Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:01:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238273.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_SRR6238273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238273.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:01:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,636,589
Mapped reads	2,433,769 / 92.31%
Unmapped reads	202,820 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,122 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	102,031 / 3.87%
Duplication rate	3.11%
Clipped reads	1,085,495 / 41.17%

2.2. ACGT Content

Number/percentage of A's	46,583,506 / 28.55%
Number/percentage of C's	30,769,583 / 18.86%
Number/percentage of T's	50,587,082 / 31%
Number/percentage of G's	35,186,132 / 21.56%
Number/percentage of N's	38,595 / 0.02%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.4606

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

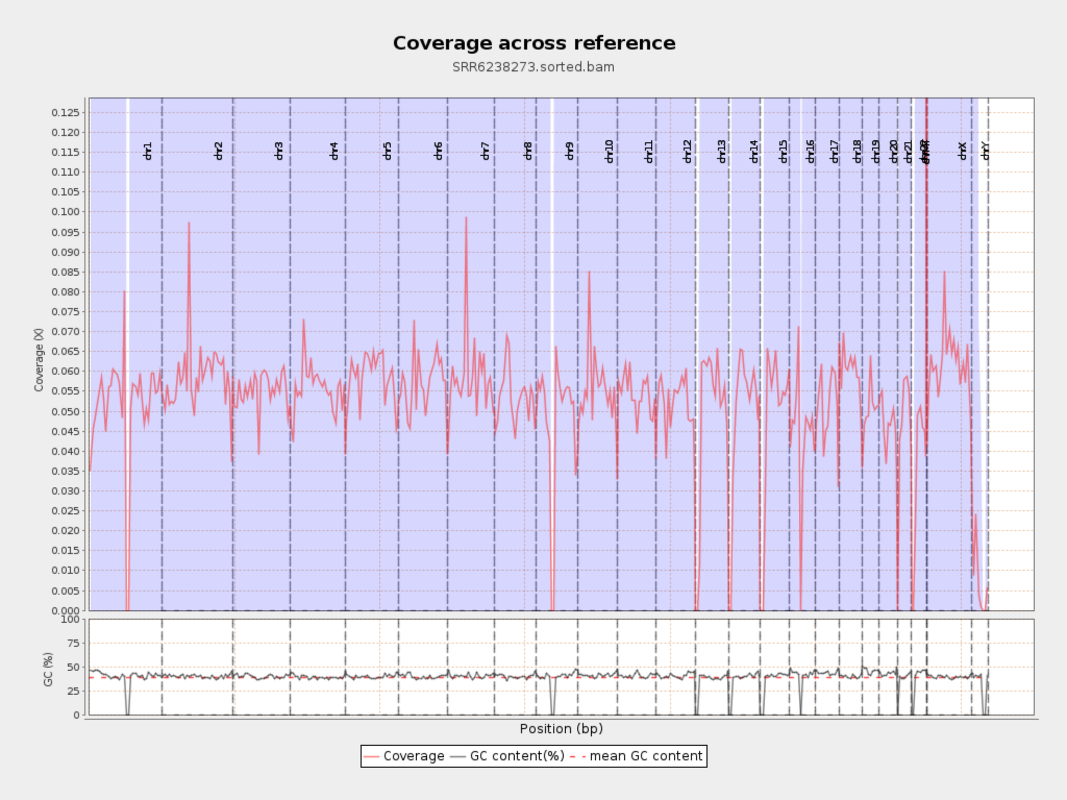
General error rate	0.89%
Mismatches	1,428,232
Insertions	13,642
Mapped reads with at least one insertion	0.56%
Deletions	50,611
Mapped reads with at least one deletion	2.05%
Homopolymer indels	46.76%

2.6. Chromosome stats

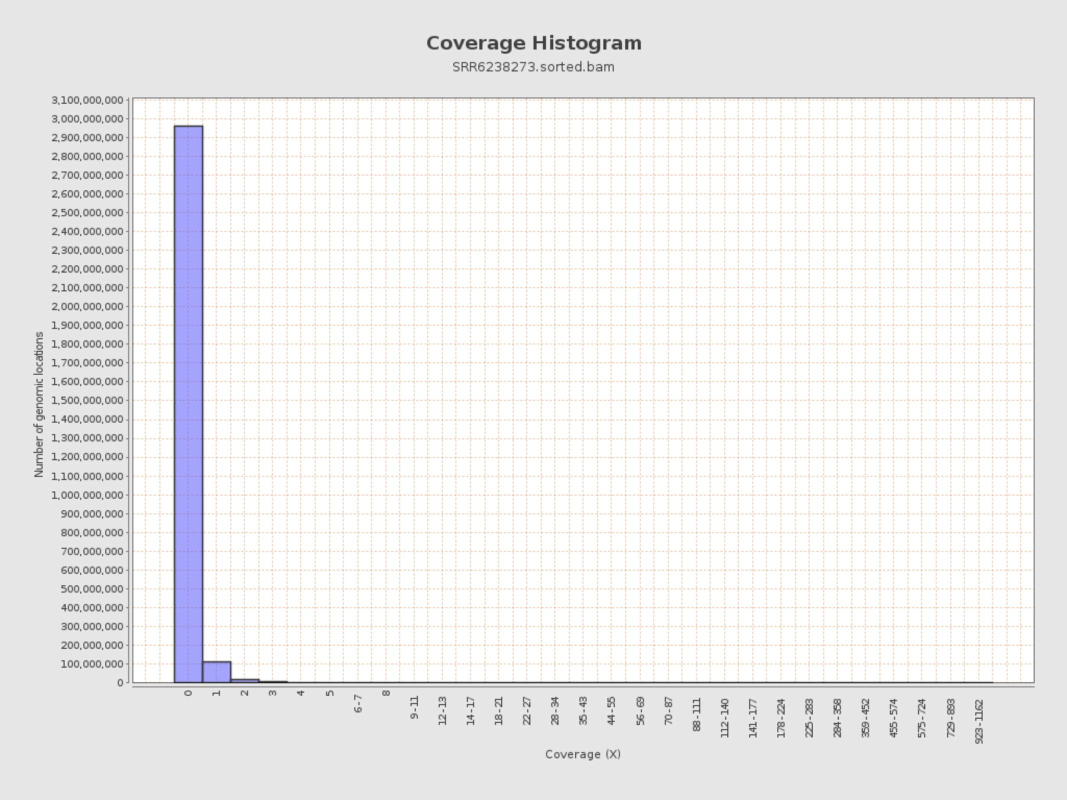
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12747254	0.0511	0.7344
chr2	243199373	14305767	0.0588	0.5162
chr3	198022430	10946697	0.0553	0.2745
chr4	191154276	10646755	0.0557	0.3045
chr5	180915260	10611235	0.0587	0.2873
chr6	171115067	9779567	0.0572	0.3568
chr7	159138663	9383888	0.059	0.7216

chr8	146364022	7790114	0.0532	0.7551
chr9	141213431	6717360	0.0476	0.4267
chr10	135534747	7588712	0.056	0.4198
chr11	135006516	7297263	0.0541	0.3794
chr12	133851895	6994800	0.0523	0.2766
chr13	115169878	5539892	0.0481	0.2574
chr14	107349540	5212811	0.0486	0.3111
chr15	102531392	4872128	0.0475	0.2605
chr16	90354753	3981728	0.0441	0.285
chr17	81195210	4138985	0.051	0.3162
chr18	78077248	4743682	0.0608	0.8445
chr19	59128983	3014173	0.051	0.5129
chr20	63025520	2934414	0.0466	0.2632
chr21	48129895	2220129	0.0461	0.2876
chr22	51304566	1721406	0.0336	0.2128
chrMT	16571	6770	0.4085	0.7561
chrX	155270560	9616072	0.0619	0.3367
chrY	59373566	436998	0.0074	0.2002

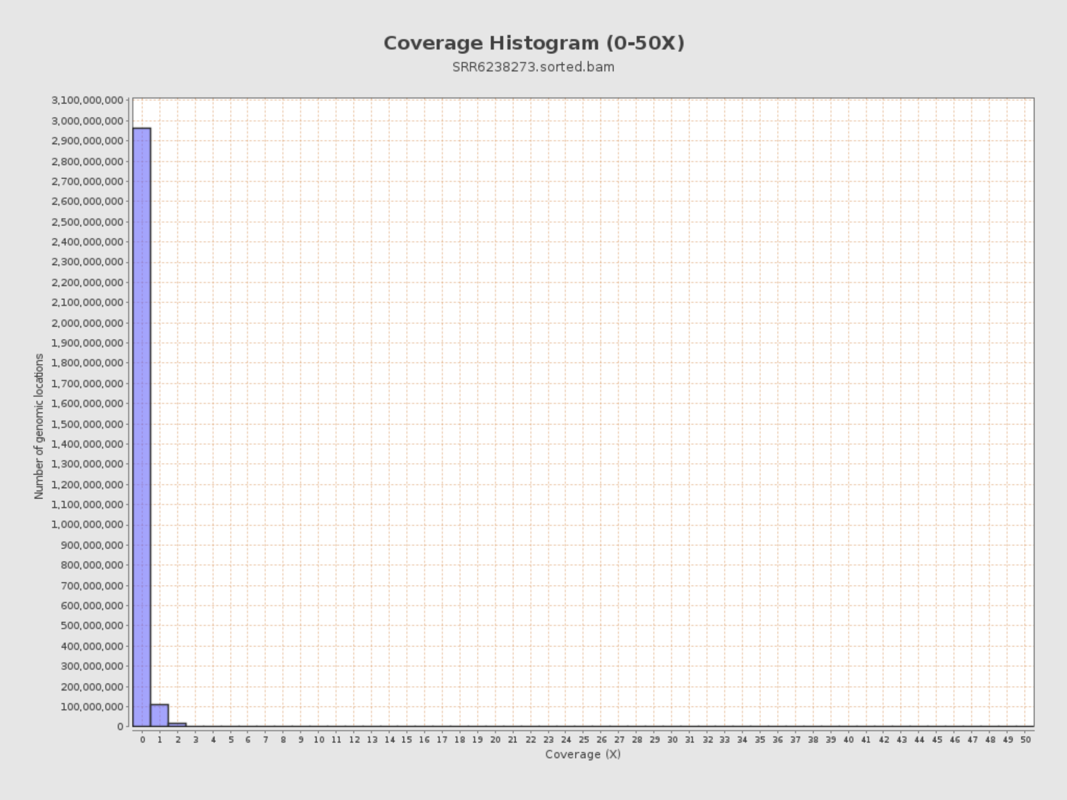
3. Results : Coverage across reference



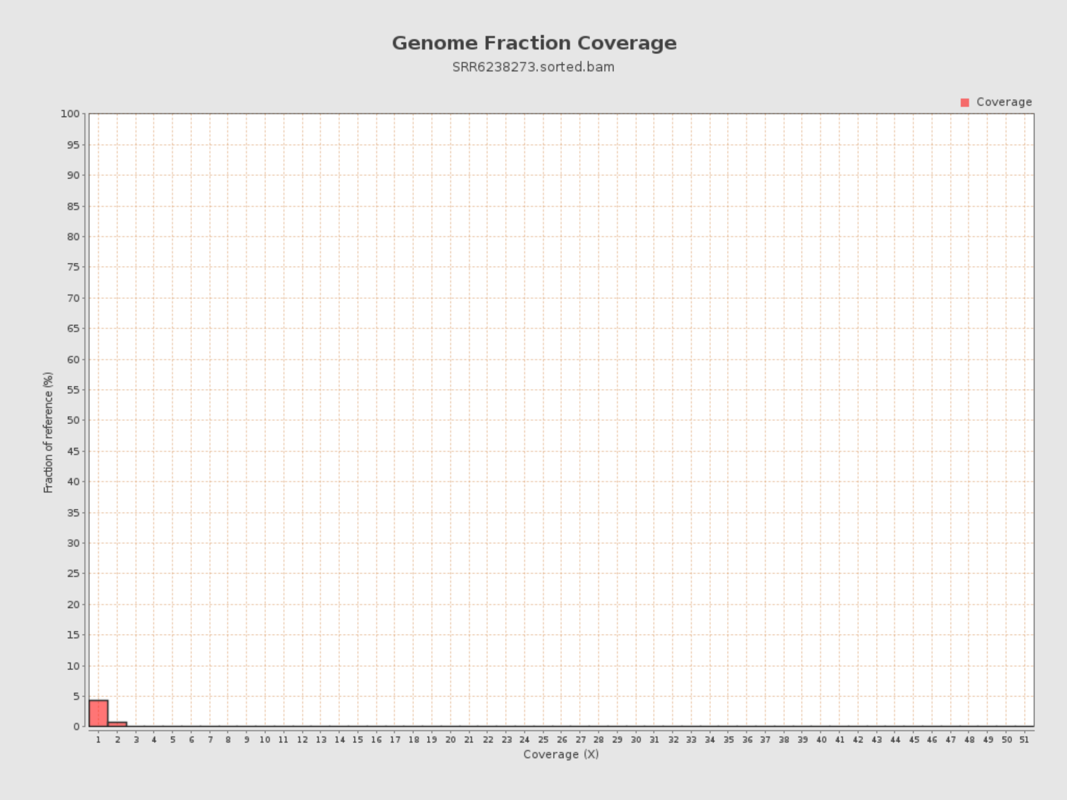
4. Results : Coverage Histogram



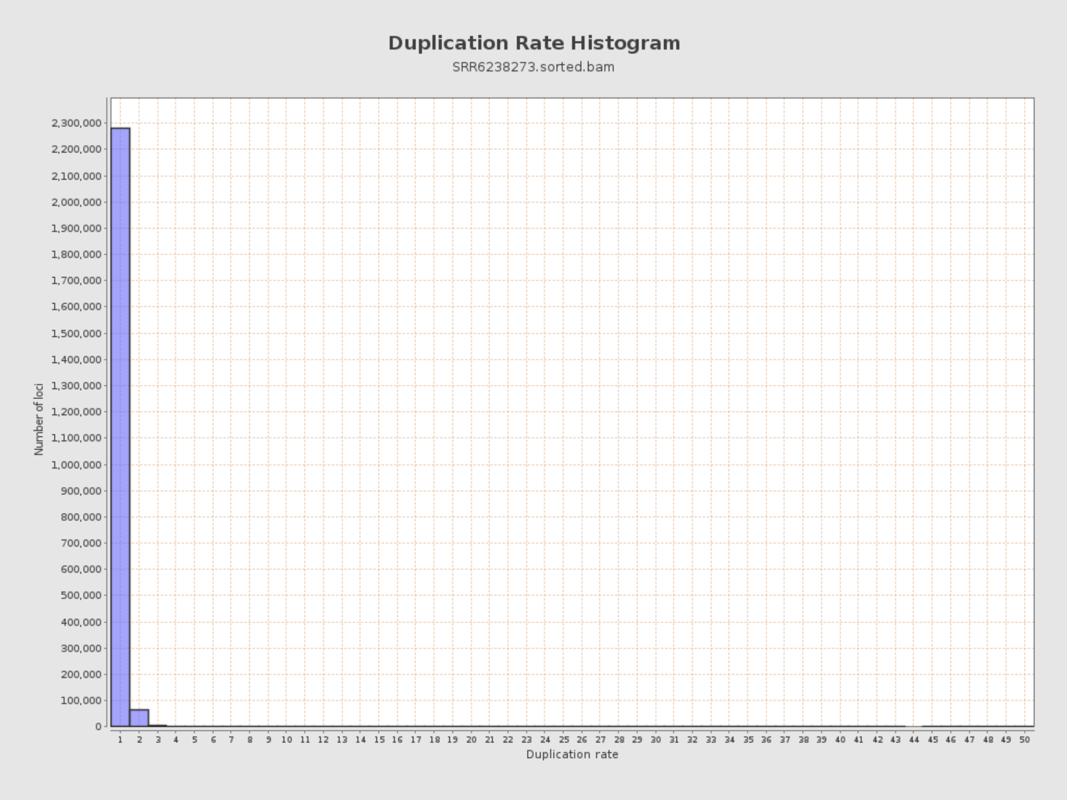
5. Results : Coverage Histogram (0-50X)



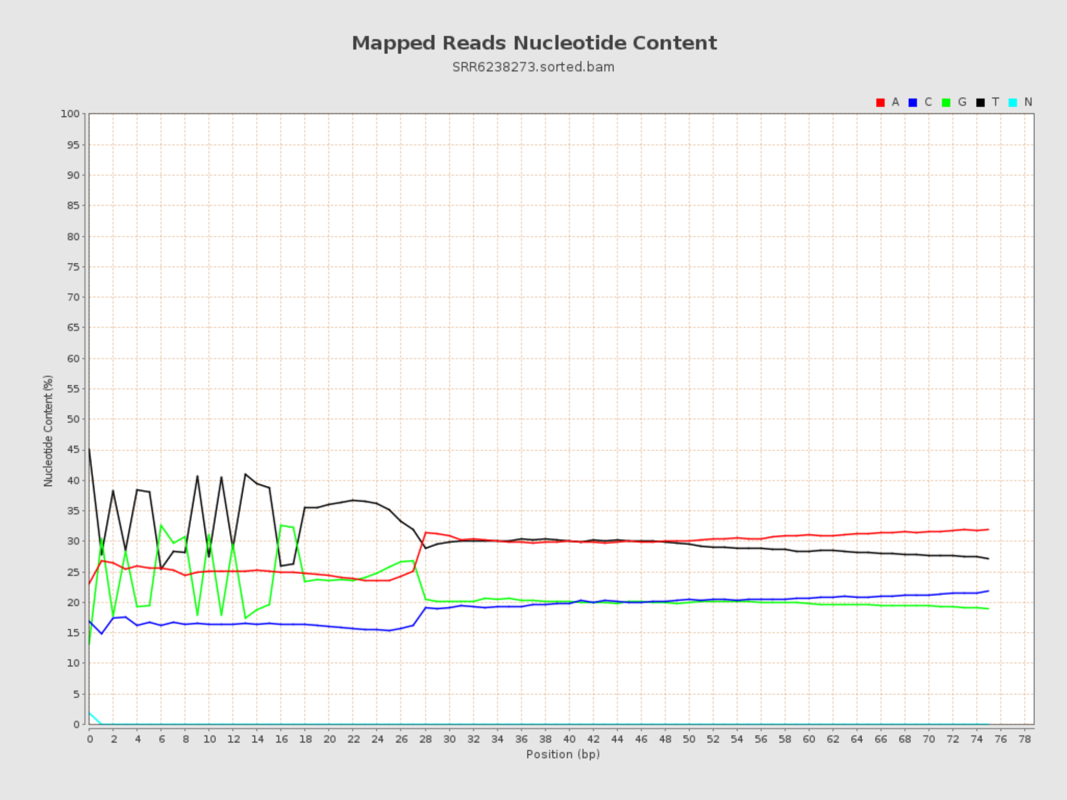
6. Results : Genome Fraction Coverage



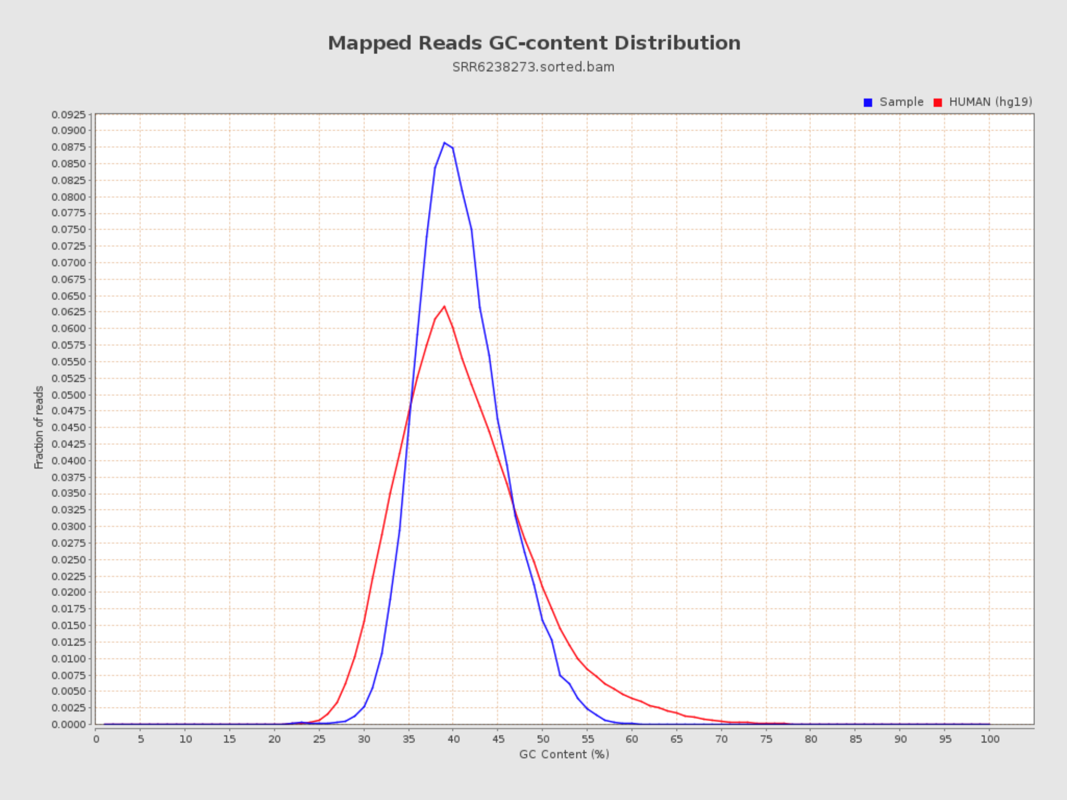
7. Results : Duplication Rate Histogram



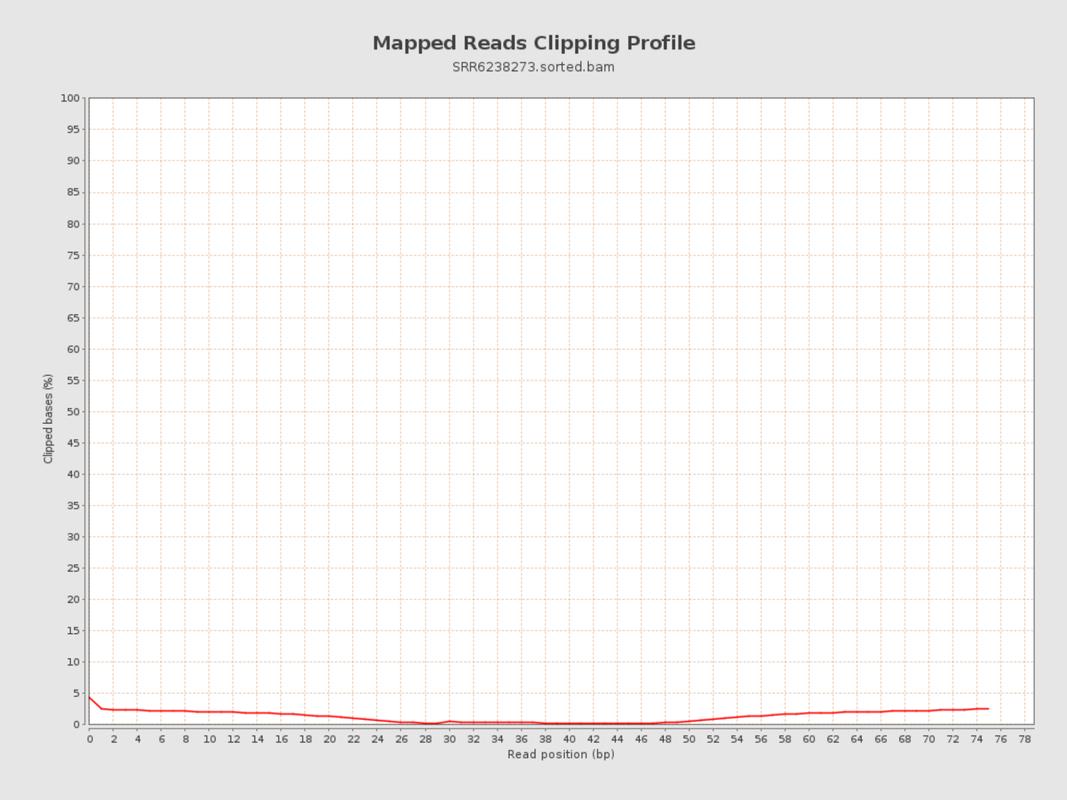
8. Results : Mapped Reads Nucleotide Content



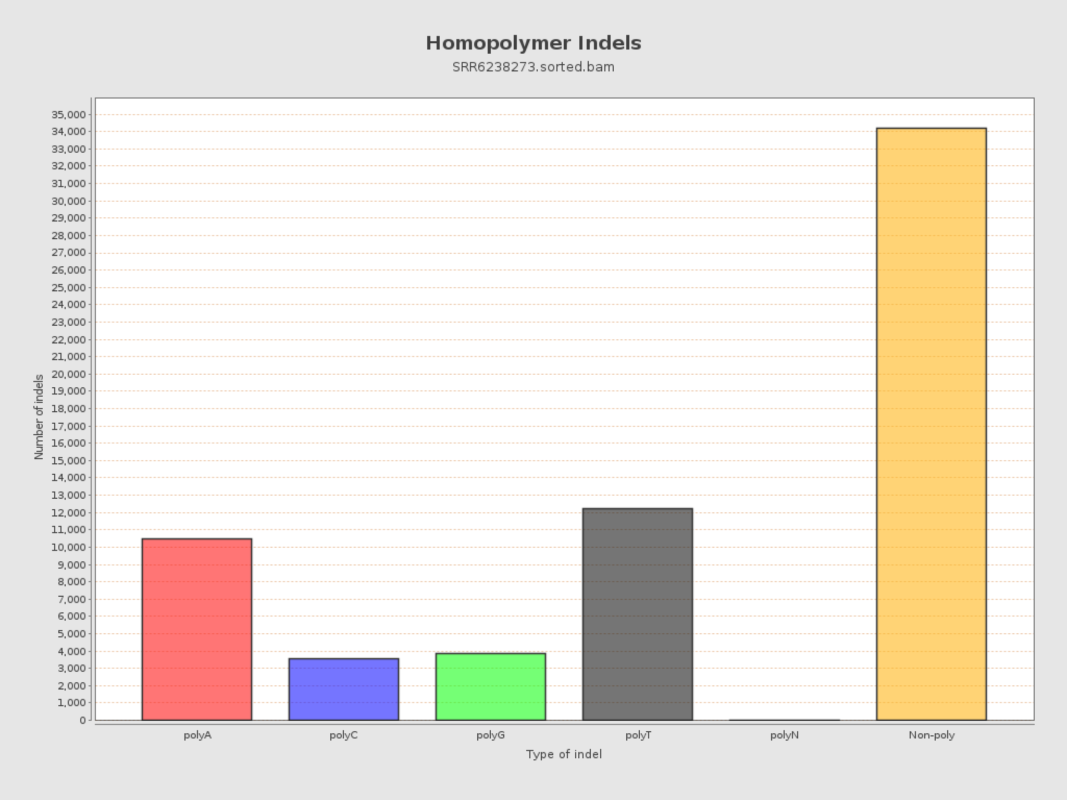
9. Results : Mapped Reads GC-content Distribution



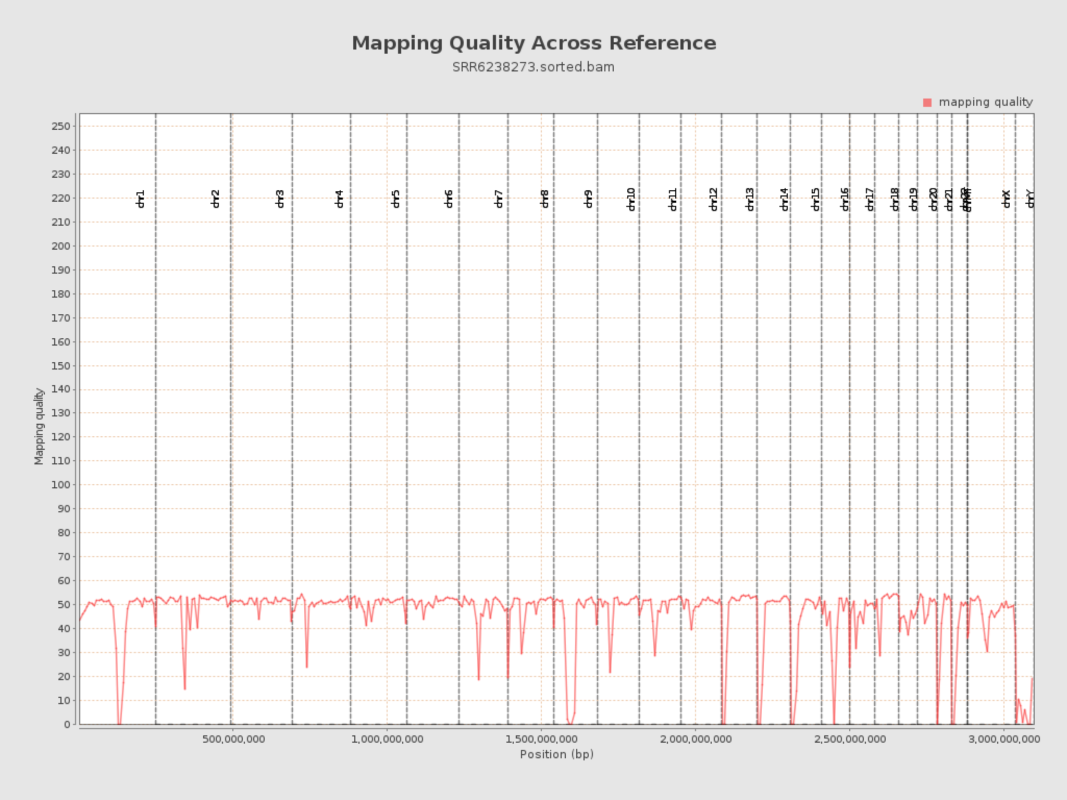
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram