Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:03:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238625.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_SRR6238625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238625.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:03:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	967,432
Mapped reads	755,203 / 78.06%
Unmapped reads	212,229 / 21.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,930 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	151,202 / 15.63%
Duplication rate	15.37%
Clipped reads	491,860 / 50.84%

2.2. ACGT Content

Number/percentage of A's	11,461,178 / 24.96%
Number/percentage of C's	7,928,856 / 17.27%
Number/percentage of T's	15,560,062 / 33.88%
Number/percentage of G's	10,969,692 / 23.89%
Number/percentage of N's	2,093 / 0%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.2716

2.4. Mapping Quality

Mean Mapping Quality	40.06

2.5. Mismatches and indels

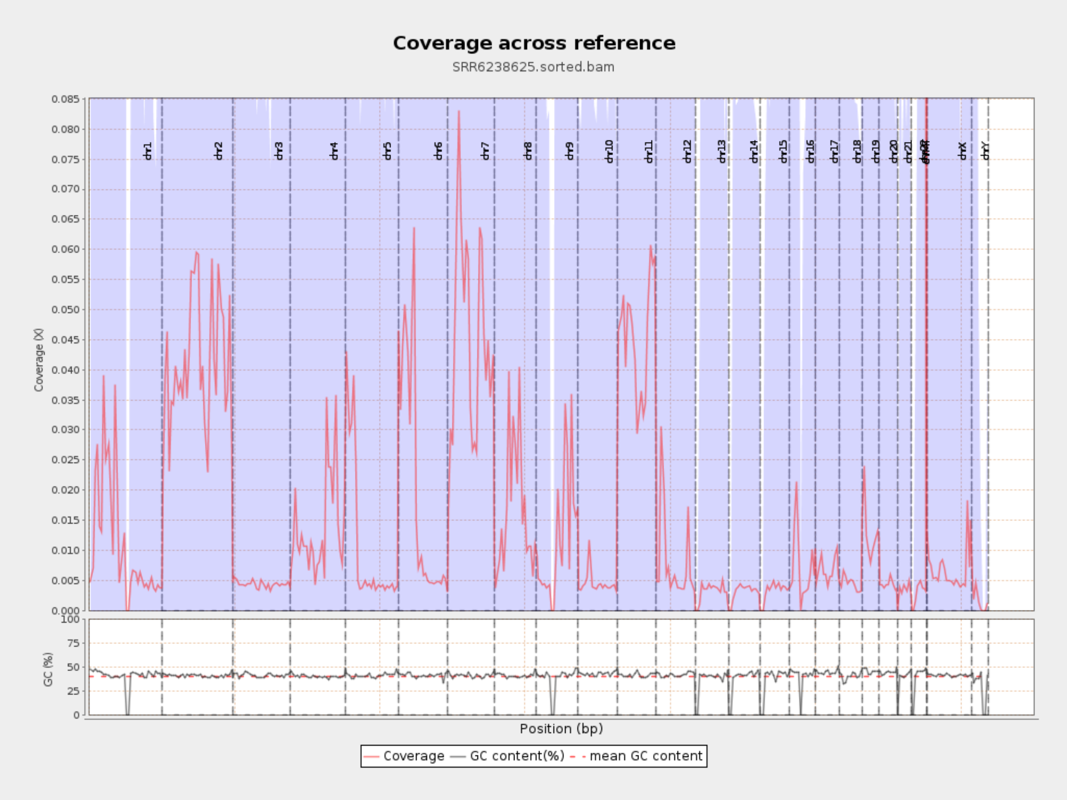
General error rate	0.7%
Mismatches	318,245
Insertions	2,838
Mapped reads with at least one insertion	0.37%
Deletions	18,667
Mapped reads with at least one deletion	2.44%
Homopolymer indels	40.82%

2.6. Chromosome stats

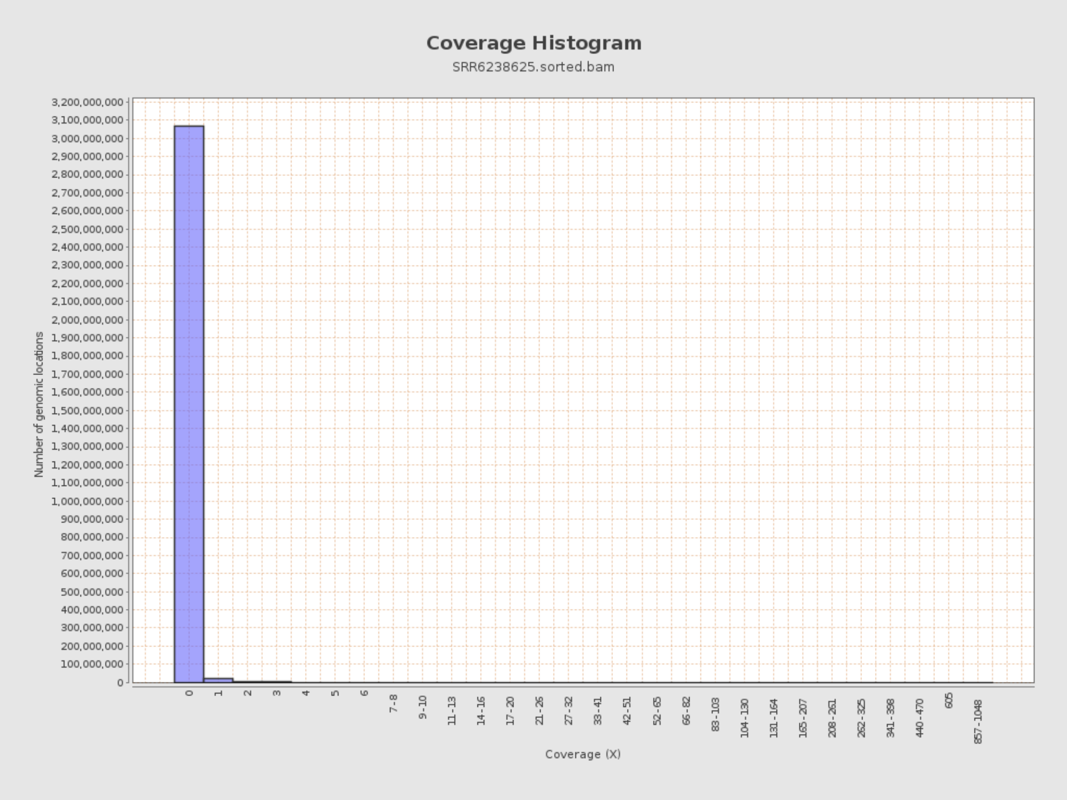
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2810805	0.0113	0.1984
chr2	243199373	10086906	0.0415	0.5613
chr3	198022430	868850	0.0044	0.097
chr4	191154276	2630136	0.0138	0.1782
chr5	180915260	1903555	0.0105	0.1565
chr6	171115067	3378286	0.0197	0.3363
chr7	159138663	7324492	0.046	0.5586

chr8	146364022	2442334	0.0167	0.2626
chr9	141213431	1664721	0.0118	0.1695
chr10	135534747	604558	0.0045	0.1051
chr11	135006516	6070237	0.045	0.3859
chr12	133851895	1039943	0.0078	0.1325
chr13	115169878	367789	0.0032	0.1218
chr14	107349540	335398	0.0031	0.1151
chr15	102531392	340065	0.0033	0.1701
chr16	90354753	670816	0.0074	0.132
chr17	81195210	545297	0.0067	0.1404
chr18	78077248	351058	0.0045	0.2809
chr19	59128983	760567	0.0129	0.1749
chr20	63025520	268726	0.0043	0.0969
chr21	48129895	161225	0.0033	0.0828
chr22	51304566	144599	0.0028	0.0762
chrMT	16571	28523	1.7213	2.2376
chrX	155270560	1060941	0.0068	0.1348
chrY	59373566	93852	0.0016	0.0873

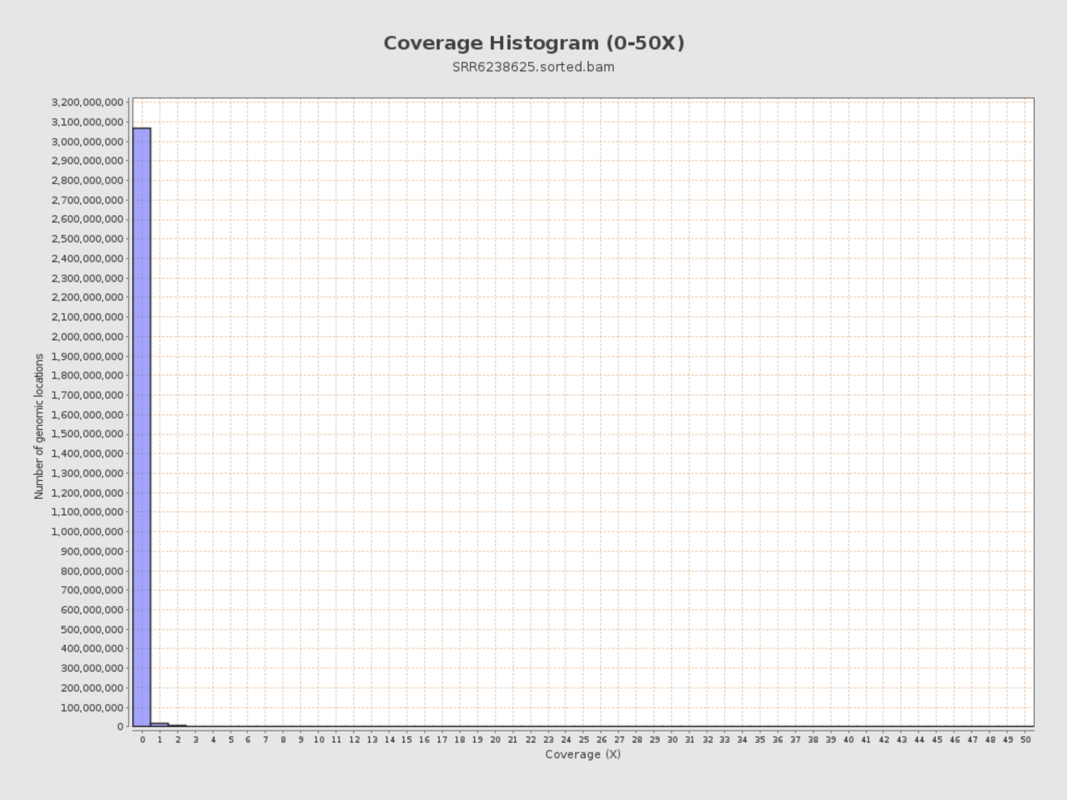
3. Results : Coverage across reference



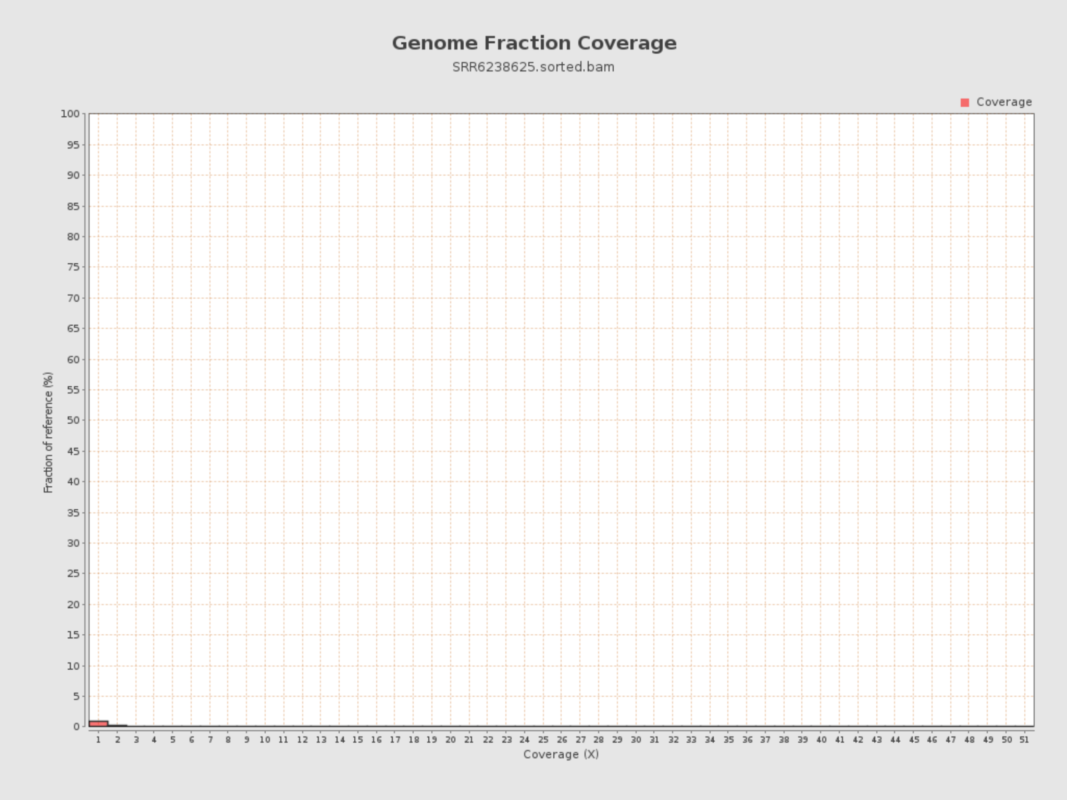
4. Results : Coverage Histogram



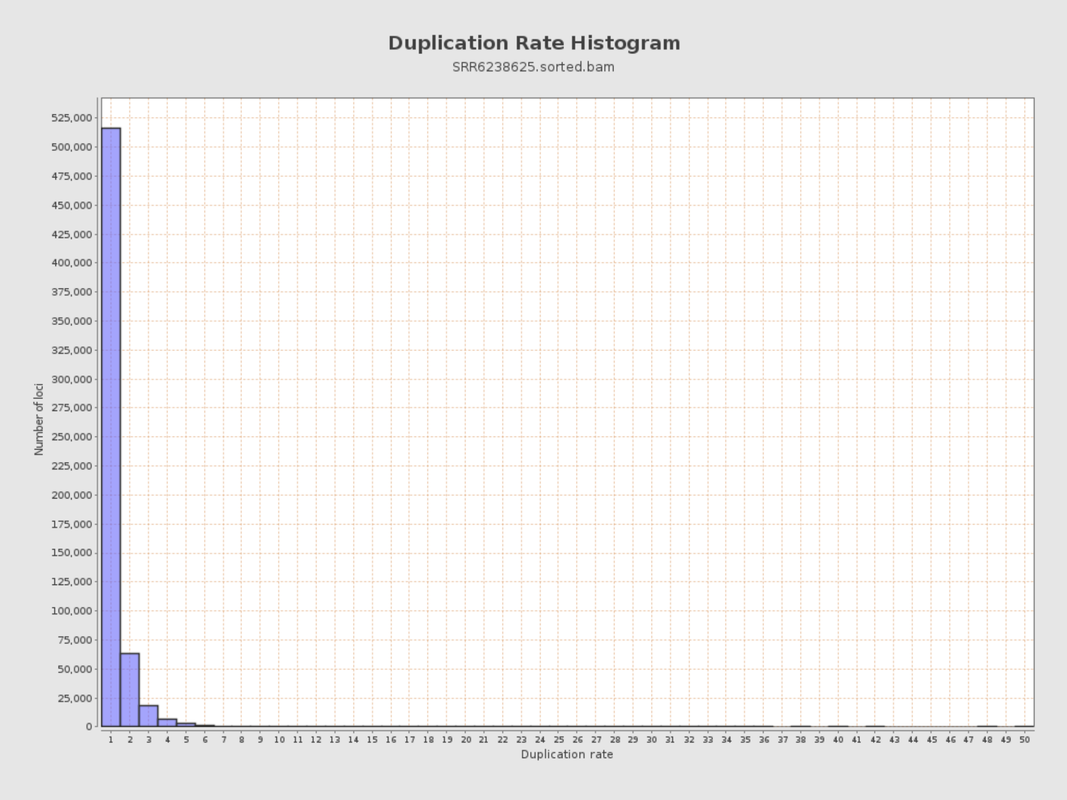
5. Results : Coverage Histogram (0-50X)



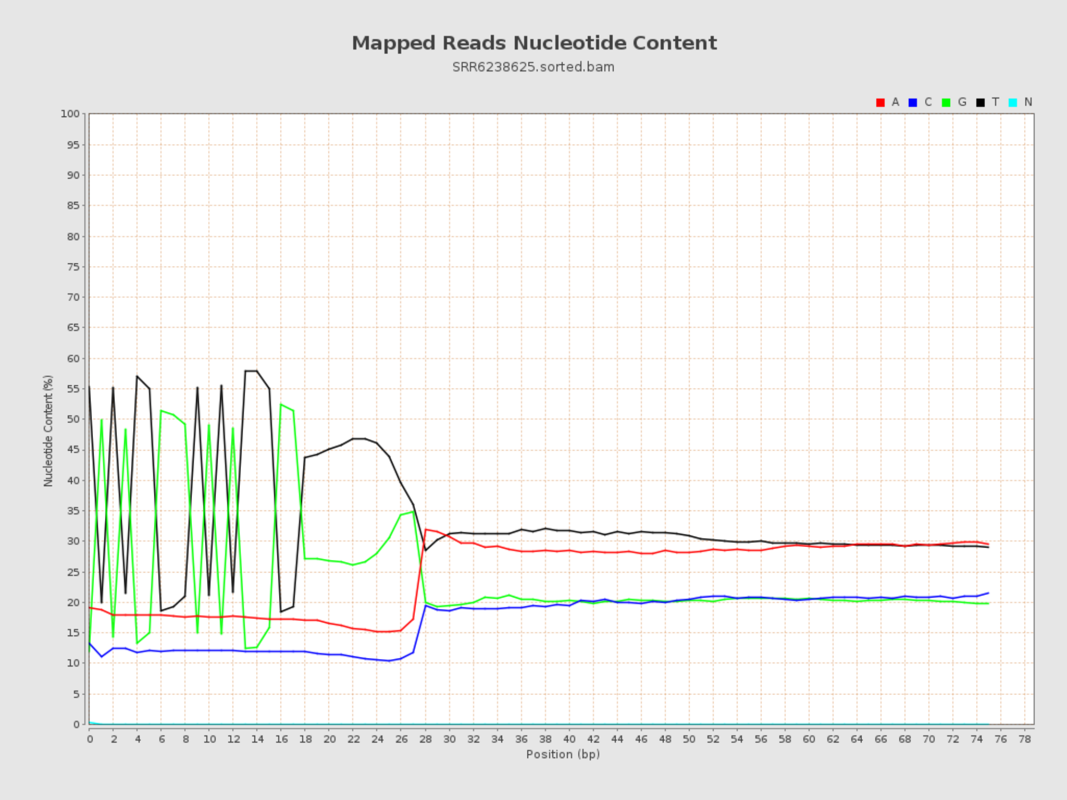
6. Results : Genome Fraction Coverage



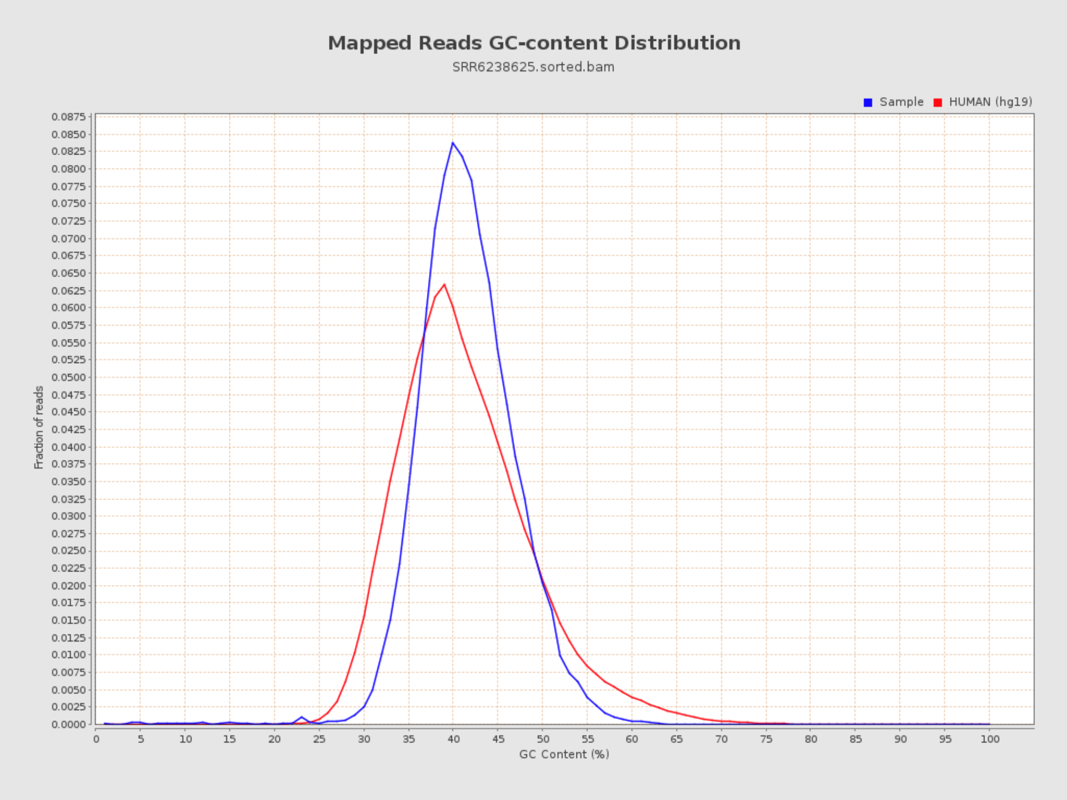
7. Results : Duplication Rate Histogram



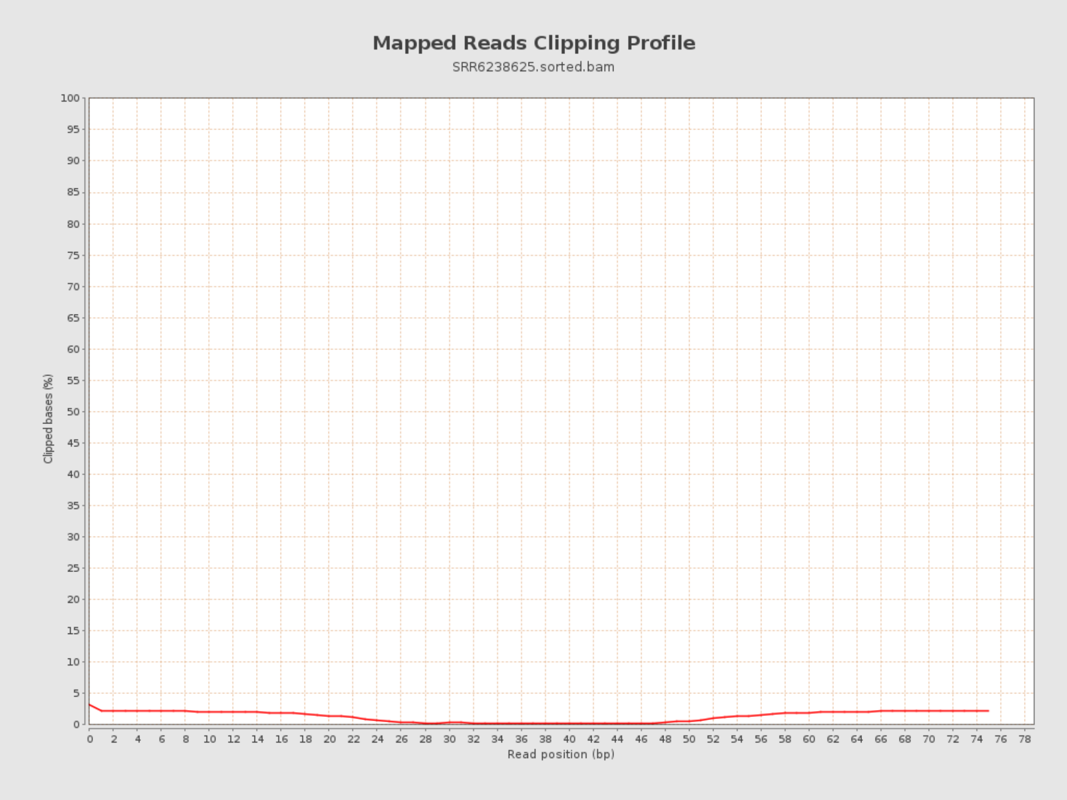
8. Results : Mapped Reads Nucleotide Content



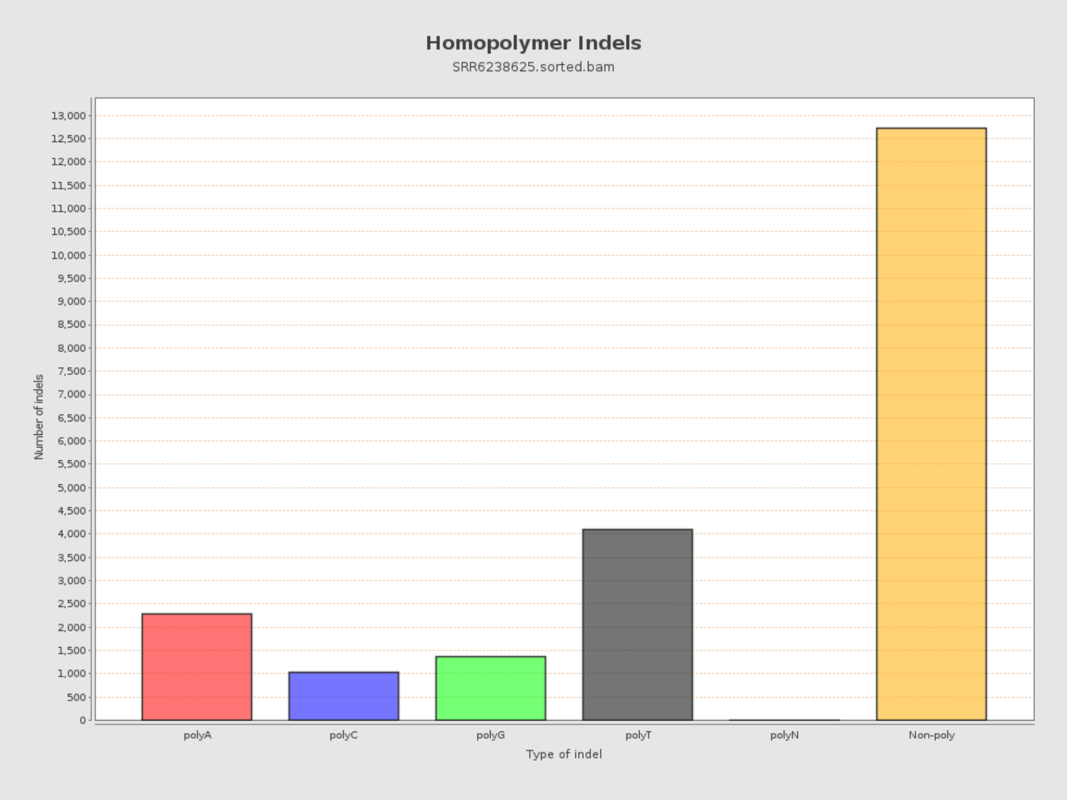
9. Results : Mapped Reads GC-content Distribution



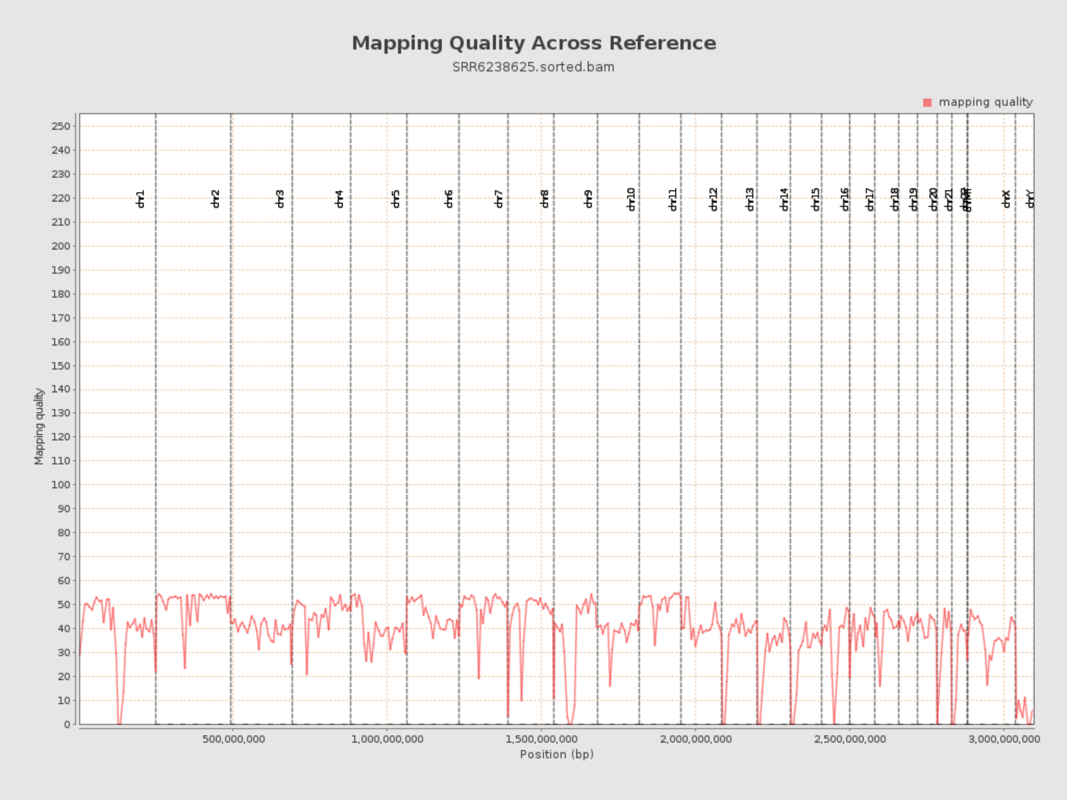
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram