Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:22:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237585.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_SRR6237585 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237585.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:22:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237585.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,013,857
Mapped reads	1,646,962 / 81.78%
Unmapped reads	366,895 / 18.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,708 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	82,269 / 4.09%
Duplication rate	3.39%
Clipped reads	1,014,848 / 50.39%

2.2. ACGT Content

Number/percentage of A's	26,733,707 / 25.72%
Number/percentage of C's	19,790,436 / 19.04%
Number/percentage of T's	31,304,155 / 30.12%
Number/percentage of G's	26,081,521 / 25.1%
Number/percentage of N's	16,895 / 0.02%
GC Percentage	44.14%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.315

2.4. Mapping Quality

Mean Mapping Quality	39.93

2.5. Mismatches and indels

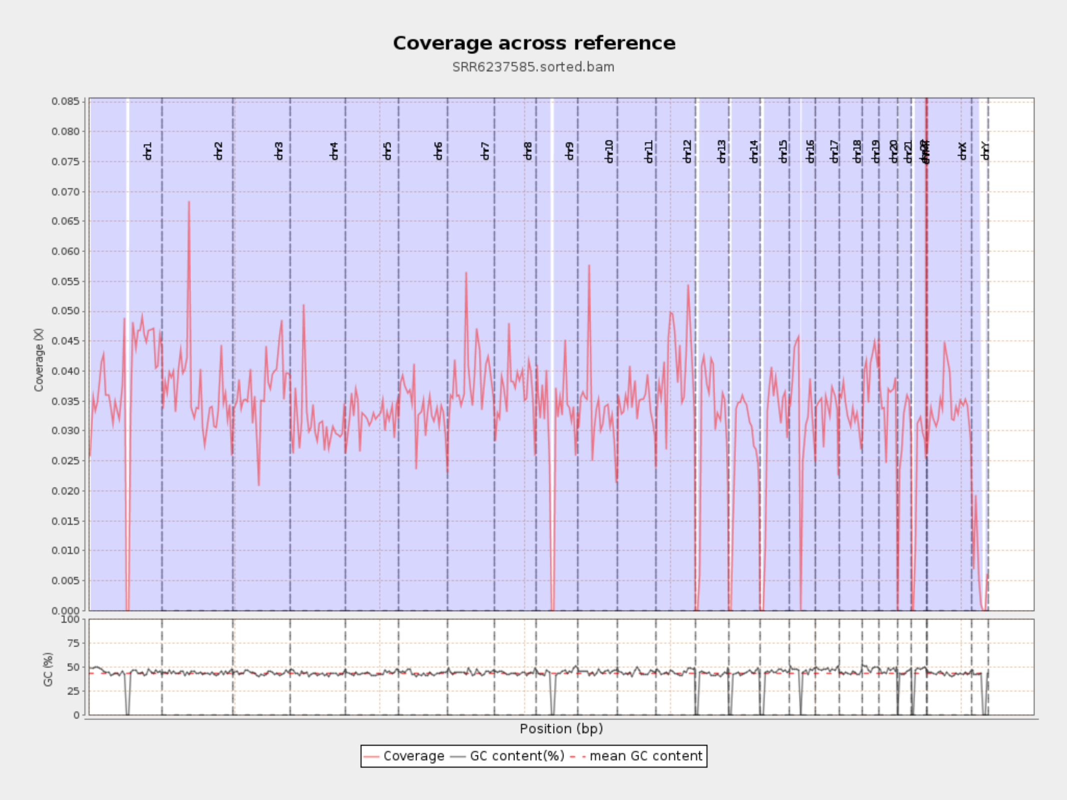
General error rate	0.95%
Mismatches	973,747
Insertions	9,700
Mapped reads with at least one insertion	0.58%
Deletions	37,205
Mapped reads with at least one deletion	2.23%
Homopolymer indels	44.69%

2.6. Chromosome stats

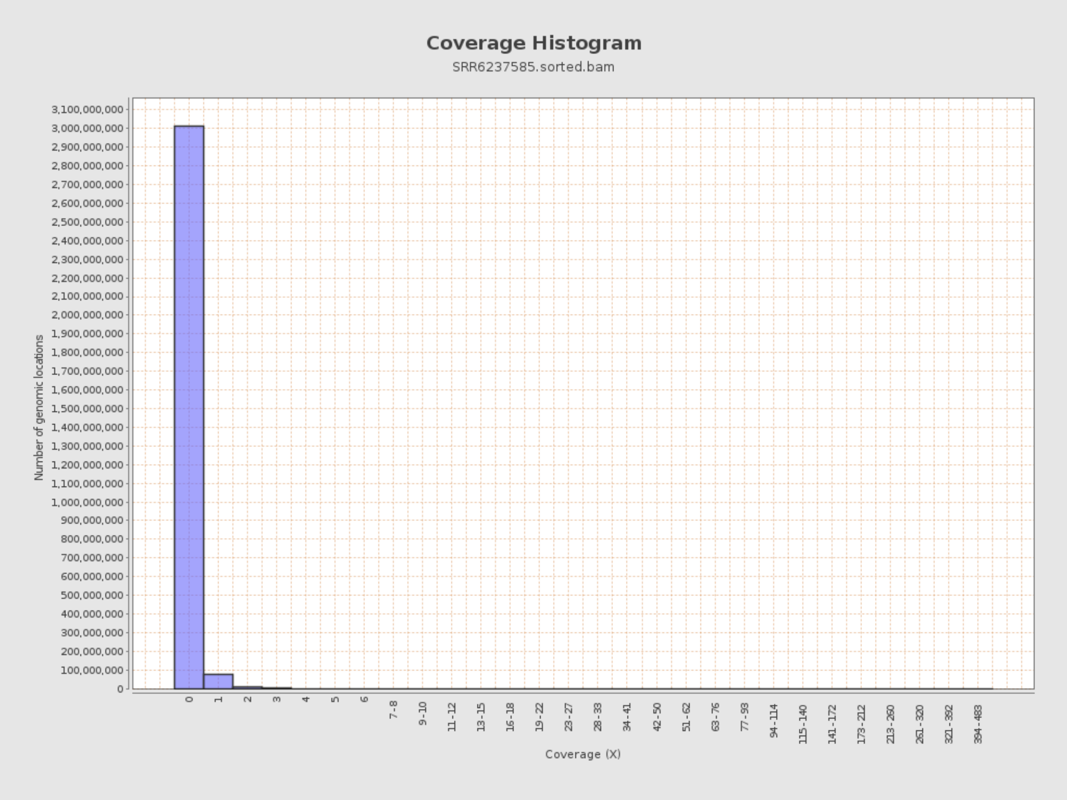
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9379688	0.0376	0.444
chr2	243199373	8915401	0.0367	0.4203
chr3	198022430	7280382	0.0368	0.2457
chr4	191154276	5968577	0.0312	0.2464
chr5	180915260	5870329	0.0324	0.2221
chr6	171115067	5764293	0.0337	0.2571
chr7	159138663	6205645	0.039	0.4497

chr8	146364022	5377628	0.0367	0.2955
chr9	141213431	4295628	0.0304	0.3191
chr10	135534747	4546712	0.0335	0.3254
chr11	135006516	4666710	0.0346	0.3502
chr12	133851895	5503033	0.0411	0.2718
chr13	115169878	3461190	0.0301	0.2228
chr14	107349540	2841806	0.0265	0.233
chr15	102531392	2914940	0.0284	0.2252
chr16	90354753	2964393	0.0328	0.2592
chr17	81195210	2718257	0.0335	0.2496
chr18	78077248	2587646	0.0331	0.4255
chr19	59128983	2395052	0.0405	0.3667
chr20	63025520	2155776	0.0342	0.242
chr21	48129895	1338948	0.0278	0.2343
chr22	51304566	1069352	0.0208	0.1872
chrMT	16571	98089	5.9193	5.1729
chrX	155270560	5297842	0.0341	0.2617
chrY	59373566	370625	0.0062	0.1486

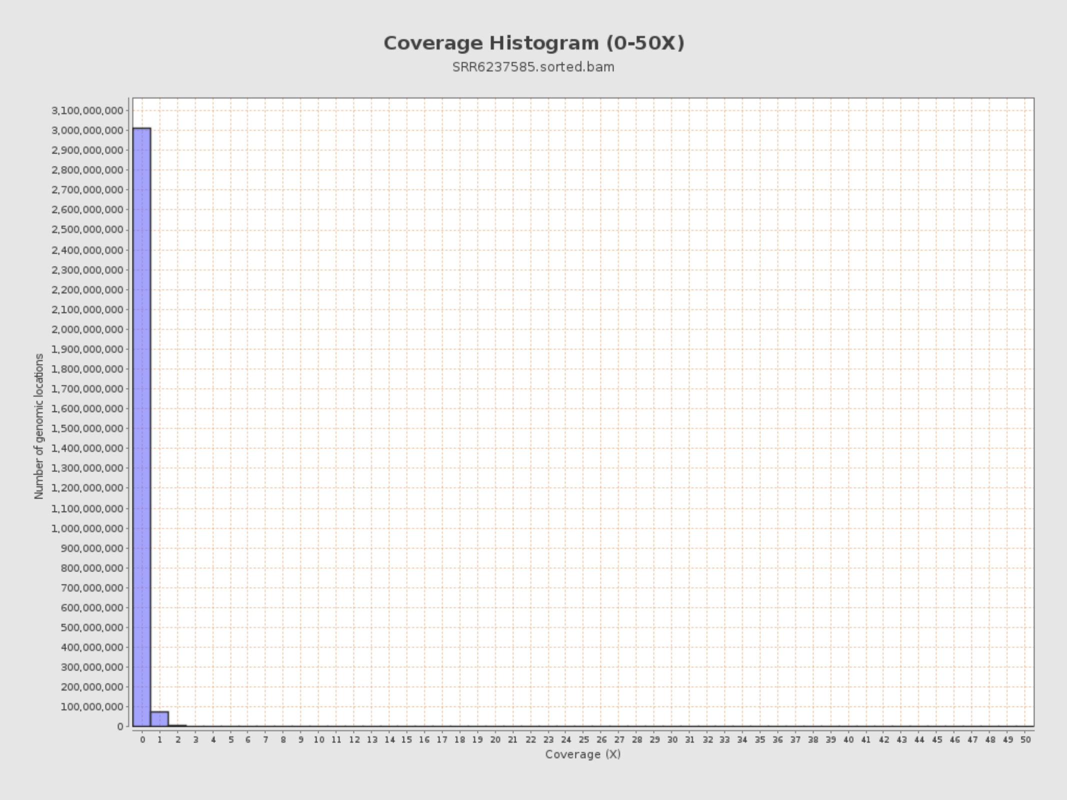
3. Results : Coverage across reference



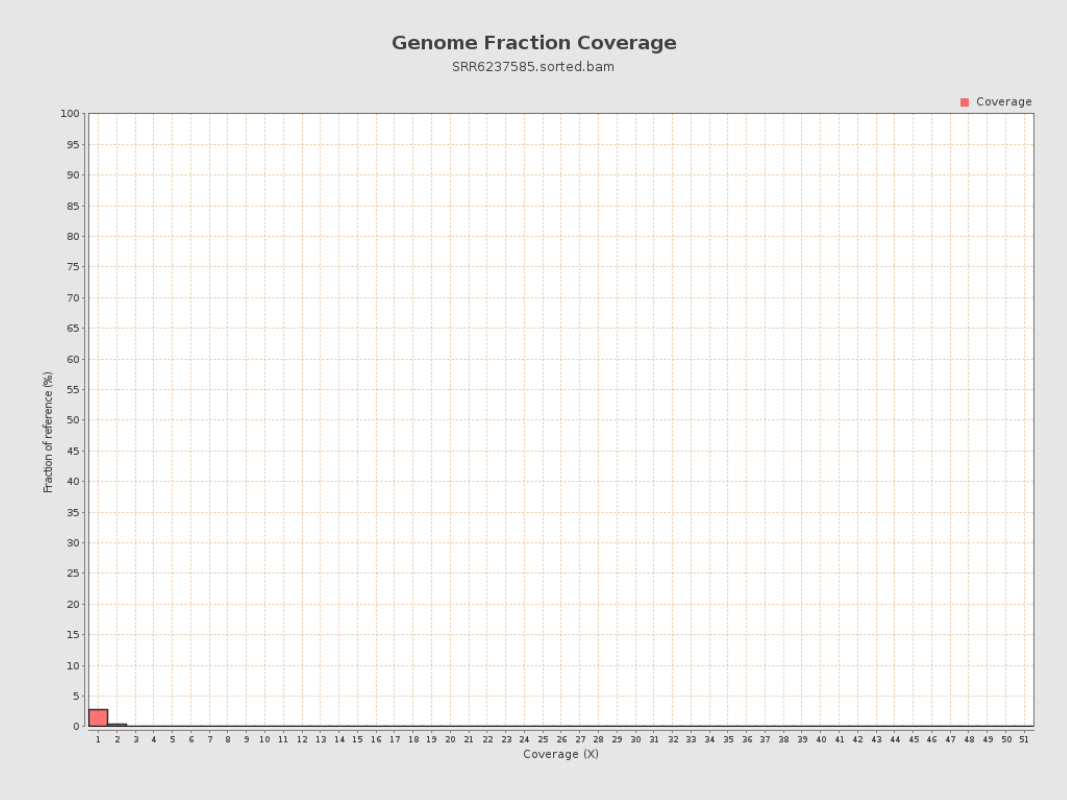
4. Results : Coverage Histogram



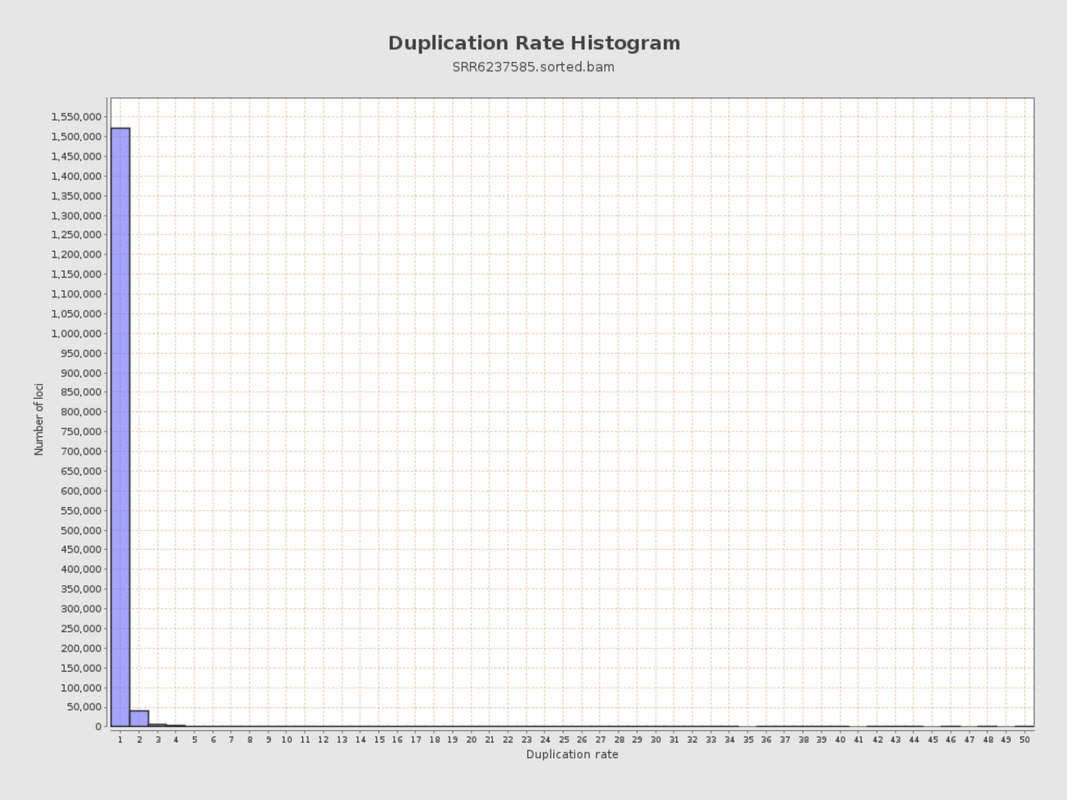
5. Results : Coverage Histogram (0-50X)



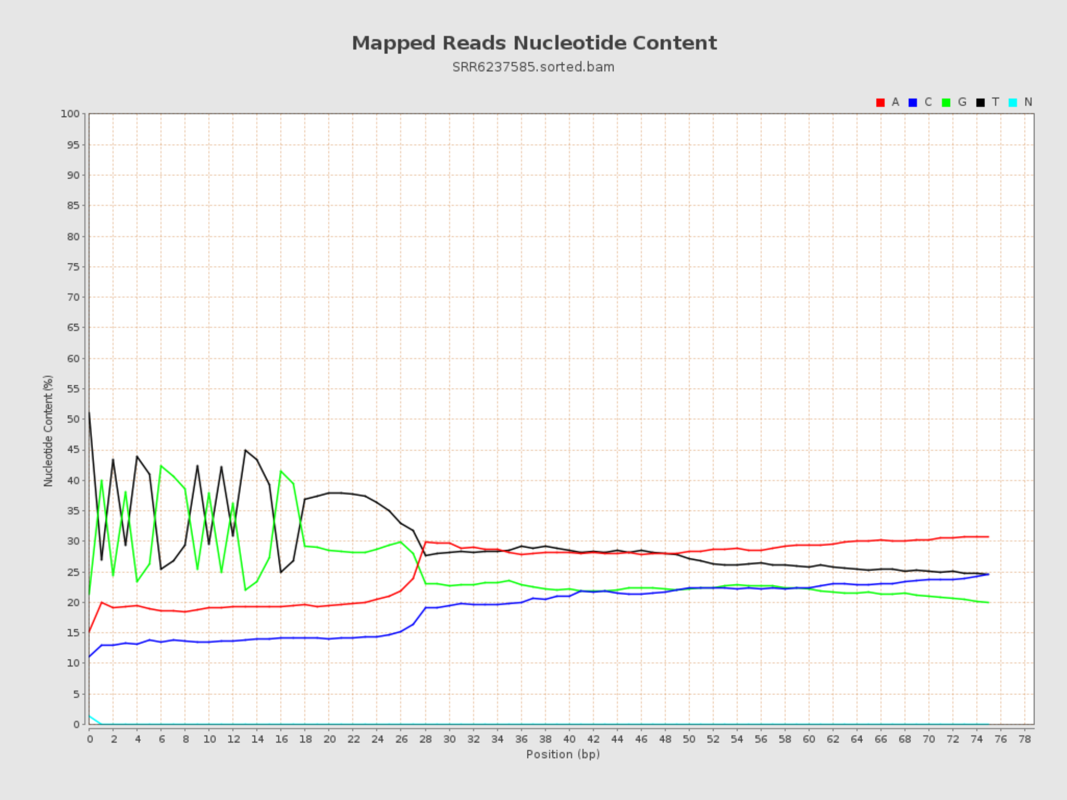
6. Results : Genome Fraction Coverage



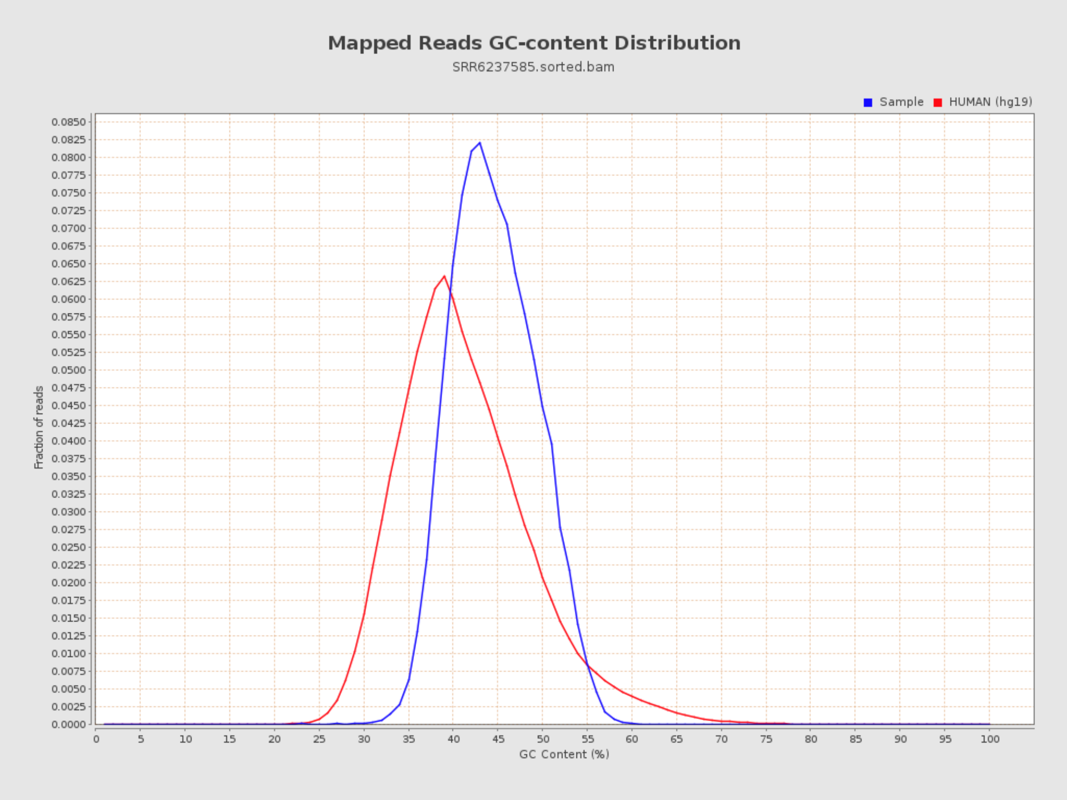
7. Results : Duplication Rate Histogram



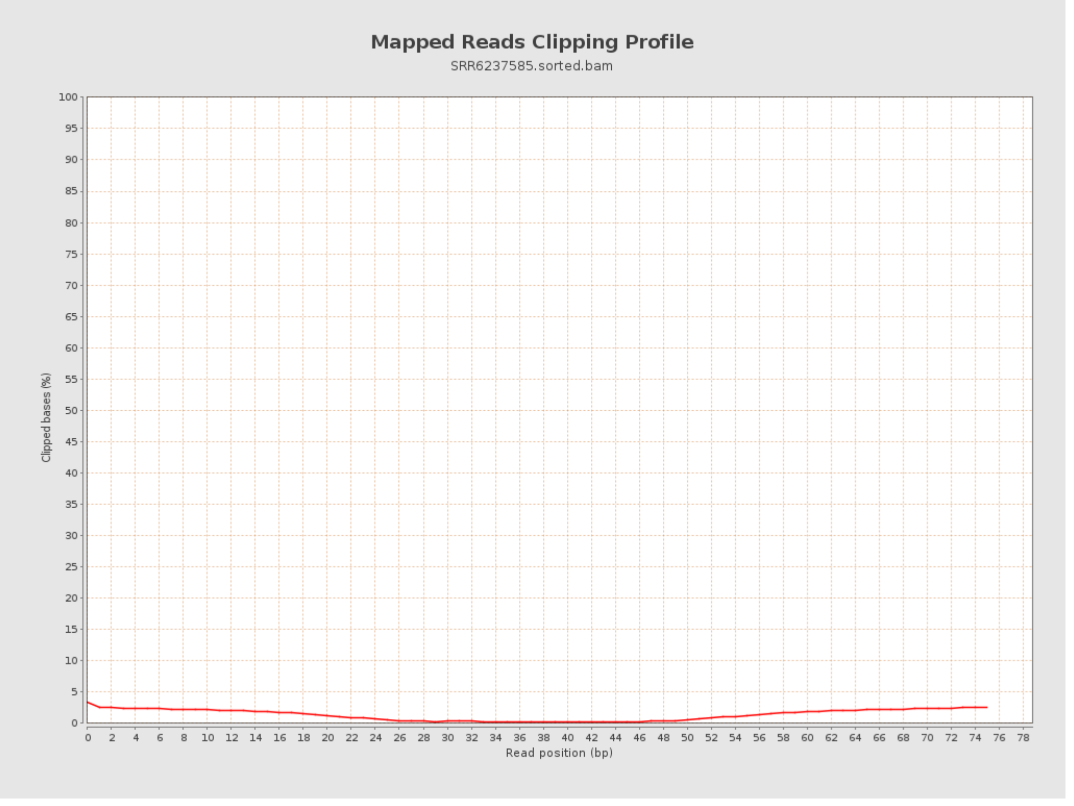
8. Results : Mapped Reads Nucleotide Content



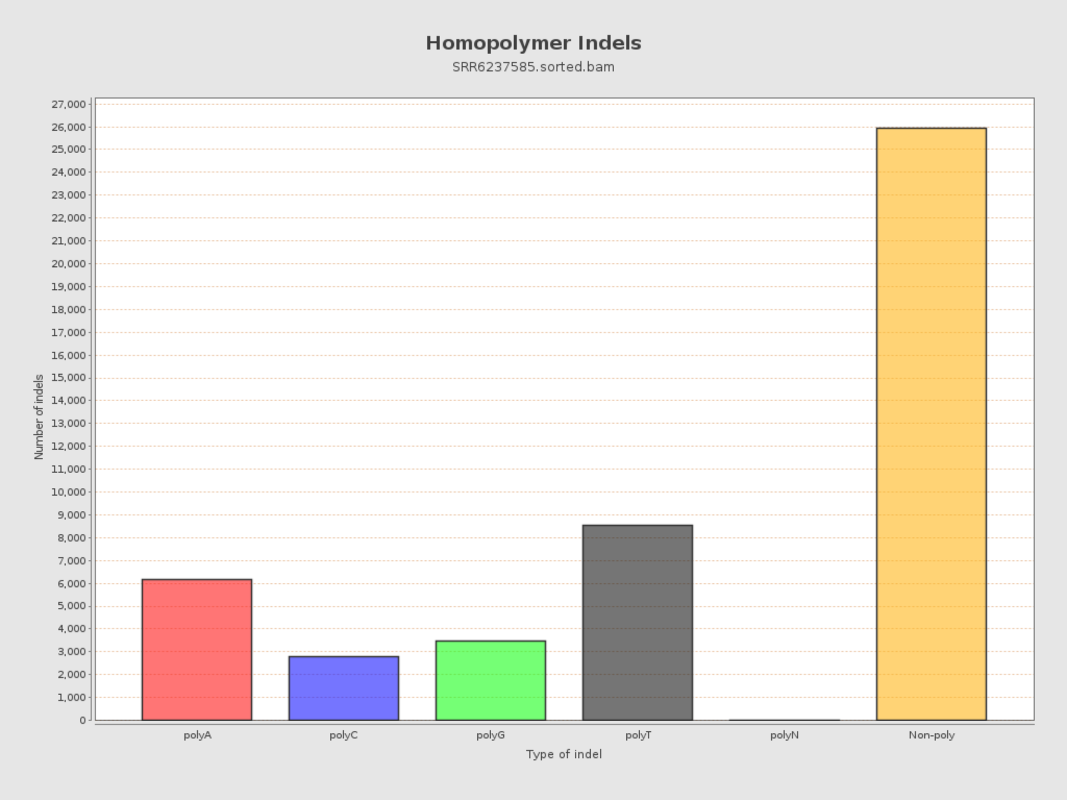
9. Results : Mapped Reads GC-content Distribution



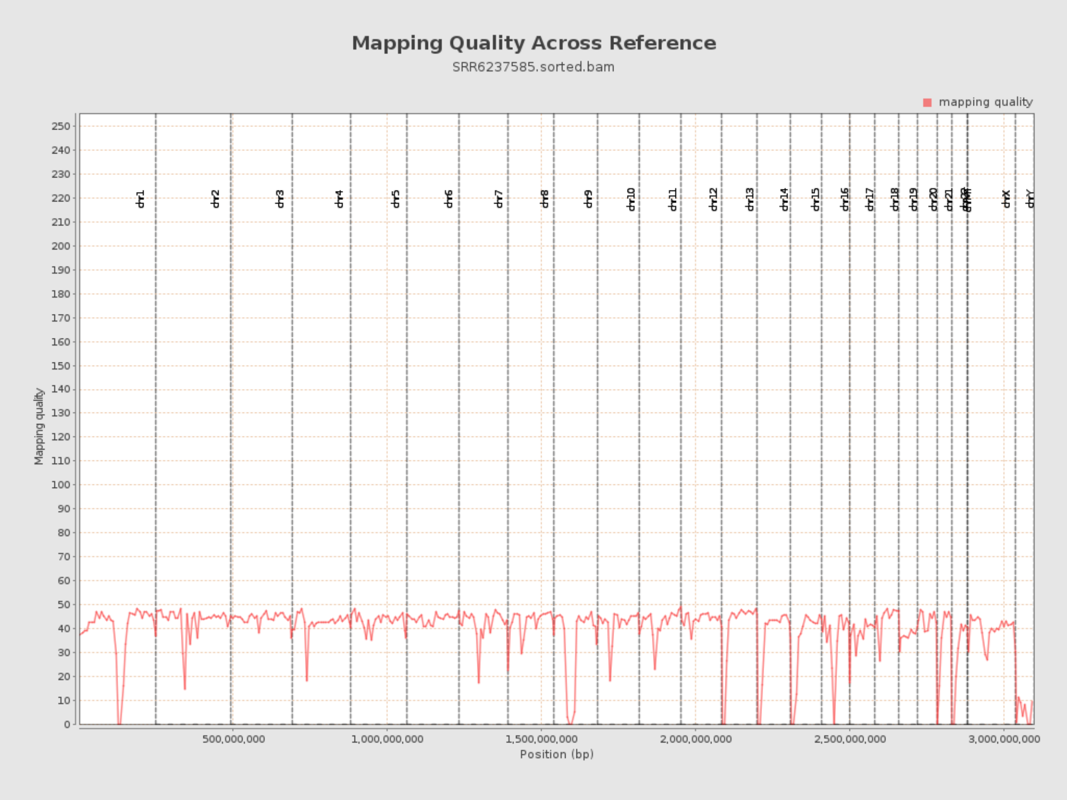
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram