Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:45:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237594.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_SRR6237594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237594.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:44:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,256,842
Mapped reads	942,636 / 75%
Unmapped reads	314,206 / 25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,183 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	52,324 / 4.16%
Duplication rate	4.02%
Clipped reads	603,606 / 48.03%

2.2. ACGT Content

Number/percentage of A's	15,400,323 / 26.47%
Number/percentage of C's	10,031,821 / 17.24%
Number/percentage of T's	18,499,776 / 31.79%
Number/percentage of G's	14,152,676 / 24.32%
Number/percentage of N's	101,724 / 0.17%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.2251

2.4. Mapping Quality

Mean Mapping Quality	42.79

2.5. Mismatches and indels

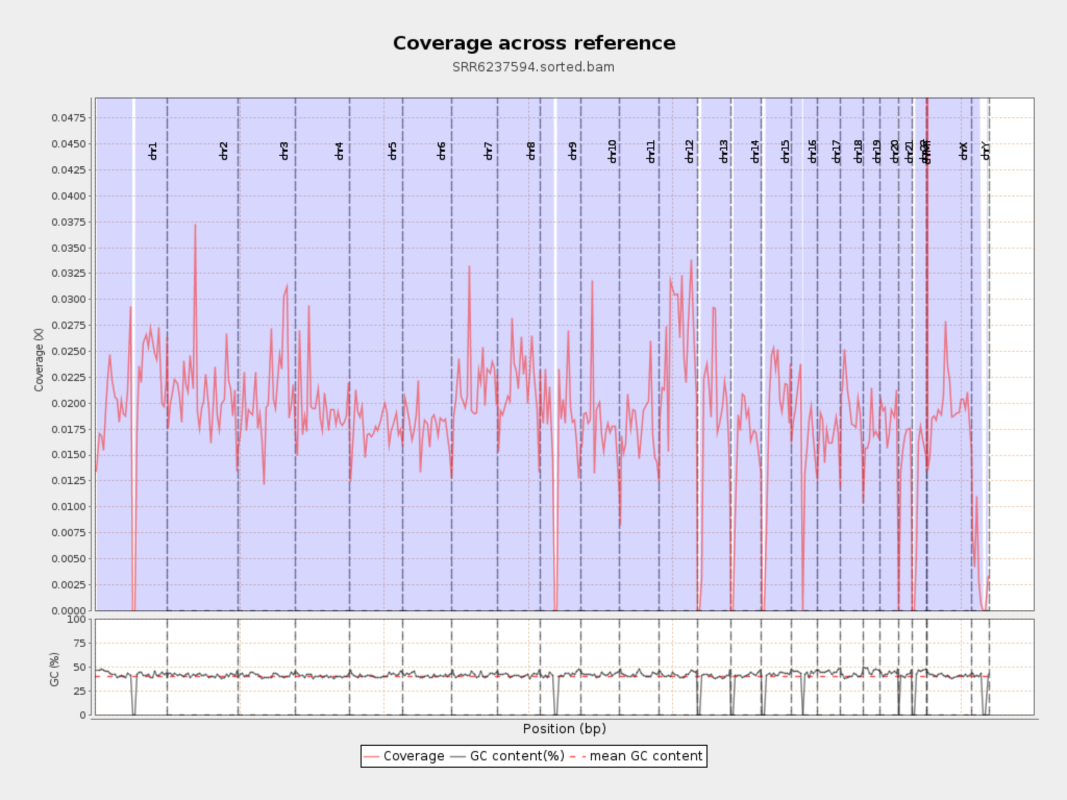
General error rate	1.03%
Mismatches	587,683
Insertions	5,732
Mapped reads with at least one insertion	0.6%
Deletions	22,964
Mapped reads with at least one deletion	2.4%
Homopolymer indels	48.16%

2.6. Chromosome stats

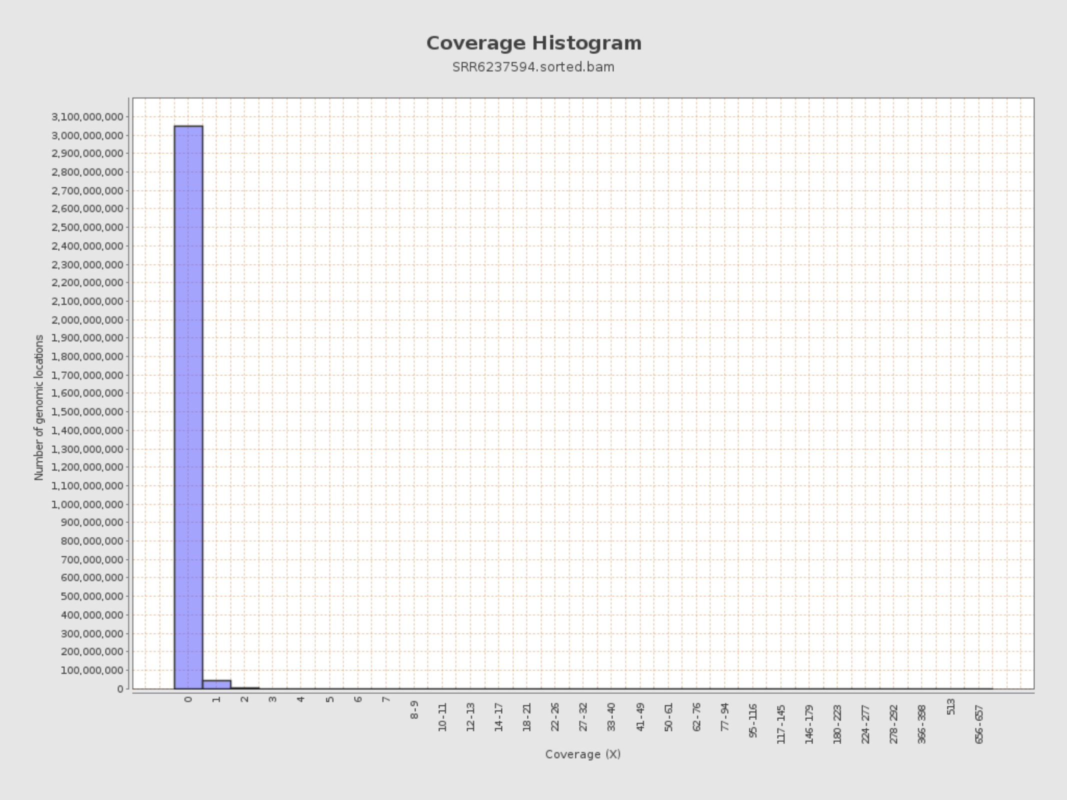
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5083447	0.0204	0.262
chr2	243199373	5118793	0.021	0.3526
chr3	198022430	4102342	0.0207	0.1765
chr4	191154276	3718173	0.0195	0.1727
chr5	180915260	3217753	0.0178	0.1576
chr6	171115067	3034926	0.0177	0.1931
chr7	159138663	3459298	0.0217	0.3034

chr8	146364022	3163771	0.0216	0.221
chr9	141213431	2418694	0.0171	0.2301
chr10	135534747	2437818	0.018	0.2008
chr11	135006516	2397012	0.0178	0.215
chr12	133851895	3494028	0.0261	0.2035
chr13	115169878	2047898	0.0178	0.1698
chr14	107349540	1598316	0.0149	0.1626
chr15	102531392	1832445	0.0179	0.1642
chr16	90354753	1474090	0.0163	0.166
chr17	81195210	1358788	0.0167	0.1664
chr18	78077248	1544161	0.0198	0.4306
chr19	59128983	1000632	0.0169	0.2066
chr20	63025520	1162784	0.0184	0.1661
chr21	48129895	690906	0.0144	0.1588
chr22	51304566	578470	0.0113	0.1271
chrMT	16571	39461	2.3813	2.2461
chrX	155270560	3043852	0.0196	0.1809
chrY	59373566	206636	0.0035	0.0913

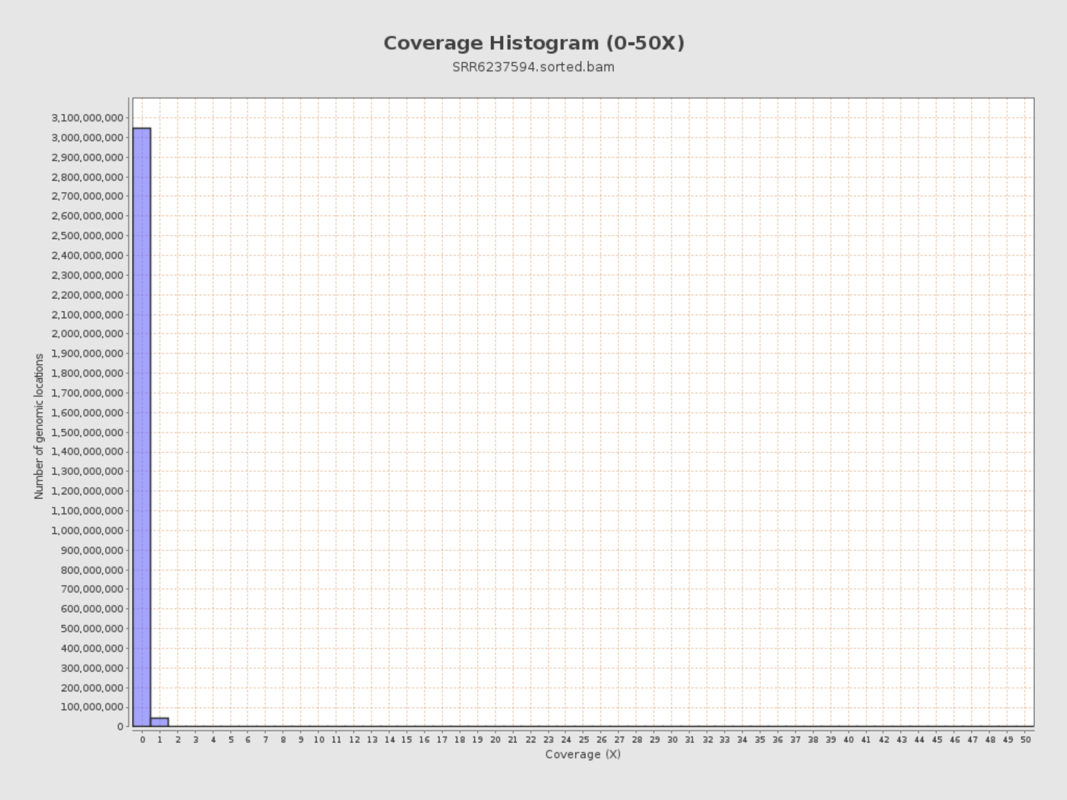
3. Results : Coverage across reference



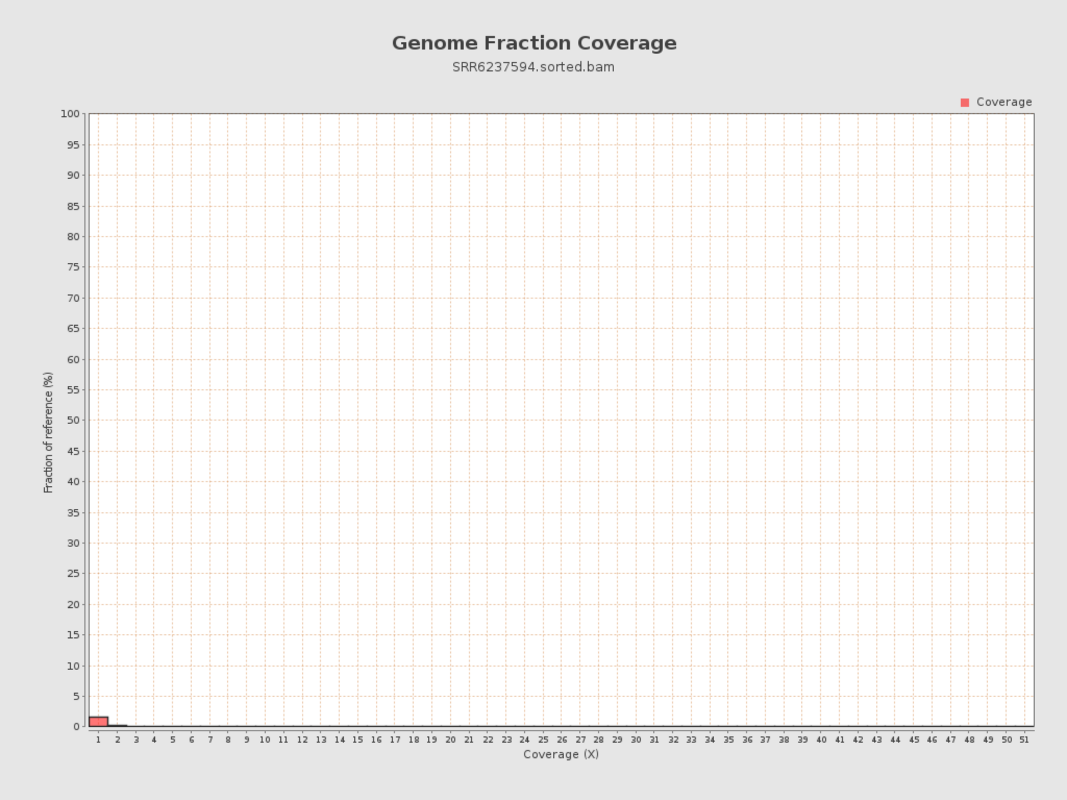
4. Results : Coverage Histogram



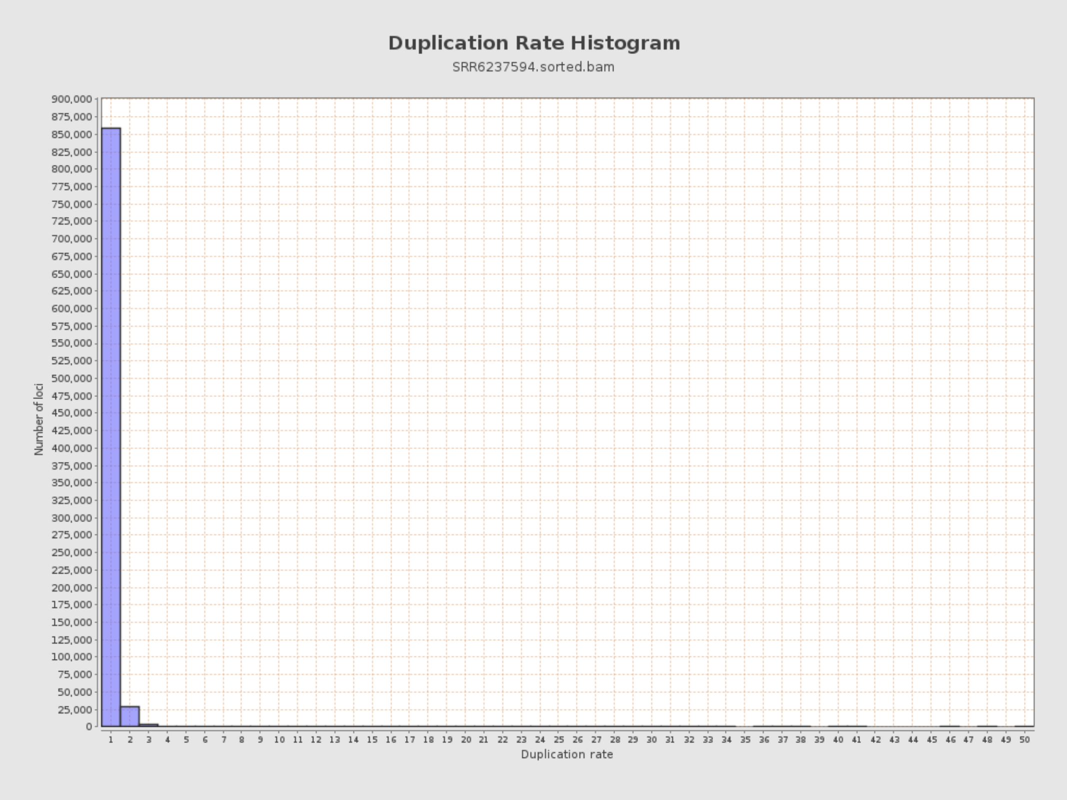
5. Results : Coverage Histogram (0-50X)



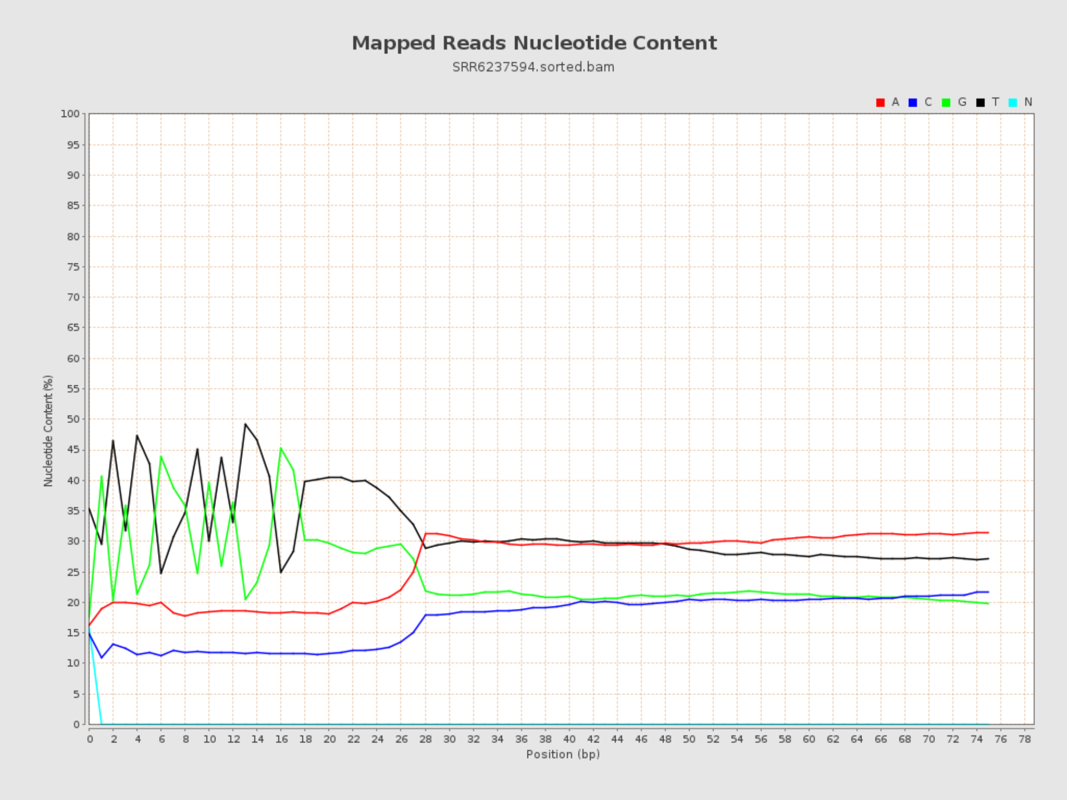
6. Results : Genome Fraction Coverage



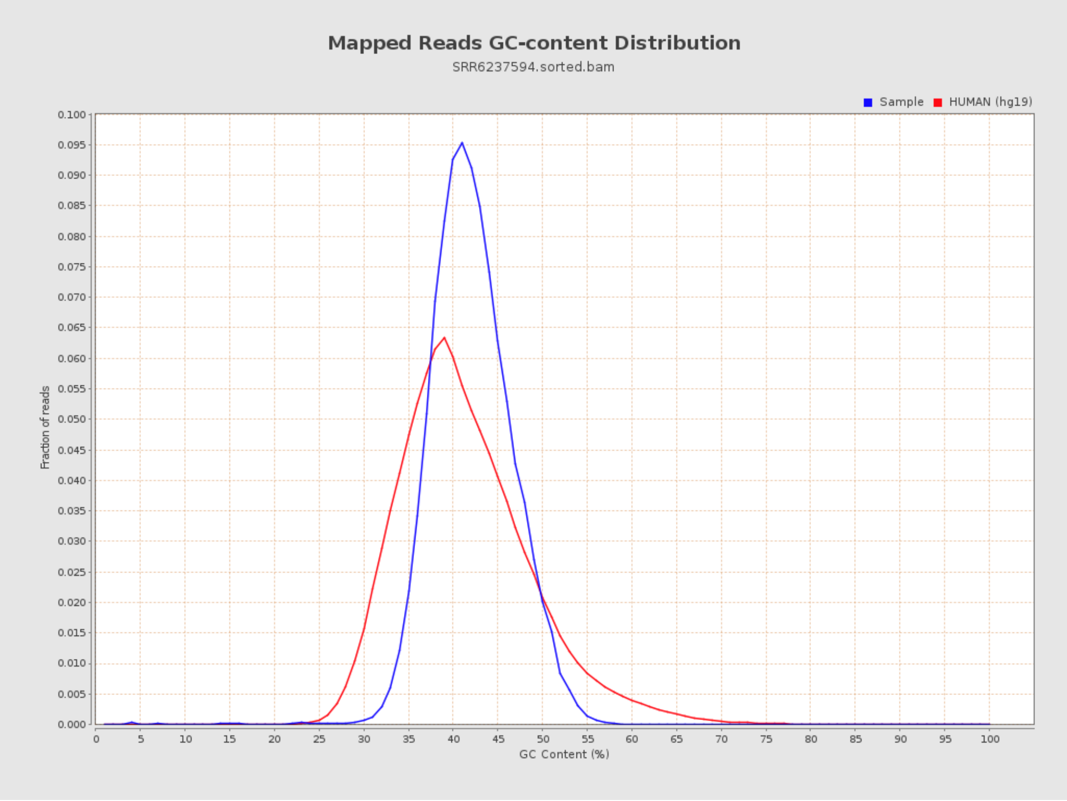
7. Results : Duplication Rate Histogram



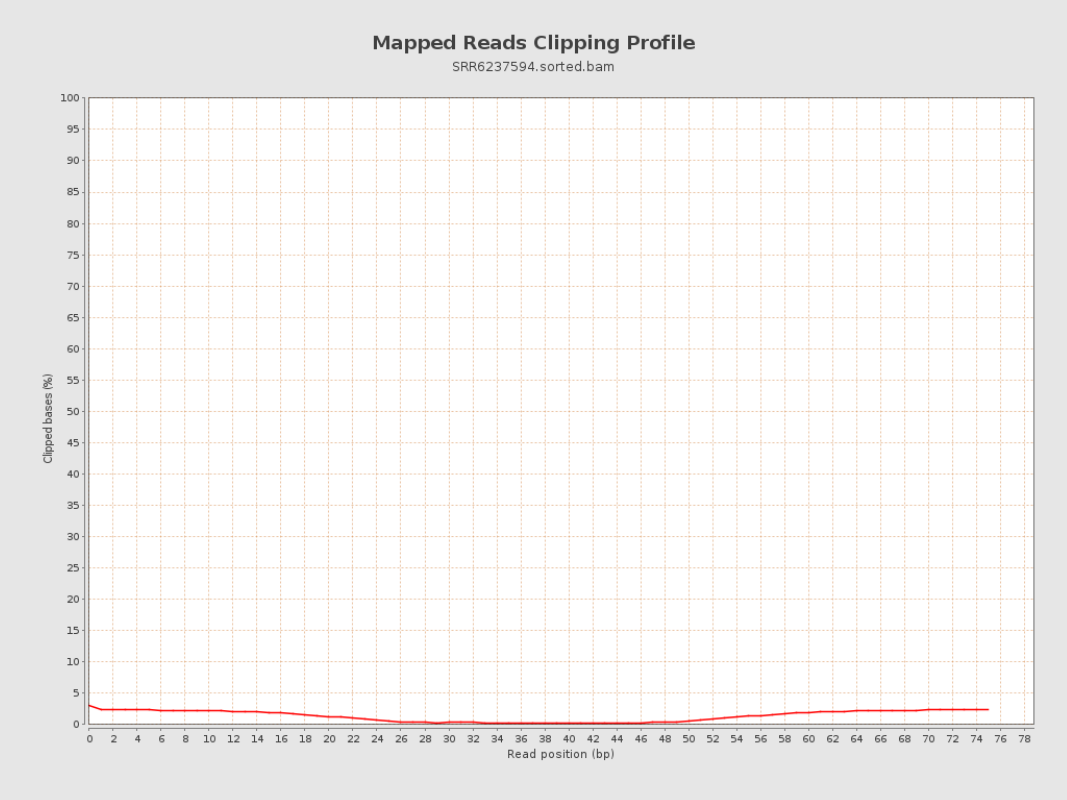
8. Results : Mapped Reads Nucleotide Content



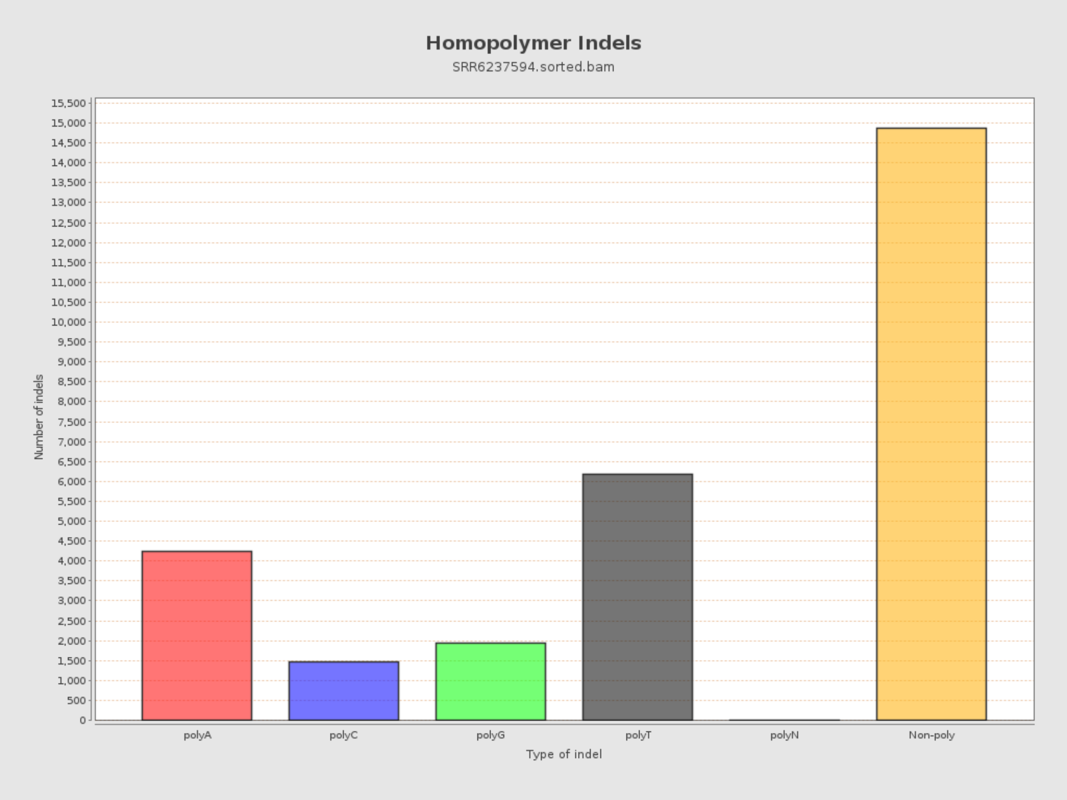
9. Results : Mapped Reads GC-content Distribution



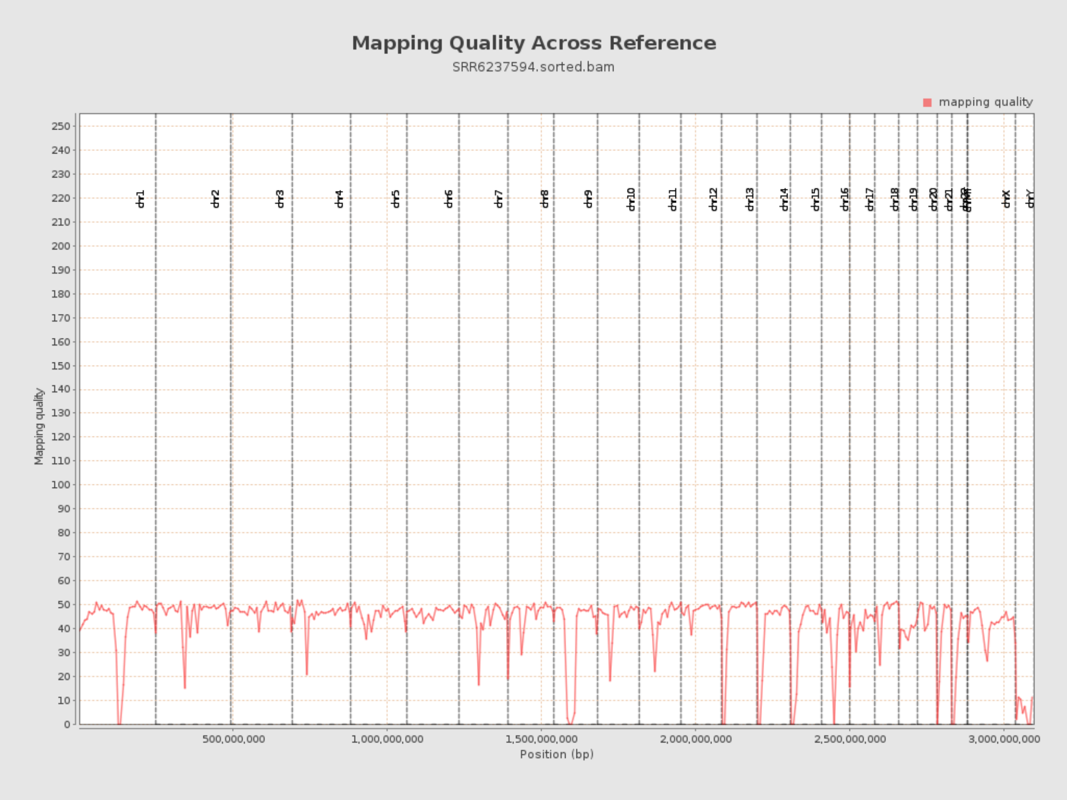
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram