Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:06:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237317.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_SRR6237317 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237317.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:06:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237317.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,571,821
Mapped reads	2,233,493 / 86.84%
Unmapped reads	338,328 / 13.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,976 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	141,927 / 5.52%
Duplication rate	4.92%
Clipped reads	1,014,906 / 39.46%

2.2. ACGT Content

Number/percentage of A's	41,395,144 / 27.82%
Number/percentage of C's	27,188,013 / 18.27%
Number/percentage of T's	47,269,734 / 31.76%
Number/percentage of G's	32,963,976 / 22.15%
Number/percentage of N's	2,264 / 0%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.4766

2.4. Mapping Quality

Mean Mapping Quality	46.44

2.5. Mismatches and indels

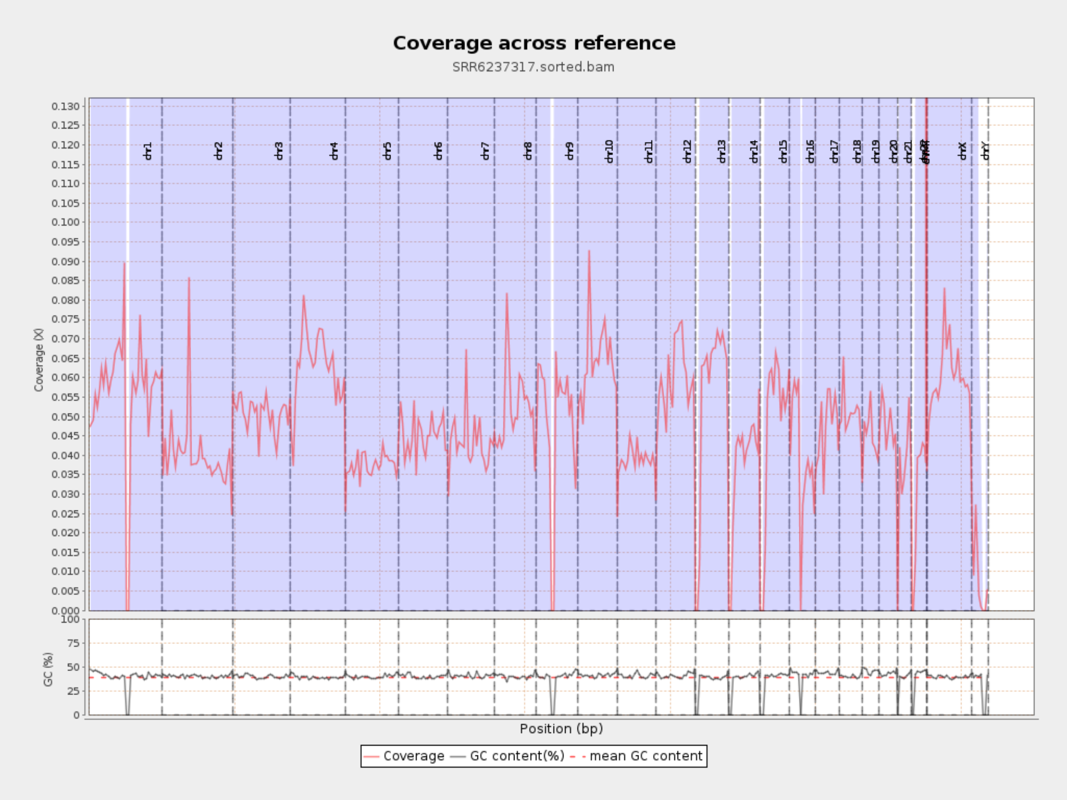
General error rate	0.81%
Mismatches	1,182,711
Insertions	11,009
Mapped reads with at least one insertion	0.49%
Deletions	35,416
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.1%

2.6. Chromosome stats

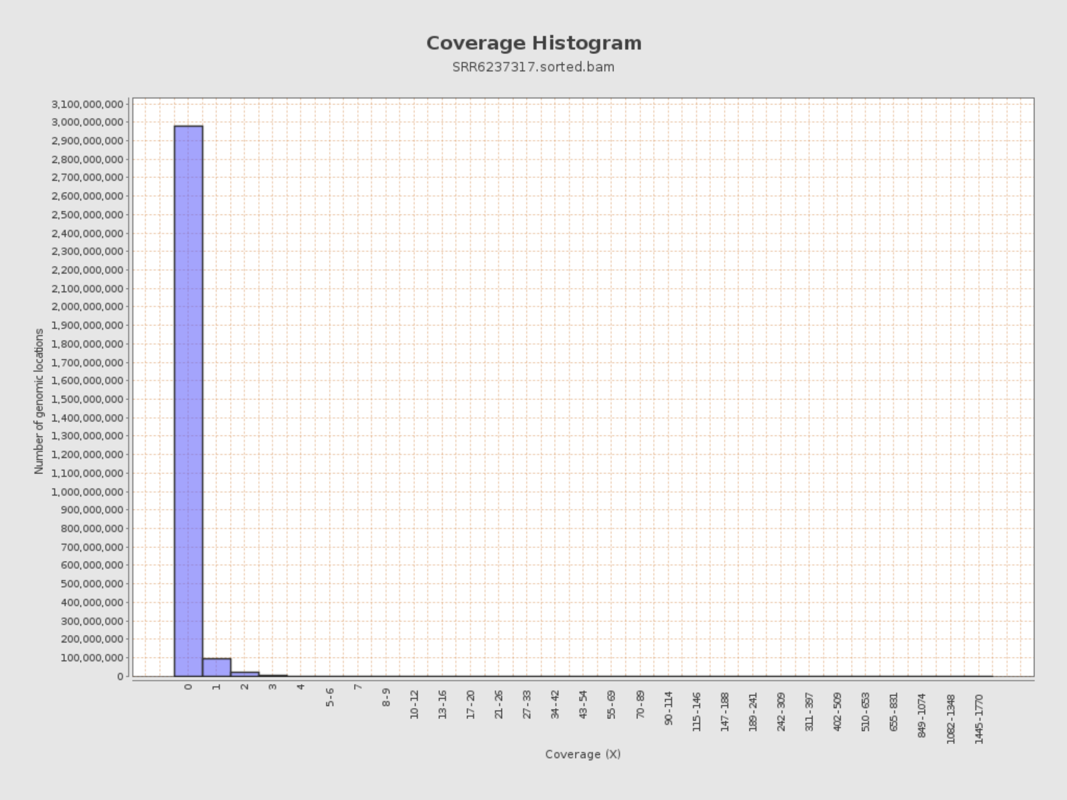
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14076496	0.0565	0.7591
chr2	243199373	9813347	0.0404	0.5037
chr3	198022430	10059798	0.0508	0.2779
chr4	191154276	12018091	0.0629	0.349
chr5	180915260	6792481	0.0375	0.2435
chr6	171115067	7748806	0.0453	0.3103
chr7	159138663	6916368	0.0435	0.4157

chr8	146364022	7584054	0.0518	1.0946
chr9	141213431	6843743	0.0485	0.4635
chr10	135534747	8738703	0.0645	0.469
chr11	135006516	5247835	0.0389	0.3331
chr12	133851895	7990997	0.0597	0.3188
chr13	115169878	6351345	0.0551	0.2897
chr14	107349540	3923183	0.0365	0.291
chr15	102531392	4763362	0.0465	0.2714
chr16	90354753	3522189	0.039	0.2779
chr17	81195210	3848885	0.0474	0.2936
chr18	78077248	3987097	0.0511	0.8129
chr19	59128983	2687243	0.0454	0.511
chr20	63025520	2987433	0.0474	0.2878
chr21	48129895	1753468	0.0364	0.279
chr22	51304566	1449612	0.0283	0.203
chrMT	16571	19231	1.1605	1.5086
chrX	155270560	9310674	0.06	0.3416
chrY	59373566	445957	0.0075	0.2479

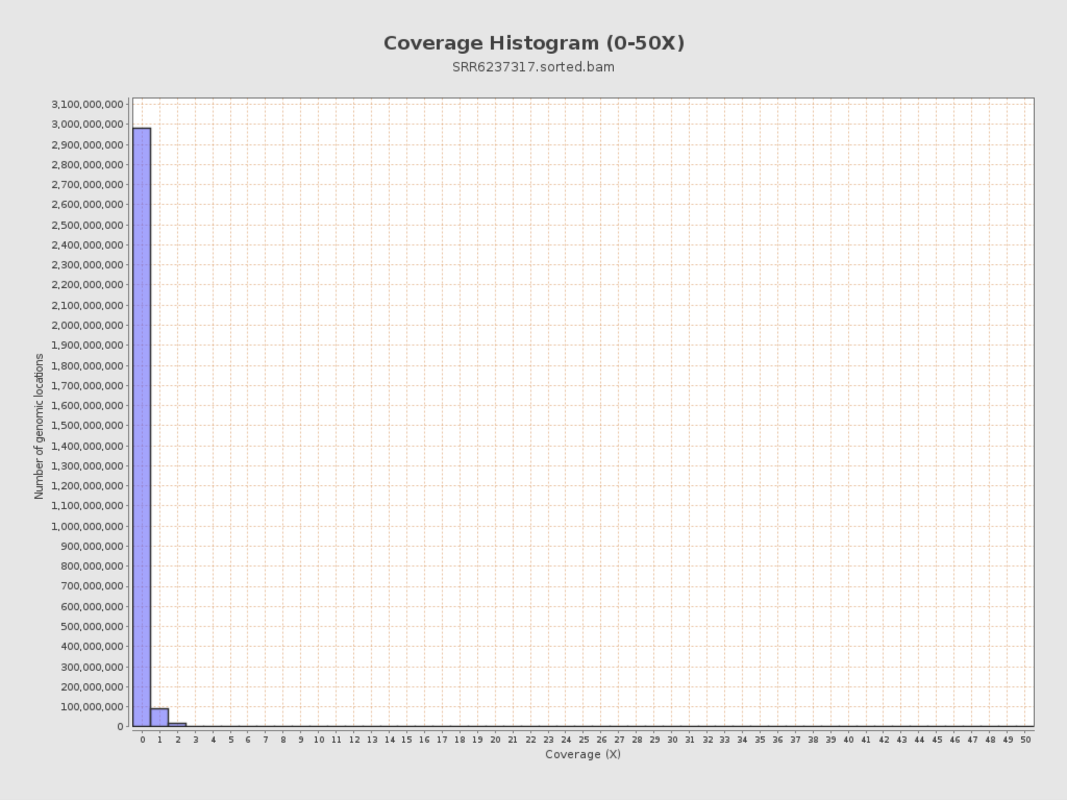
3. Results : Coverage across reference



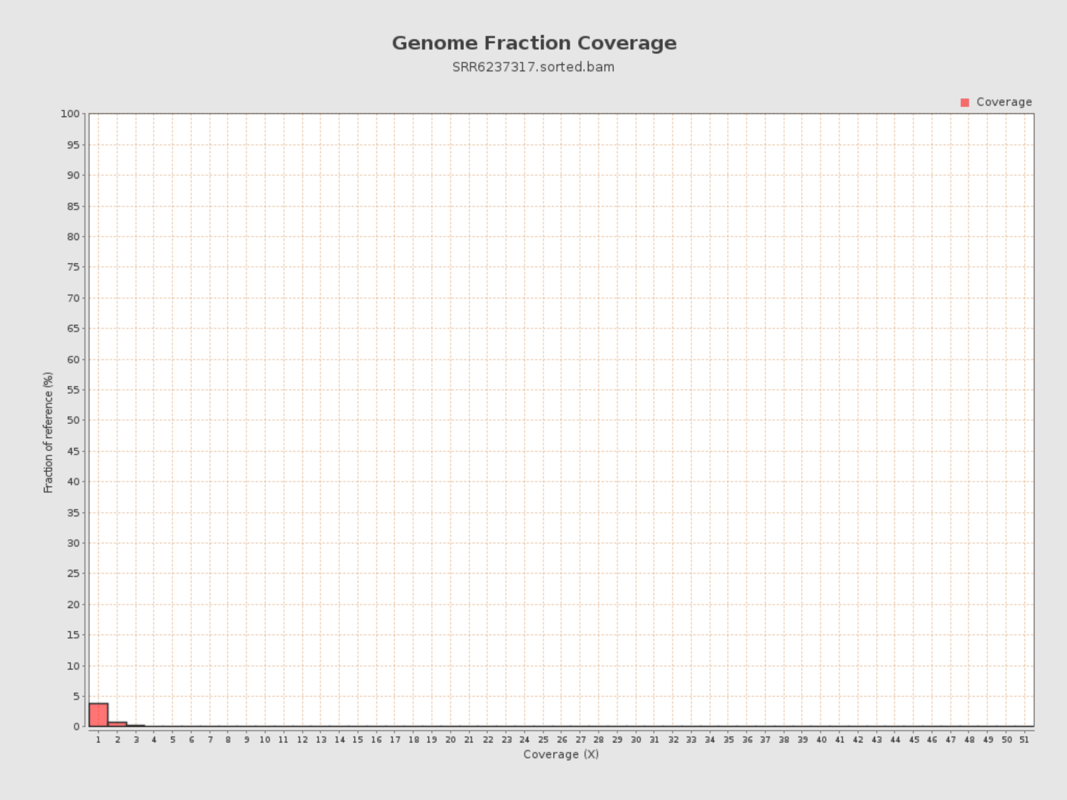
4. Results : Coverage Histogram



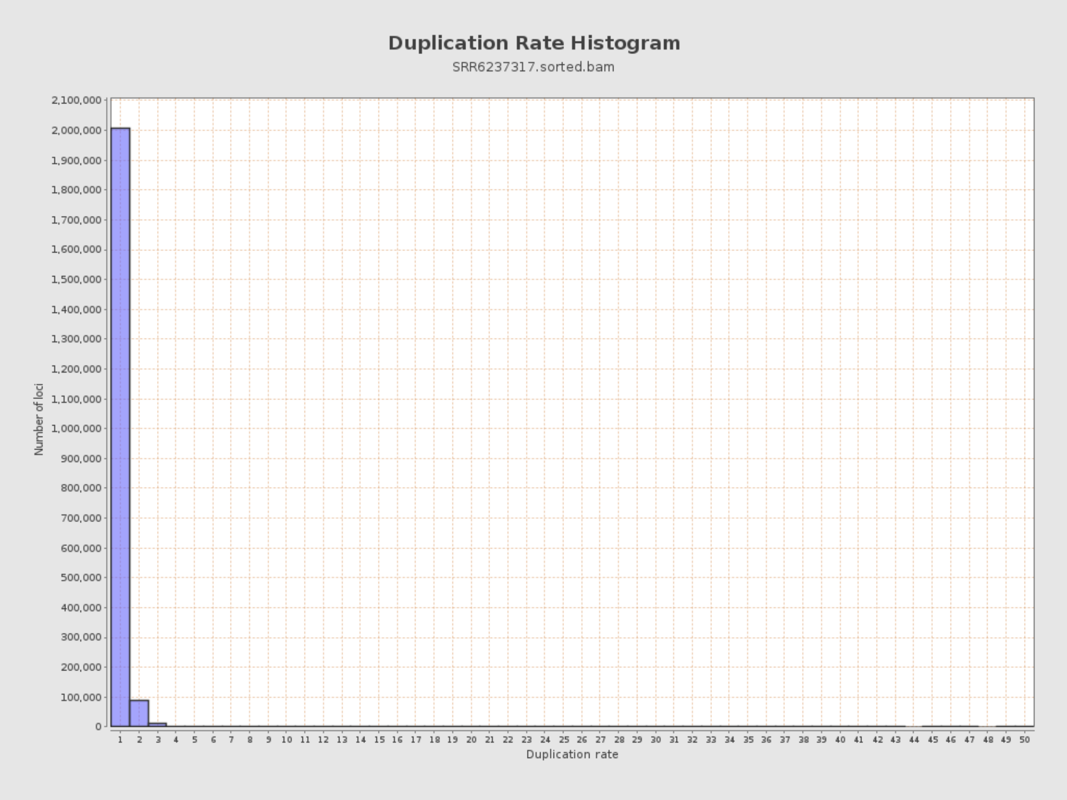
5. Results : Coverage Histogram (0-50X)



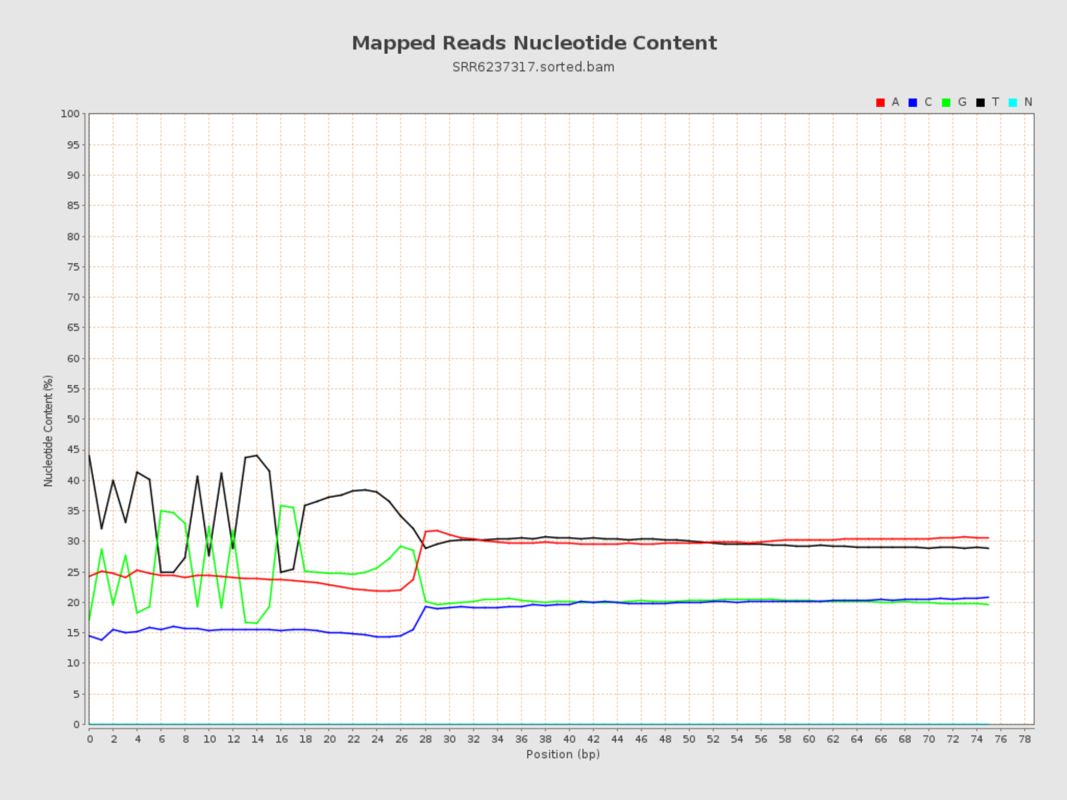
6. Results : Genome Fraction Coverage



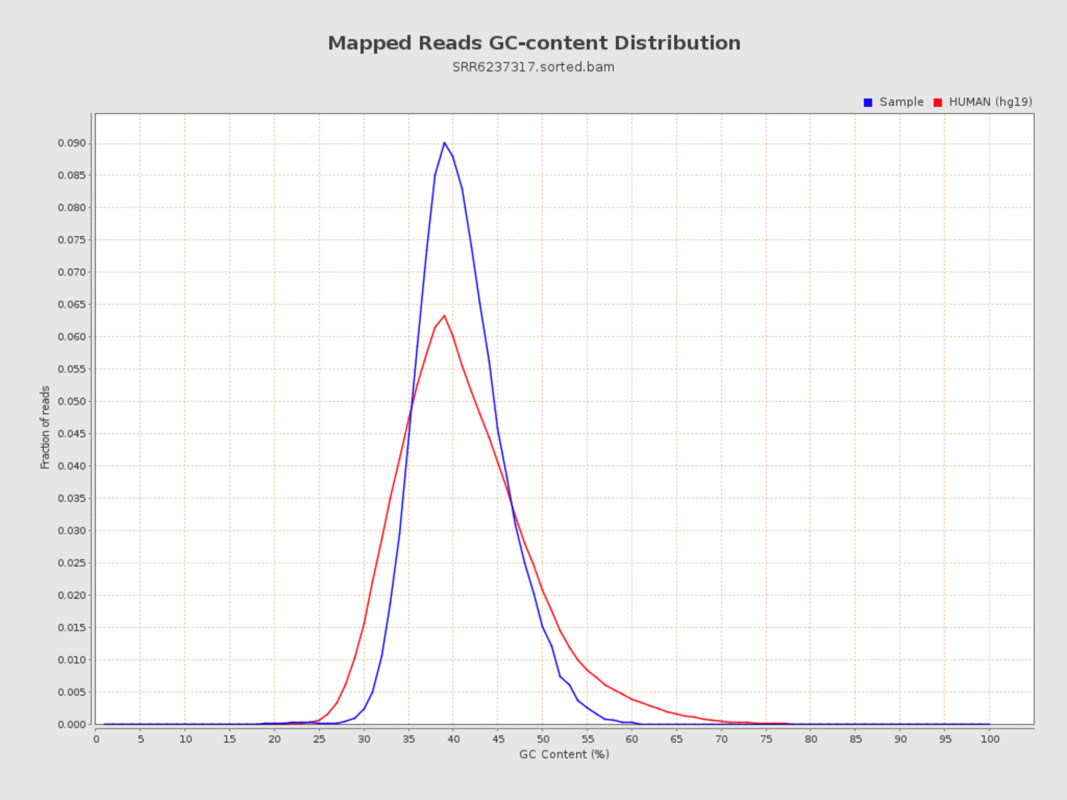
7. Results : Duplication Rate Histogram



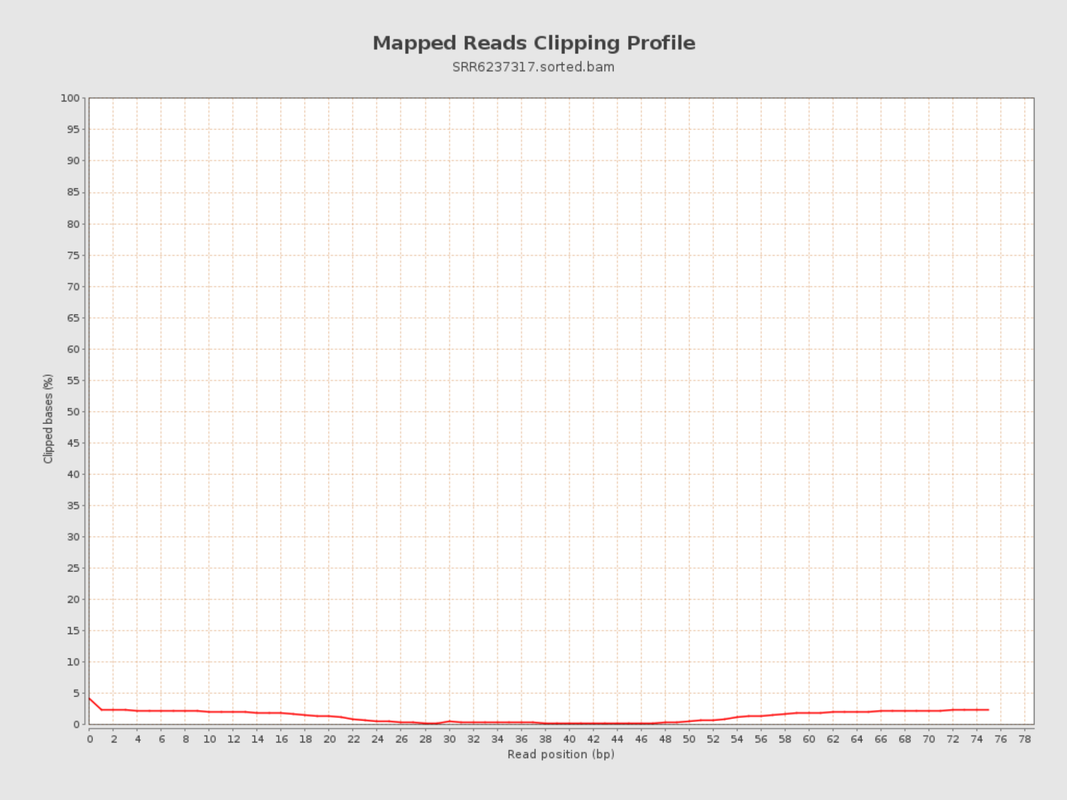
8. Results : Mapped Reads Nucleotide Content



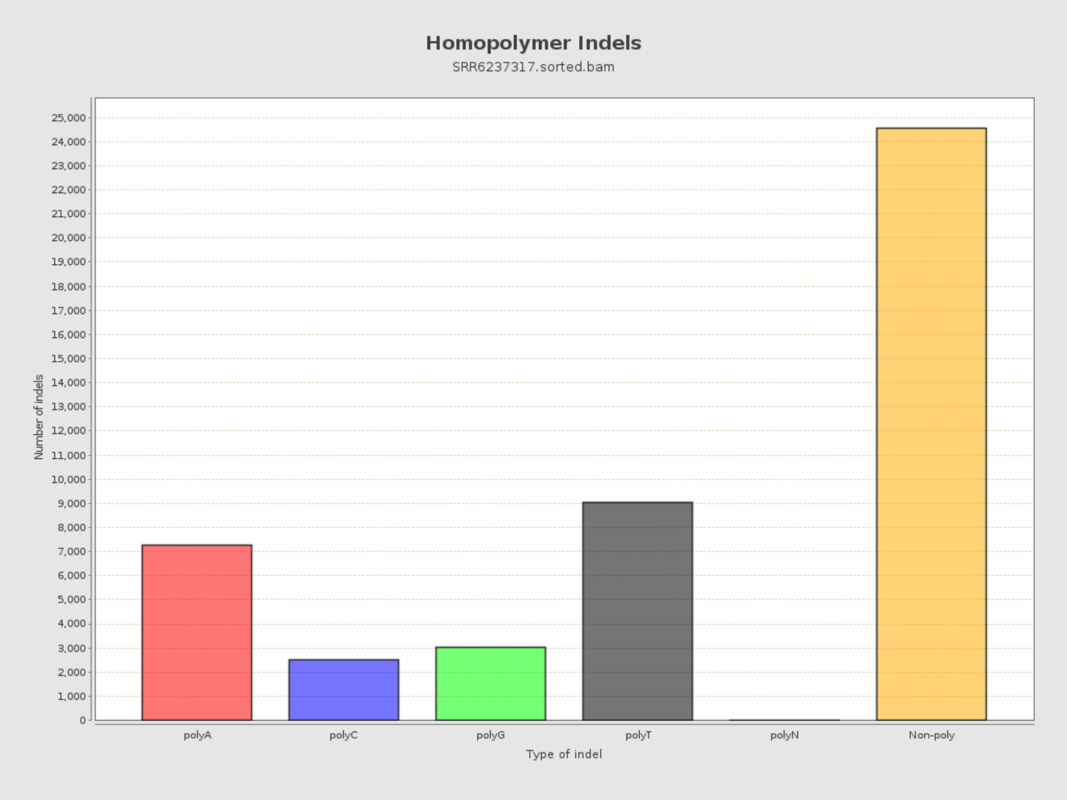
9. Results : Mapped Reads GC-content Distribution



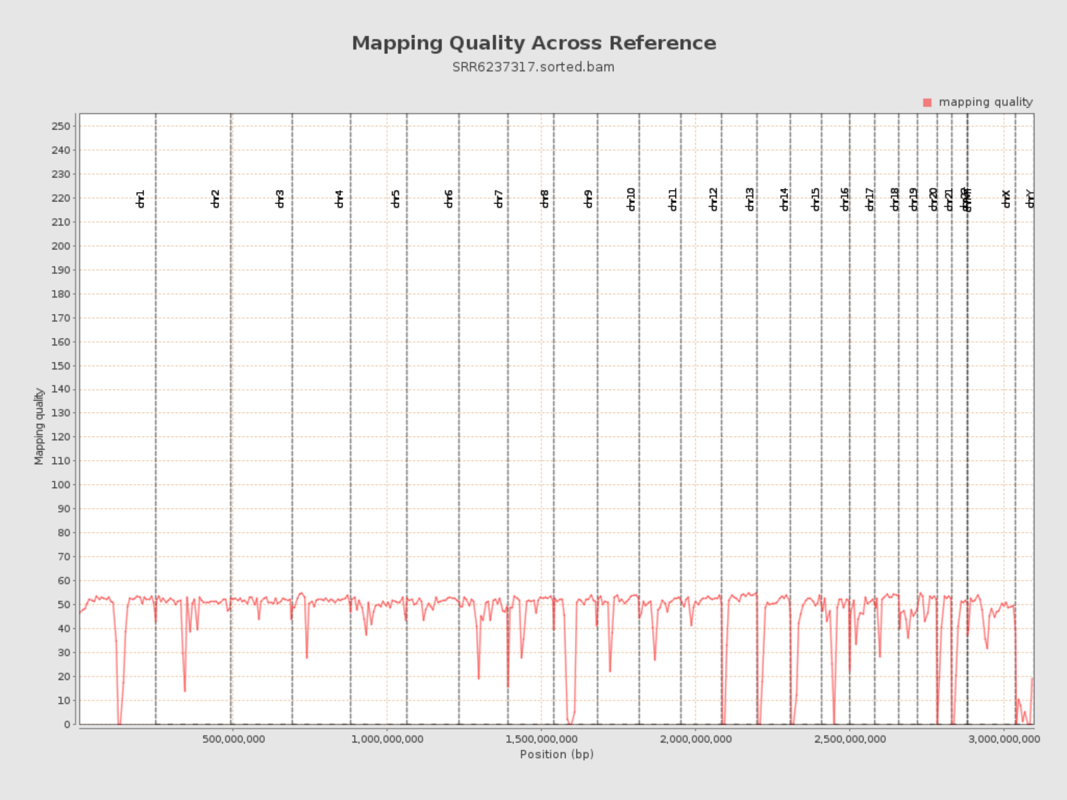
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram