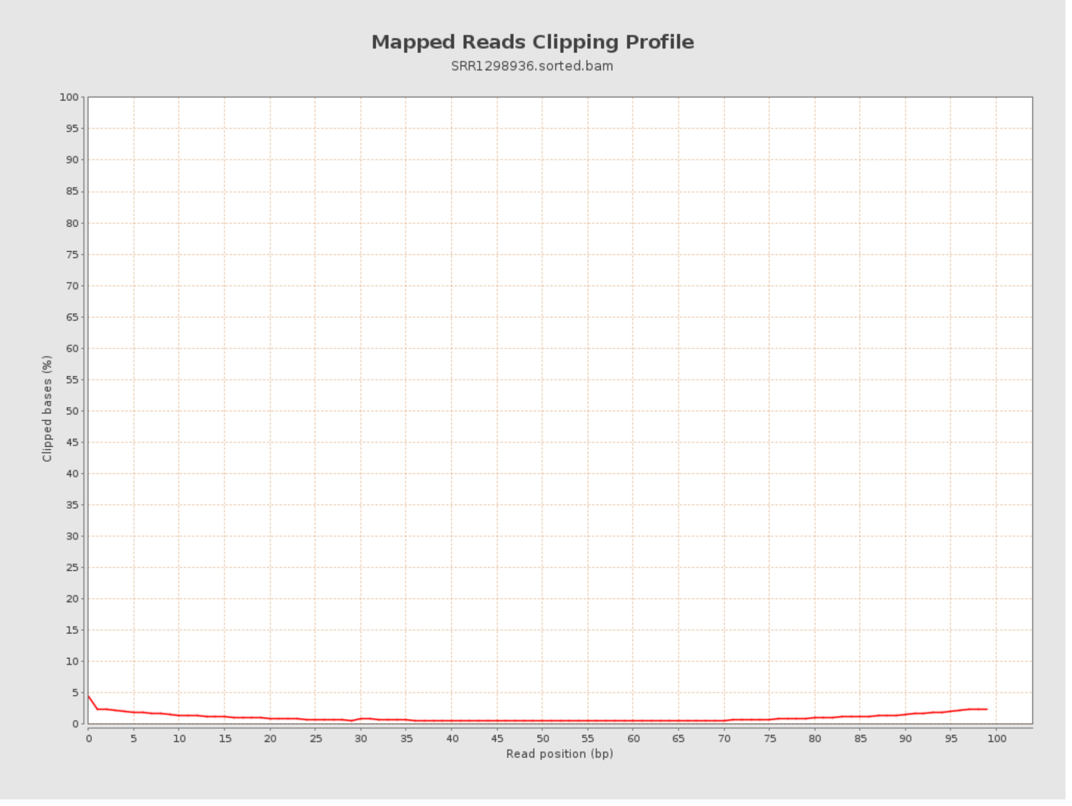
8. Results : Mapped Reads Nucleotide Content



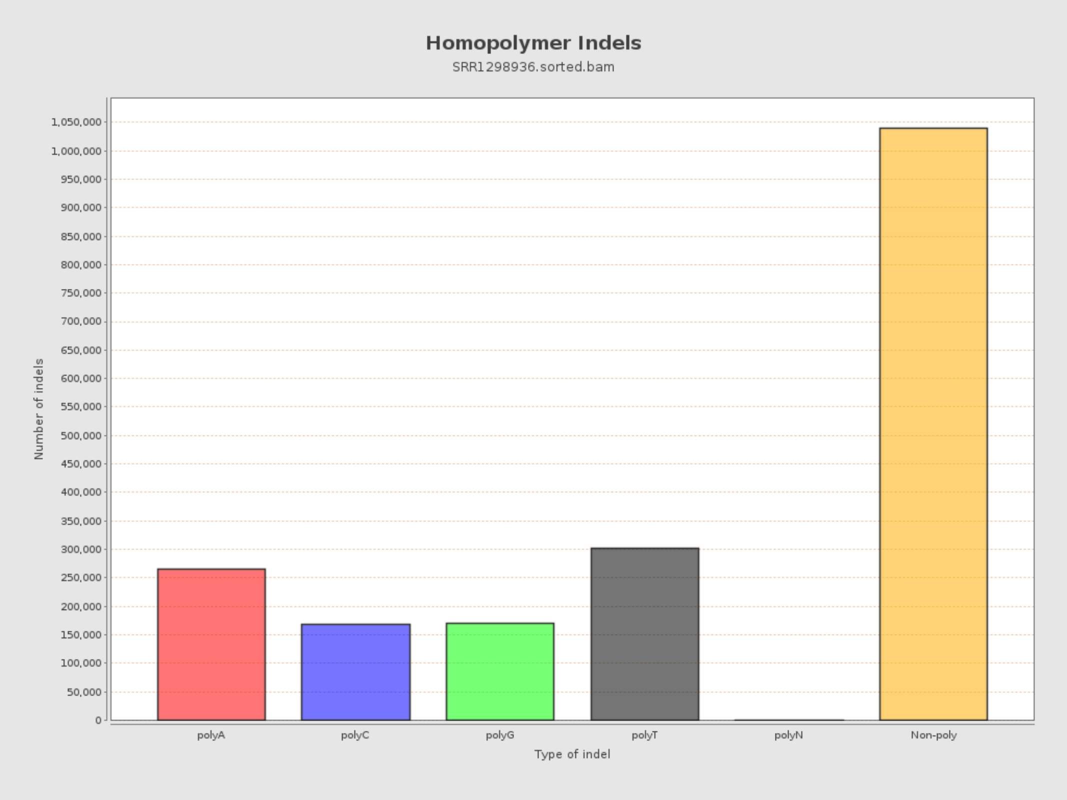
9. Results : Mapped Reads GC-content Distribution



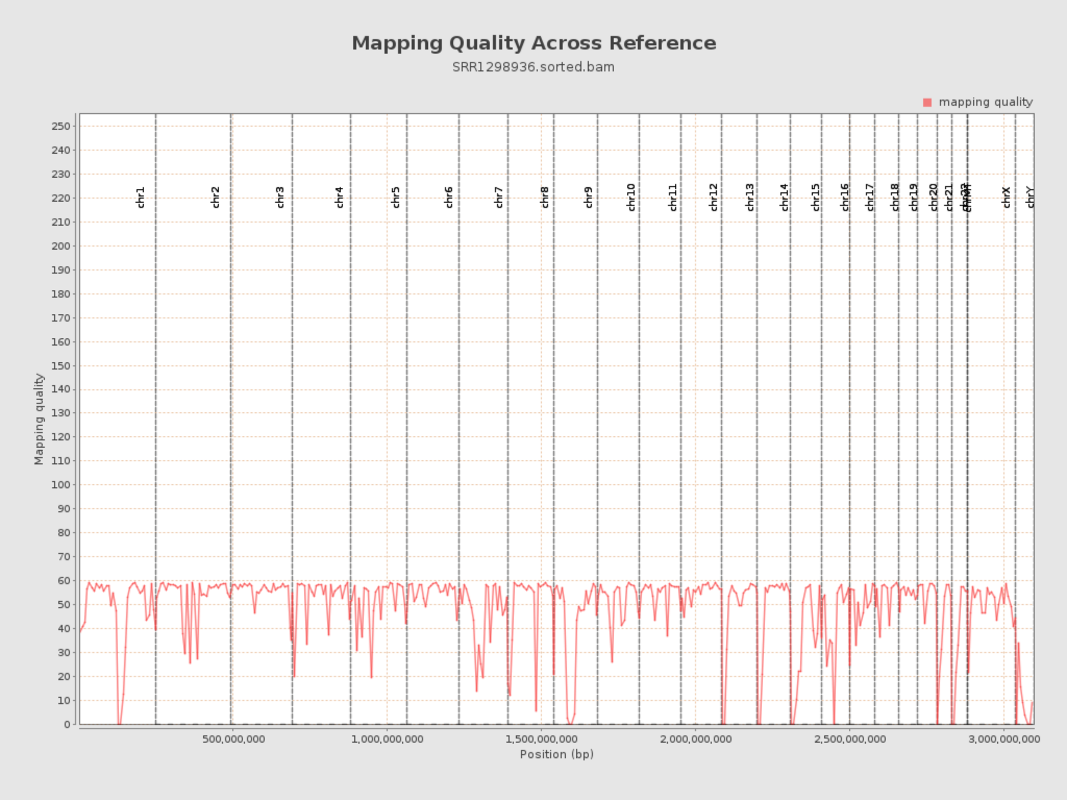
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram