Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 01:19:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237303.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_SRR6237303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237303.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 01:19:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,687,382
Mapped reads	1,964,804 / 73.11%
Unmapped reads	722,578 / 26.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,192 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	606,537 / 22.57%
Duplication rate	20.42%
Clipped reads	1,206,617 / 44.9%

2.2. ACGT Content

Number/percentage of A's	32,065,689 / 26.05%
Number/percentage of C's	21,446,536 / 17.42%
Number/percentage of T's	40,970,925 / 33.29%
Number/percentage of G's	28,582,965 / 23.22%
Number/percentage of N's	13,618 / 0.01%
GC Percentage	40.65%

2.3. Coverage

Mean	0.0398

Standard Deviation	0.6105

2.4. Mapping Quality

Mean Mapping Quality	41.14

2.5. Mismatches and indels

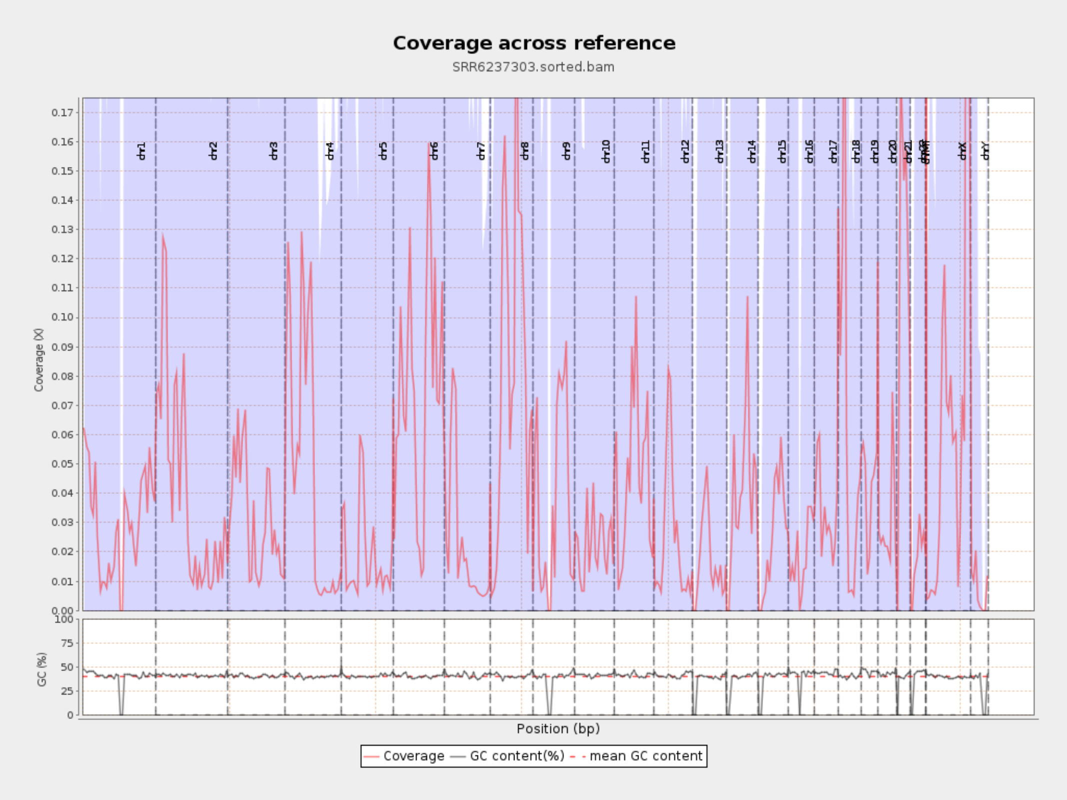
General error rate	0.61%
Mismatches	740,347
Insertions	8,469
Mapped reads with at least one insertion	0.43%
Deletions	34,026
Mapped reads with at least one deletion	1.71%
Homopolymer indels	42.45%

2.6. Chromosome stats

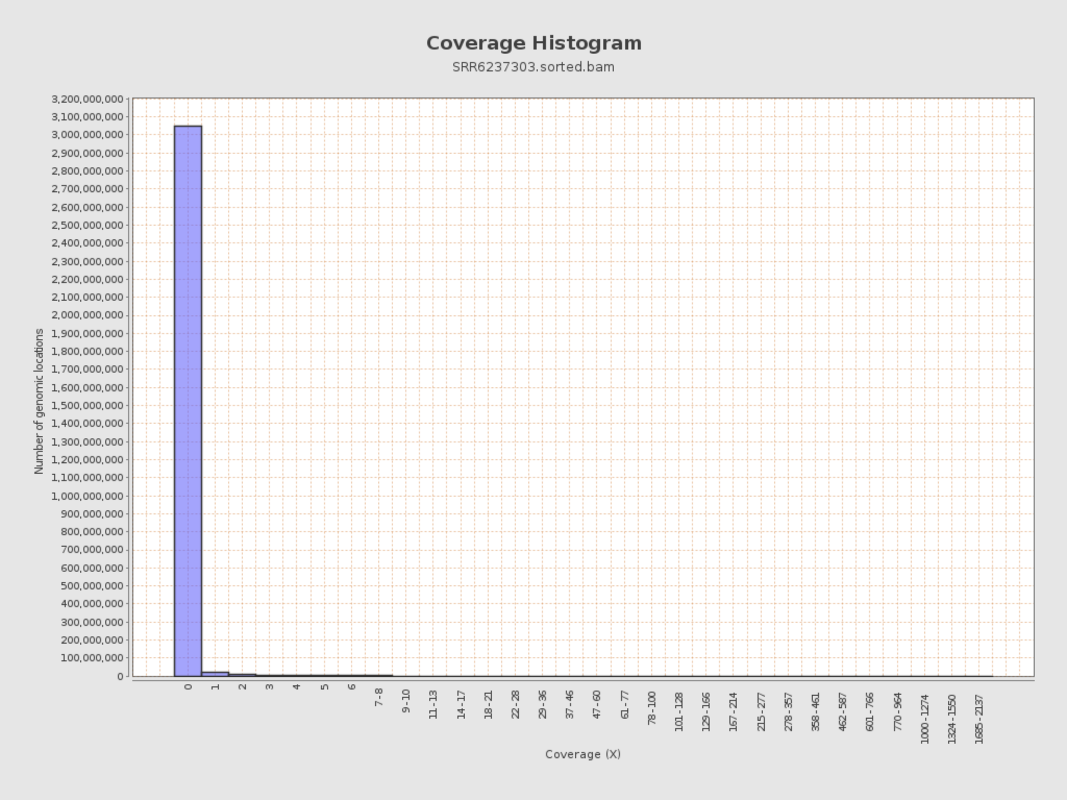
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7489815	0.03	0.4113
chr2	243199373	9714658	0.0399	0.9322
chr3	198022430	6260474	0.0316	0.3733
chr4	191154276	9341191	0.0489	0.4829
chr5	180915260	3447962	0.0191	0.2842
chr6	171115067	13042829	0.0762	0.7883
chr7	159138663	3444439	0.0216	0.3531

chr8	146364022	12340457	0.0843	1.521
chr9	141213431	5363858	0.038	0.5218
chr10	135534747	3035398	0.0224	0.4064
chr11	135006516	6272260	0.0465	0.5094
chr12	133851895	3279429	0.0245	0.346
chr13	115169878	1943869	0.0169	0.2855
chr14	107349540	4470947	0.0416	0.429
chr15	102531392	2580881	0.0252	0.3426
chr16	90354753	1662316	0.0184	0.2877
chr17	81195210	2722805	0.0335	0.4125
chr18	78077248	5329040	0.0683	0.8824
chr19	59128983	2586249	0.0437	0.5434
chr20	63025520	1970574	0.0313	0.3842
chr21	48129895	5513469	0.1146	0.7297
chr22	51304566	905908	0.0177	0.2669
chrMT	16571	46709	2.8187	4.1037
chrX	155270560	9938832	0.064	0.5869
chrY	59373566	433979	0.0073	0.1894

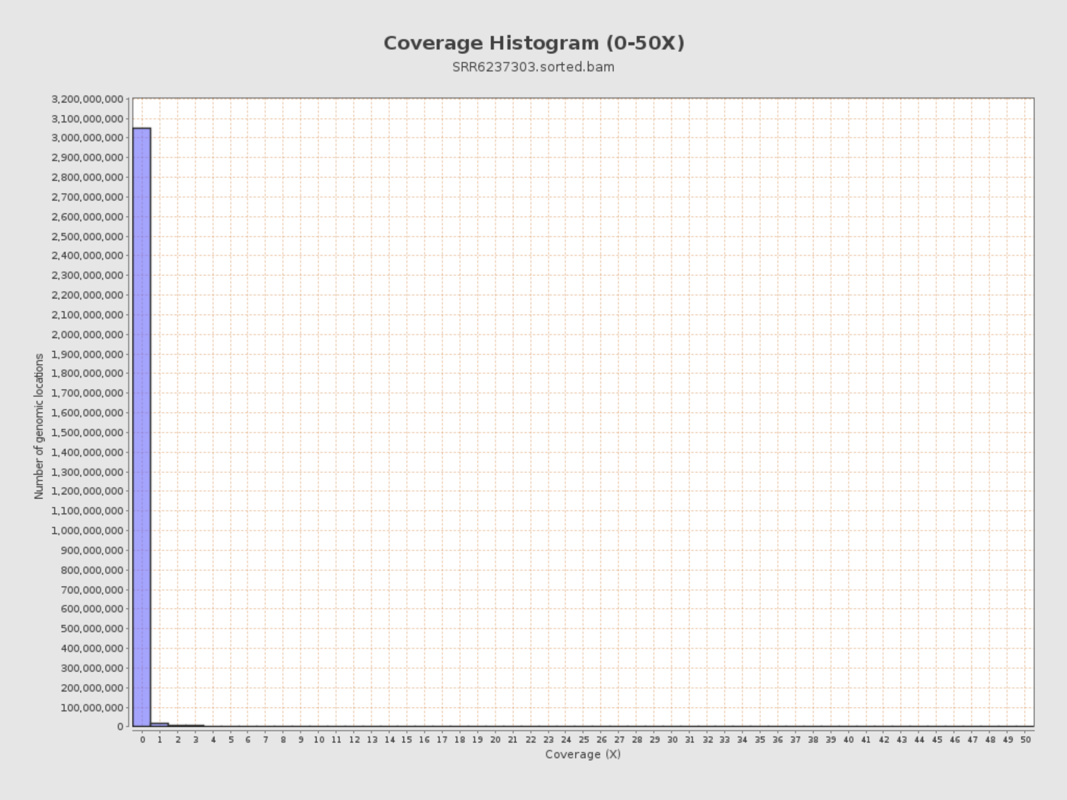
3. Results : Coverage across reference



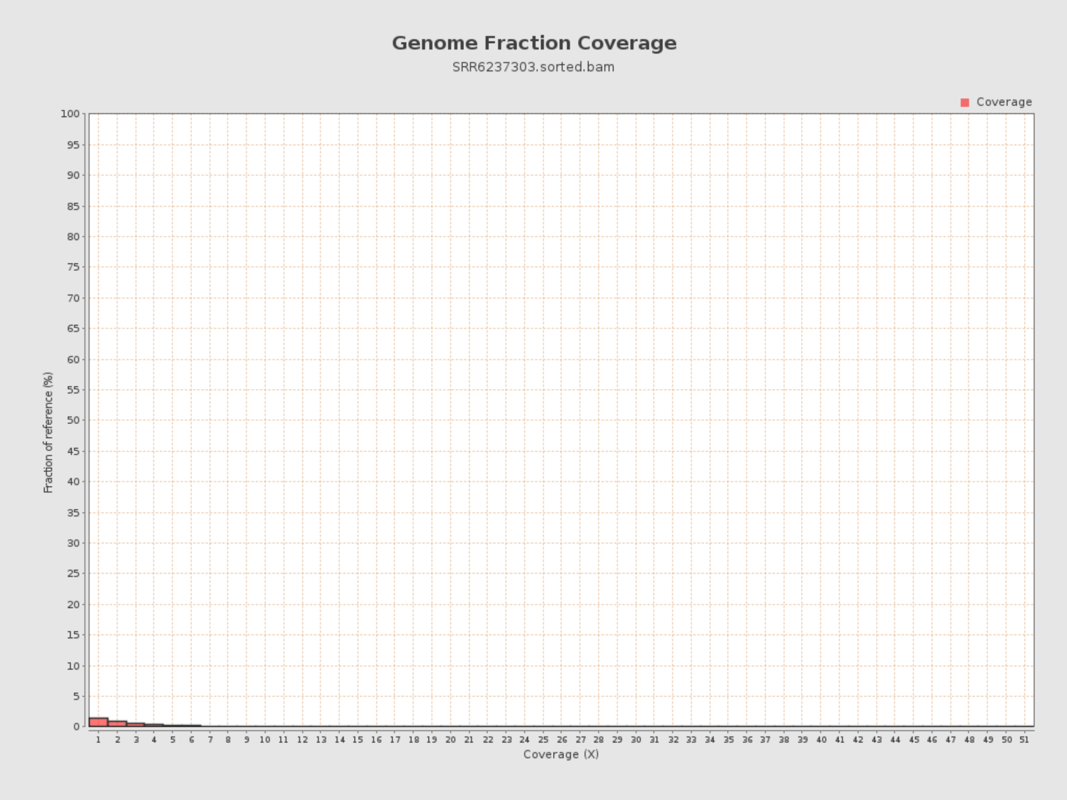
4. Results : Coverage Histogram



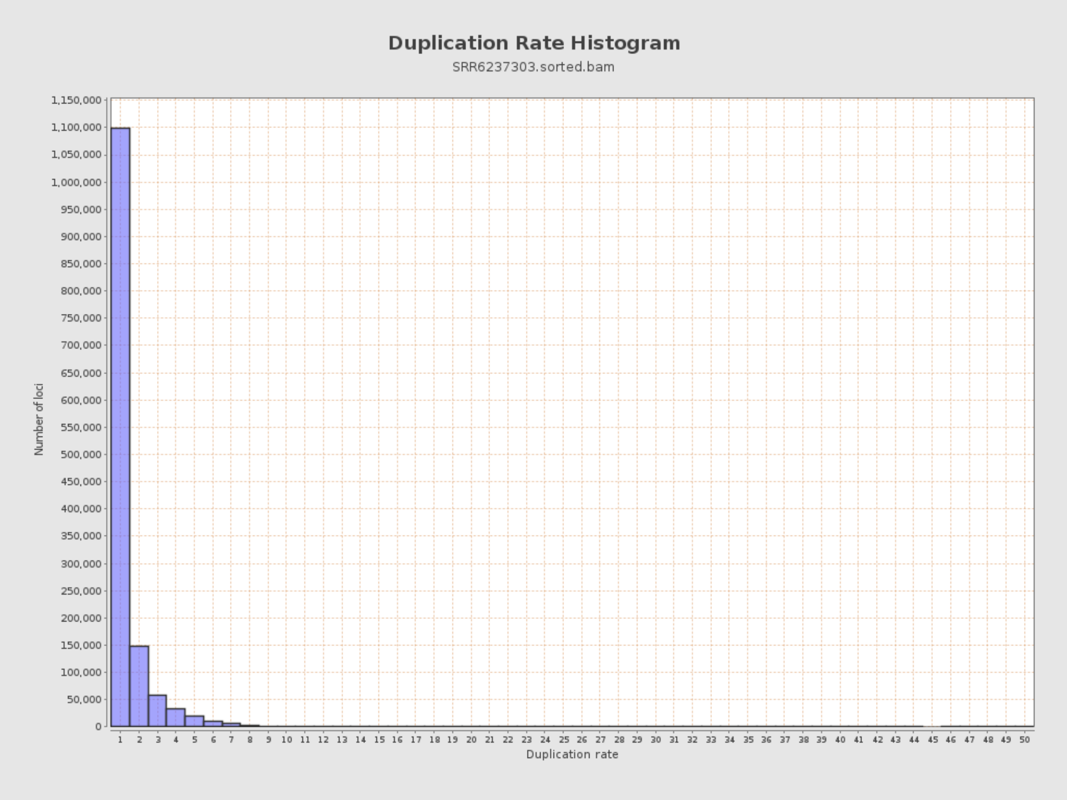
5. Results : Coverage Histogram (0-50X)



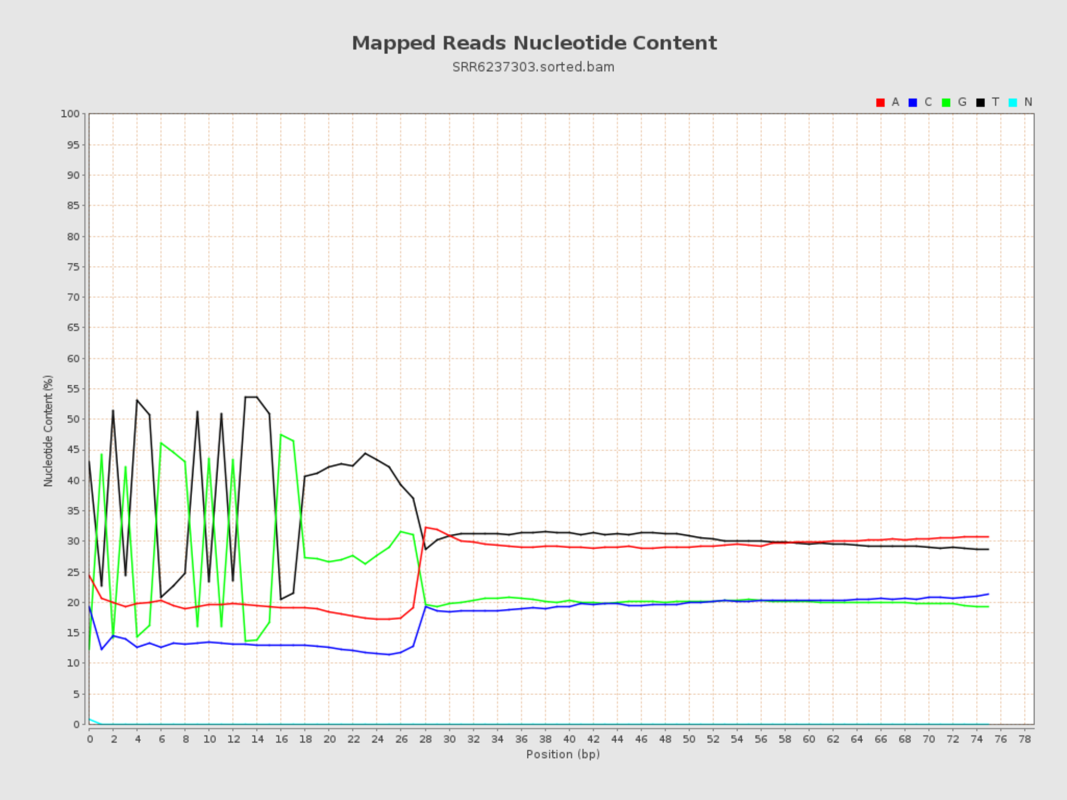
6. Results : Genome Fraction Coverage



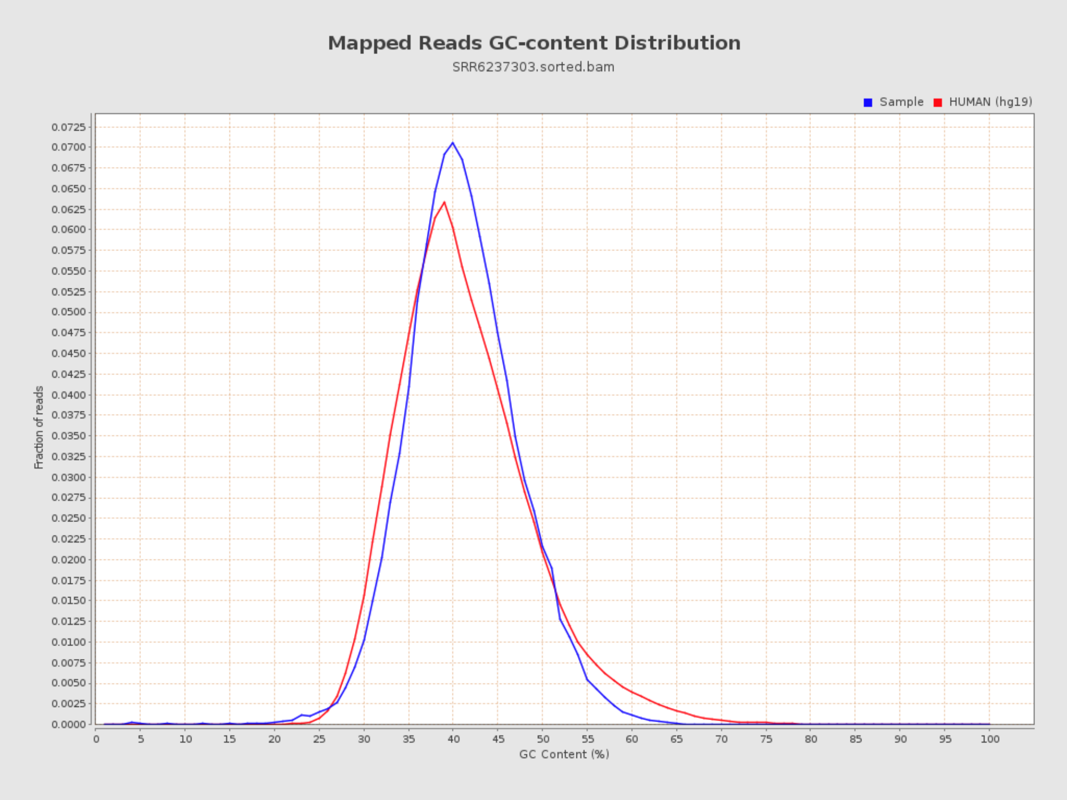
7. Results : Duplication Rate Histogram



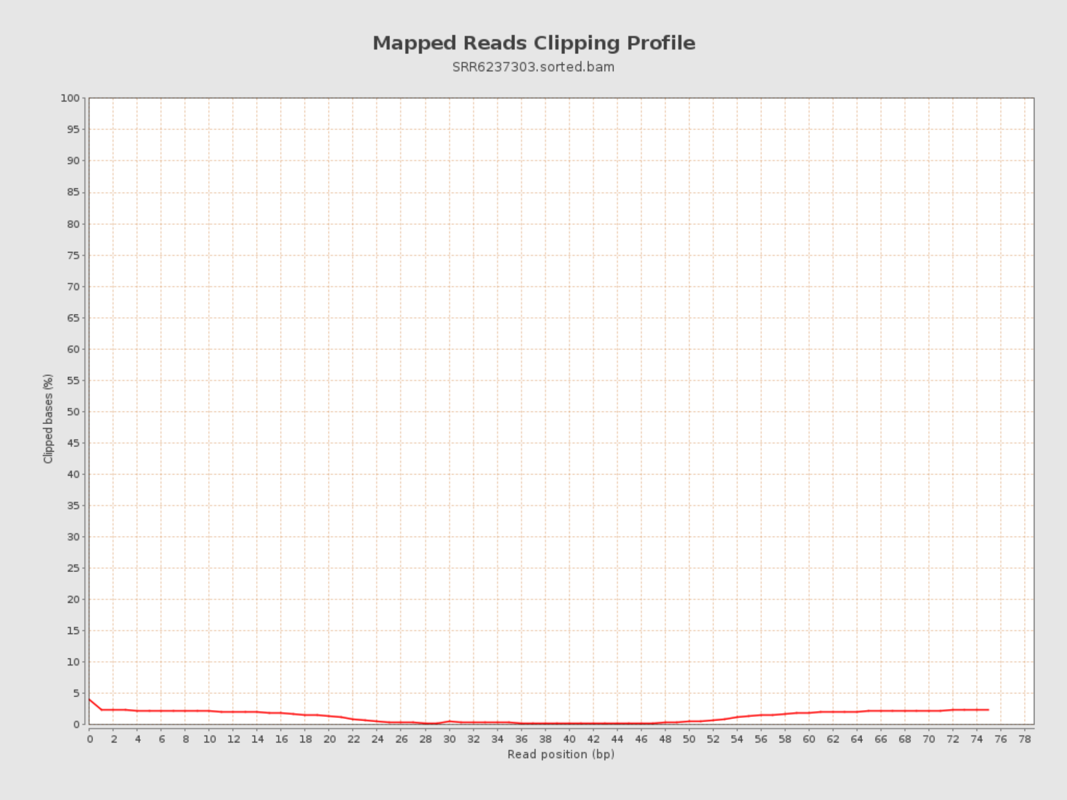
8. Results : Mapped Reads Nucleotide Content



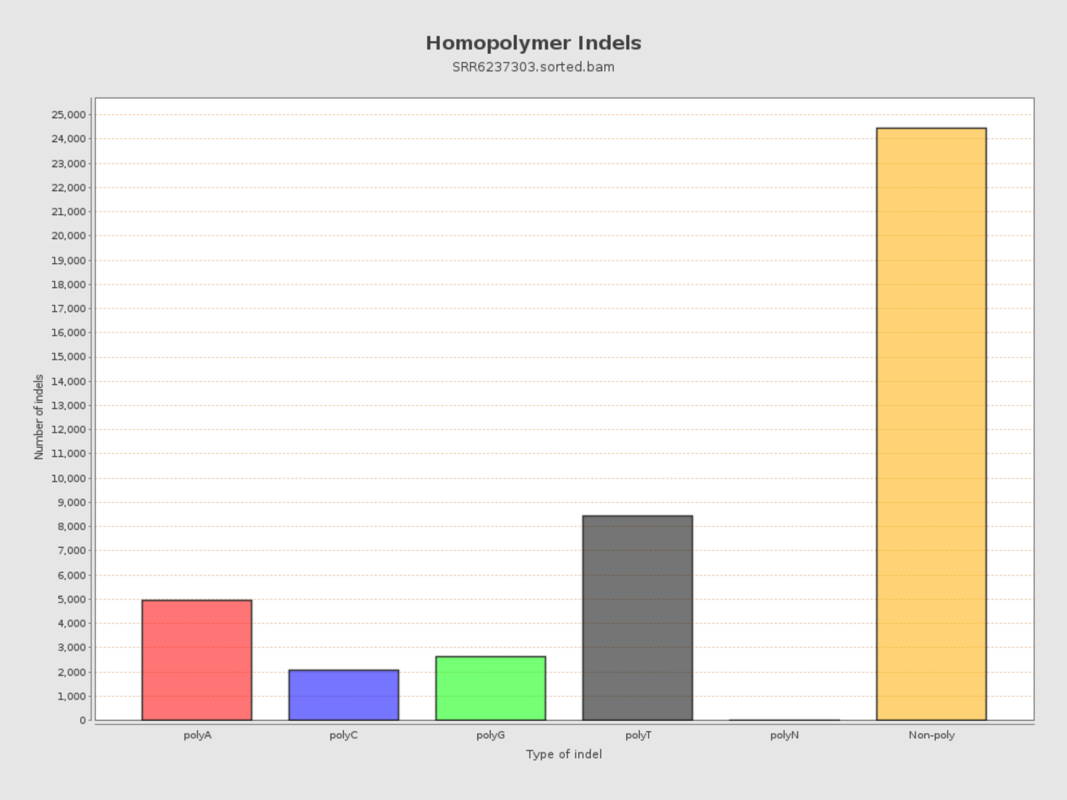
9. Results : Mapped Reads GC-content Distribution



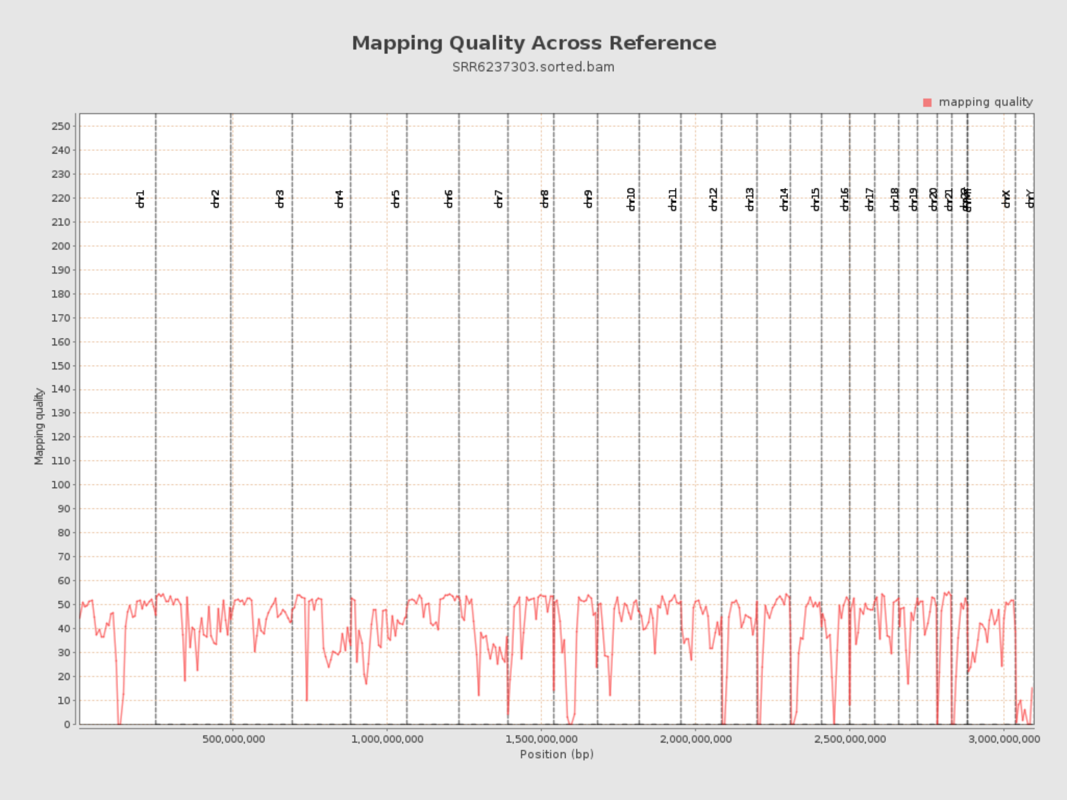
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram