Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:47:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240214.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_SRR6240214 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240214.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:47:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240214.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,645,109
Mapped reads	2,752,194 / 75.5%
Unmapped reads	892,915 / 24.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,788 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	502,829 / 13.79%
Duplication rate	12.83%
Clipped reads	1,544,719 / 42.38%

2.2. ACGT Content

Number/percentage of A's	48,815,379 / 27.63%
Number/percentage of C's	32,591,067 / 18.45%
Number/percentage of T's	55,947,583 / 31.67%
Number/percentage of G's	39,279,206 / 22.24%
Number/percentage of N's	16,376 / 0.01%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.6168

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

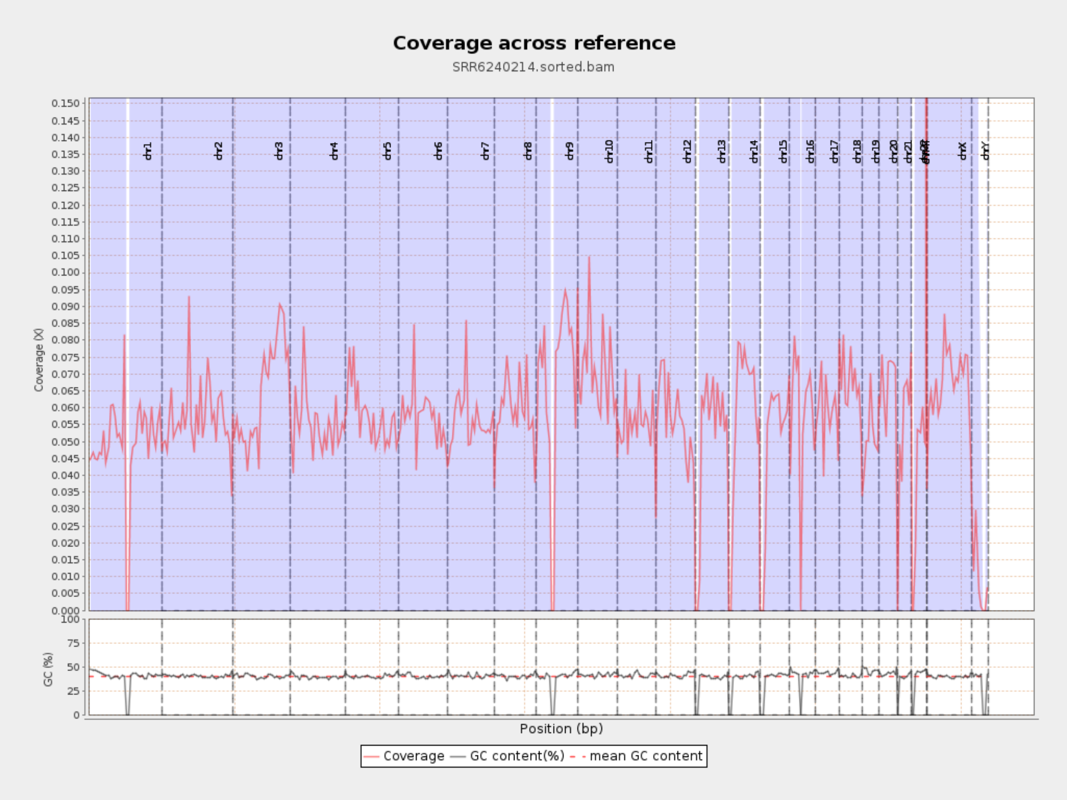
General error rate	0.86%
Mismatches	1,495,331
Insertions	13,129
Mapped reads with at least one insertion	0.47%
Deletions	44,949
Mapped reads with at least one deletion	1.61%
Homopolymer indels	46.75%

2.6. Chromosome stats

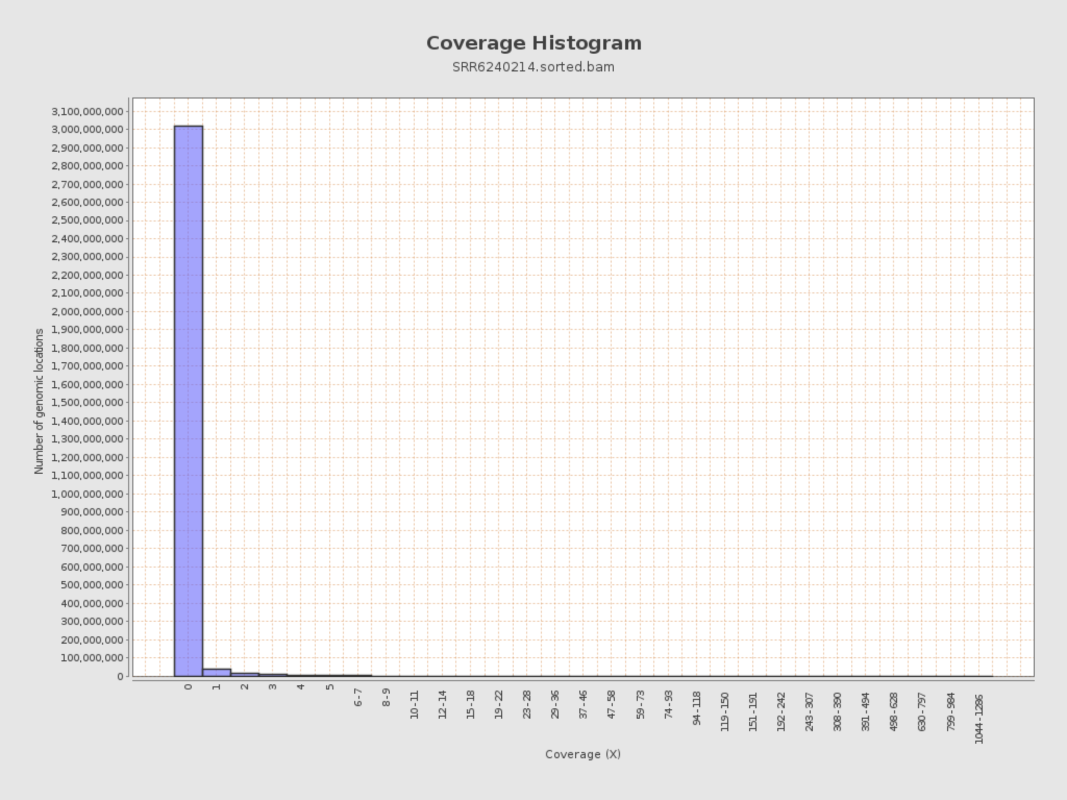
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12329268	0.0495	0.8586
chr2	243199373	13920679	0.0572	0.7055
chr3	198022430	12785602	0.0646	0.4988
chr4	191154276	10496513	0.0549	0.4845
chr5	180915260	10421865	0.0576	0.4654
chr6	171115067	9827369	0.0574	0.5406
chr7	159138663	9025159	0.0567	0.6385

chr8	146364022	8664823	0.0592	0.8994
chr9	141213431	9595495	0.068	0.665
chr10	135534747	9606321	0.0709	0.6209
chr11	135006516	7507208	0.0556	0.5531
chr12	133851895	7537618	0.0563	0.4692
chr13	115169878	5793989	0.0503	0.4401
chr14	107349540	6159988	0.0574	0.5059
chr15	102531392	4930203	0.0481	0.4456
chr16	90354753	5300608	0.0587	0.499
chr17	81195210	4738652	0.0584	0.4855
chr18	78077248	5286840	0.0677	1.1154
chr19	59128983	3042372	0.0515	0.6754
chr20	63025520	4190352	0.0665	0.5155
chr21	48129895	2556927	0.0531	0.4641
chr22	51304566	1907207	0.0372	0.3645
chrMT	16571	140070	8.4527	7.2779
chrX	155270560	10433089	0.0672	0.5422
chrY	59373566	529464	0.0089	0.2273

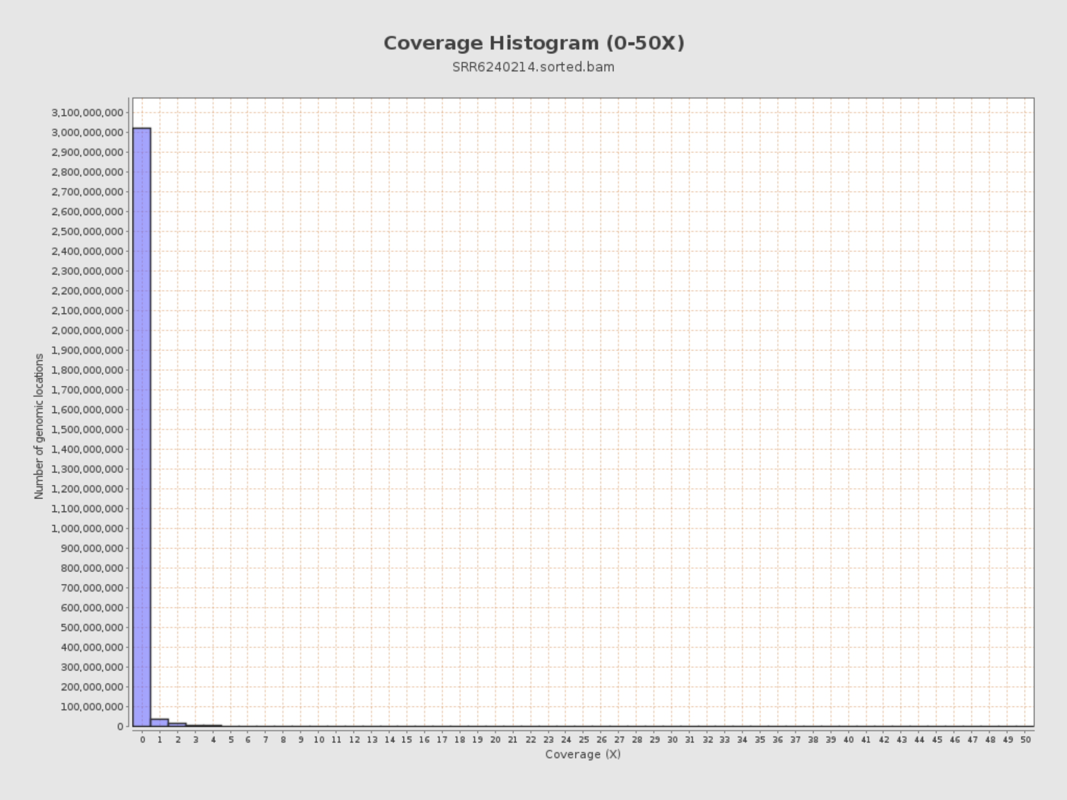
3. Results : Coverage across reference



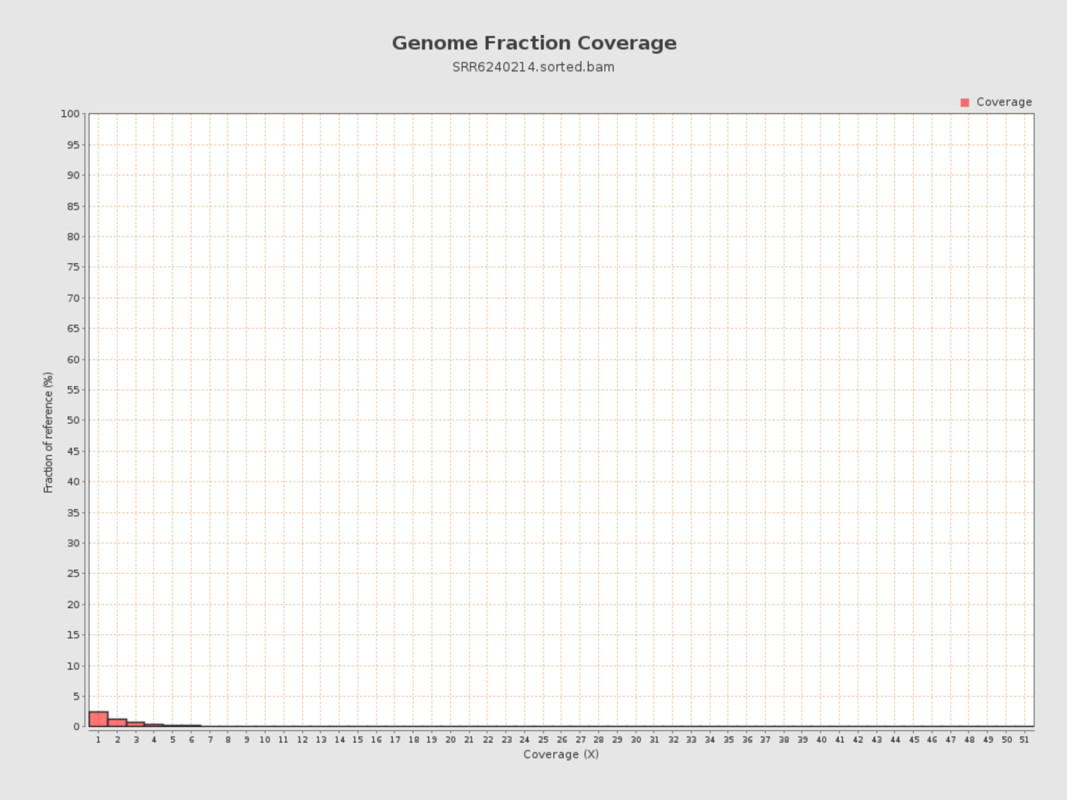
4. Results : Coverage Histogram



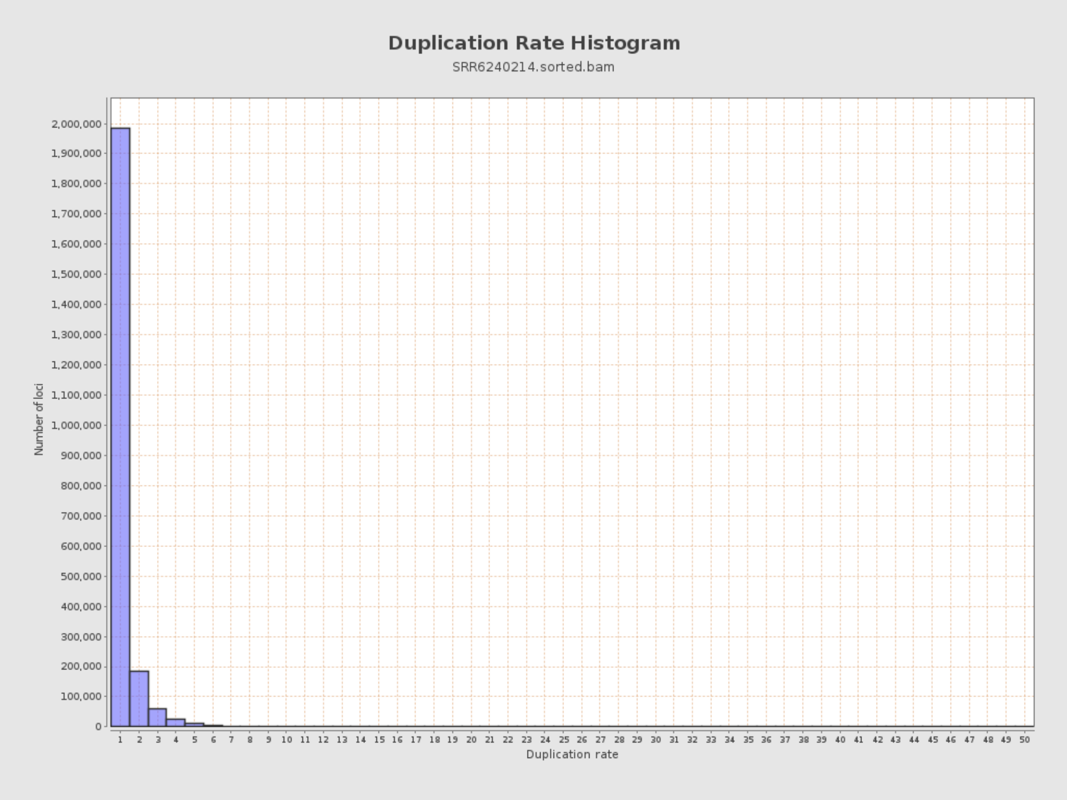
5. Results : Coverage Histogram (0-50X)



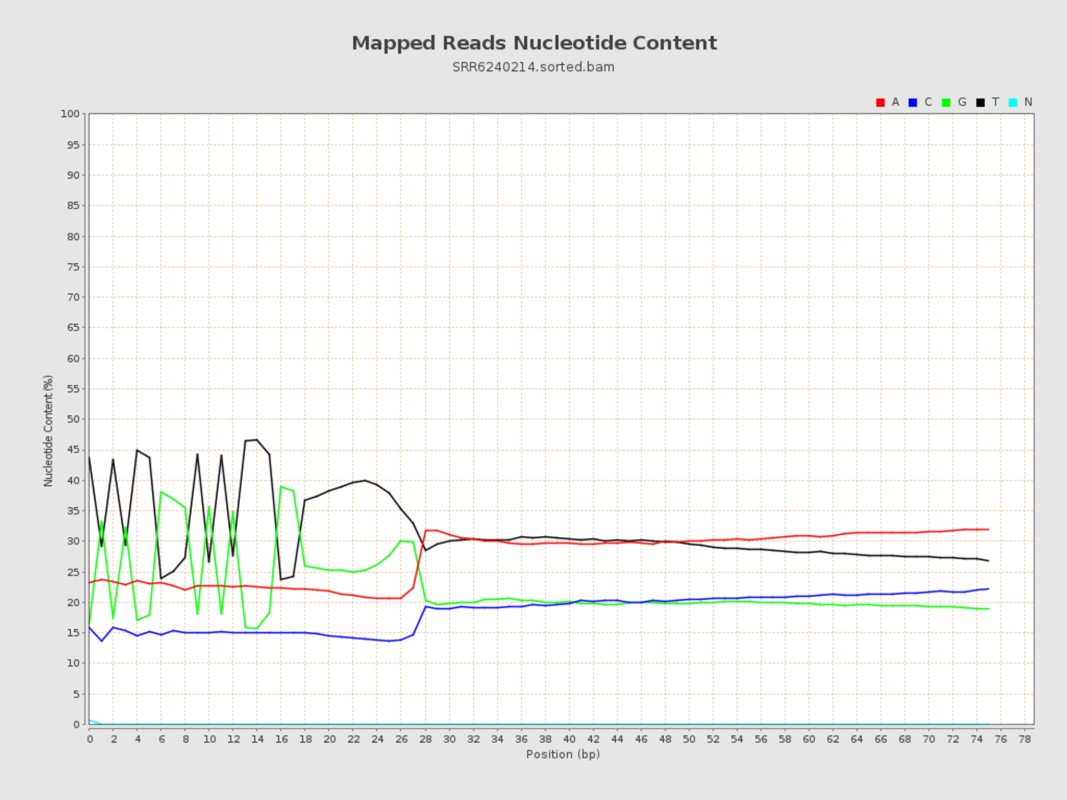
6. Results : Genome Fraction Coverage



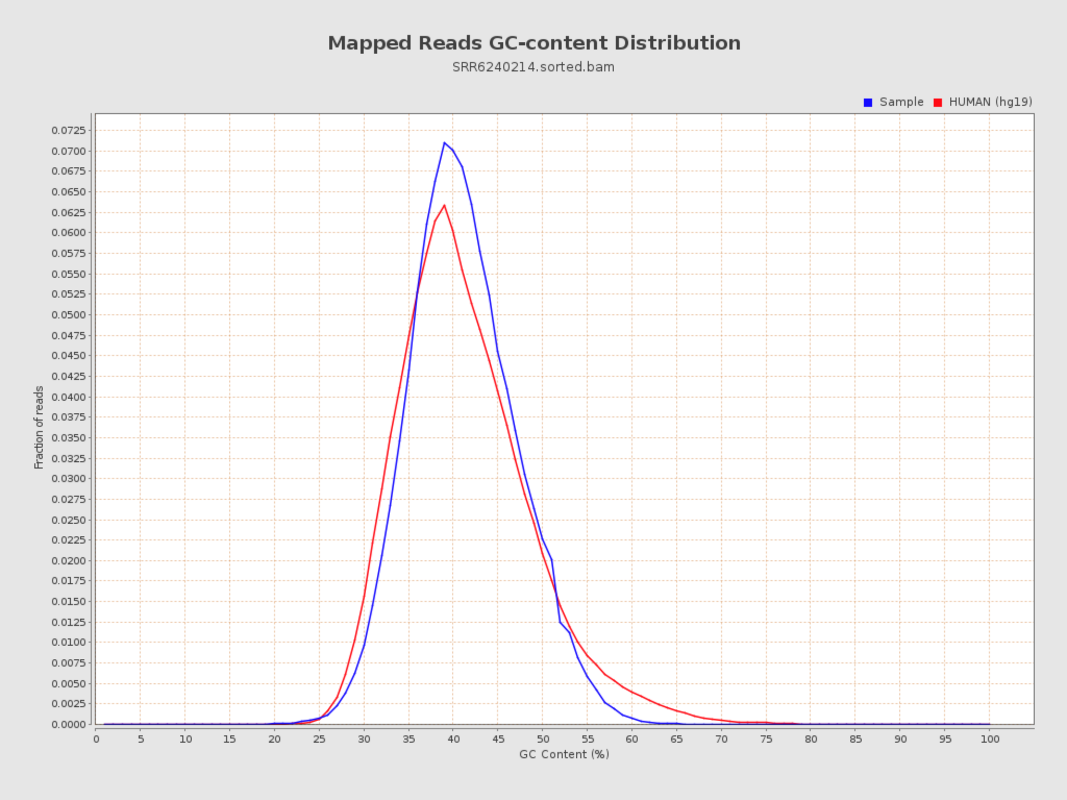
7. Results : Duplication Rate Histogram



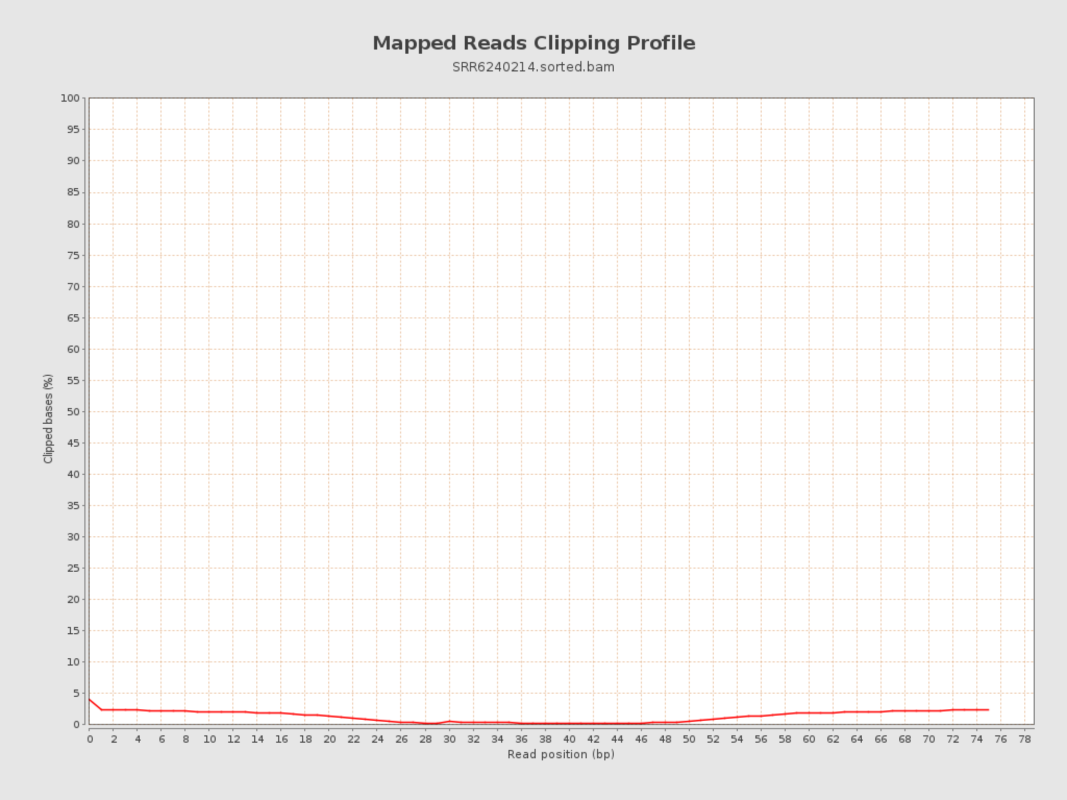
8. Results : Mapped Reads Nucleotide Content



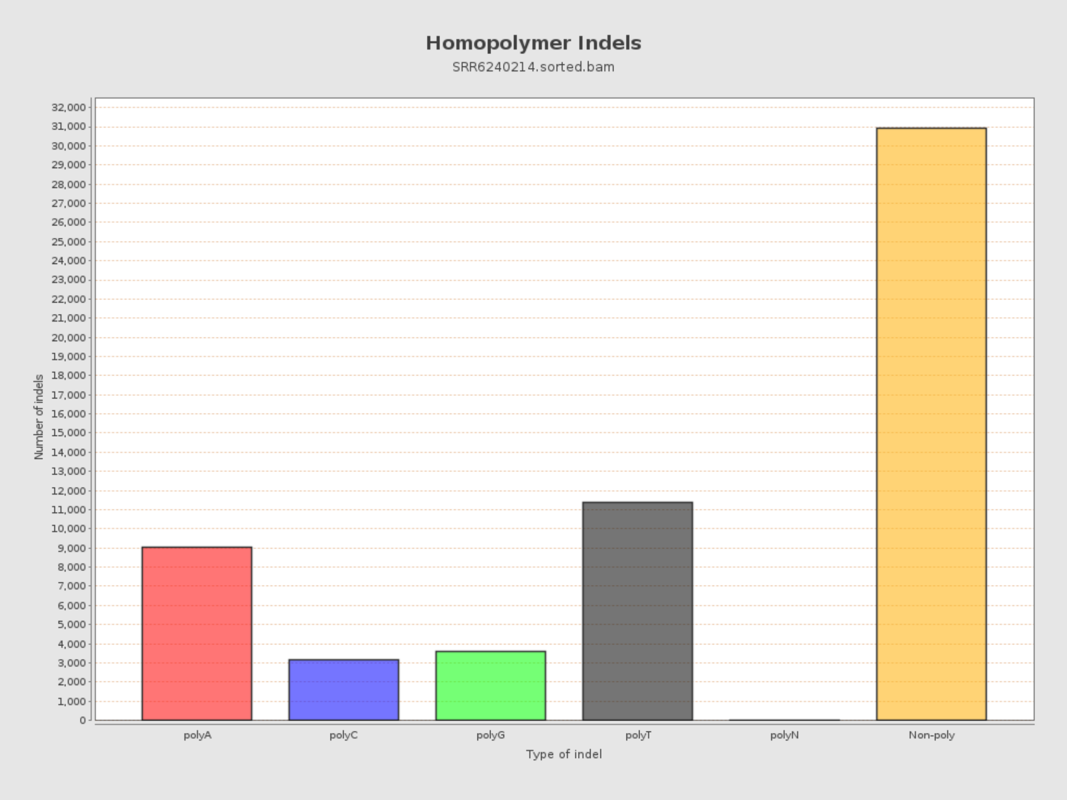
9. Results : Mapped Reads GC-content Distribution



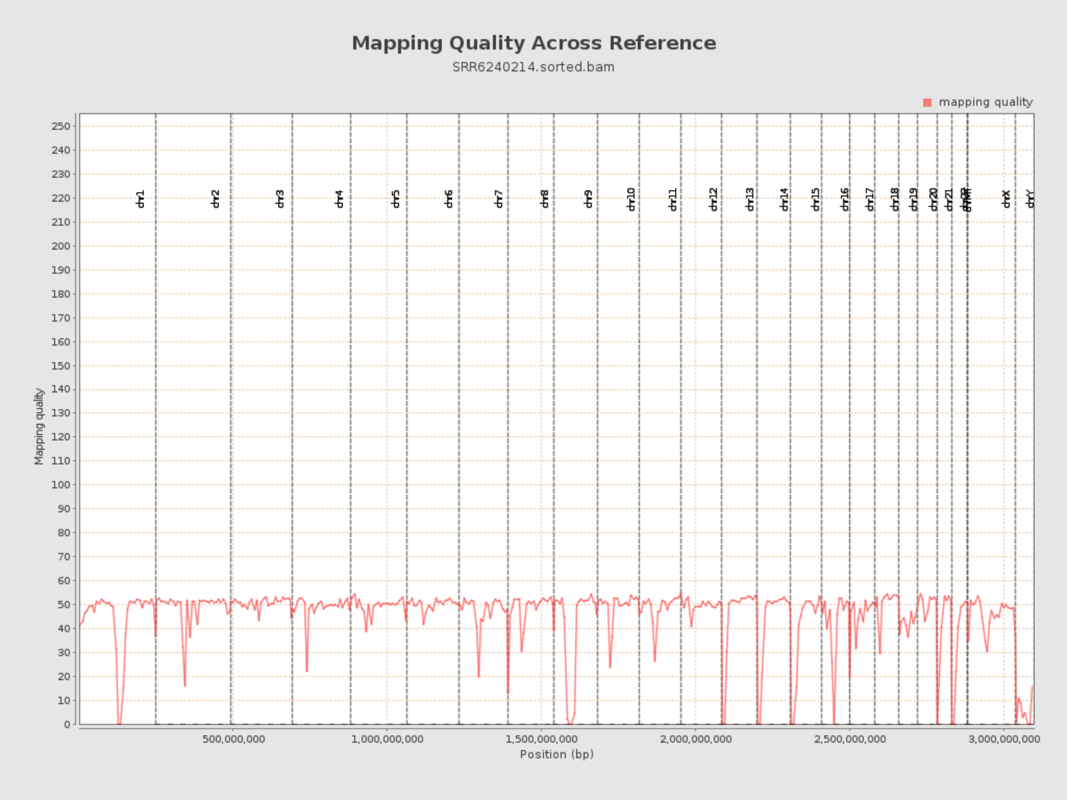
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram