Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:55:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238525.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_SRR6238525 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238525.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:55:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238525.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,258,765
Mapped reads	2,840,784 / 87.17%
Unmapped reads	417,981 / 12.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,837 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	647,506 / 19.87%
Duplication rate	17.56%
Clipped reads	1,780,604 / 54.64%

2.2. ACGT Content

Number/percentage of A's	42,886,952 / 24.45%
Number/percentage of C's	31,594,070 / 18.01%
Number/percentage of T's	57,982,696 / 33.05%
Number/percentage of G's	42,966,687 / 24.49%
Number/percentage of N's	11,923 / 0.01%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0567

Standard Deviation	0.7591

2.4. Mapping Quality

Mean Mapping Quality	40.79

2.5. Mismatches and indels

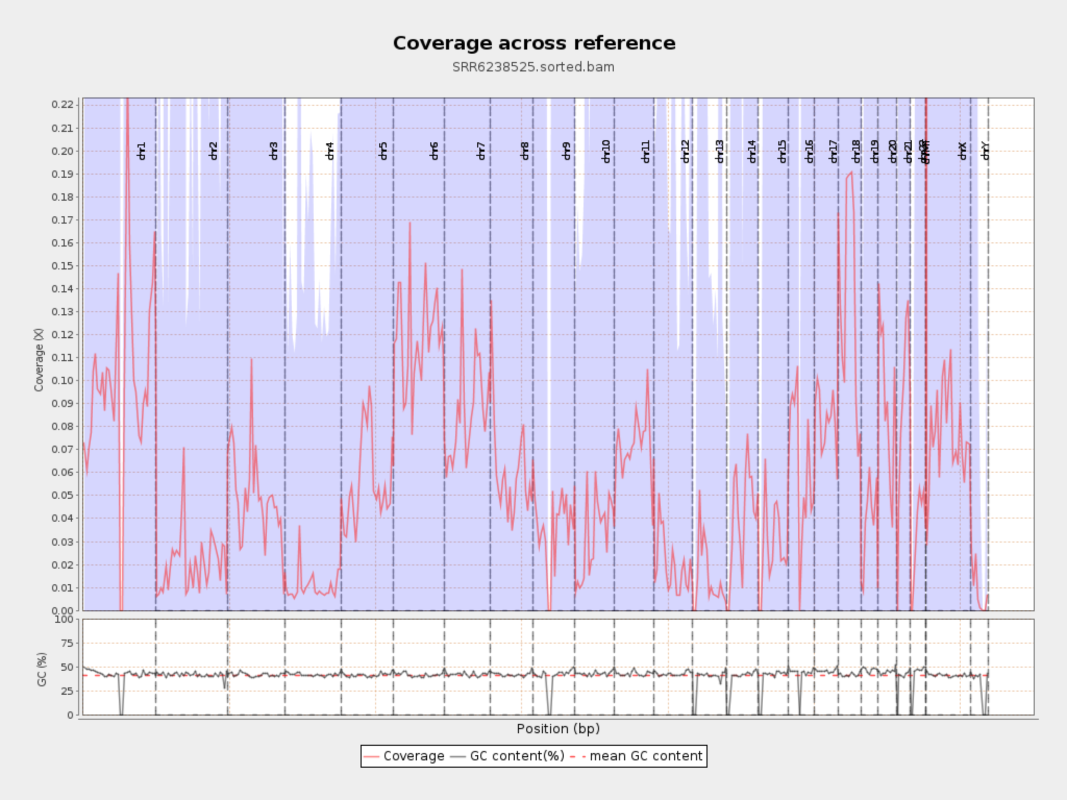
General error rate	0.62%
Mismatches	1,065,229
Insertions	10,967
Mapped reads with at least one insertion	0.38%
Deletions	51,603
Mapped reads with at least one deletion	1.8%
Homopolymer indels	41.1%

2.6. Chromosome stats

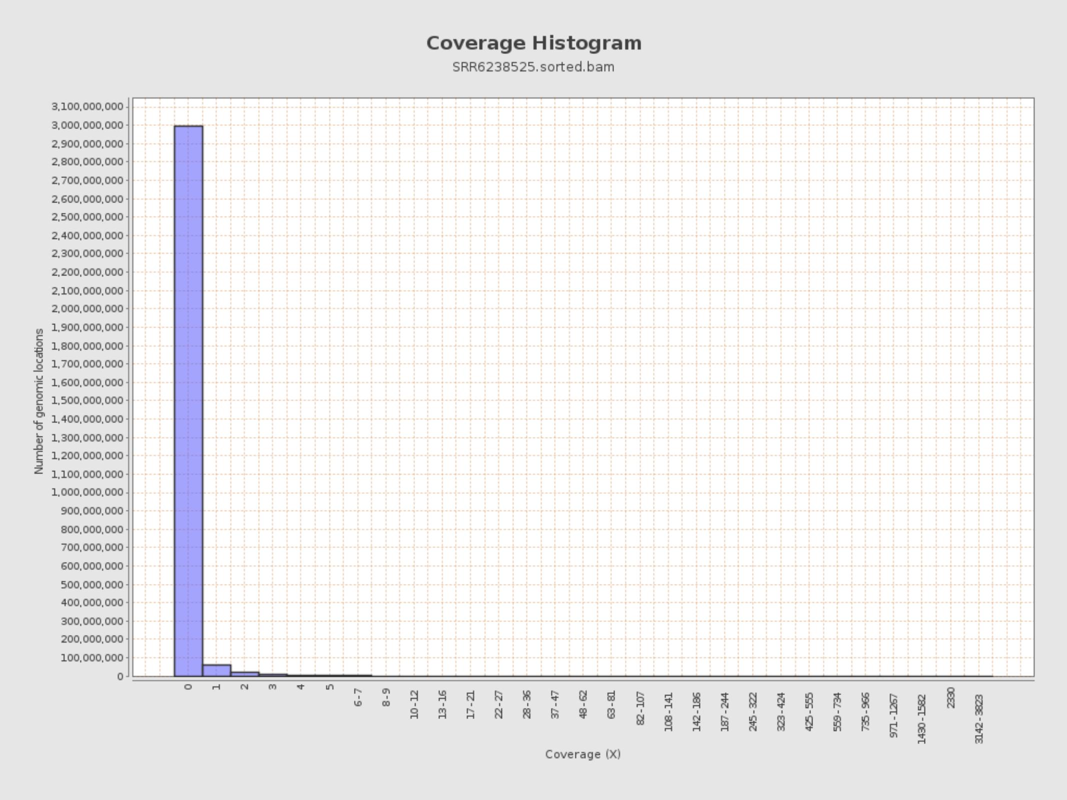
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25059295	0.1005	0.9628
chr2	243199373	5080120	0.0209	1.7084
chr3	198022430	9865307	0.0498	0.3683
chr4	191154276	2022948	0.0106	0.1711
chr5	180915260	10243722	0.0566	0.3856
chr6	171115067	20451109	0.1195	0.9652
chr7	159138663	13907992	0.0874	1.0028

chr8	146364022	8763486	0.0599	0.5345
chr9	141213431	4938608	0.035	0.4375
chr10	135534747	4307008	0.0318	0.4286
chr11	135006516	9720025	0.072	0.528
chr12	133851895	2634426	0.0197	0.2382
chr13	115169878	1658778	0.0144	0.3631
chr14	107349540	4412423	0.0411	0.3426
chr15	102531392	2872459	0.028	0.3814
chr16	90354753	5502046	0.0609	0.4517
chr17	81195210	6856779	0.0844	0.5093
chr18	78077248	10594239	0.1357	1.3306
chr19	59128983	2356667	0.0399	0.6438
chr20	63025520	5803207	0.0921	0.518
chr21	48129895	4231094	0.0879	0.4989
chr22	51304566	1705547	0.0332	0.2956
chrMT	16571	127967	7.7223	5.6146
chrX	155270560	11915886	0.0767	0.4932
chrY	59373566	499957	0.0084	0.2544

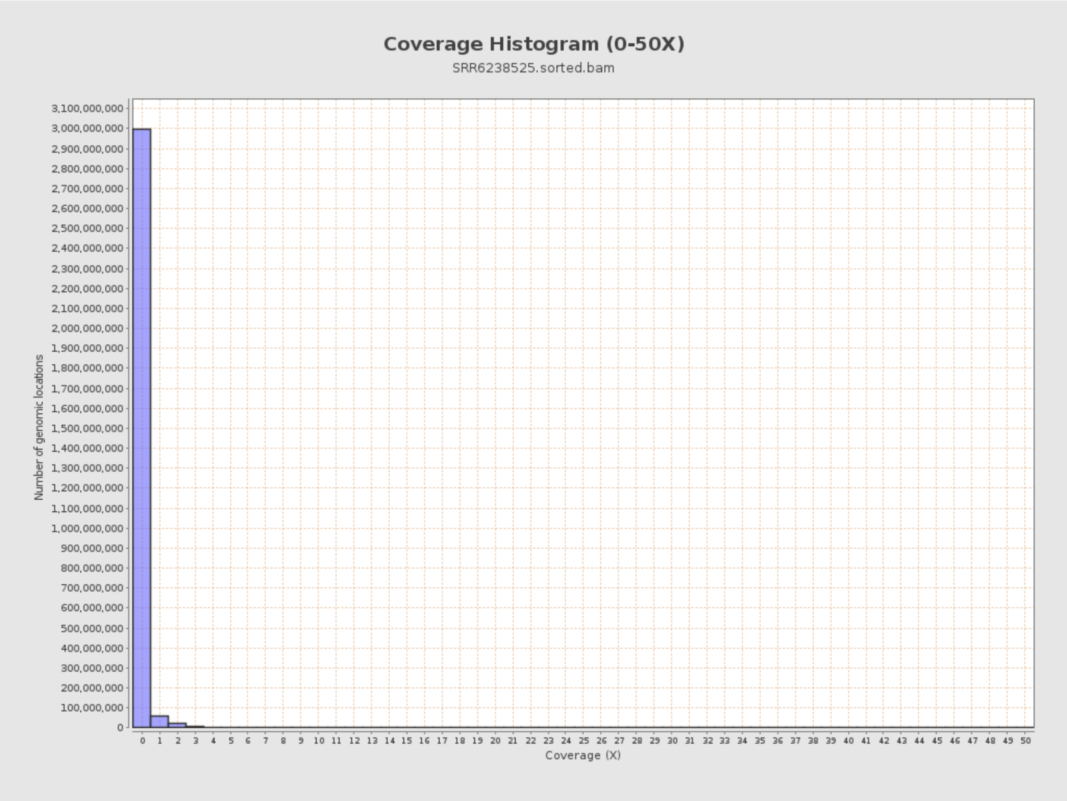
3. Results : Coverage across reference



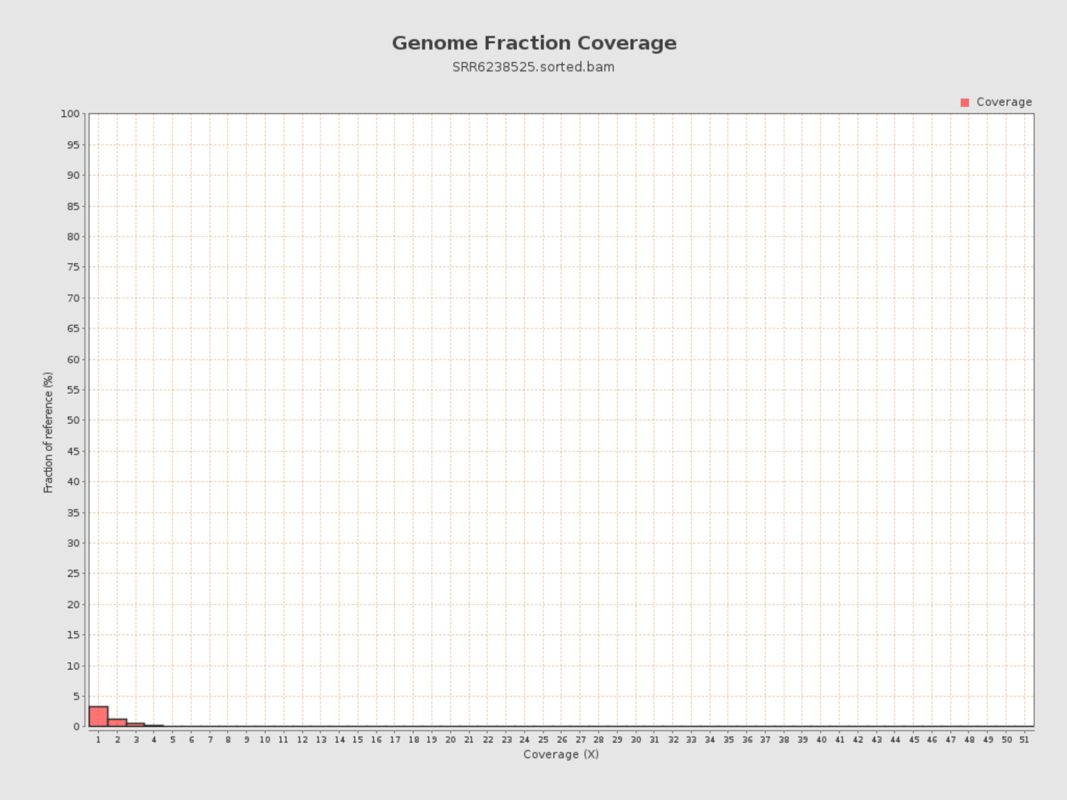
4. Results : Coverage Histogram



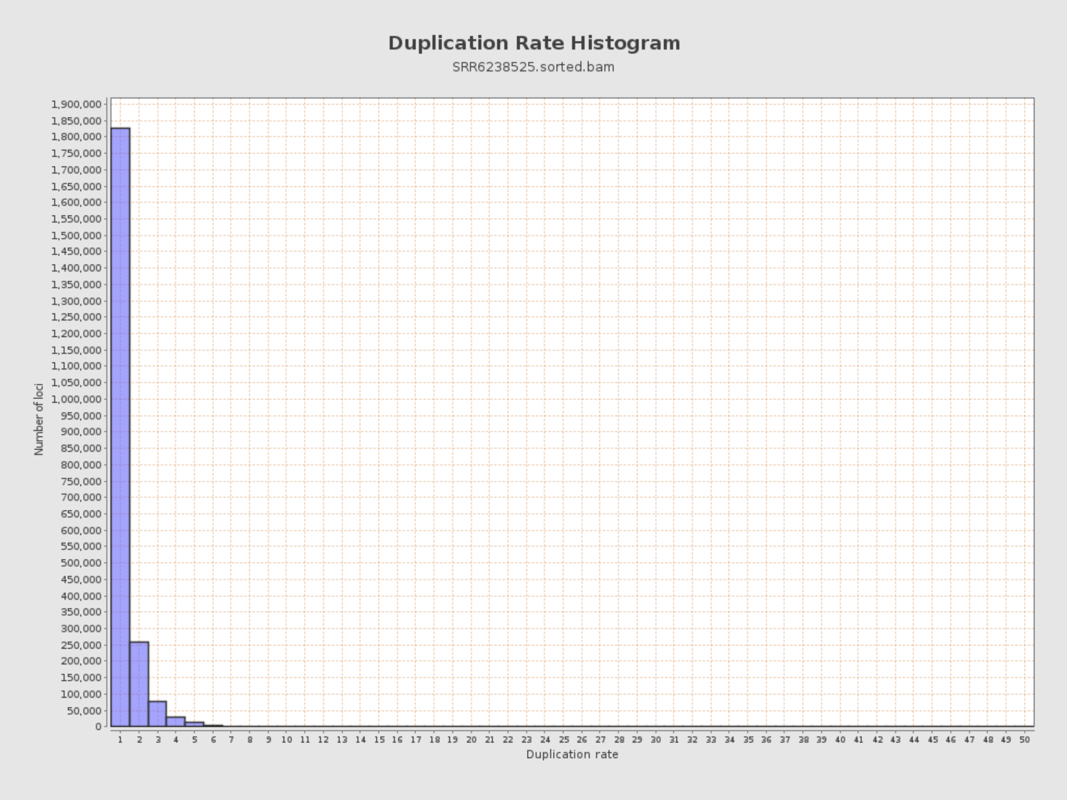
5. Results : Coverage Histogram (0-50X)



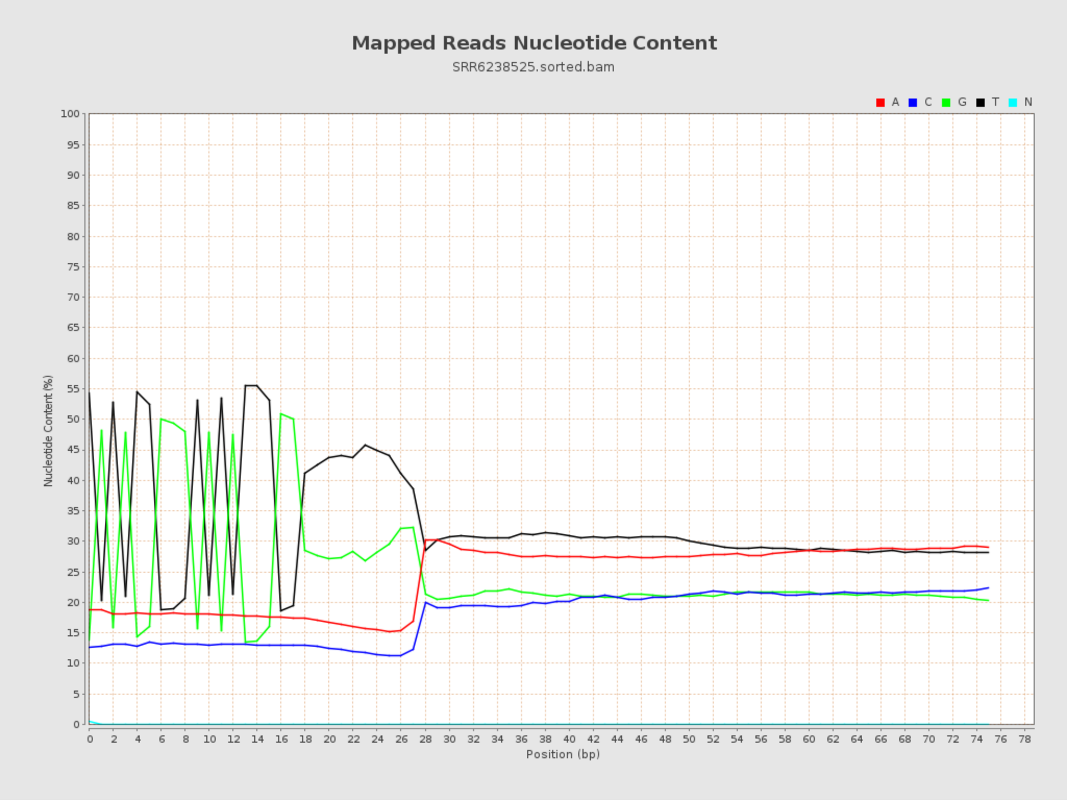
6. Results : Genome Fraction Coverage



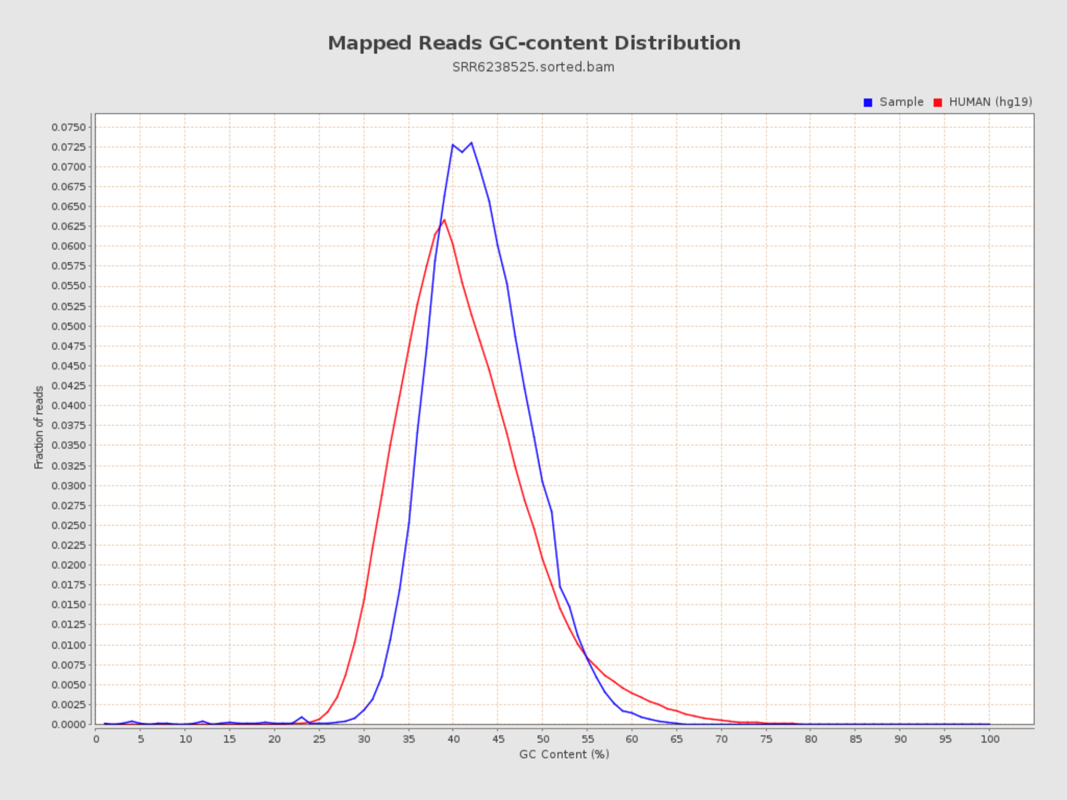
7. Results : Duplication Rate Histogram



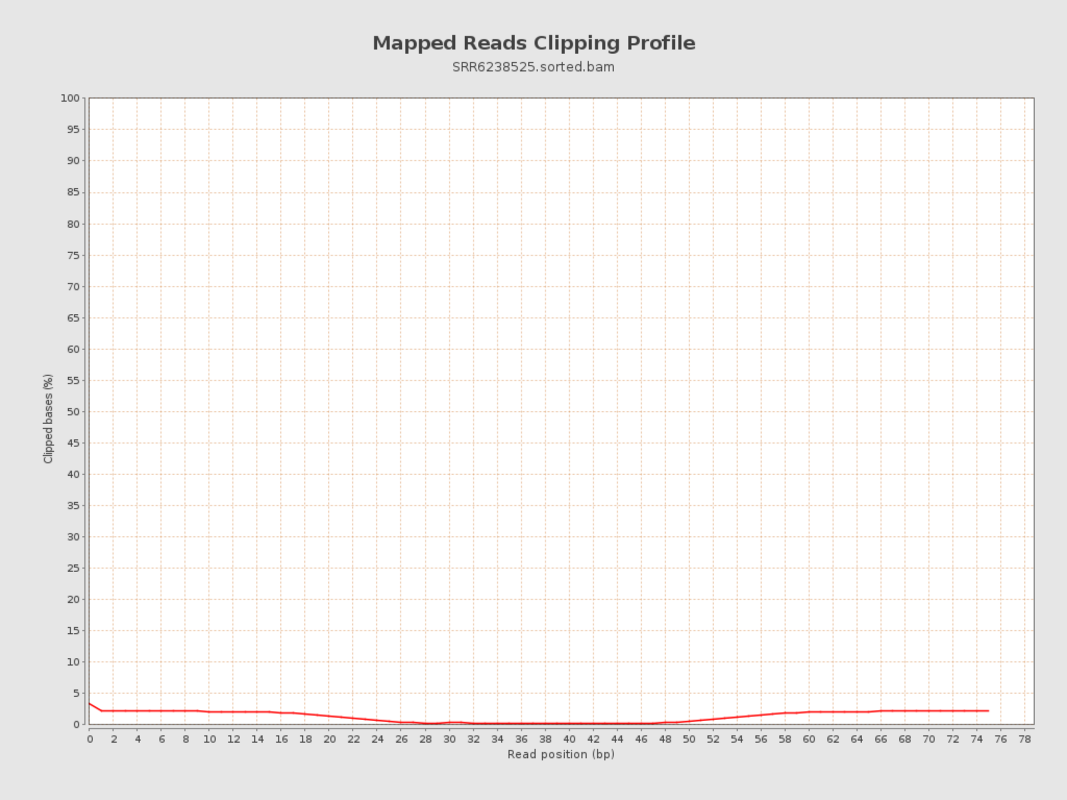
8. Results : Mapped Reads Nucleotide Content



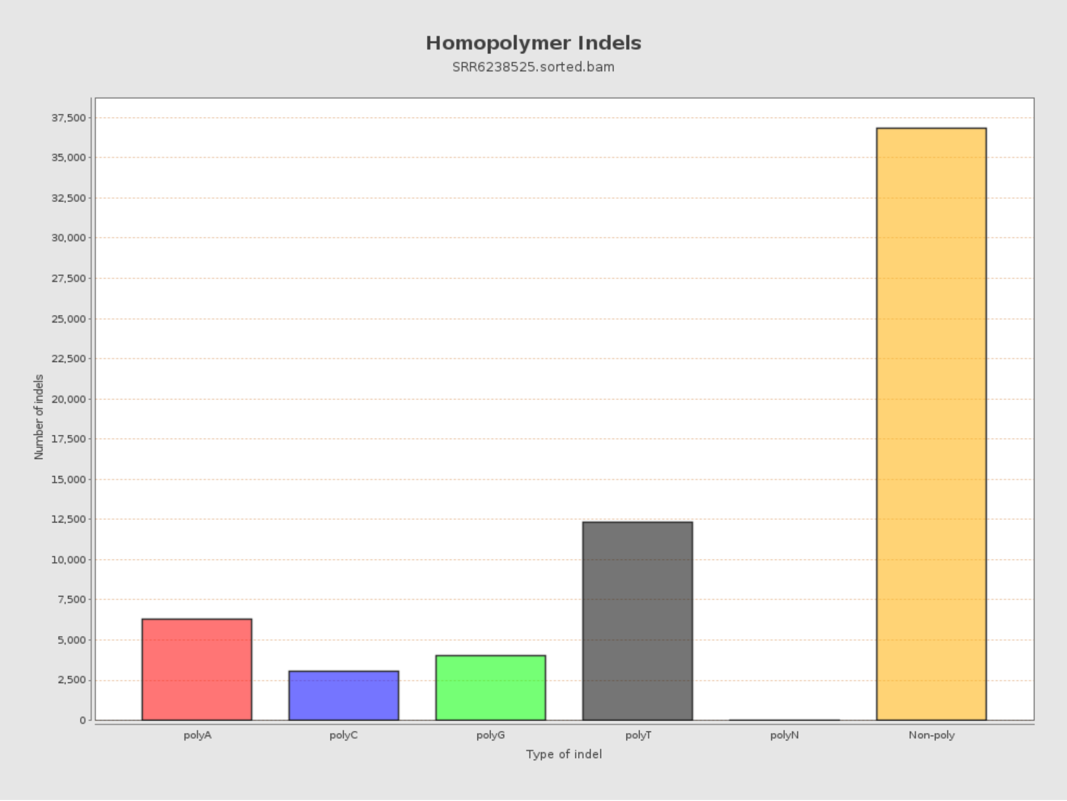
9. Results : Mapped Reads GC-content Distribution



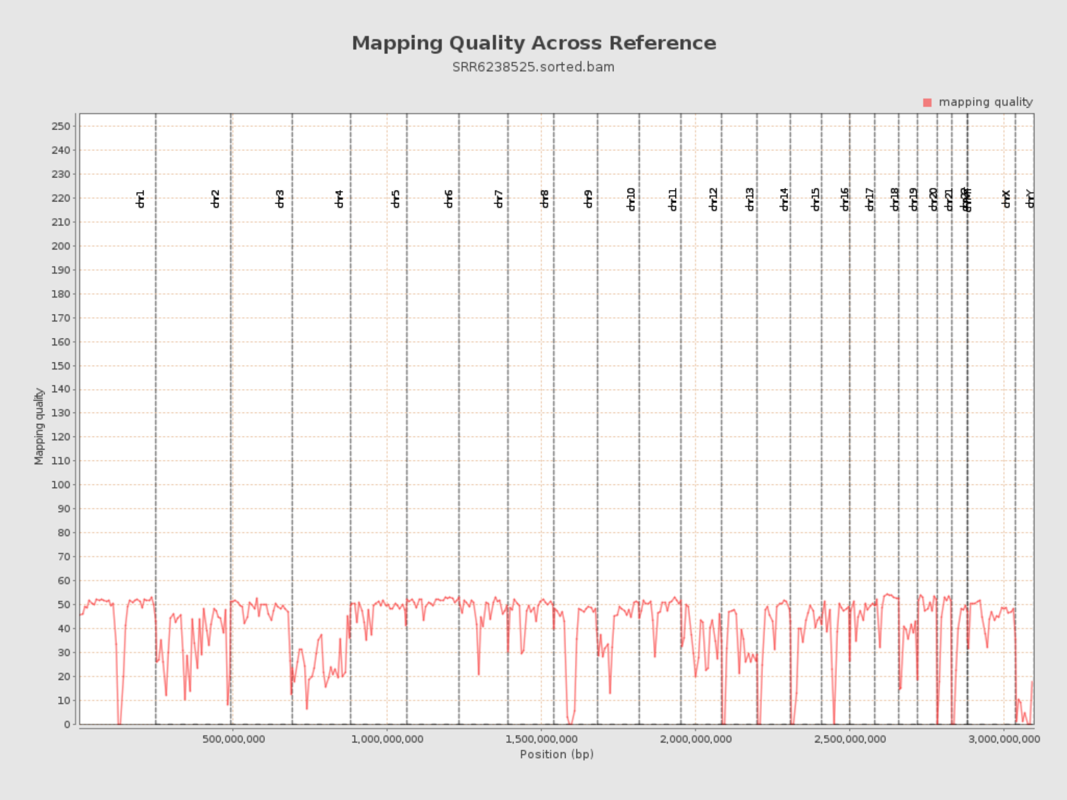
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram