Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:06:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238626.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_SRR6238626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238626.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:06:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,012,124
Mapped reads	2,345,171 / 77.86%
Unmapped reads	666,953 / 22.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,772 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	1,100,179 / 36.53%
Duplication rate	24.24%
Clipped reads	1,689,111 / 56.08%

2.2. ACGT Content

Number/percentage of A's	34,014,213 / 24.3%
Number/percentage of C's	23,741,036 / 16.96%
Number/percentage of T's	48,349,769 / 34.55%
Number/percentage of G's	33,844,178 / 24.18%
Number/percentage of N's	2,988 / 0%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.9091

2.4. Mapping Quality

Mean Mapping Quality	43.72

2.5. Mismatches and indels

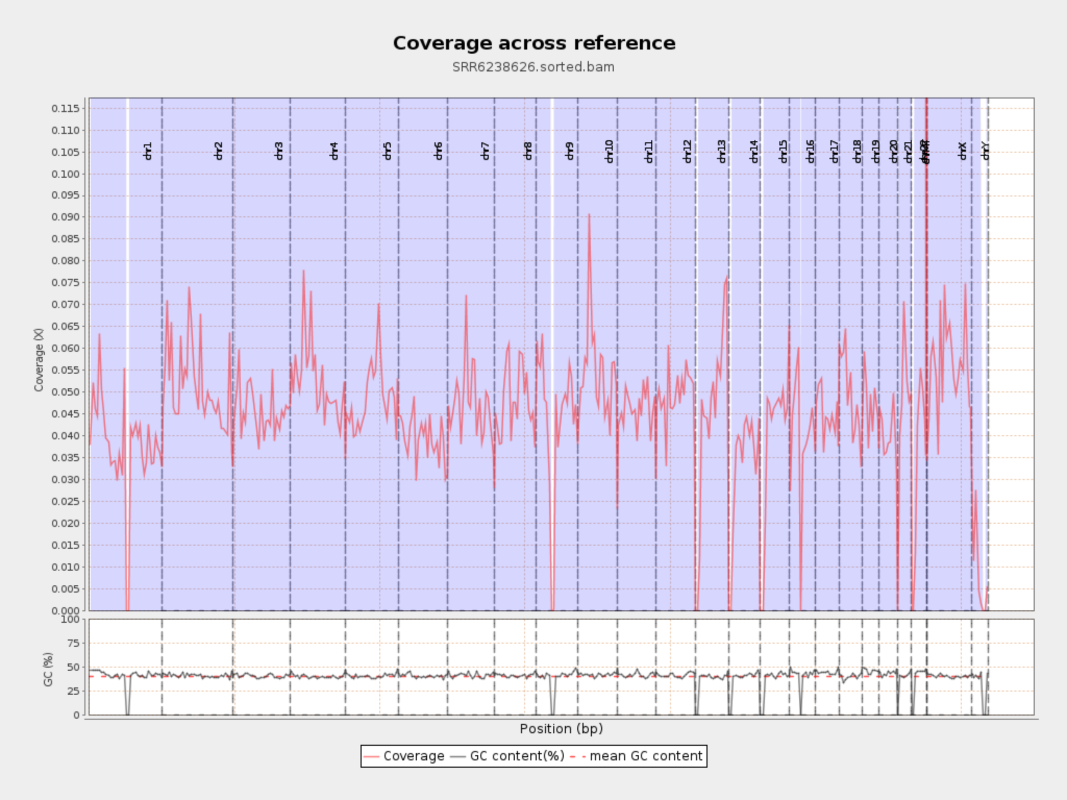
General error rate	0.58%
Mismatches	790,368
Insertions	9,951
Mapped reads with at least one insertion	0.42%
Deletions	32,597
Mapped reads with at least one deletion	1.38%
Homopolymer indels	41.65%

2.6. Chromosome stats

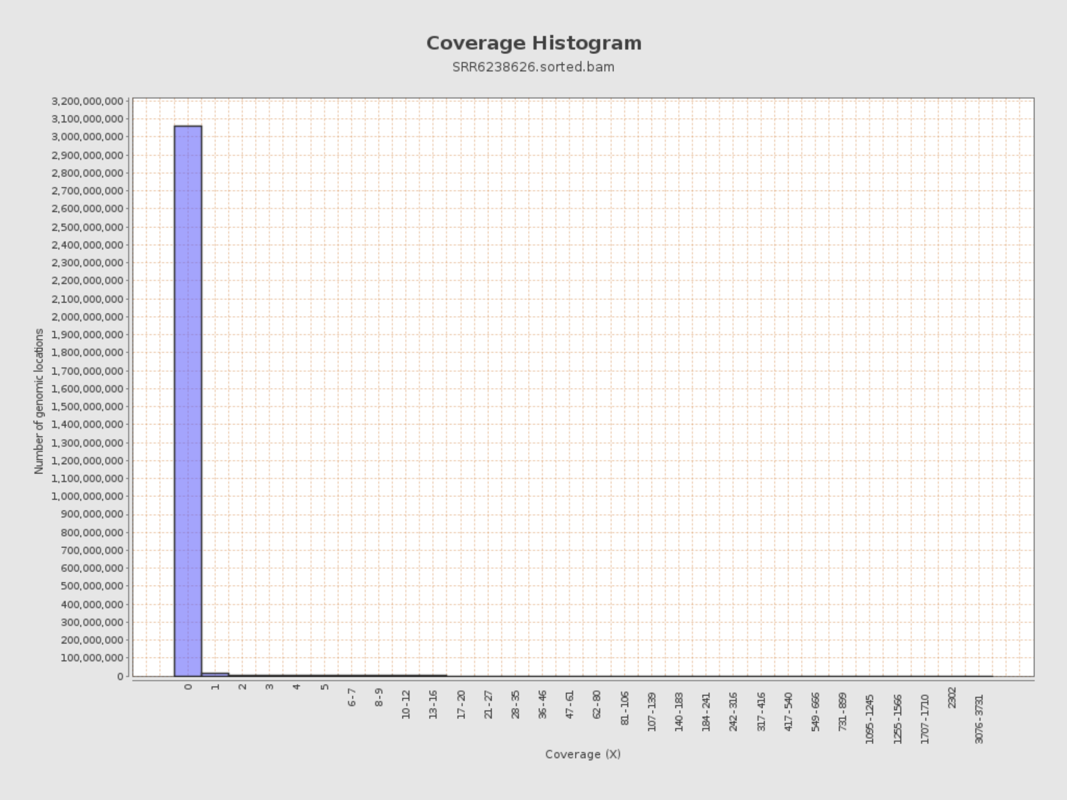
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9365488	0.0376	0.7391
chr2	243199373	12611098	0.0519	1.8031
chr3	198022430	9006521	0.0455	0.6861
chr4	191154276	10068759	0.0527	0.739
chr5	180915260	8801842	0.0487	0.7015
chr6	171115067	6785813	0.0397	0.8475
chr7	159138663	7605869	0.0478	0.8382

chr8	146364022	6987767	0.0477	0.7895
chr9	141213431	6089588	0.0431	0.697
chr10	135534747	7436045	0.0549	0.8206
chr11	135006516	6190384	0.0459	0.6929
chr12	133851895	6632898	0.0496	0.7208
chr13	115169878	5181692	0.045	0.8141
chr14	107349540	3495331	0.0326	0.5975
chr15	102531392	3978060	0.0388	0.7093
chr16	90354753	3656971	0.0405	0.6512
chr17	81195210	3633309	0.0447	0.6562
chr18	78077248	3879554	0.0497	1.8709
chr19	59128983	2786931	0.0471	0.7943
chr20	63025520	2536308	0.0402	0.6491
chr21	48129895	2239726	0.0465	0.7136
chr22	51304566	1663352	0.0324	0.5549
chrMT	16571	224105	13.5239	15.247
chrX	155270560	8661477	0.0558	0.7771
chrY	59373566	488051	0.0082	0.3385

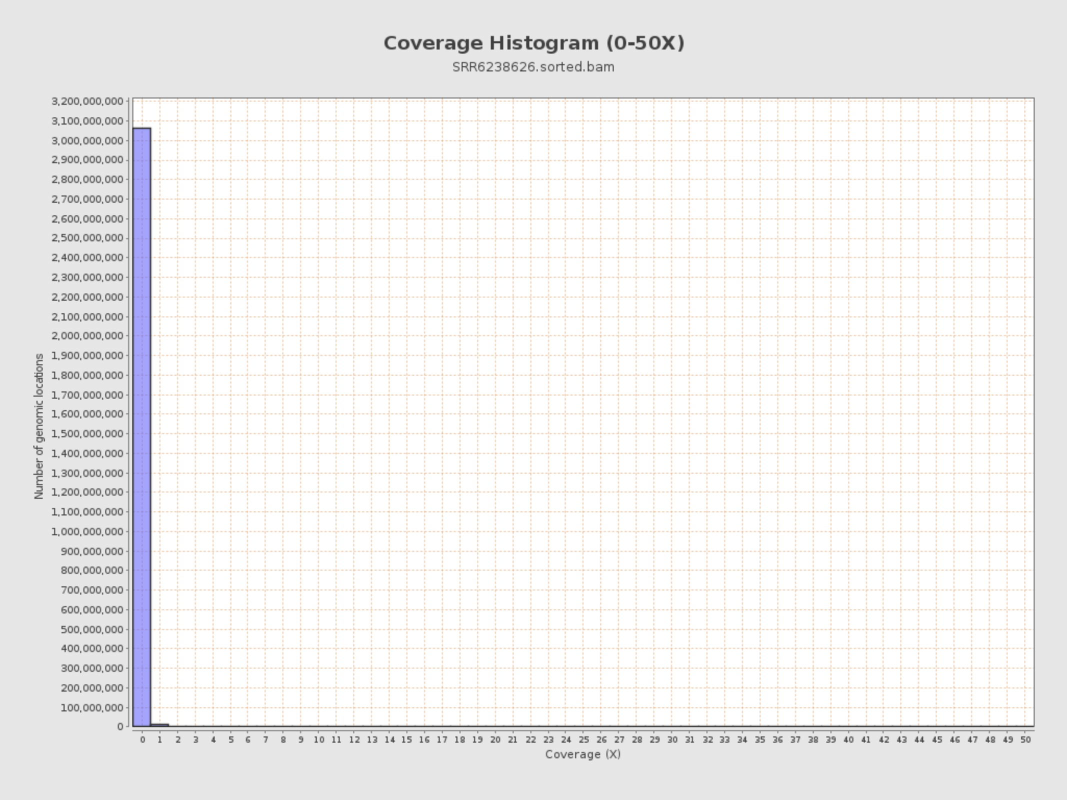
3. Results : Coverage across reference



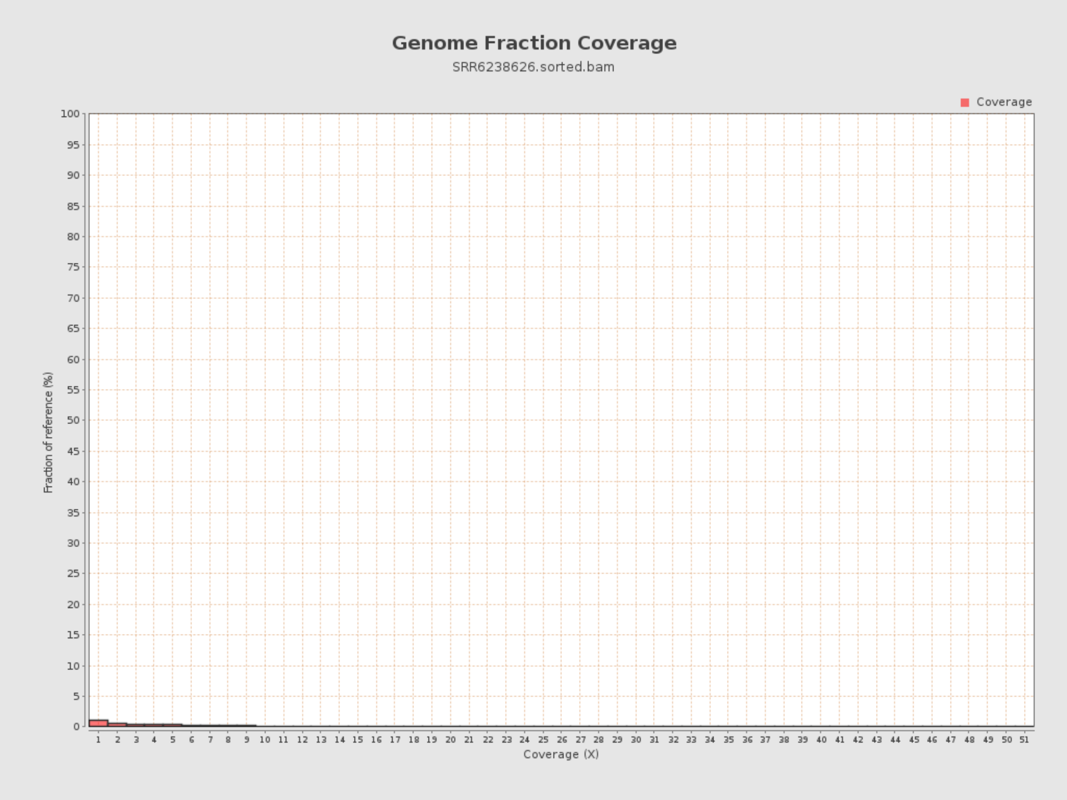
4. Results : Coverage Histogram



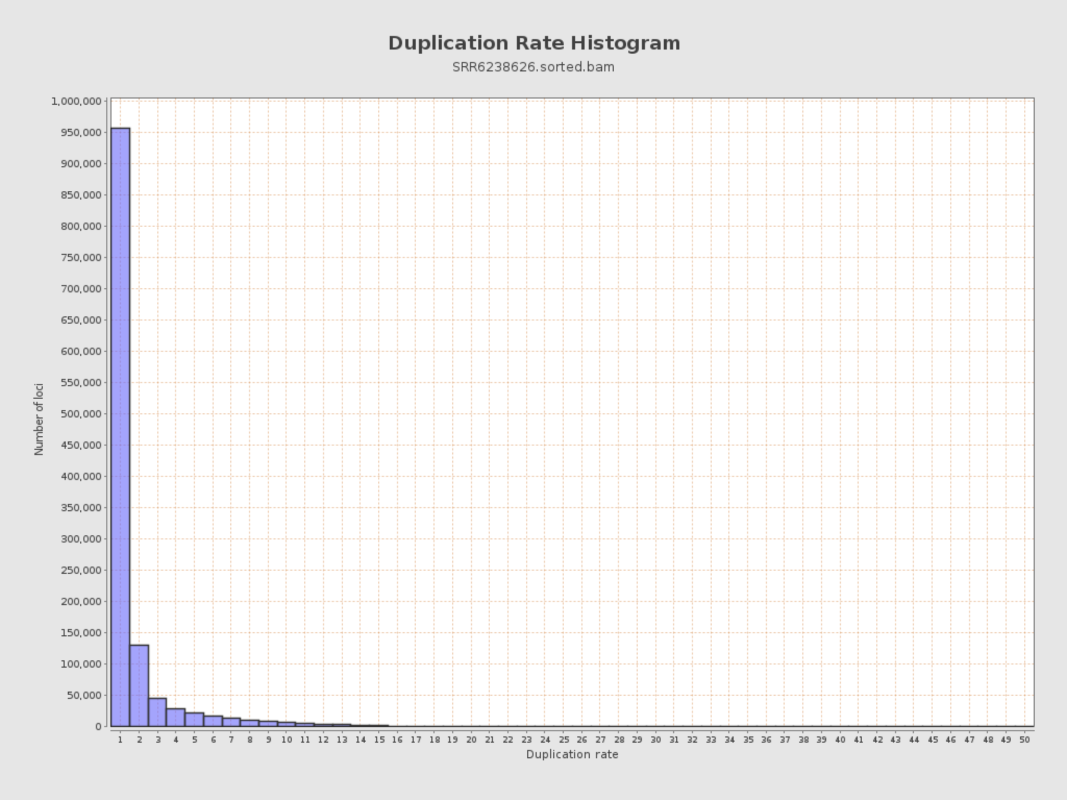
5. Results : Coverage Histogram (0-50X)



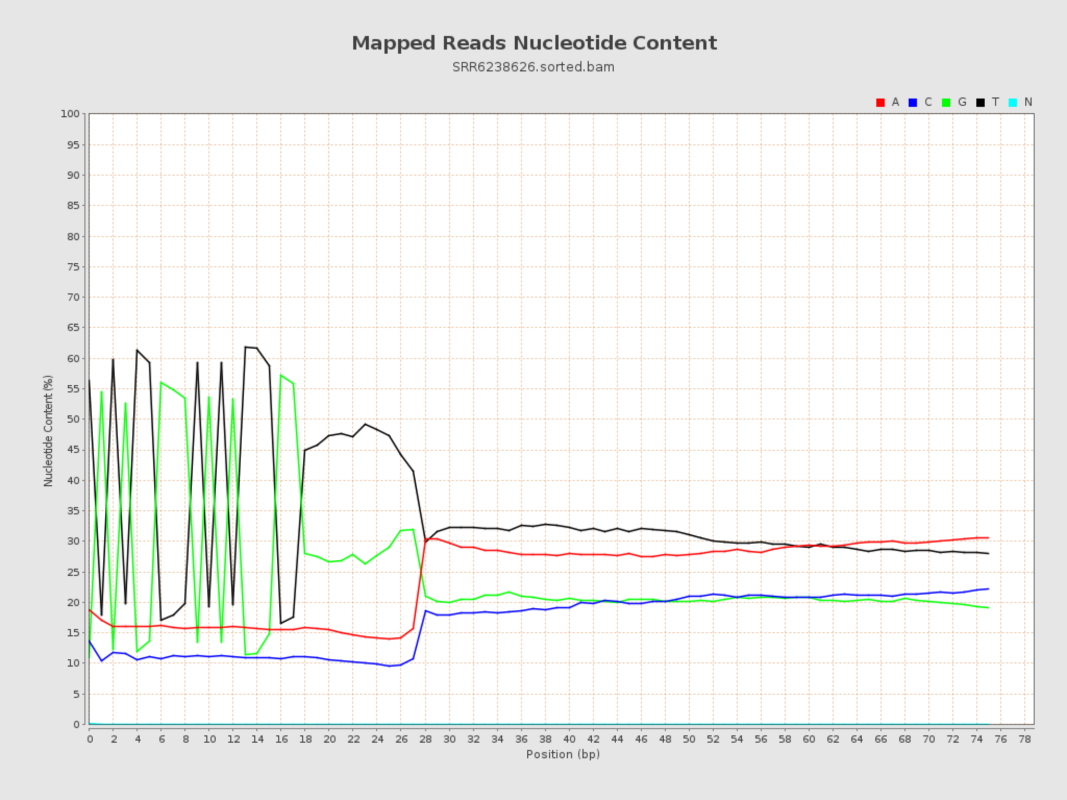
6. Results : Genome Fraction Coverage



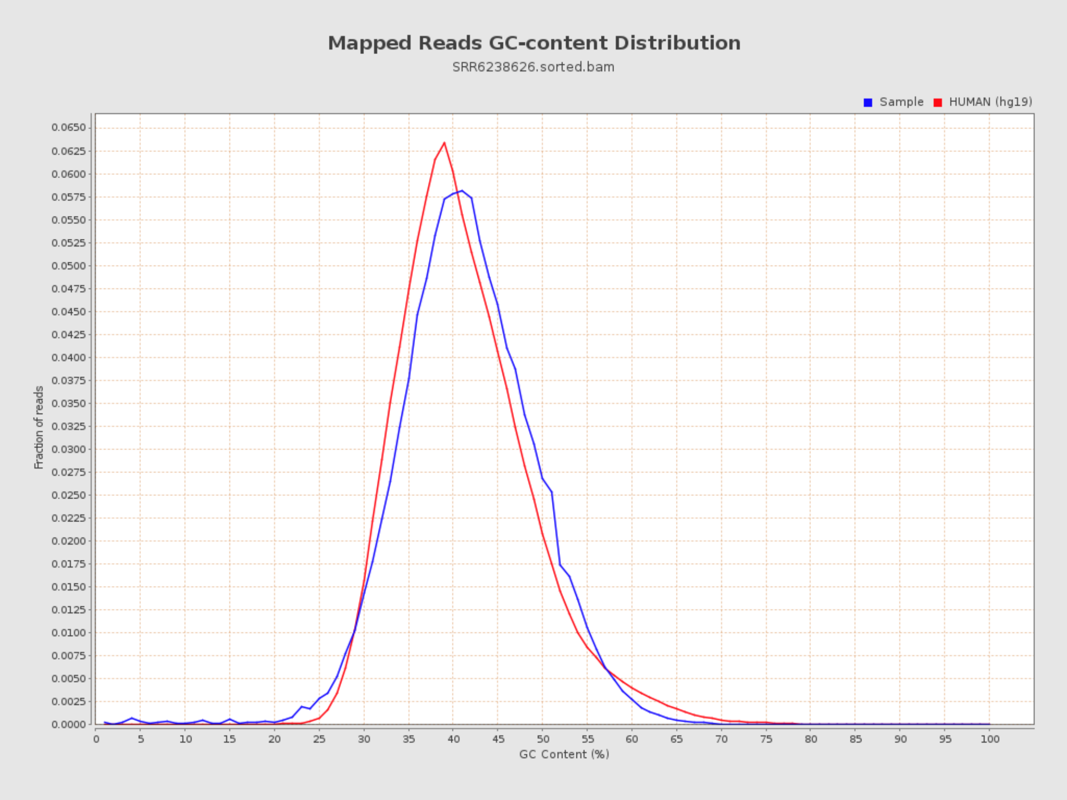
7. Results : Duplication Rate Histogram



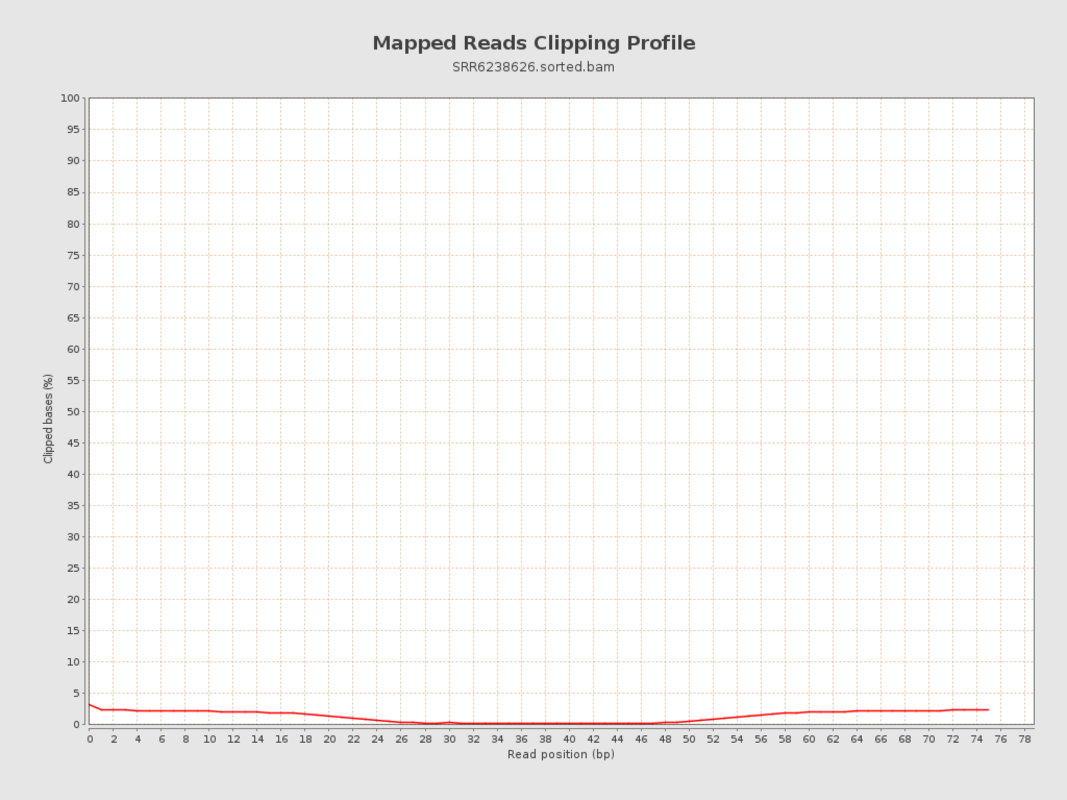
8. Results : Mapped Reads Nucleotide Content



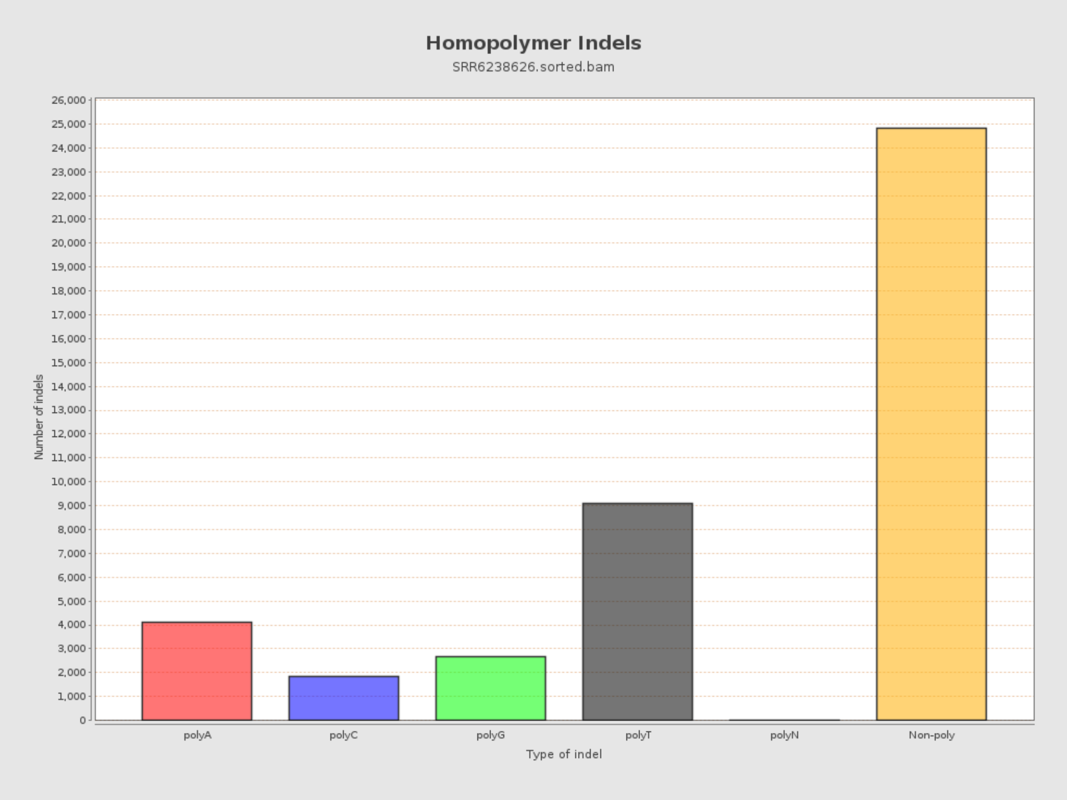
9. Results : Mapped Reads GC-content Distribution



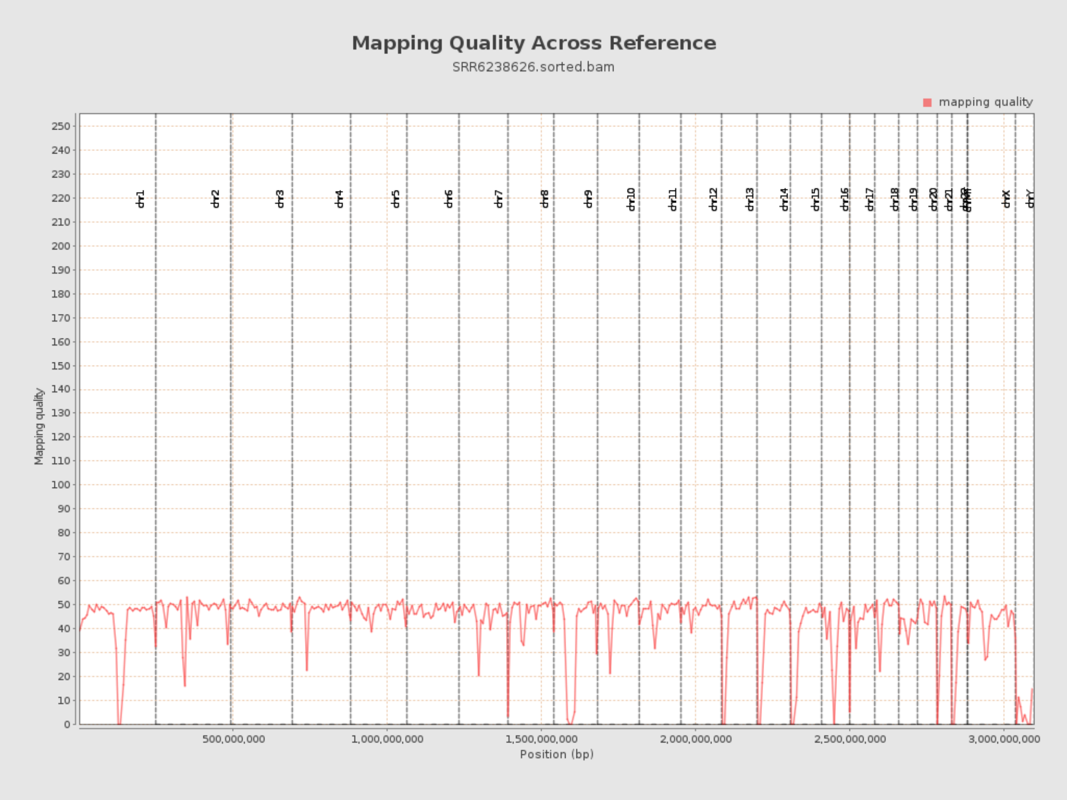
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram