Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:53:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237313.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_SRR6237313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237313.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:53:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,415,371
Mapped reads	2,182,173 / 90.35%
Unmapped reads	233,198 / 9.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,537 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	87,759 / 3.63%
Duplication rate	2.73%
Clipped reads	855,470 / 35.42%

2.2. ACGT Content

Number/percentage of A's	42,128,131 / 28.39%
Number/percentage of C's	27,305,887 / 18.4%
Number/percentage of T's	46,641,318 / 31.43%
Number/percentage of G's	32,297,929 / 21.77%
Number/percentage of N's	2,637 / 0%
GC Percentage	40.17%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.4784

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

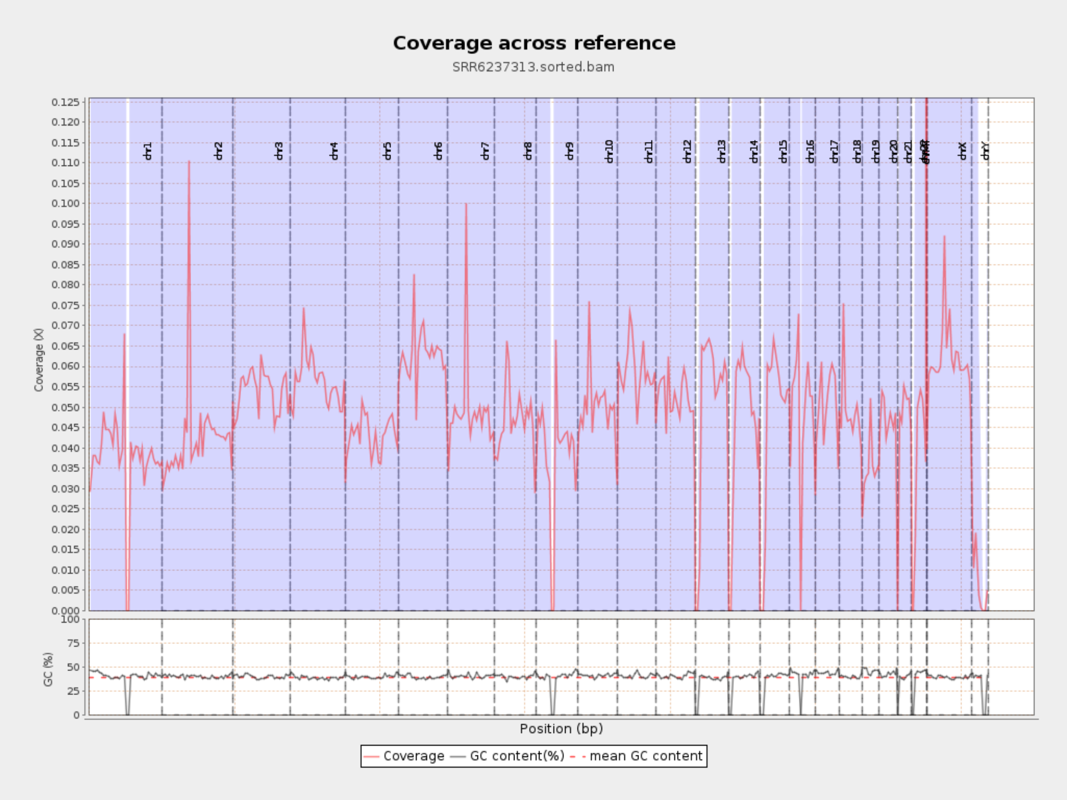
General error rate	0.77%
Mismatches	1,121,440
Insertions	11,388
Mapped reads with at least one insertion	0.52%
Deletions	32,012
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.88%

2.6. Chromosome stats

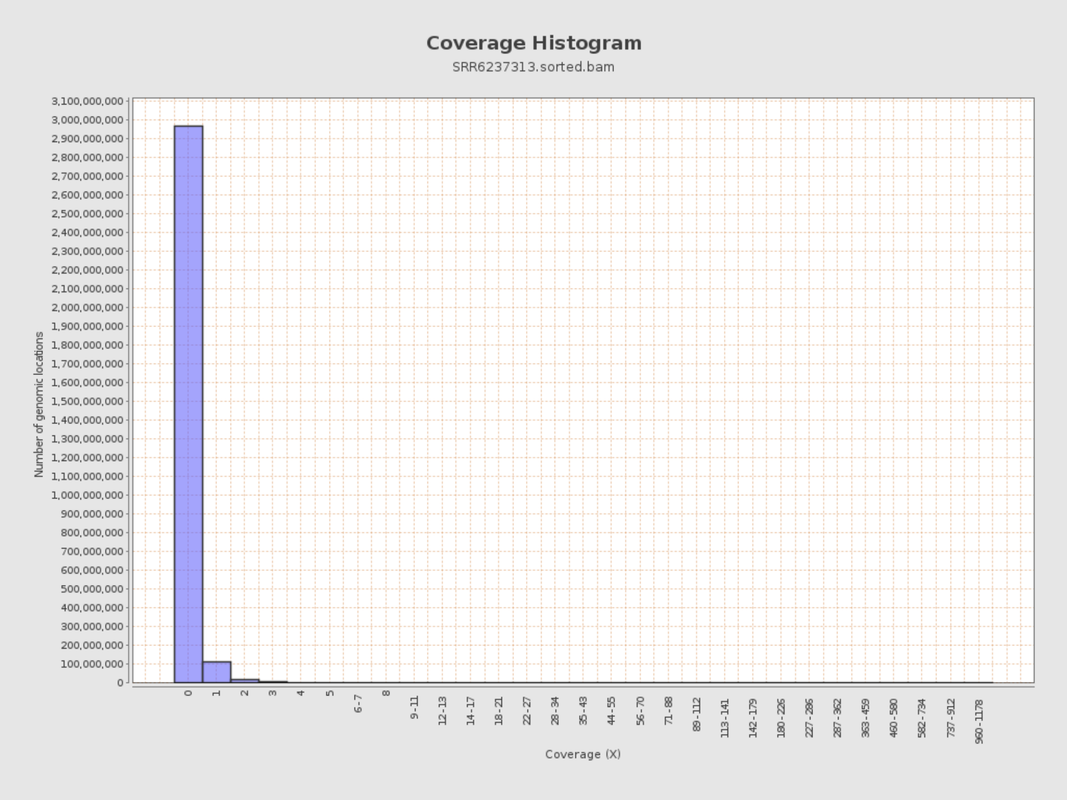
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9364047	0.0376	0.6705
chr2	243199373	10380940	0.0427	0.5651
chr3	198022430	10696075	0.054	0.2608
chr4	191154276	10791081	0.0565	0.2911
chr5	180915260	7810623	0.0432	0.2351
chr6	171115067	10717930	0.0626	0.3973
chr7	159138663	7868423	0.0494	0.7528

chr8	146364022	6825291	0.0466	0.7896
chr9	141213431	5400585	0.0382	0.4963
chr10	135534747	6838970	0.0505	0.3916
chr11	135006516	7911489	0.0586	0.5715
chr12	133851895	7013823	0.0524	0.2651
chr13	115169878	5793188	0.0503	0.2528
chr14	107349540	4868764	0.0454	0.2746
chr15	102531392	4752284	0.0463	0.2577
chr16	90354753	4436440	0.0491	0.2965
chr17	81195210	4103971	0.0505	0.3201
chr18	78077248	3865698	0.0495	1.0059
chr19	59128983	2100733	0.0355	0.4962
chr20	63025520	2930831	0.0465	0.2697
chr21	48129895	2178345	0.0453	0.2678
chr22	51304566	1760727	0.0343	0.2054
chrMT	16571	10161	0.6132	0.855
chrX	155270560	9614185	0.0619	0.3381
chrY	59373566	397247	0.0067	0.1458

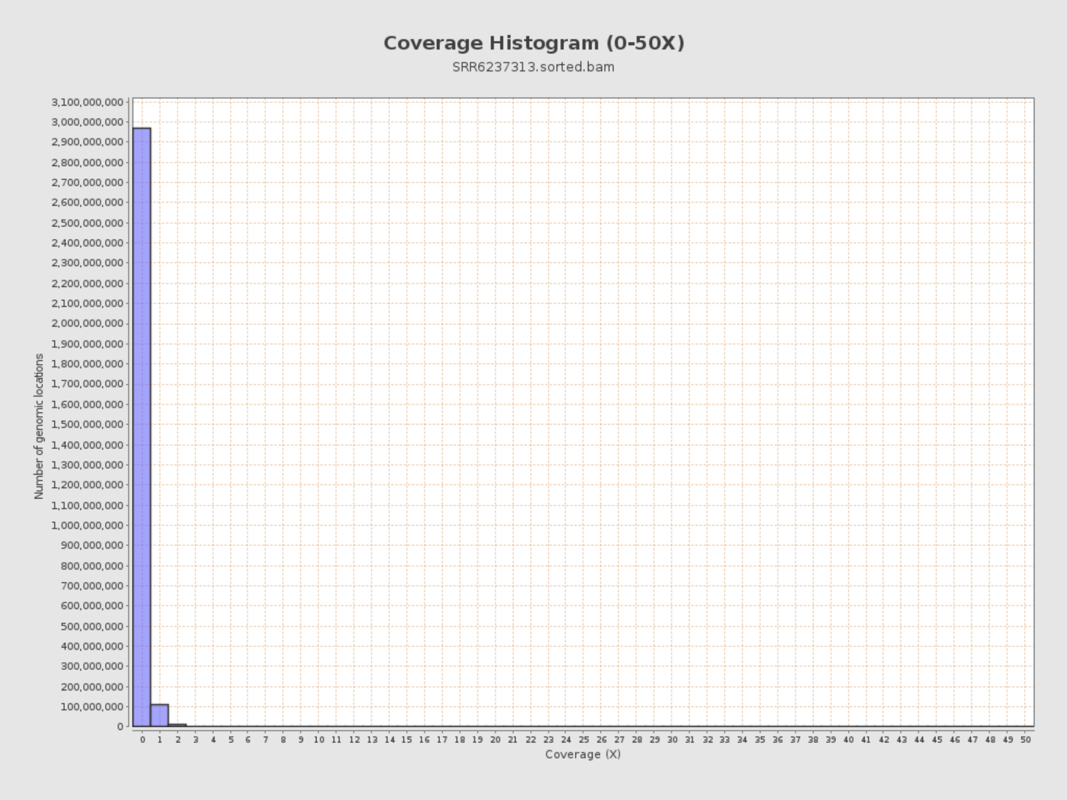
3. Results : Coverage across reference



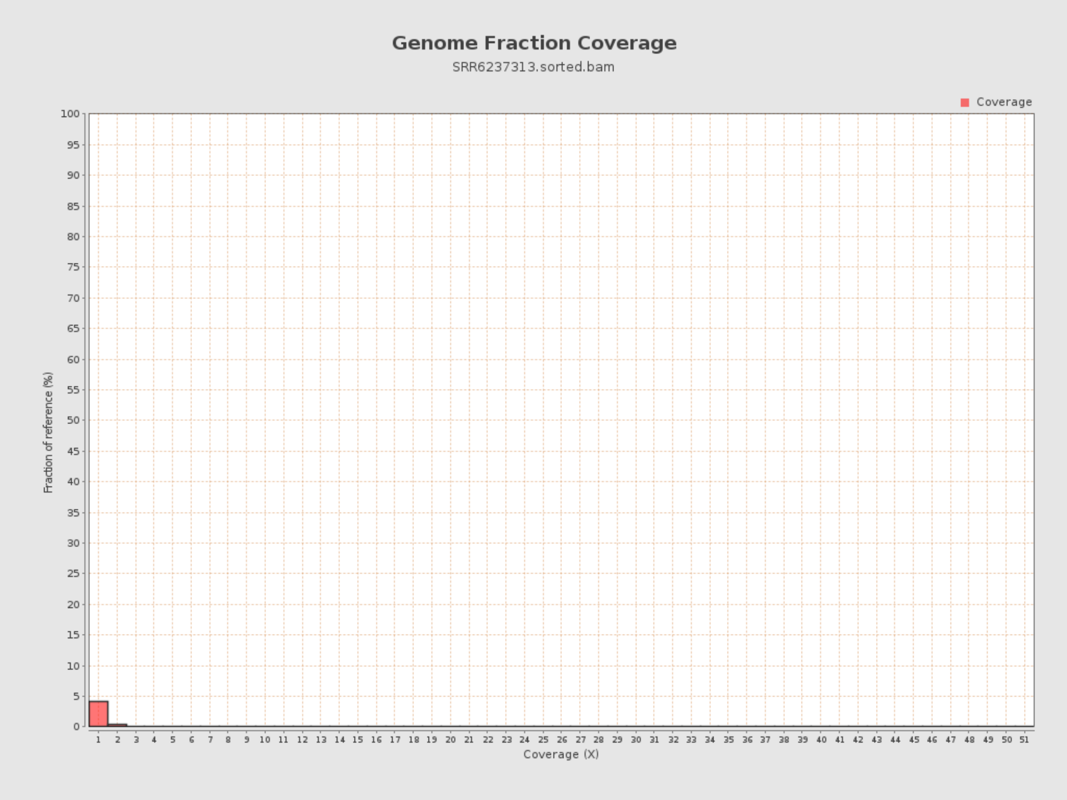
4. Results : Coverage Histogram



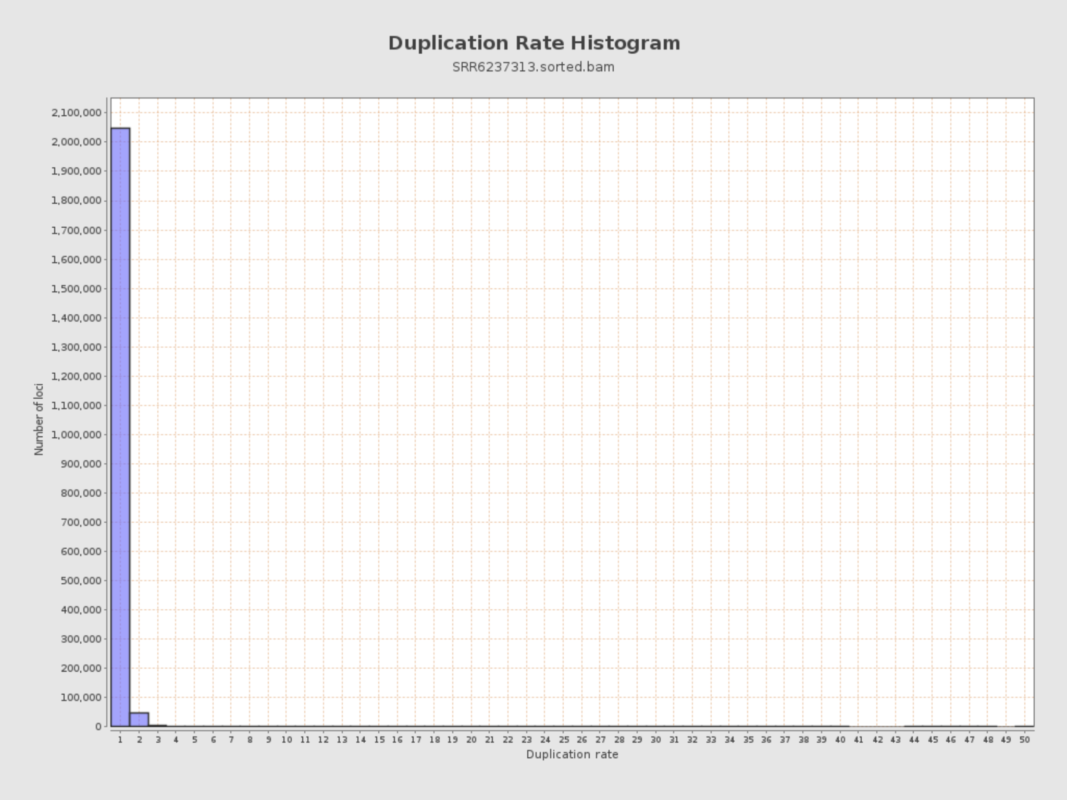
5. Results : Coverage Histogram (0-50X)



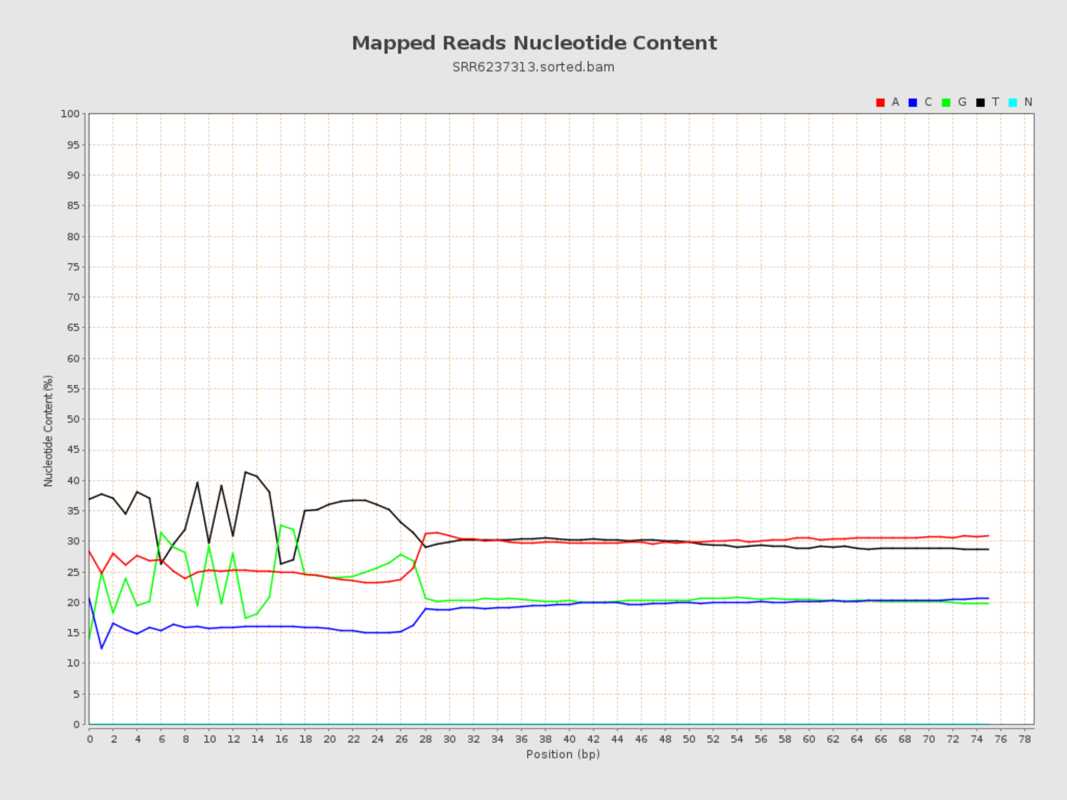
6. Results : Genome Fraction Coverage



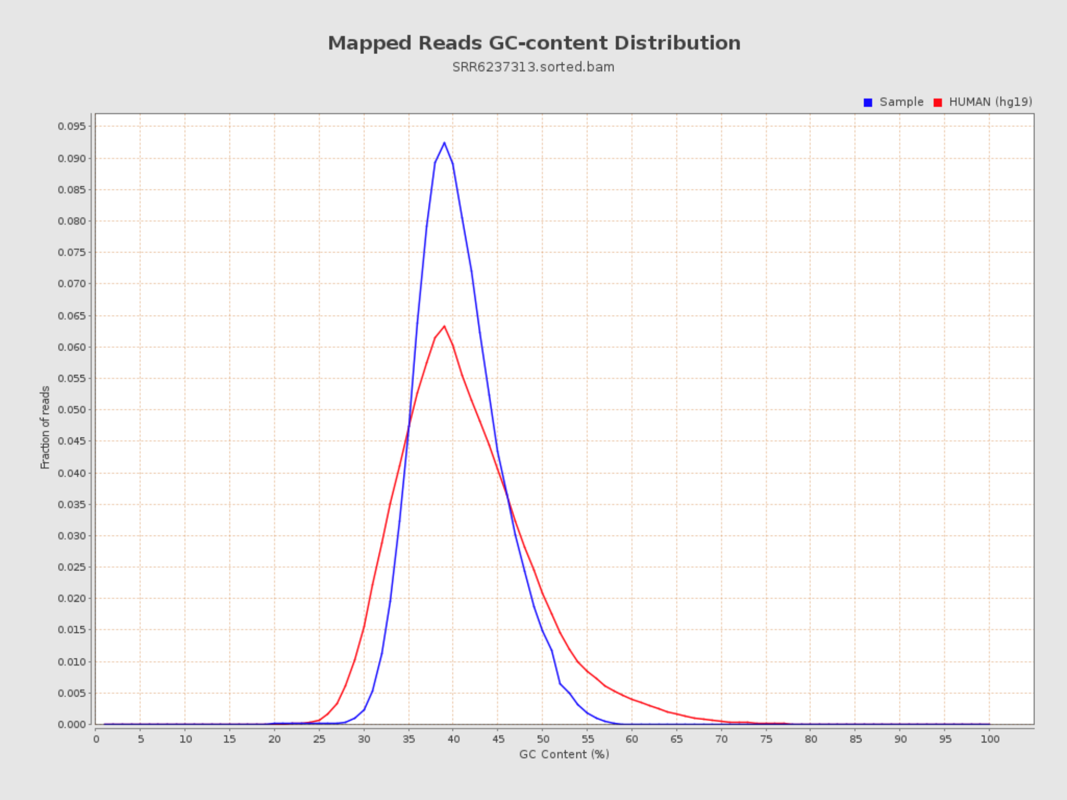
7. Results : Duplication Rate Histogram



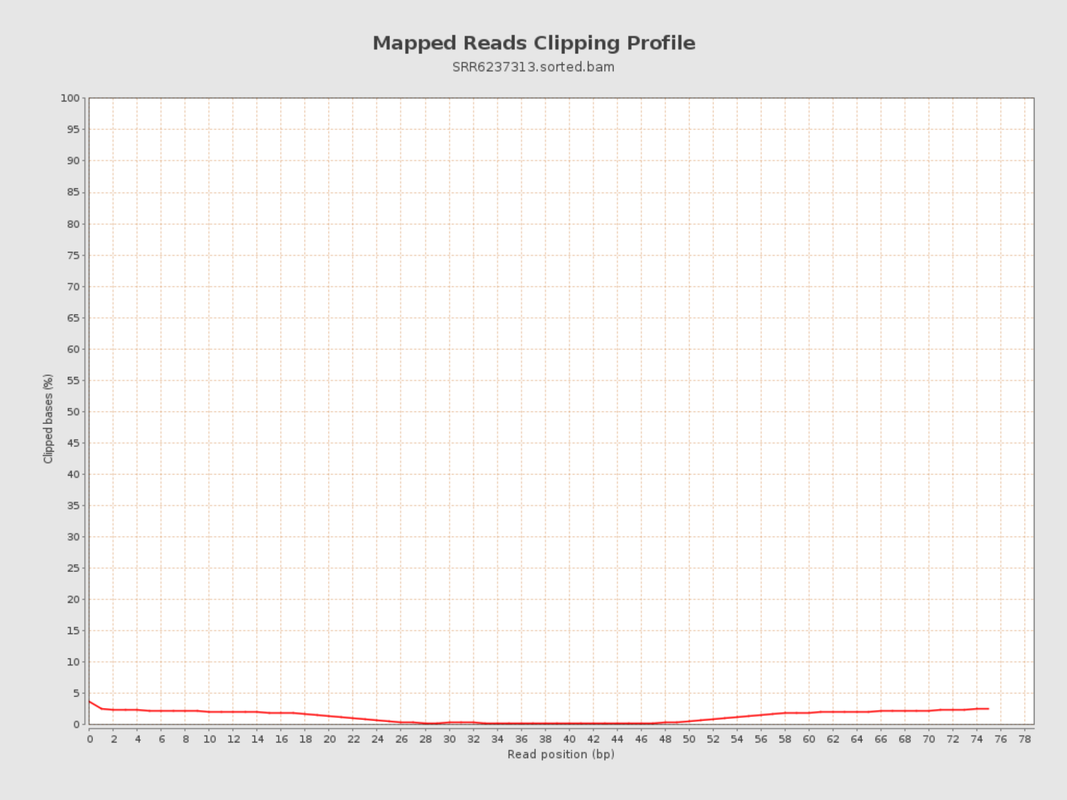
8. Results : Mapped Reads Nucleotide Content



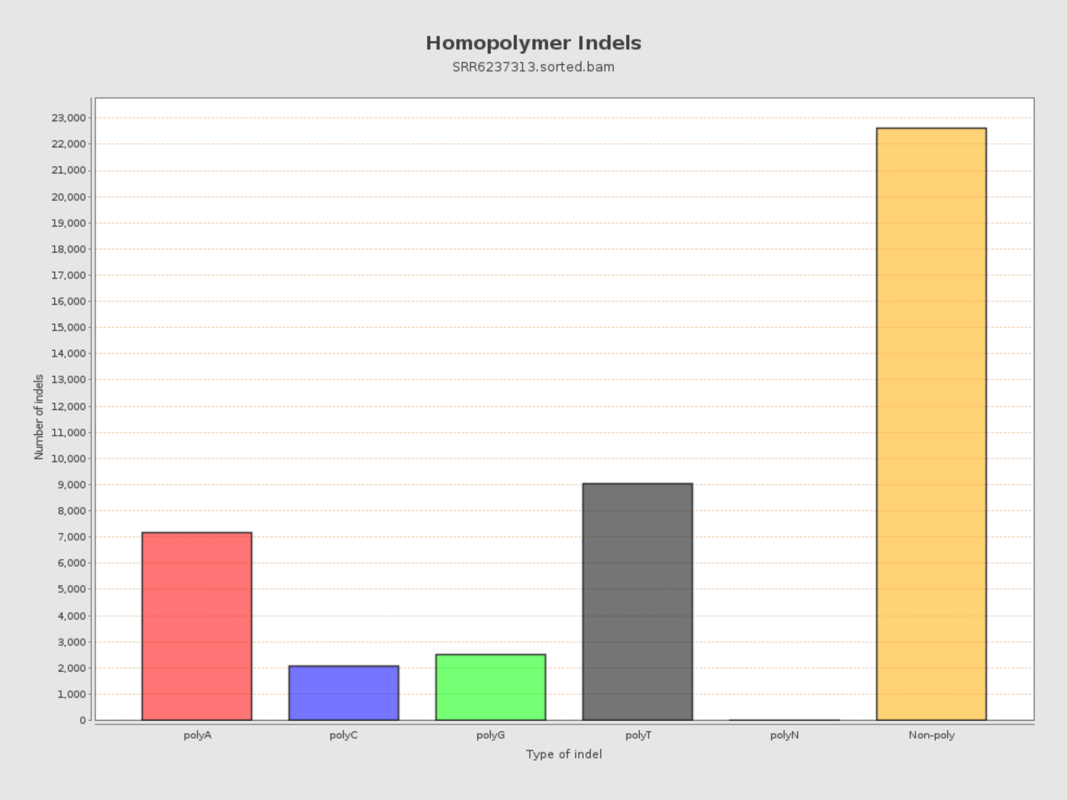
9. Results : Mapped Reads GC-content Distribution



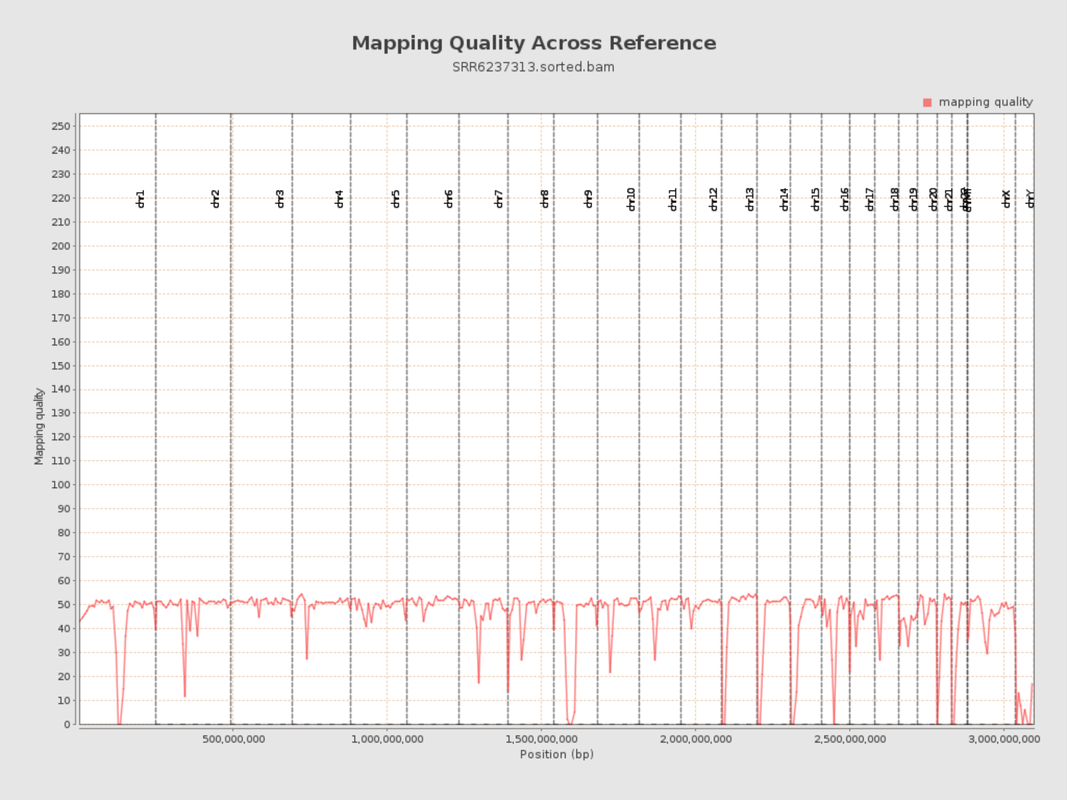
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram