Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:48:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238620.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_SRR6238620 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238620.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:48:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238620.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,192,433
Mapped reads	1,981,106 / 90.36%
Unmapped reads	211,327 / 9.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,346 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	469,160 / 21.4%
Duplication rate	18.14%
Clipped reads	1,248,995 / 56.97%

2.2. ACGT Content

Number/percentage of A's	30,346,844 / 24.81%
Number/percentage of C's	21,552,325 / 17.62%
Number/percentage of T's	41,007,390 / 33.53%
Number/percentage of G's	29,405,055 / 24.04%
Number/percentage of N's	6,075 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0395

Standard Deviation	0.5783

2.4. Mapping Quality

Mean Mapping Quality	38.87

2.5. Mismatches and indels

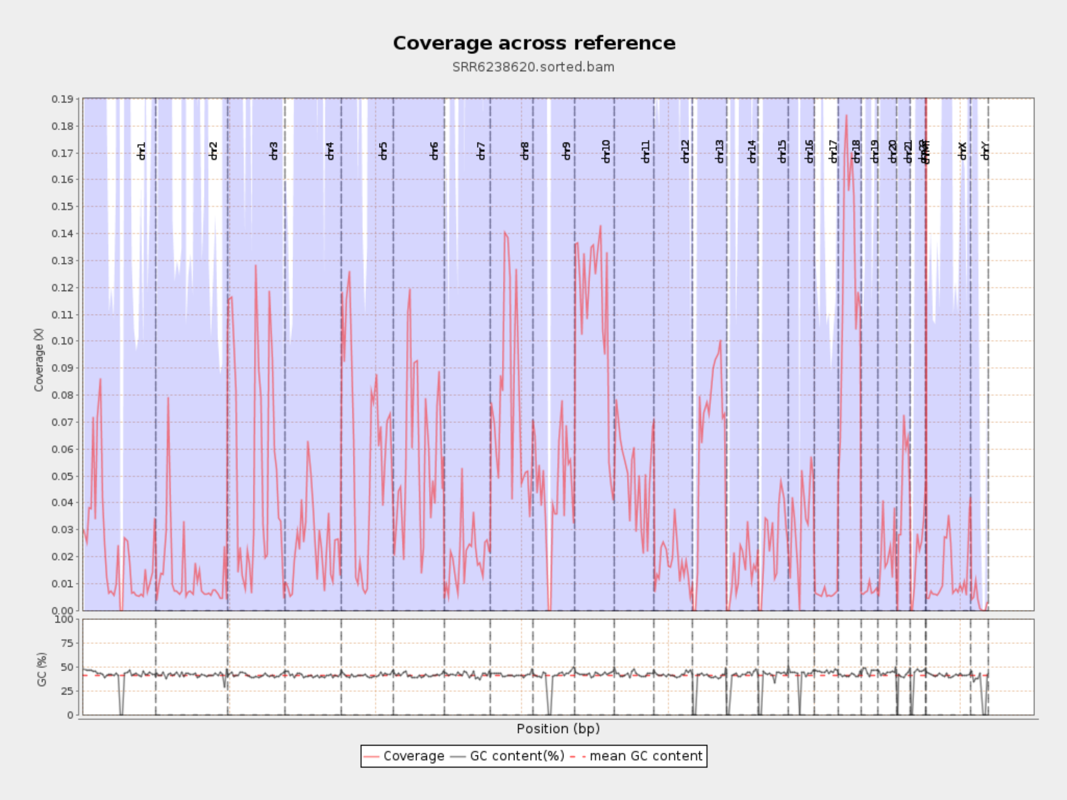
General error rate	0.57%
Mismatches	689,589
Insertions	7,589
Mapped reads with at least one insertion	0.38%
Deletions	33,344
Mapped reads with at least one deletion	1.67%
Homopolymer indels	41.51%

2.6. Chromosome stats

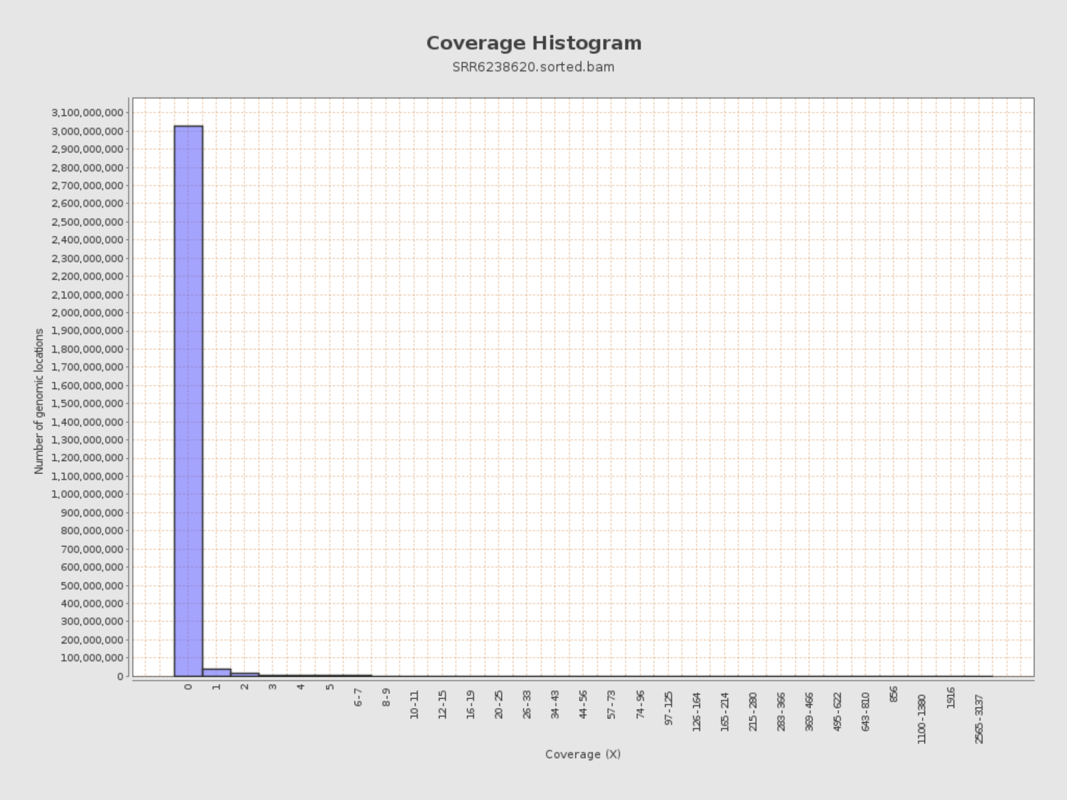
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5559446	0.0223	0.2631
chr2	243199373	3231232	0.0133	1.3978
chr3	198022430	10457881	0.0528	0.3905
chr4	191154276	4602638	0.0241	0.2549
chr5	180915260	10733983	0.0593	0.4121
chr6	171115067	9782255	0.0572	0.6432
chr7	159138663	3215053	0.0202	0.427

chr8	146364022	11298151	0.0772	0.6087
chr9	141213431	6211769	0.044	0.4173
chr10	135534747	15312455	0.113	0.6158
chr11	135006516	6731379	0.0499	0.4084
chr12	133851895	2342361	0.0175	0.2318
chr13	115169878	7684043	0.0667	0.5148
chr14	107349540	1611508	0.015	0.2203
chr15	102531392	2577305	0.0251	0.3675
chr16	90354753	3000960	0.0332	0.3355
chr17	81195210	491190	0.006	0.1296
chr18	78077248	10212744	0.1308	1.235
chr19	59128983	441128	0.0075	0.2683
chr20	63025520	1397781	0.0222	0.2528
chr21	48129895	2153962	0.0448	0.3663
chr22	51304566	1016426	0.0198	0.2286
chrMT	16571	6429	0.388	0.7694
chrX	155270560	2096680	0.0135	0.208
chrY	59373566	204920	0.0035	0.2092

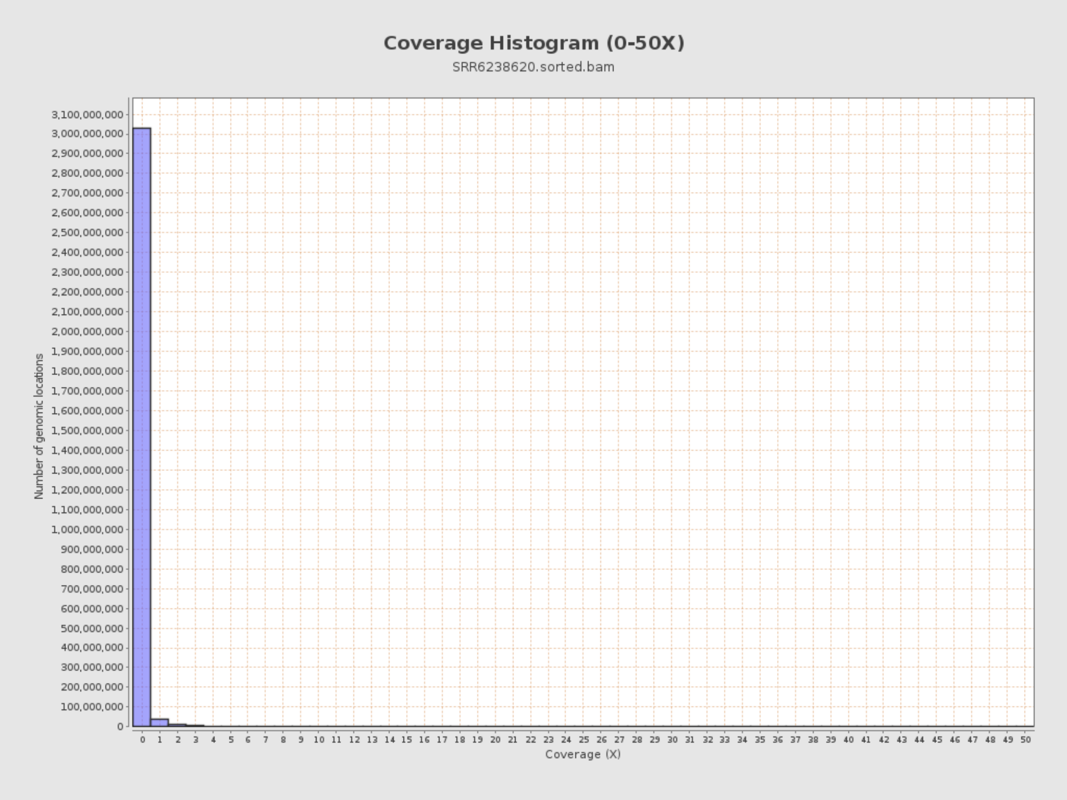
3. Results : Coverage across reference



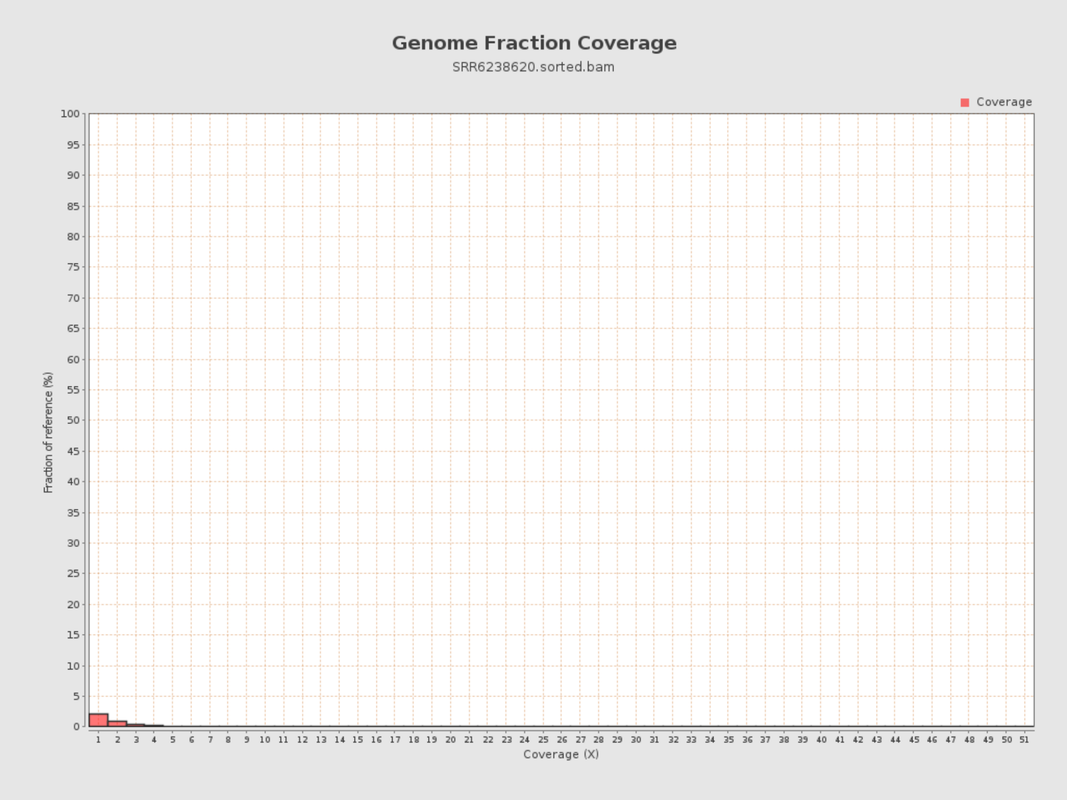
4. Results : Coverage Histogram



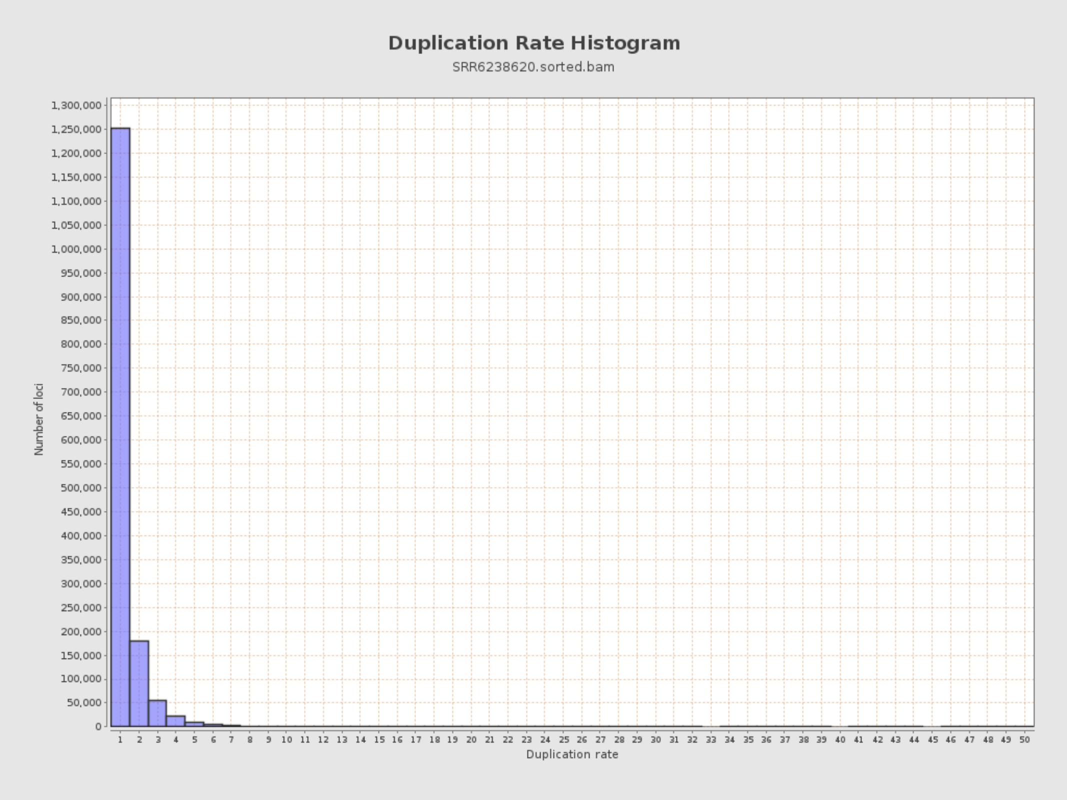
5. Results : Coverage Histogram (0-50X)



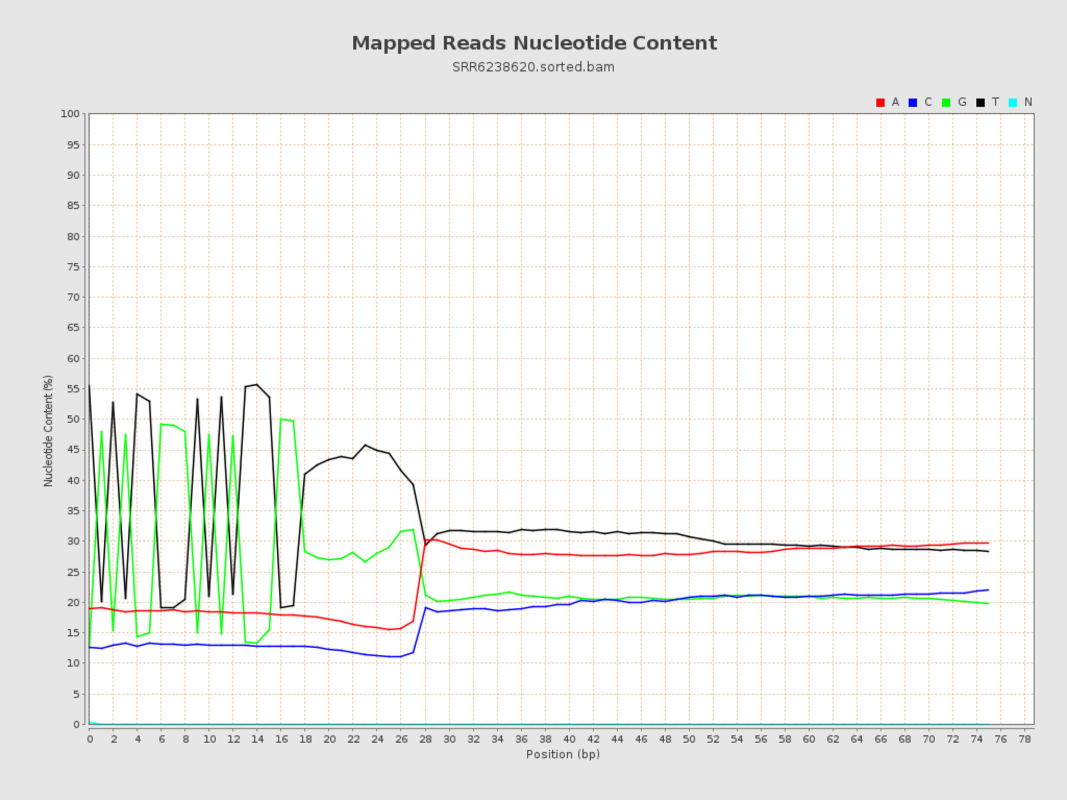
6. Results : Genome Fraction Coverage



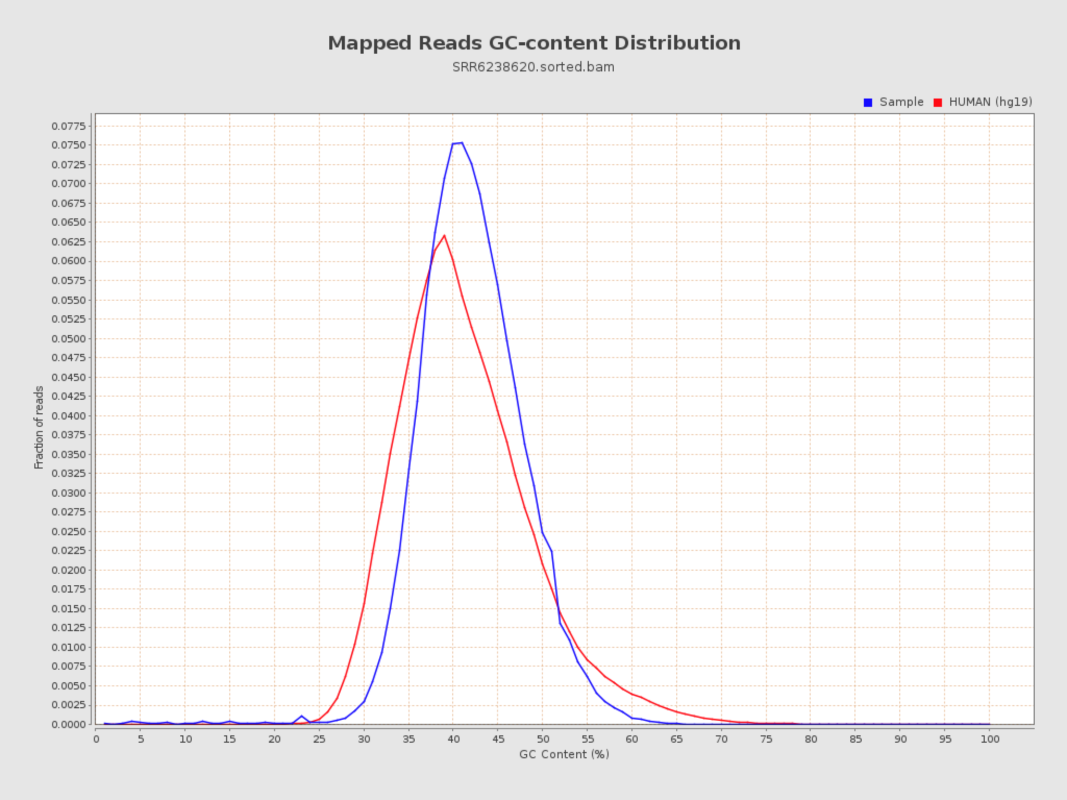
7. Results : Duplication Rate Histogram



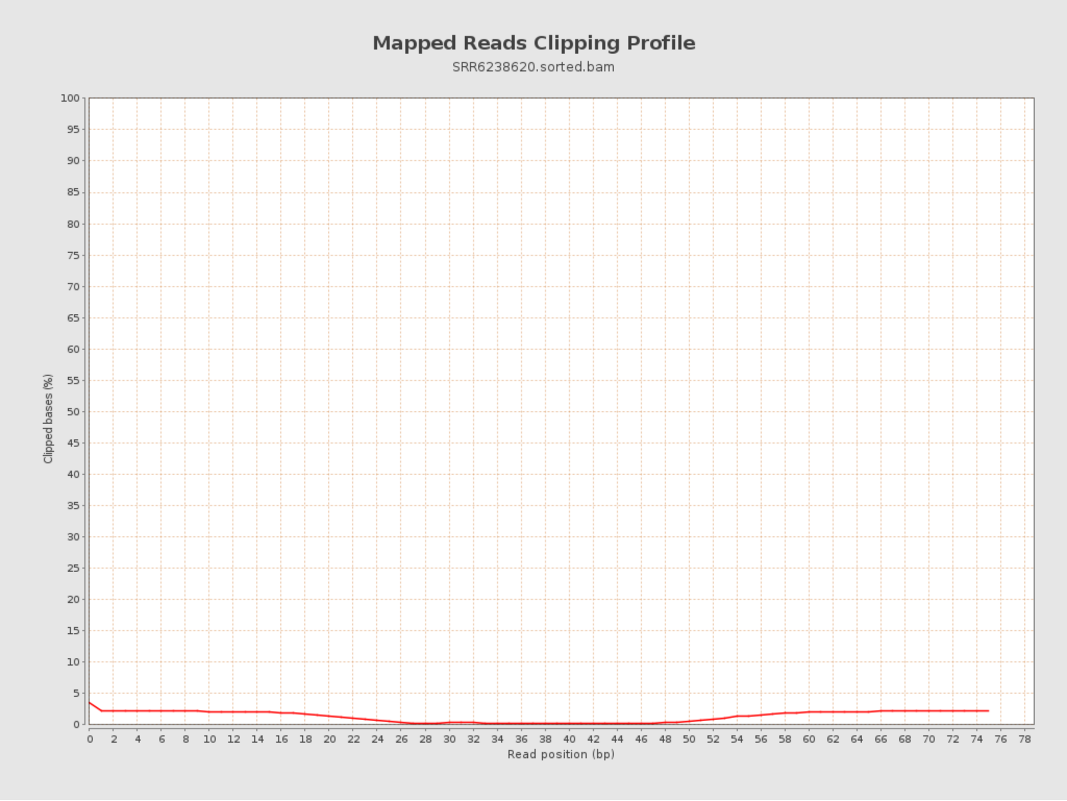
8. Results : Mapped Reads Nucleotide Content



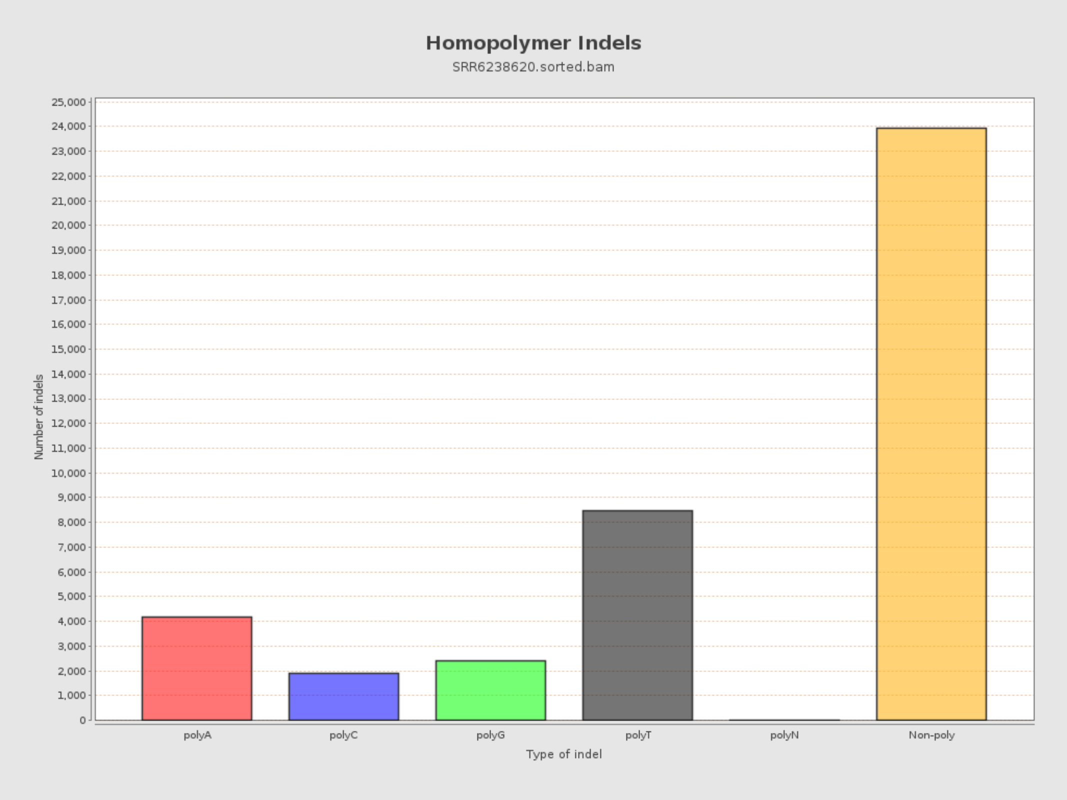
9. Results : Mapped Reads GC-content Distribution



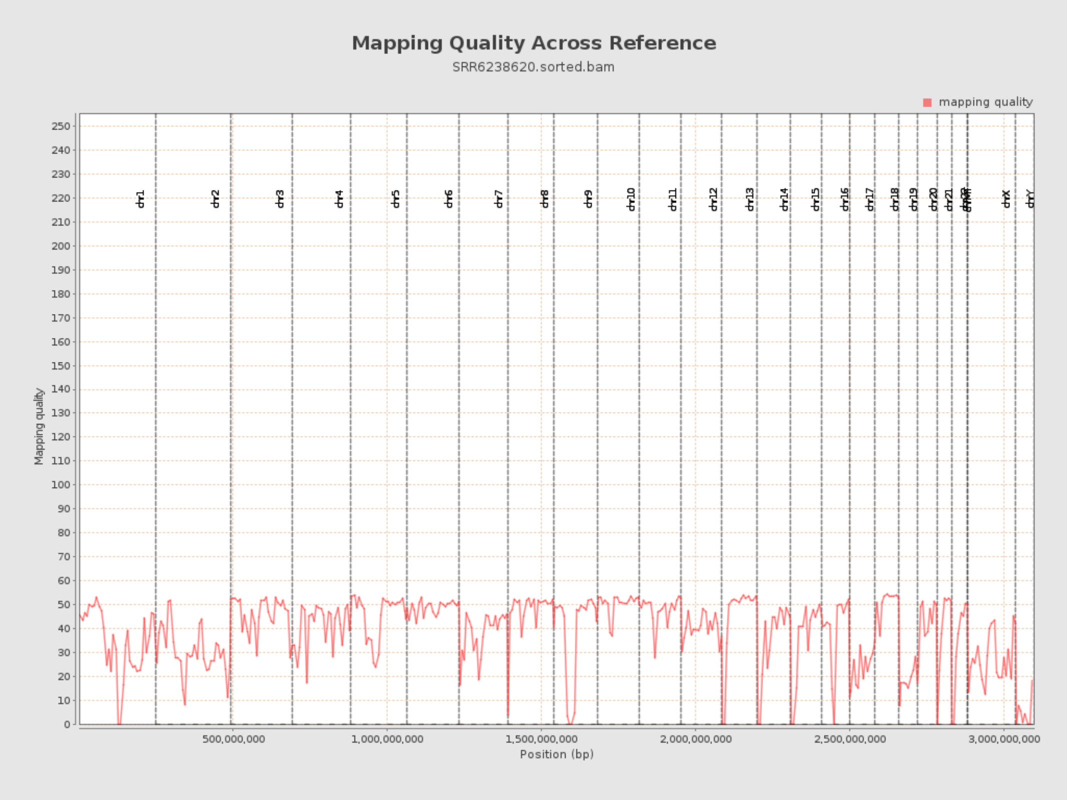
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram