Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 22:24:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238613.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_SRR6238613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238613.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 22:24:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,619,033
Mapped reads	2,395,143 / 66.18%
Unmapped reads	1,223,890 / 33.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,003 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	604,974 / 16.72%
Duplication rate	18.93%
Clipped reads	1,531,735 / 42.32%

2.2. ACGT Content

Number/percentage of A's	36,387,341 / 24.72%
Number/percentage of C's	26,367,990 / 17.91%
Number/percentage of T's	48,676,442 / 33.07%
Number/percentage of G's	35,769,287 / 24.3%
Number/percentage of N's	7,368 / 0.01%
GC Percentage	42.21%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.612

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

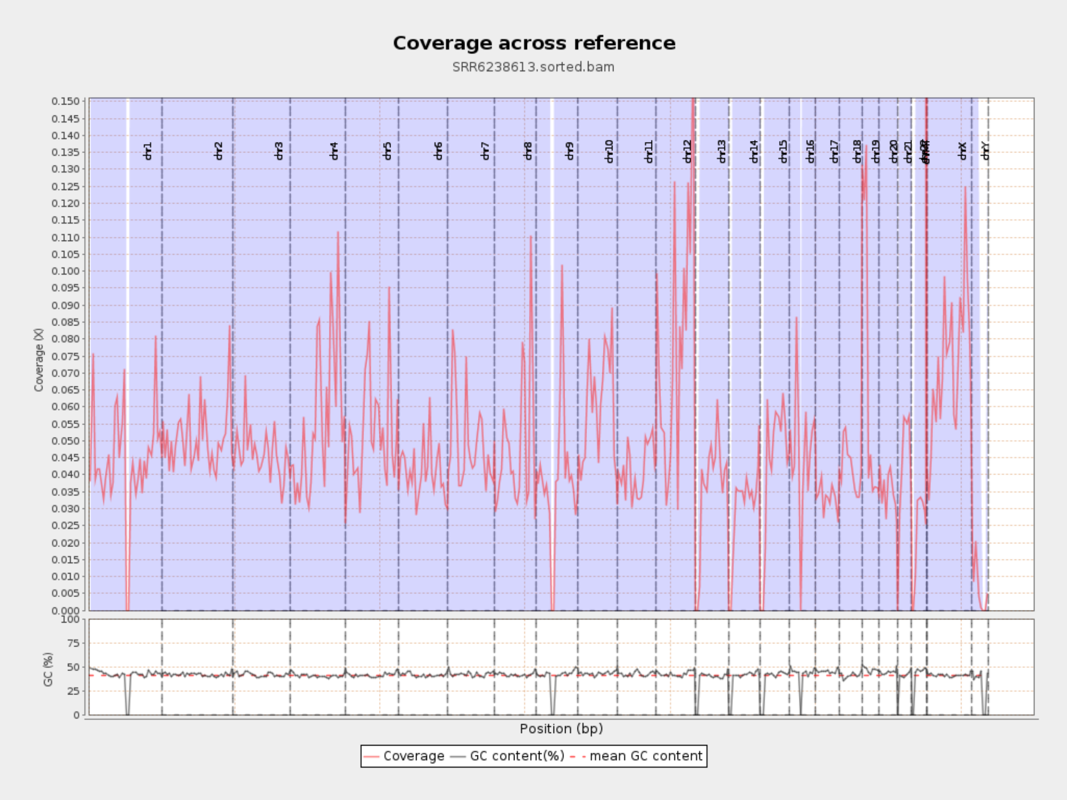
General error rate	0.55%
Mismatches	794,384
Insertions	9,619
Mapped reads with at least one insertion	0.4%
Deletions	34,713
Mapped reads with at least one deletion	1.44%
Homopolymer indels	43.05%

2.6. Chromosome stats

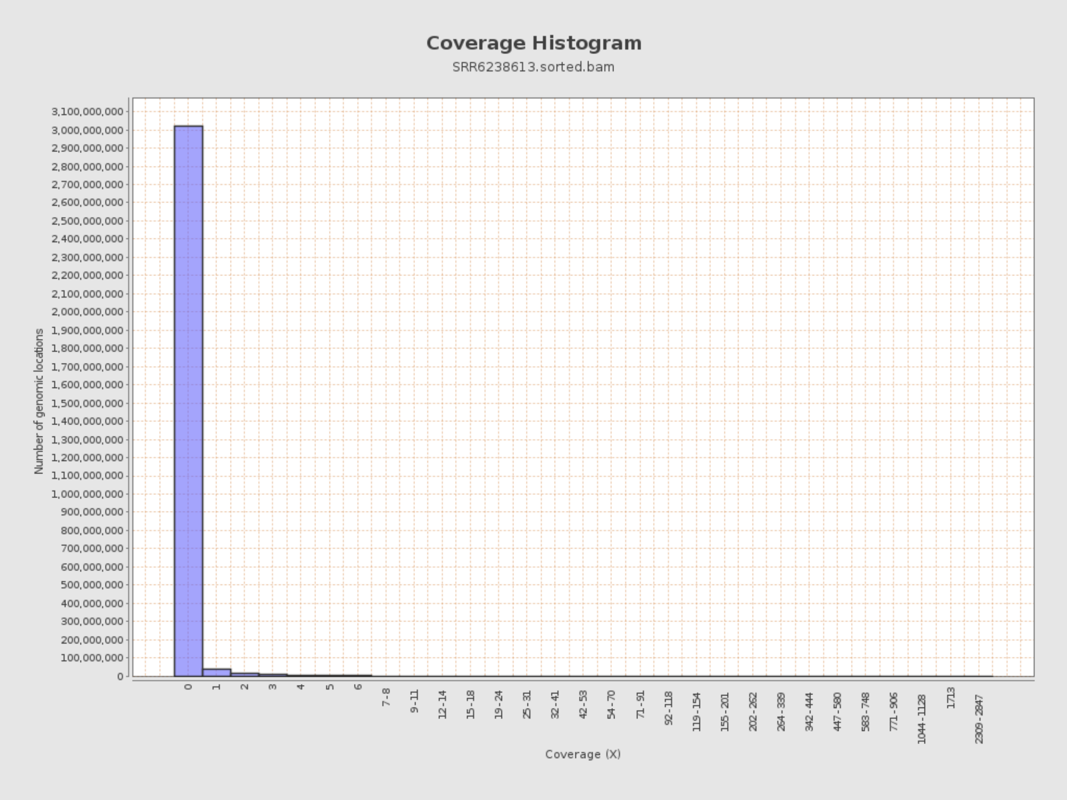
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10947330	0.0439	0.6304
chr2	243199373	12372455	0.0509	1.2982
chr3	198022430	9166056	0.0463	0.3939
chr4	191154276	10718368	0.0561	0.4357
chr5	180915260	9428767	0.0521	0.414
chr6	171115067	7046053	0.0412	0.5442
chr7	159138663	7925165	0.0498	0.626

chr8	146364022	7033364	0.0481	0.5066
chr9	141213431	5399785	0.0382	0.4086
chr10	135534747	8191353	0.0604	0.529
chr11	135006516	5573329	0.0413	0.4025
chr12	133851895	10616766	0.0793	0.5283
chr13	115169878	4133626	0.0359	0.4337
chr14	107349540	3171671	0.0295	0.3189
chr15	102531392	4397366	0.0429	0.4586
chr16	90354753	4213395	0.0466	0.4242
chr17	81195210	2666882	0.0328	0.3323
chr18	78077248	3274111	0.0419	1.2505
chr19	59128983	3932006	0.0665	0.573
chr20	63025520	2221949	0.0353	0.346
chr21	48129895	2028234	0.0421	0.3774
chr22	51304566	1113455	0.0217	0.257
chrMT	16571	40098	2.4198	2.8431
chrX	155270560	11271851	0.0726	0.496
chrY	59373566	385037	0.0065	0.2431

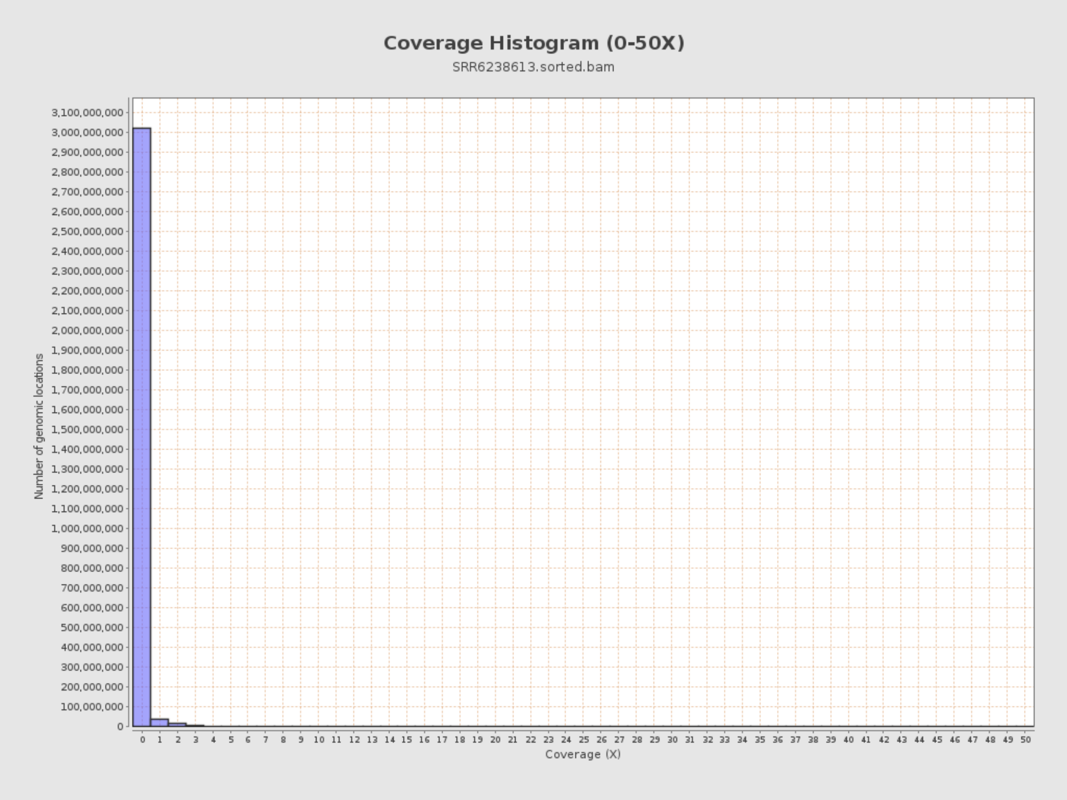
3. Results : Coverage across reference



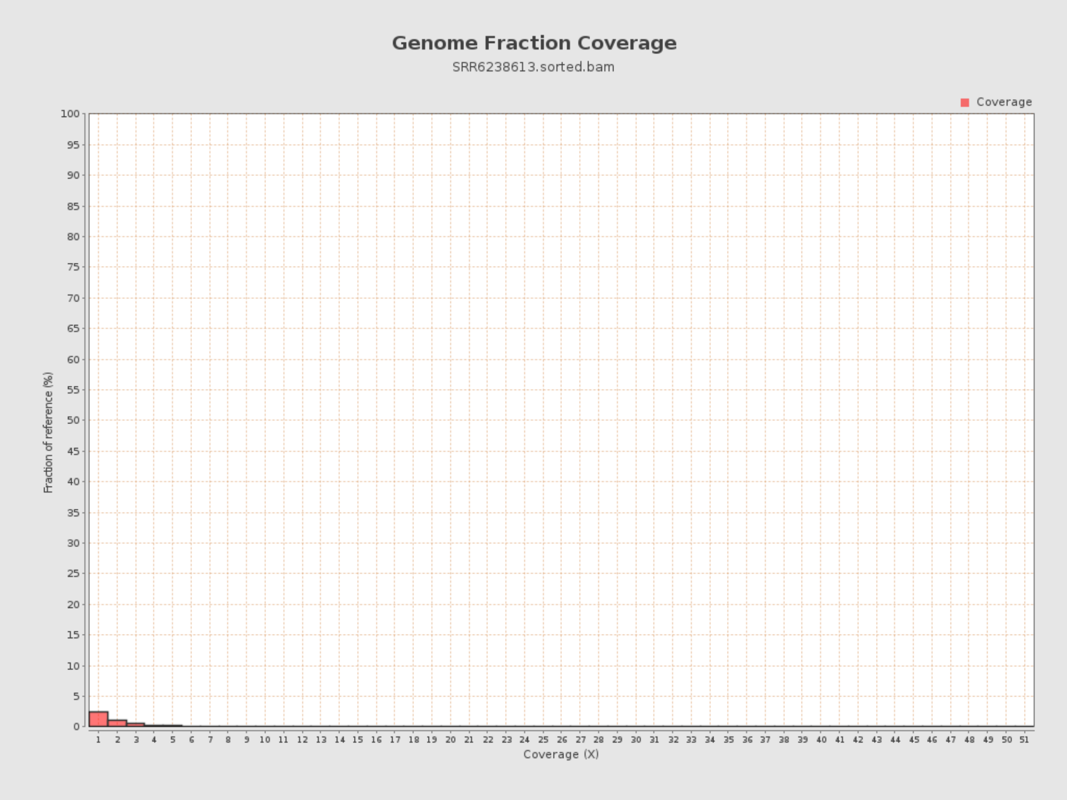
4. Results : Coverage Histogram



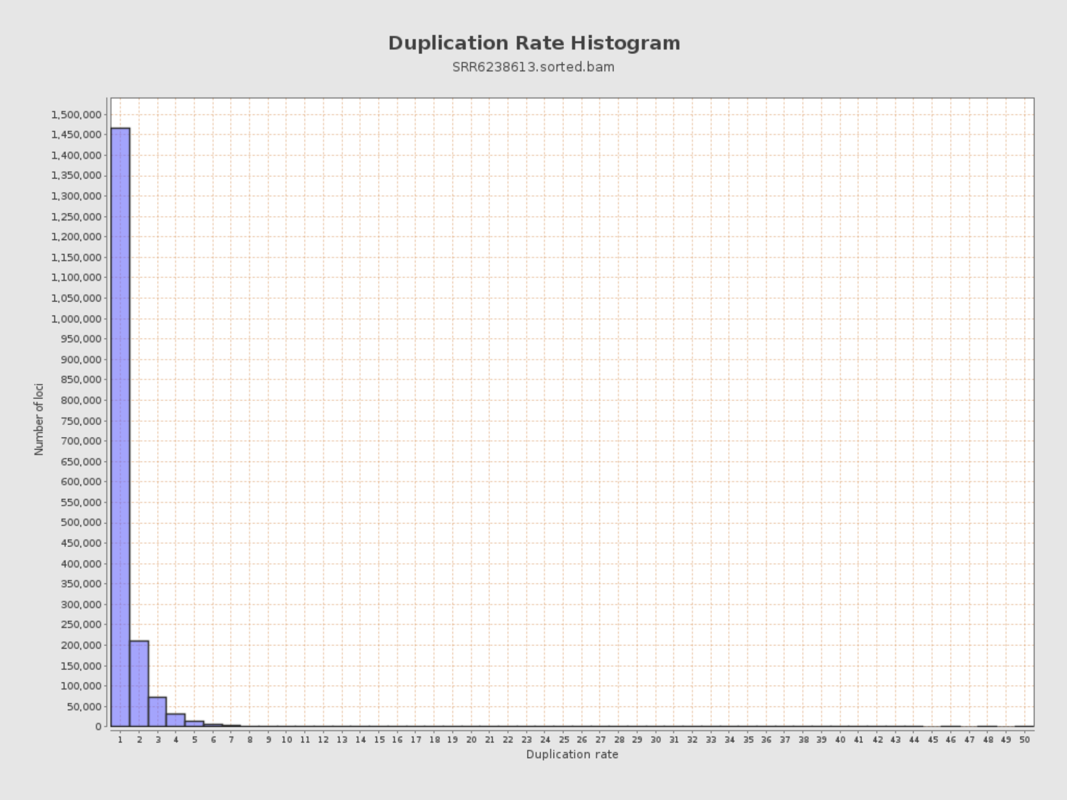
5. Results : Coverage Histogram (0-50X)



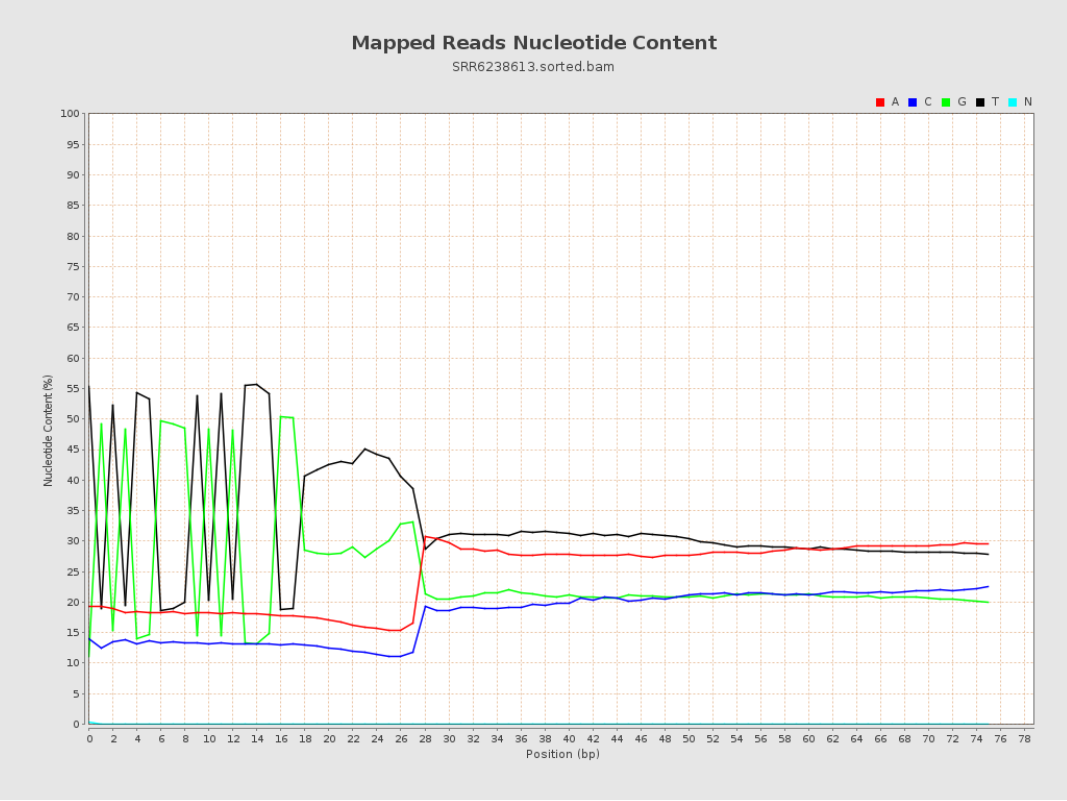
6. Results : Genome Fraction Coverage



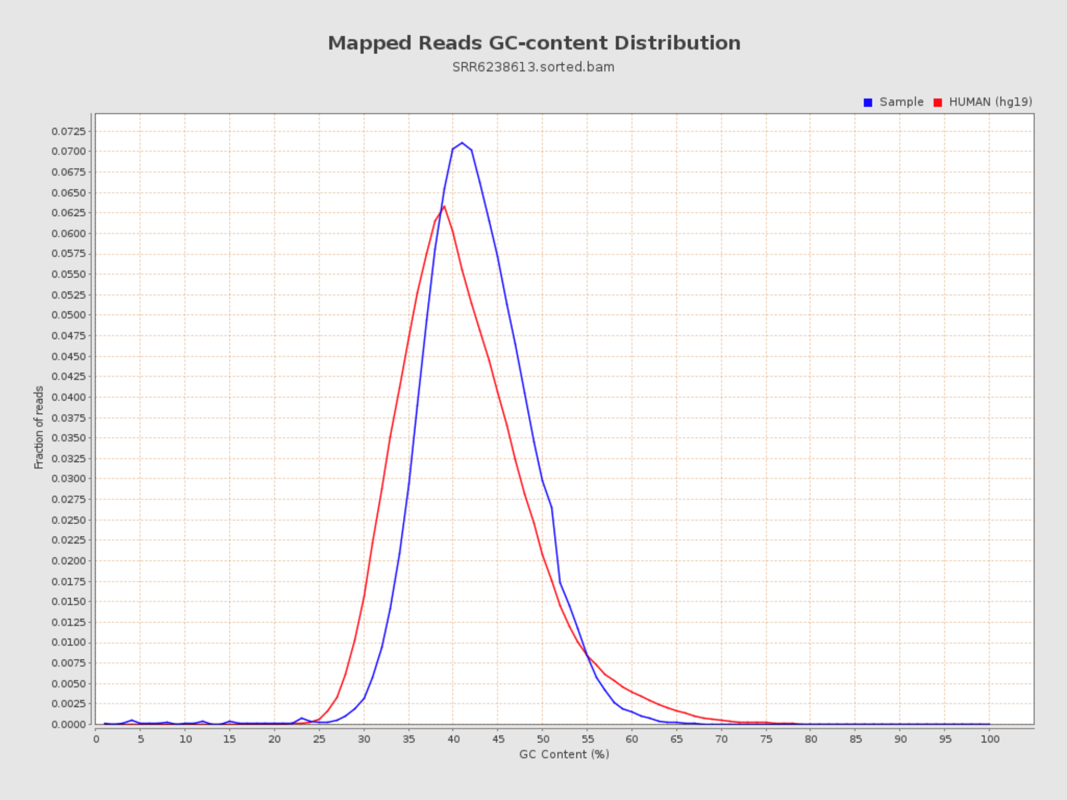
7. Results : Duplication Rate Histogram



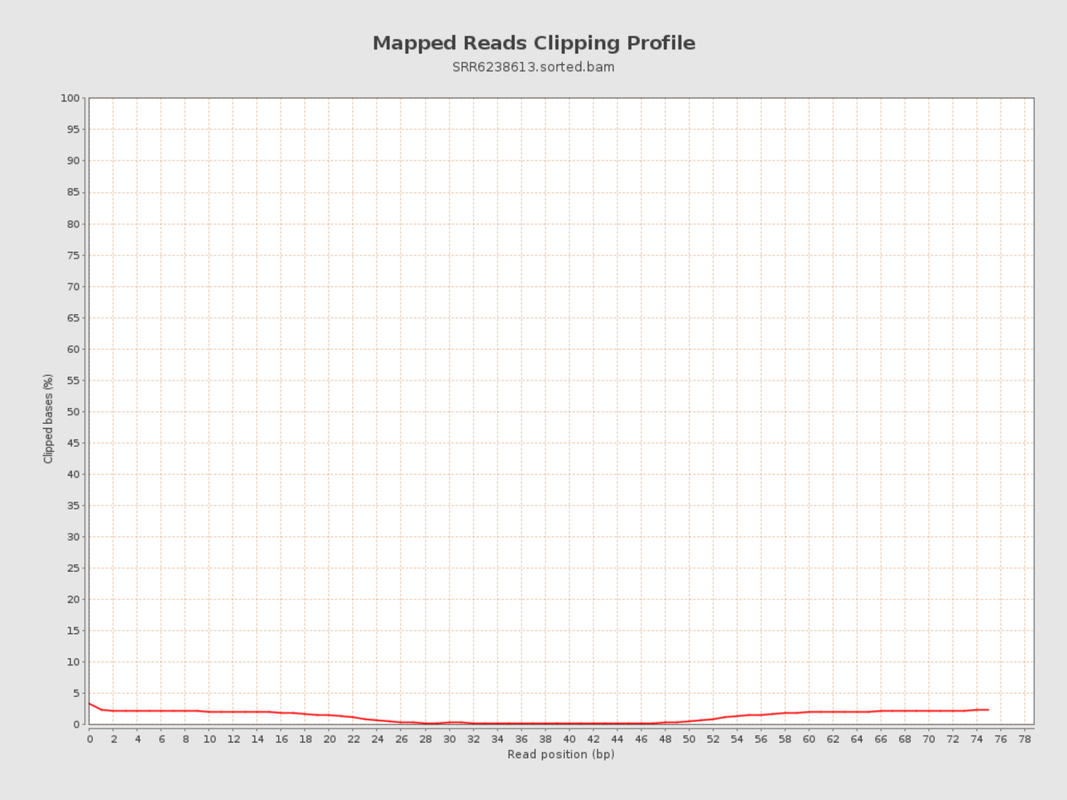
8. Results : Mapped Reads Nucleotide Content



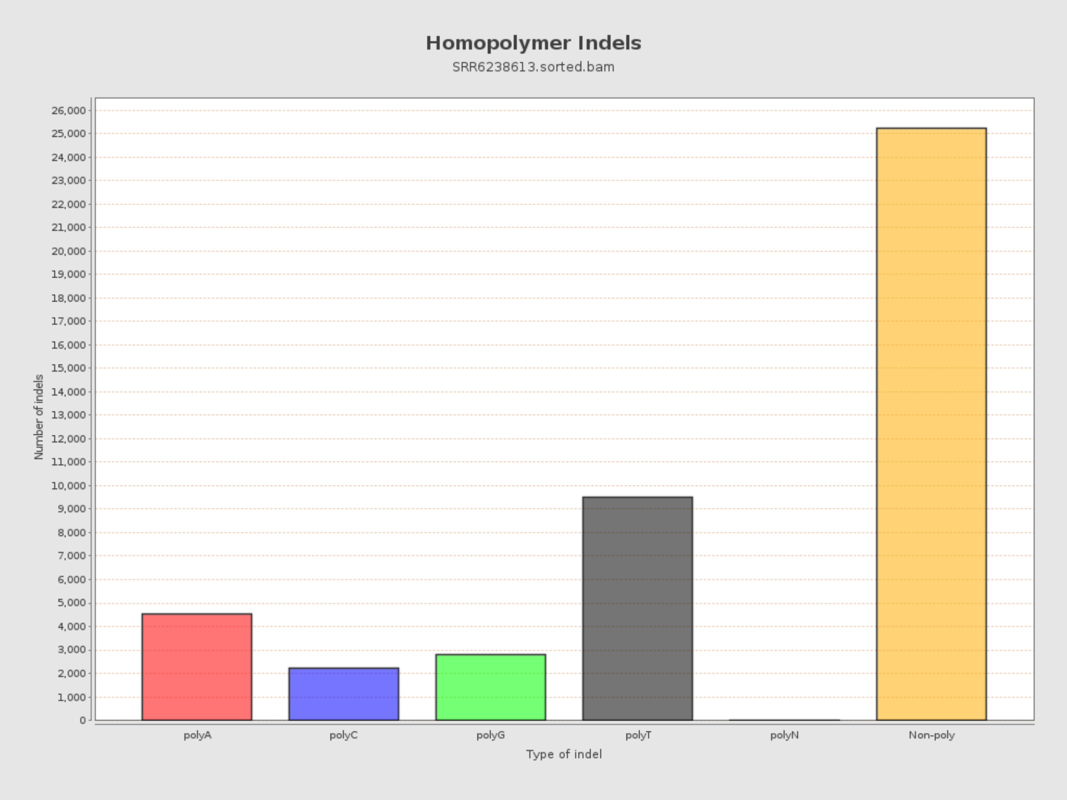
9. Results : Mapped Reads GC-content Distribution



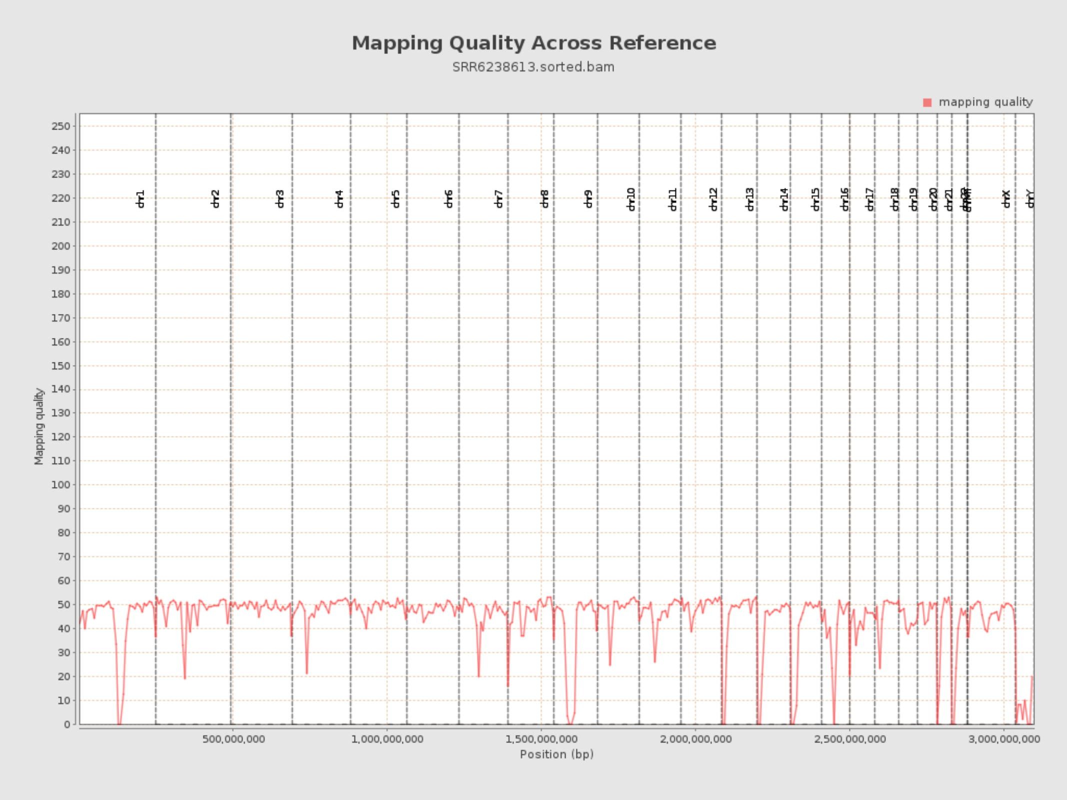
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram