Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:36:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238664.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_SRR6238664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:36:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,508,477
Mapped reads	2,350,195 / 93.69%
Unmapped reads	158,282 / 6.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,815 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	365,289 / 14.56%
Duplication rate	13.34%
Clipped reads	1,432,037 / 57.09%

2.2. ACGT Content

Number/percentage of A's	35,600,815 / 24.19%
Number/percentage of C's	26,381,518 / 17.92%
Number/percentage of T's	49,067,953 / 33.34%
Number/percentage of G's	36,127,863 / 24.55%
Number/percentage of N's	7,471 / 0.01%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.5875

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

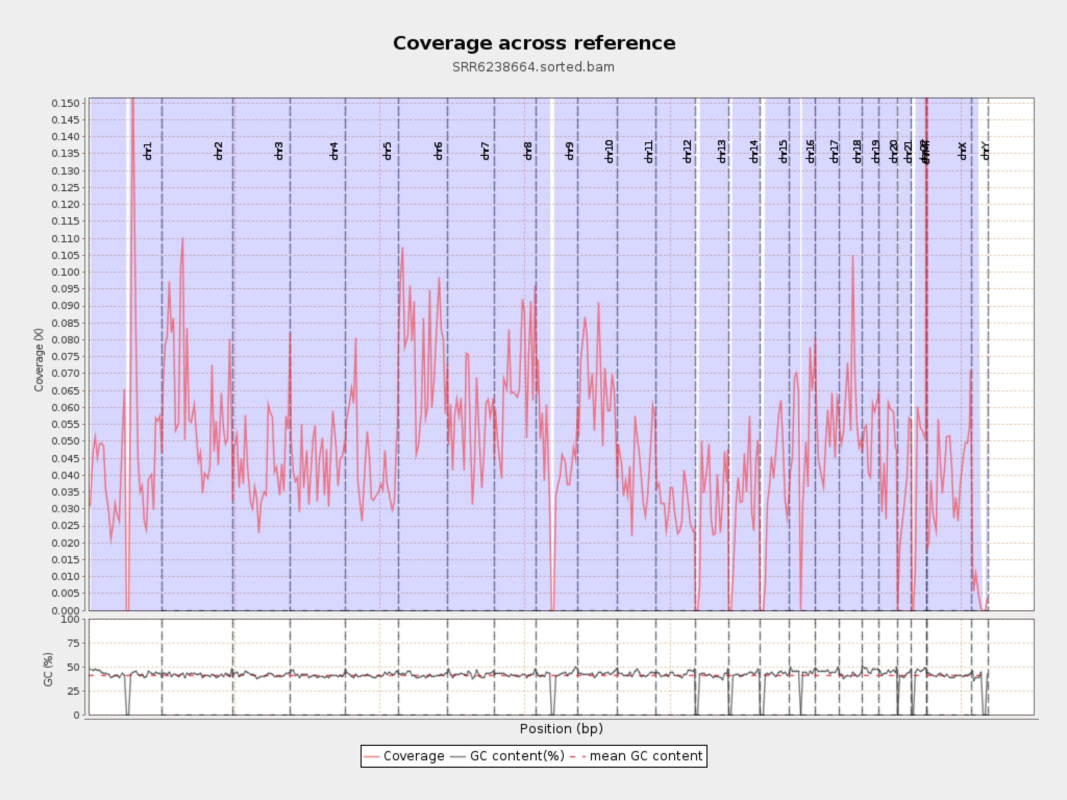
General error rate	0.54%
Mismatches	782,130
Insertions	9,460
Mapped reads with at least one insertion	0.4%
Deletions	39,401
Mapped reads with at least one deletion	1.66%
Homopolymer indels	41.76%

2.6. Chromosome stats

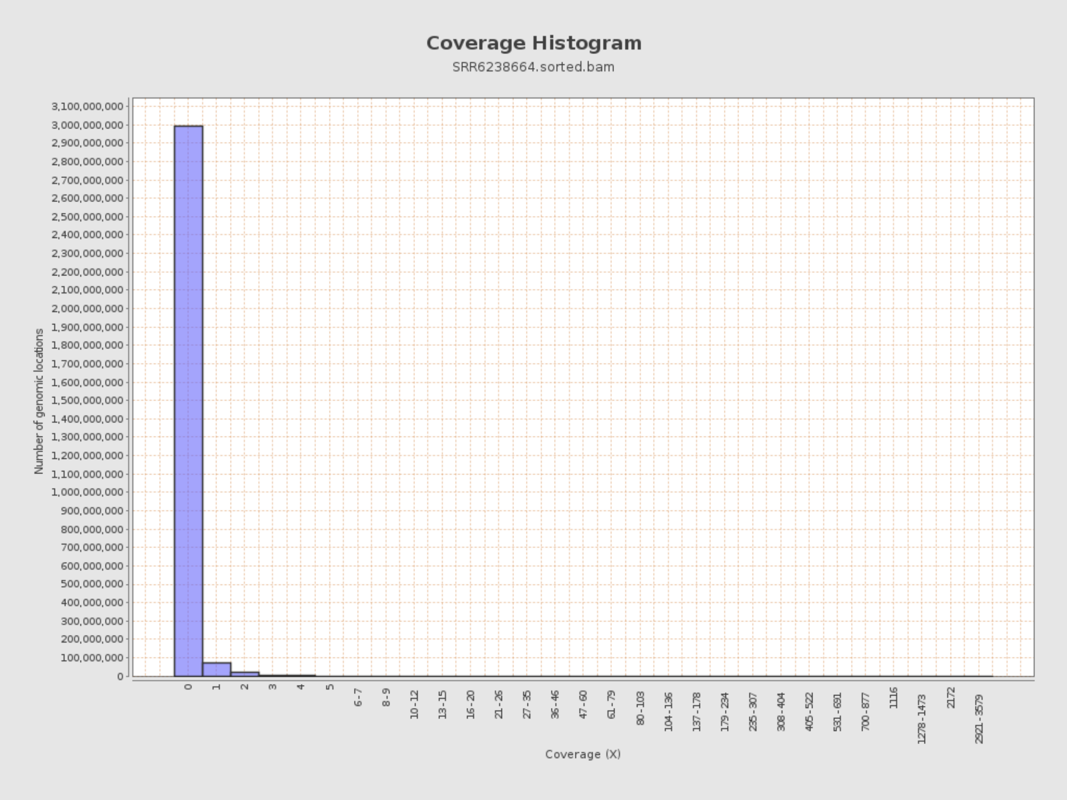
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10883621	0.0437	0.4667
chr2	243199373	15124460	0.0622	1.5639
chr3	198022430	8417835	0.0425	0.2956
chr4	191154276	8280748	0.0433	0.2949
chr5	180915260	7912751	0.0437	0.2939
chr6	171115067	13184393	0.077	0.6284
chr7	159138663	8766624	0.0551	0.5577

chr8	146364022	9888646	0.0676	0.4465
chr9	141213431	5734417	0.0406	0.3118
chr10	135534747	9193167	0.0678	0.382
chr11	135006516	5694932	0.0422	0.2934
chr12	133851895	4096465	0.0306	0.2459
chr13	115169878	3460978	0.0301	0.3709
chr14	107349540	3371106	0.0314	0.2524
chr15	102531392	3477976	0.0339	0.3636
chr16	90354753	4730176	0.0524	0.3382
chr17	81195210	4184527	0.0515	0.3168
chr18	78077248	4853998	0.0622	1.0028
chr19	59128983	3140577	0.0531	0.3955
chr20	63025520	2959334	0.047	0.3002
chr21	48129895	1586157	0.033	0.263
chr22	51304566	1894111	0.0369	0.267
chrMT	16571	17043	1.0285	1.4106
chrX	155270560	6130479	0.0395	0.2782
chrY	59373566	267483	0.0045	0.209

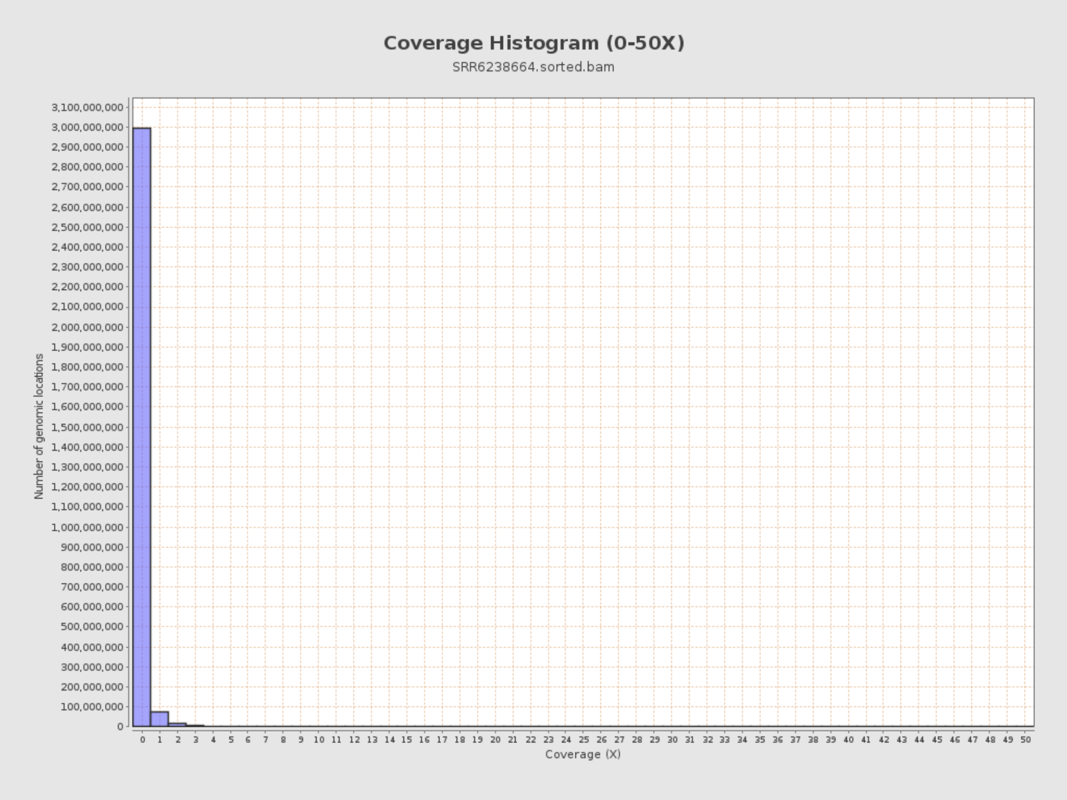
3. Results : Coverage across reference



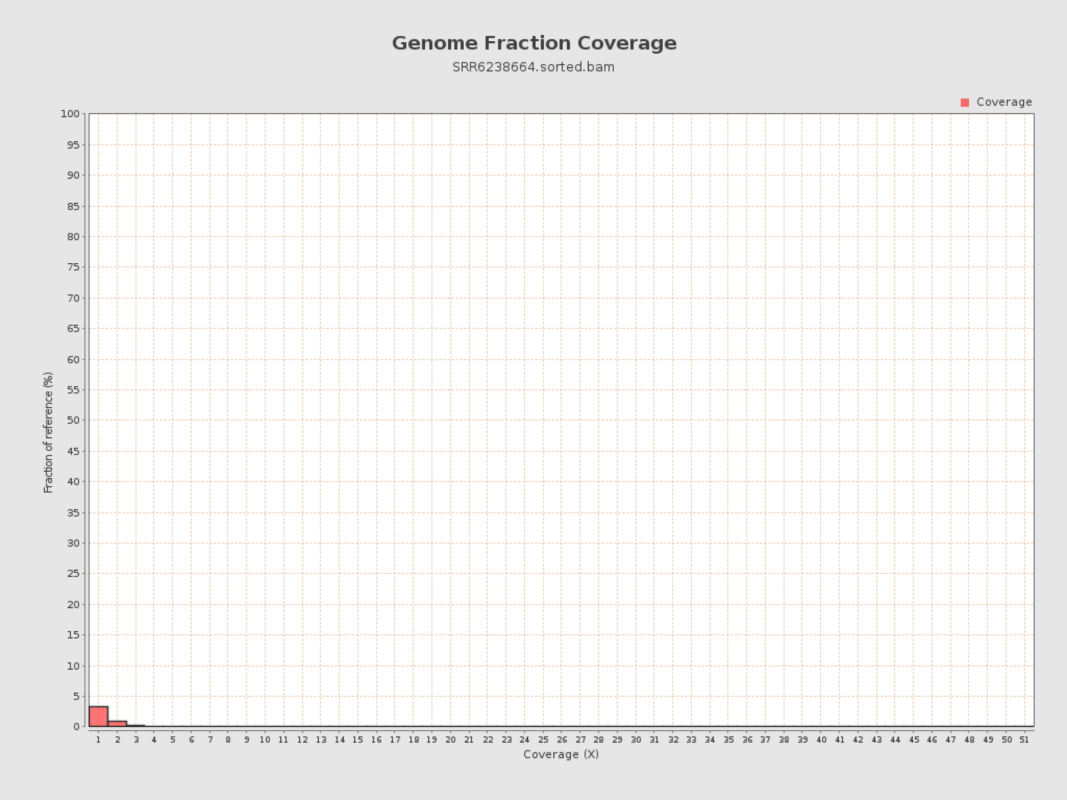
4. Results : Coverage Histogram



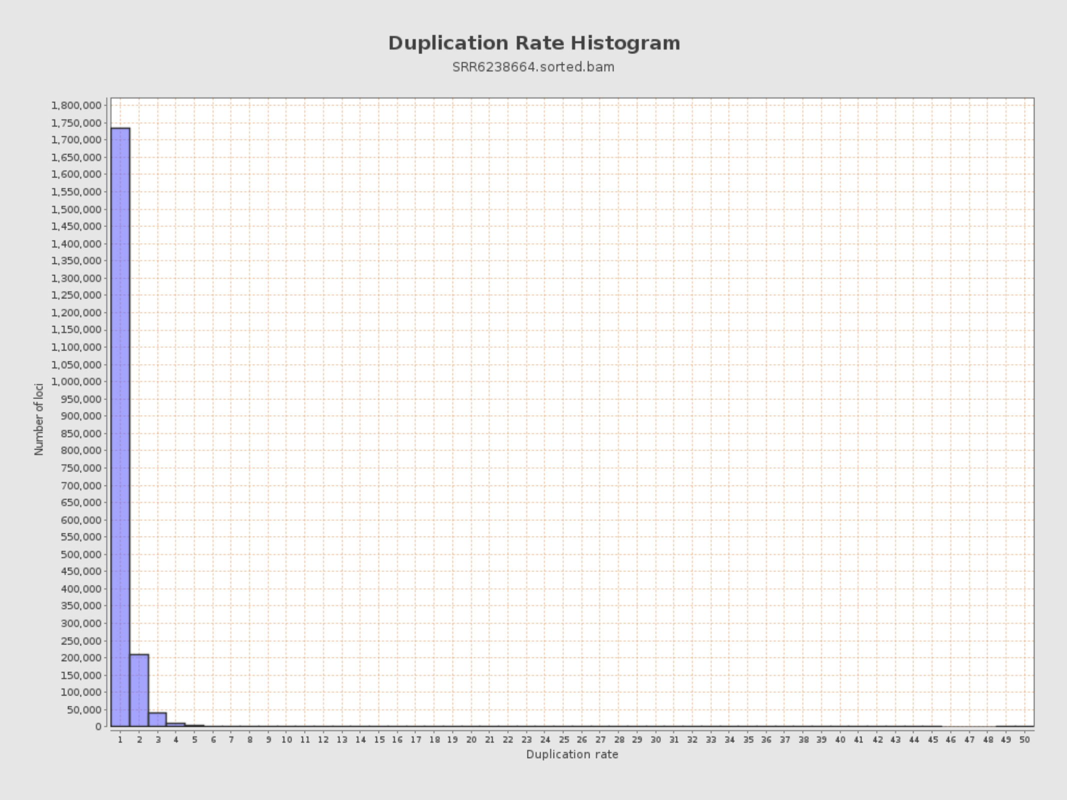
5. Results : Coverage Histogram (0-50X)



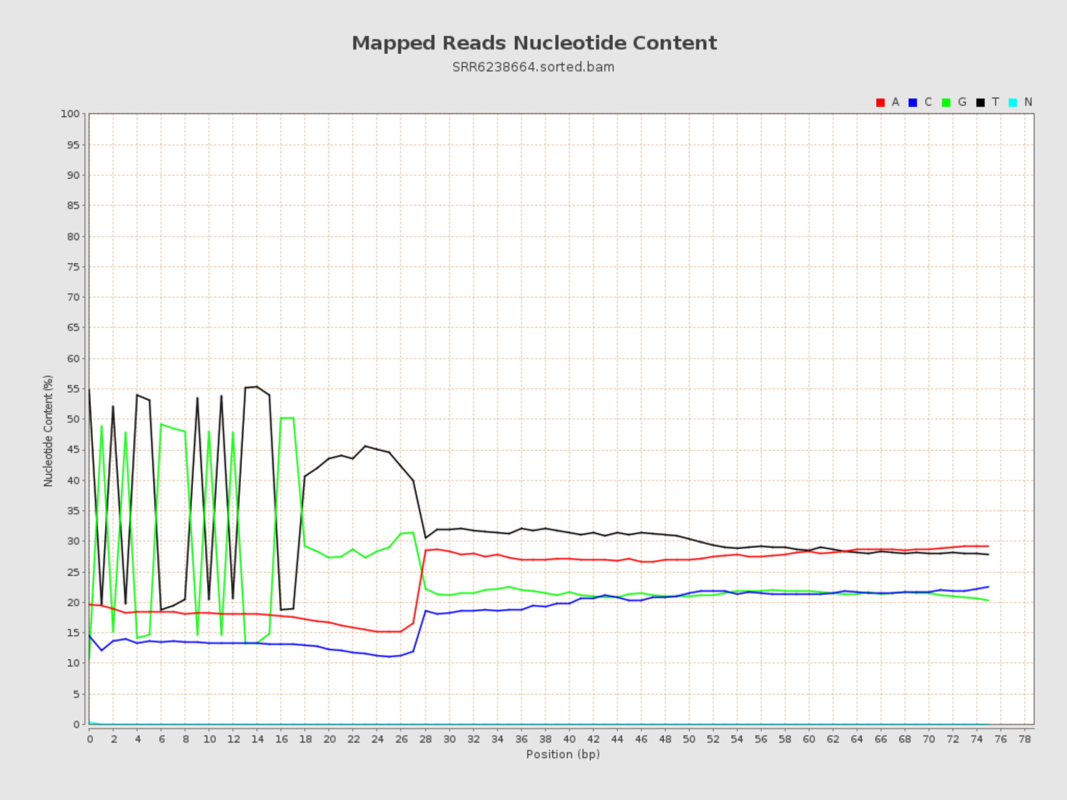
6. Results : Genome Fraction Coverage



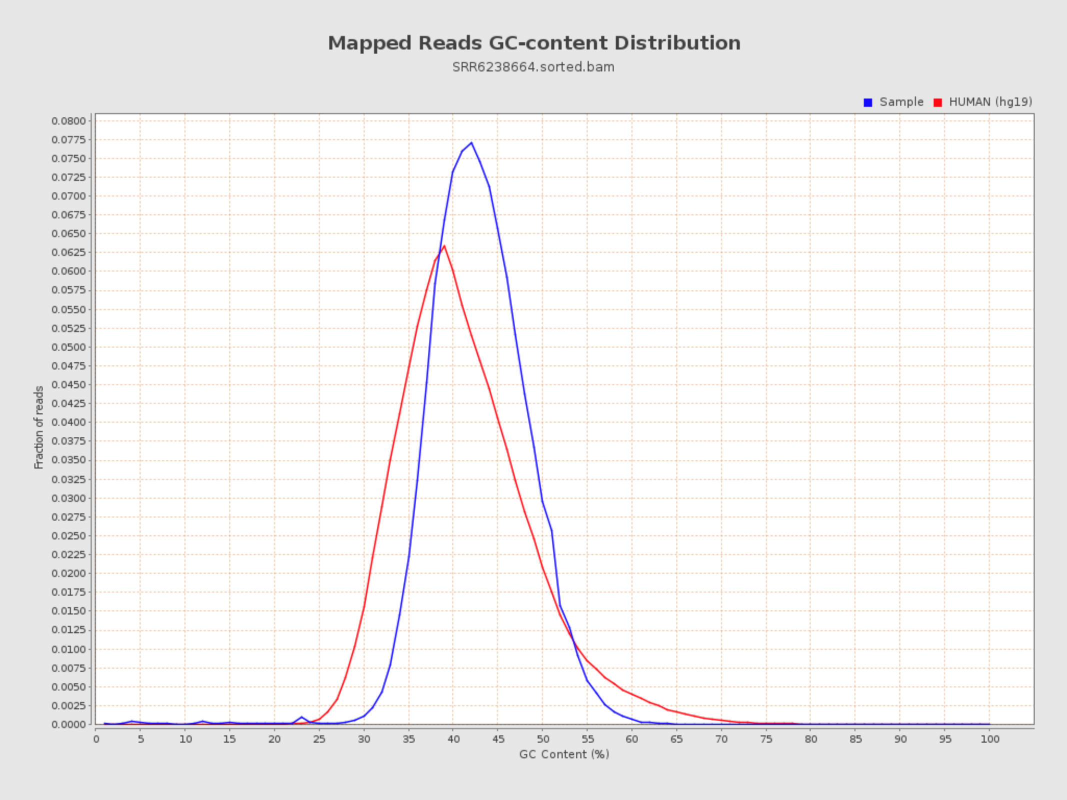
7. Results : Duplication Rate Histogram



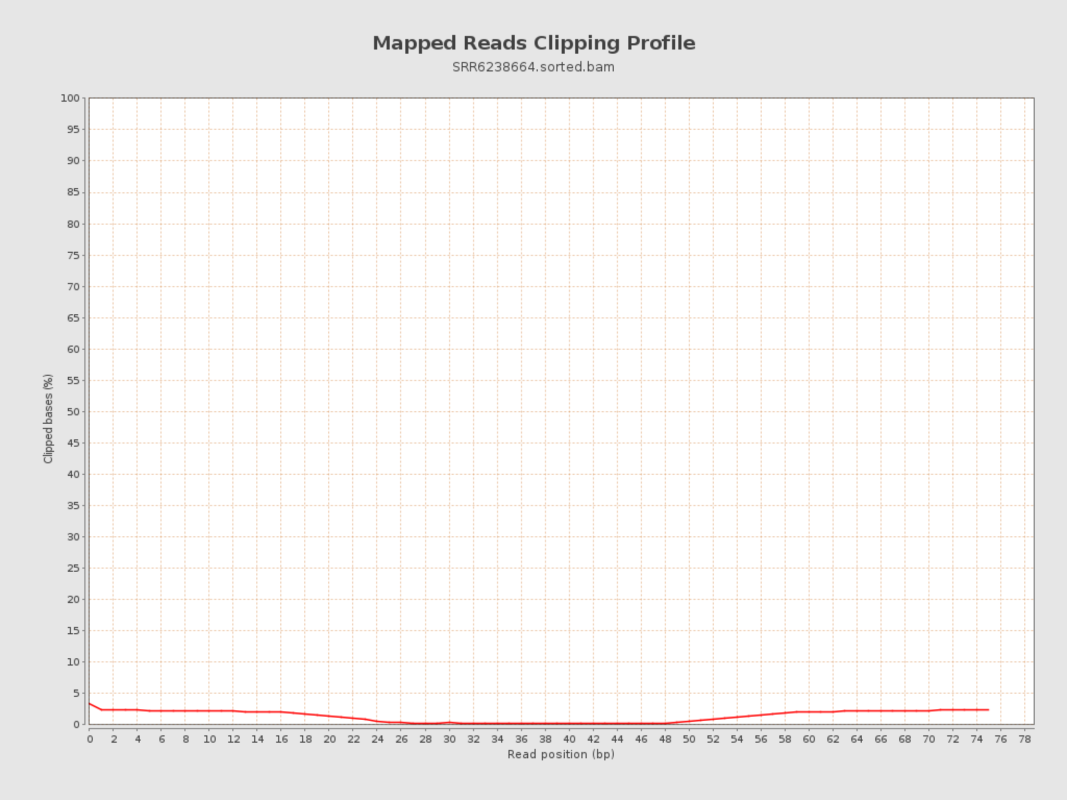
8. Results : Mapped Reads Nucleotide Content



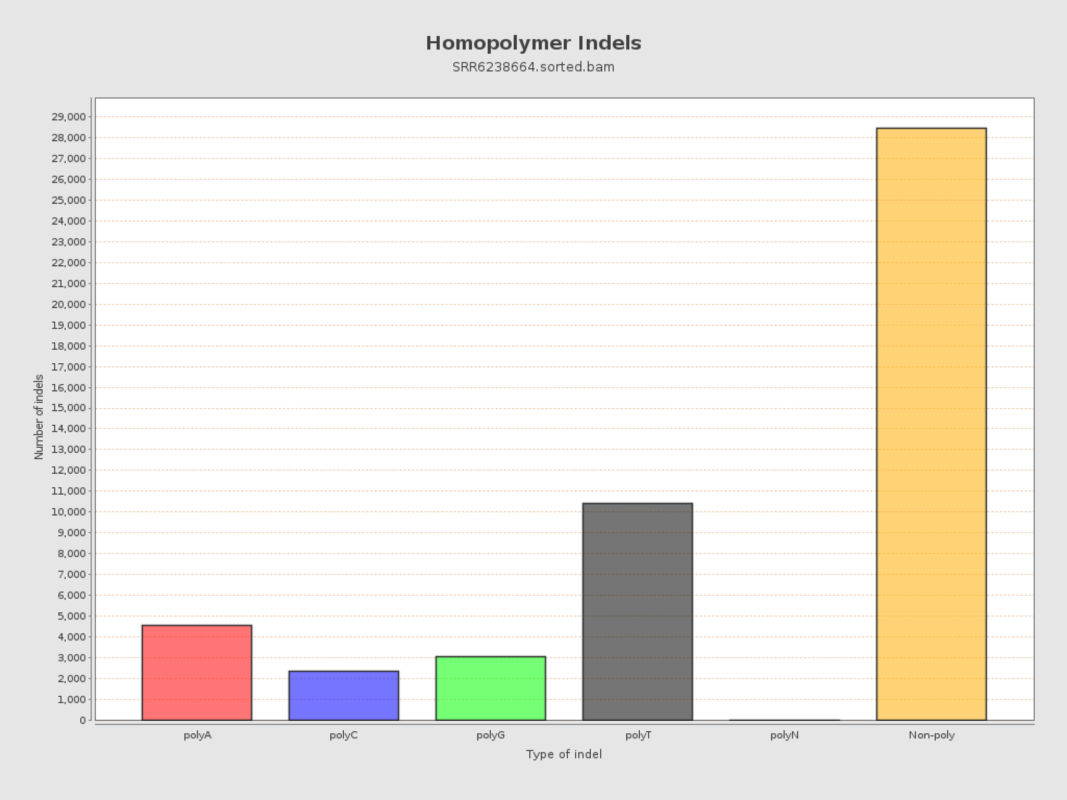
9. Results : Mapped Reads GC-content Distribution



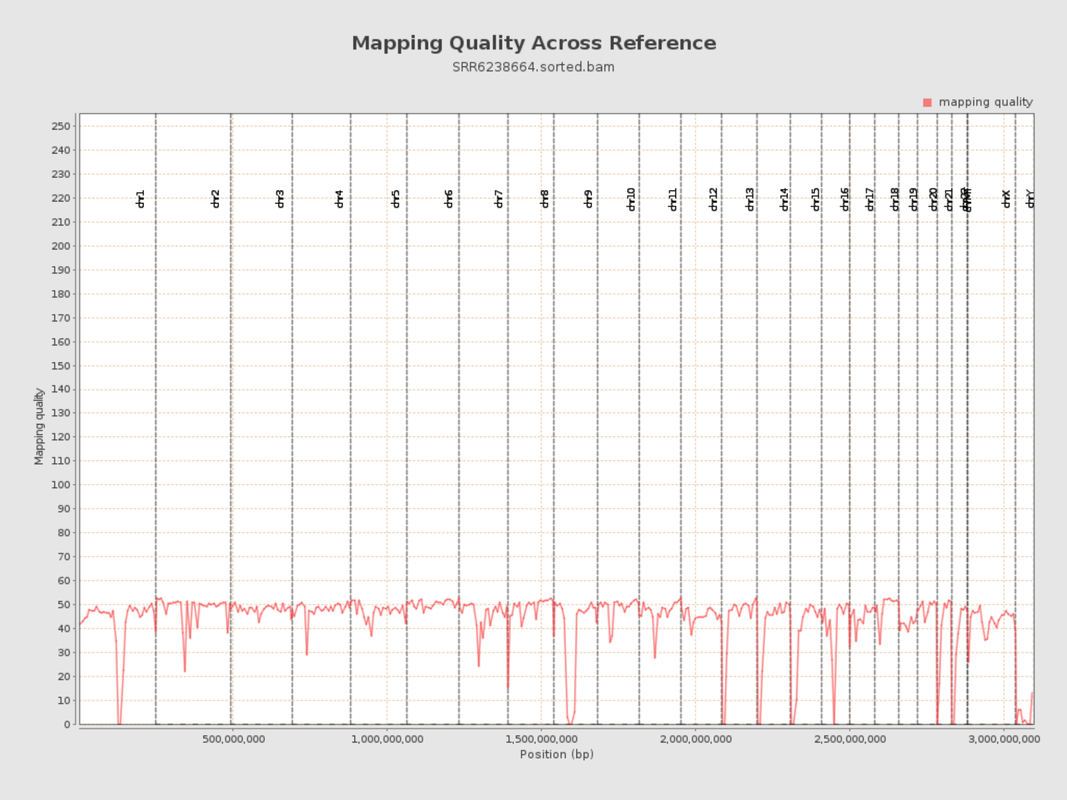
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram