Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:13:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238257.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_SRR6238257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:13:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,990,832
Mapped reads	1,691,531 / 84.97%
Unmapped reads	299,301 / 15.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,015 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	161,374 / 8.11%
Duplication rate	7.76%
Clipped reads	959,569 / 48.2%

2.2. ACGT Content

Number/percentage of A's	30,213,252 / 27.79%
Number/percentage of C's	21,333,536 / 19.63%
Number/percentage of T's	33,150,740 / 30.5%
Number/percentage of G's	23,979,890 / 22.06%
Number/percentage of N's	25,215 / 0.02%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.3213

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

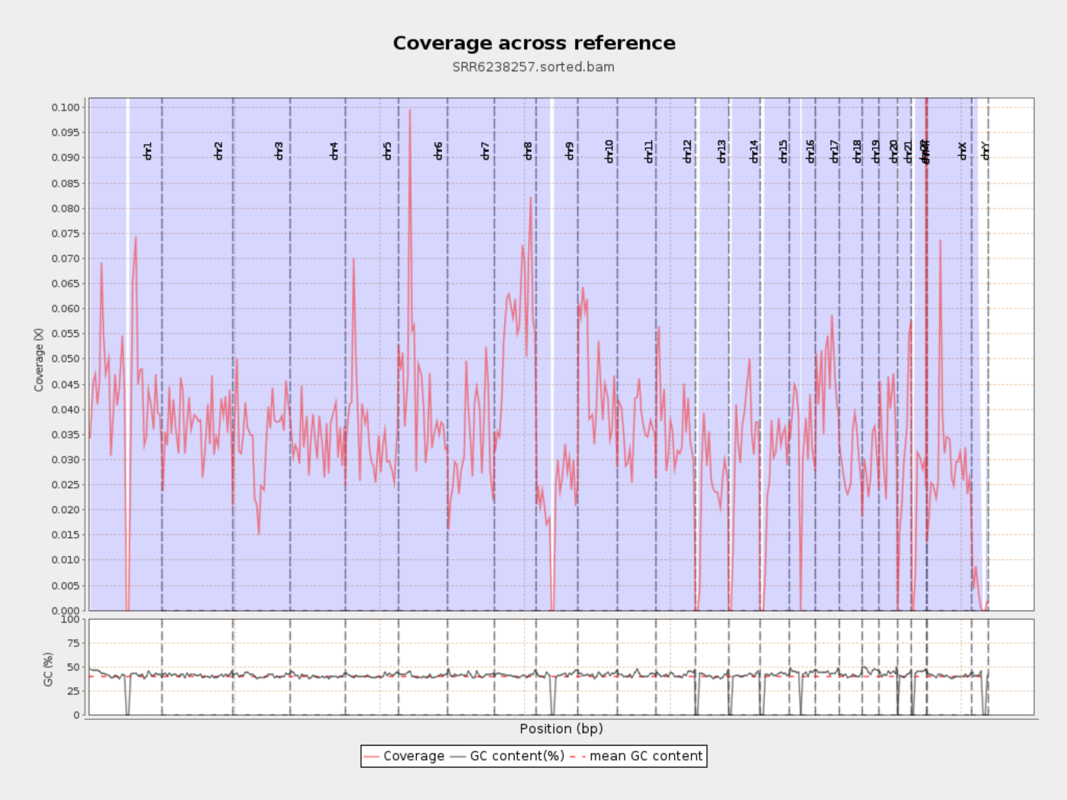
General error rate	0.94%
Mismatches	1,012,522
Insertions	8,664
Mapped reads with at least one insertion	0.51%
Deletions	36,915
Mapped reads with at least one deletion	2.16%
Homopolymer indels	47.89%

2.6. Chromosome stats

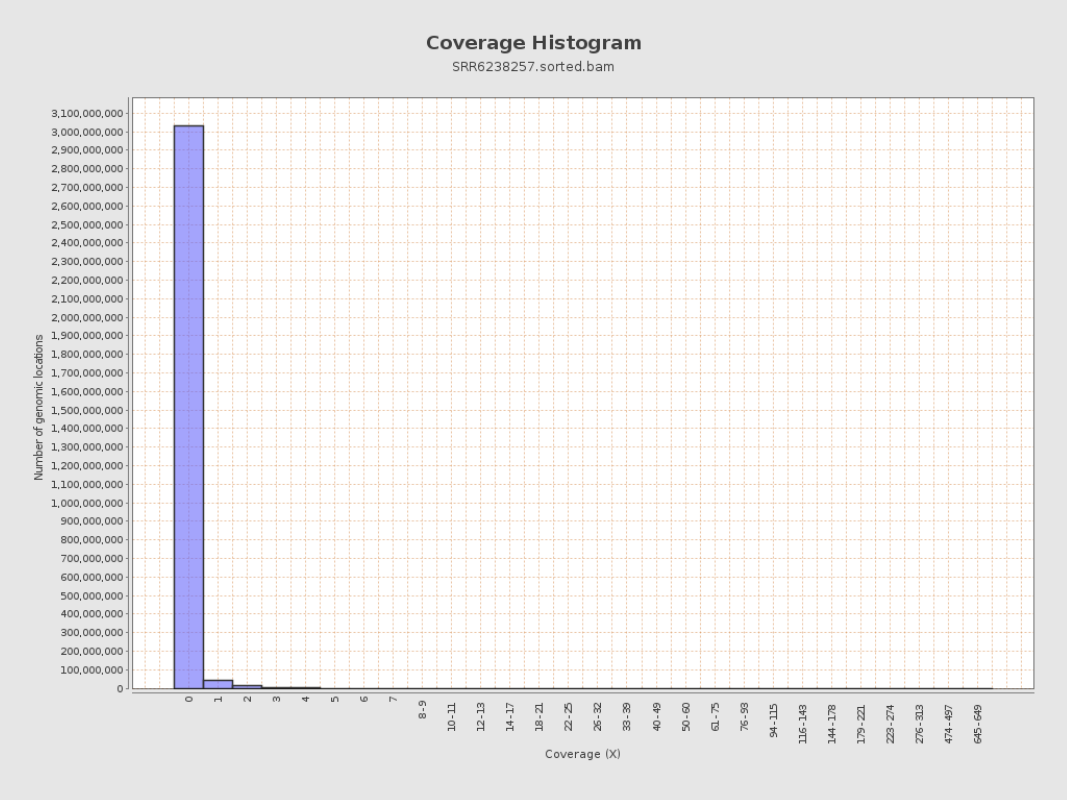
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10558327	0.0424	0.374
chr2	243199373	9022075	0.0371	0.4064
chr3	198022430	6820490	0.0344	0.2832
chr4	191154276	6516676	0.0341	0.285
chr5	180915260	6387537	0.0353	0.2861
chr6	171115067	7471179	0.0437	0.3425
chr7	159138663	5290786	0.0332	0.3908

chr8	146364022	8262753	0.0565	0.4142
chr9	141213431	3110909	0.022	0.249
chr10	135534747	6274132	0.0463	0.3422
chr11	135006516	4888026	0.0362	0.3222
chr12	133851895	4904106	0.0366	0.2921
chr13	115169878	2669113	0.0232	0.2339
chr14	107349540	3334318	0.0311	0.2925
chr15	102531392	2642249	0.0258	0.2764
chr16	90354753	3039210	0.0336	0.2783
chr17	81195210	3820894	0.0471	0.3416
chr18	78077248	2341146	0.03	0.3653
chr19	59128983	1705692	0.0288	0.2997
chr20	63025520	2324678	0.0369	0.2936
chr21	48129895	1502343	0.0312	0.2705
chr22	51304566	1031428	0.0201	0.2088
chrMT	16571	45550	2.7488	3.1191
chrX	155270560	4616175	0.0297	0.2695
chrY	59373566	186084	0.0031	0.0779

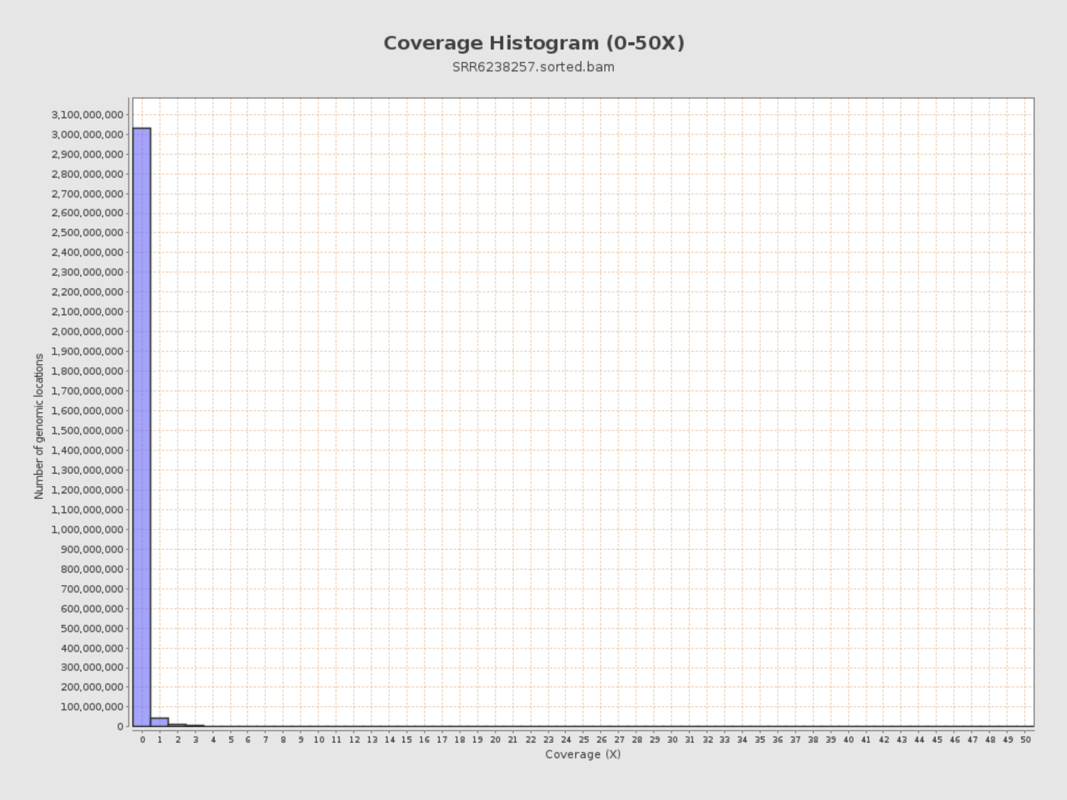
3. Results : Coverage across reference



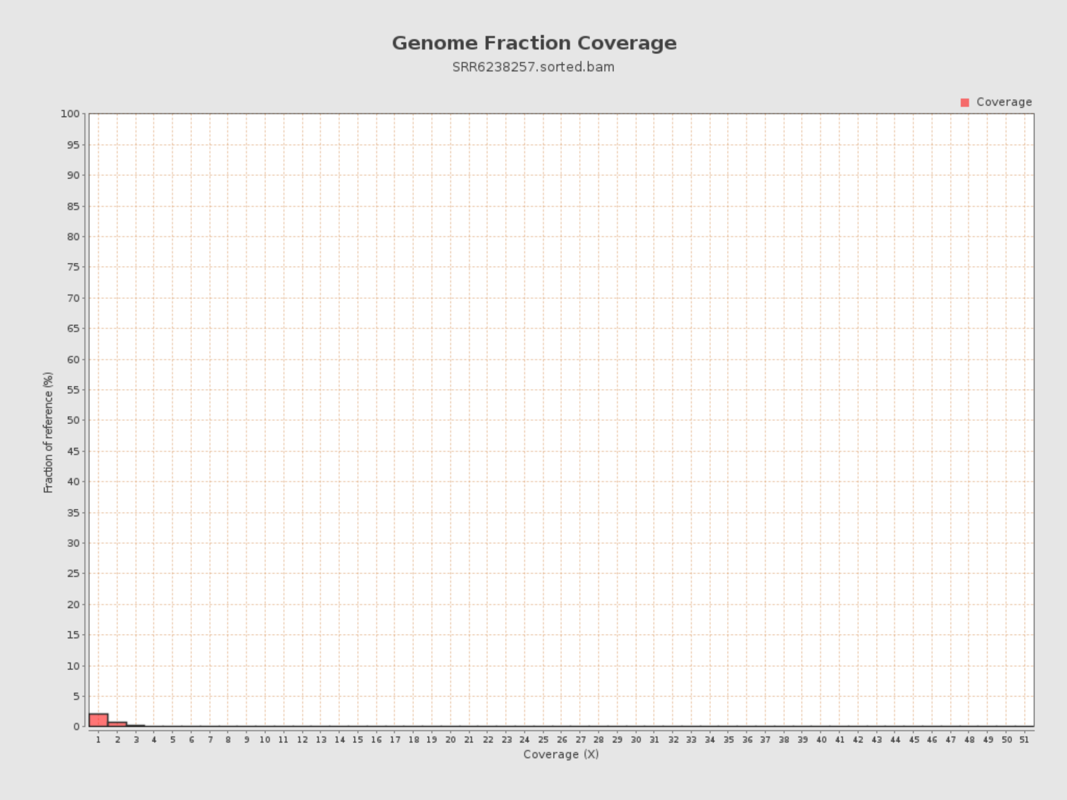
4. Results : Coverage Histogram



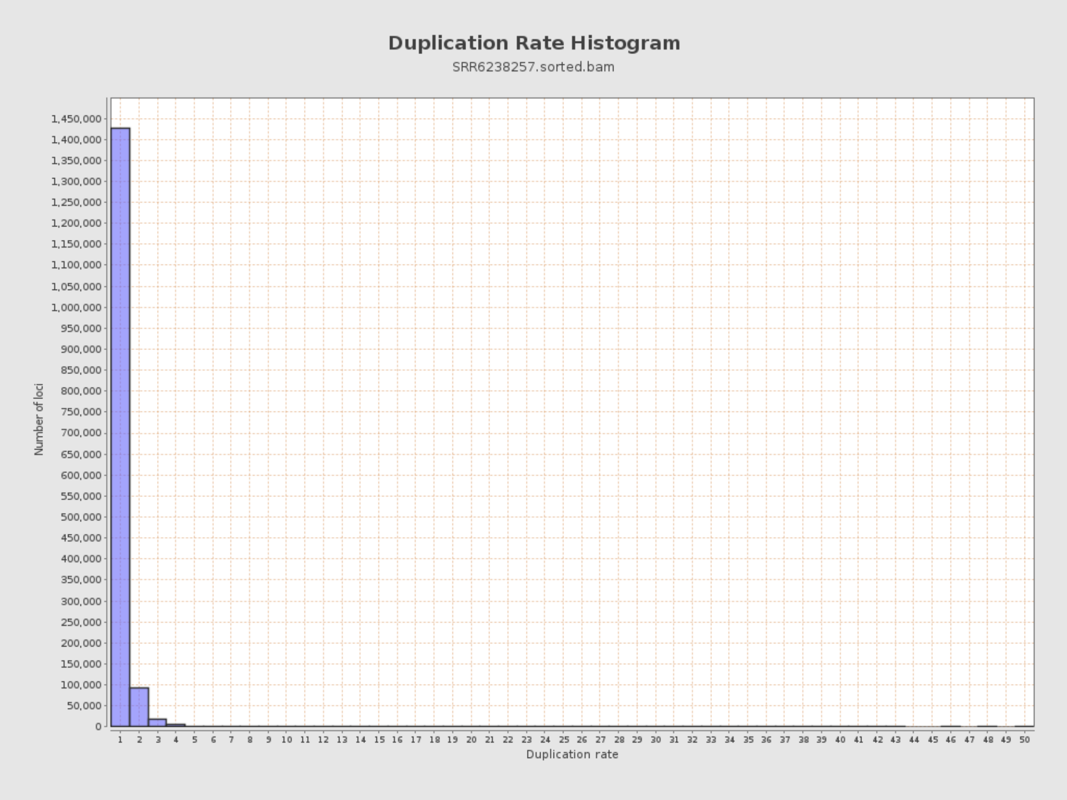
5. Results : Coverage Histogram (0-50X)



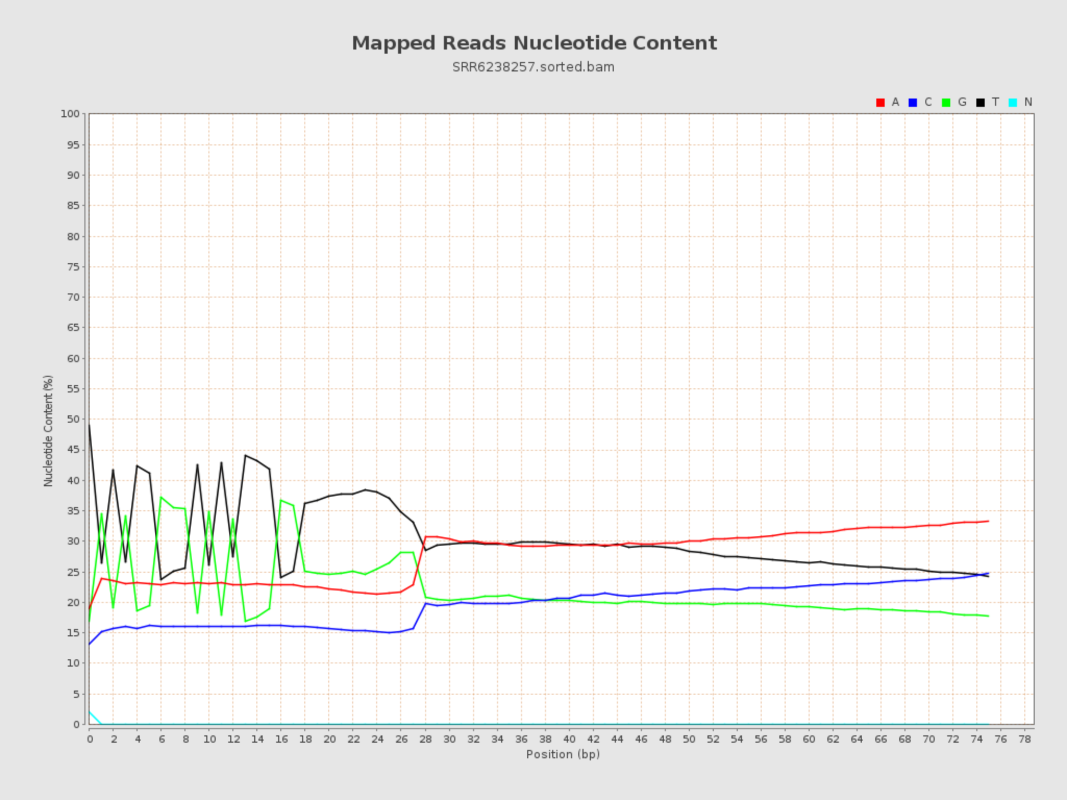
6. Results : Genome Fraction Coverage



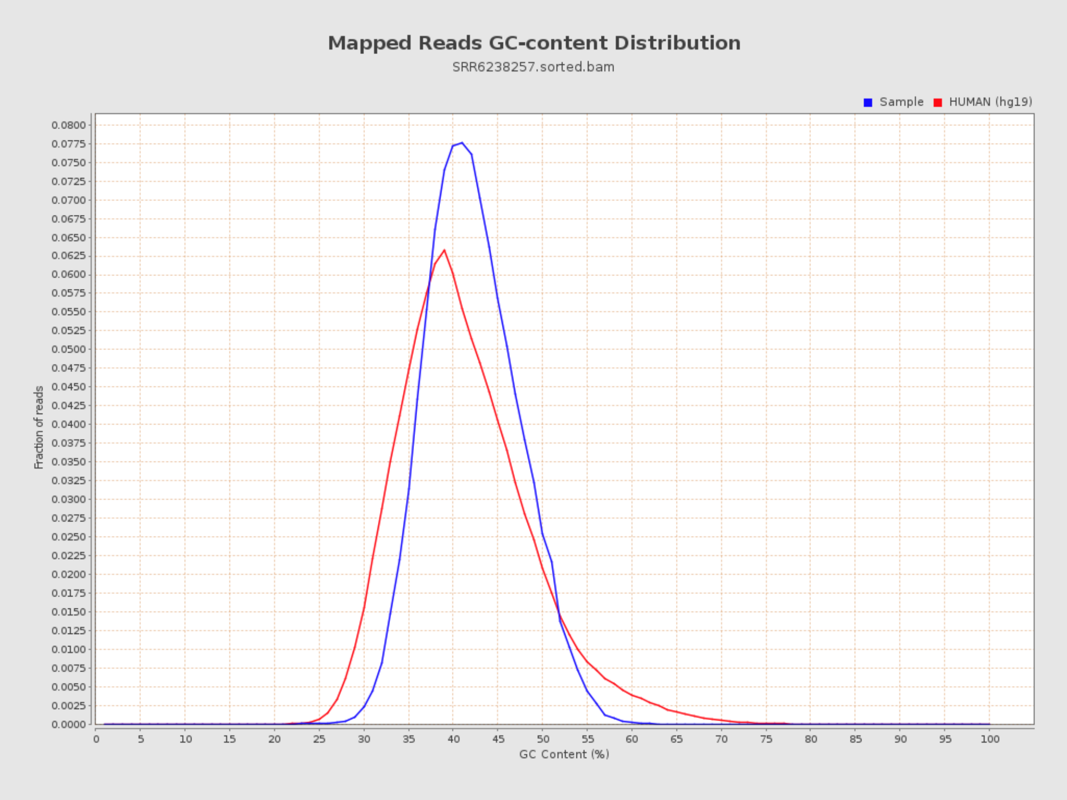
7. Results : Duplication Rate Histogram



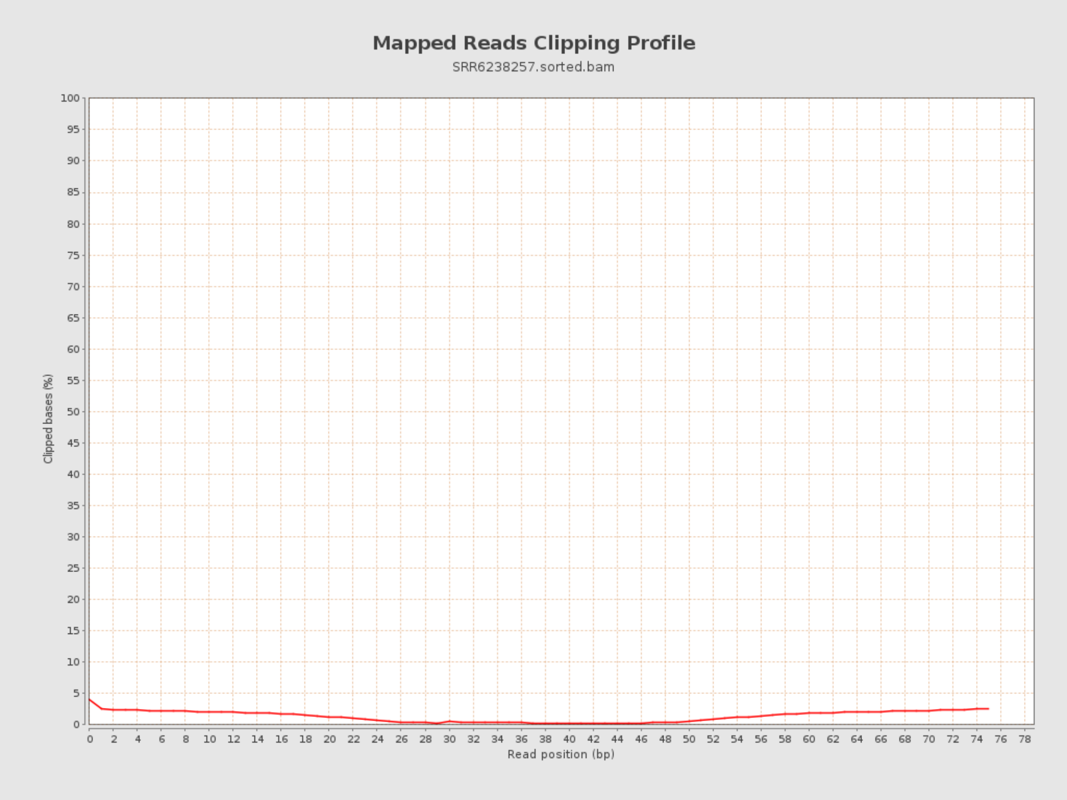
8. Results : Mapped Reads Nucleotide Content



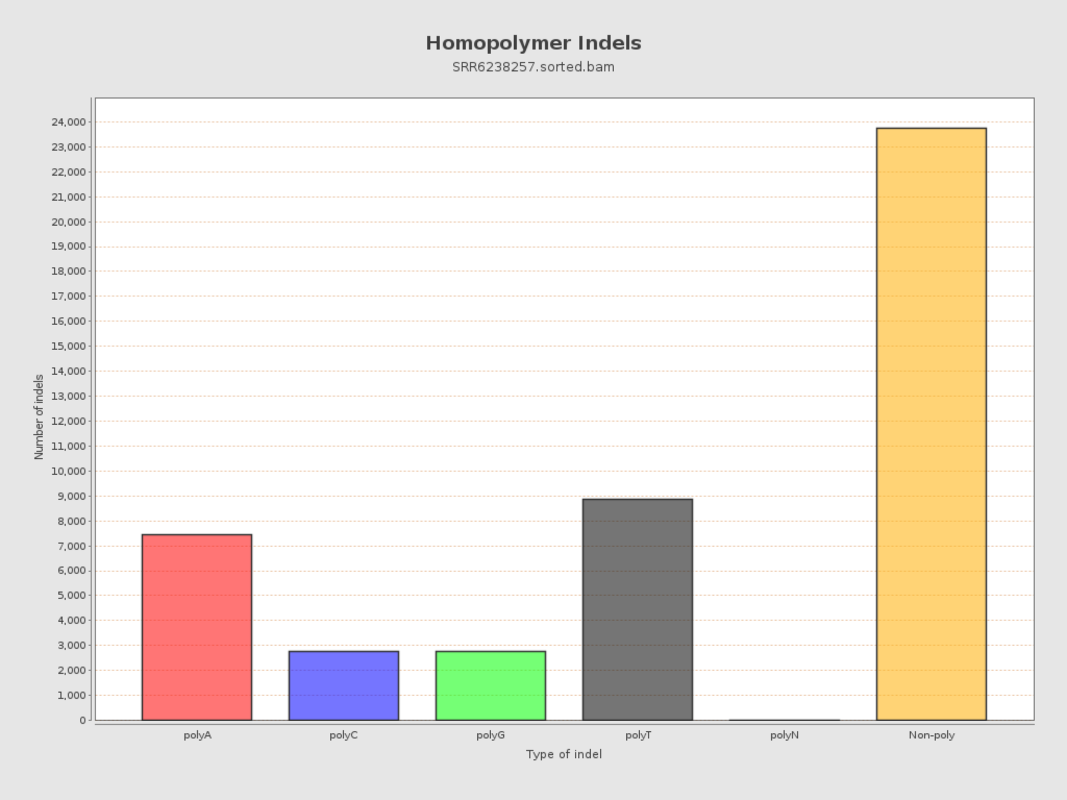
9. Results : Mapped Reads GC-content Distribution



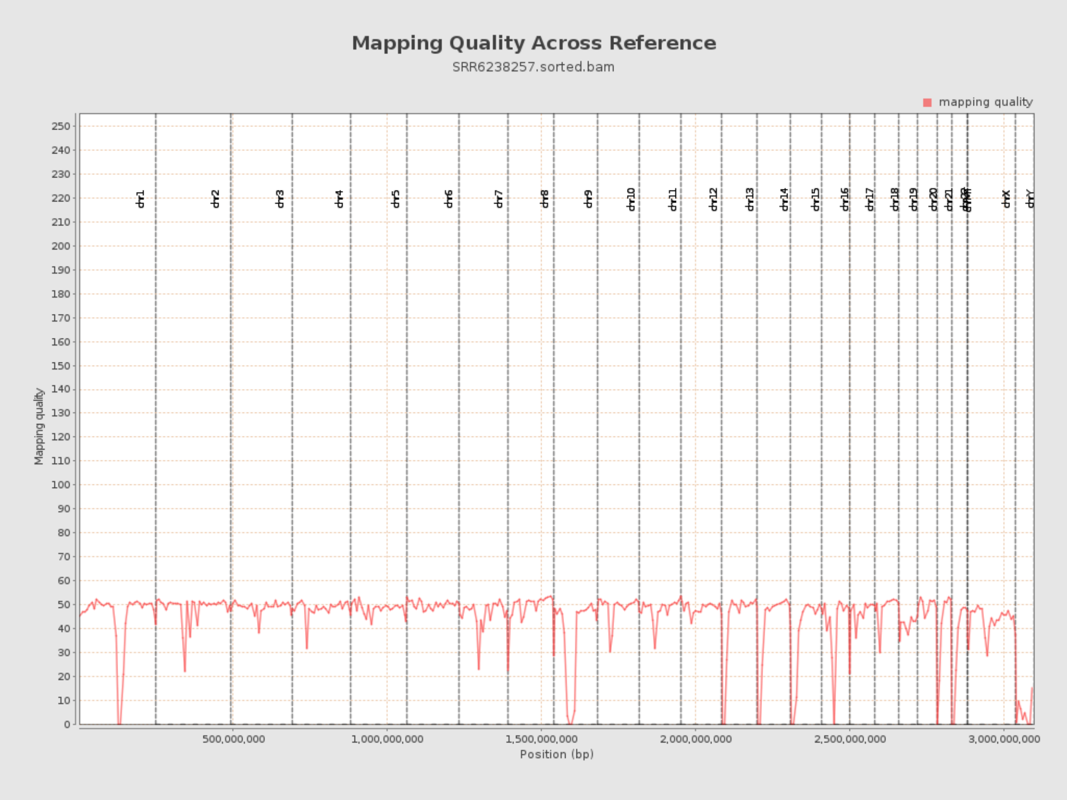
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram