Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:01:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230388.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_SRR6230388 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230388.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:01:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230388.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,328,927
Mapped reads	1,583,916 / 68.01%
Unmapped reads	745,011 / 31.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,167 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	104,621 / 4.49%
Duplication rate	5.35%
Clipped reads	902,325 / 38.74%

2.2. ACGT Content

Number/percentage of A's	26,592,665 / 26.45%
Number/percentage of C's	16,929,862 / 16.84%
Number/percentage of T's	34,386,837 / 34.2%
Number/percentage of G's	22,451,811 / 22.33%
Number/percentage of N's	178,431 / 0.18%
GC Percentage	39.17%

2.3. Coverage

Mean	0.0325

Standard Deviation	0.3702

2.4. Mapping Quality

Mean Mapping Quality	44.94

2.5. Mismatches and indels

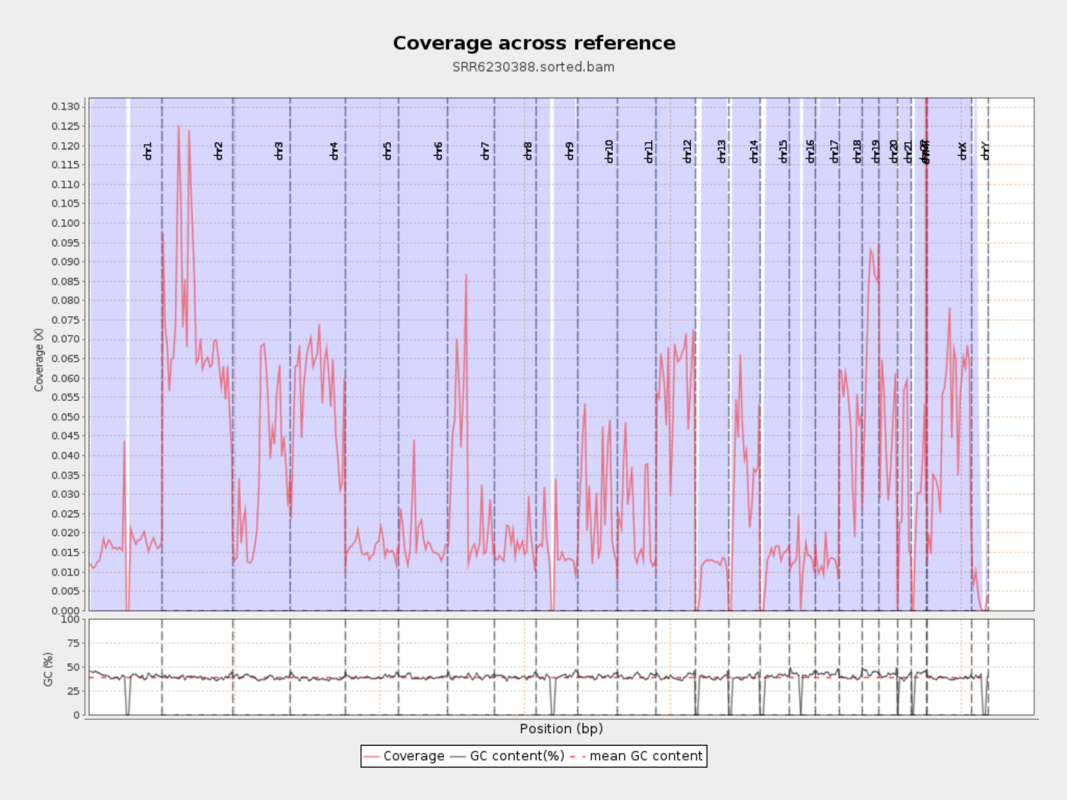
General error rate	1.13%
Mismatches	1,125,401
Insertions	8,553
Mapped reads with at least one insertion	0.54%
Deletions	27,992
Mapped reads with at least one deletion	1.75%
Homopolymer indels	48.84%

2.6. Chromosome stats

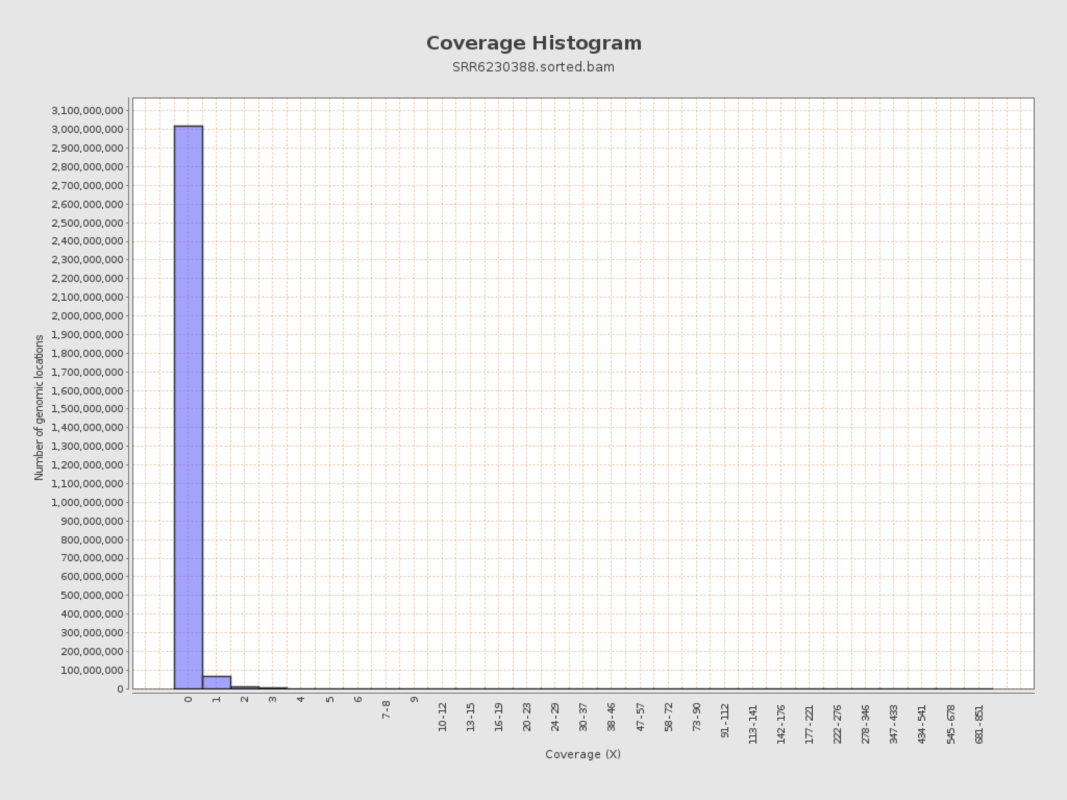
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4066283	0.0163	0.6785
chr2	243199373	17760498	0.073	0.4854
chr3	198022430	6954121	0.0351	0.2267
chr4	191154276	10844961	0.0567	0.2921
chr5	180915260	2908758	0.0161	0.1552
chr6	171115067	3193918	0.0187	0.2087
chr7	159138663	5225055	0.0328	0.7391

chr8	146364022	2460384	0.0168	0.3085
chr9	141213431	2061917	0.0146	0.2843
chr10	135534747	3891894	0.0287	0.2521
chr11	135006516	3210447	0.0238	0.2937
chr12	133851895	7921059	0.0592	0.2981
chr13	115169878	1203619	0.0105	0.1203
chr14	107349540	3718871	0.0346	0.2328
chr15	102531392	1245893	0.0122	0.1325
chr16	90354753	1149981	0.0127	0.1491
chr17	81195210	1010721	0.0124	0.1437
chr18	78077248	3843146	0.0492	0.5139
chr19	59128983	4496607	0.076	0.4252
chr20	63025520	2880684	0.0457	0.2618
chr21	48129895	1438941	0.0299	0.2134
chr22	51304566	1376402	0.0268	0.1948
chrMT	16571	76767	4.6326	3.9554
chrX	155270560	7409718	0.0477	0.3055
chrY	59373566	233554	0.0039	0.0837

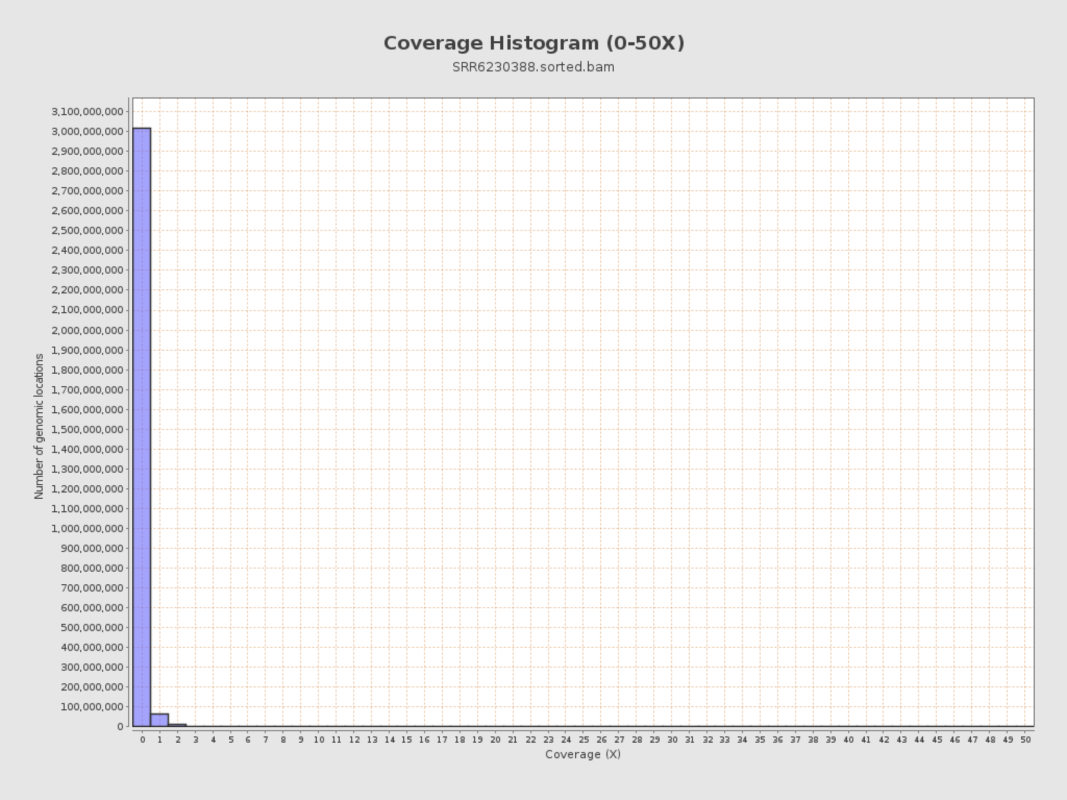
3. Results : Coverage across reference



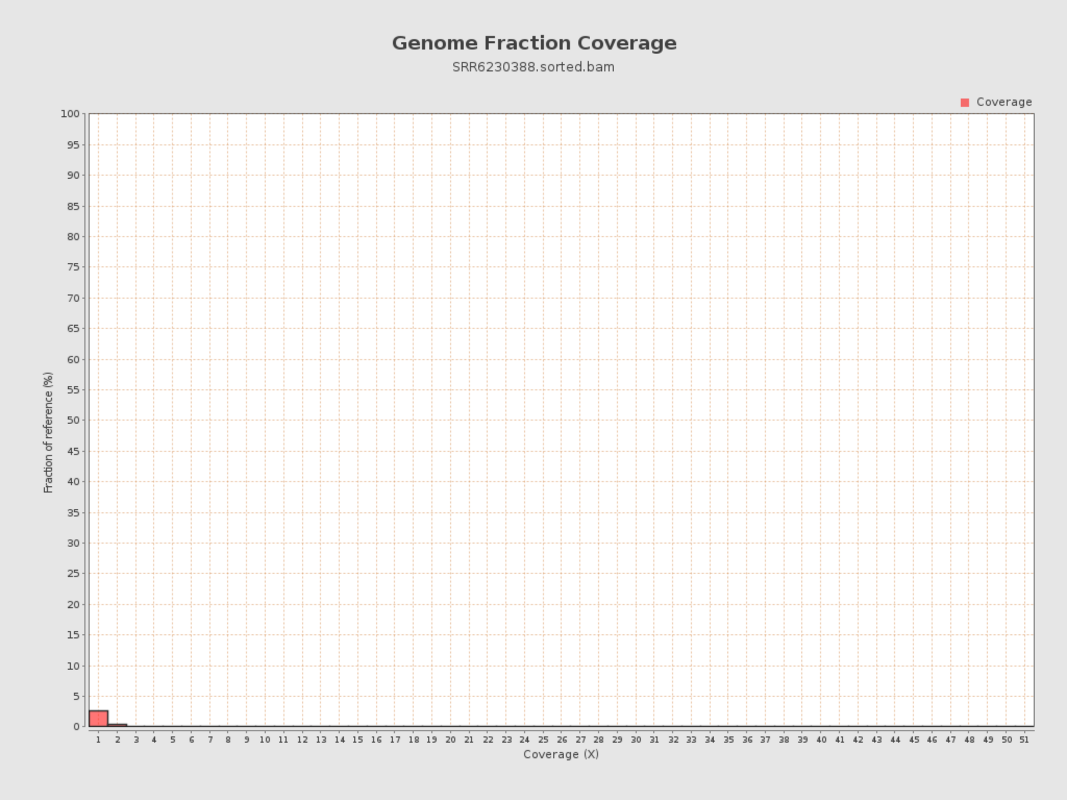
4. Results : Coverage Histogram



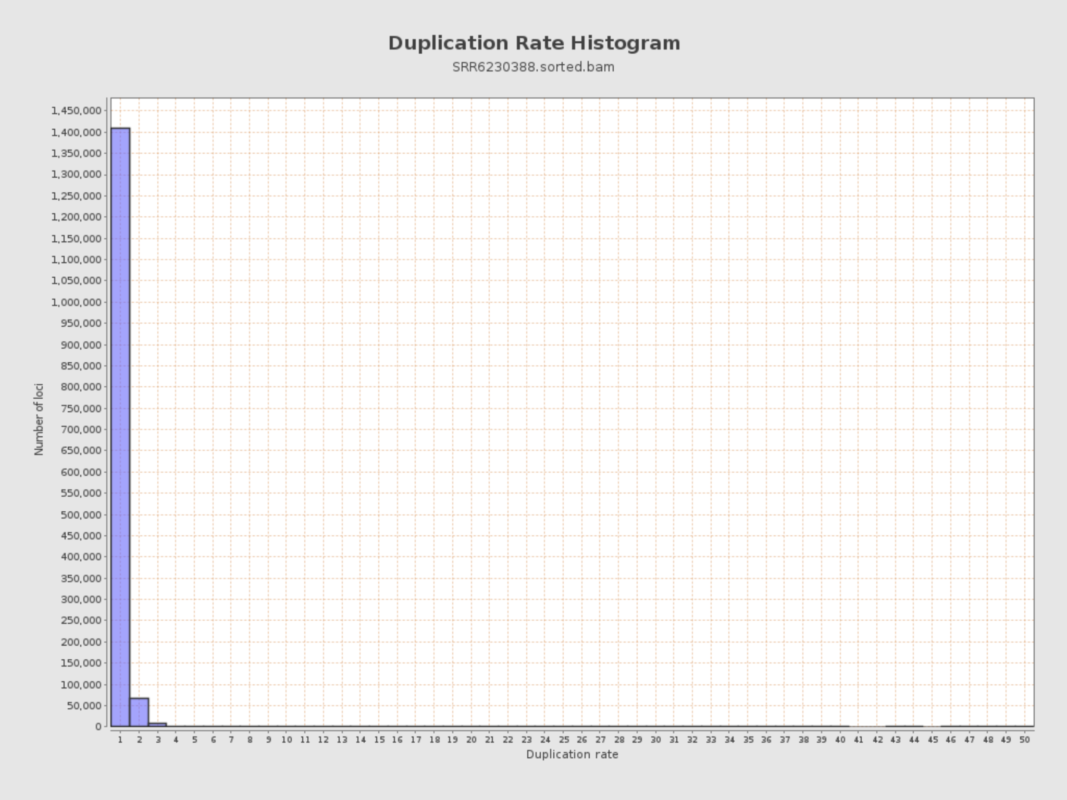
5. Results : Coverage Histogram (0-50X)



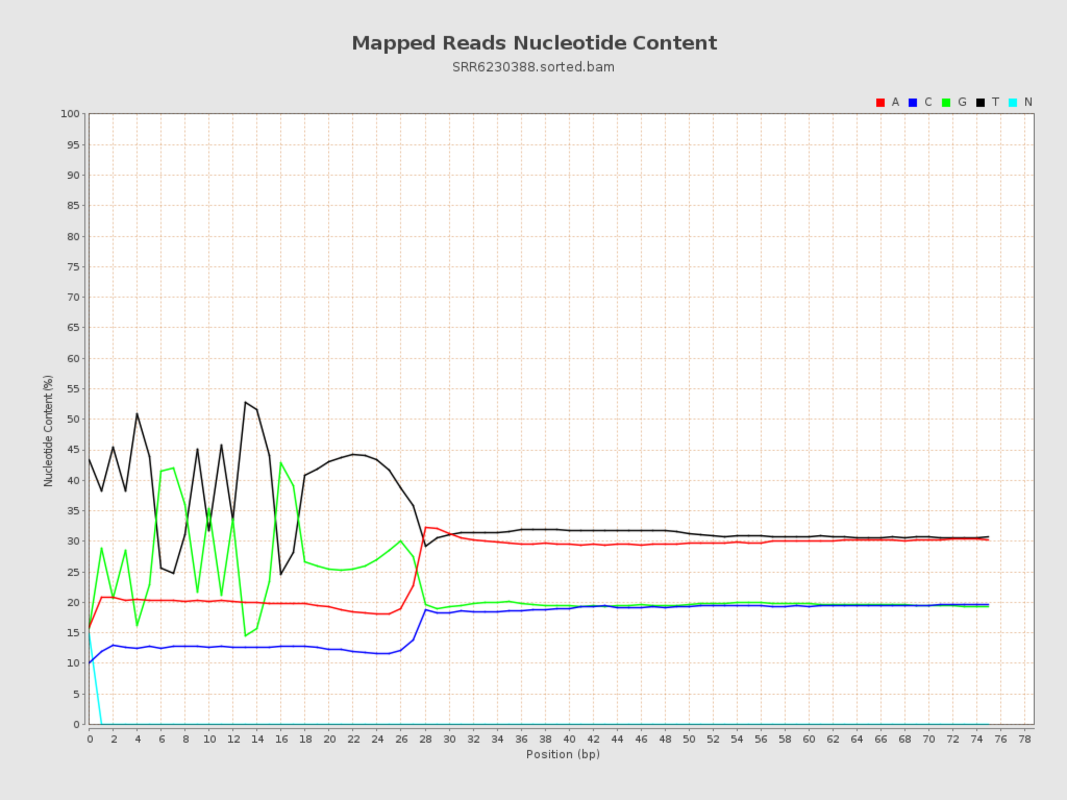
6. Results : Genome Fraction Coverage



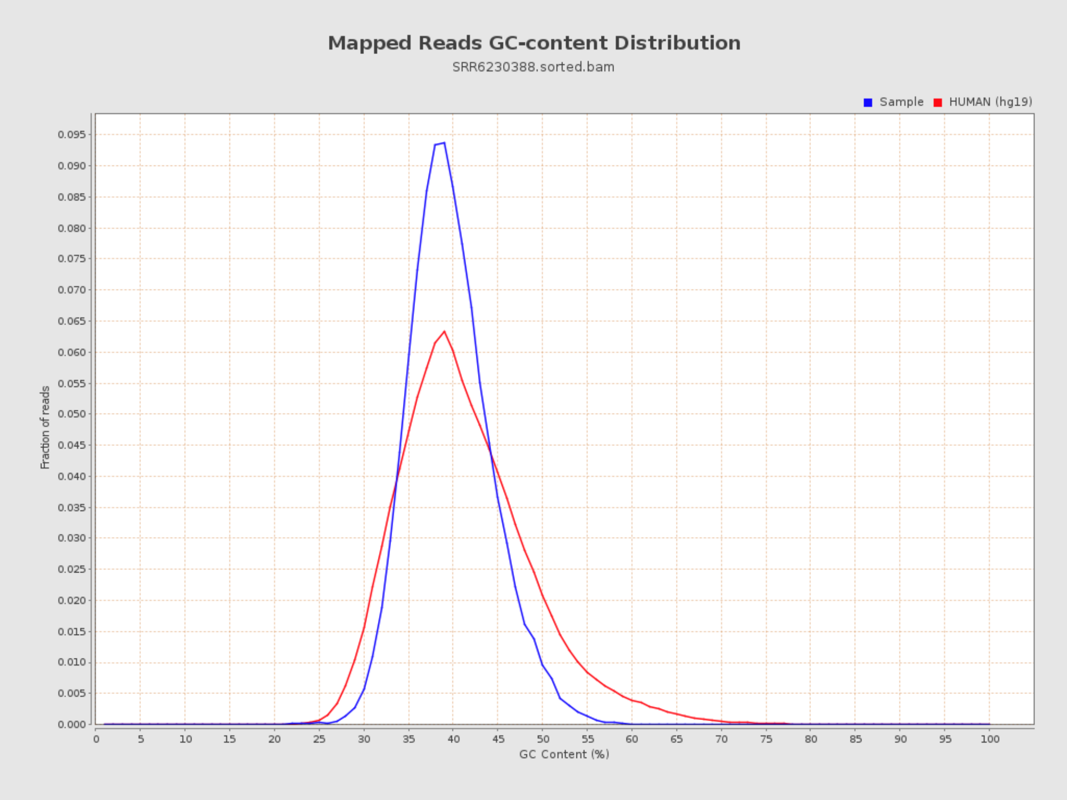
7. Results : Duplication Rate Histogram



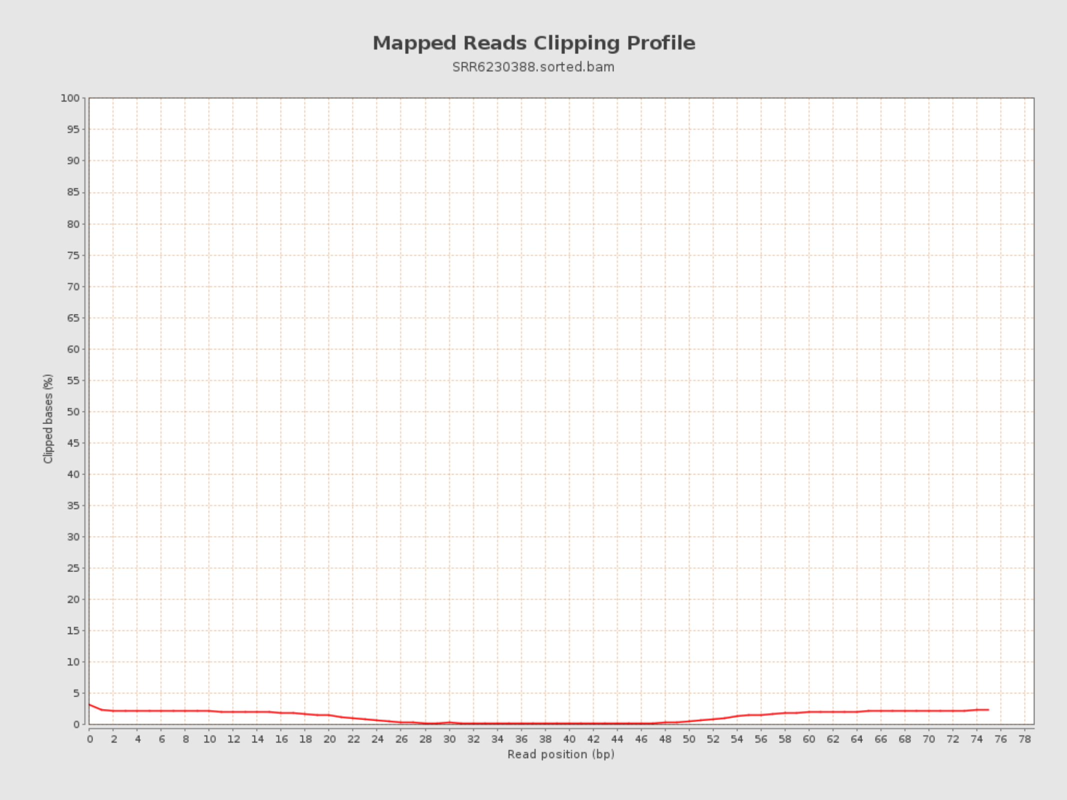
8. Results : Mapped Reads Nucleotide Content



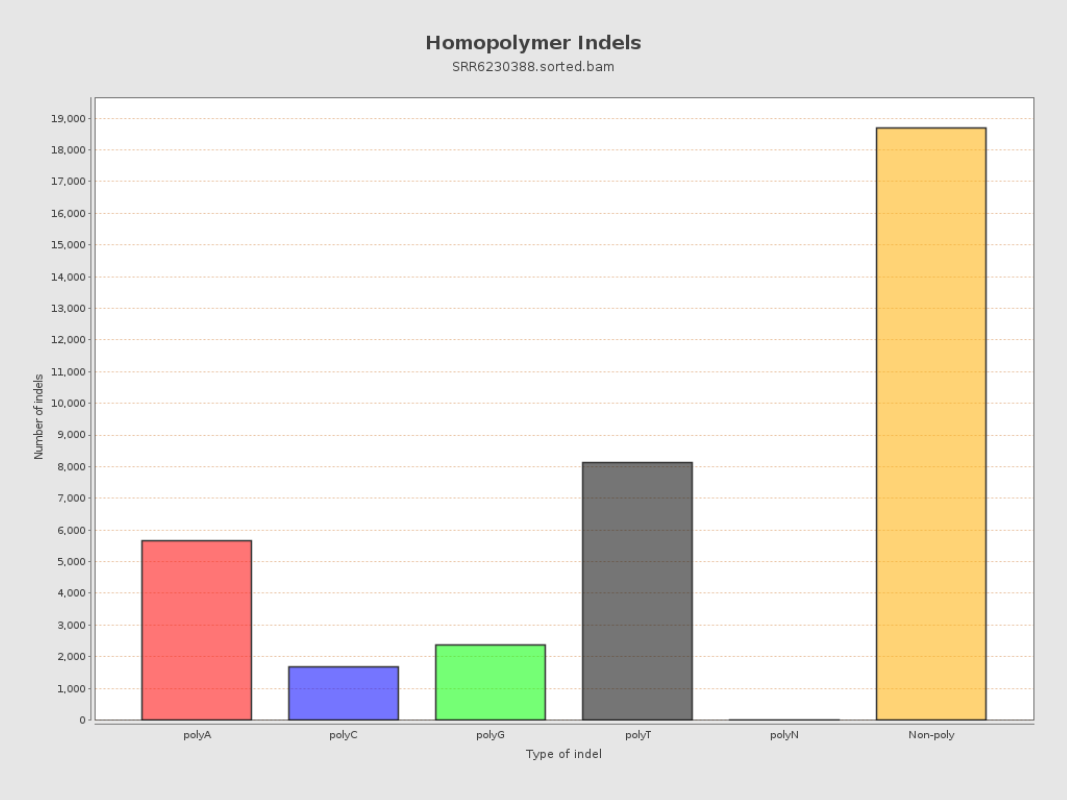
9. Results : Mapped Reads GC-content Distribution



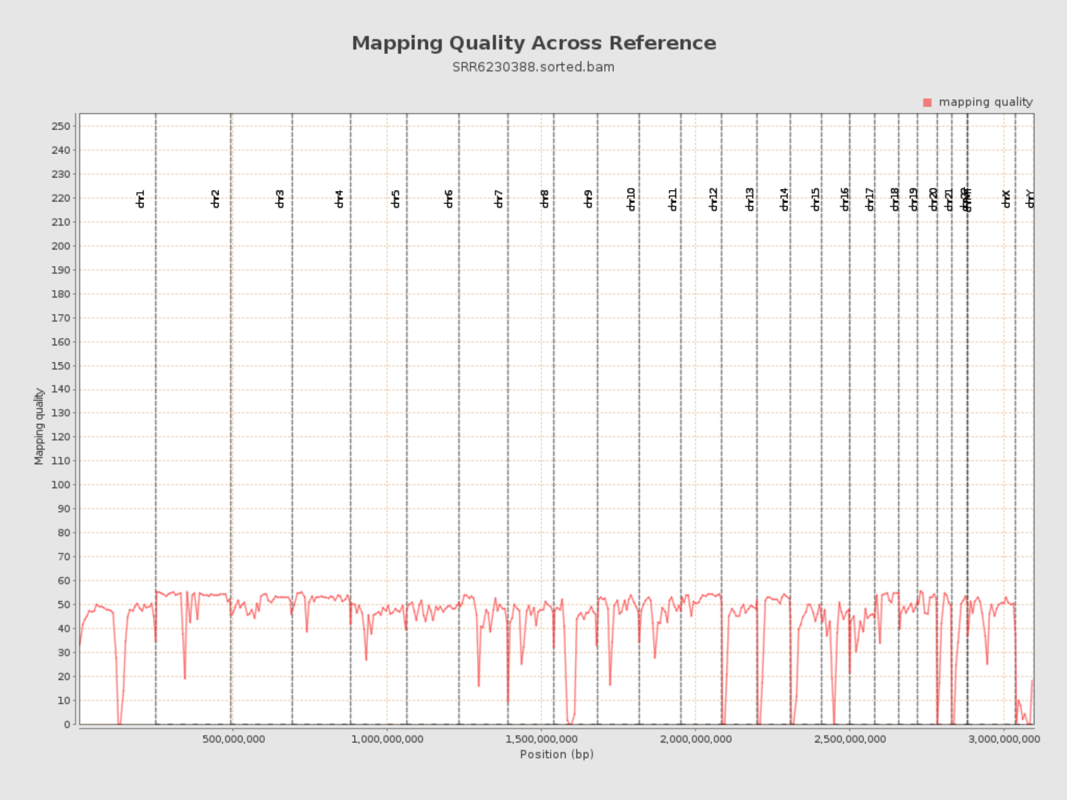
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram