Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:45:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238637.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_SRR6238637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238637.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:45:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,840,315
Mapped reads	3,499,229 / 91.12%
Unmapped reads	341,086 / 8.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,903 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	756,751 / 19.71%
Duplication rate	16.81%
Clipped reads	2,270,615 / 59.13%

2.2. ACGT Content

Number/percentage of A's	55,910,848 / 25.96%
Number/percentage of C's	39,595,092 / 18.38%
Number/percentage of T's	69,698,411 / 32.36%
Number/percentage of G's	50,167,285 / 23.29%
Number/percentage of N's	11,042 / 0.01%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0696

Standard Deviation	0.784

2.4. Mapping Quality

Mean Mapping Quality	41.97

2.5. Mismatches and indels

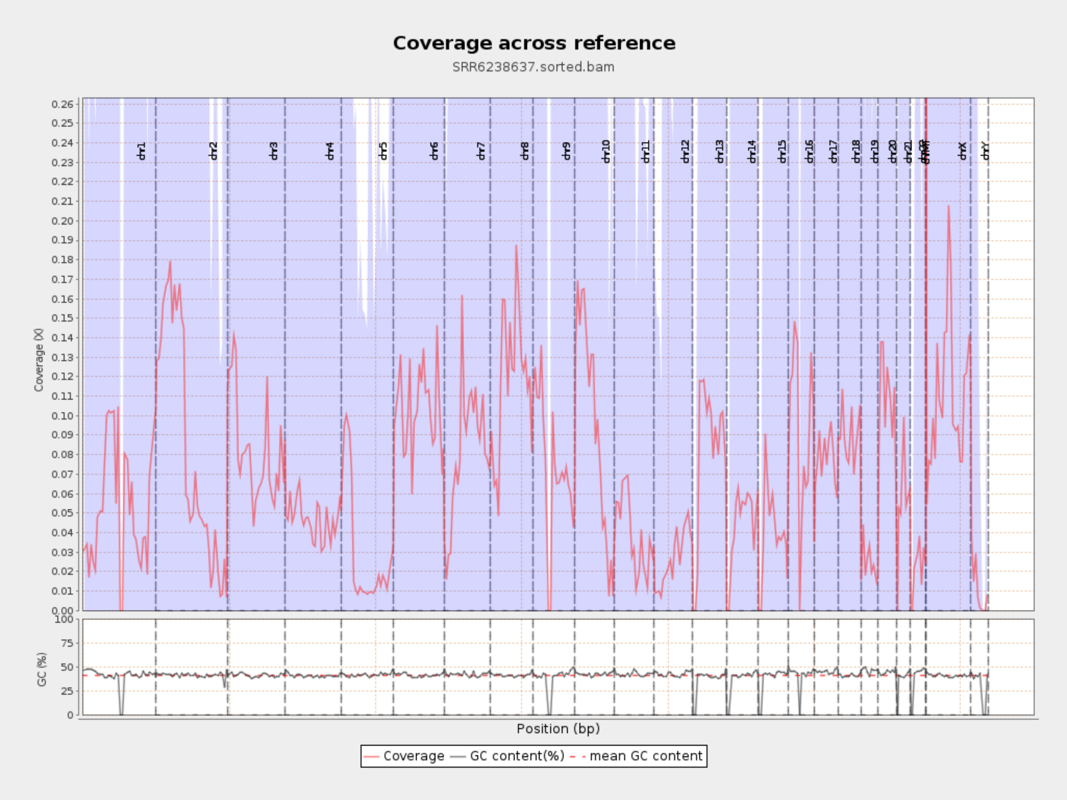
General error rate	0.57%
Mismatches	1,194,406
Insertions	13,895
Mapped reads with at least one insertion	0.39%
Deletions	51,371
Mapped reads with at least one deletion	1.46%
Homopolymer indels	42.05%

2.6. Chromosome stats

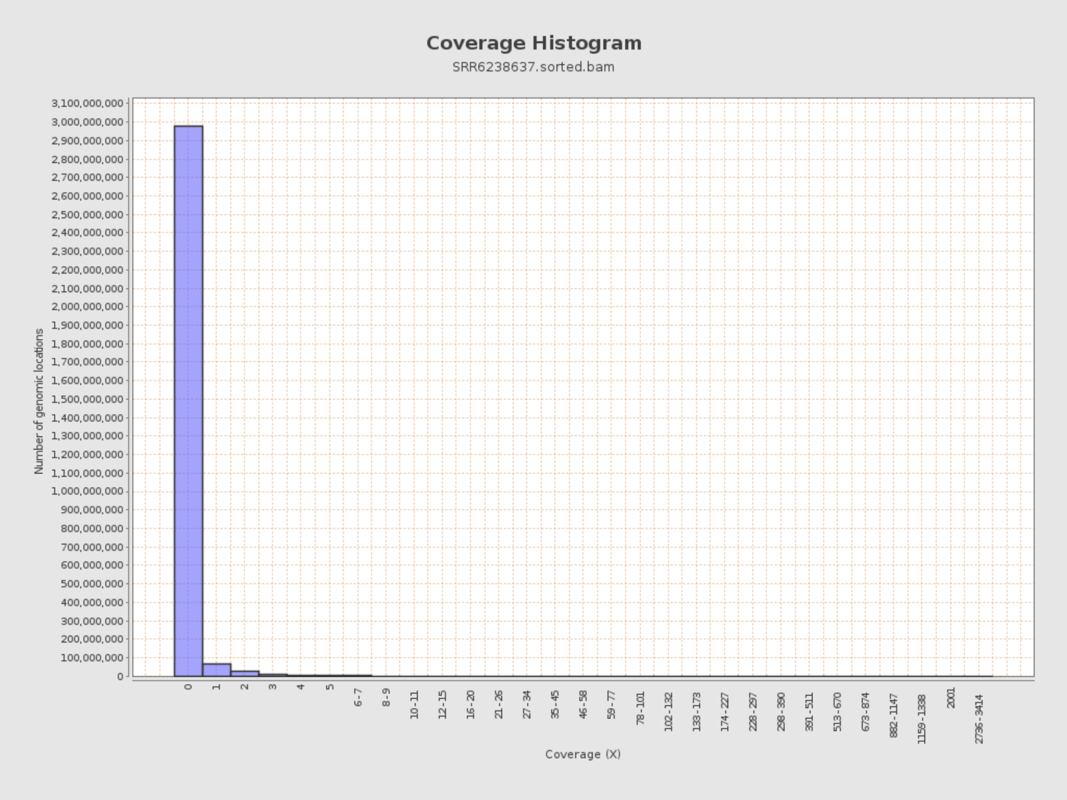
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13304367	0.0534	0.661
chr2	243199373	20614755	0.0848	1.6276
chr3	198022430	16250735	0.0821	0.4839
chr4	191154276	8949178	0.0468	0.3727
chr5	180915260	5281219	0.0292	0.2939
chr6	171115067	17780972	0.1039	0.8058
chr7	159138663	13019966	0.0818	1.2628

chr8	146364022	17441611	0.1192	0.8328
chr9	141213431	10543077	0.0747	0.7144
chr10	135534747	13066455	0.0964	0.6155
chr11	135006516	5242095	0.0388	0.4367
chr12	133851895	3578690	0.0267	0.3051
chr13	115169878	9610704	0.0834	0.5802
chr14	107349540	4720095	0.044	0.4287
chr15	102531392	4131076	0.0403	0.4411
chr16	90354753	8193394	0.0907	0.572
chr17	81195210	6403429	0.0789	0.481
chr18	78077248	6999184	0.0896	1.5484
chr19	59128983	1476222	0.025	0.5999
chr20	63025520	6954319	0.1103	0.5707
chr21	48129895	2734068	0.0568	0.4322
chr22	51304566	1089545	0.0212	0.2329
chrMT	16571	26875	1.6218	2.3809
chrX	155270560	17398656	0.1121	0.61
chrY	59373566	659557	0.0111	0.283

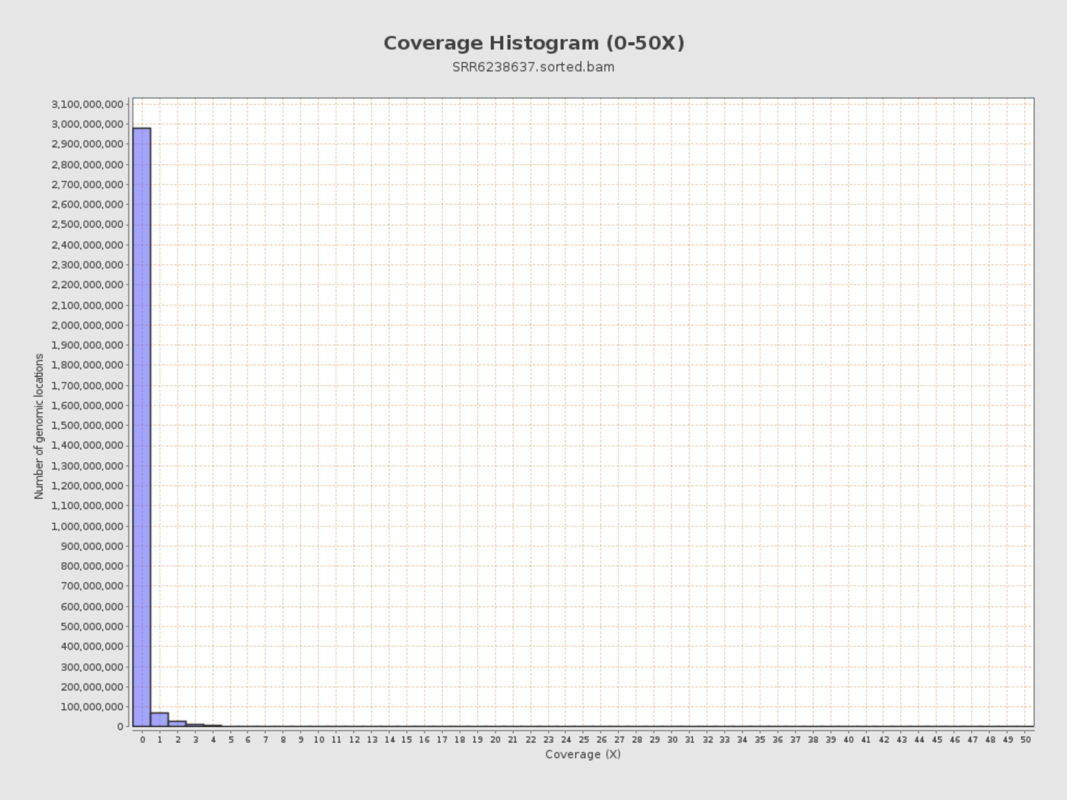
3. Results : Coverage across reference



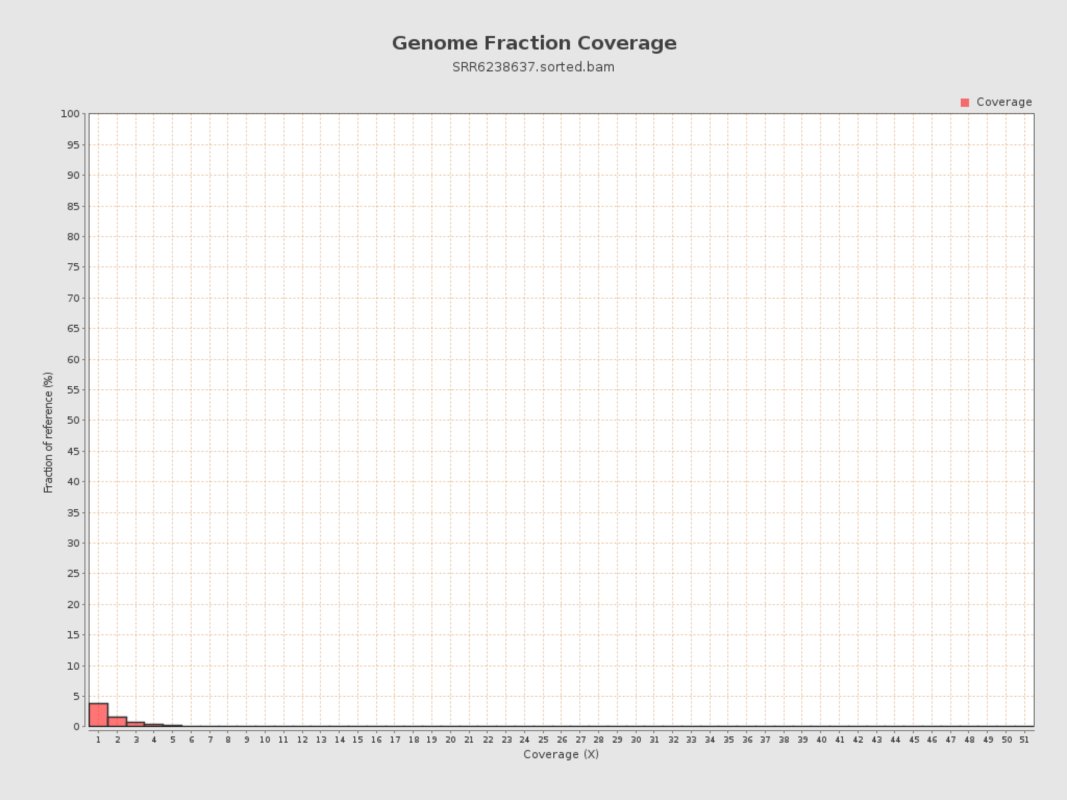
4. Results : Coverage Histogram



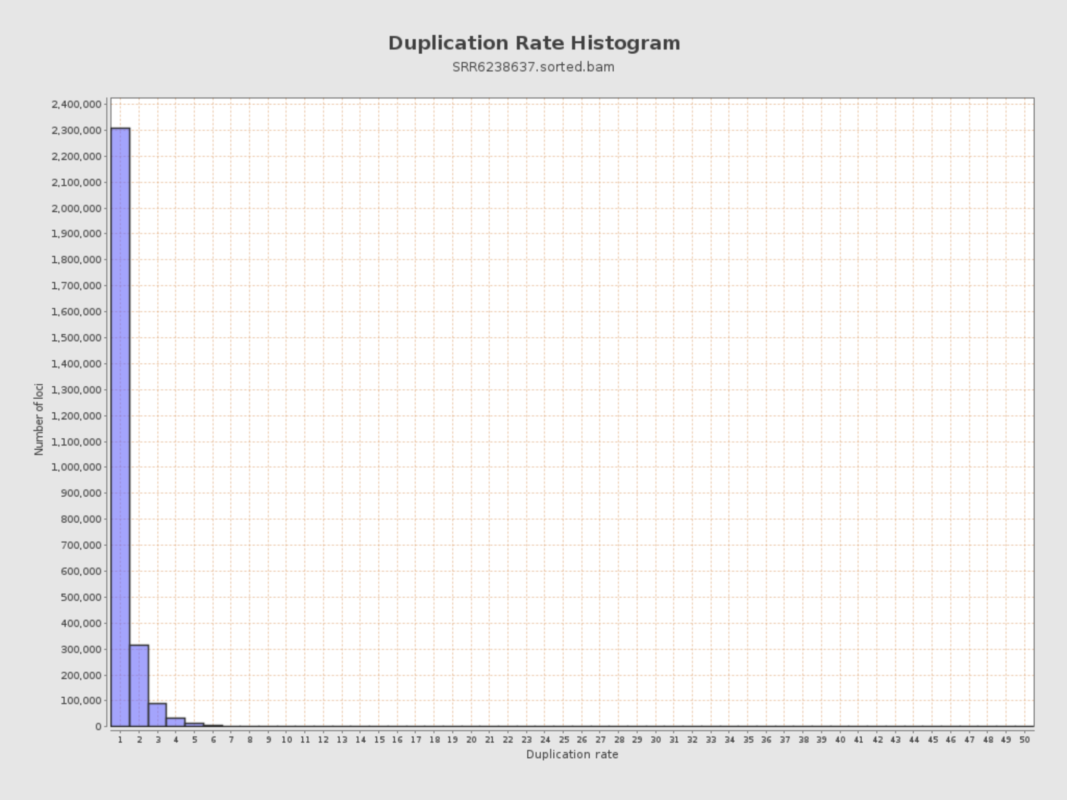
5. Results : Coverage Histogram (0-50X)



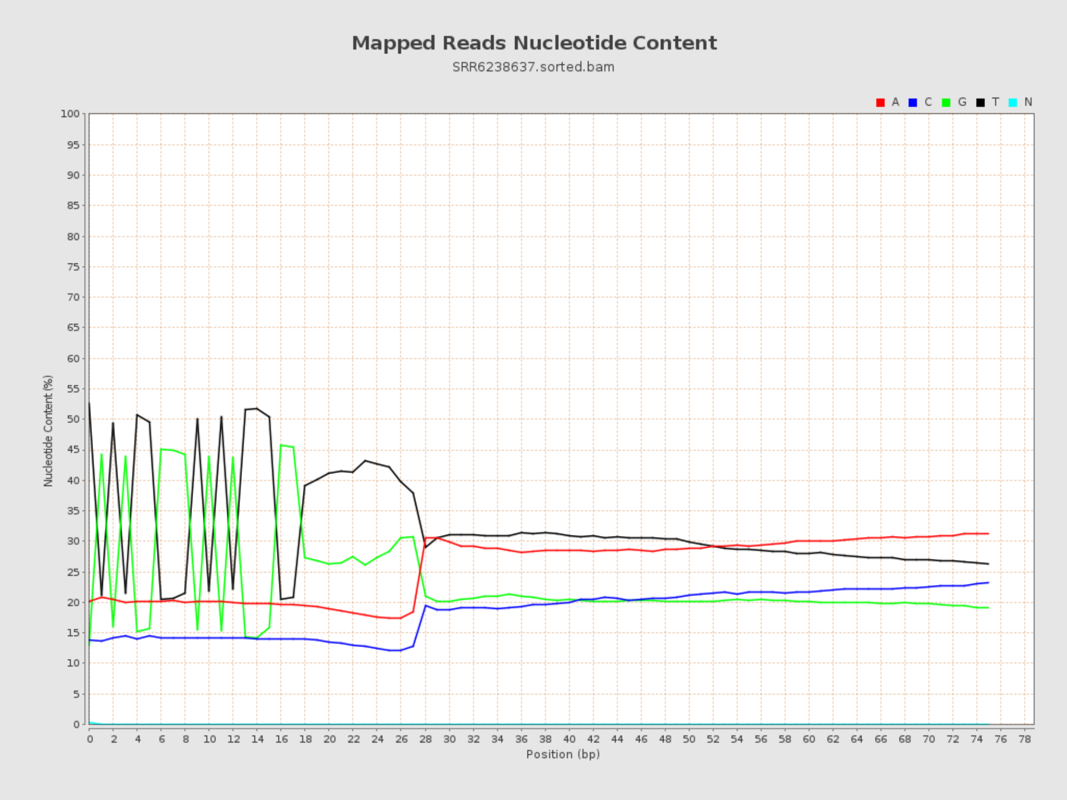
6. Results : Genome Fraction Coverage



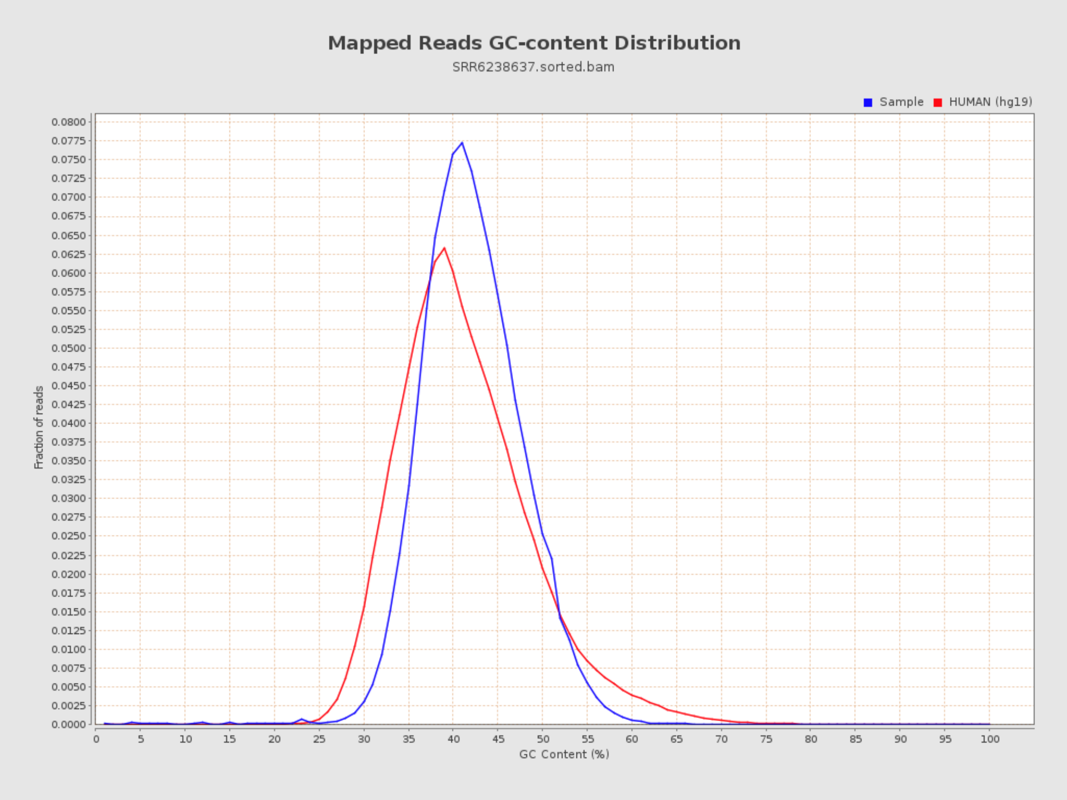
7. Results : Duplication Rate Histogram



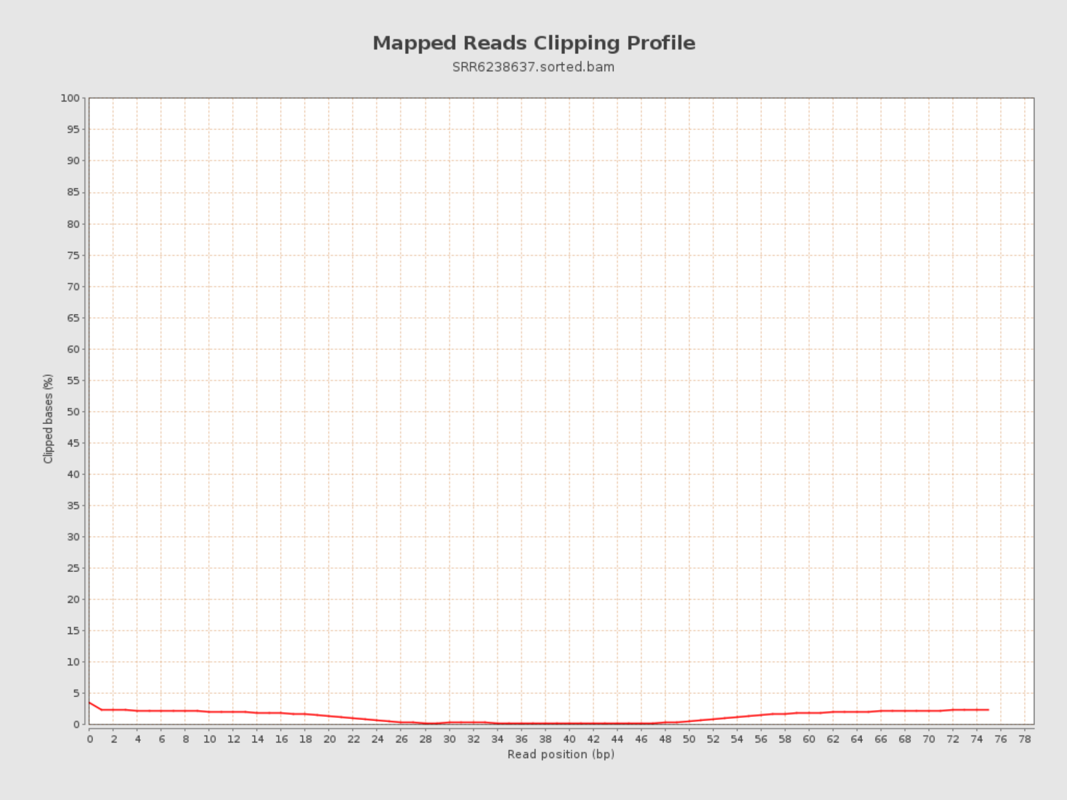
8. Results : Mapped Reads Nucleotide Content



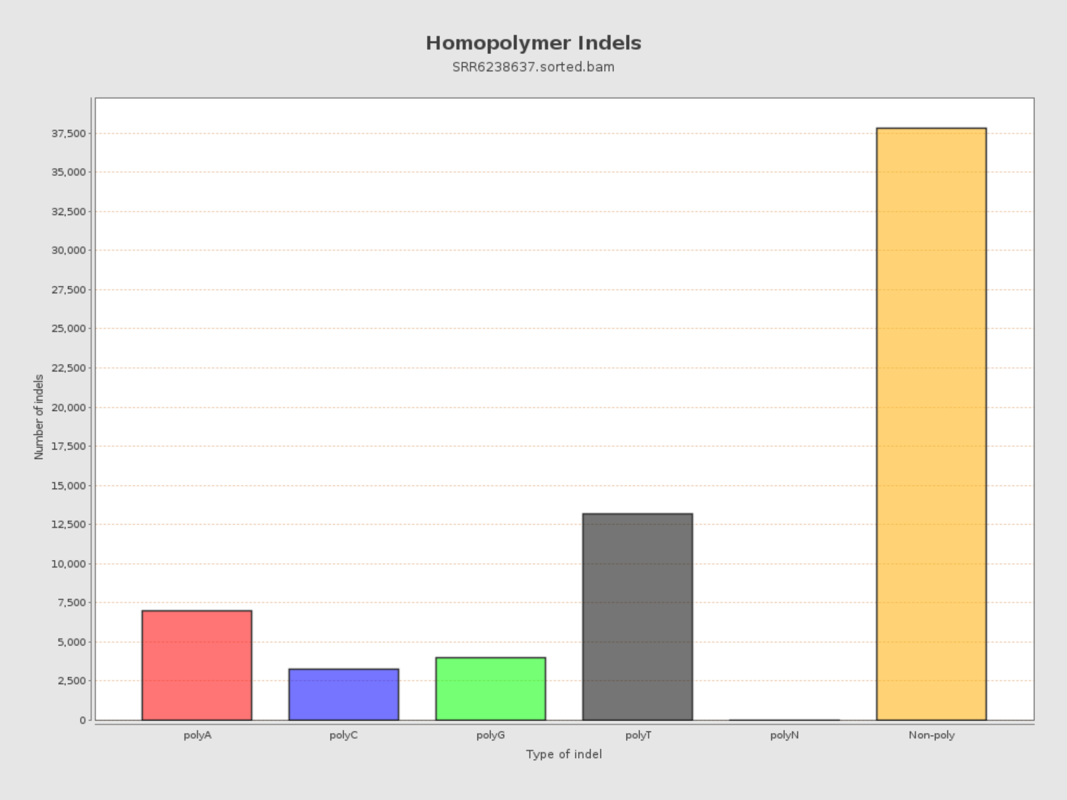
9. Results : Mapped Reads GC-content Distribution



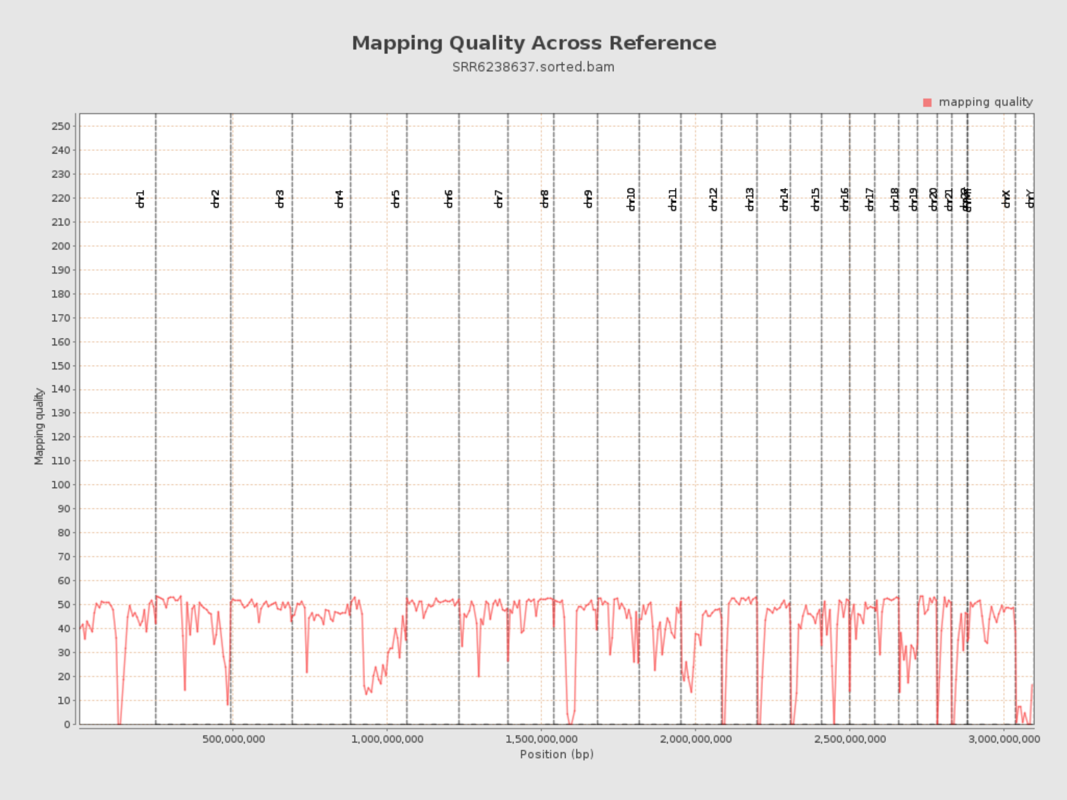
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram