Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:08:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237834.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_SRR6237834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237834.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:08:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237834.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,775,833
Mapped reads	2,180,493 / 78.55%
Unmapped reads	595,340 / 21.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,626 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	197,983 / 7.13%
Duplication rate	7.29%
Clipped reads	1,185,479 / 42.71%

2.2. ACGT Content

Number/percentage of A's	38,836,038 / 27.86%
Number/percentage of C's	25,259,904 / 18.12%
Number/percentage of T's	44,469,204 / 31.9%
Number/percentage of G's	30,728,032 / 22.04%
Number/percentage of N's	109,401 / 0.08%
GC Percentage	40.16%

2.3. Coverage

Mean	0.0451

Standard Deviation	0.4039

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

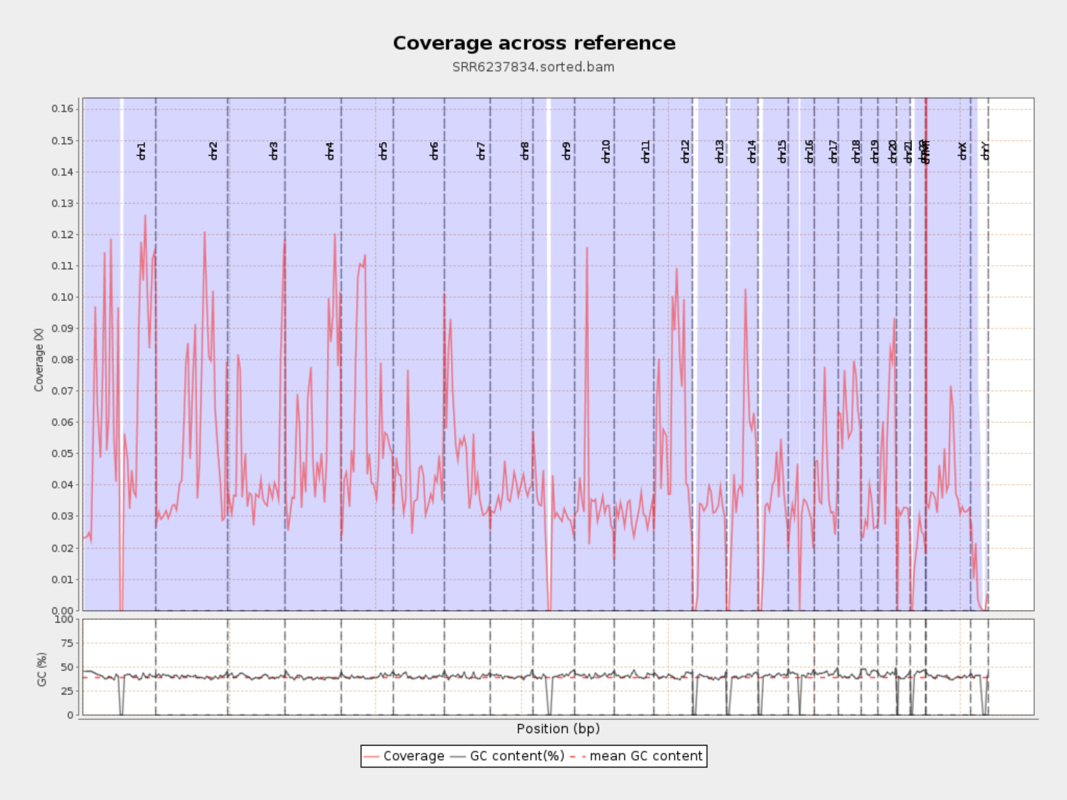
General error rate	0.83%
Mismatches	1,138,997
Insertions	11,706
Mapped reads with at least one insertion	0.53%
Deletions	42,526
Mapped reads with at least one deletion	1.93%
Homopolymer indels	48.32%

2.6. Chromosome stats

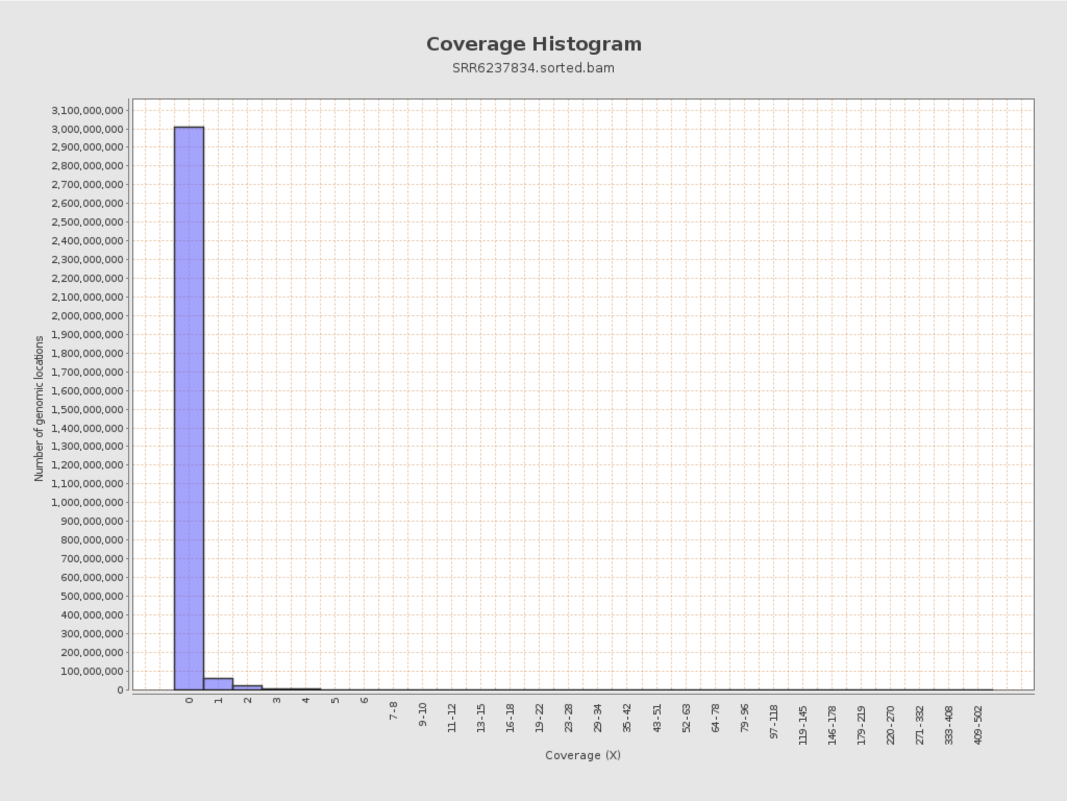
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16295383	0.0654	0.543
chr2	243199373	13390913	0.0551	0.4362
chr3	198022430	9004136	0.0455	0.335
chr4	191154276	11022316	0.0577	0.3705
chr5	180915260	10622475	0.0587	0.3569
chr6	171115067	7024628	0.0411	0.3324
chr7	159138663	8109091	0.051	0.4144

chr8	146364022	5546785	0.0379	0.3847
chr9	141213431	4174906	0.0296	0.3398
chr10	135534747	5039947	0.0372	0.7647
chr11	135006516	4137251	0.0306	0.3172
chr12	133851895	8292870	0.062	0.3676
chr13	115169878	3241033	0.0281	0.25
chr14	107349540	4907729	0.0457	0.324
chr15	102531392	3192112	0.0311	0.2625
chr16	90354753	2599696	0.0288	0.2804
chr17	81195210	3365856	0.0415	0.3068
chr18	78077248	5042948	0.0646	0.7105
chr19	59128983	1739805	0.0294	0.3534
chr20	63025520	3820451	0.0606	0.3653
chr21	48129895	1362032	0.0283	0.2657
chr22	51304566	924429	0.018	0.1904
chrMT	16571	38013	2.2939	2.7311
chrX	155270560	6115941	0.0394	0.3151
chrY	59373566	460655	0.0078	0.1654

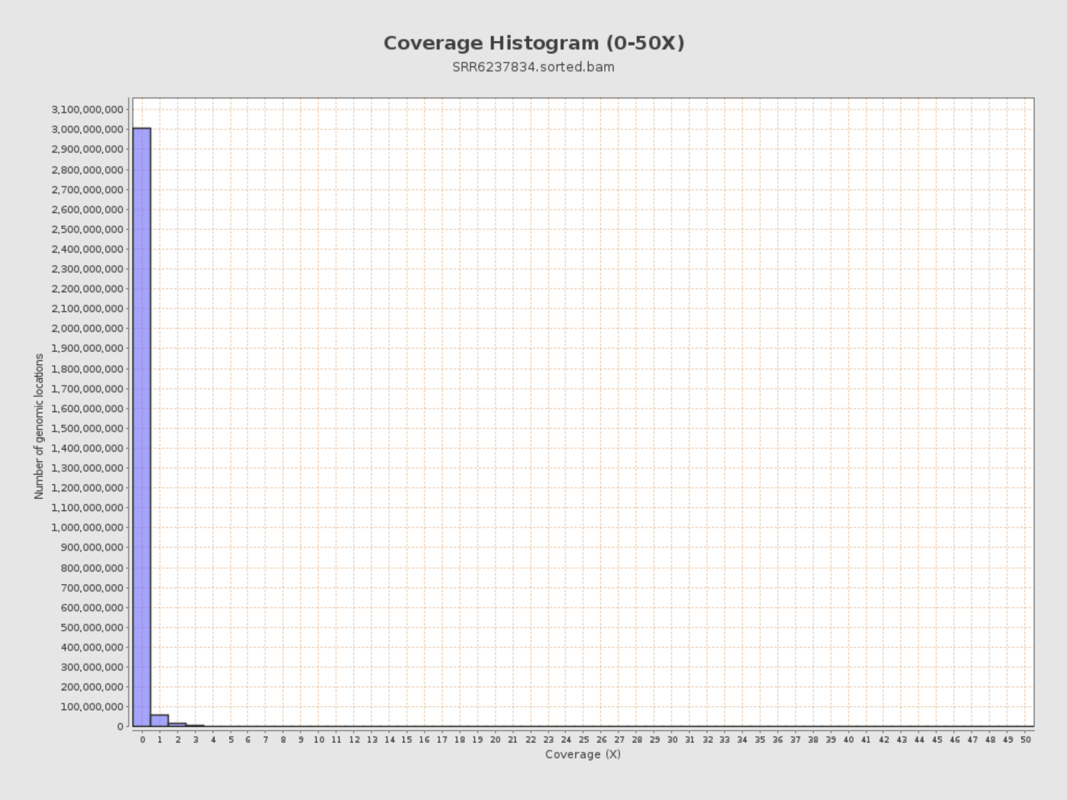
3. Results : Coverage across reference



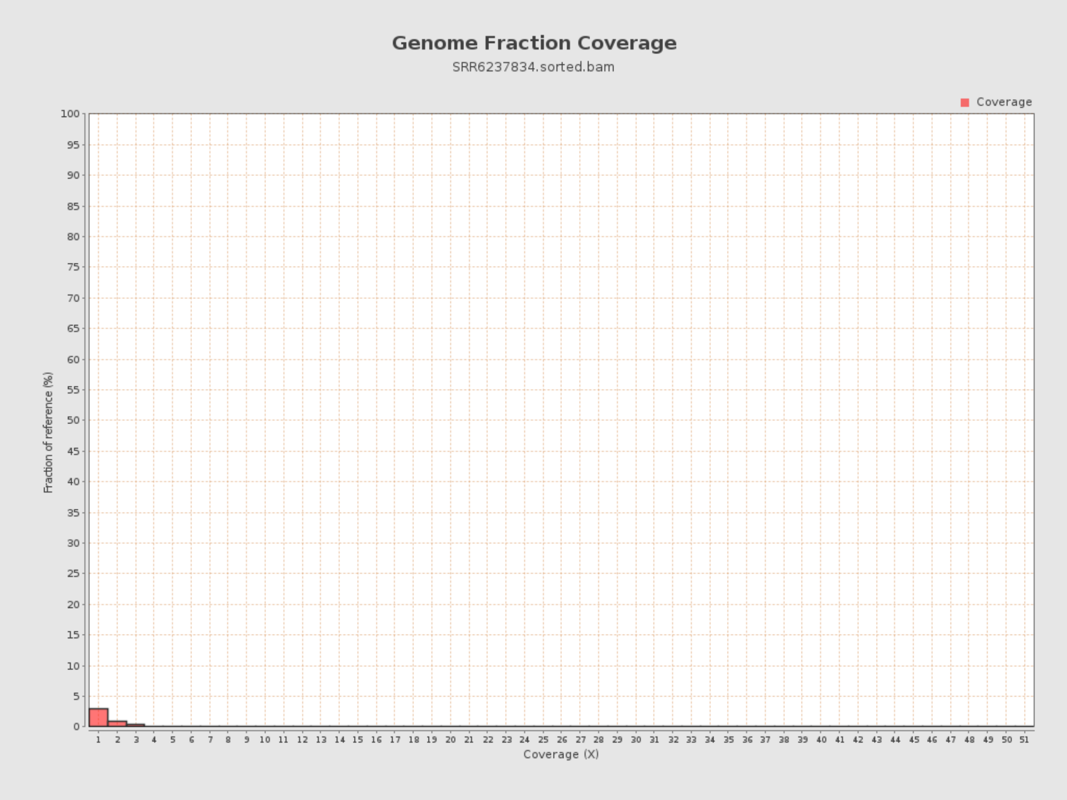
4. Results : Coverage Histogram



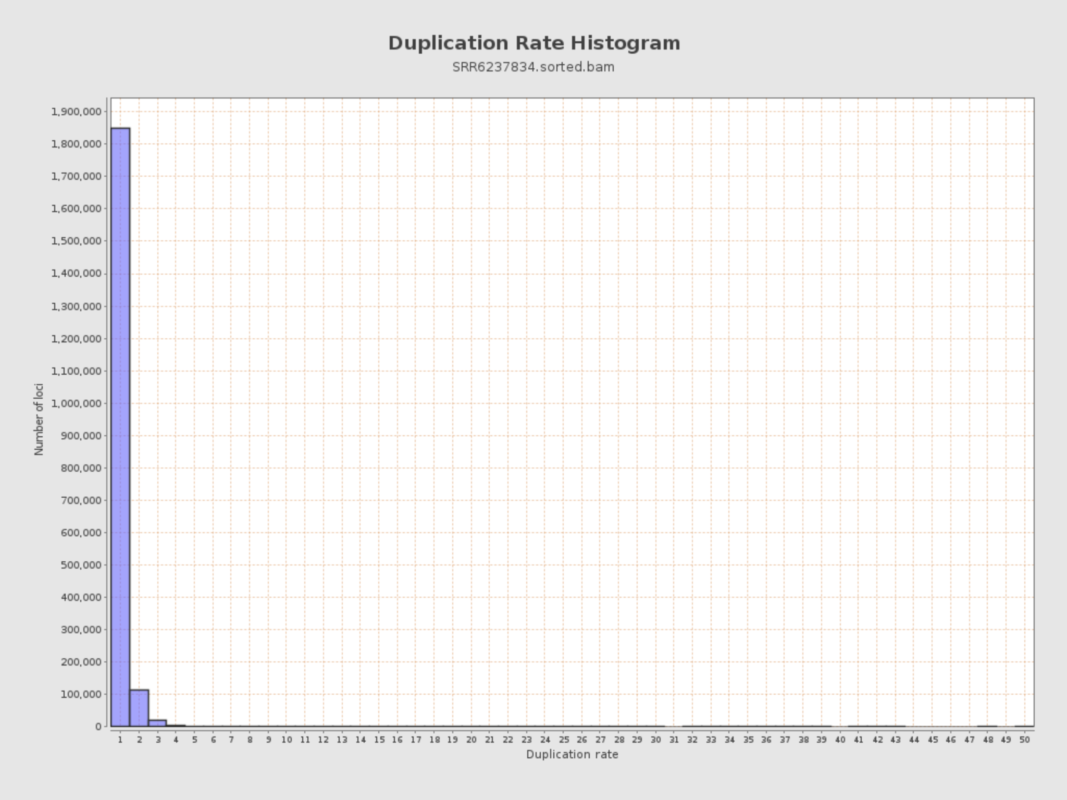
5. Results : Coverage Histogram (0-50X)



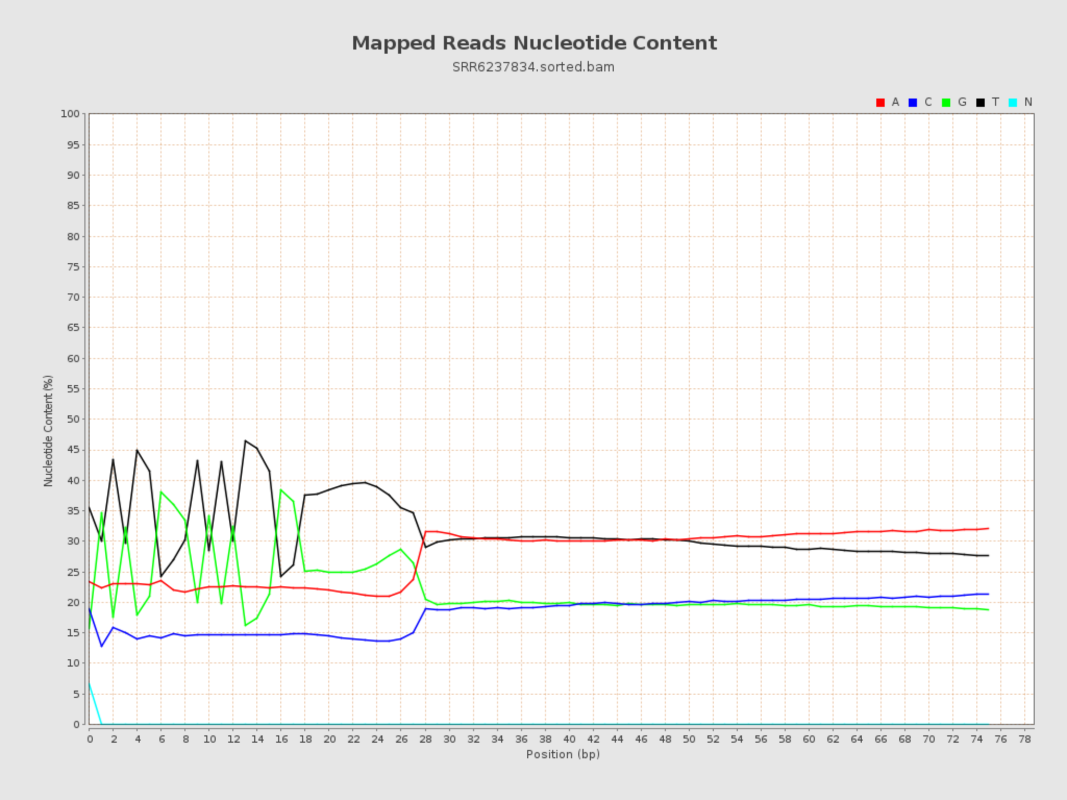
6. Results : Genome Fraction Coverage



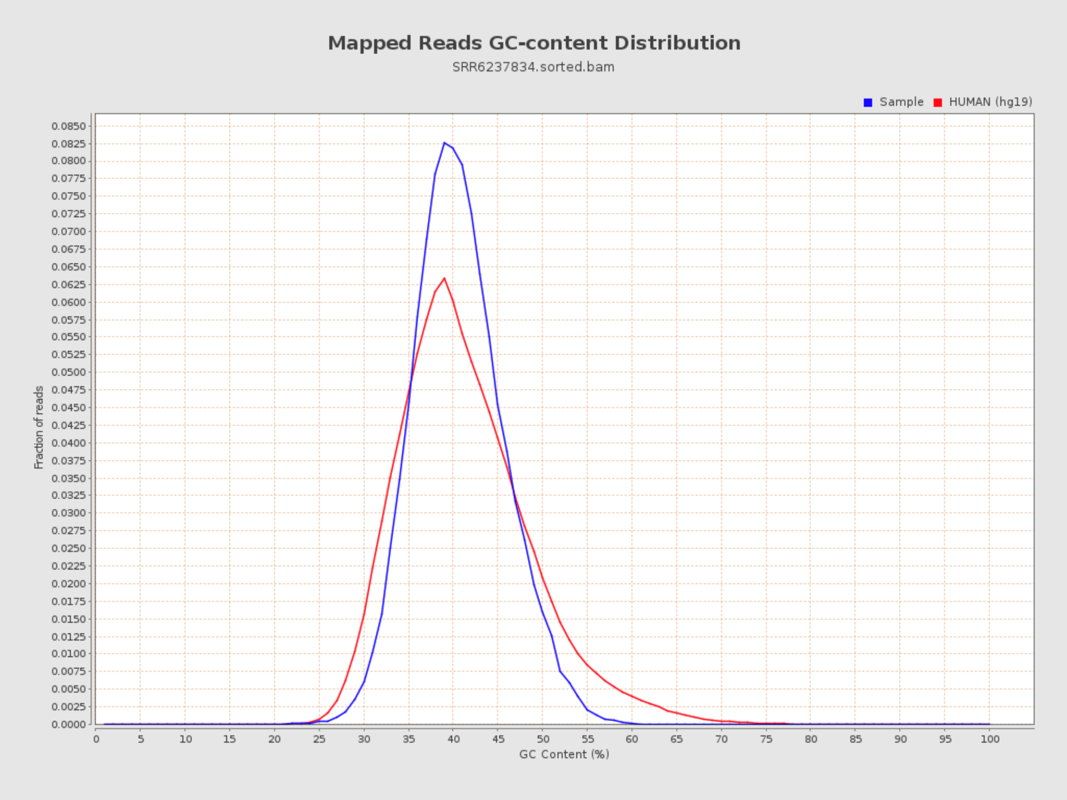
7. Results : Duplication Rate Histogram



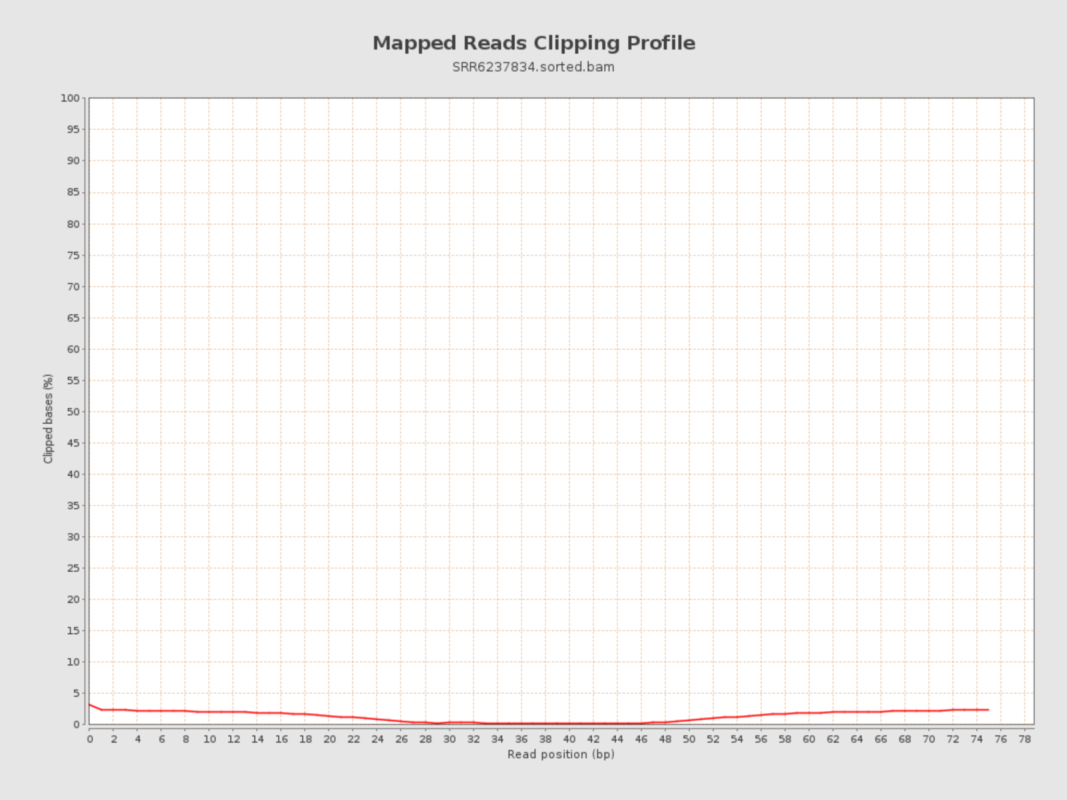
8. Results : Mapped Reads Nucleotide Content



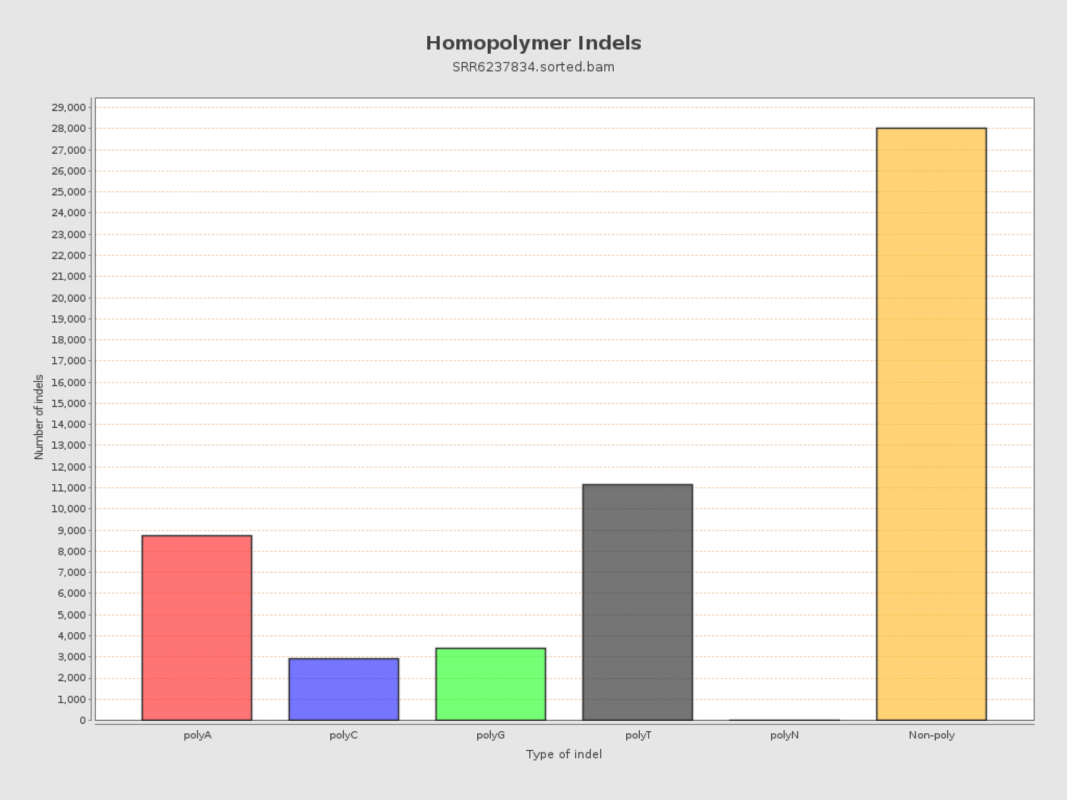
9. Results : Mapped Reads GC-content Distribution



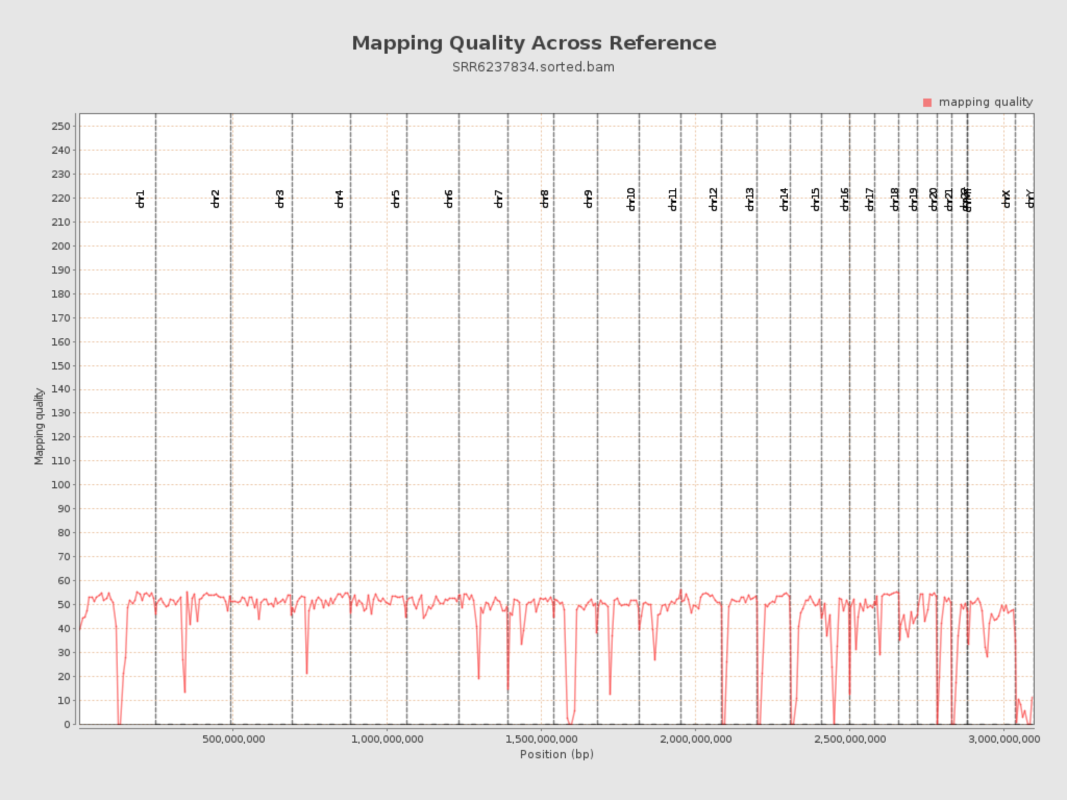
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram