Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 00:18:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238643.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_SRR6238643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238643.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 00:18:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,798,311
Mapped reads	2,778,199 / 73.14%
Unmapped reads	1,020,112 / 26.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,620 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,113,670 / 29.32%
Duplication rate	20.62%
Clipped reads	1,650,447 / 43.45%

2.2. ACGT Content

Number/percentage of A's	43,795,625 / 25.23%
Number/percentage of C's	30,914,725 / 17.81%
Number/percentage of T's	57,601,643 / 33.18%
Number/percentage of G's	41,262,995 / 23.77%
Number/percentage of N's	4,363 / 0%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0561

Standard Deviation	0.9659

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Mismatches and indels

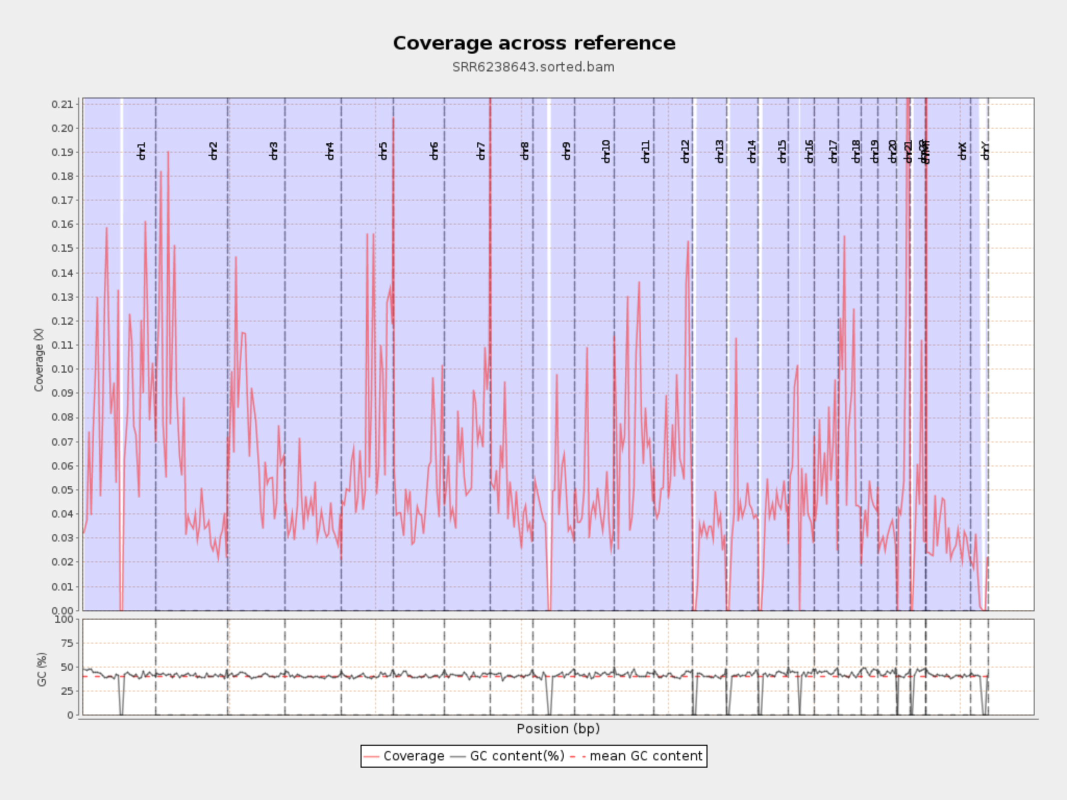
General error rate	0.55%
Mismatches	933,685
Insertions	12,583
Mapped reads with at least one insertion	0.45%
Deletions	41,787
Mapped reads with at least one deletion	1.49%
Homopolymer indels	43.95%

2.6. Chromosome stats

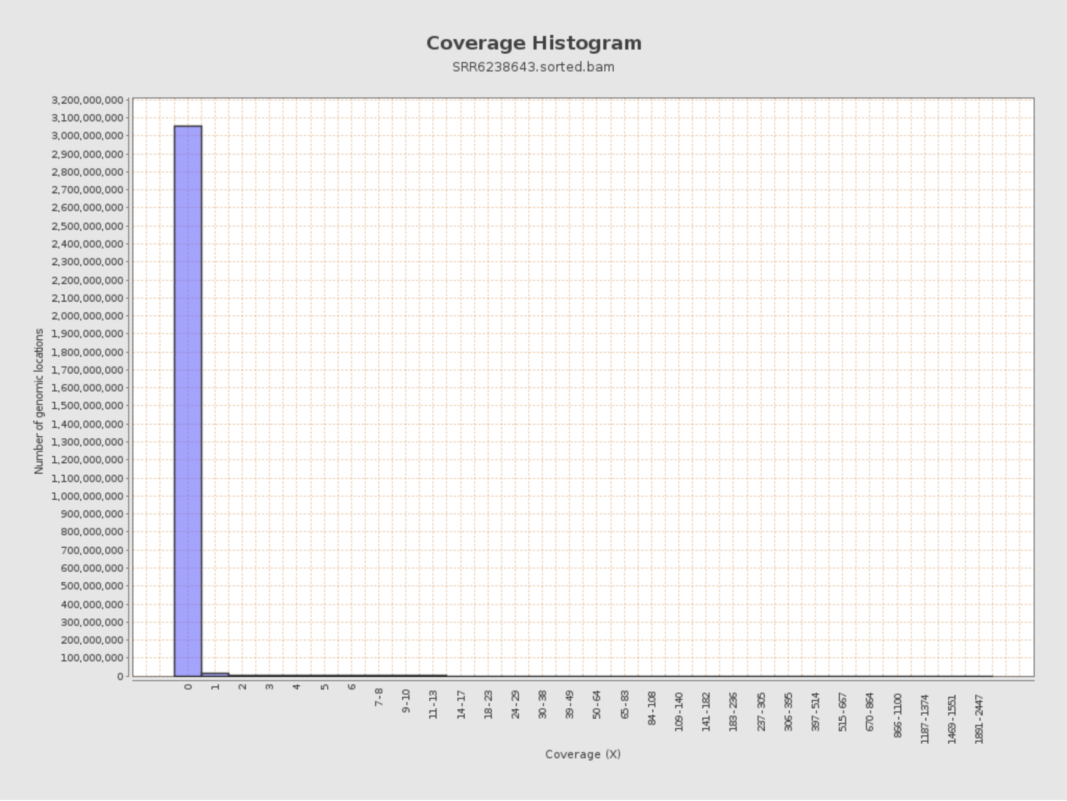
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21141165	0.0848	1.2899
chr2	243199373	15244837	0.0627	1.505
chr3	198022430	14491946	0.0732	0.8823
chr4	191154276	7454160	0.039	0.6325
chr5	180915260	14171604	0.0783	0.8978
chr6	171115067	8460101	0.0494	0.8336
chr7	159138663	10625816	0.0668	0.9294

chr8	146364022	6914525	0.0472	0.9432
chr9	141213431	6060894	0.0429	0.6937
chr10	135534747	5992611	0.0442	0.9088
chr11	135006516	9856712	0.073	0.8854
chr12	133851895	9264952	0.0692	0.8597
chr13	115169878	3316346	0.0288	0.6697
chr14	107349540	4408708	0.0411	1.01
chr15	102531392	3690337	0.036	1.2911
chr16	90354753	4569457	0.0506	0.7309
chr17	81195210	4900549	0.0604	0.7985
chr18	78077248	6626453	0.0849	1.3526
chr19	59128983	2415036	0.0408	0.848
chr20	63025520	1915876	0.0304	0.5401
chr21	48129895	4508945	0.0937	0.9985
chr22	51304566	2126085	0.0414	0.6284
chrMT	16571	114863	6.9316	9.7841
chrX	155270560	4597531	0.0296	0.6234
chrY	59373566	783698	0.0132	0.3446

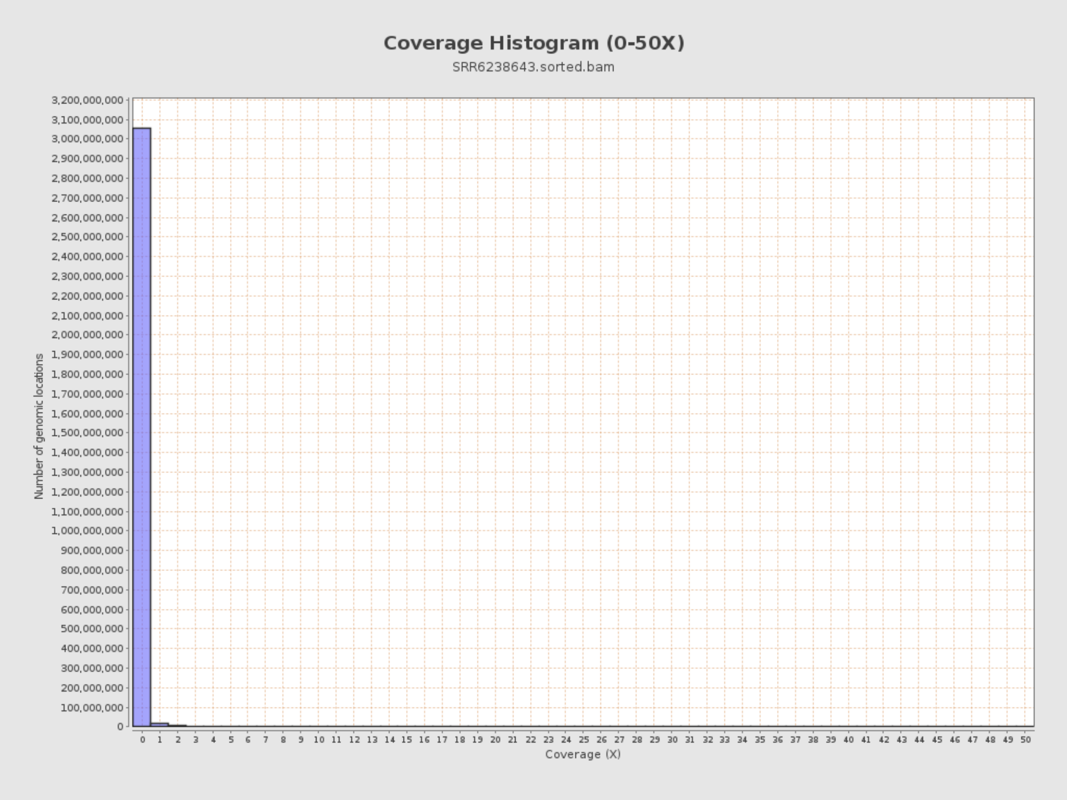
3. Results : Coverage across reference



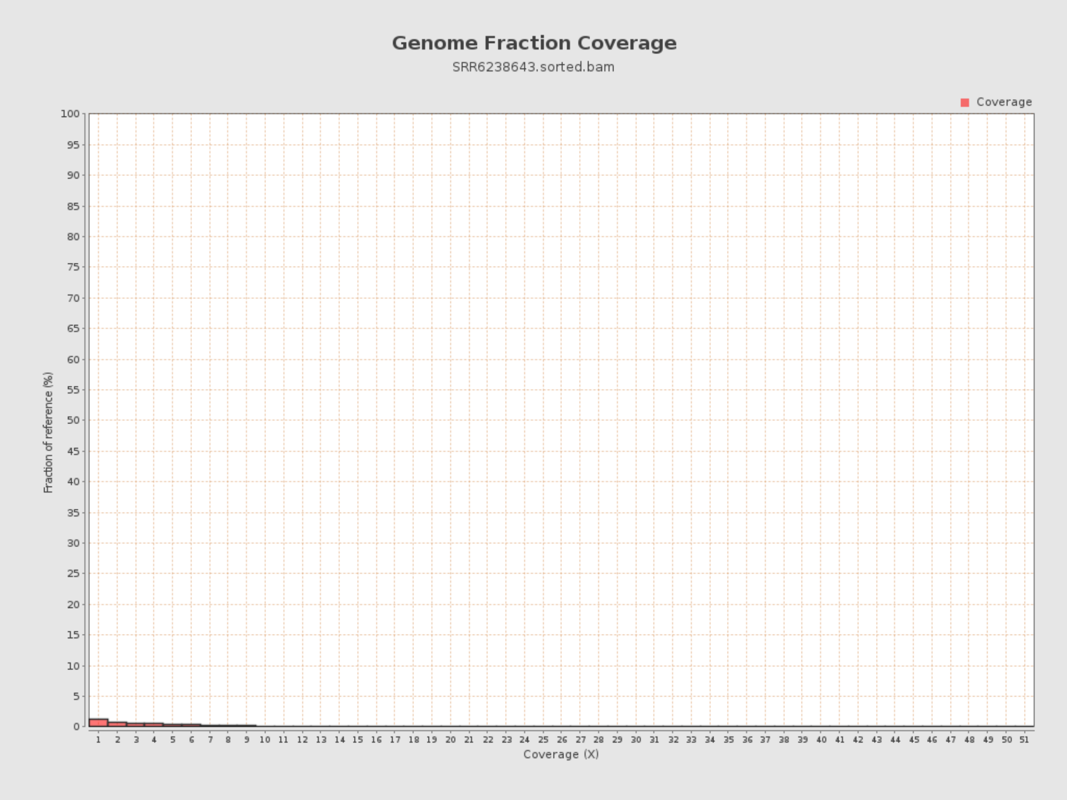
4. Results : Coverage Histogram



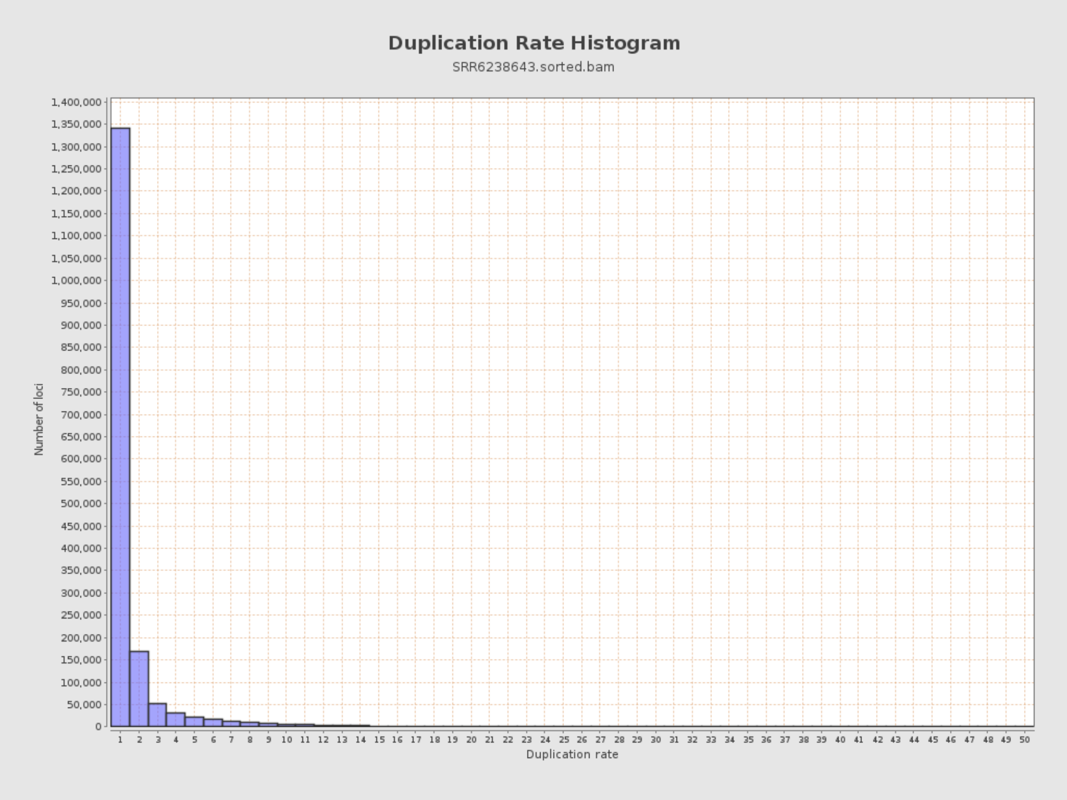
5. Results : Coverage Histogram (0-50X)



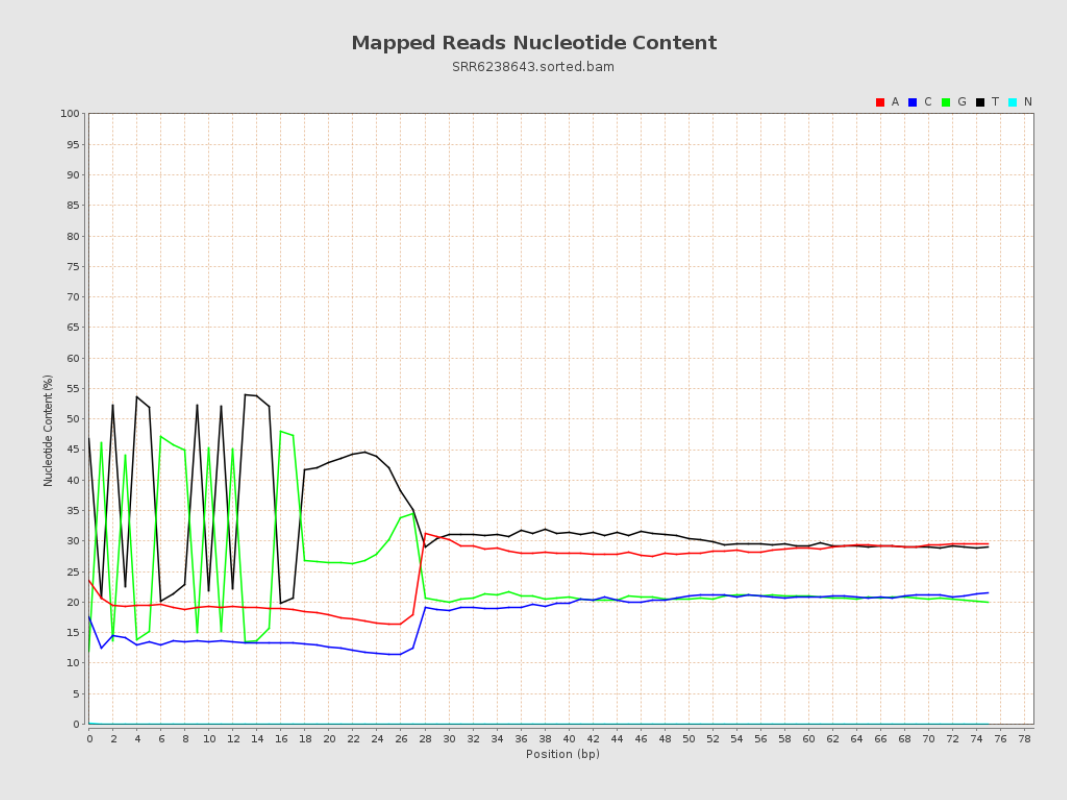
6. Results : Genome Fraction Coverage



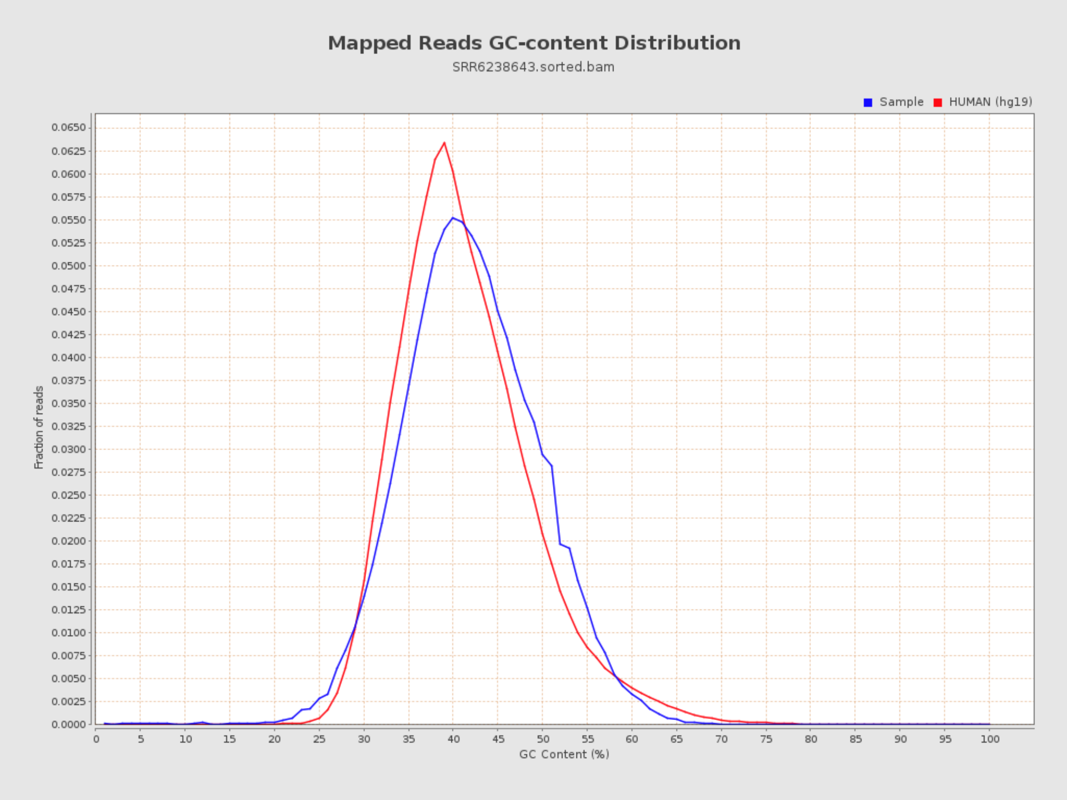
7. Results : Duplication Rate Histogram



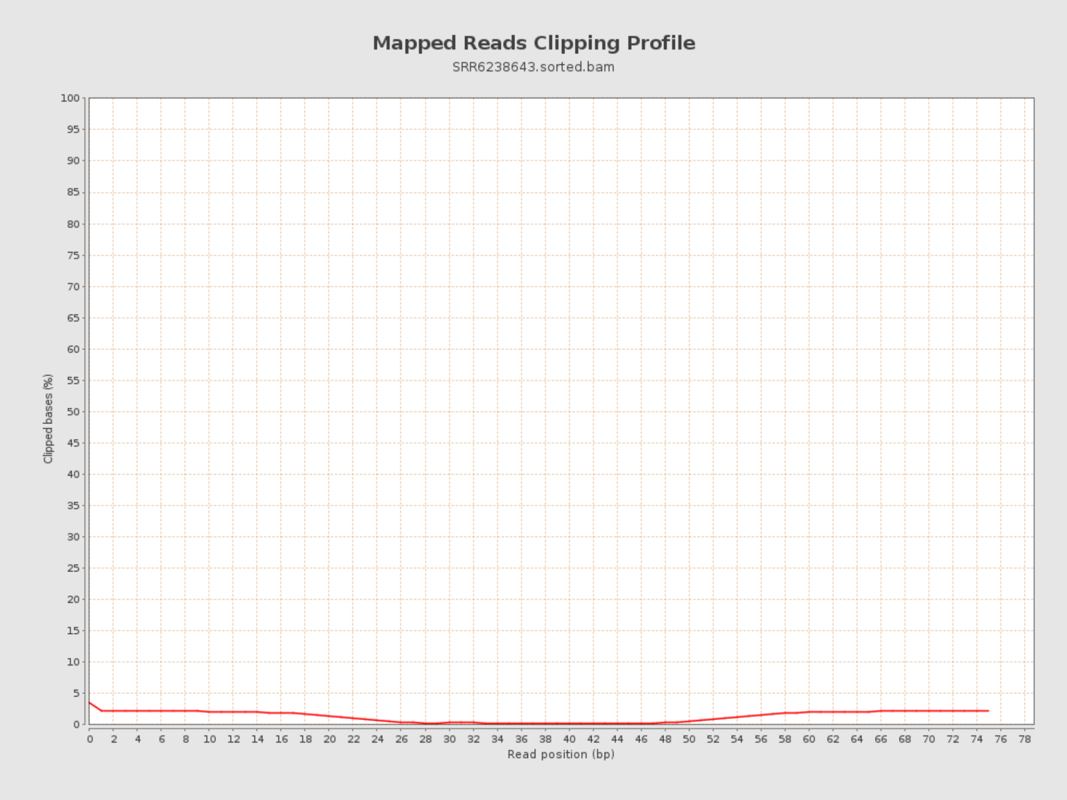
8. Results : Mapped Reads Nucleotide Content



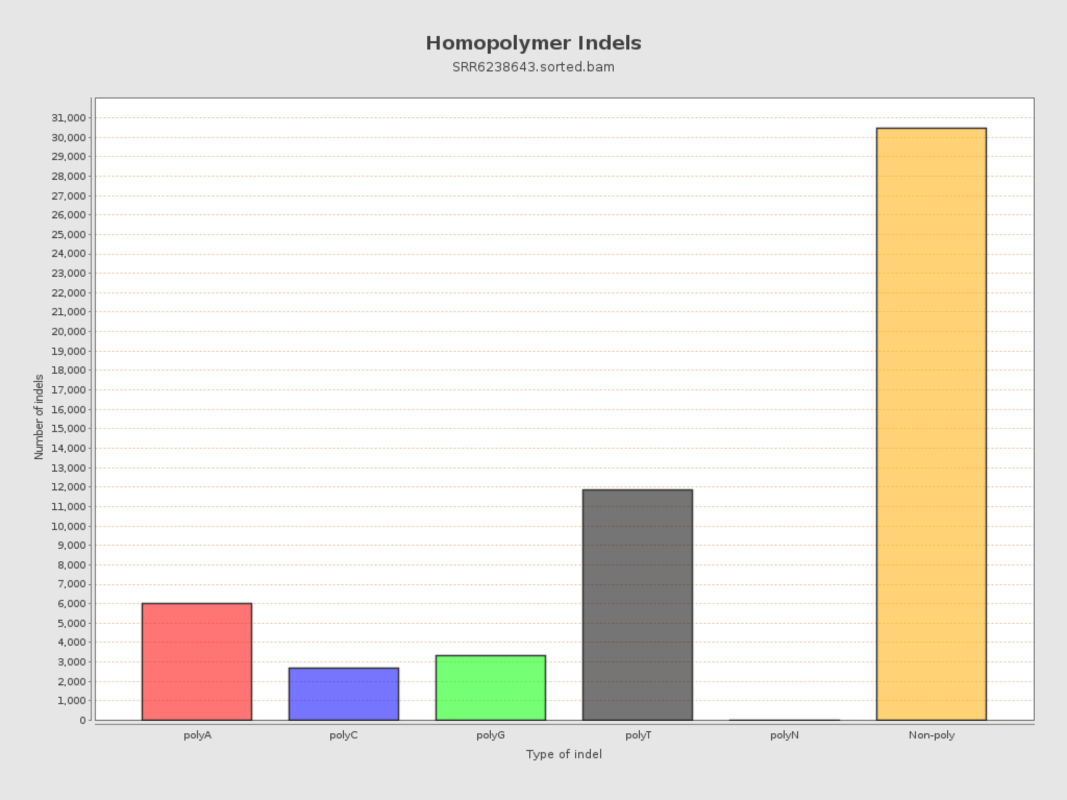
9. Results : Mapped Reads GC-content Distribution



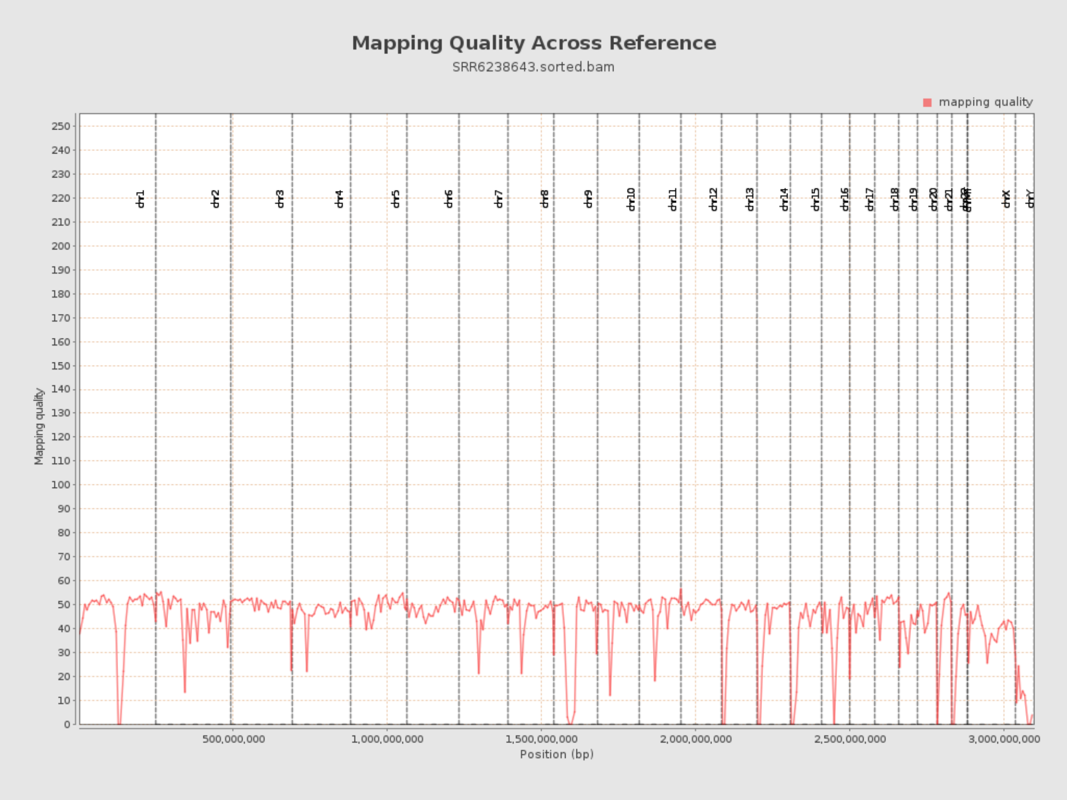
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram