Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:49:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237596.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_SRR6237596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237596.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:49:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,224,823
Mapped reads	978,079 / 79.85%
Unmapped reads	246,744 / 20.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,113 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	69,380 / 5.66%
Duplication rate	6.07%
Clipped reads	615,327 / 50.24%

2.2. ACGT Content

Number/percentage of A's	16,534,971 / 27.19%
Number/percentage of C's	10,515,762 / 17.29%
Number/percentage of T's	19,904,238 / 32.73%
Number/percentage of G's	13,745,550 / 22.6%
Number/percentage of N's	107,065 / 0.18%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0197

Standard Deviation	0.2067

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

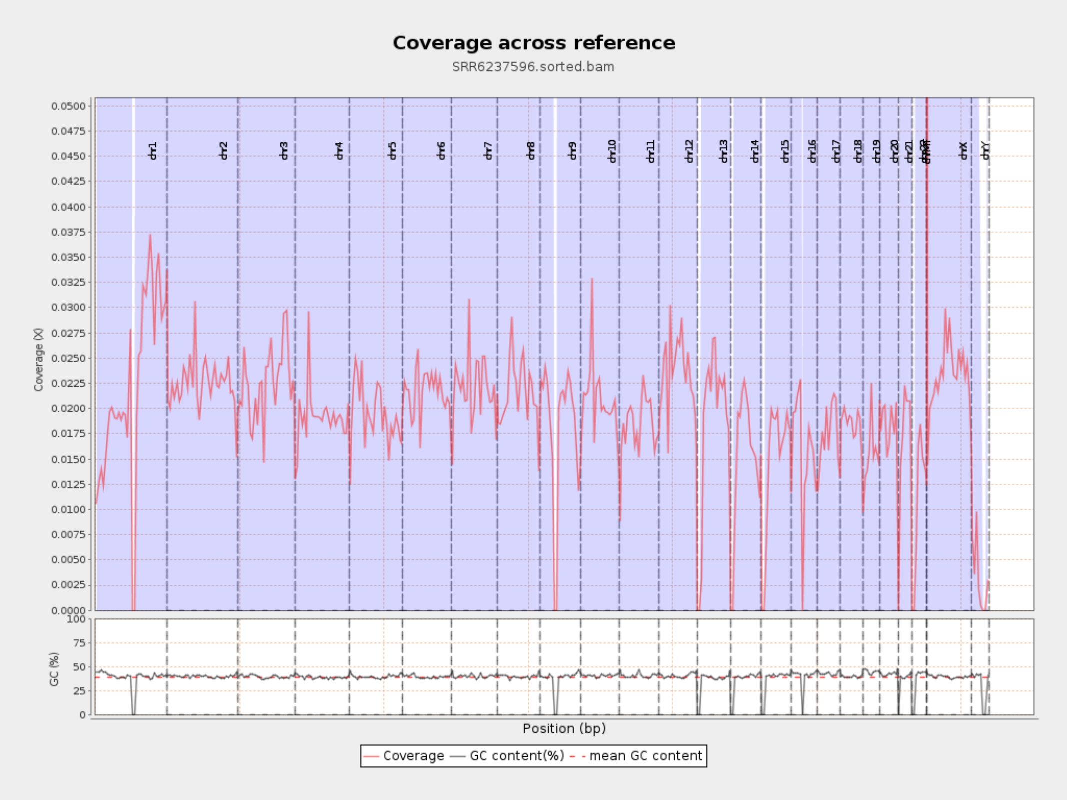
General error rate	1.02%
Mismatches	611,068
Insertions	5,243
Mapped reads with at least one insertion	0.53%
Deletions	22,507
Mapped reads with at least one deletion	2.27%
Homopolymer indels	49.69%

2.6. Chromosome stats

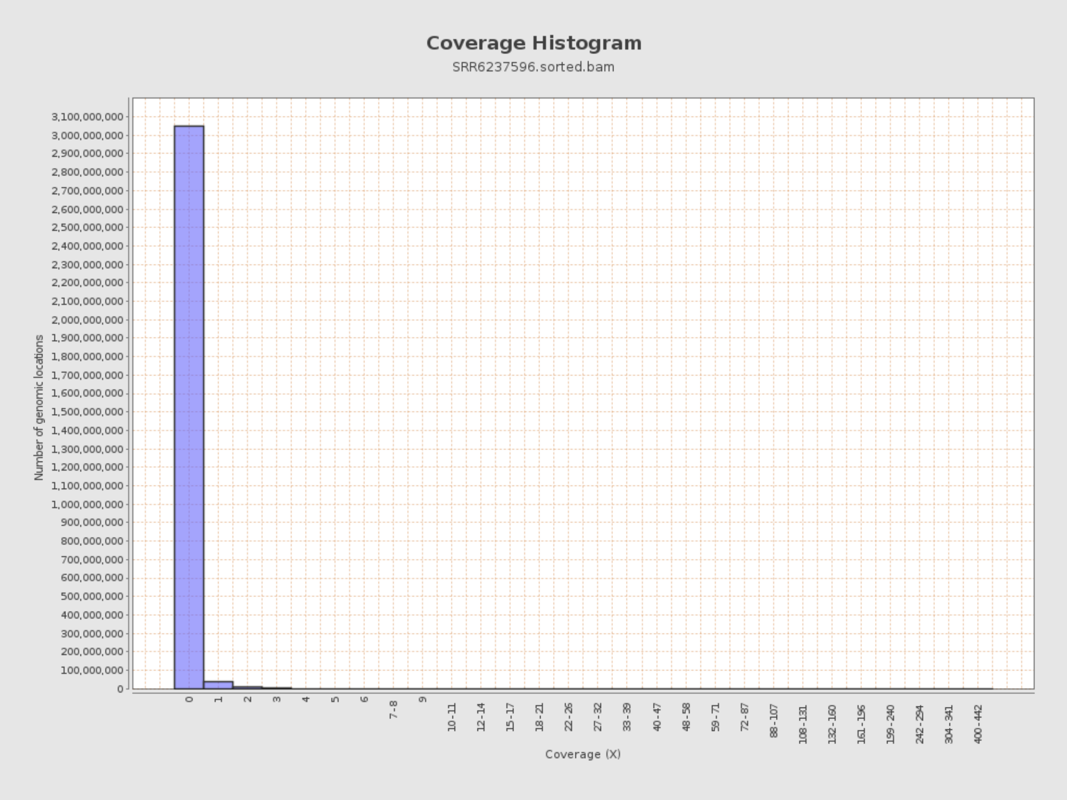
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5518004	0.0221	0.2692
chr2	243199373	5471577	0.0225	0.2329
chr3	198022430	4454665	0.0225	0.1856
chr4	191154276	3657345	0.0191	0.177
chr5	180915260	3549637	0.0196	0.1711
chr6	171115067	3691702	0.0216	0.1903
chr7	159138663	3504998	0.022	0.2484

chr8	146364022	3165791	0.0216	0.3206
chr9	141213431	2553641	0.0181	0.1878
chr10	135534747	2811913	0.0207	0.2101
chr11	135006516	2483590	0.0184	0.191
chr12	133851895	3161647	0.0236	0.1911
chr13	115169878	2120882	0.0184	0.1688
chr14	107349540	1604334	0.0149	0.1593
chr15	102531392	1505440	0.0147	0.1483
chr16	90354753	1395255	0.0154	0.1572
chr17	81195210	1408600	0.0173	0.1678
chr18	78077248	1450933	0.0186	0.2666
chr19	59128983	933931	0.0158	0.1973
chr20	63025520	1141687	0.0181	0.168
chr21	48129895	809292	0.0168	0.1634
chr22	51304566	567150	0.0111	0.1267
chrMT	16571	53517	3.2296	3.0618
chrX	155270560	3643830	0.0235	0.1934
chrY	59373566	183766	0.0031	0.0862

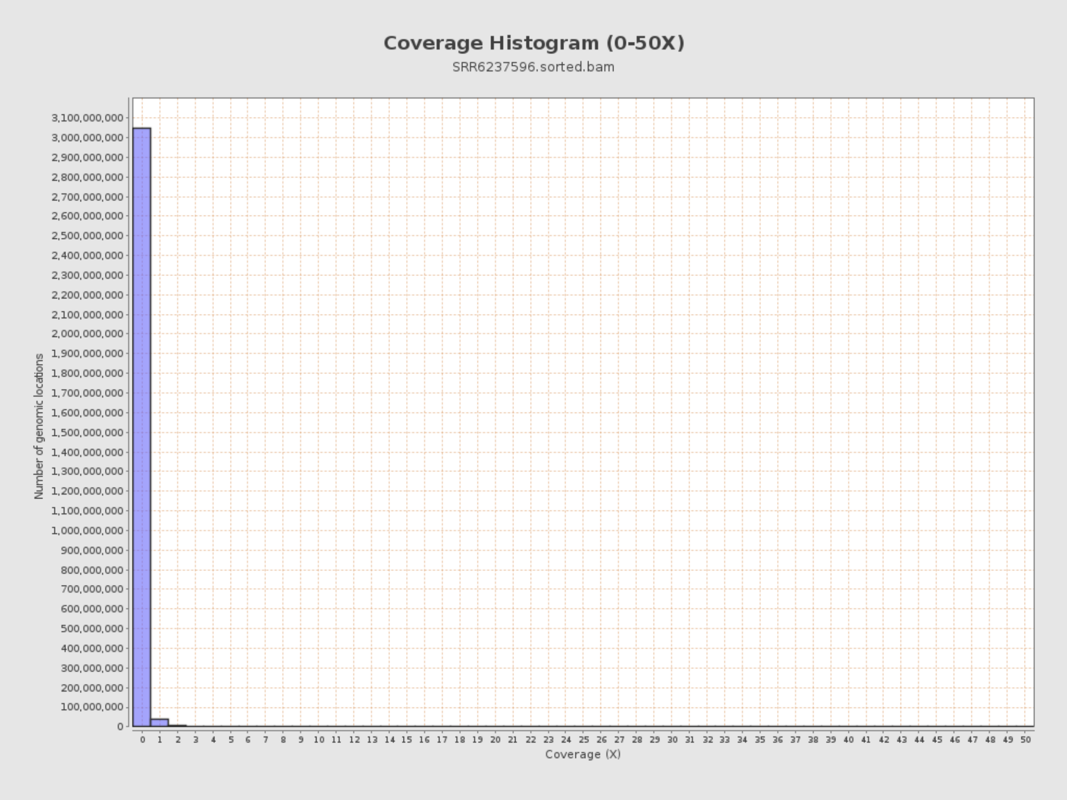
3. Results : Coverage across reference



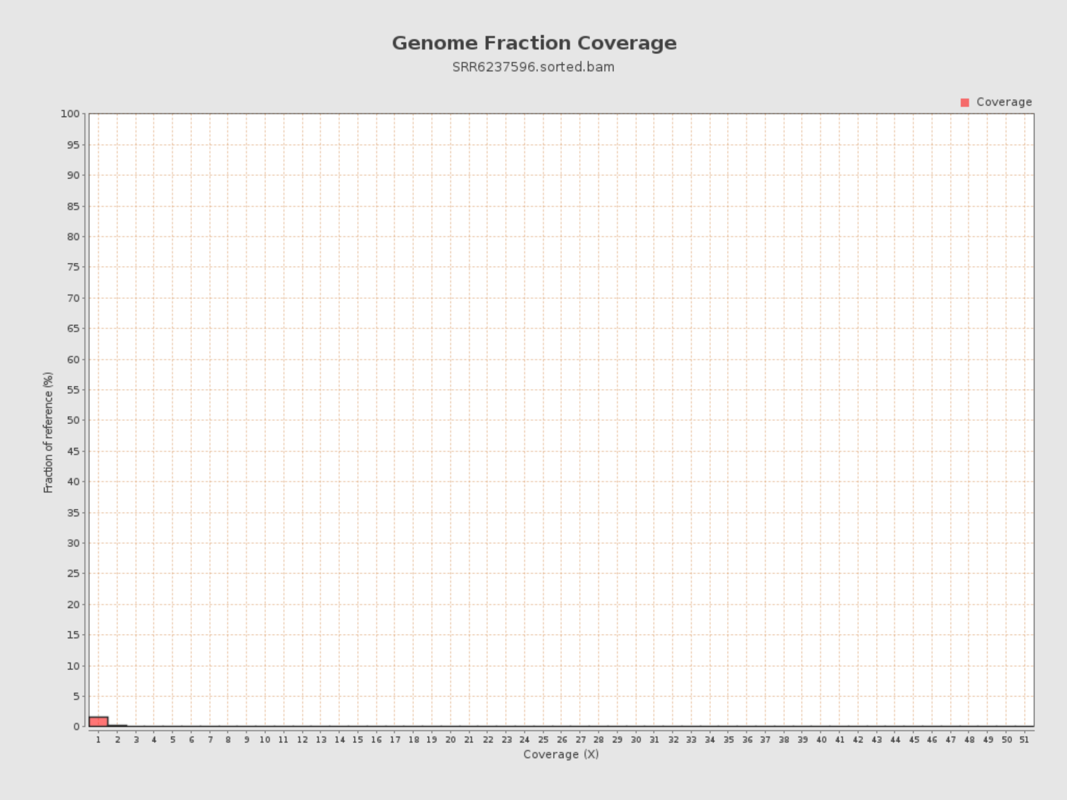
4. Results : Coverage Histogram



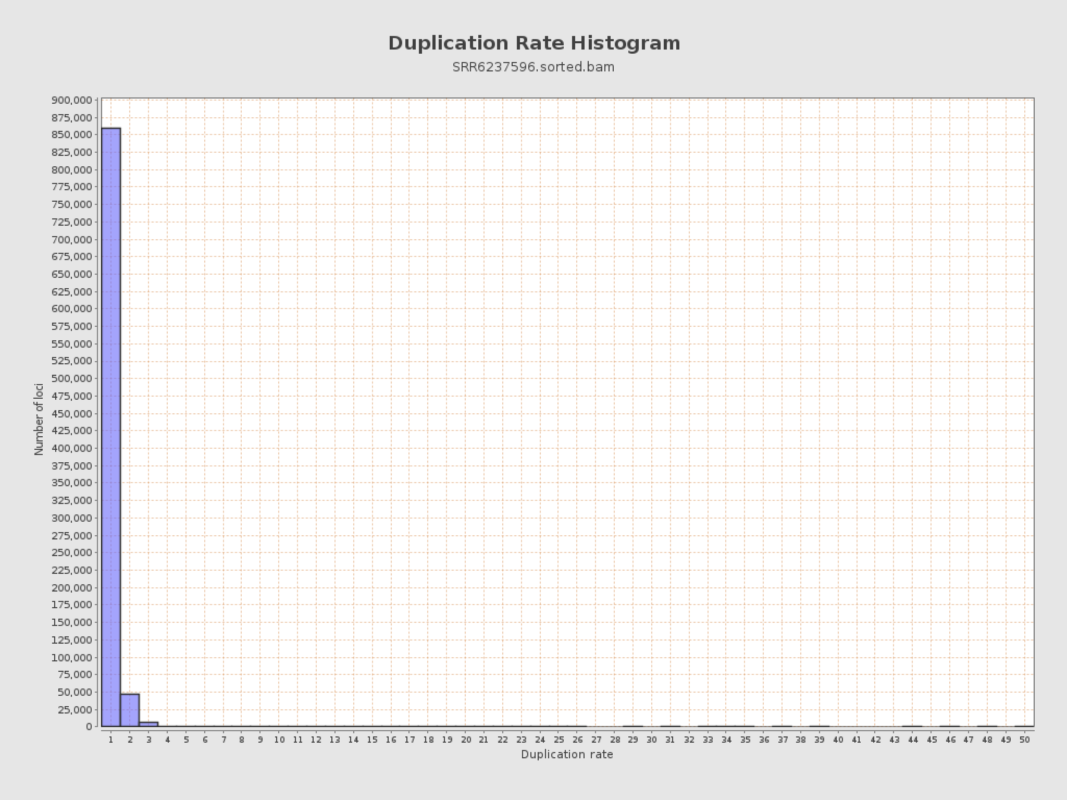
5. Results : Coverage Histogram (0-50X)



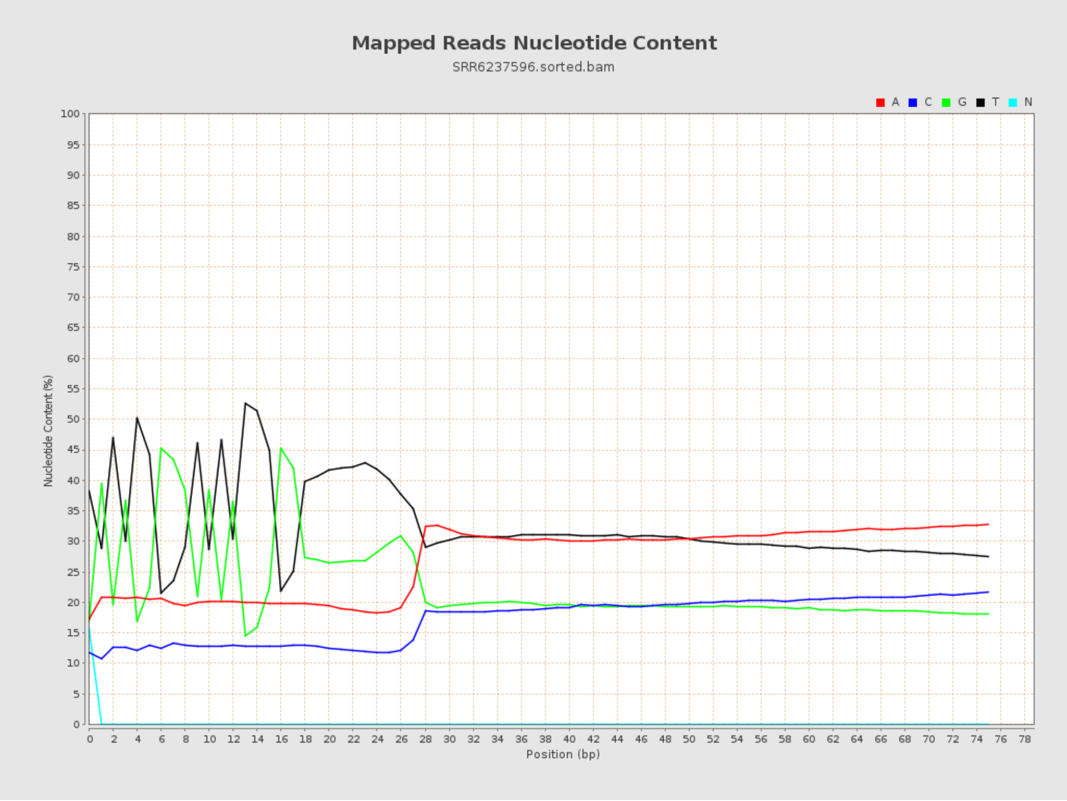
6. Results : Genome Fraction Coverage



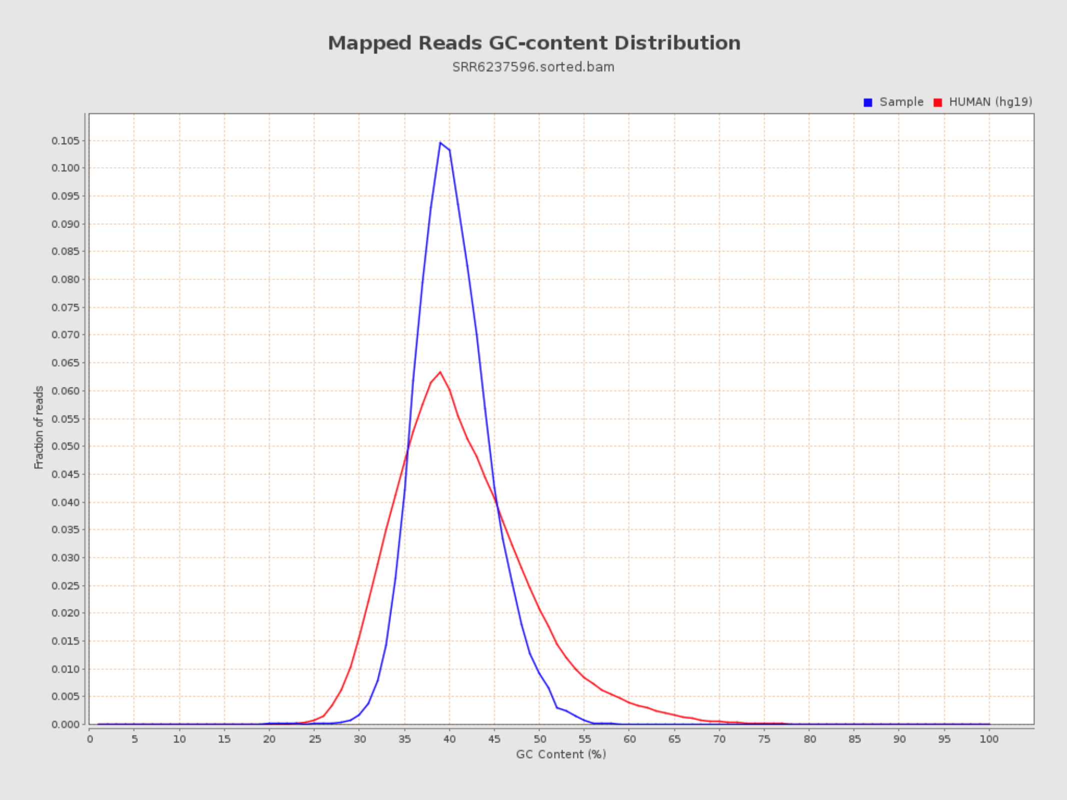
7. Results : Duplication Rate Histogram



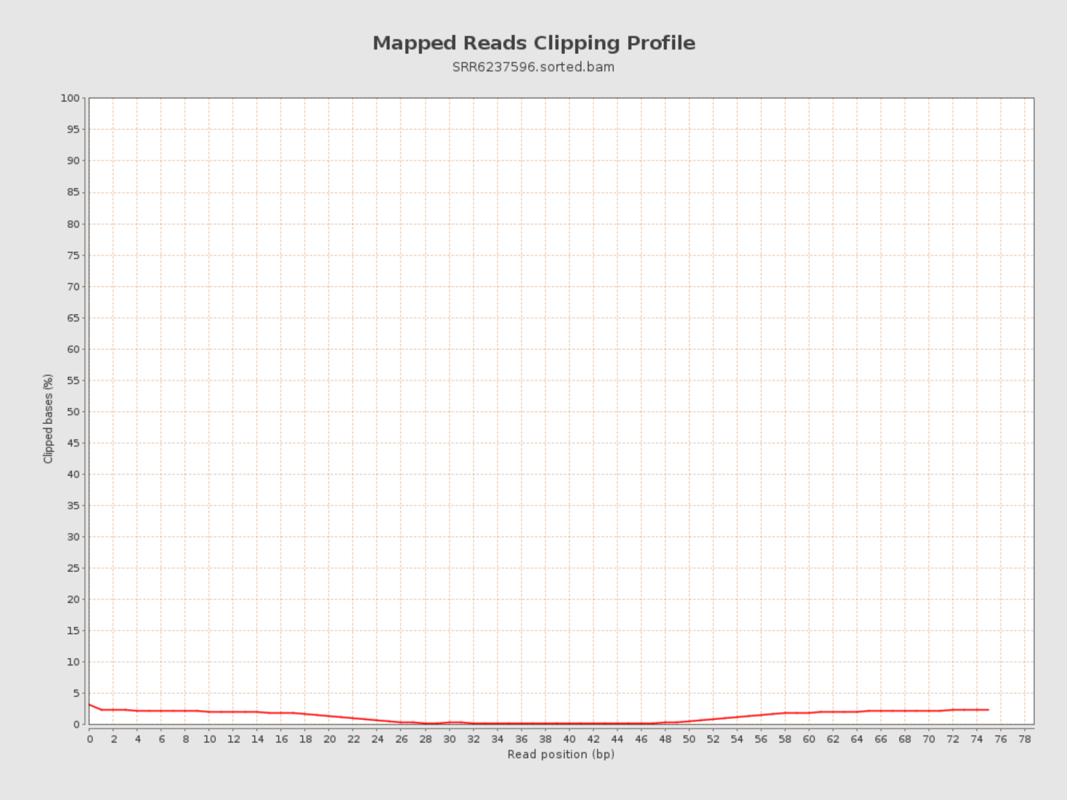
8. Results : Mapped Reads Nucleotide Content



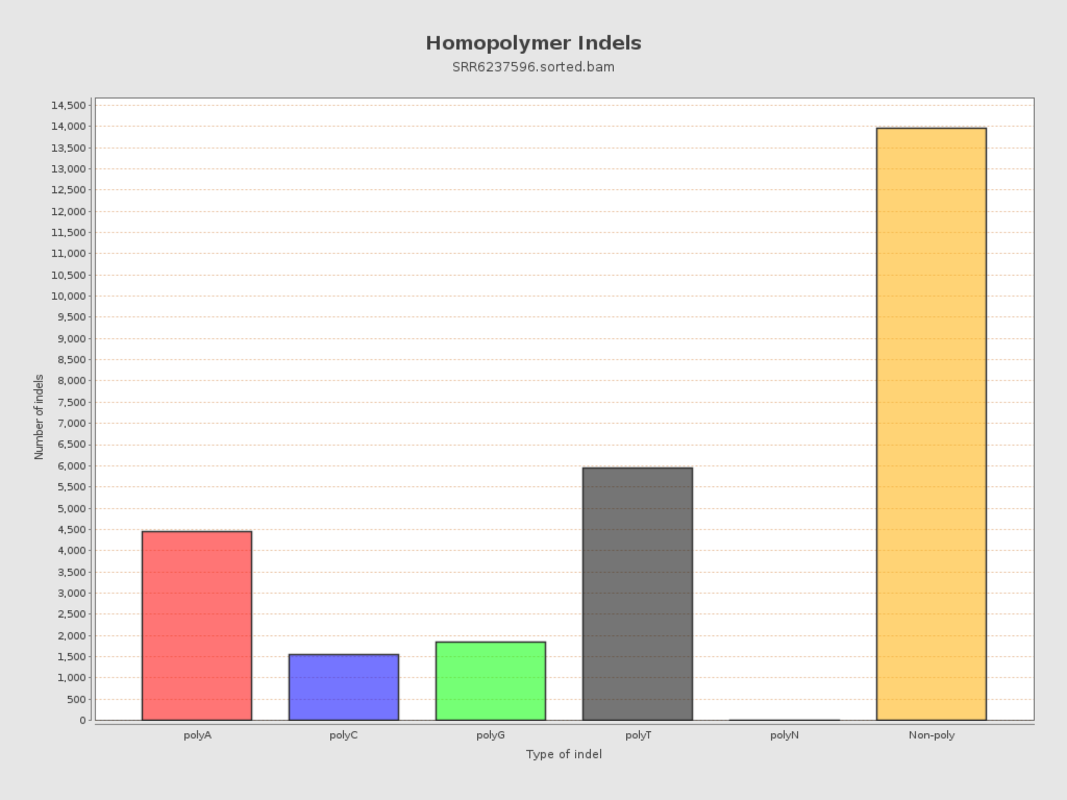
9. Results : Mapped Reads GC-content Distribution



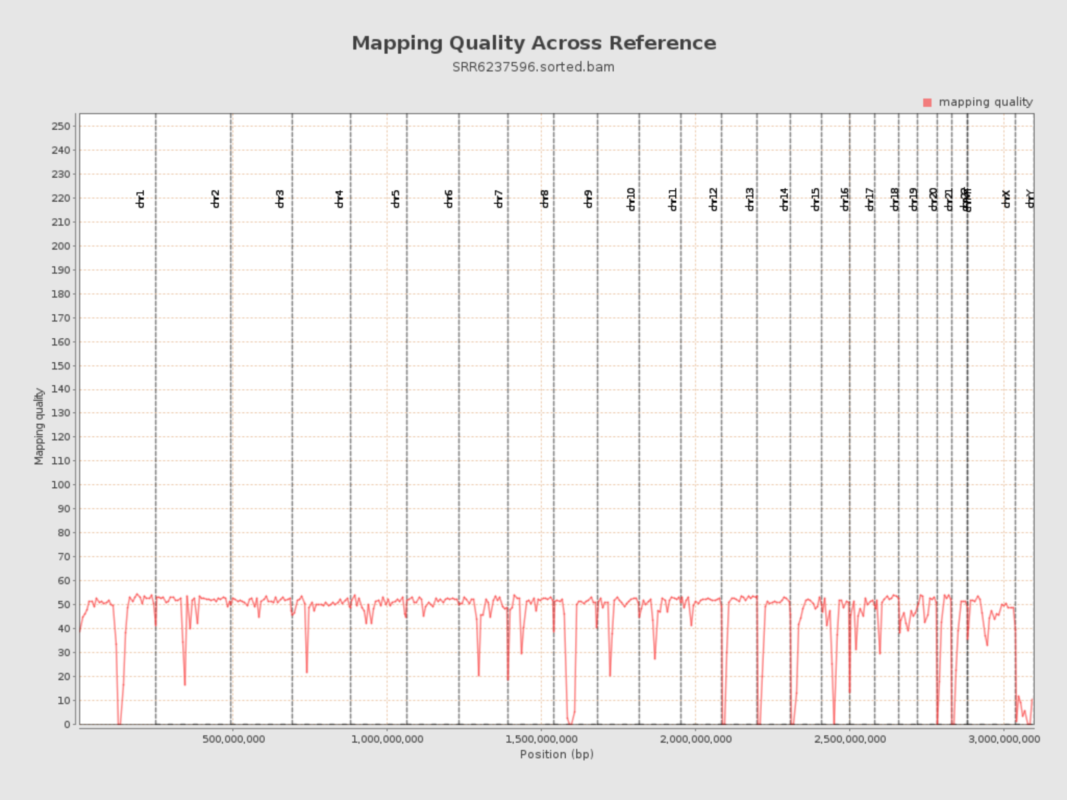
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram