Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:52:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230385.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_SRR6230385 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230385.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:52:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230385.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,552,555
Mapped reads	2,130,047 / 83.45%
Unmapped reads	422,508 / 16.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,132 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	101,753 / 3.99%
Duplication rate	3.75%
Clipped reads	1,030,307 / 40.36%

2.2. ACGT Content

Number/percentage of A's	37,876,339 / 27.16%
Number/percentage of C's	24,347,797 / 17.46%
Number/percentage of T's	45,774,350 / 32.83%
Number/percentage of G's	31,174,821 / 22.36%
Number/percentage of N's	266,487 / 0.19%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.3997

2.4. Mapping Quality

Mean Mapping Quality	46.88

2.5. Mismatches and indels

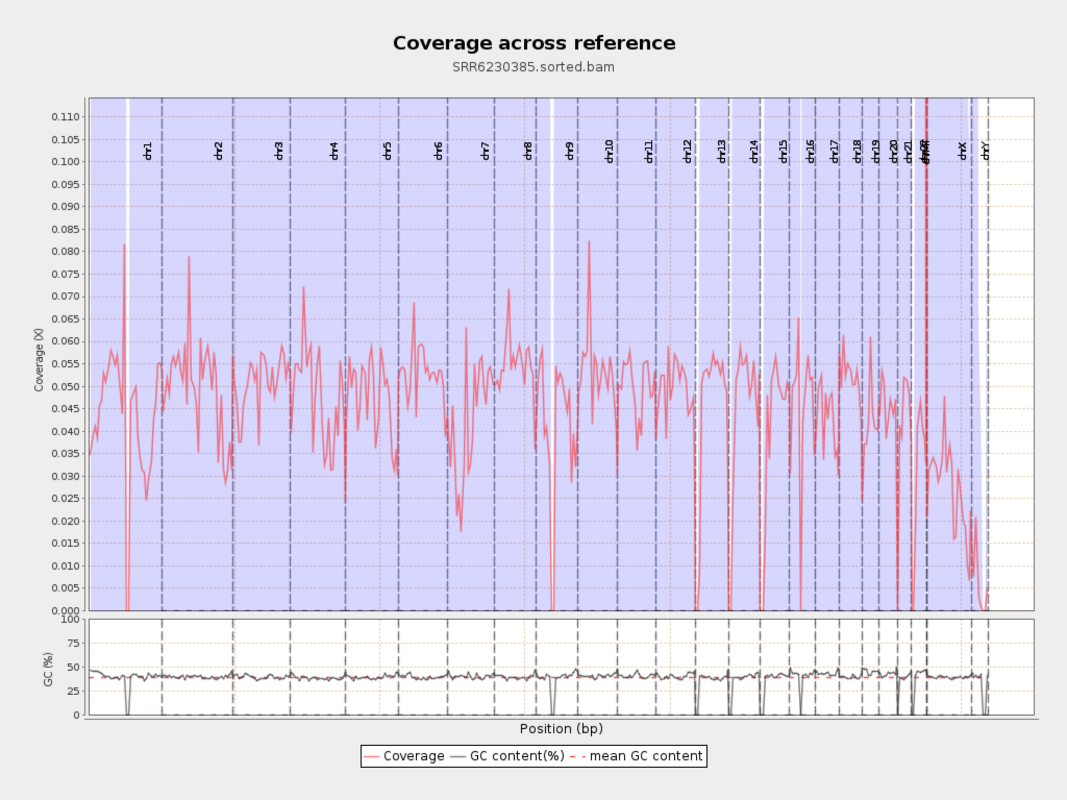
General error rate	0.94%
Mismatches	1,285,296
Insertions	12,524
Mapped reads with at least one insertion	0.58%
Deletions	37,838
Mapped reads with at least one deletion	1.76%
Homopolymer indels	48.1%

2.6. Chromosome stats

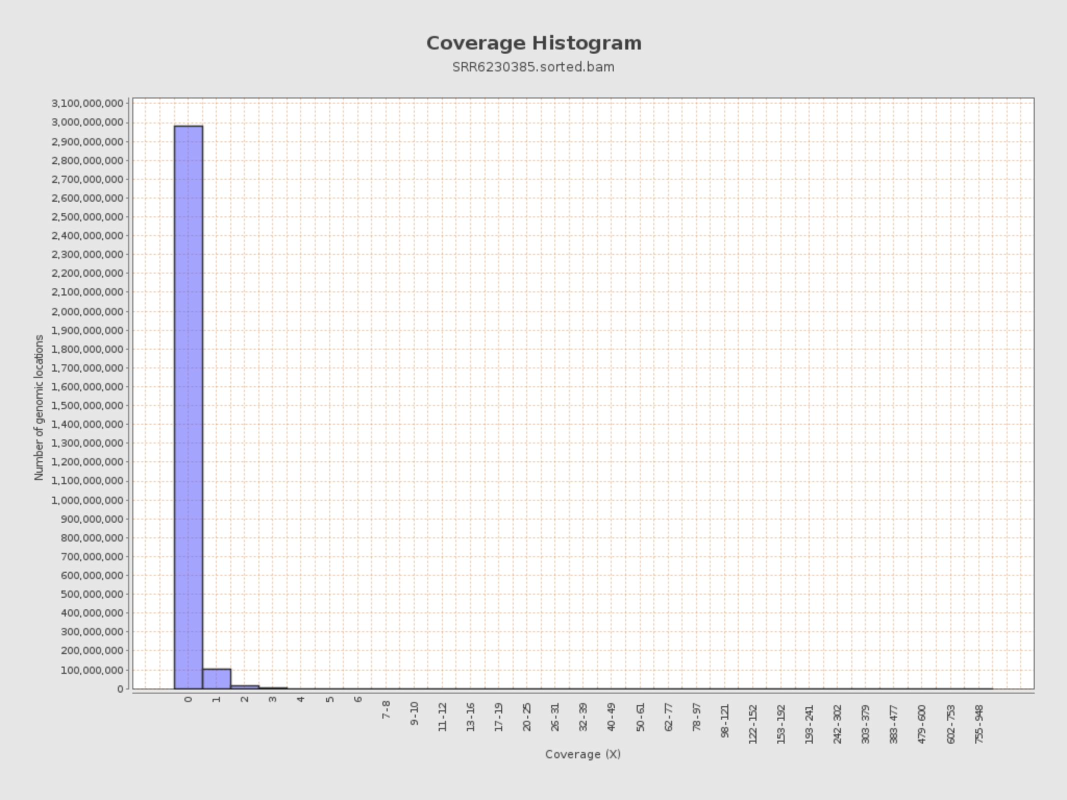
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10713829	0.043	0.7378
chr2	243199373	11985824	0.0493	0.4163
chr3	198022430	10058391	0.0508	0.2609
chr4	191154276	9126667	0.0477	0.2723
chr5	180915260	8619551	0.0476	0.2516
chr6	171115067	9051468	0.0529	0.3228
chr7	159138663	6666980	0.0419	0.4109

chr8	146364022	8014624	0.0548	0.6427
chr9	141213431	5730005	0.0406	0.3954
chr10	135534747	7299925	0.0539	0.3945
chr11	135006516	6723884	0.0498	0.3677
chr12	133851895	6625335	0.0495	0.2596
chr13	115169878	5078018	0.0441	0.2399
chr14	107349540	4689714	0.0437	0.2538
chr15	102531392	4046467	0.0395	0.228
chr16	90354753	4082607	0.0452	0.2776
chr17	81195210	3464930	0.0427	0.2696
chr18	78077248	4089107	0.0524	0.6776
chr19	59128983	2499814	0.0423	0.4983
chr20	63025520	2833359	0.045	0.2553
chr21	48129895	1980709	0.0412	0.2552
chr22	51304566	1487776	0.029	0.1946
chrMT	16571	110505	6.6686	4.1883
chrX	155270560	4185487	0.027	0.224
chrY	59373566	337875	0.0057	0.1625

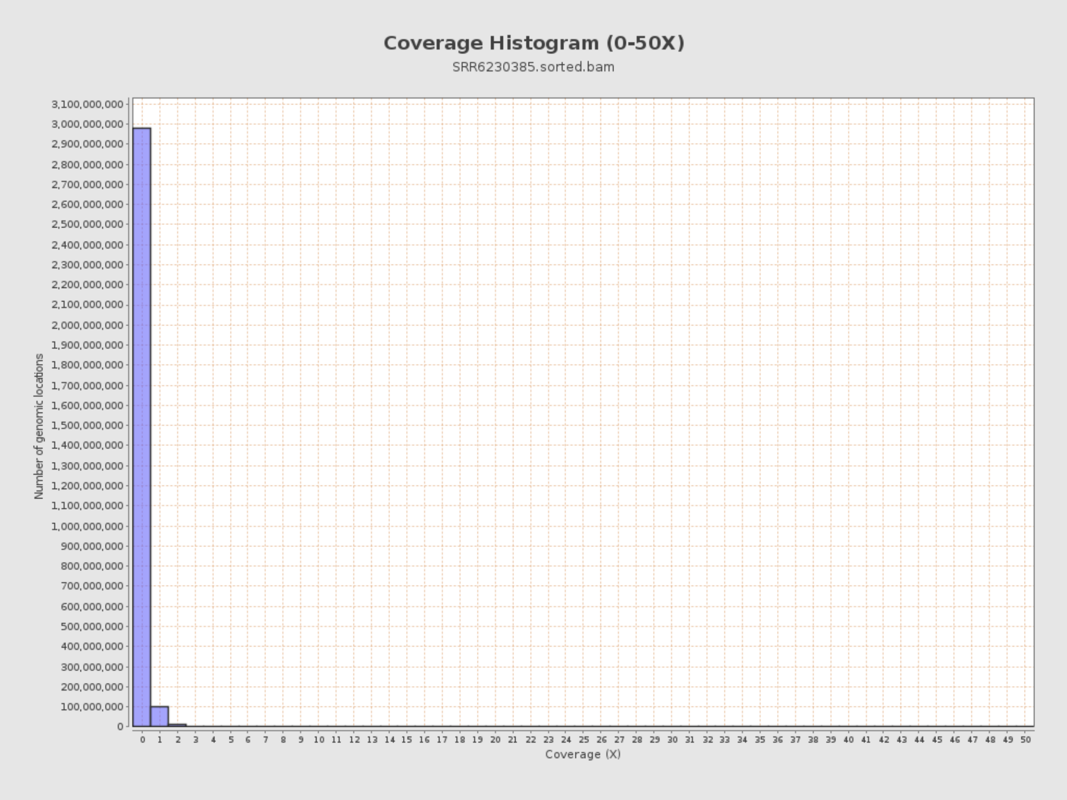
3. Results : Coverage across reference



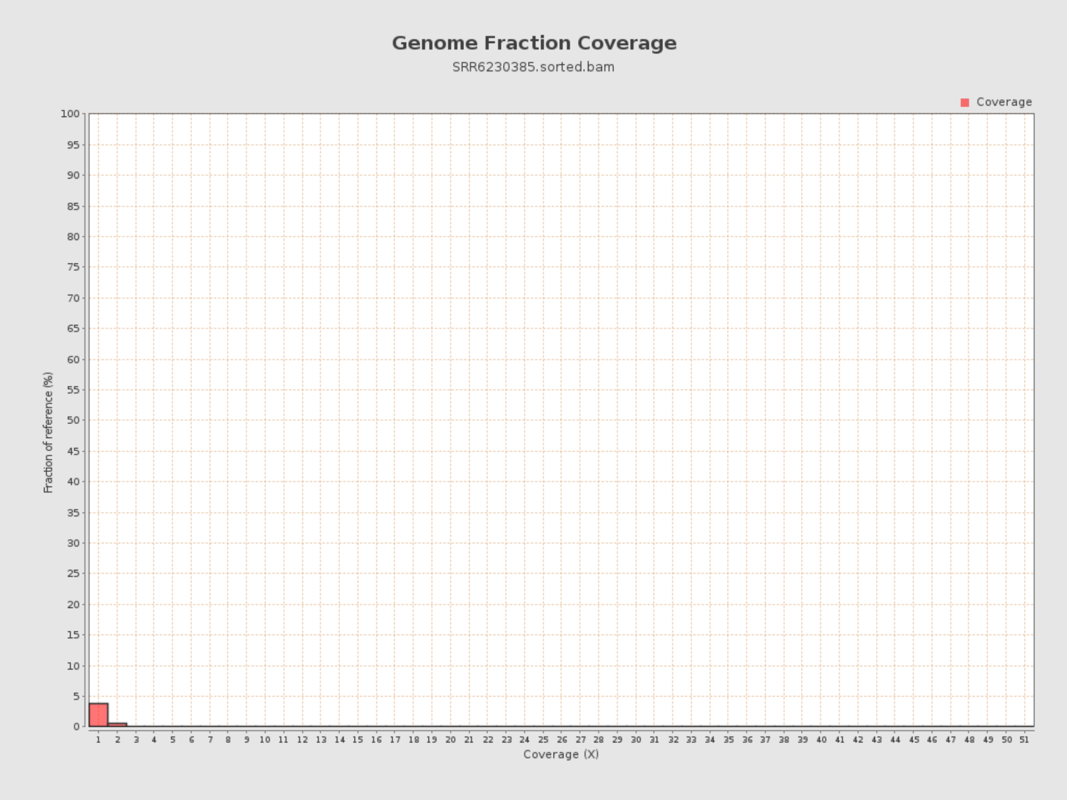
4. Results : Coverage Histogram



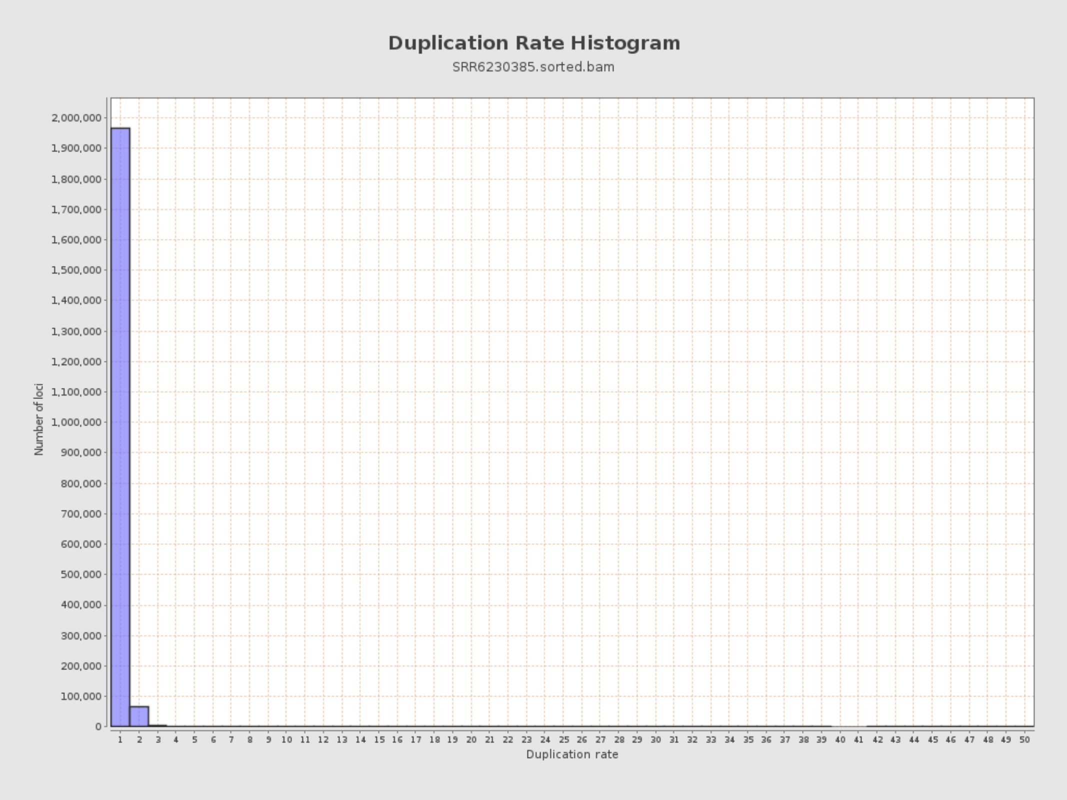
5. Results : Coverage Histogram (0-50X)



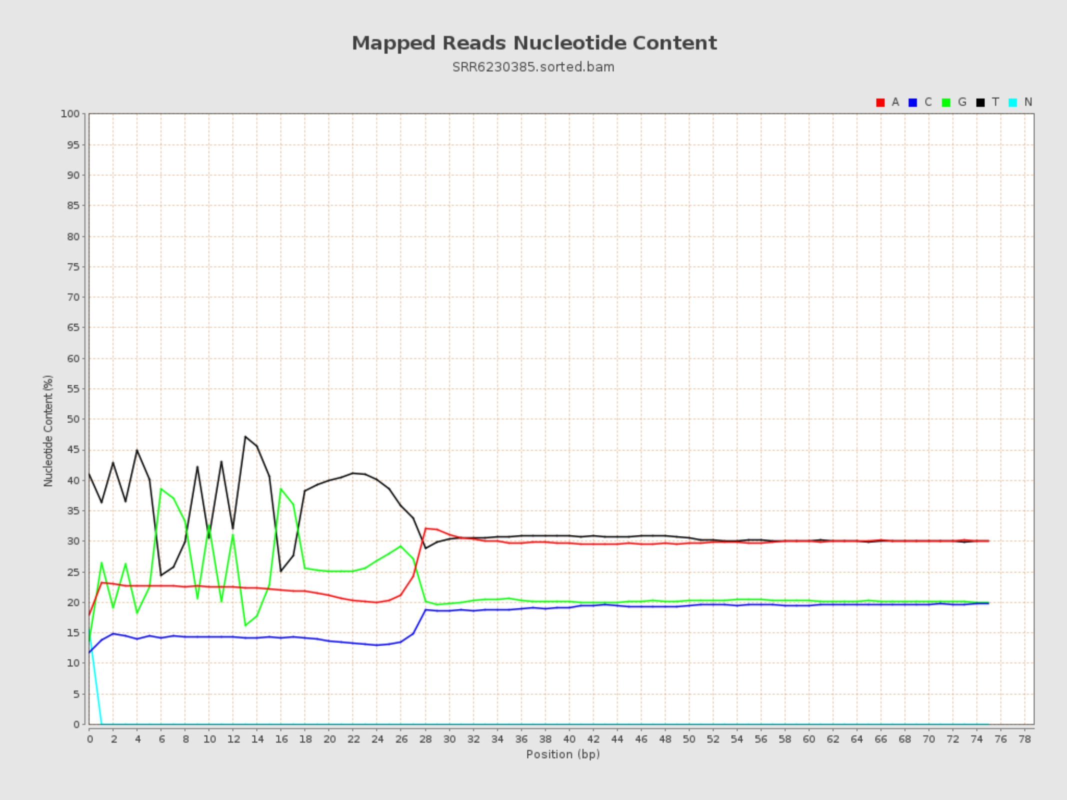
6. Results : Genome Fraction Coverage



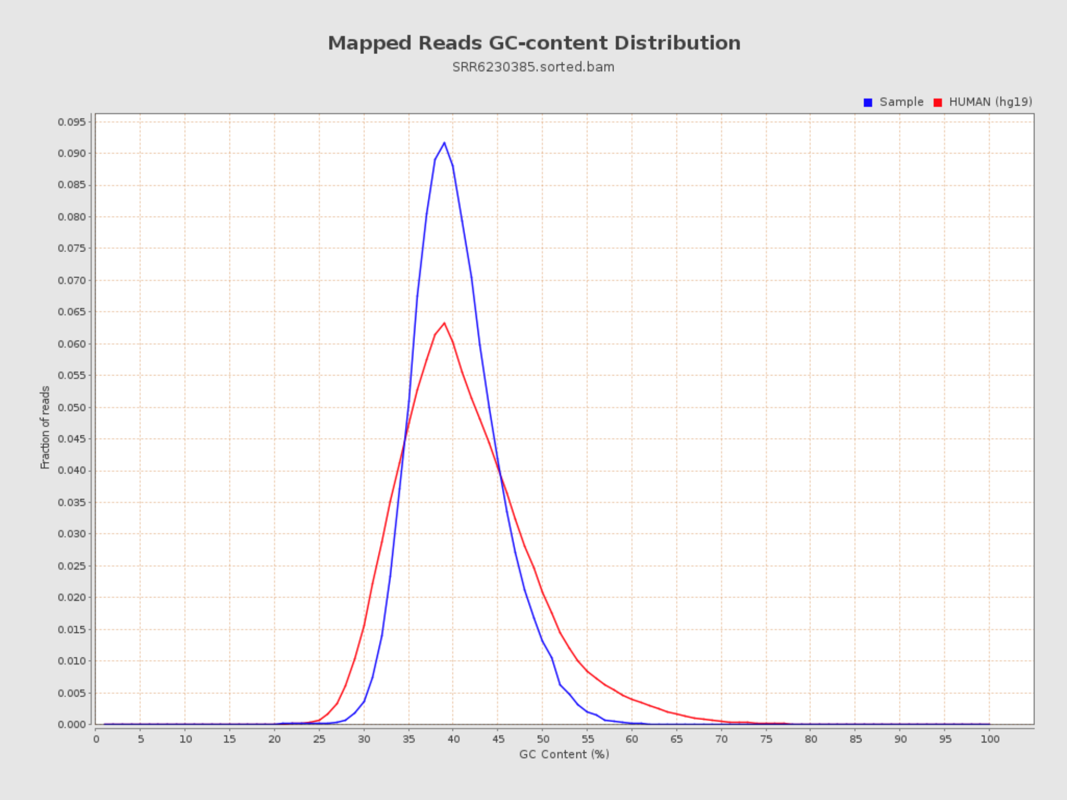
7. Results : Duplication Rate Histogram



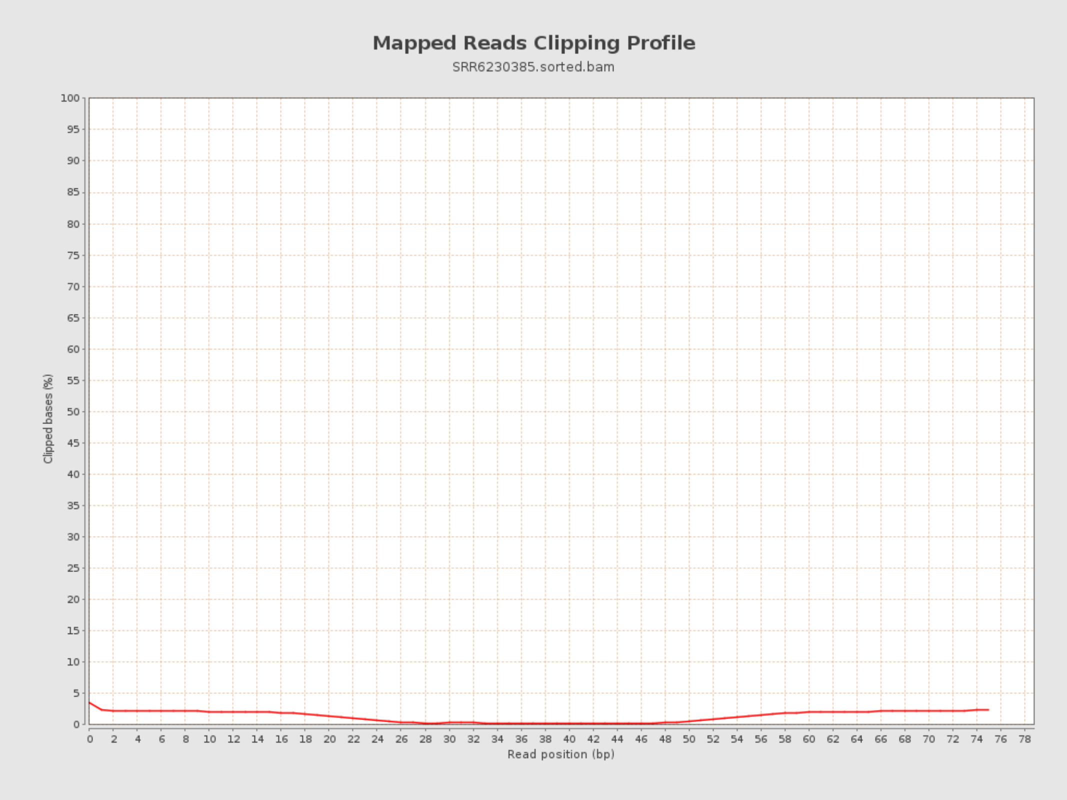
8. Results : Mapped Reads Nucleotide Content



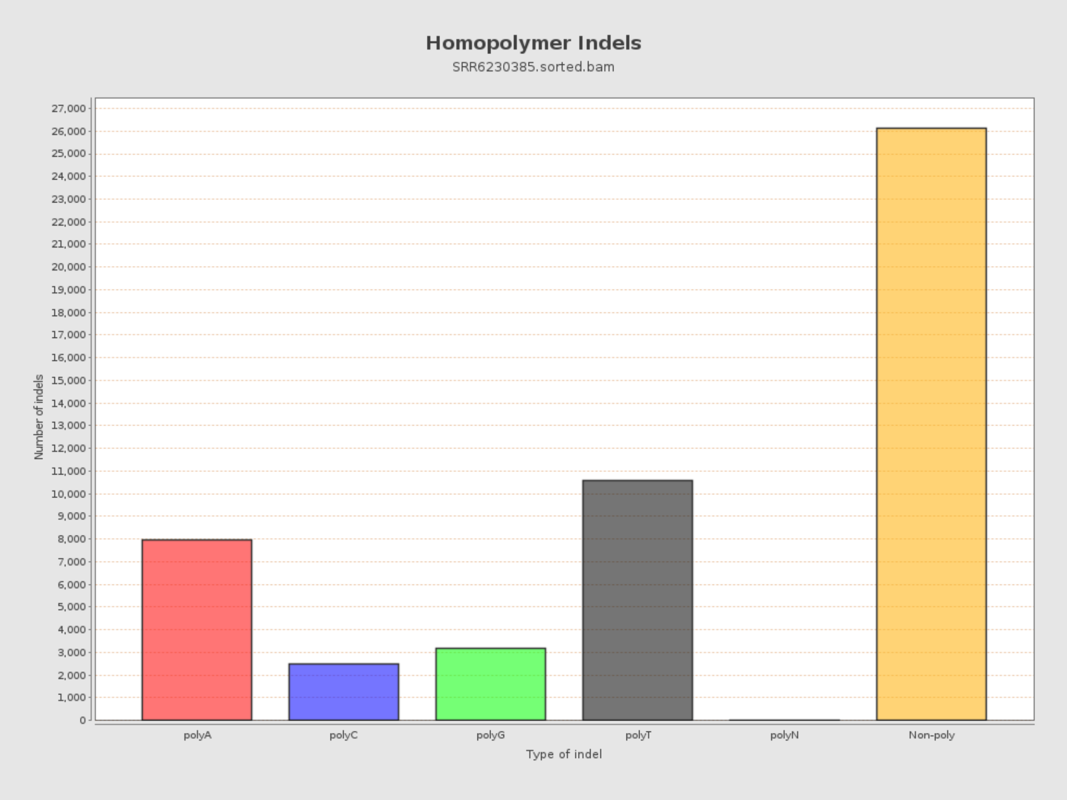
9. Results : Mapped Reads GC-content Distribution



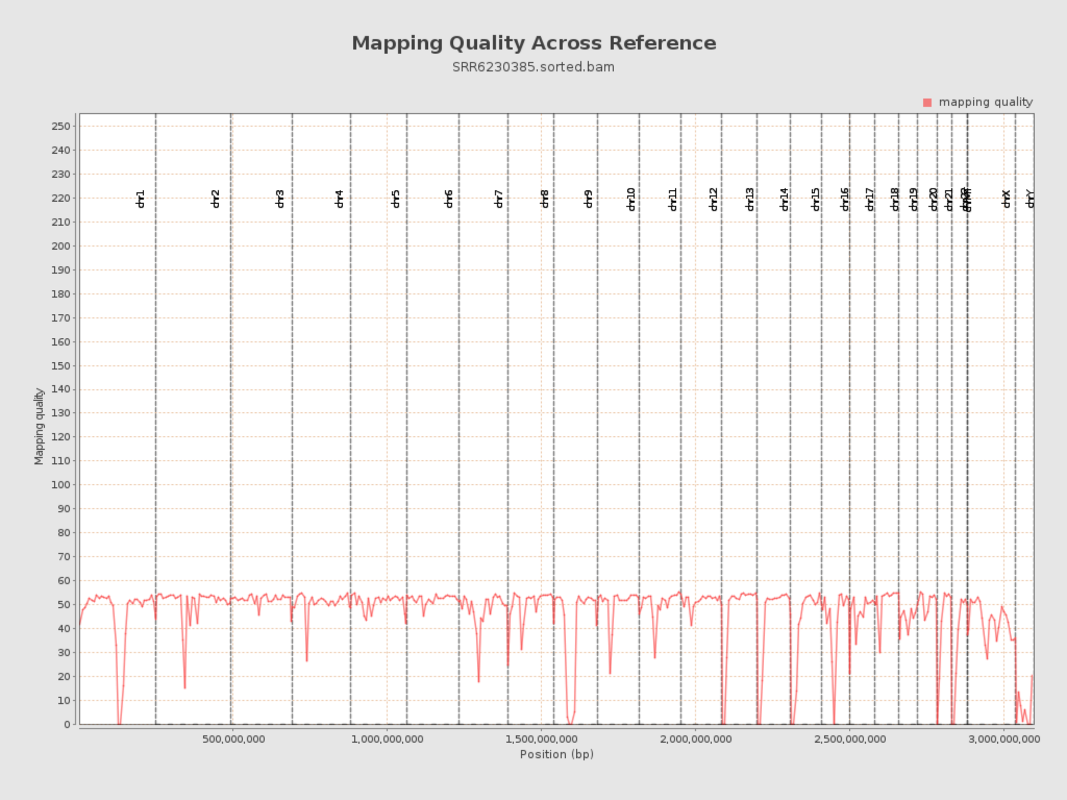
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram