Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:17:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237818.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_SRR6237818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:17:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,209,236
Mapped reads	2,337,475 / 72.84%
Unmapped reads	871,761 / 27.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,620 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	394,813 / 12.3%
Duplication rate	12.25%
Clipped reads	689,490 / 21.48%

2.2. ACGT Content

Number/percentage of A's	47,515,550 / 29.03%
Number/percentage of C's	31,351,516 / 19.16%
Number/percentage of T's	50,361,010 / 30.77%
Number/percentage of G's	34,148,592 / 20.87%
Number/percentage of N's	284,395 / 0.17%
GC Percentage	40.02%

2.3. Coverage

Mean	0.0529

Standard Deviation	0.863

2.4. Mapping Quality

Mean Mapping Quality	47.18

2.5. Mismatches and indels

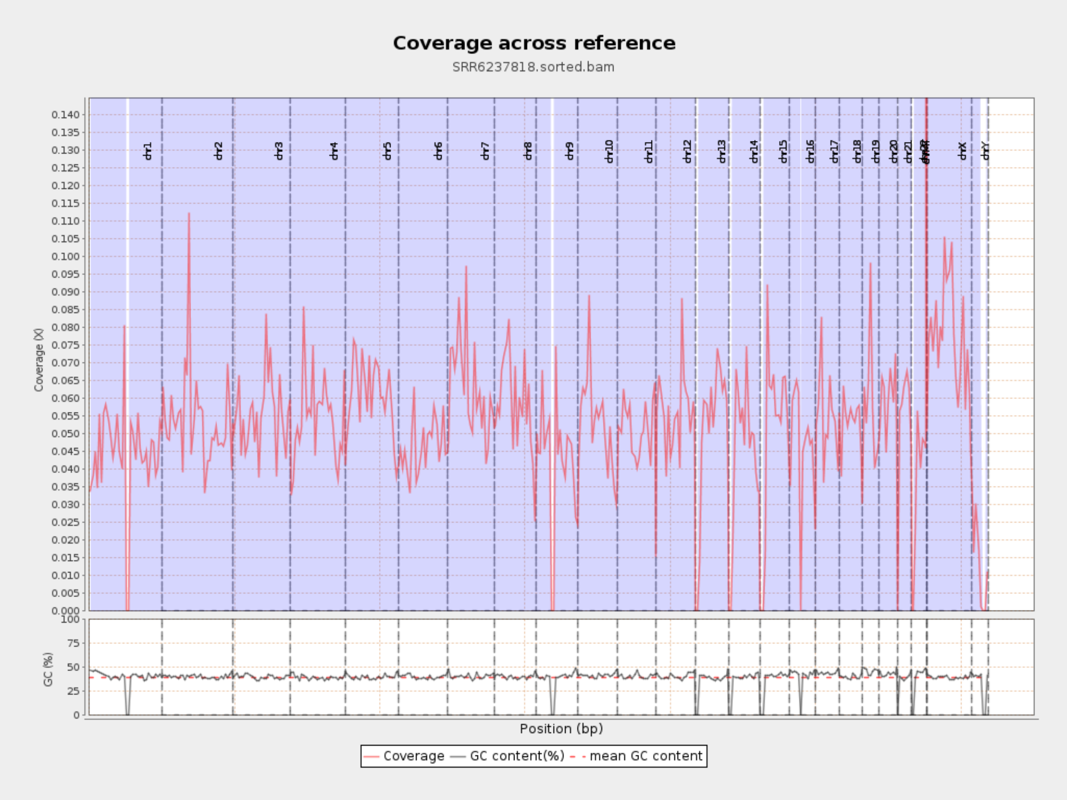
General error rate	0.86%
Mismatches	1,382,922
Insertions	13,670
Mapped reads with at least one insertion	0.58%
Deletions	38,139
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.21%

2.6. Chromosome stats

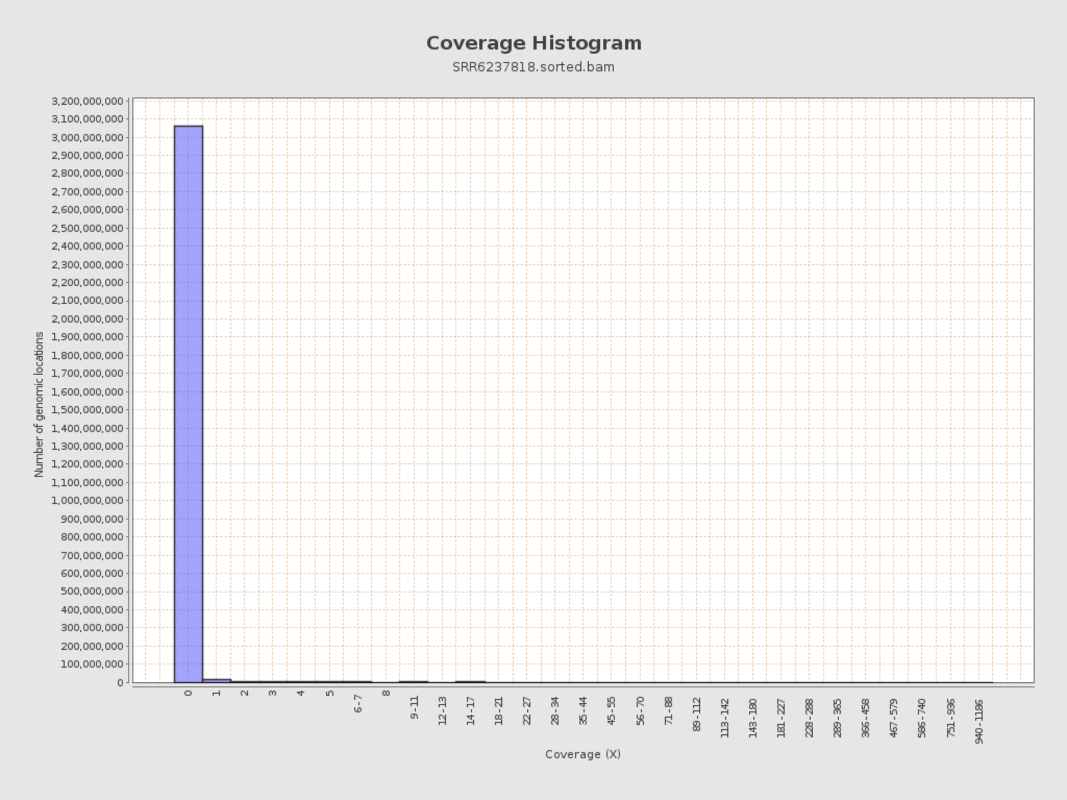
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11003168	0.0441	1.1534
chr2	243199373	13245312	0.0545	0.9004
chr3	198022430	10992072	0.0555	0.8067
chr4	191154276	10352677	0.0542	0.7983
chr5	180915260	11004730	0.0608	0.8304
chr6	171115067	7948091	0.0464	0.7428
chr7	159138663	10085635	0.0634	1.0344

chr8	146364022	8559863	0.0585	0.9364
chr9	141213431	5993227	0.0424	0.7199
chr10	135534747	7249353	0.0535	0.8746
chr11	135006516	6936706	0.0514	0.7774
chr12	133851895	7548609	0.0564	0.8064
chr13	115169878	5753738	0.05	0.7548
chr14	107349540	4689232	0.0437	0.7172
chr15	102531392	5161108	0.0503	0.7532
chr16	90354753	4220812	0.0467	0.7304
chr17	81195210	4392510	0.0541	0.8091
chr18	78077248	4203547	0.0538	1.0326
chr19	59128983	3456323	0.0585	1.0049
chr20	63025520	3808699	0.0604	0.843
chr21	48129895	2617703	0.0544	0.7661
chr22	51304566	1759788	0.0343	0.5961
chrMT	16571	52572	3.1725	5.0133
chrX	155270560	11952616	0.077	0.9503
chrY	59373566	743007	0.0125	0.3451

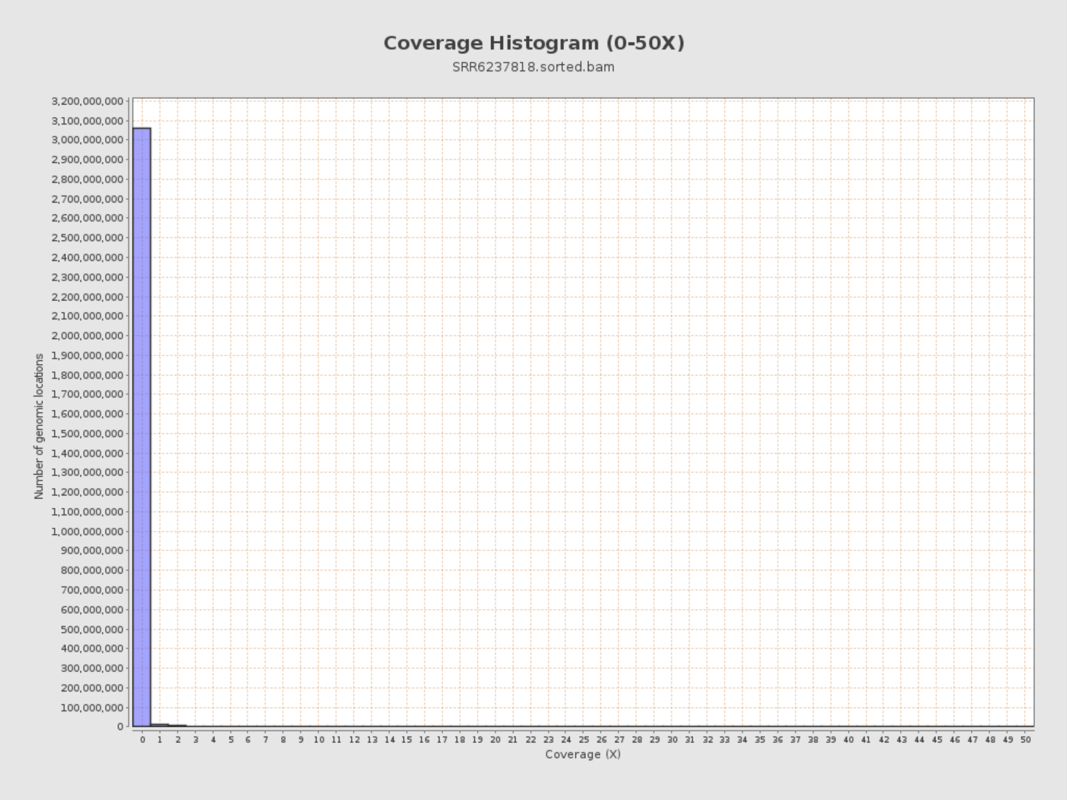
3. Results : Coverage across reference



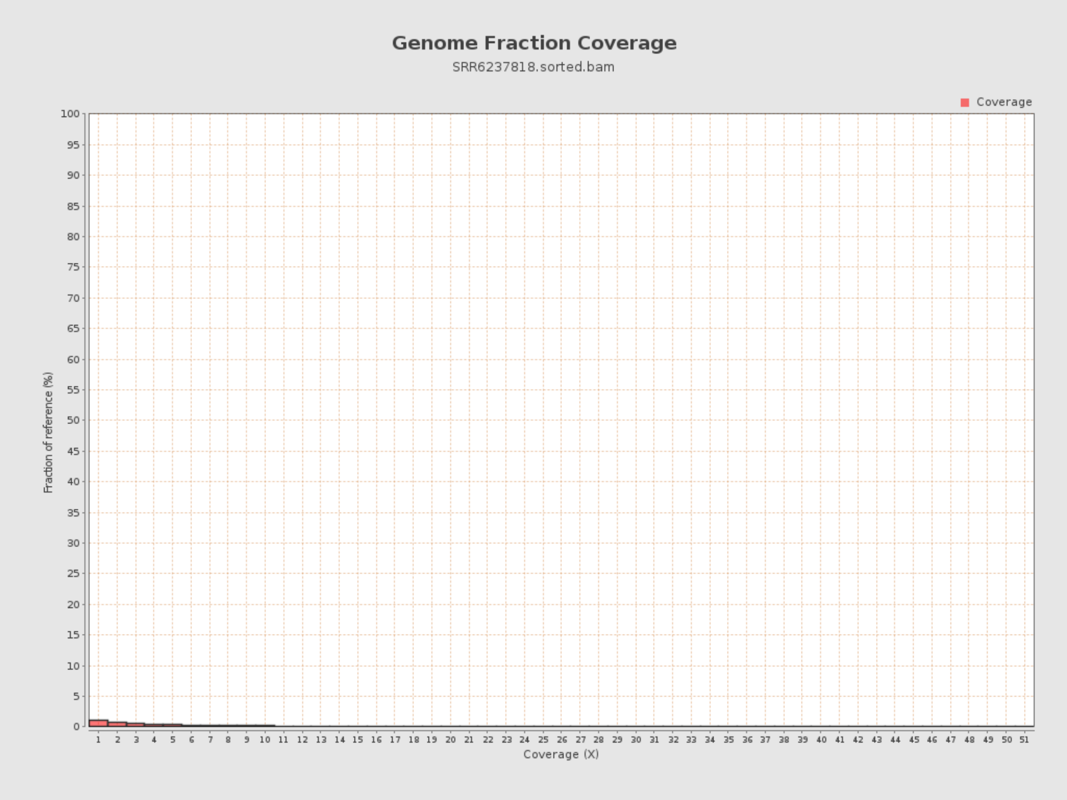
4. Results : Coverage Histogram



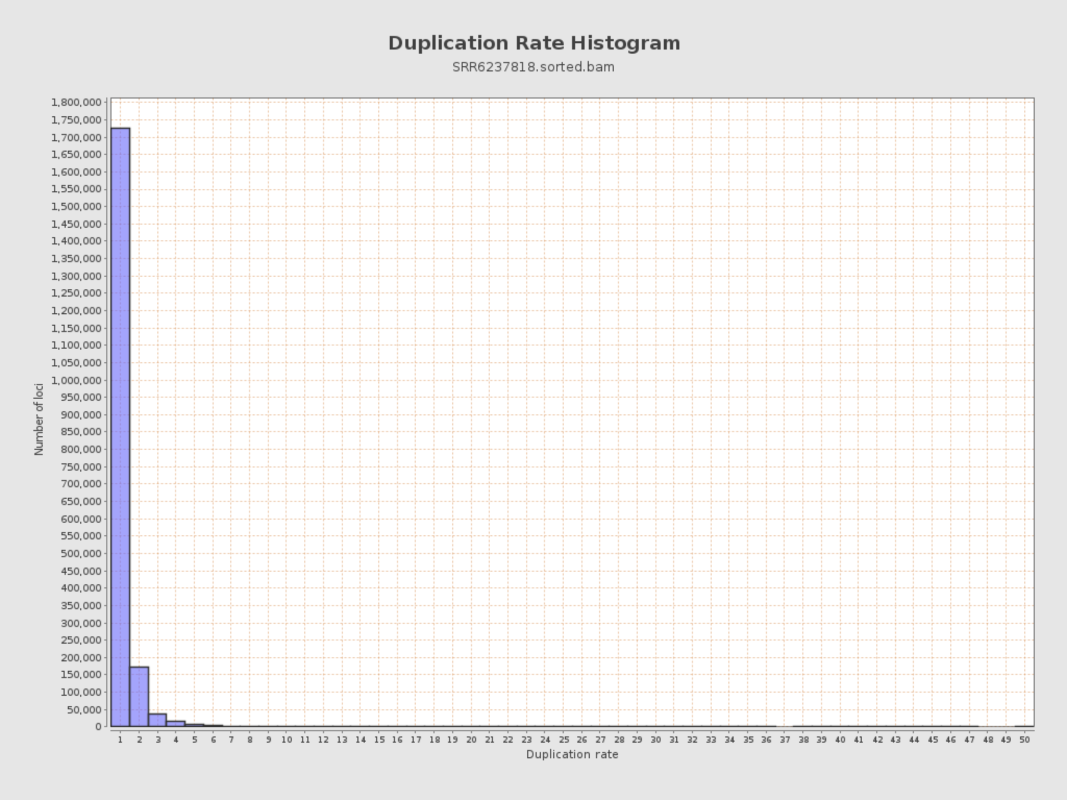
5. Results : Coverage Histogram (0-50X)



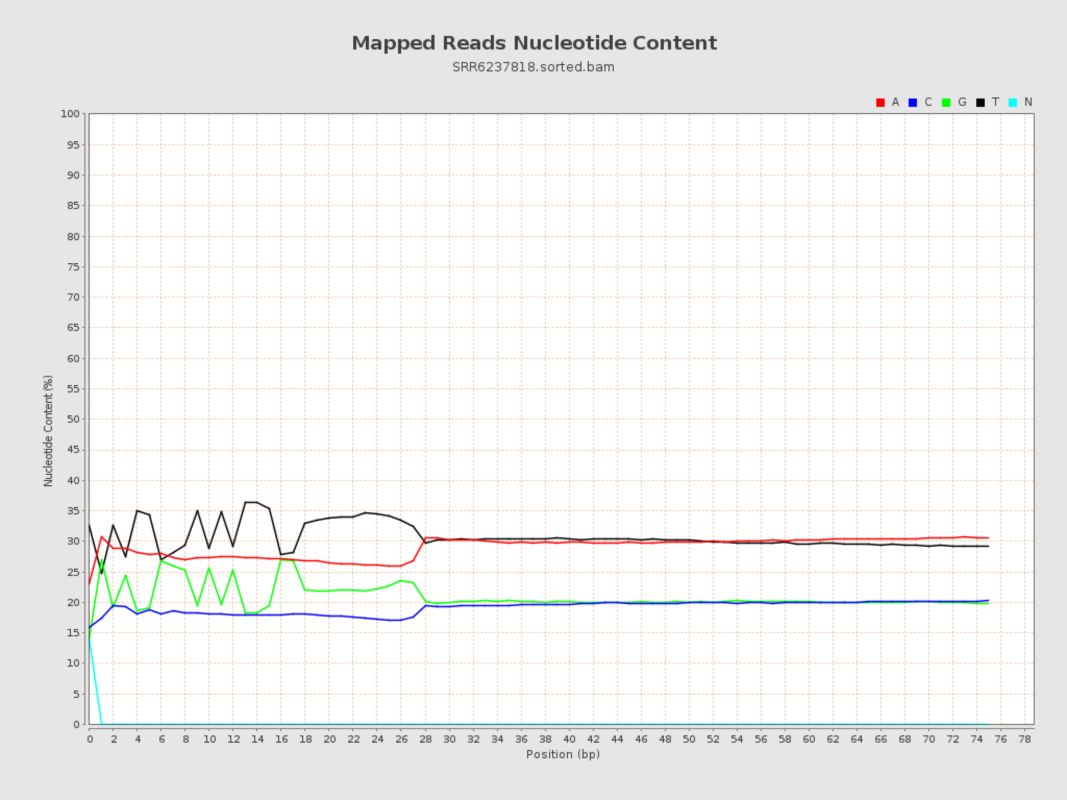
6. Results : Genome Fraction Coverage



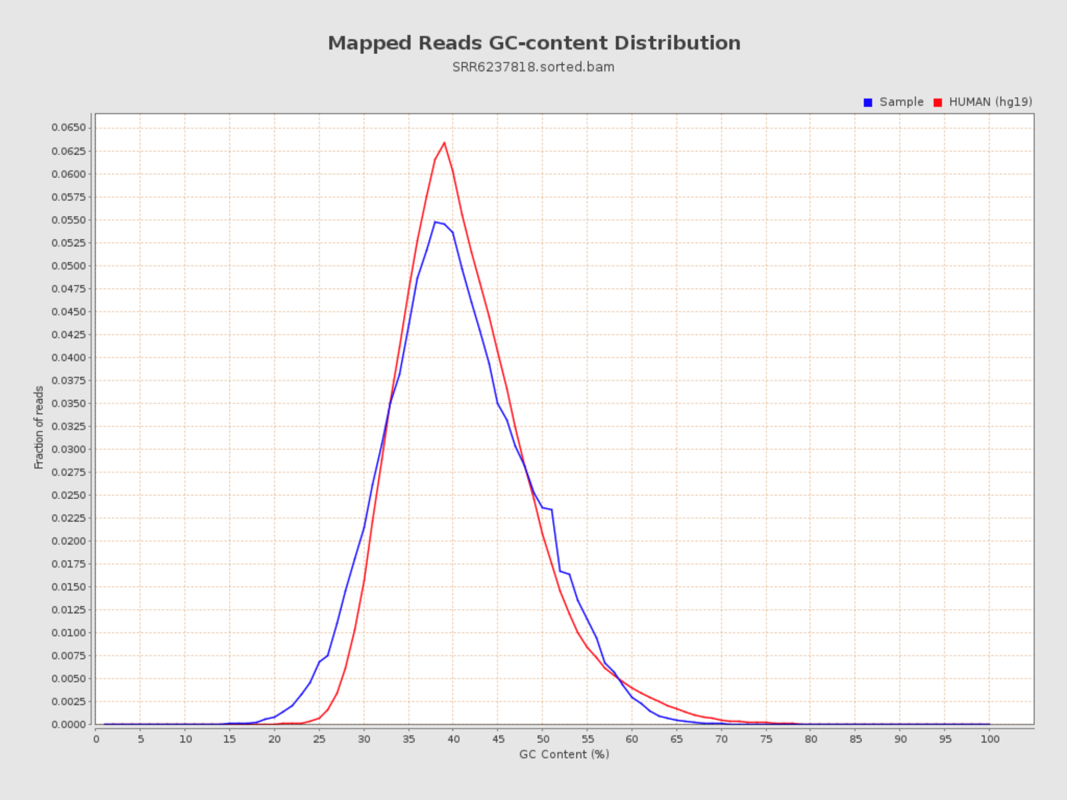
7. Results : Duplication Rate Histogram



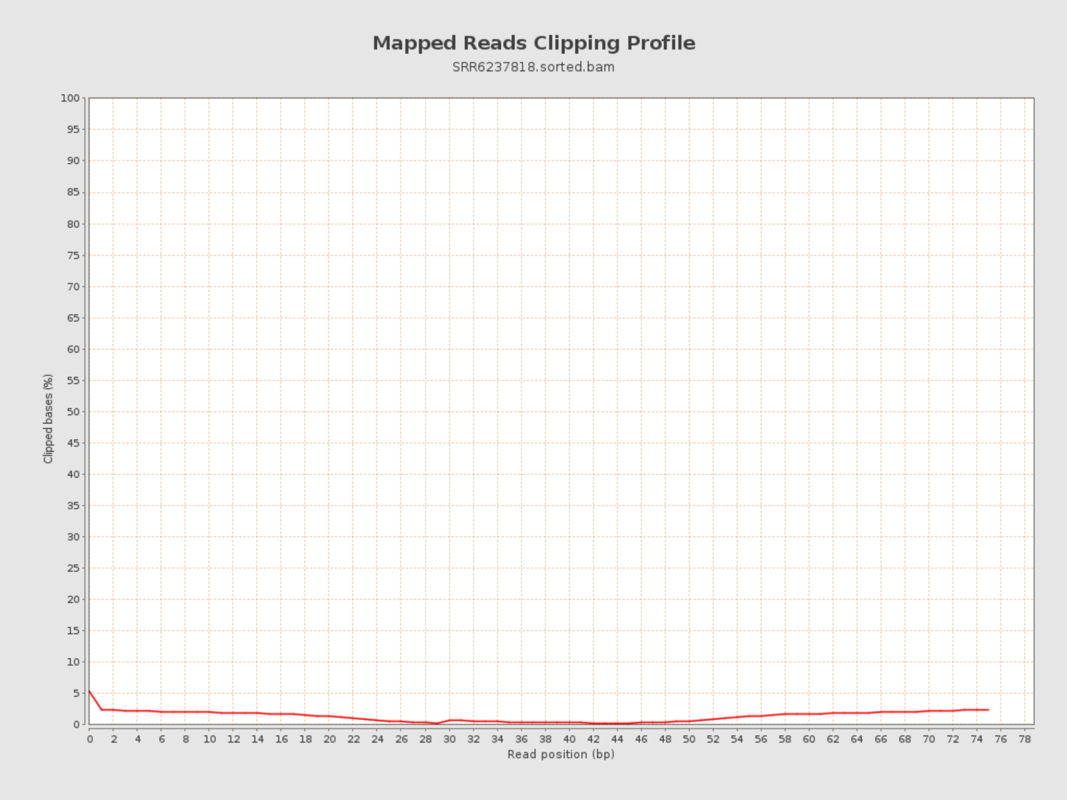
8. Results : Mapped Reads Nucleotide Content



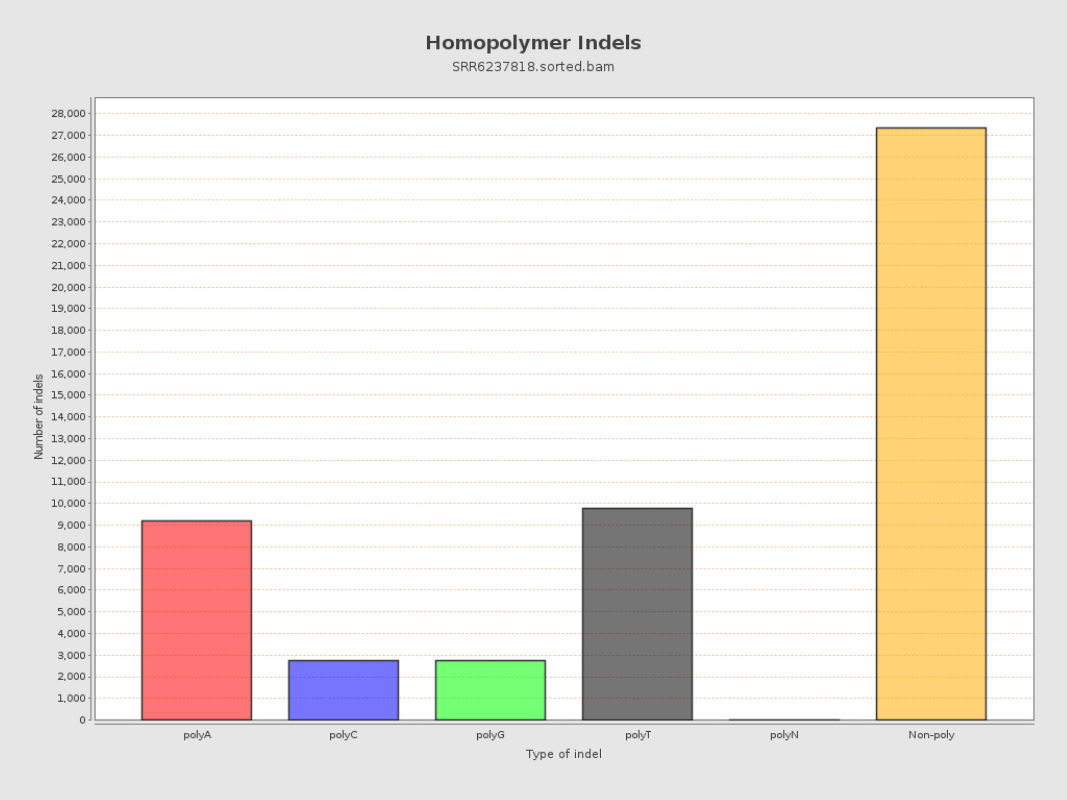
9. Results : Mapped Reads GC-content Distribution



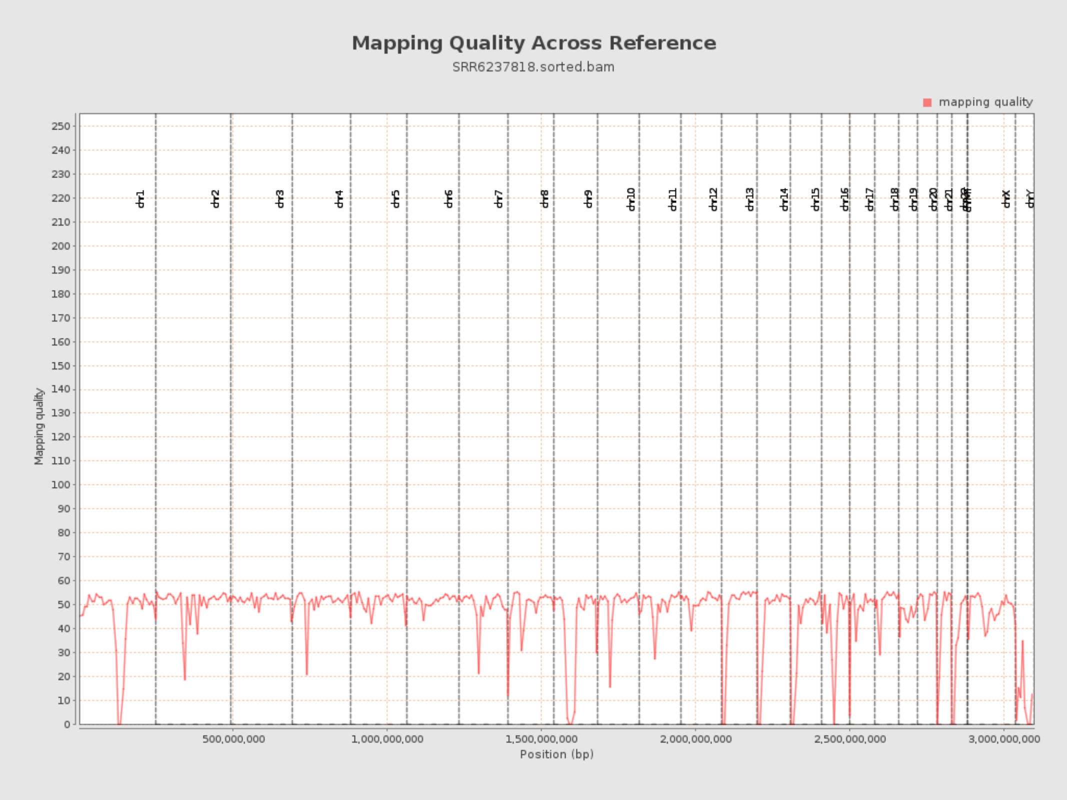
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram