Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:54:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234088.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_SRR6234088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:54:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	936,572
Mapped reads	642,258 / 68.58%
Unmapped reads	294,314 / 31.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,189 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	14,936 / 1.59%
Duplication rate	1.83%
Clipped reads	359,157 / 38.35%

2.2. ACGT Content

Number/percentage of A's	11,459,008 / 28.21%
Number/percentage of C's	6,691,255 / 16.47%
Number/percentage of T's	13,091,966 / 32.23%
Number/percentage of G's	9,374,315 / 23.08%
Number/percentage of N's	7,594 / 0.02%
GC Percentage	39.55%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1541

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

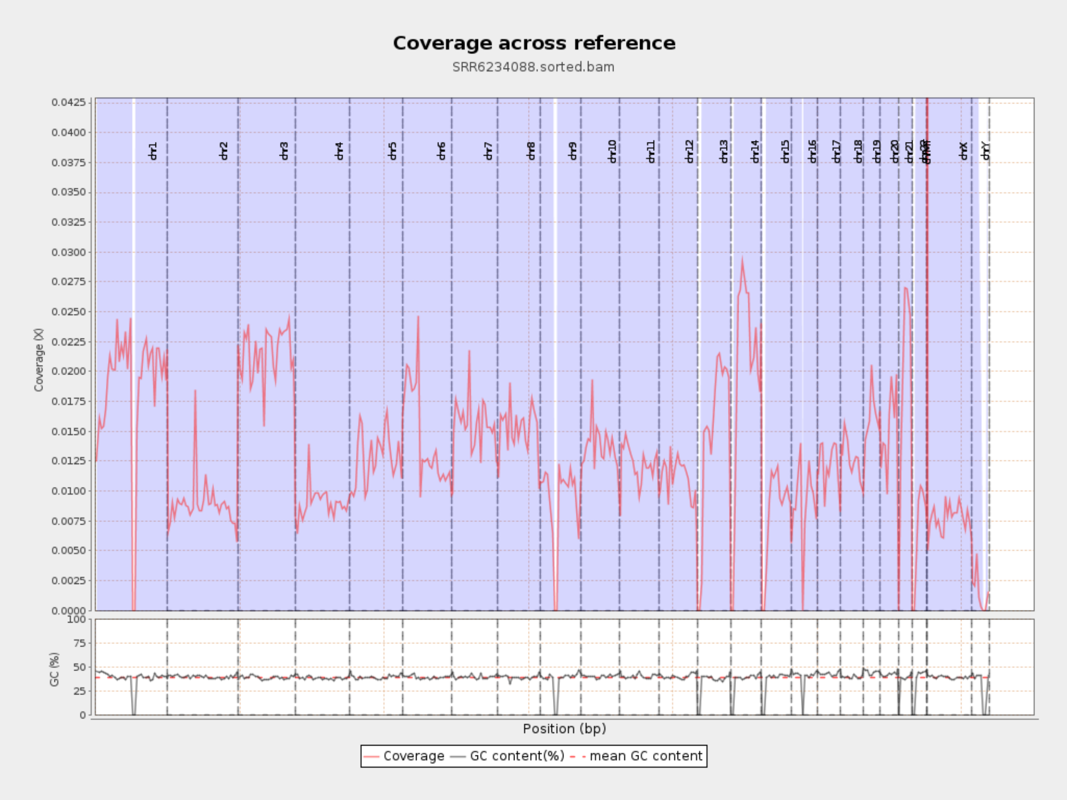
General error rate	0.96%
Mismatches	383,707
Insertions	3,150
Mapped reads with at least one insertion	0.49%
Deletions	11,951
Mapped reads with at least one deletion	1.84%
Homopolymer indels	45.71%

2.6. Chromosome stats

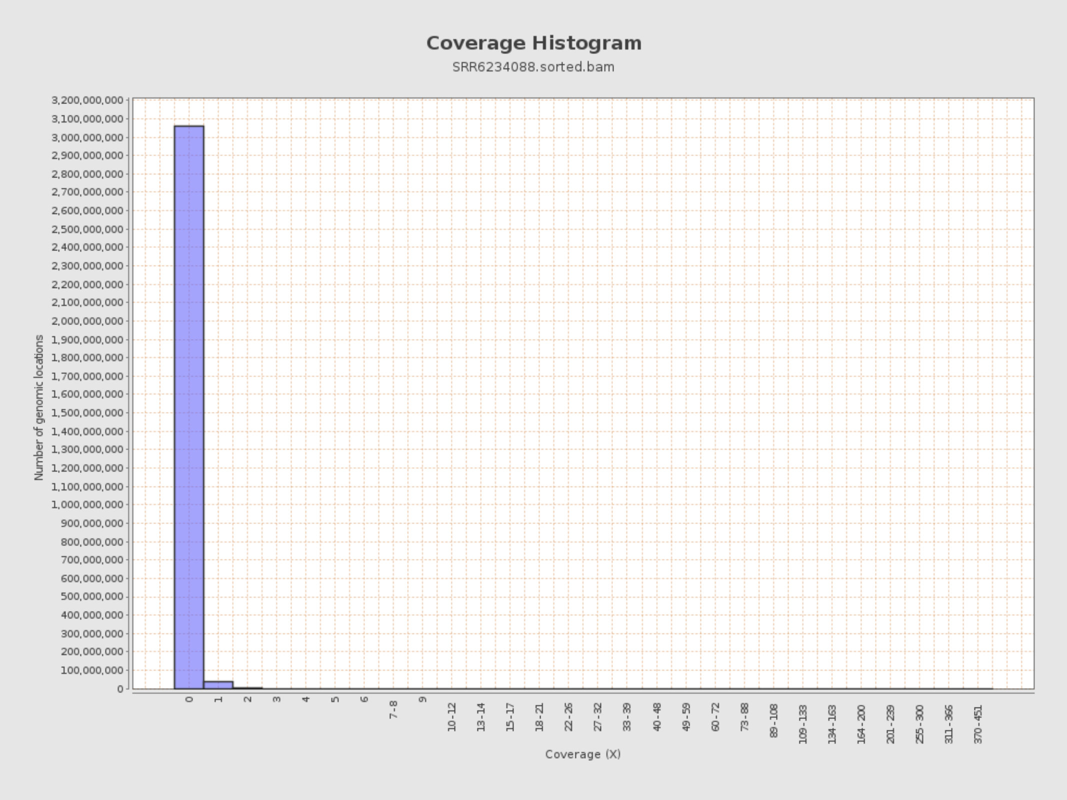
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4661447	0.0187	0.2401
chr2	243199373	2161162	0.0089	0.1294
chr3	198022430	4269926	0.0216	0.1544
chr4	191154276	1722859	0.009	0.101
chr5	180915260	2327373	0.0129	0.1192
chr6	171115067	2481335	0.0145	0.1359
chr7	159138663	2473821	0.0155	0.1727

chr8	146364022	2221301	0.0152	0.3012
chr9	141213431	1283577	0.0091	0.1161
chr10	135534747	1857342	0.0137	0.1378
chr11	135006516	1662950	0.0123	0.1308
chr12	133851895	1489853	0.0111	0.1107
chr13	115169878	1710712	0.0149	0.1278
chr14	107349540	2158762	0.0201	0.1514
chr15	102531392	852542	0.0083	0.0954
chr16	90354753	801787	0.0089	0.1036
chr17	81195210	987101	0.0122	0.1194
chr18	78077248	992691	0.0127	0.1981
chr19	59128983	954651	0.0161	0.1569
chr20	63025520	947669	0.015	0.1295
chr21	48129895	947478	0.0197	0.149
chr22	51304566	346288	0.0067	0.0861
chrMT	16571	37690	2.2745	2.1746
chrX	155270560	1205495	0.0078	0.0969
chrY	59373566	88795	0.0015	0.046

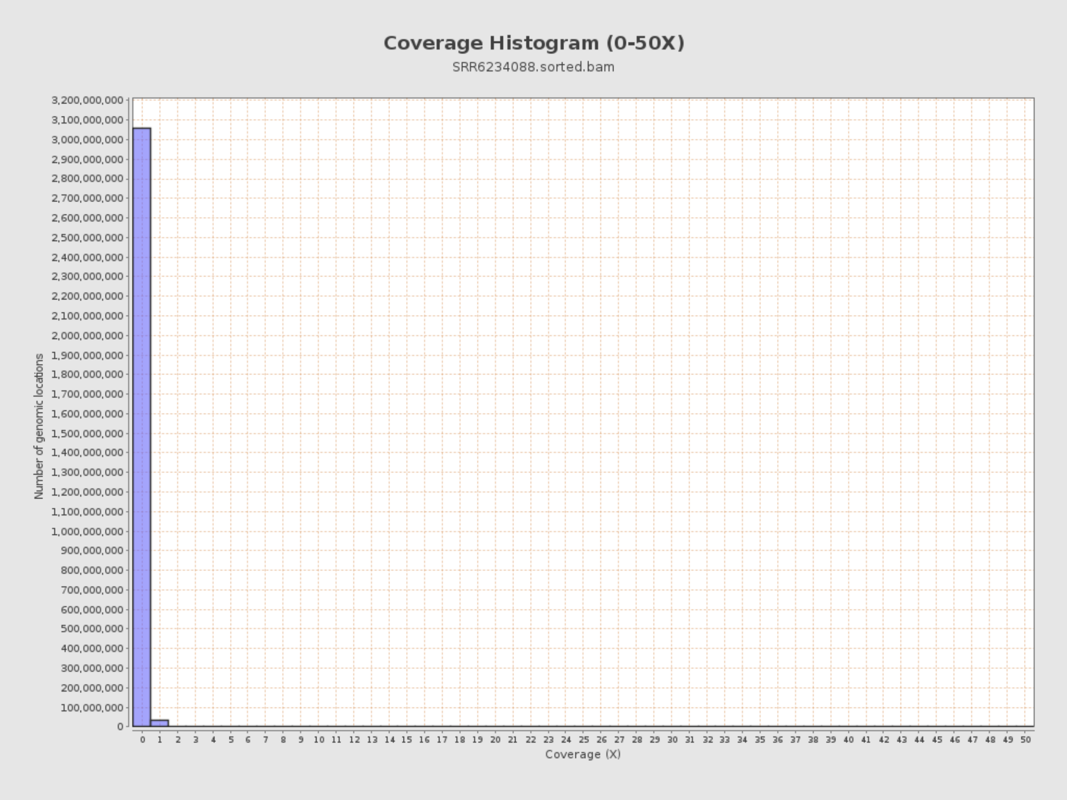
3. Results : Coverage across reference



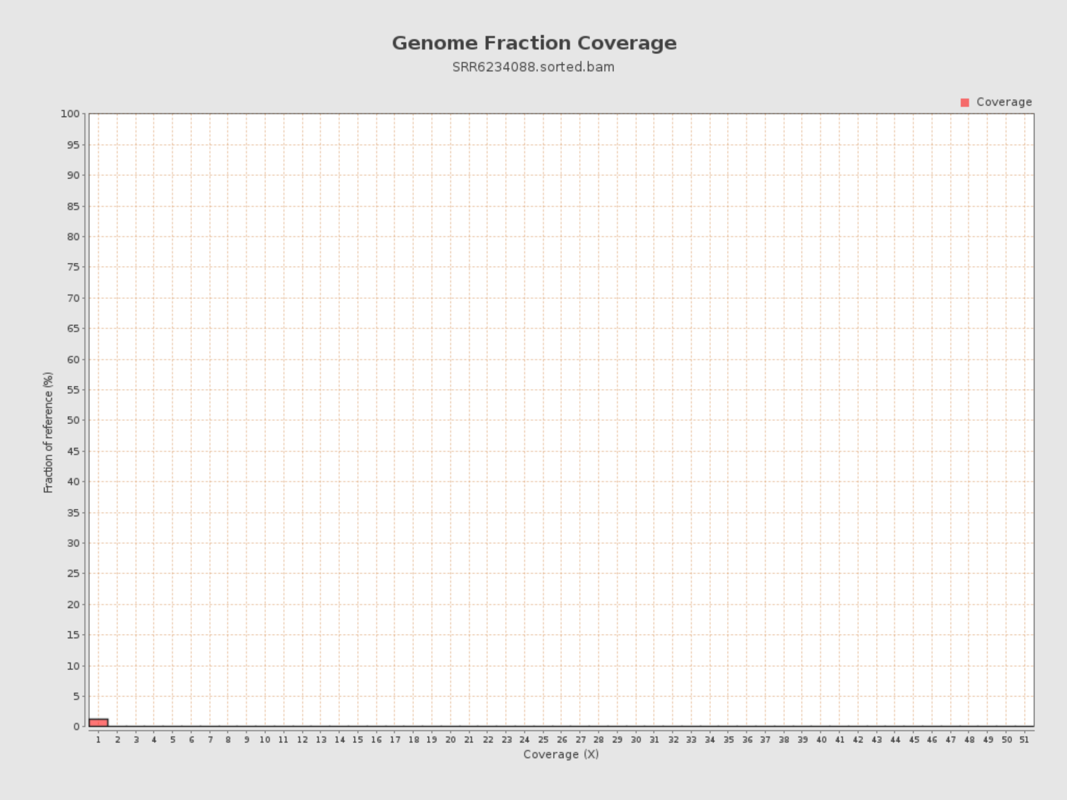
4. Results : Coverage Histogram



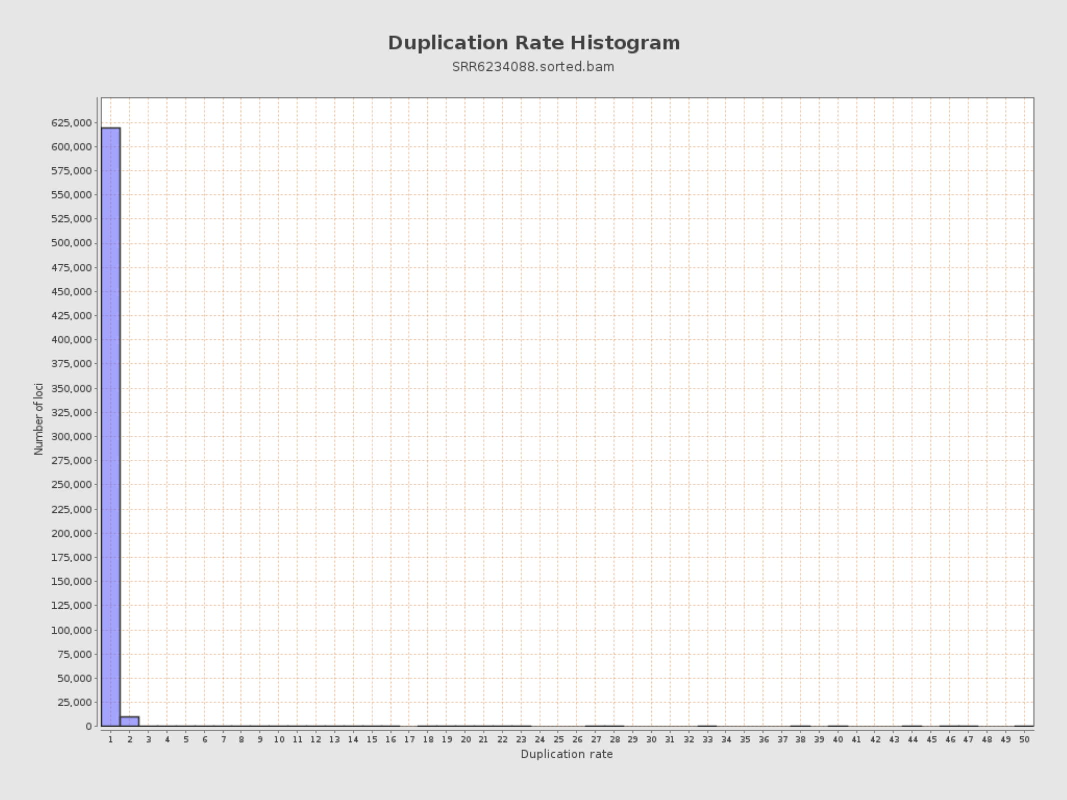
5. Results : Coverage Histogram (0-50X)



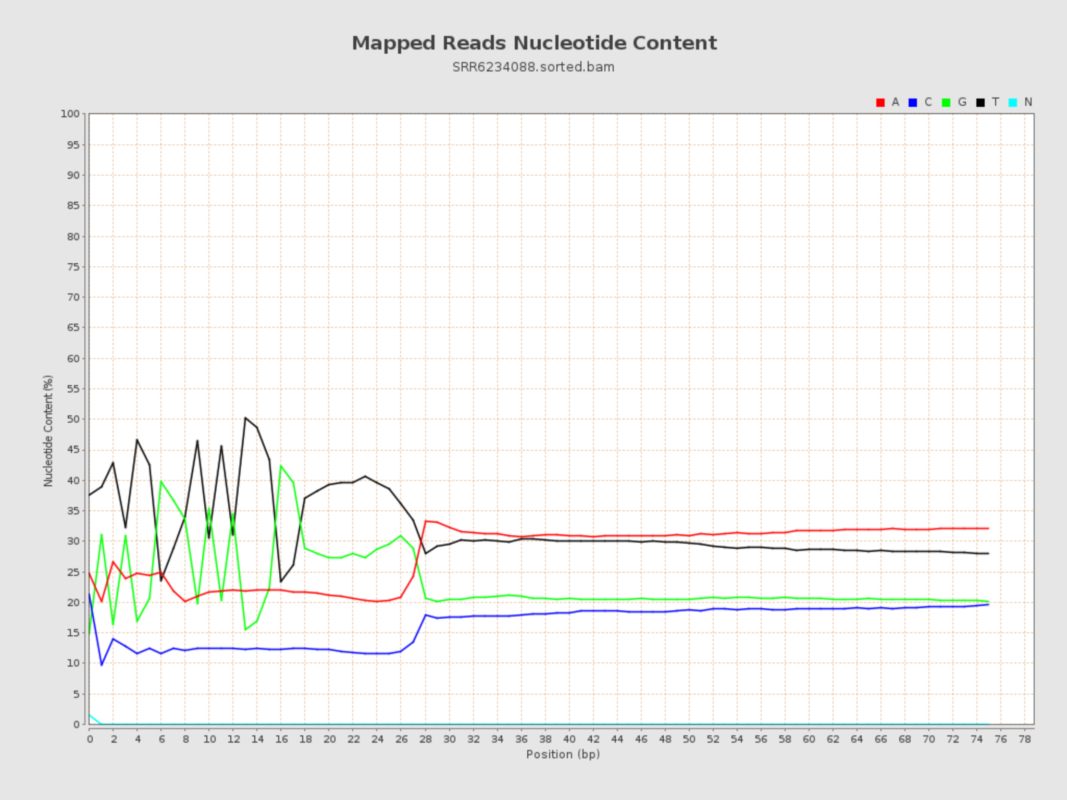
6. Results : Genome Fraction Coverage



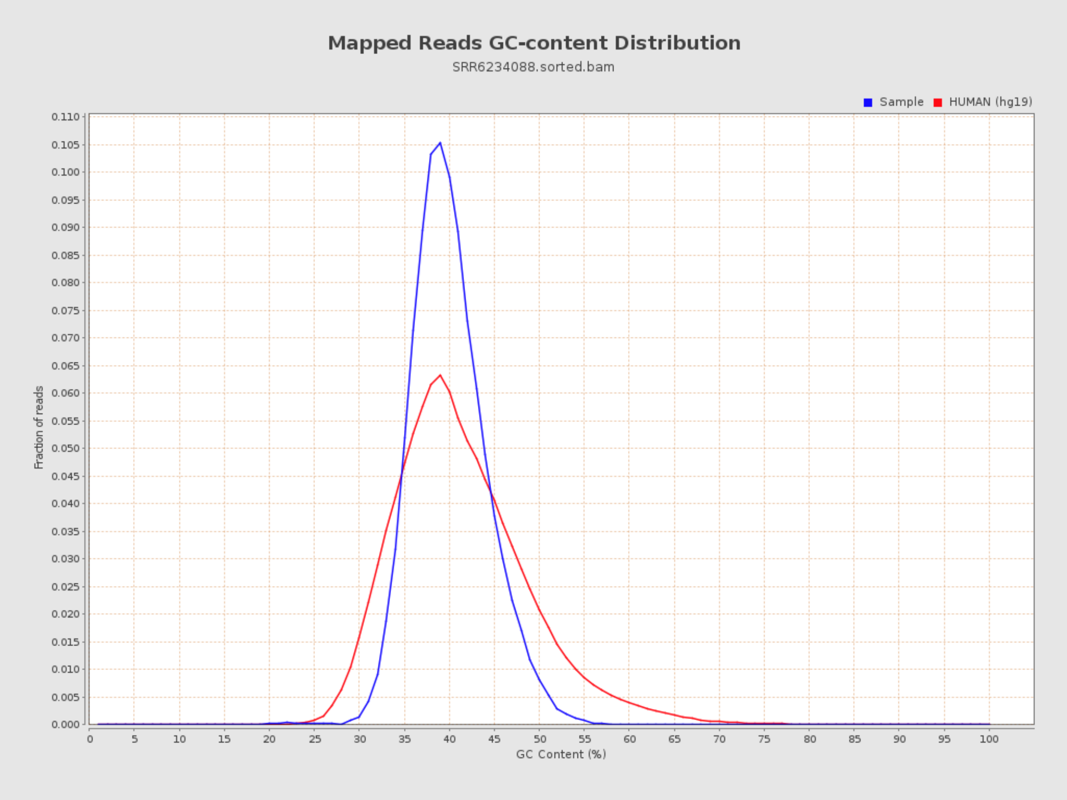
7. Results : Duplication Rate Histogram



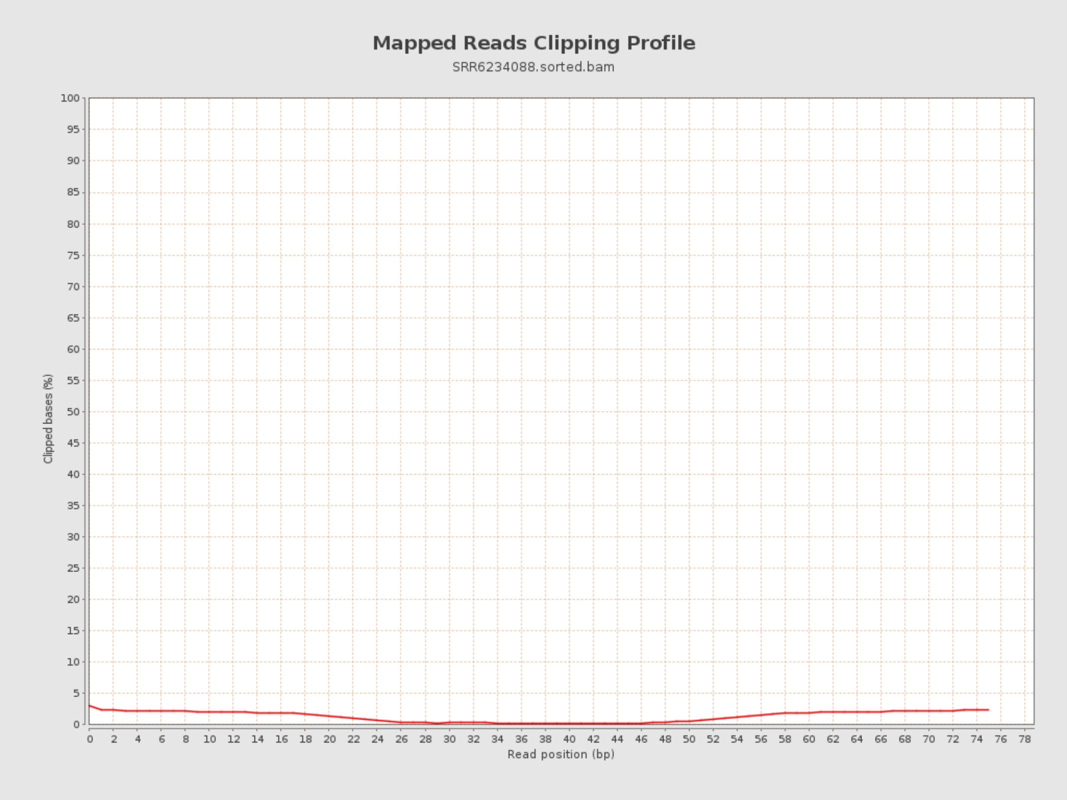
8. Results : Mapped Reads Nucleotide Content



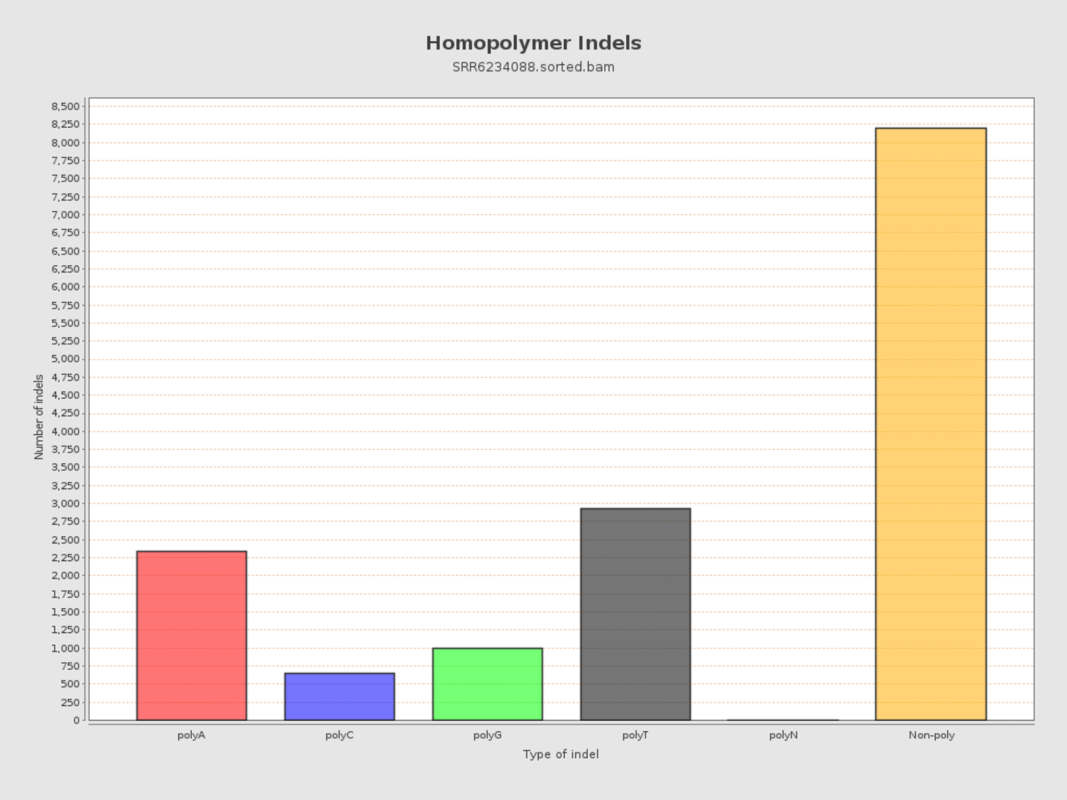
9. Results : Mapped Reads GC-content Distribution



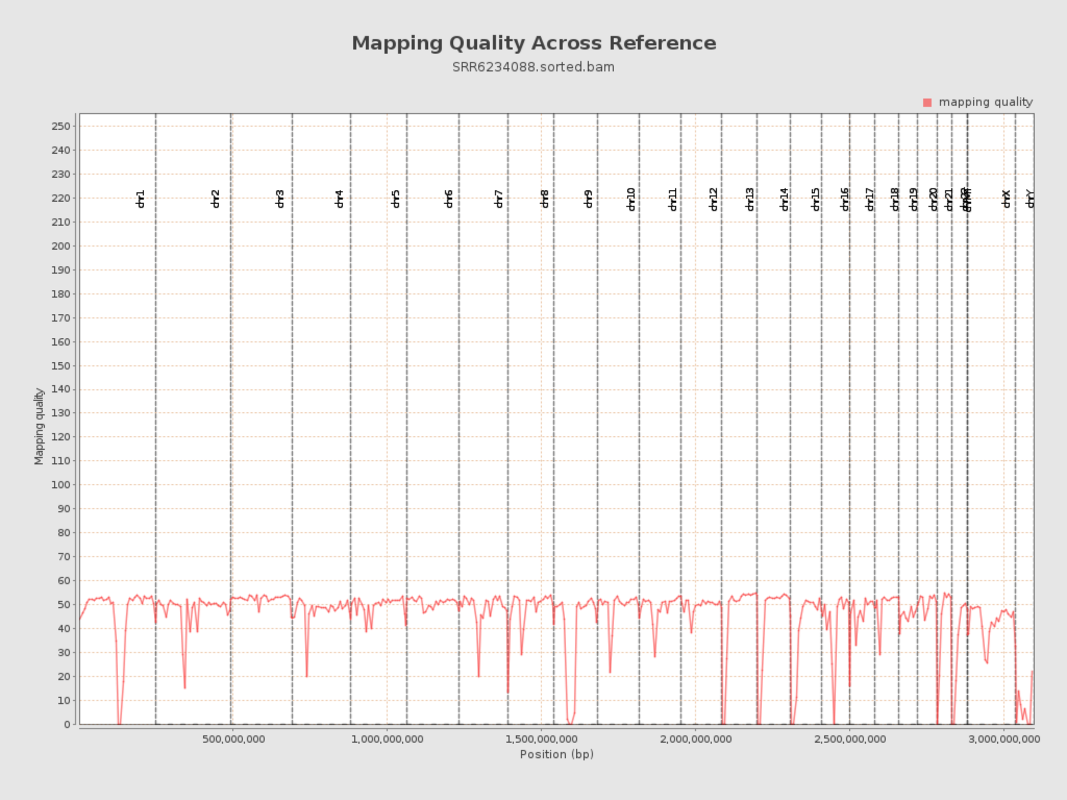
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram