Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:34:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238536.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_SRR6238536 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238536.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:34:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238536.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,331,031
Mapped reads	2,835,133 / 85.11%
Unmapped reads	495,898 / 14.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,073 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,162,220 / 34.89%
Duplication rate	20.69%
Clipped reads	1,890,281 / 56.75%

2.2. ACGT Content

Number/percentage of A's	43,588,492 / 25.23%
Number/percentage of C's	30,094,947 / 17.42%
Number/percentage of T's	58,694,375 / 33.97%
Number/percentage of G's	40,399,355 / 23.38%
Number/percentage of N's	3,972 / 0%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0558

Standard Deviation	1.1312

2.4. Mapping Quality

Mean Mapping Quality	42.74

2.5. Mismatches and indels

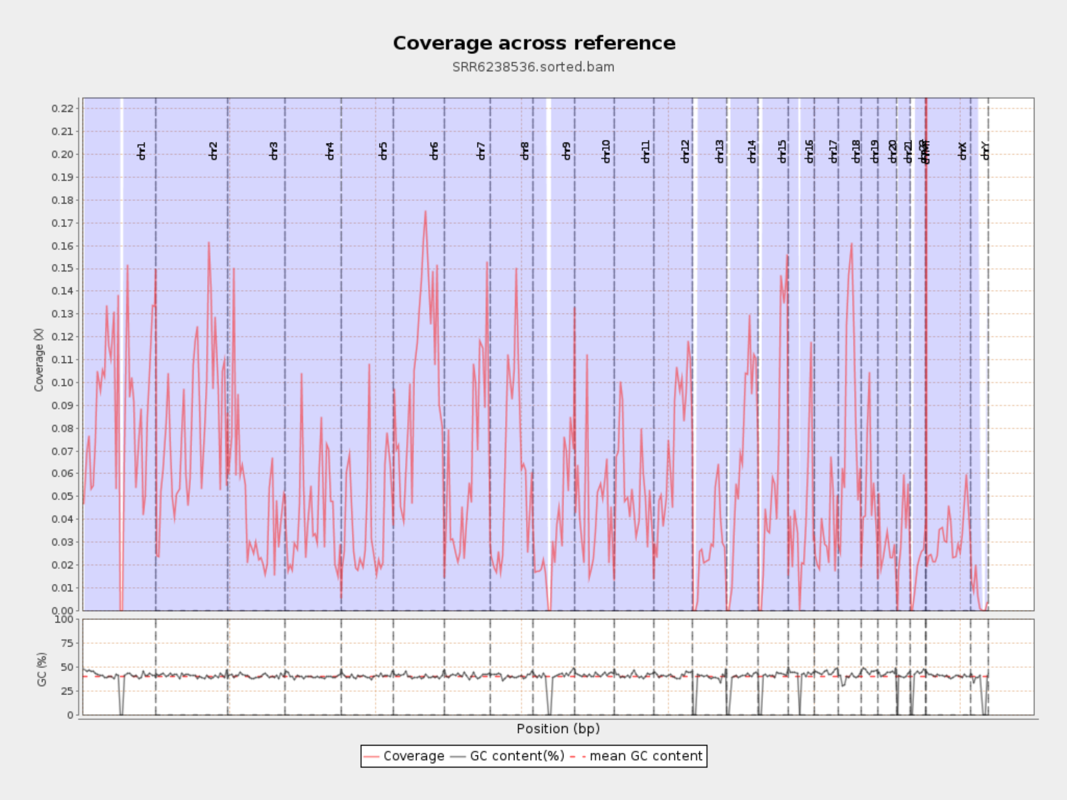
General error rate	0.62%
Mismatches	1,055,197
Insertions	10,027
Mapped reads with at least one insertion	0.35%
Deletions	54,674
Mapped reads with at least one deletion	1.91%
Homopolymer indels	41.42%

2.6. Chromosome stats

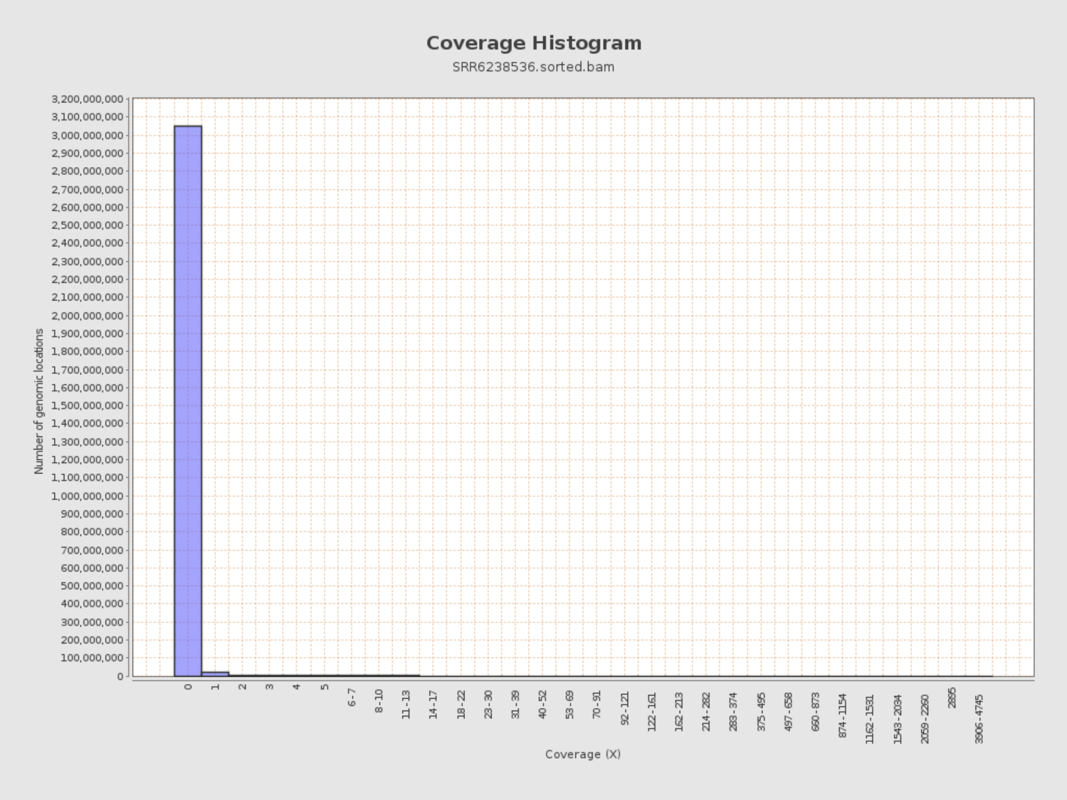
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21465756	0.0861	1.6439
chr2	243199373	19769030	0.0813	2.2486
chr3	198022430	9281657	0.0469	0.6605
chr4	191154276	7995770	0.0418	0.591
chr5	180915260	7061108	0.039	0.5924
chr6	171115067	17736373	0.1037	1.1858
chr7	159138663	9994747	0.0628	0.8274

chr8	146364022	9032213	0.0617	0.868
chr9	141213431	5000260	0.0354	0.5536
chr10	135534747	5847567	0.0431	0.8242
chr11	135006516	7312007	0.0542	0.7458
chr12	133851895	9664507	0.0722	0.8079
chr13	115169878	3095596	0.0269	0.77
chr14	107349540	7321694	0.0682	0.7904
chr15	102531392	6531754	0.0637	0.8399
chr16	90354753	3425838	0.0379	0.5822
chr17	81195210	2677001	0.033	0.527
chr18	78077248	6811583	0.0872	2.89
chr19	59128983	3161263	0.0535	1.1989
chr20	63025520	1738296	0.0276	0.4633
chr21	48129895	1629538	0.0339	0.5332
chr22	51304566	870100	0.017	0.3493
chrMT	16571	168624	10.1758	11.2714
chrX	155270560	4911655	0.0316	0.5085
chrY	59373566	367812	0.0062	0.342

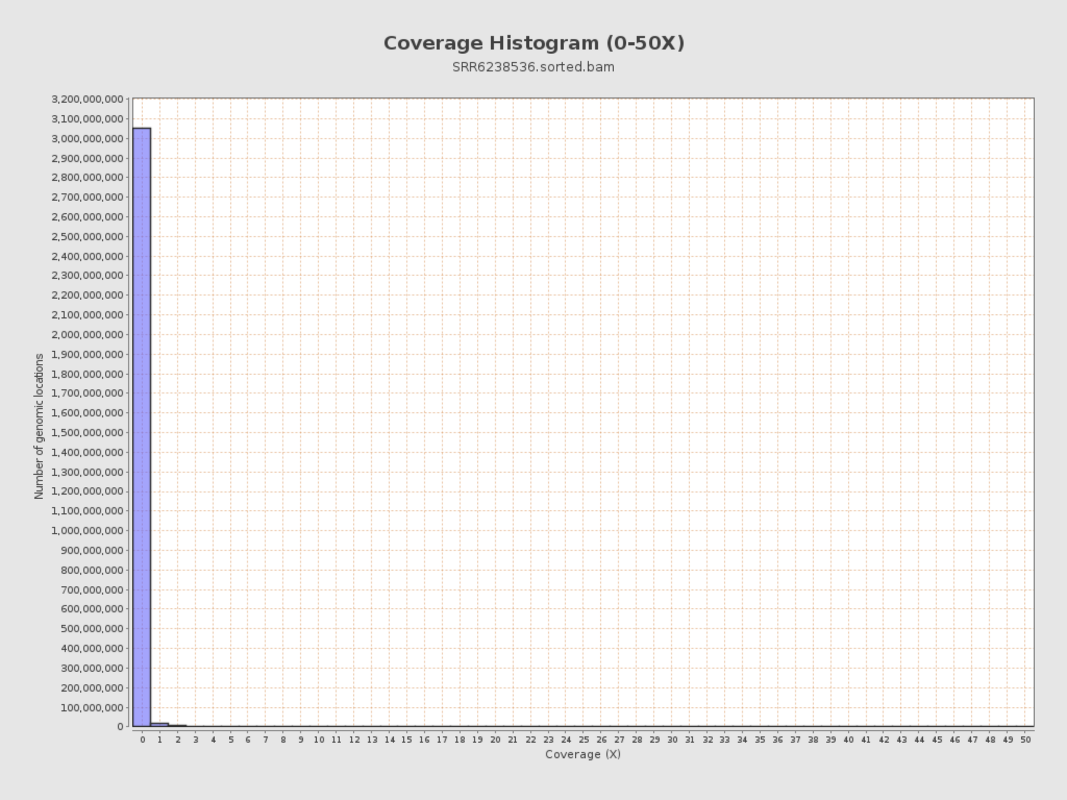
3. Results : Coverage across reference



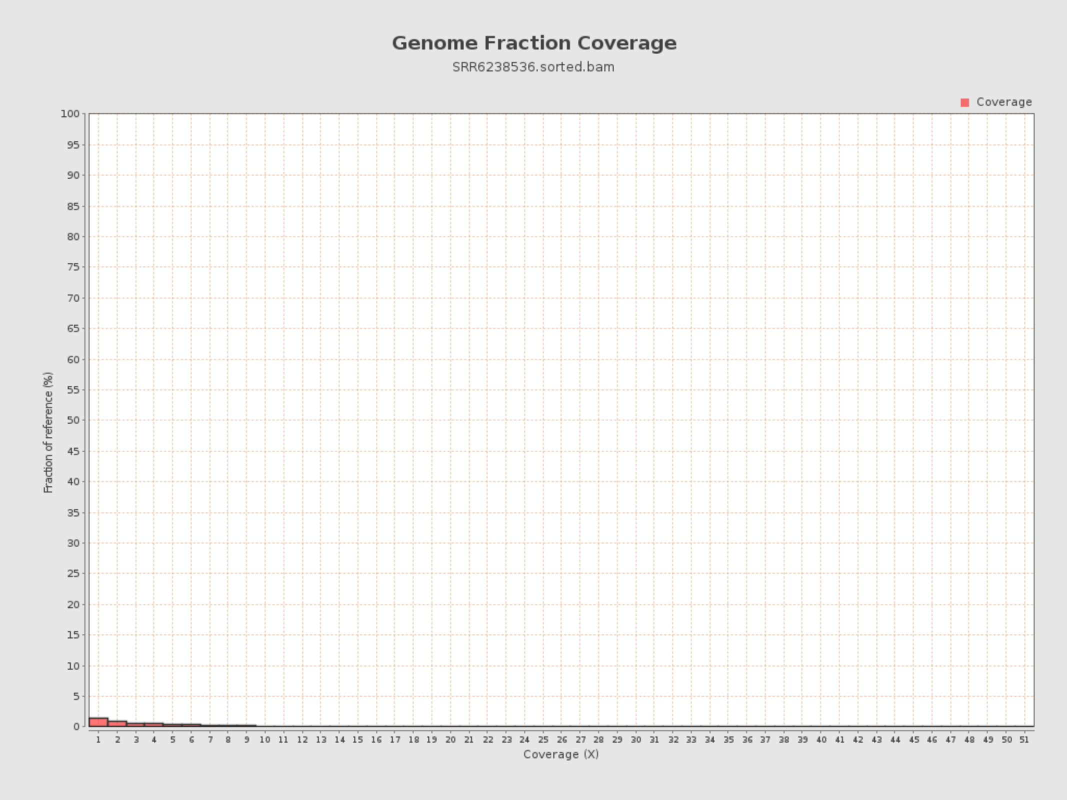
4. Results : Coverage Histogram



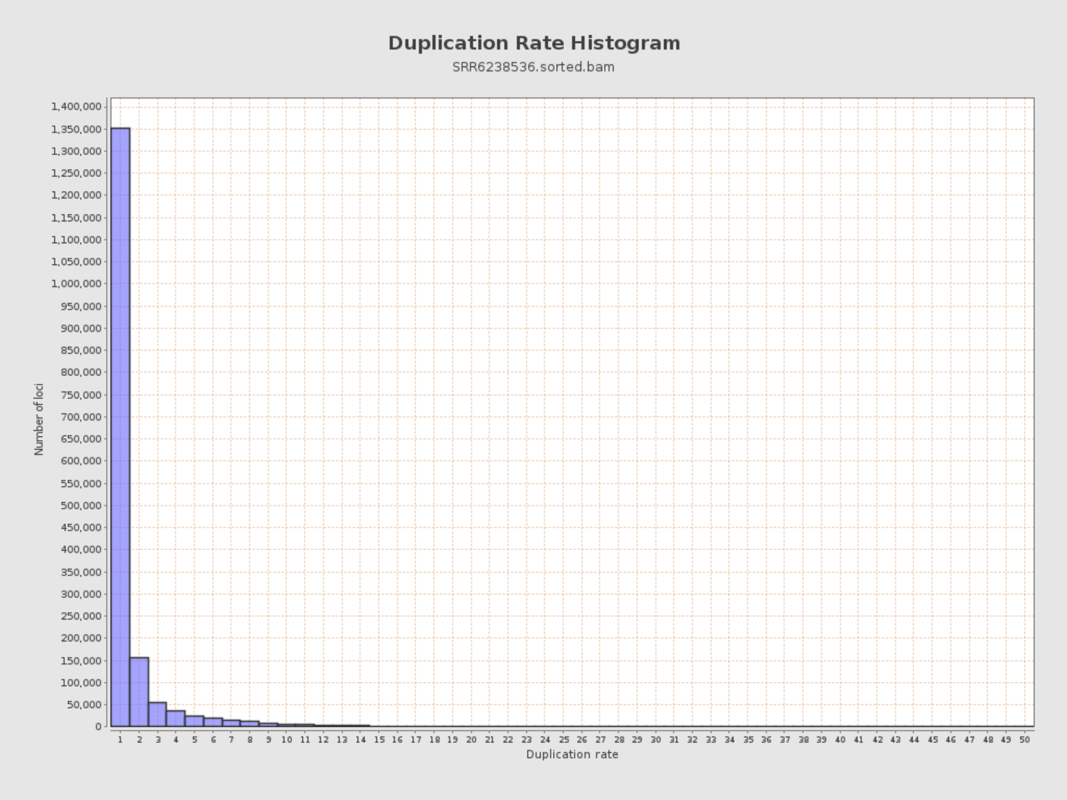
5. Results : Coverage Histogram (0-50X)



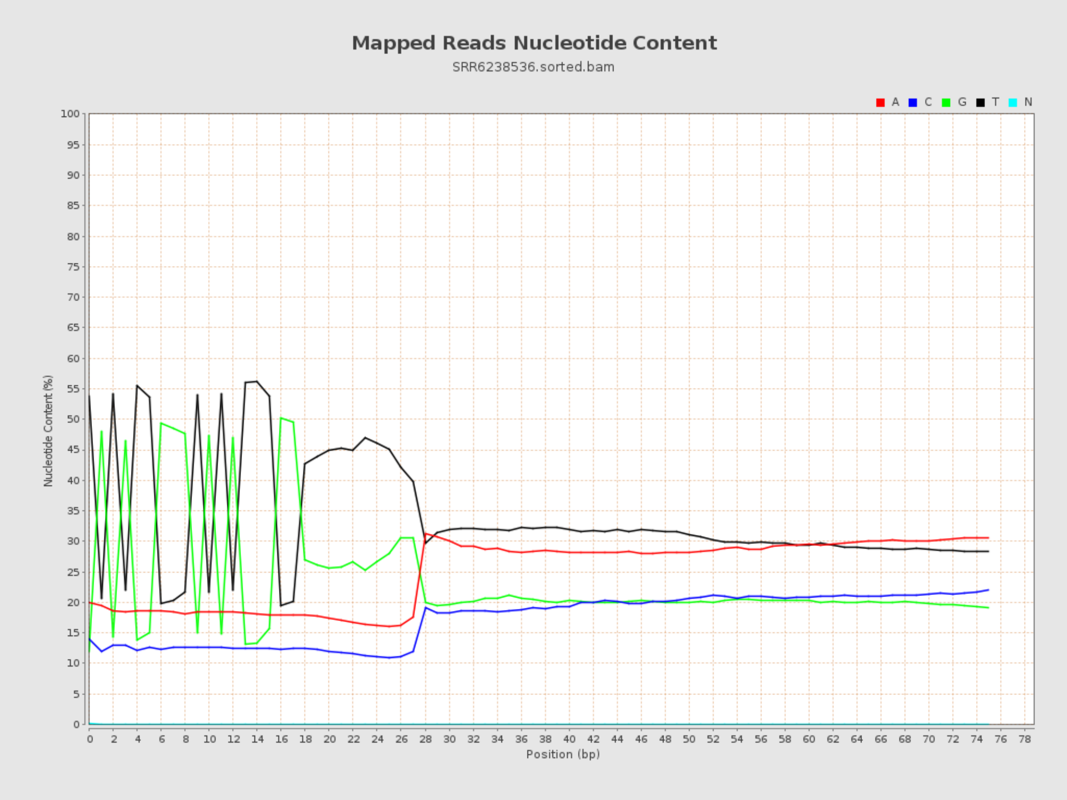
6. Results : Genome Fraction Coverage



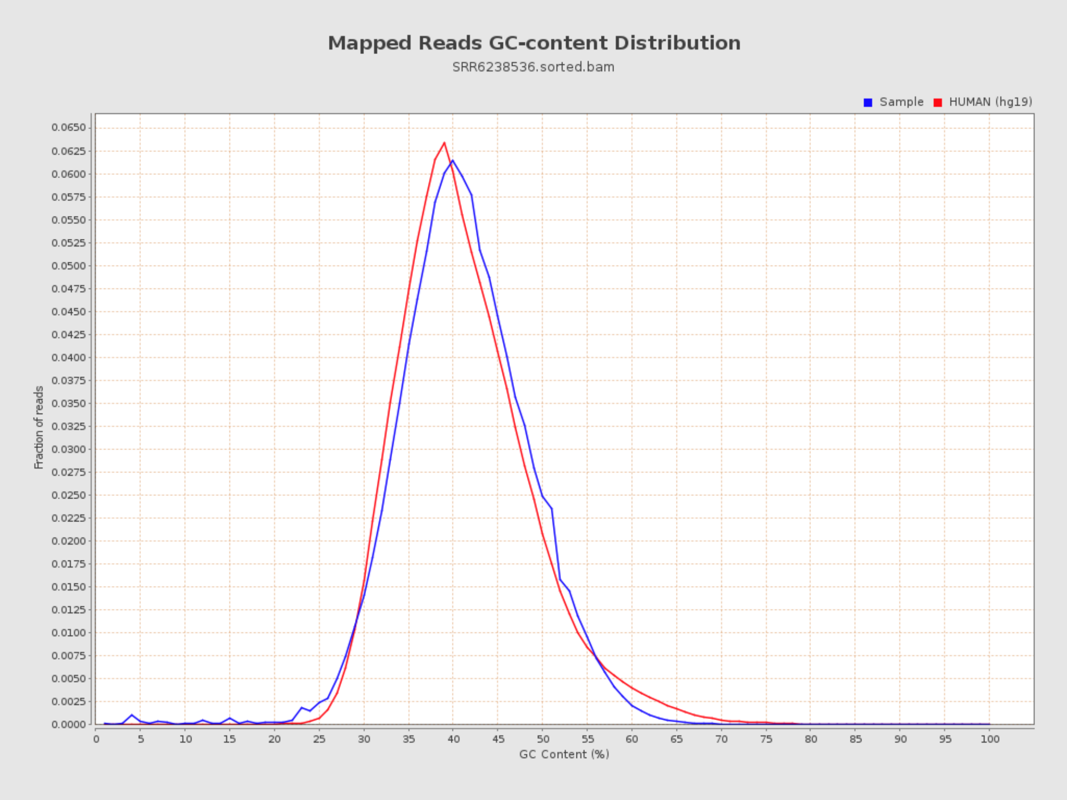
7. Results : Duplication Rate Histogram



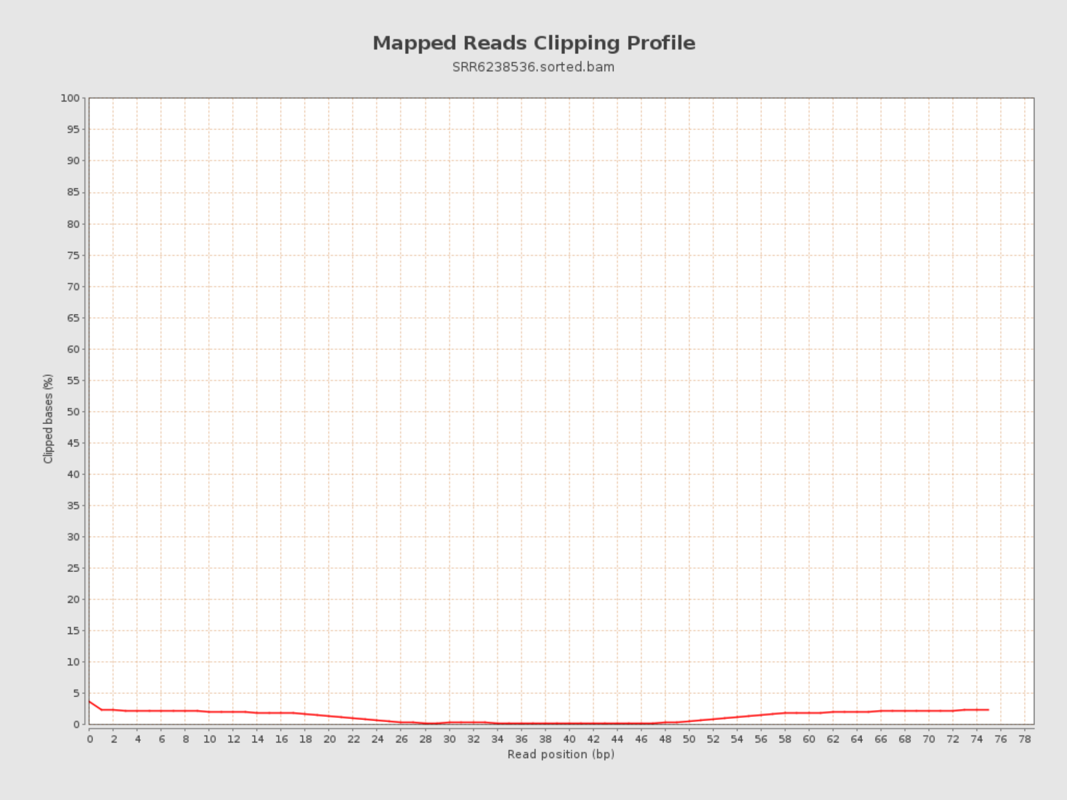
8. Results : Mapped Reads Nucleotide Content



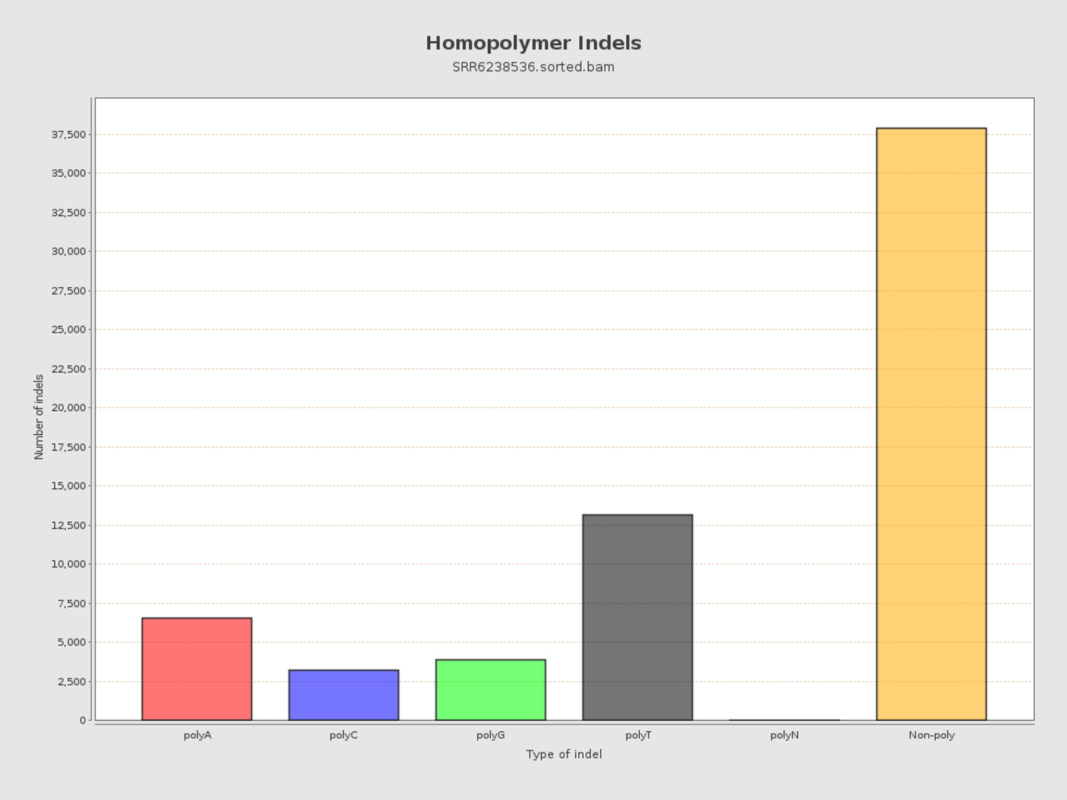
9. Results : Mapped Reads GC-content Distribution



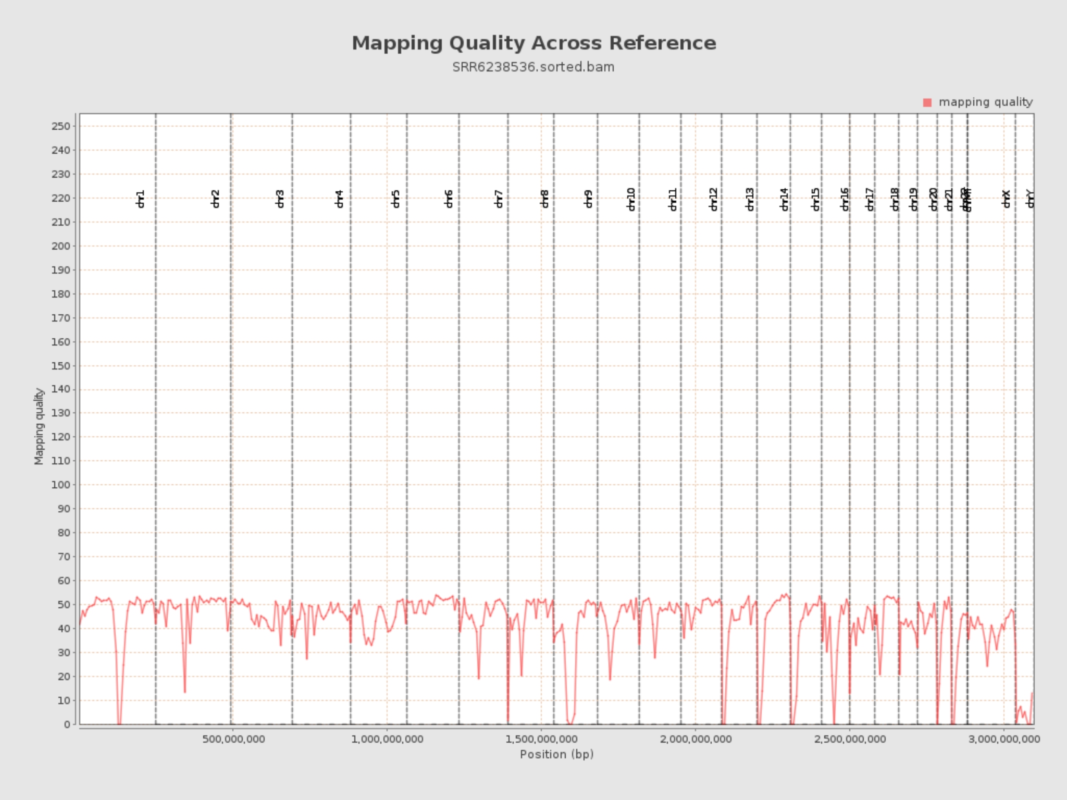
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram