Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 19:21:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230360.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_SRR6230360 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230360.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 19:21:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230360.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,953,318
Mapped reads	3,533,192 / 89.37%
Unmapped reads	420,126 / 10.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,416 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	161,458 / 4.08%
Duplication rate	3.24%
Clipped reads	1,780,732 / 45.04%

2.2. ACGT Content

Number/percentage of A's	63,590,969 / 27.55%
Number/percentage of C's	43,415,551 / 18.81%
Number/percentage of T's	70,905,036 / 30.72%
Number/percentage of G's	52,795,638 / 22.88%
Number/percentage of N's	93,281 / 0.04%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0746

Standard Deviation	0.5977

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

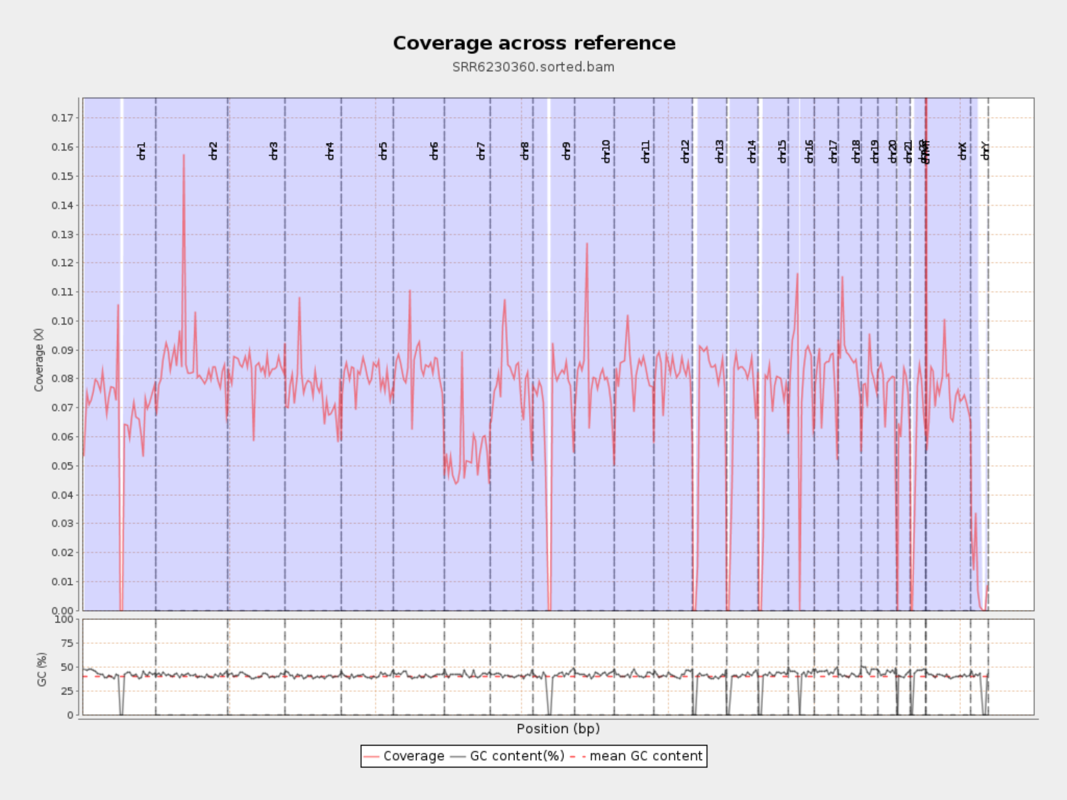
General error rate	0.88%
Mismatches	2,002,659
Insertions	20,124
Mapped reads with at least one insertion	0.56%
Deletions	58,770
Mapped reads with at least one deletion	1.65%
Homopolymer indels	45.56%

2.6. Chromosome stats

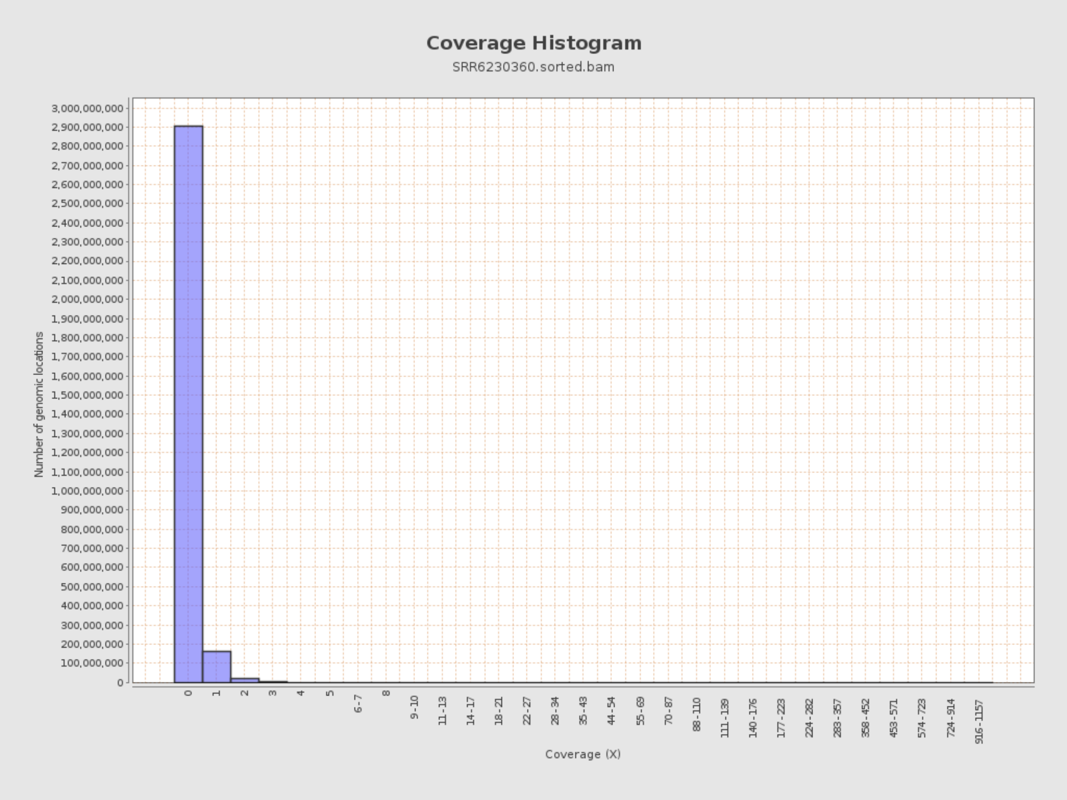
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16805168	0.0674	0.9523
chr2	243199373	20864229	0.0858	0.8725
chr3	198022430	16513285	0.0834	0.3362
chr4	191154276	14493863	0.0758	0.3724
chr5	180915260	14566958	0.0805	0.3323
chr6	171115067	14411131	0.0842	0.4675
chr7	159138663	8458096	0.0531	0.5643

chr8	146364022	11591561	0.0792	0.7374
chr9	141213431	9635283	0.0682	0.6558
chr10	135534747	10957578	0.0808	0.6094
chr11	135006516	11160371	0.0827	0.6511
chr12	133851895	11089160	0.0828	0.348
chr13	115169878	8173162	0.071	0.3086
chr14	107349540	7379224	0.0687	0.3652
chr15	102531392	6487145	0.0633	0.3055
chr16	90354753	7102250	0.0786	0.45
chr17	81195210	6576981	0.081	0.3855
chr18	78077248	6961426	0.0892	1.2893
chr19	59128983	4666236	0.0789	0.7385
chr20	63025520	4875834	0.0774	0.3555
chr21	48129895	3111264	0.0646	0.353
chr22	51304566	2741163	0.0534	0.2684
chrMT	16571	22022	1.3289	1.5287
chrX	155270560	11623407	0.0749	0.3996
chrY	59373566	630857	0.0106	0.2476

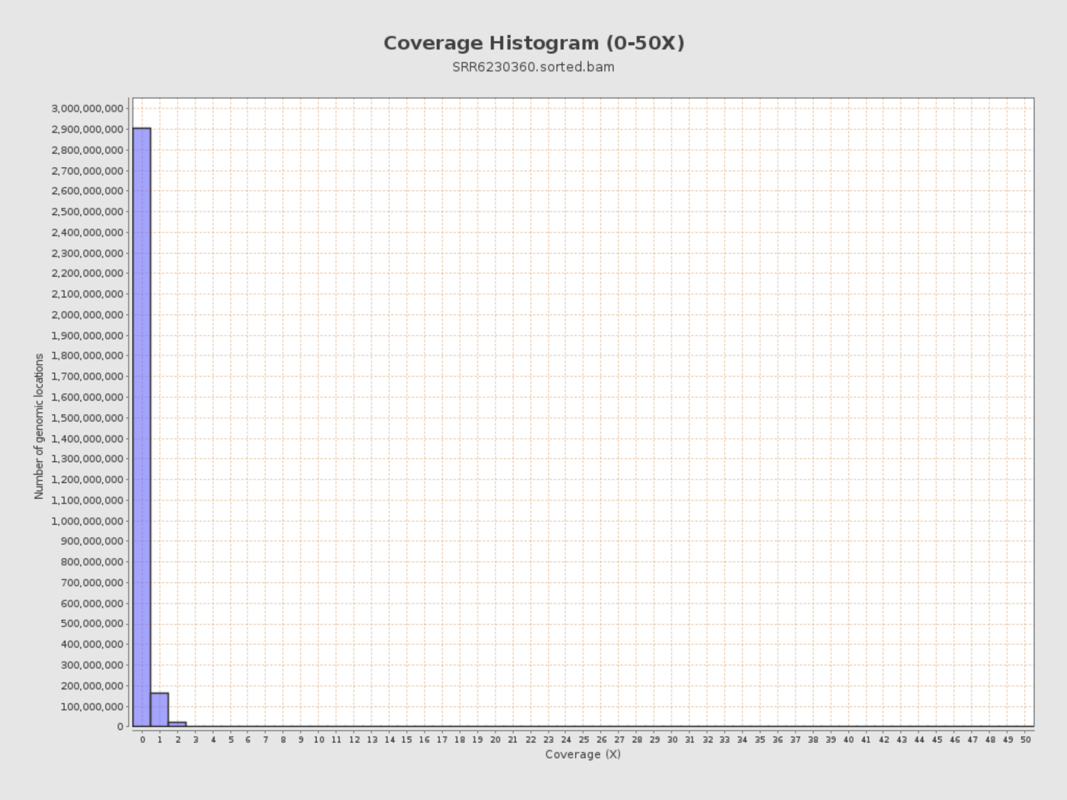
3. Results : Coverage across reference



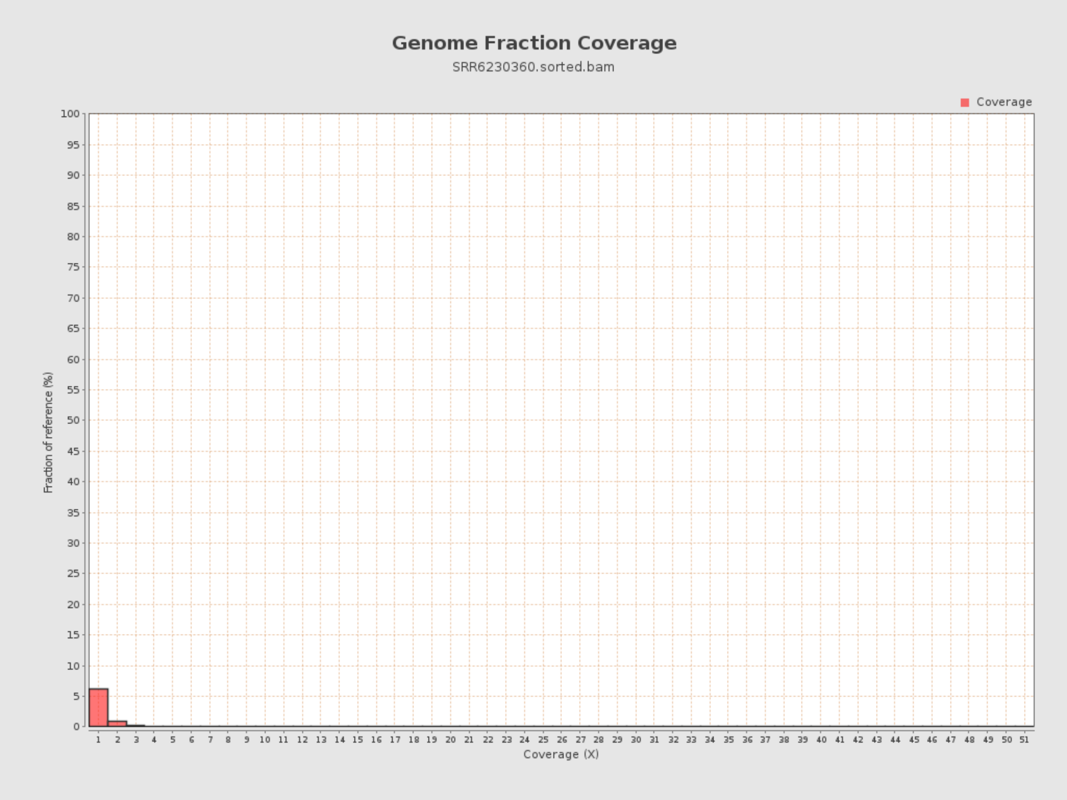
4. Results : Coverage Histogram



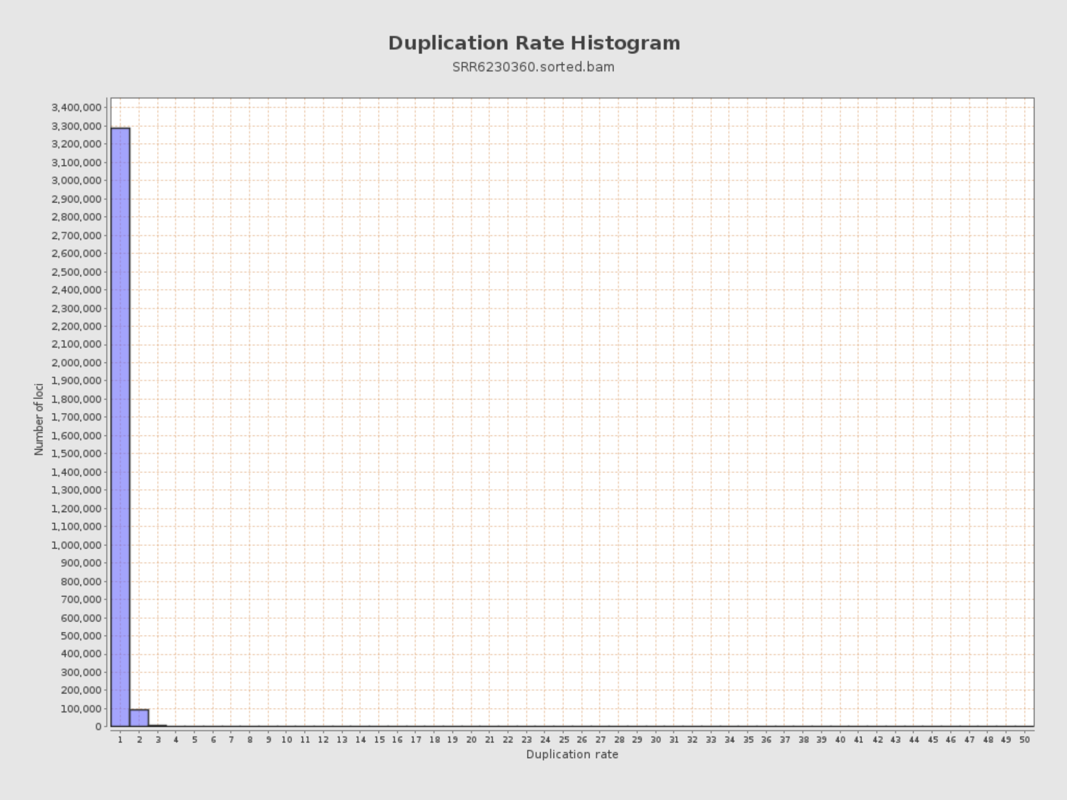
5. Results : Coverage Histogram (0-50X)



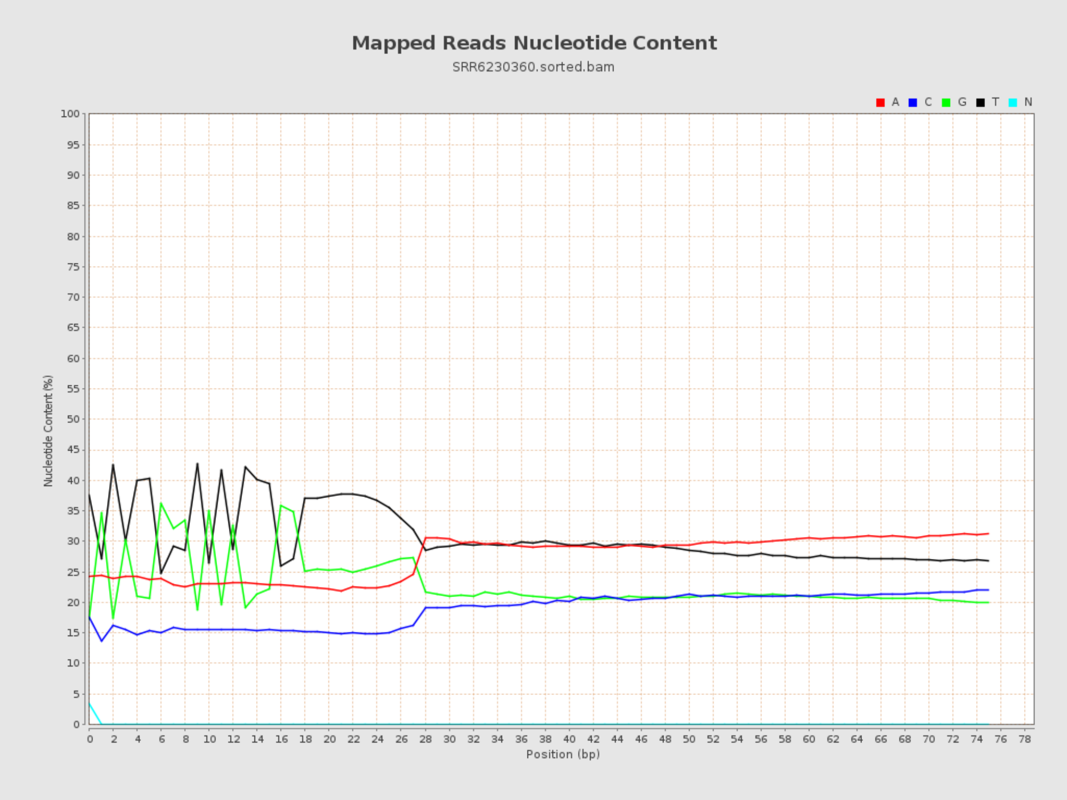
6. Results : Genome Fraction Coverage



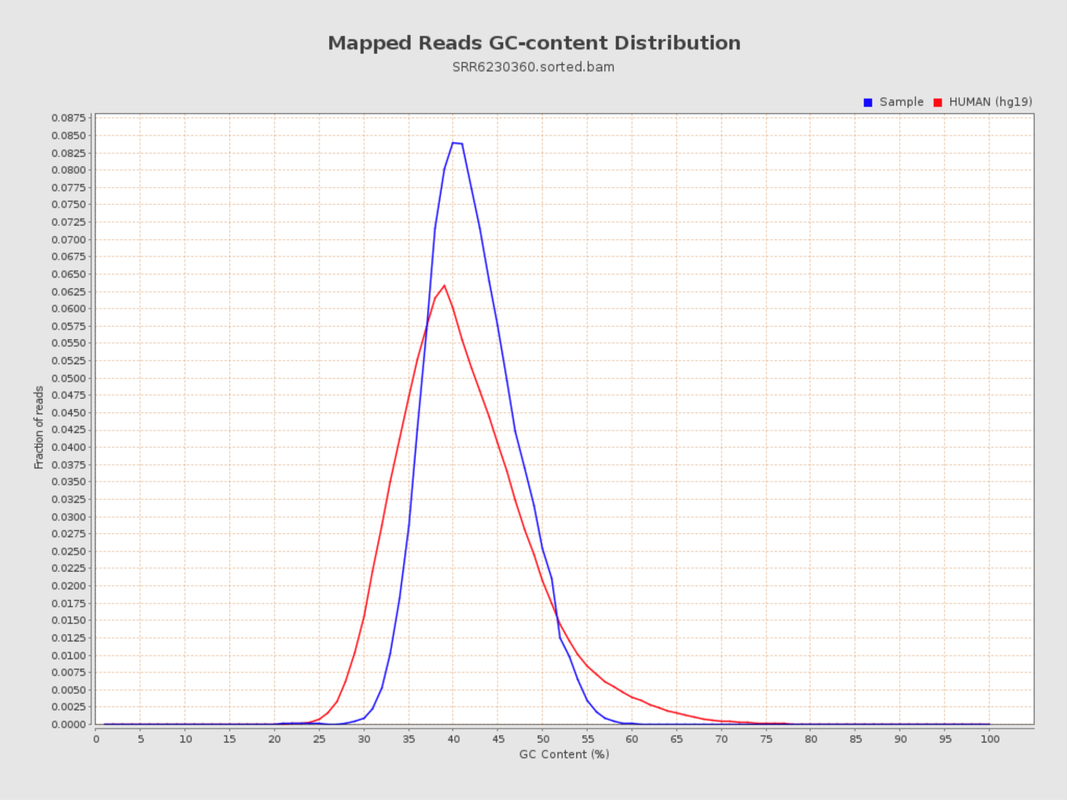
7. Results : Duplication Rate Histogram



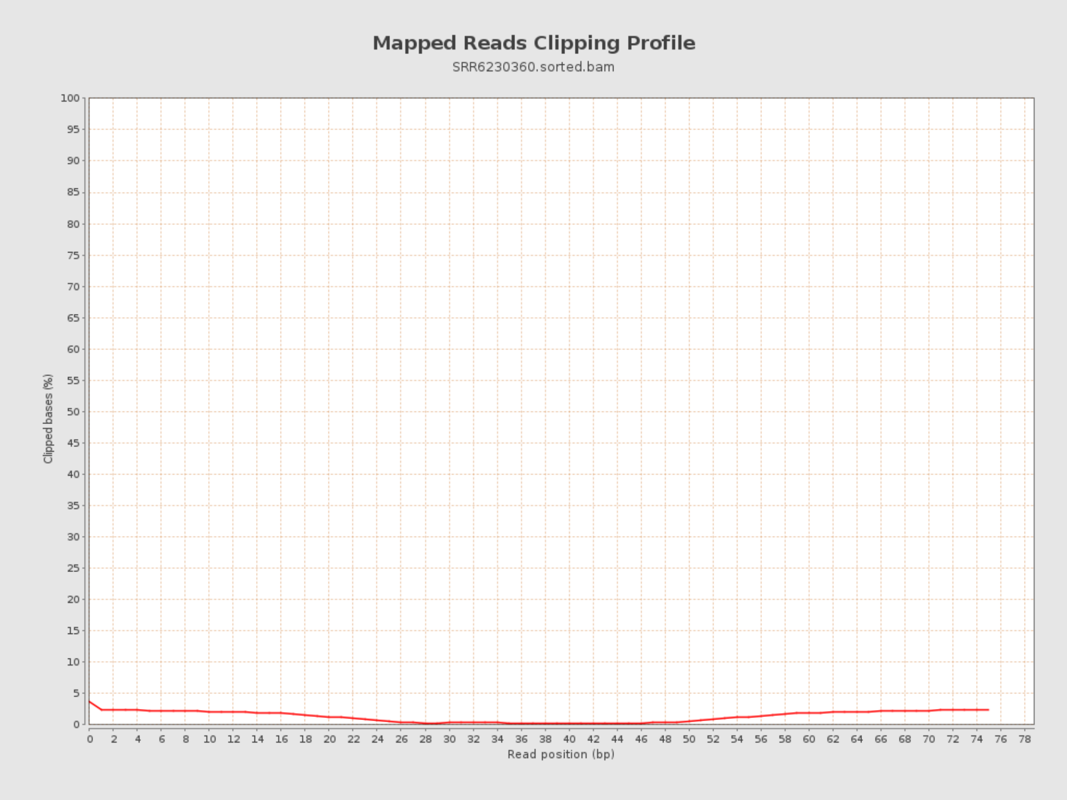
8. Results : Mapped Reads Nucleotide Content



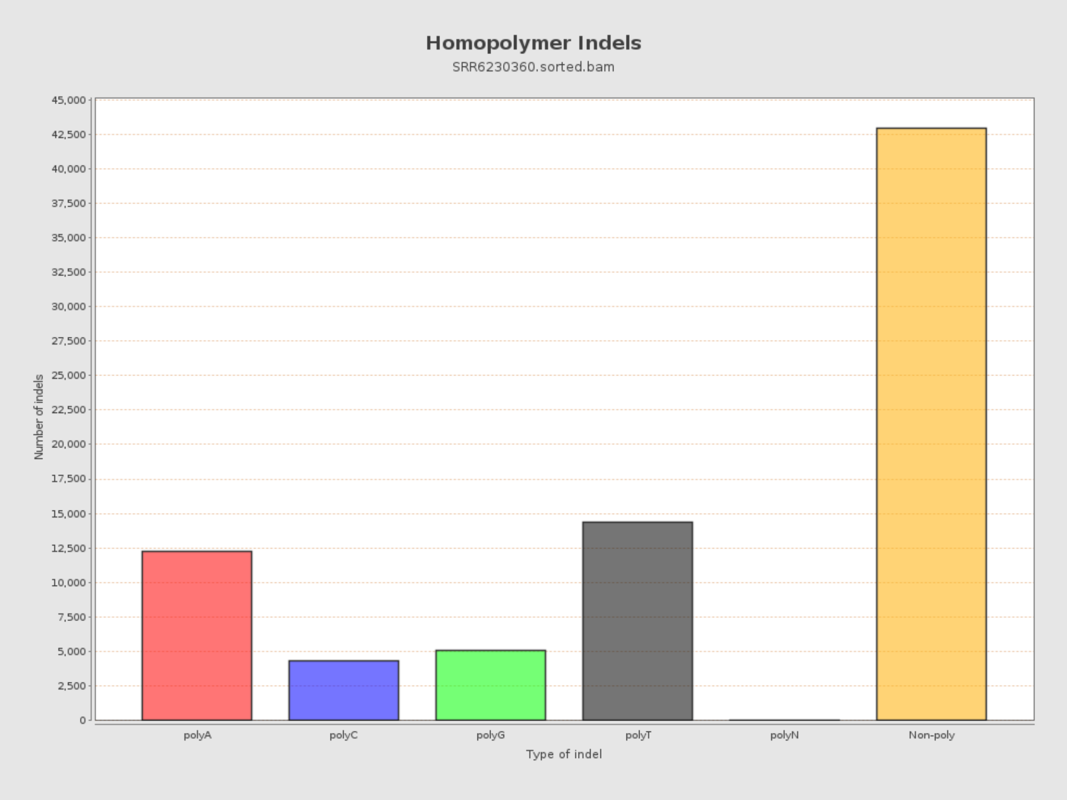
9. Results : Mapped Reads GC-content Distribution



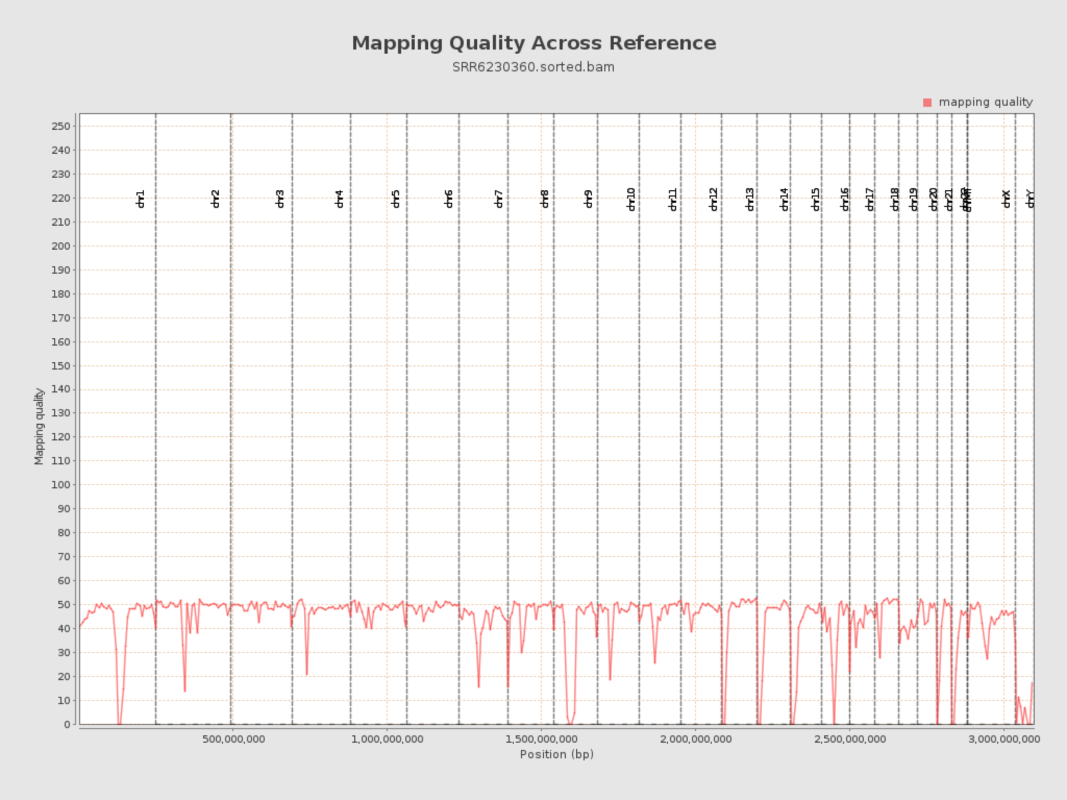
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram