Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:29:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238662.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_SRR6238662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238662.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:29:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,353,792
Mapped reads	2,139,215 / 90.88%
Unmapped reads	214,577 / 9.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,934 / 0.68%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	264,456 / 11.24%
Duplication rate	10.71%
Clipped reads	1,367,434 / 58.09%

2.2. ACGT Content

Number/percentage of A's	32,895,490 / 25.06%
Number/percentage of C's	22,854,338 / 17.41%
Number/percentage of T's	43,949,962 / 33.48%
Number/percentage of G's	31,579,211 / 24.05%
Number/percentage of N's	6,570 / 0.01%
GC Percentage	41.46%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.4476

2.4. Mapping Quality

Mean Mapping Quality	44.9

2.5. Mismatches and indels

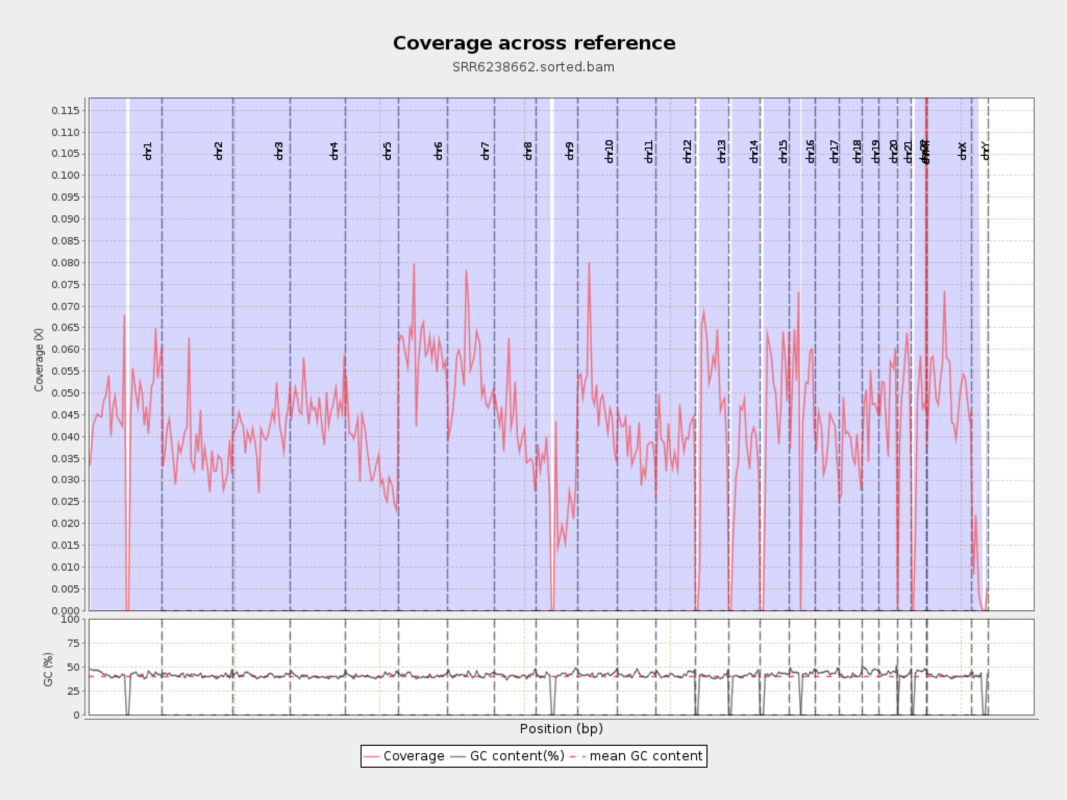
General error rate	0.6%
Mismatches	770,190
Insertions	8,494
Mapped reads with at least one insertion	0.39%
Deletions	39,714
Mapped reads with at least one deletion	1.84%
Homopolymer indels	42.11%

2.6. Chromosome stats

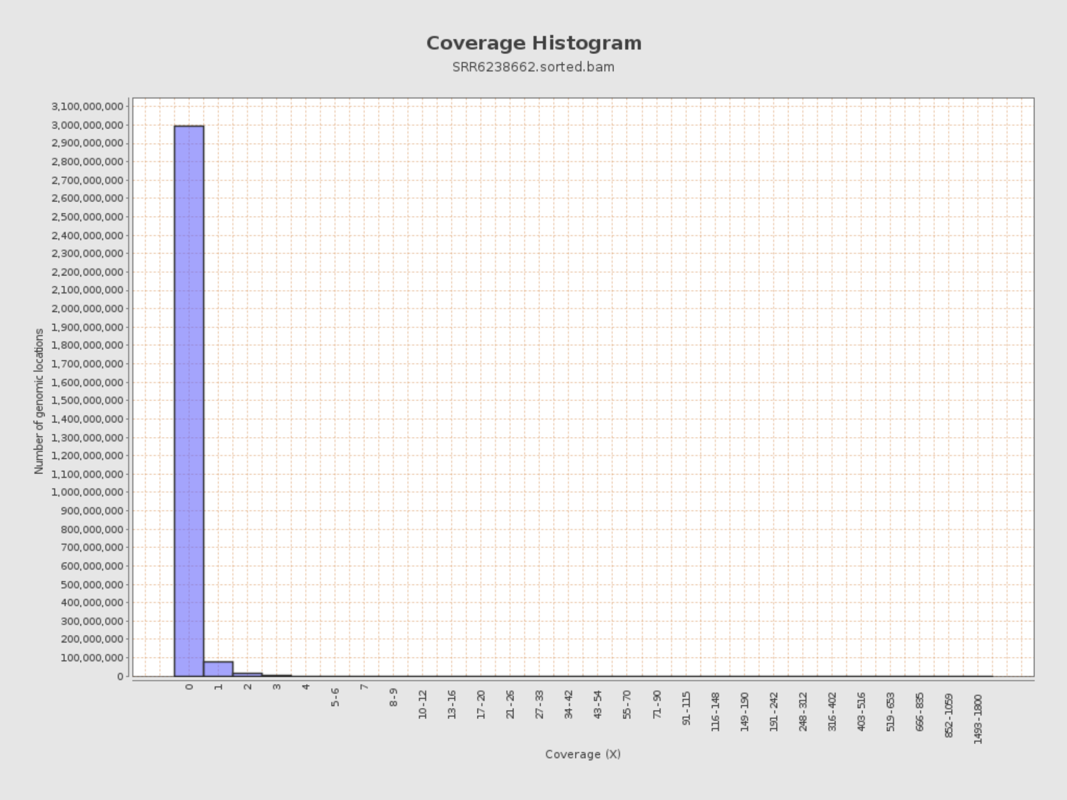
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11315254	0.0454	0.63
chr2	243199373	8895135	0.0366	0.8341
chr3	198022430	8175012	0.0413	0.2564
chr4	191154276	9003286	0.0471	0.282
chr5	180915260	6221280	0.0344	0.2343
chr6	171115067	10315290	0.0603	0.452
chr7	159138663	8740031	0.0549	0.5333

chr8	146364022	6153198	0.042	0.5757
chr9	141213431	3492404	0.0247	0.3119
chr10	135534747	6681035	0.0493	0.3792
chr11	135006516	5120161	0.0379	0.3016
chr12	133851895	5261472	0.0393	0.2546
chr13	115169878	5249551	0.0456	0.3062
chr14	107349540	3519142	0.0328	0.2441
chr15	102531392	4577684	0.0446	0.3079
chr16	90354753	4468168	0.0495	0.3189
chr17	81195210	3150735	0.0388	0.2633
chr18	78077248	2852750	0.0365	0.7792
chr19	59128983	2750779	0.0465	0.4685
chr20	63025520	3132488	0.0497	0.2908
chr21	48129895	2188838	0.0455	0.2808
chr22	51304566	1777566	0.0346	0.2317
chrMT	16571	12395	0.748	1.0884
chrX	155270560	7903468	0.0509	0.3008
chrY	59373566	398211	0.0067	0.2081

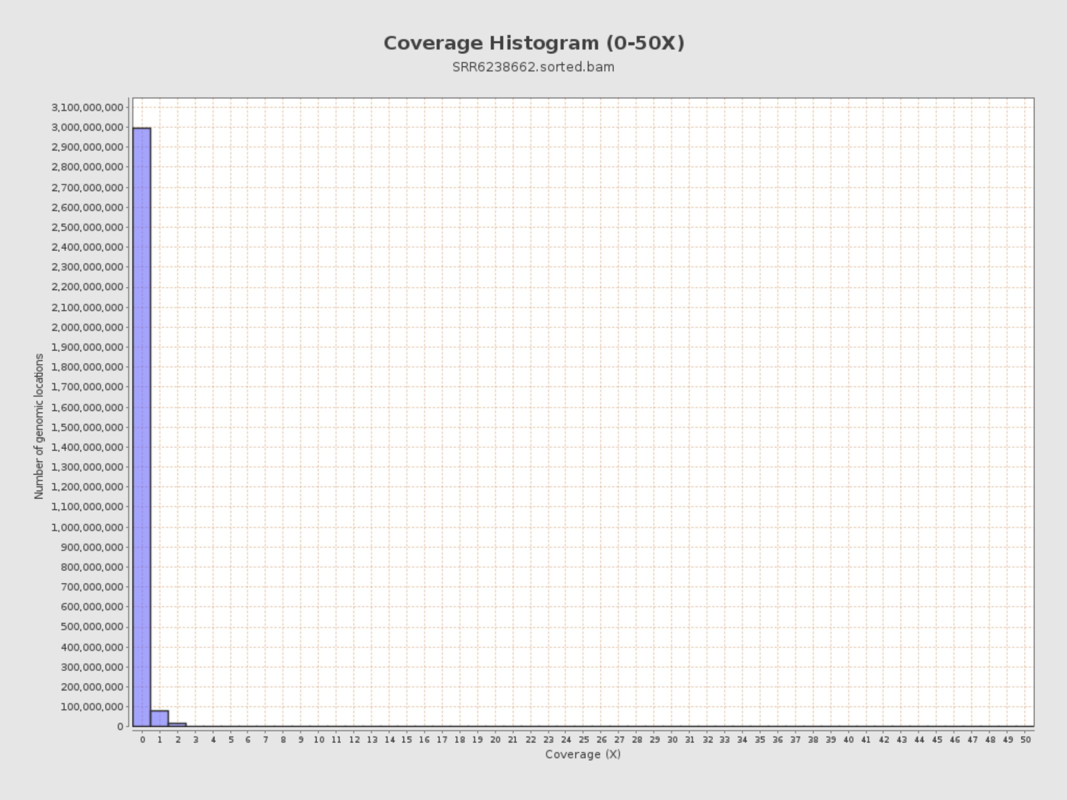
3. Results : Coverage across reference



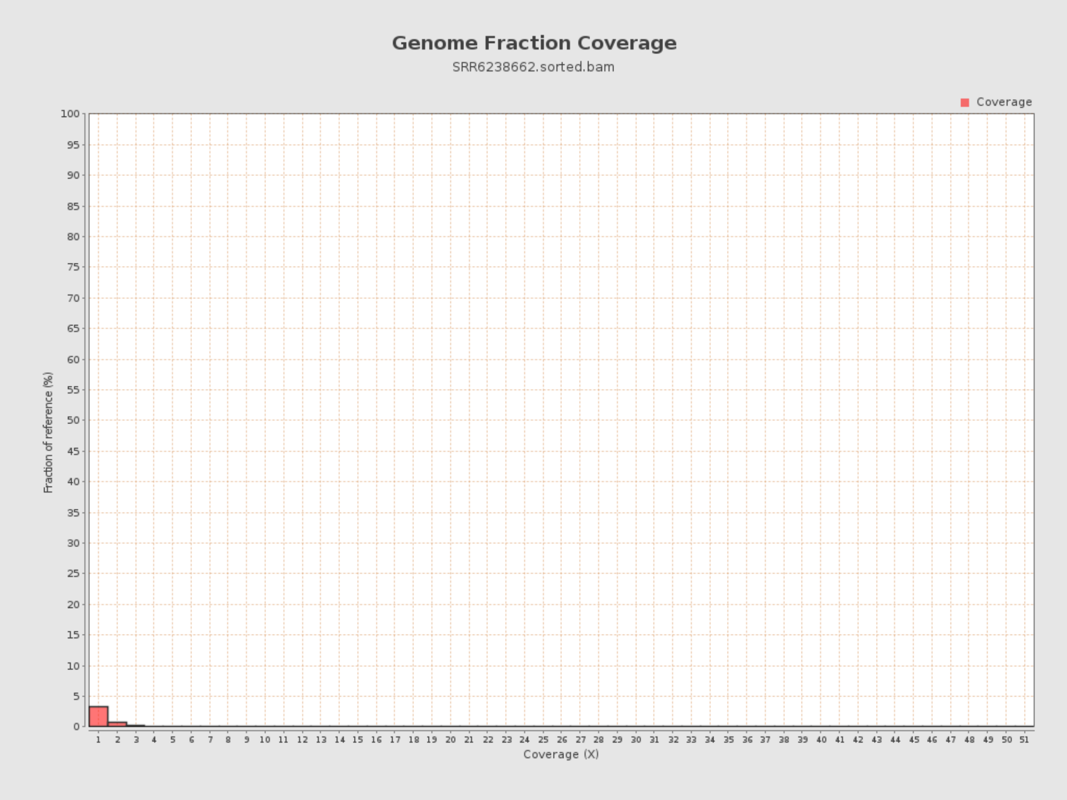
4. Results : Coverage Histogram



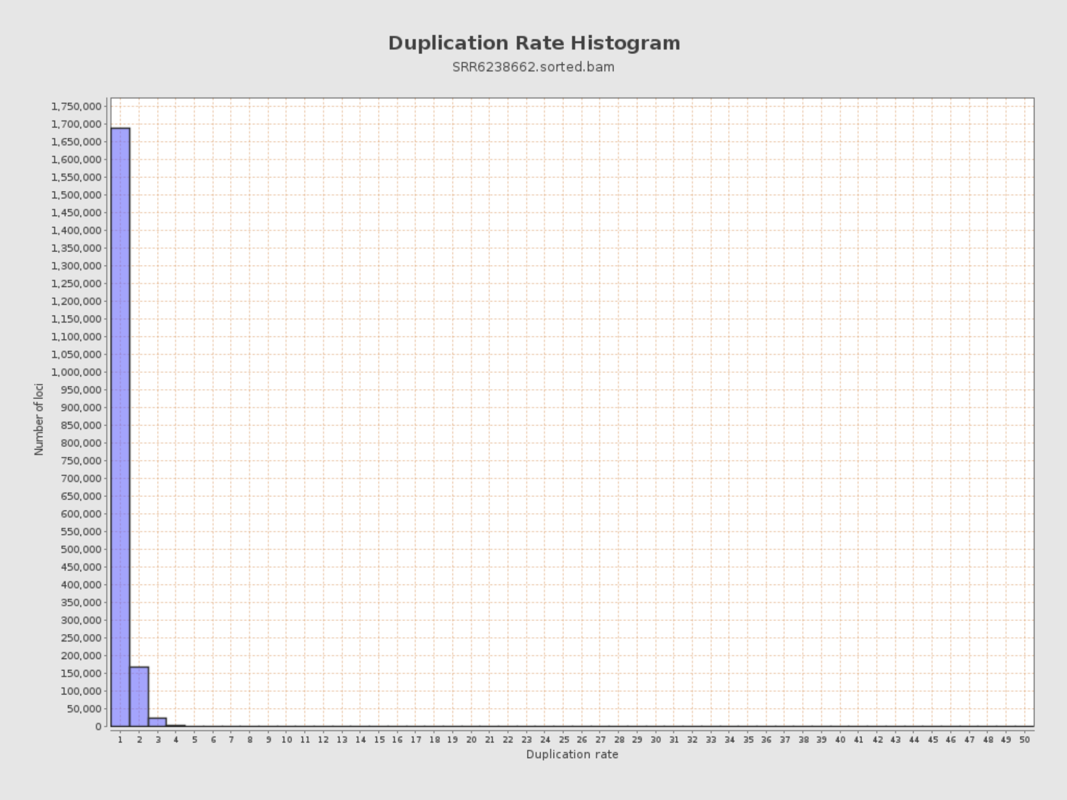
5. Results : Coverage Histogram (0-50X)



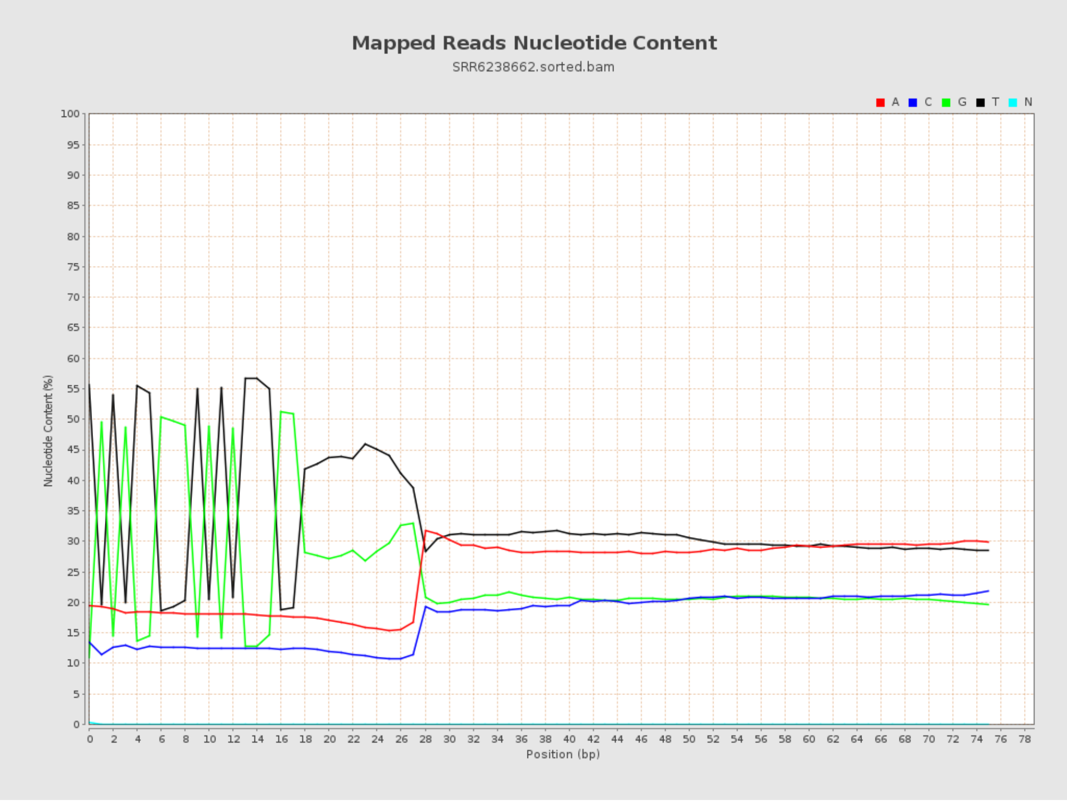
6. Results : Genome Fraction Coverage



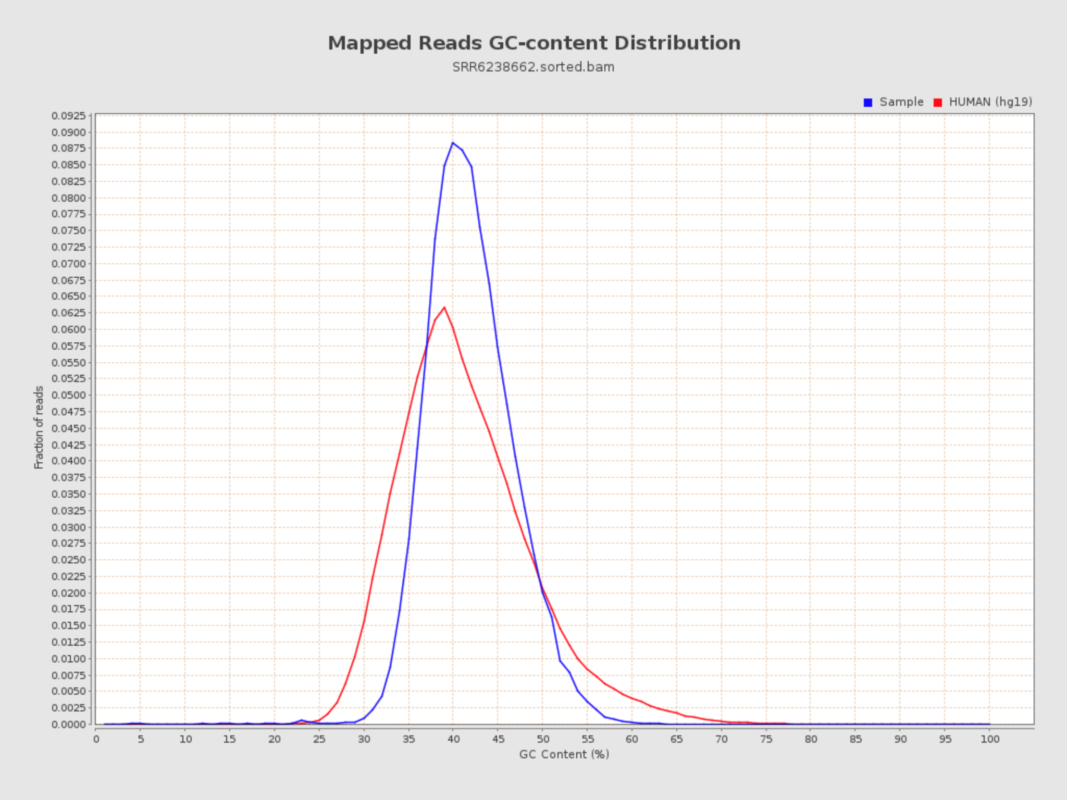
7. Results : Duplication Rate Histogram



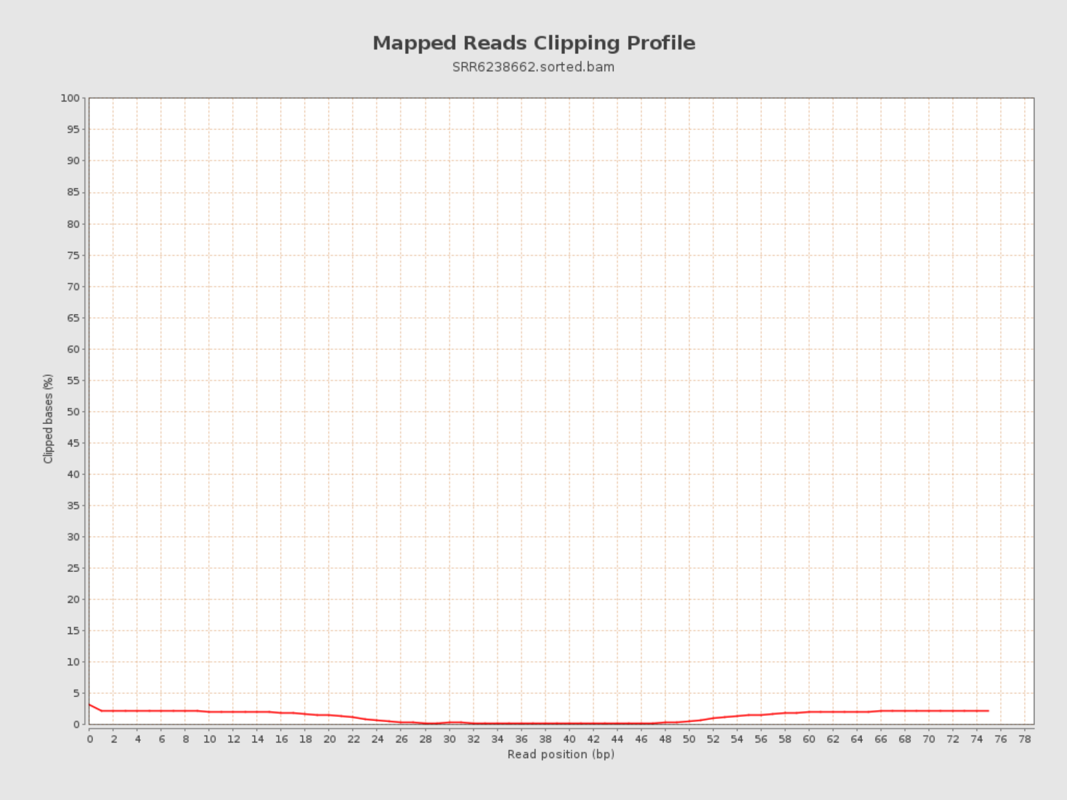
8. Results : Mapped Reads Nucleotide Content



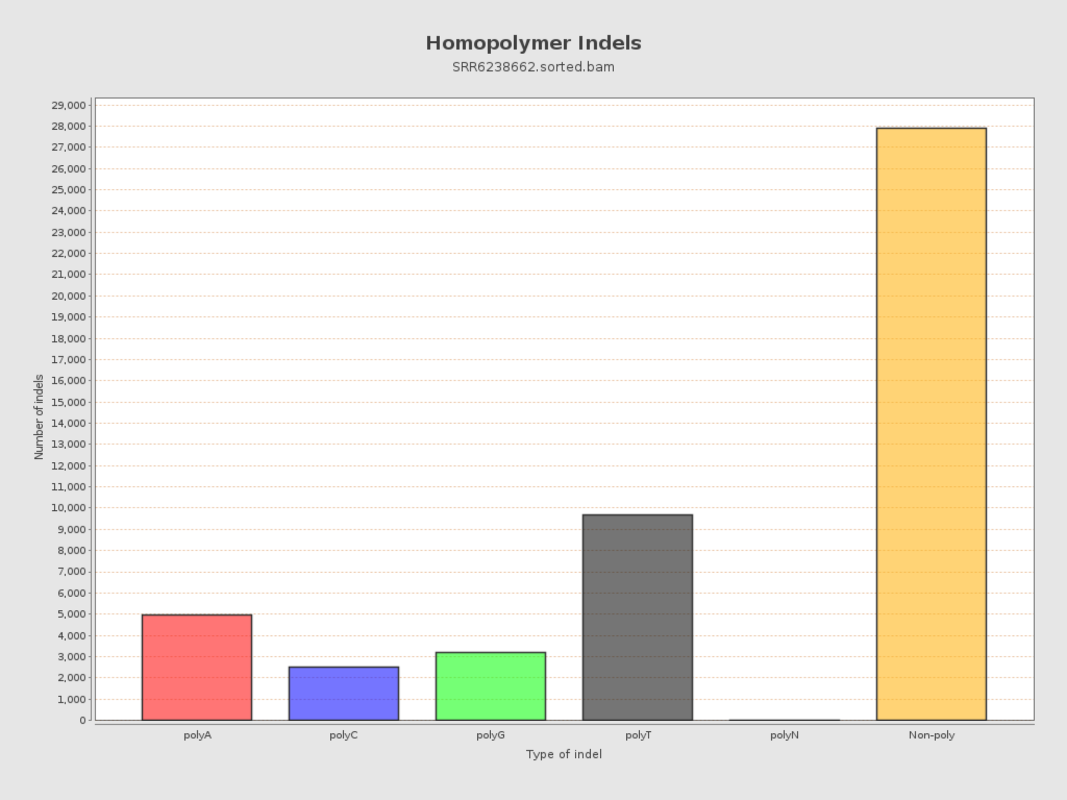
9. Results : Mapped Reads GC-content Distribution



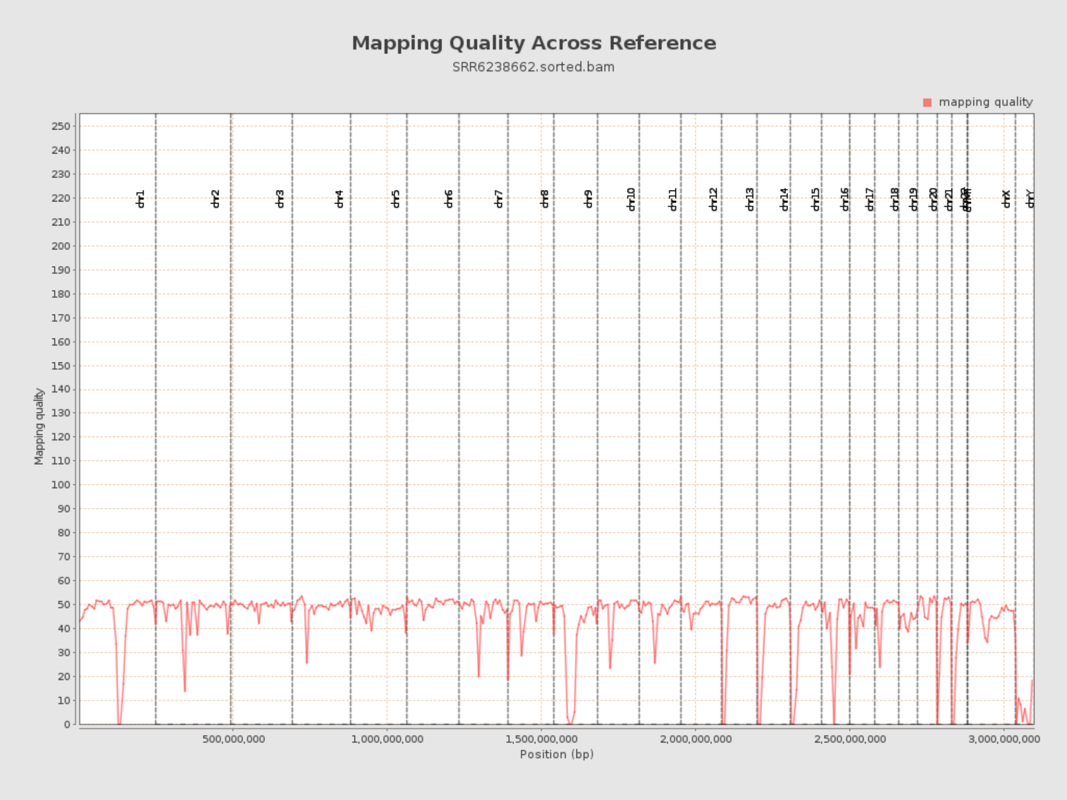
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram