Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:39:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238617.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_SRR6238617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238617.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:39:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,356,829
Mapped reads	3,748,719 / 86.04%
Unmapped reads	608,110 / 13.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,333 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,668,498 / 38.3%
Duplication rate	21.62%
Clipped reads	2,262,576 / 51.93%

2.2. ACGT Content

Number/percentage of A's	58,970,700 / 25.19%
Number/percentage of C's	41,244,158 / 17.62%
Number/percentage of T's	78,680,090 / 33.61%
Number/percentage of G's	55,179,838 / 23.57%
Number/percentage of N's	5,747 / 0%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0756

Standard Deviation	1.2784

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

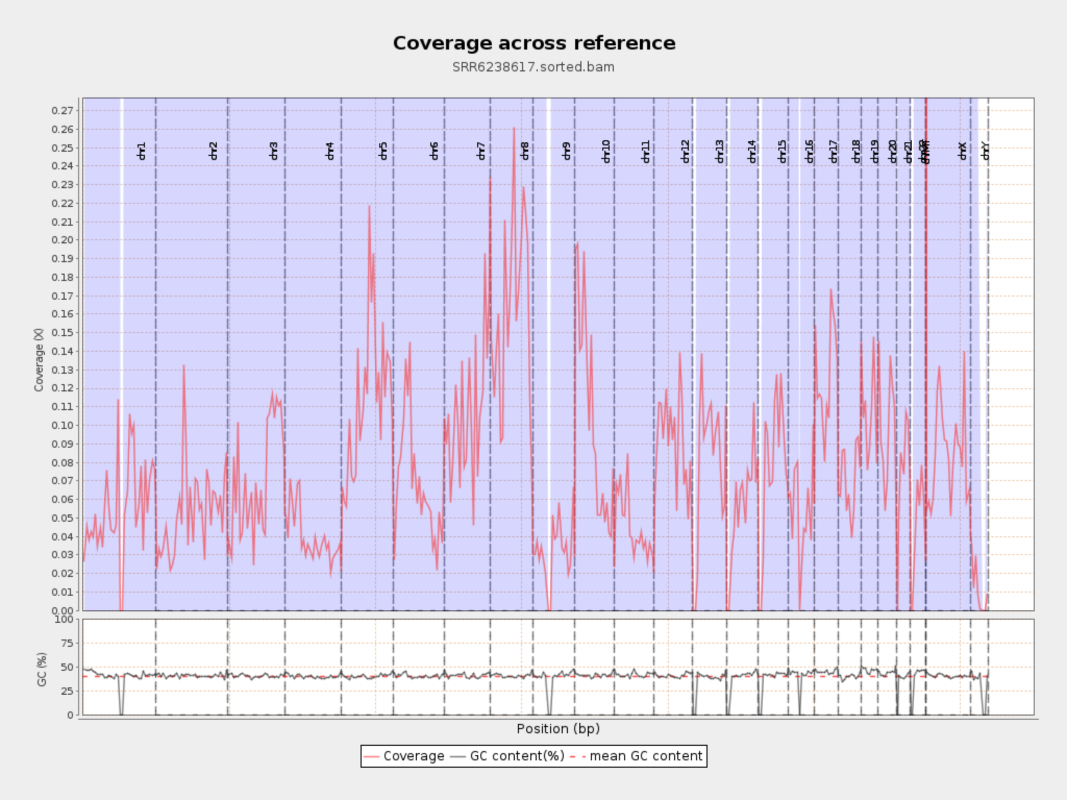
General error rate	0.52%
Mismatches	1,186,295
Insertions	15,627
Mapped reads with at least one insertion	0.41%
Deletions	52,276
Mapped reads with at least one deletion	1.38%
Homopolymer indels	43.62%

2.6. Chromosome stats

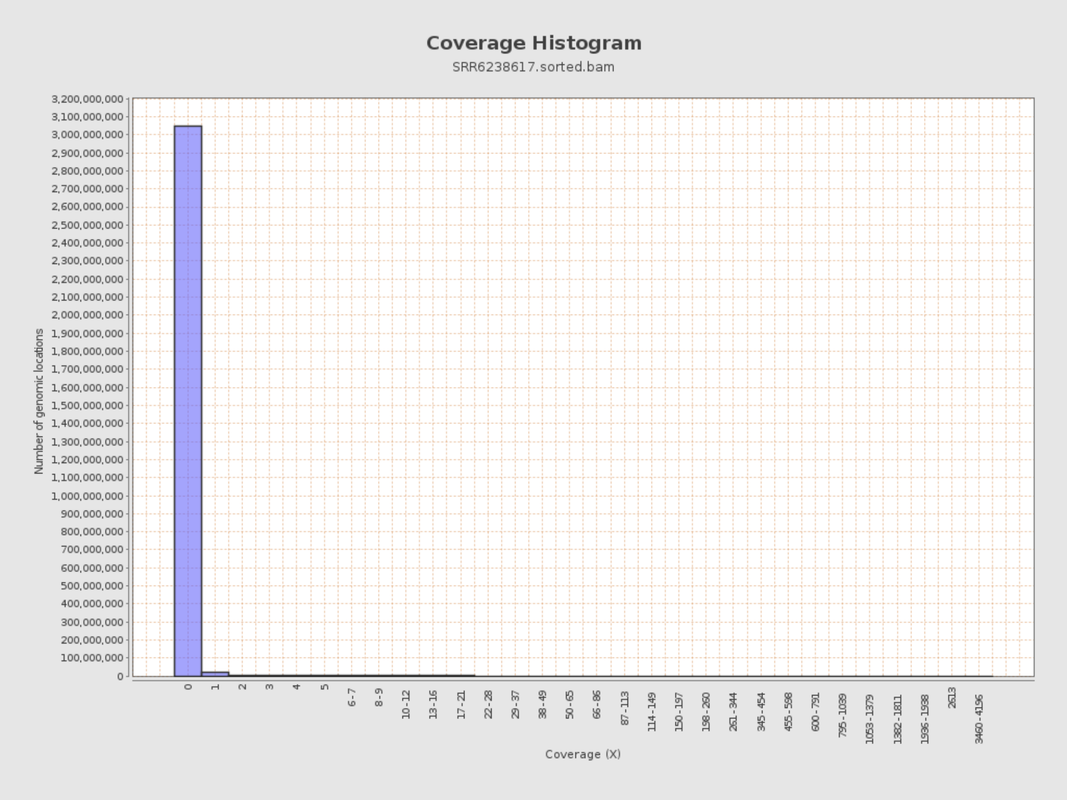
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13935046	0.0559	1.5364
chr2	243199373	12962436	0.0533	2.0486
chr3	198022430	13850045	0.0699	0.9589
chr4	191154276	7605159	0.0398	0.6803
chr5	180915260	20634870	0.1141	1.2187
chr6	171115067	11662264	0.0682	1.2109
chr7	159138663	17007674	0.1069	1.3724

chr8	146364022	23972529	0.1638	1.5635
chr9	141213431	4546169	0.0322	0.6789
chr10	135534747	13951908	0.1029	1.2401
chr11	135006516	6130465	0.0454	0.7475
chr12	133851895	12162808	0.0909	1.0712
chr13	115169878	9121177	0.0792	1.1283
chr14	107349540	6022626	0.0561	0.8677
chr15	102531392	7859522	0.0767	1.0672
chr16	90354753	4766459	0.0528	0.826
chr17	81195210	10461470	0.1288	1.2801
chr18	78077248	5490843	0.0703	2.5346
chr19	59128983	6222808	0.1052	1.4249
chr20	63025520	6214984	0.0986	1.1327
chr21	48129895	3573140	0.0742	0.9987
chr22	51304566	2326995	0.0454	0.7235
chrMT	16571	48488	2.9261	5.8346
chrX	155270560	12982670	0.0836	1.0439
chrY	59373566	658483	0.0111	0.4316

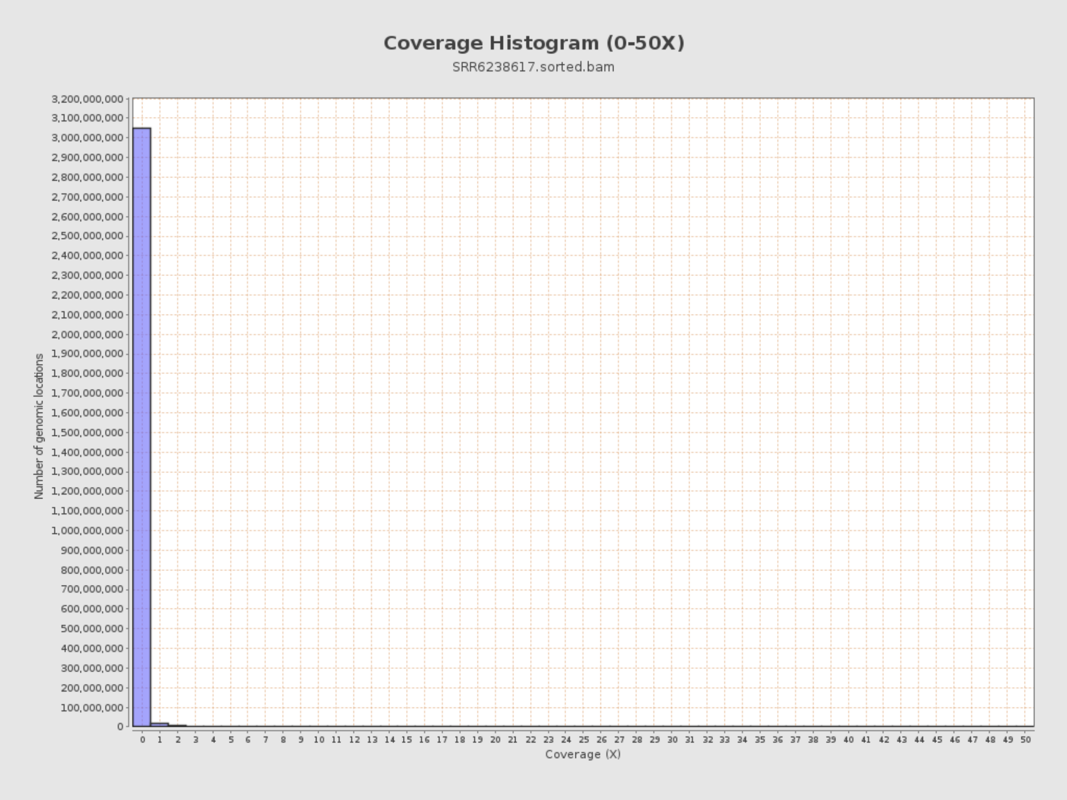
3. Results : Coverage across reference



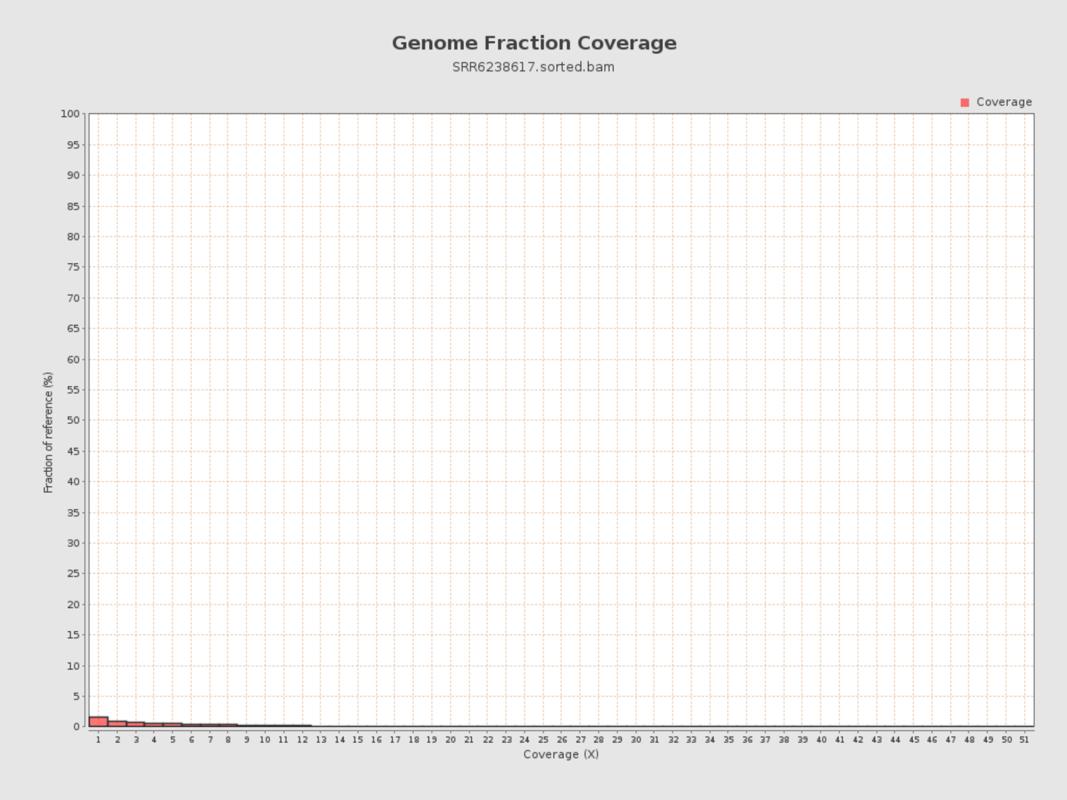
4. Results : Coverage Histogram



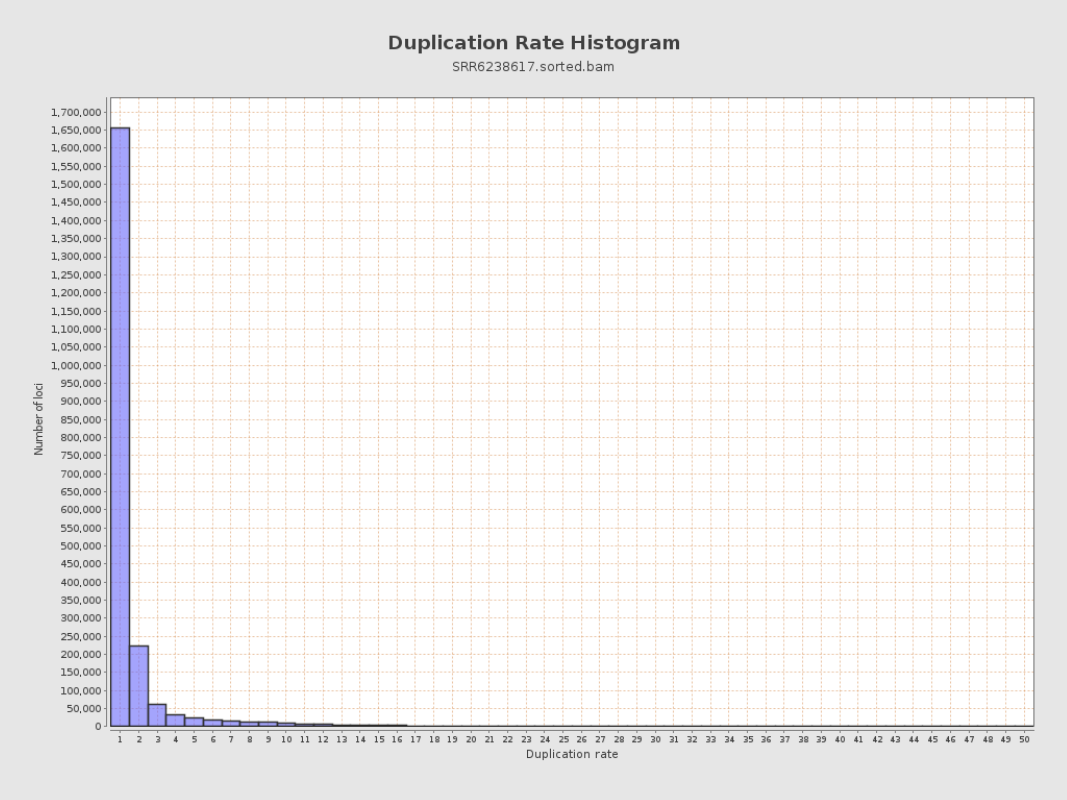
5. Results : Coverage Histogram (0-50X)



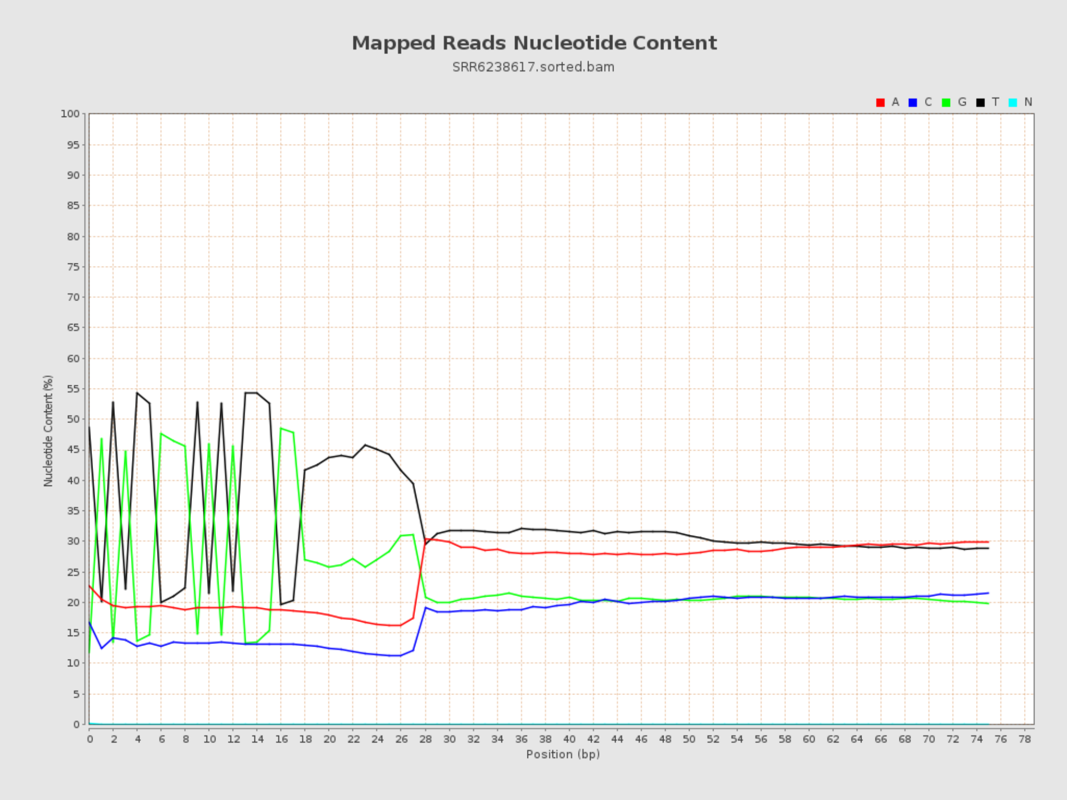
6. Results : Genome Fraction Coverage



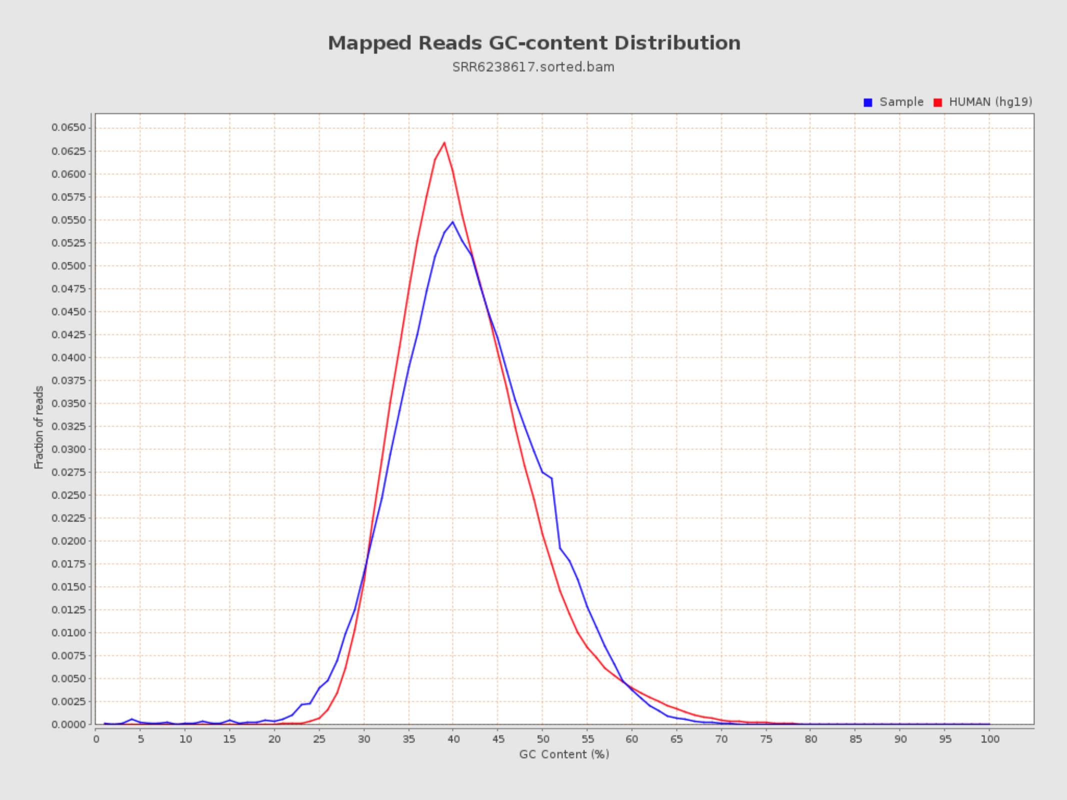
7. Results : Duplication Rate Histogram



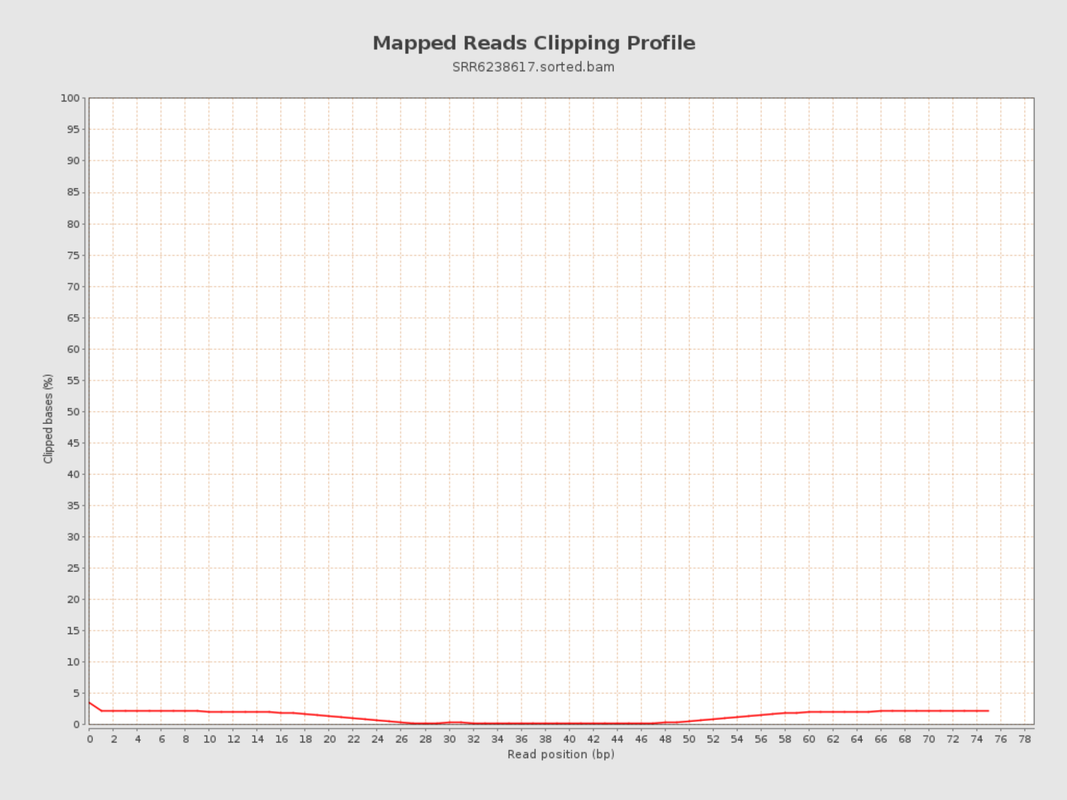
8. Results : Mapped Reads Nucleotide Content



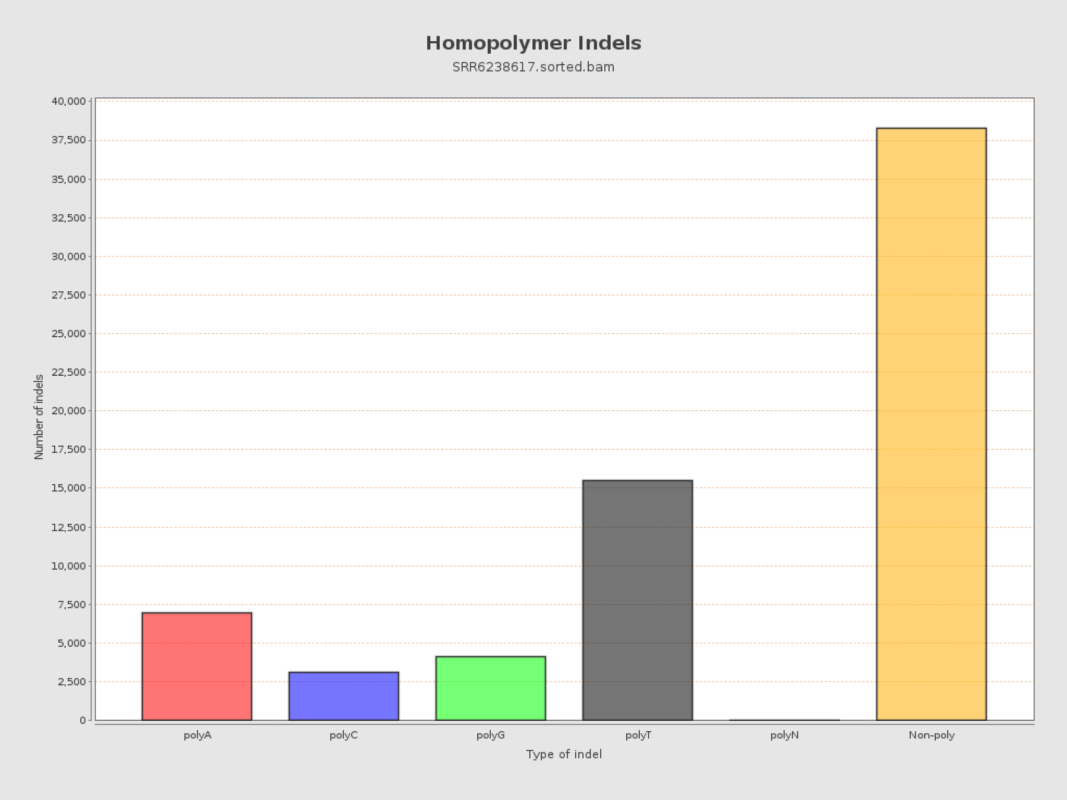
9. Results : Mapped Reads GC-content Distribution



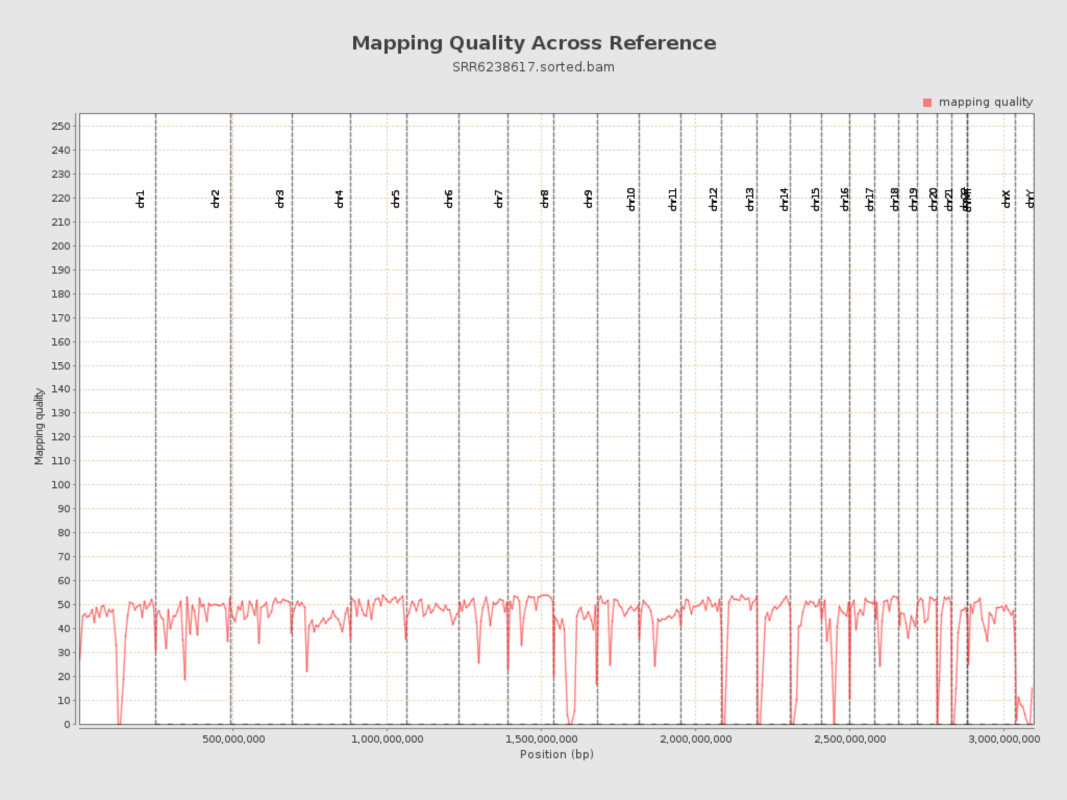
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram