Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:42:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230382.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_SRR6230382 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230382.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:42:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230382.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,303,771
Mapped reads	2,772,076 / 83.91%
Unmapped reads	531,695 / 16.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,069 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	130,962 / 3.96%
Duplication rate	3.54%
Clipped reads	1,328,163 / 40.2%

2.2. ACGT Content

Number/percentage of A's	49,078,339 / 26.96%
Number/percentage of C's	31,733,720 / 17.43%
Number/percentage of T's	60,338,711 / 33.14%
Number/percentage of G's	40,557,044 / 22.28%
Number/percentage of N's	348,292 / 0.19%
GC Percentage	39.71%

2.3. Coverage

Mean	0.0588

Standard Deviation	0.4908

2.4. Mapping Quality

Mean Mapping Quality	46.7

2.5. Mismatches and indels

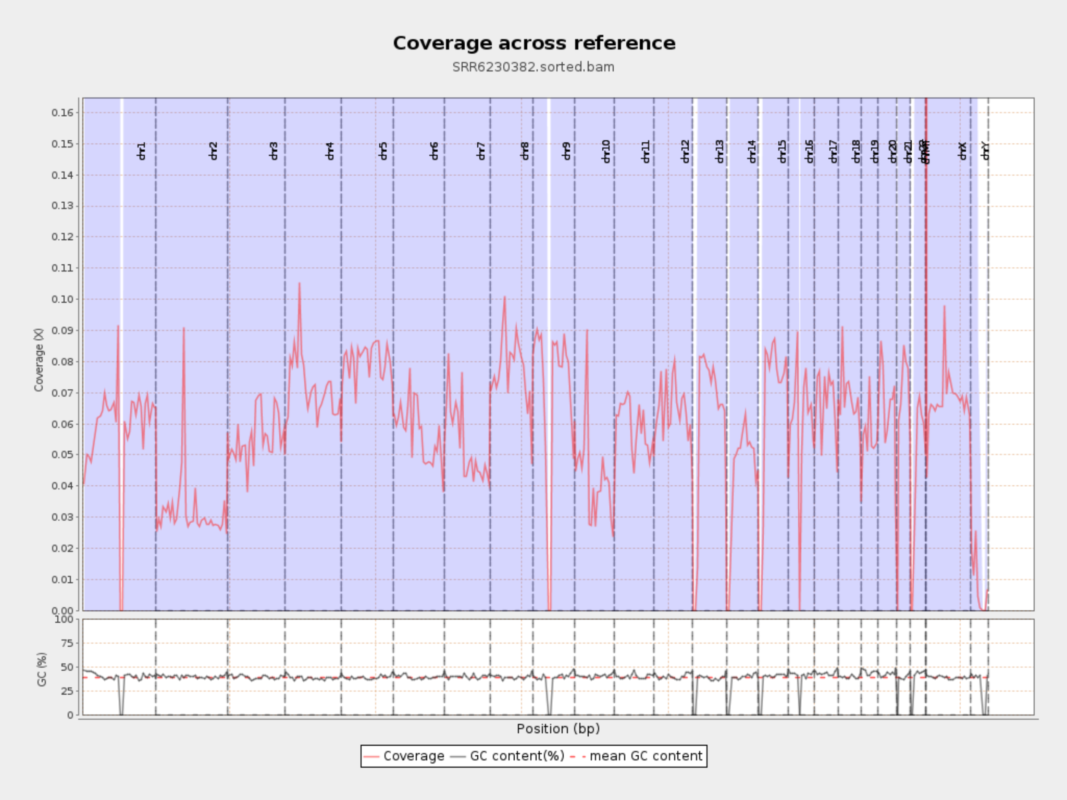
General error rate	0.98%
Mismatches	1,745,228
Insertions	16,572
Mapped reads with at least one insertion	0.59%
Deletions	46,707
Mapped reads with at least one deletion	1.67%
Homopolymer indels	48.21%

2.6. Chromosome stats

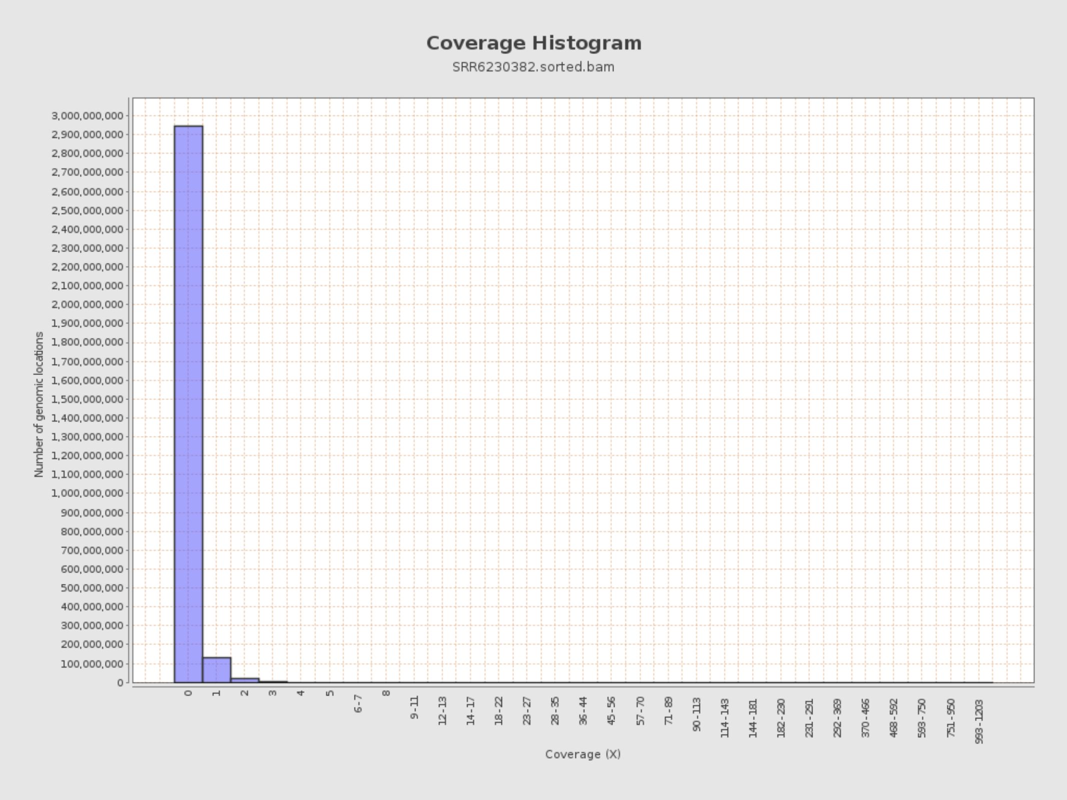
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14465764	0.058	0.7527
chr2	243199373	7857496	0.0323	0.5272
chr3	198022430	11023363	0.0557	0.2749
chr4	191154276	13785670	0.0721	0.3433
chr5	180915260	14469410	0.08	0.3304
chr6	171115067	9739485	0.0569	0.3809
chr7	159138663	8487088	0.0533	0.4748

chr8	146364022	11343769	0.0775	0.8258
chr9	141213431	9912068	0.0702	0.6139
chr10	135534747	5759615	0.0425	0.4441
chr11	135006516	7954846	0.0589	0.449
chr12	133851895	8697545	0.065	0.3097
chr13	115169878	7058908	0.0613	0.2852
chr14	107349540	4733832	0.0441	0.2946
chr15	102531392	6606495	0.0644	0.2955
chr16	90354753	5349061	0.0592	0.3552
chr17	81195210	5470077	0.0674	0.3351
chr18	78077248	5374268	0.0688	1.0958
chr19	59128983	3322354	0.0562	0.5472
chr20	63025520	4250043	0.0674	0.332
chr21	48129895	3136266	0.0652	0.3497
chr22	51304566	2275580	0.0444	0.2442
chrMT	16571	49071	2.9613	2.5989
chrX	155270560	10527867	0.0678	0.366
chrY	59373566	483357	0.0081	0.1849

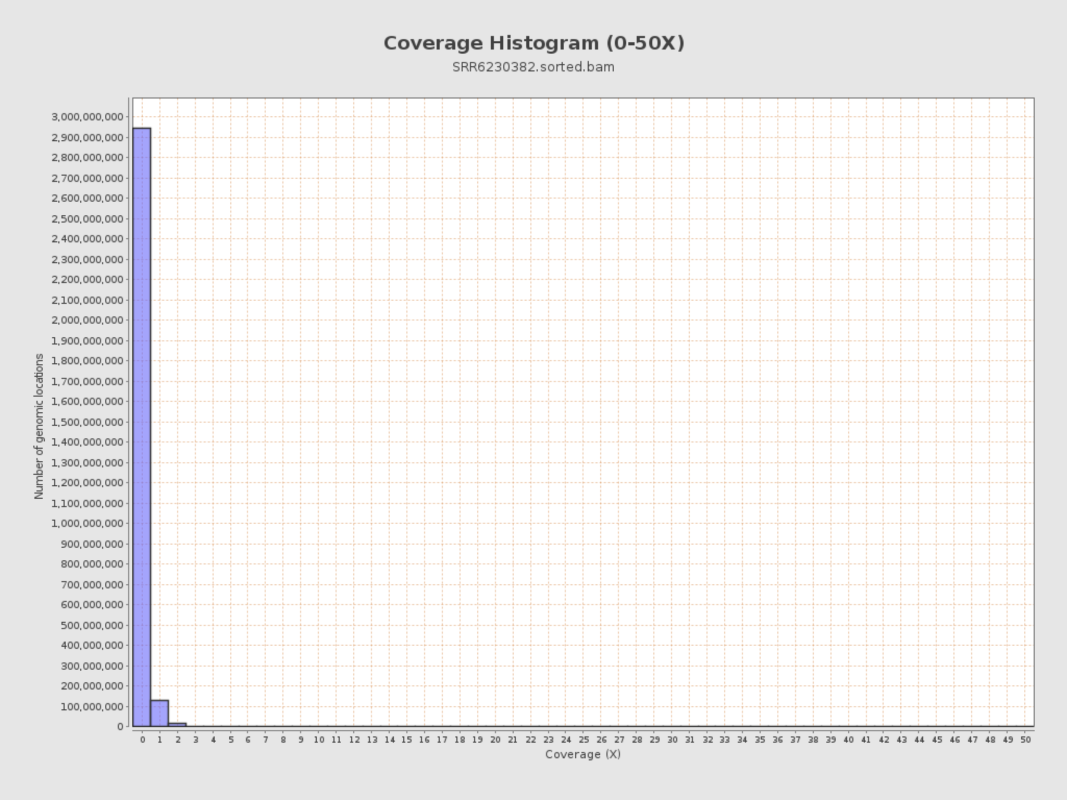
3. Results : Coverage across reference



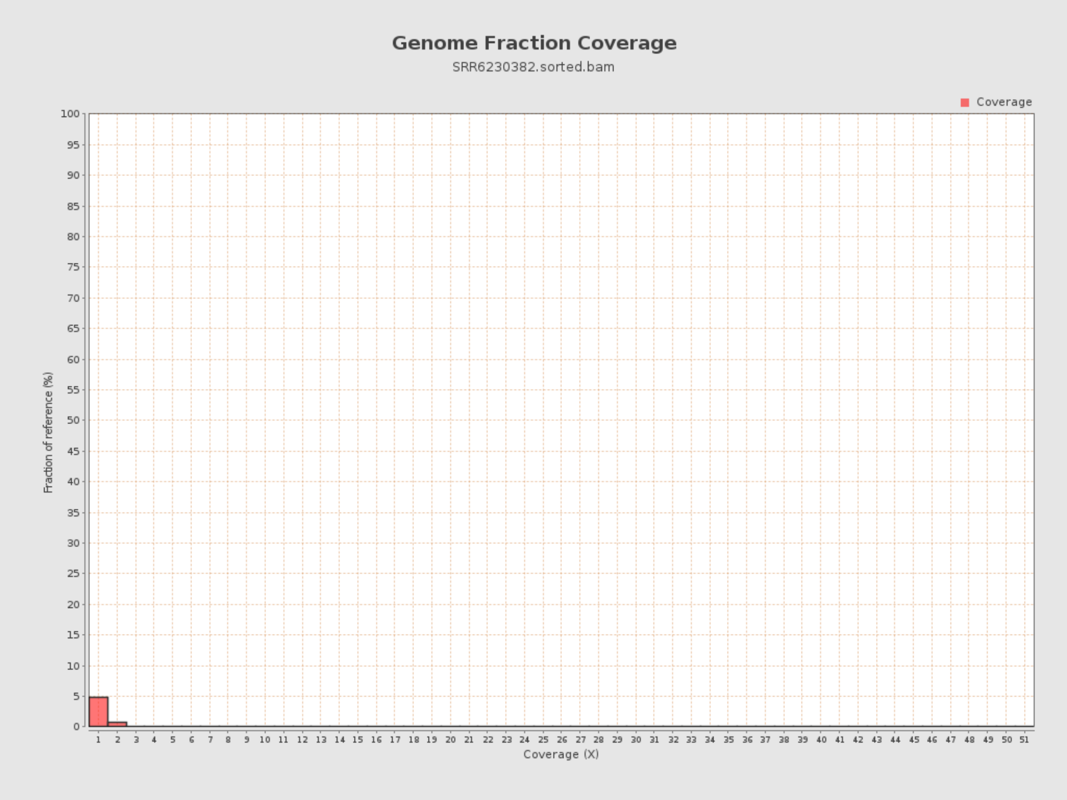
4. Results : Coverage Histogram



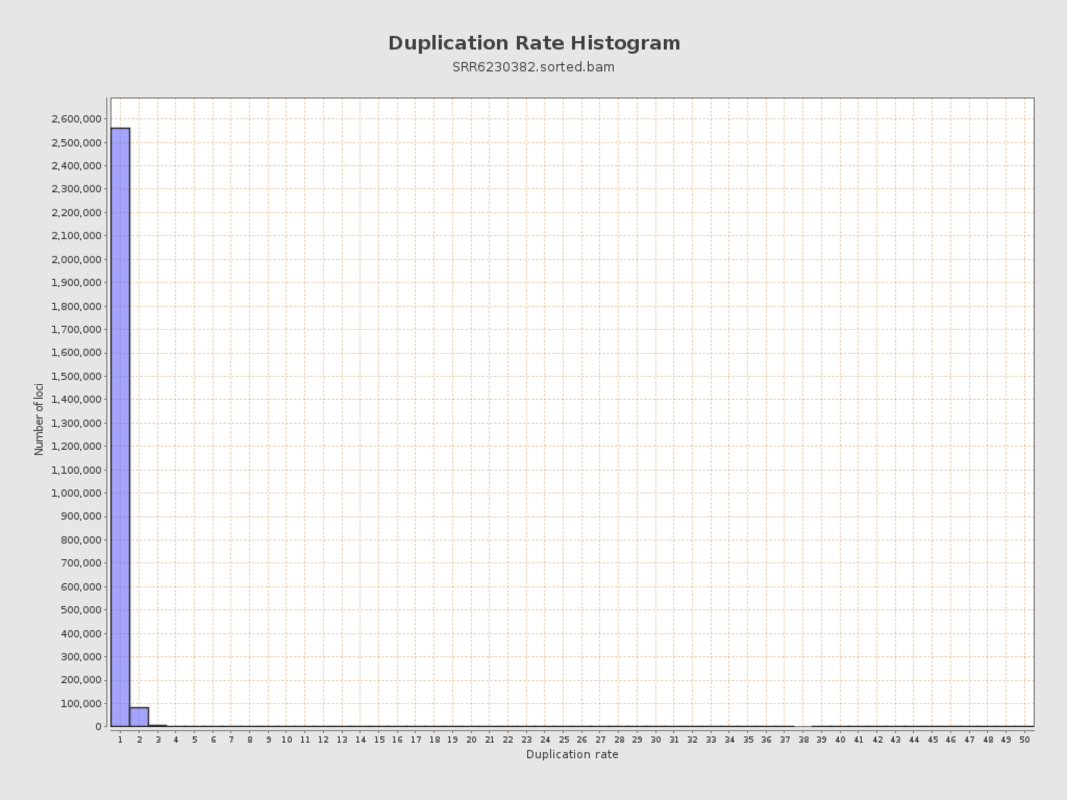
5. Results : Coverage Histogram (0-50X)



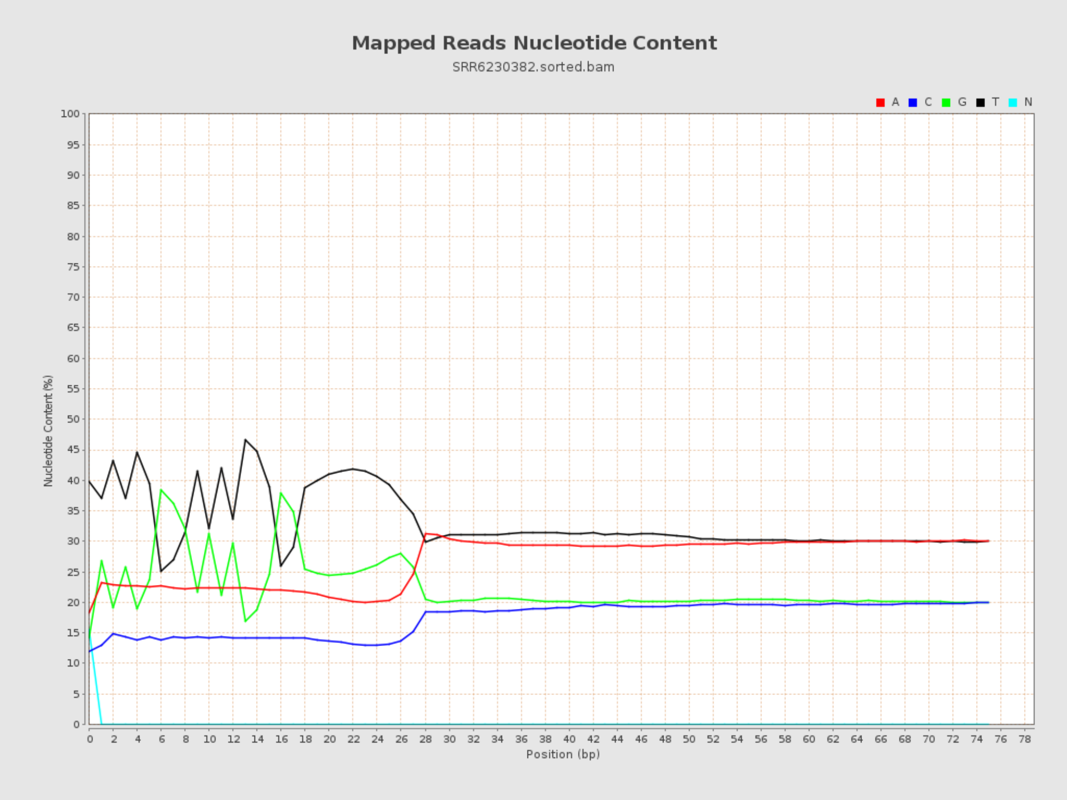
6. Results : Genome Fraction Coverage



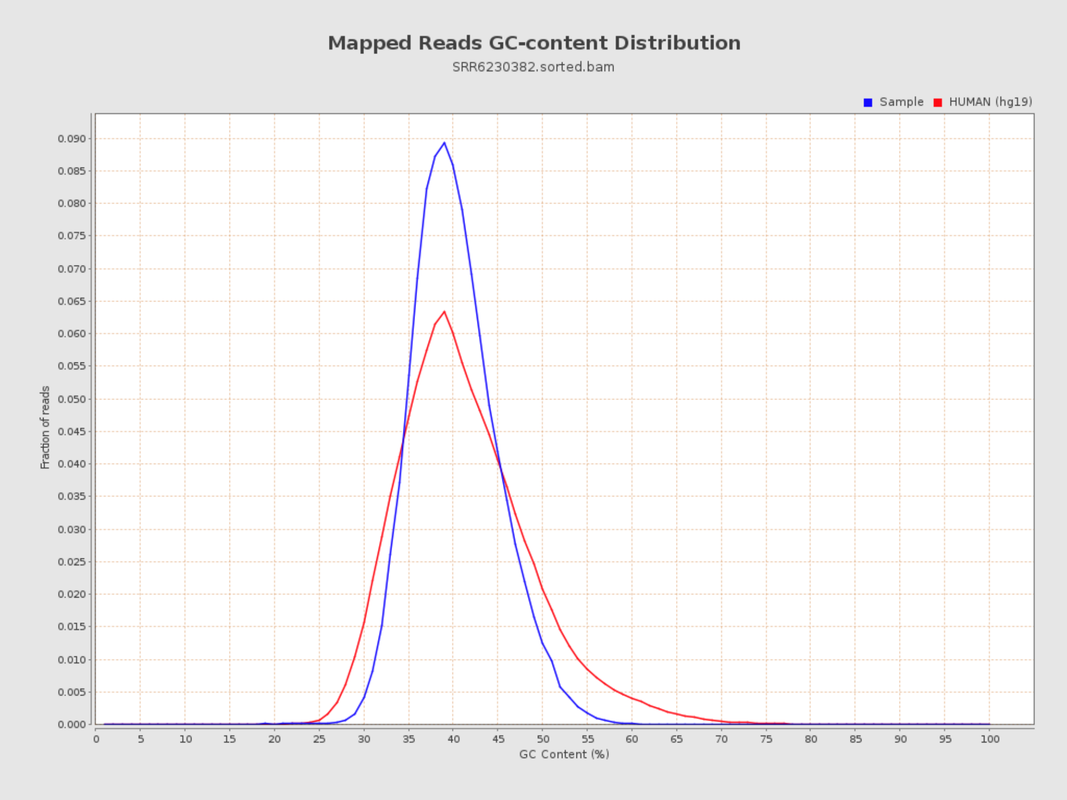
7. Results : Duplication Rate Histogram



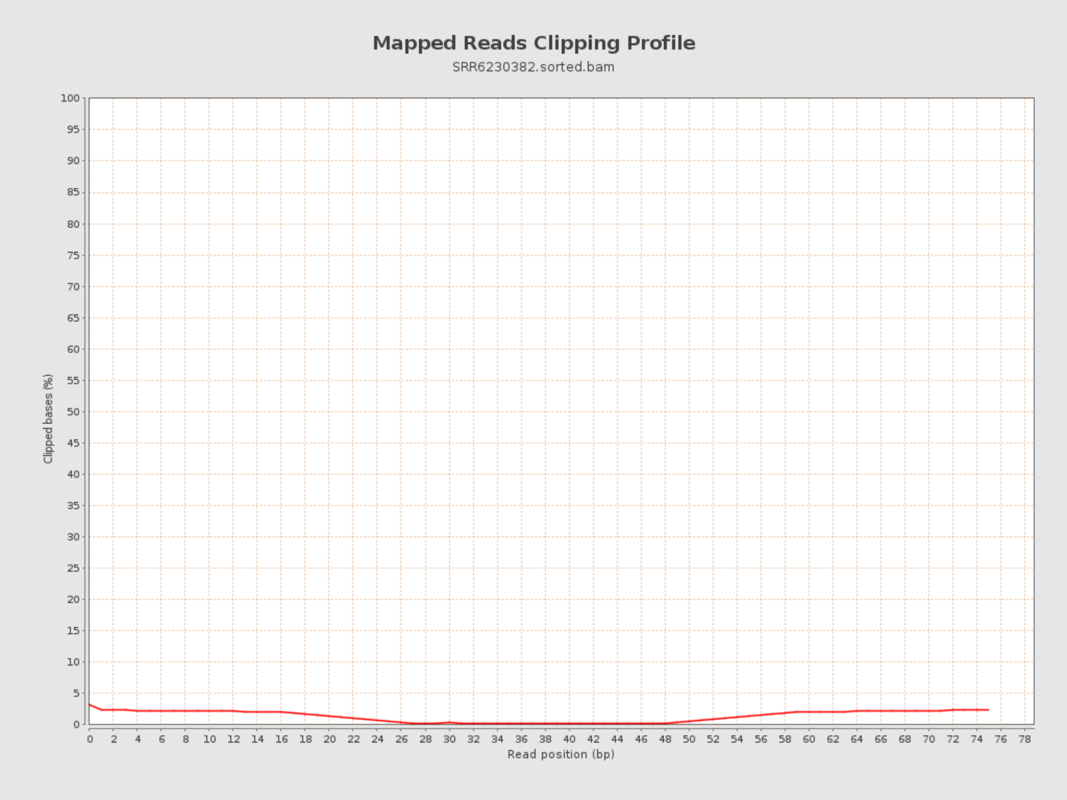
8. Results : Mapped Reads Nucleotide Content



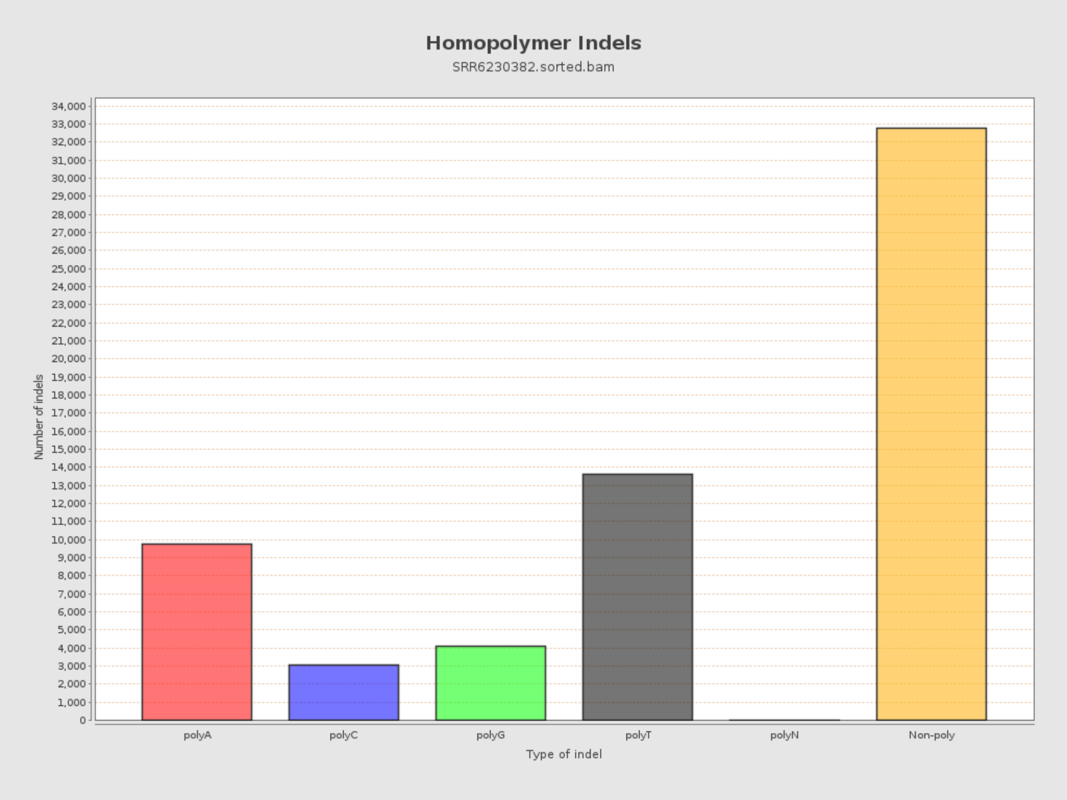
9. Results : Mapped Reads GC-content Distribution



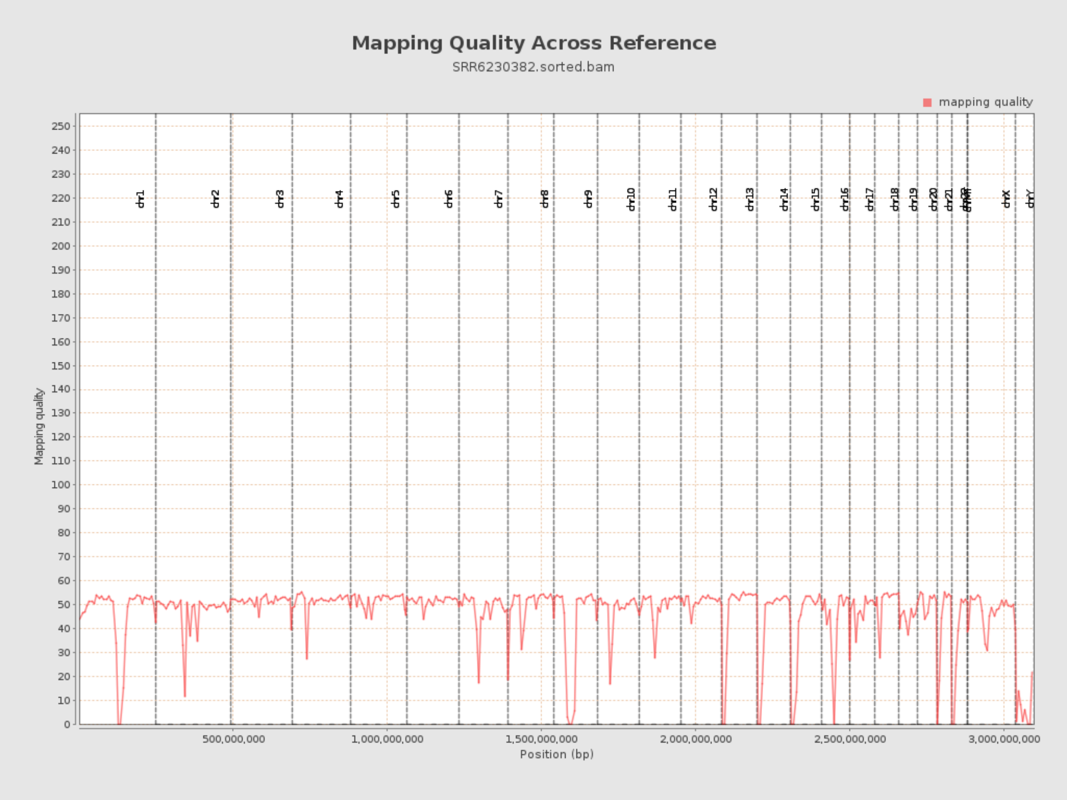
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram