Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:04:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236111.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_SRR6236111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:04:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,416,049
Mapped reads	3,968,454 / 89.86%
Unmapped reads	447,595 / 10.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,572 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	267,812 / 6.06%
Duplication rate	5.31%
Clipped reads	1,728,497 / 39.14%

2.2. ACGT Content

Number/percentage of A's	75,217,512 / 28.36%
Number/percentage of C's	48,921,667 / 18.45%
Number/percentage of T's	83,705,733 / 31.57%
Number/percentage of G's	57,330,814 / 21.62%
Number/percentage of N's	2,501 / 0%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0857

Standard Deviation	0.7158

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

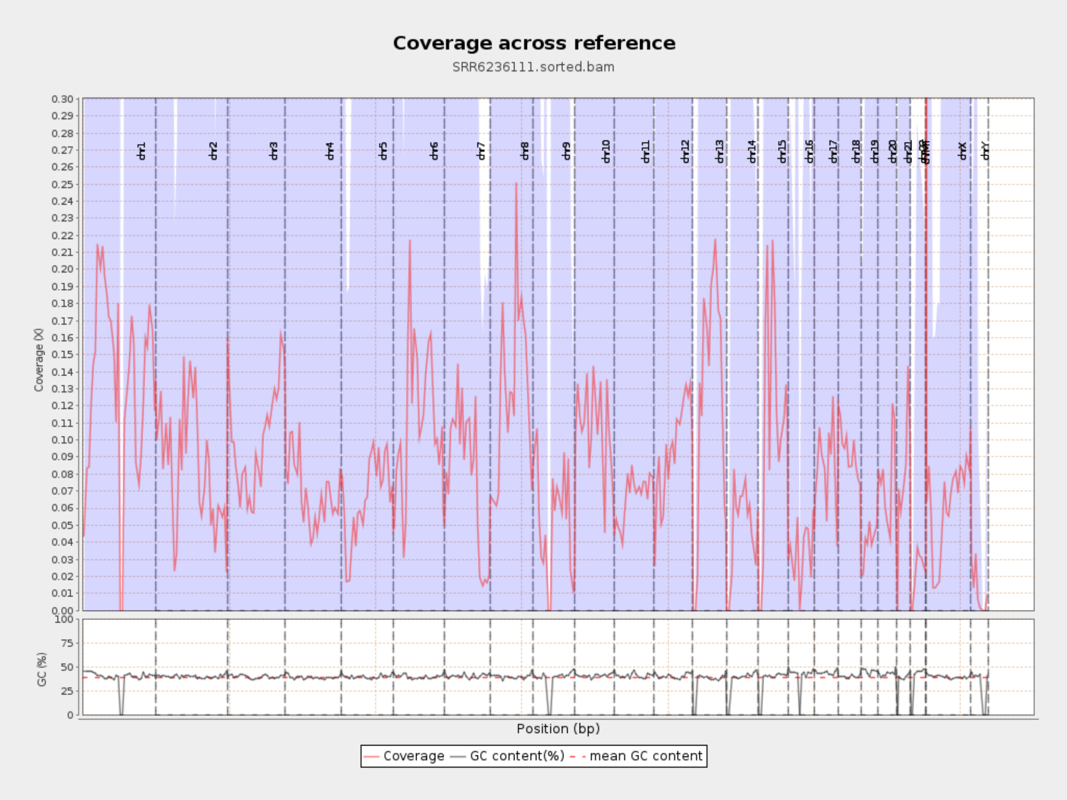
General error rate	0.73%
Mismatches	1,905,767
Insertions	19,298
Mapped reads with at least one insertion	0.48%
Deletions	76,814
Mapped reads with at least one deletion	1.91%
Homopolymer indels	46.95%

2.6. Chromosome stats

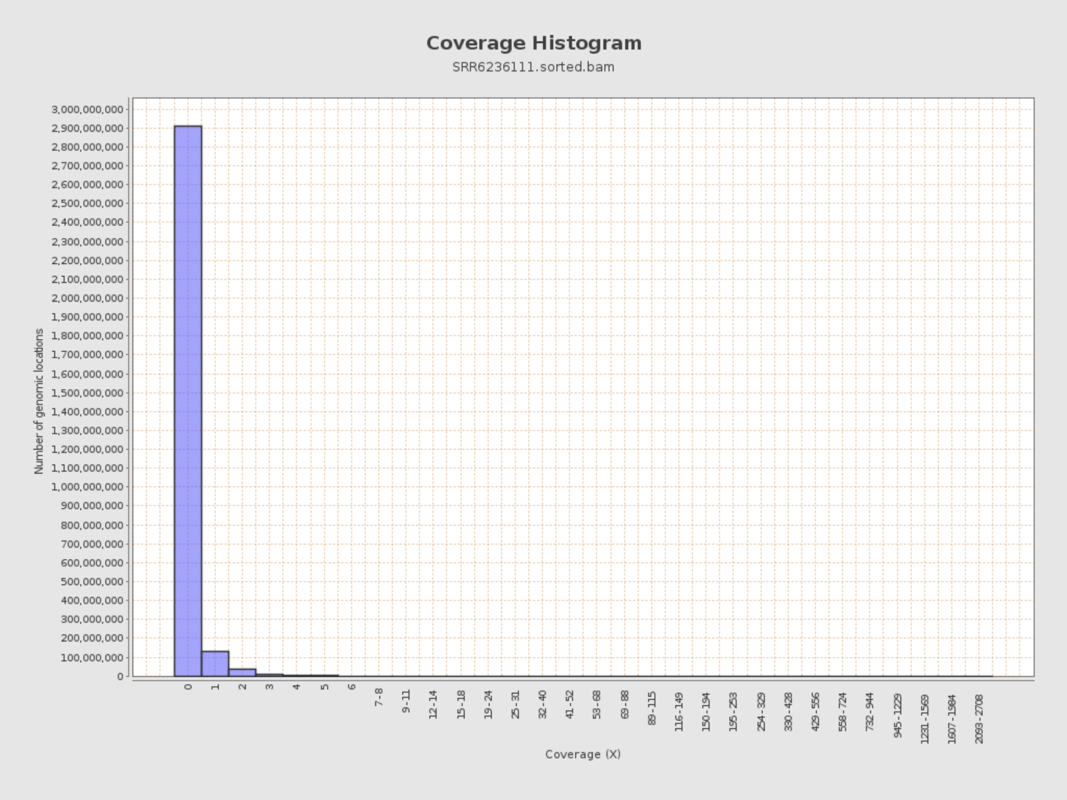
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33414297	0.1341	1.1985
chr2	243199373	20810087	0.0856	0.7283
chr3	198022430	19763360	0.0998	0.4217
chr4	191154276	13137533	0.0687	0.3923
chr5	180915260	12008734	0.0664	0.3452
chr6	171115067	19555710	0.1143	0.7289
chr7	159138663	12549015	0.0789	0.696

chr8	146364022	18787659	0.1284	1.8315
chr9	141213431	7546659	0.0534	0.4792
chr10	135534747	14621374	0.1079	0.6287
chr11	135006516	8976153	0.0665	0.4601
chr12	133851895	12704061	0.0949	0.4179
chr13	115169878	14731383	0.1279	0.4896
chr14	107349540	5155290	0.048	0.3077
chr15	102531392	11470075	0.1119	0.4625
chr16	90354753	3045694	0.0337	0.3029
chr17	81195210	6977727	0.0859	0.4613
chr18	78077248	7300698	0.0935	0.7886
chr19	59128983	2423204	0.041	0.7129
chr20	63025520	4885886	0.0775	0.3823
chr21	48129895	3849244	0.08	0.4132
chr22	51304566	1126380	0.022	0.1882
chrMT	16571	272017	16.4152	10.0186
chrX	155270560	9554623	0.0615	0.3604
chrY	59373566	645412	0.0109	0.2472

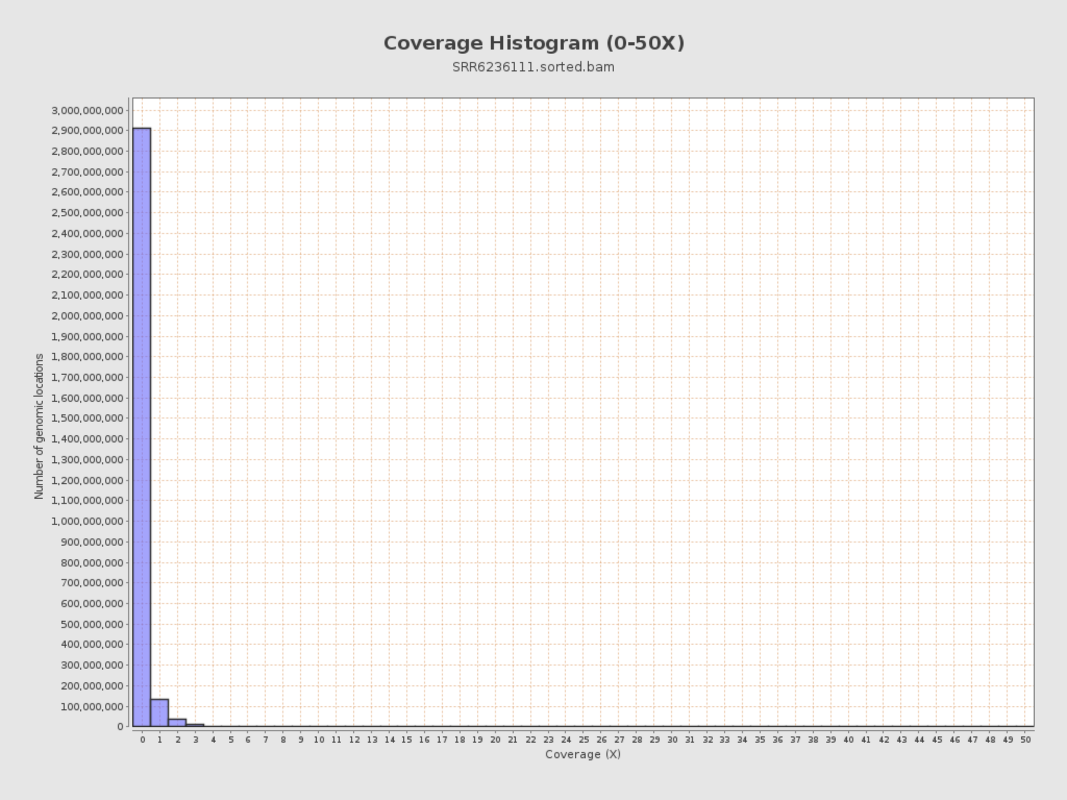
3. Results : Coverage across reference



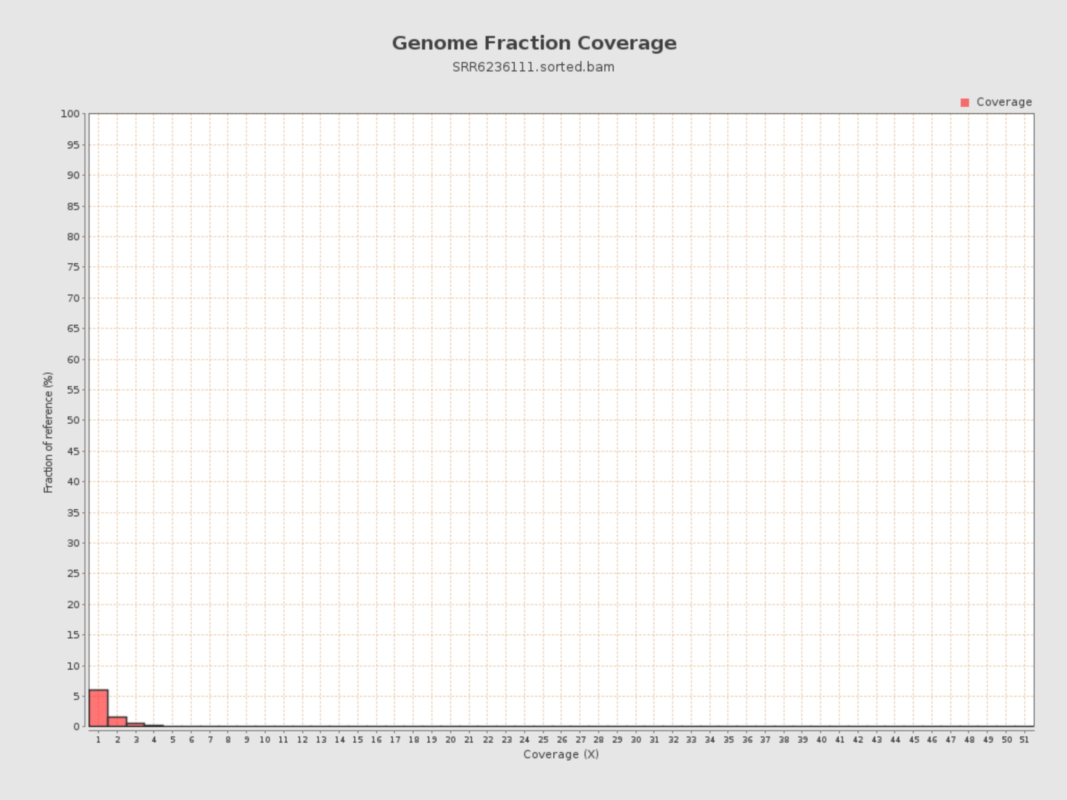
4. Results : Coverage Histogram



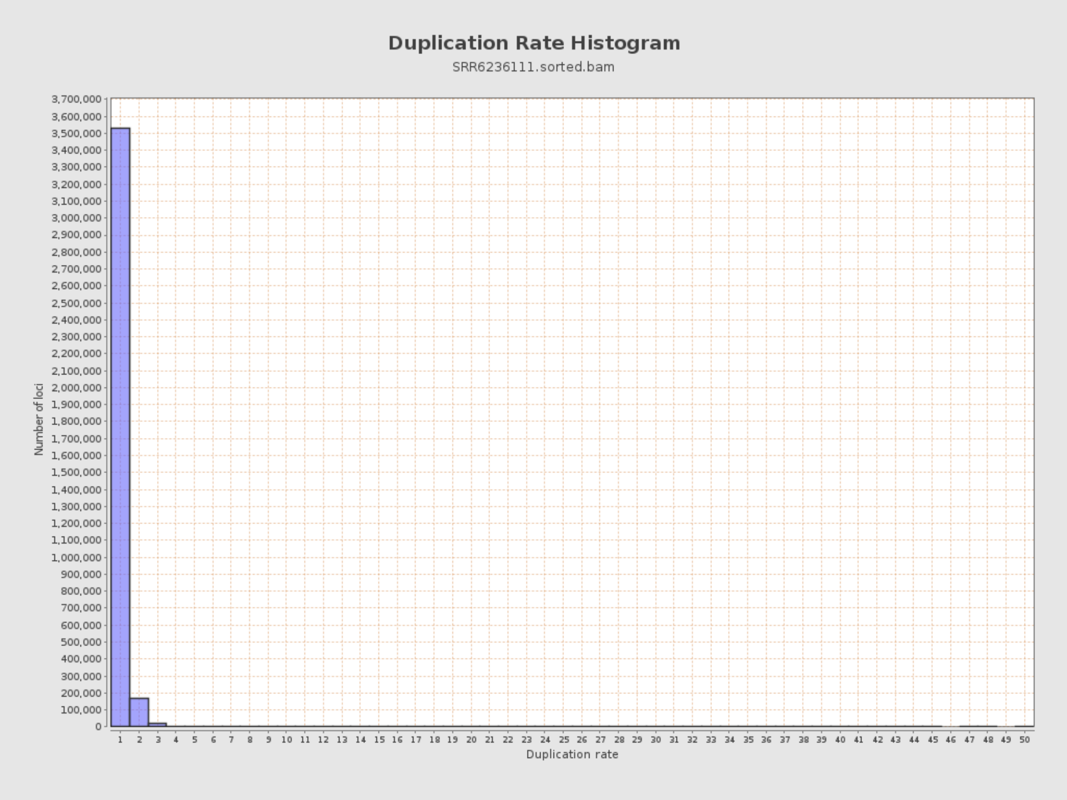
5. Results : Coverage Histogram (0-50X)



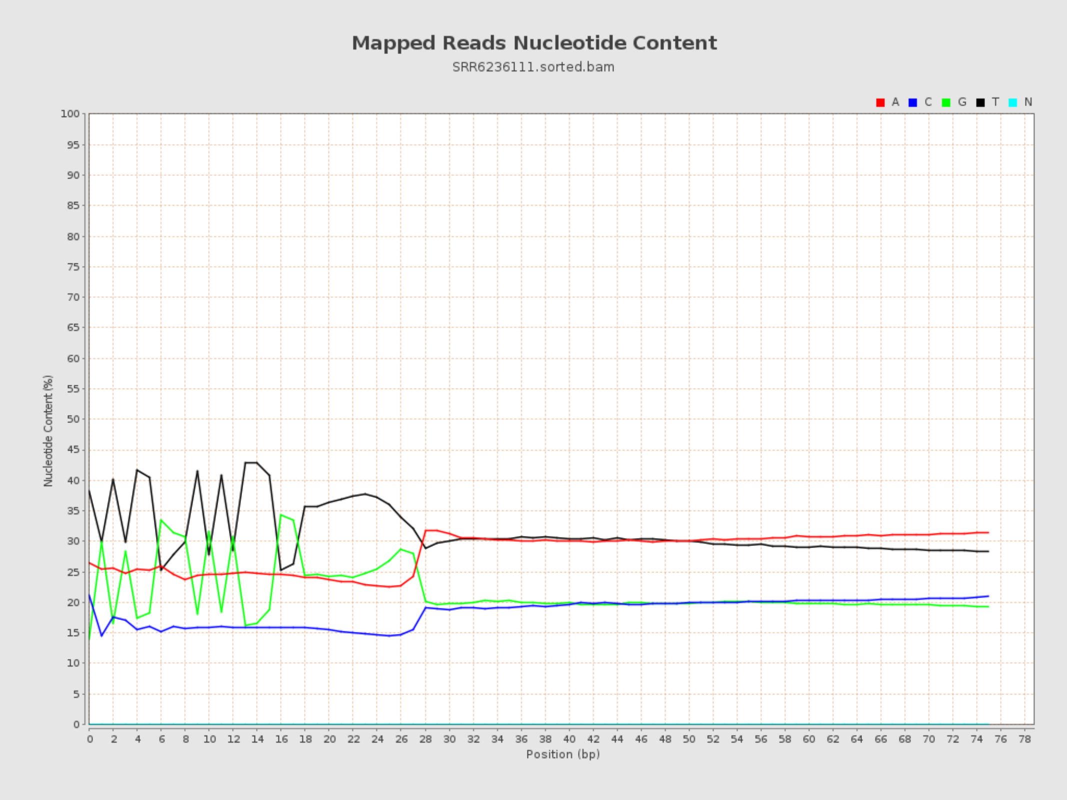
6. Results : Genome Fraction Coverage



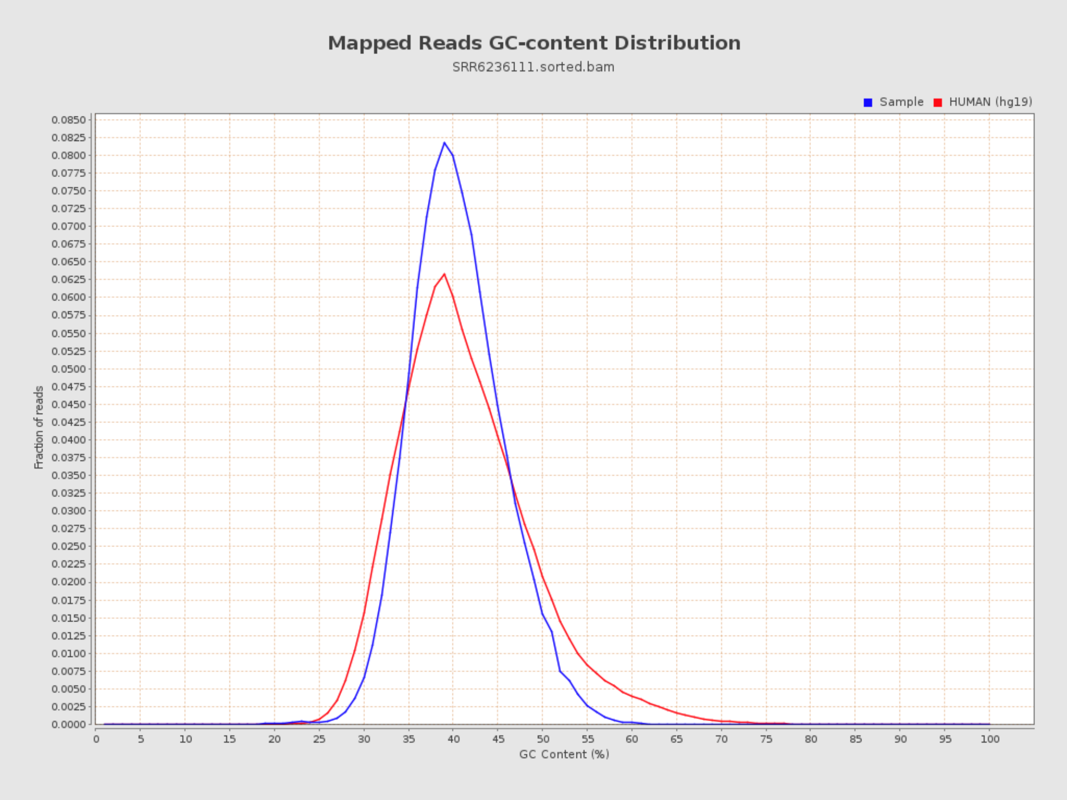
7. Results : Duplication Rate Histogram



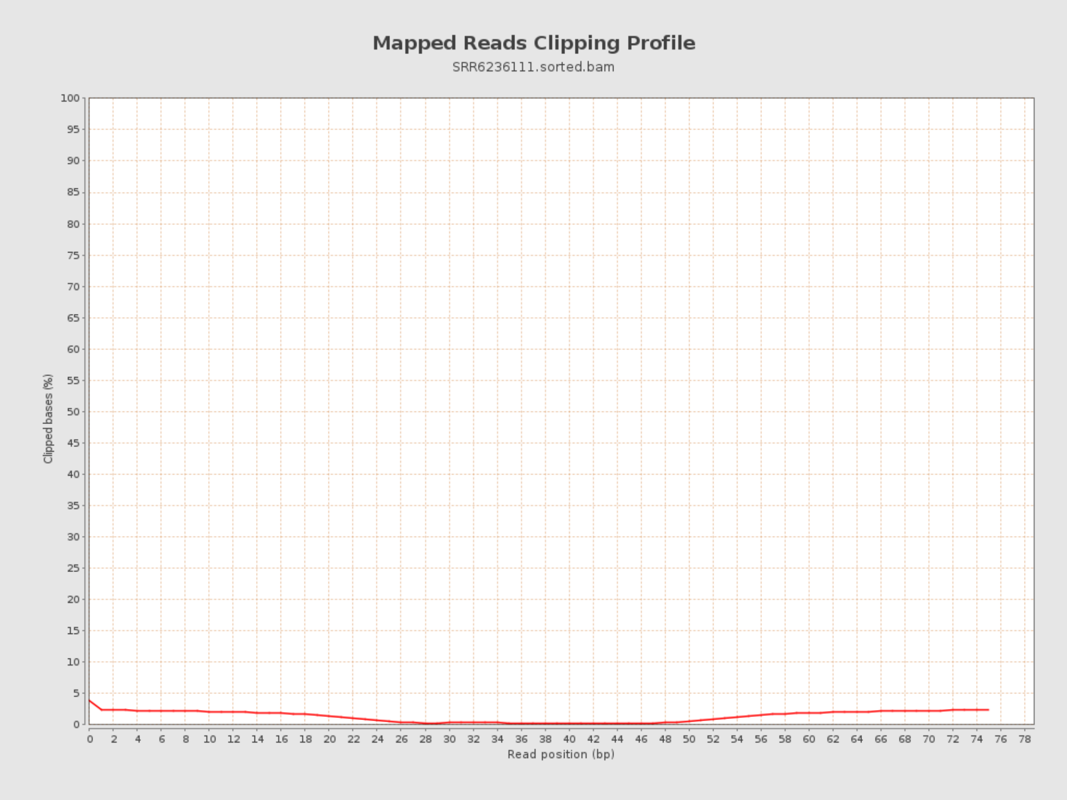
8. Results : Mapped Reads Nucleotide Content



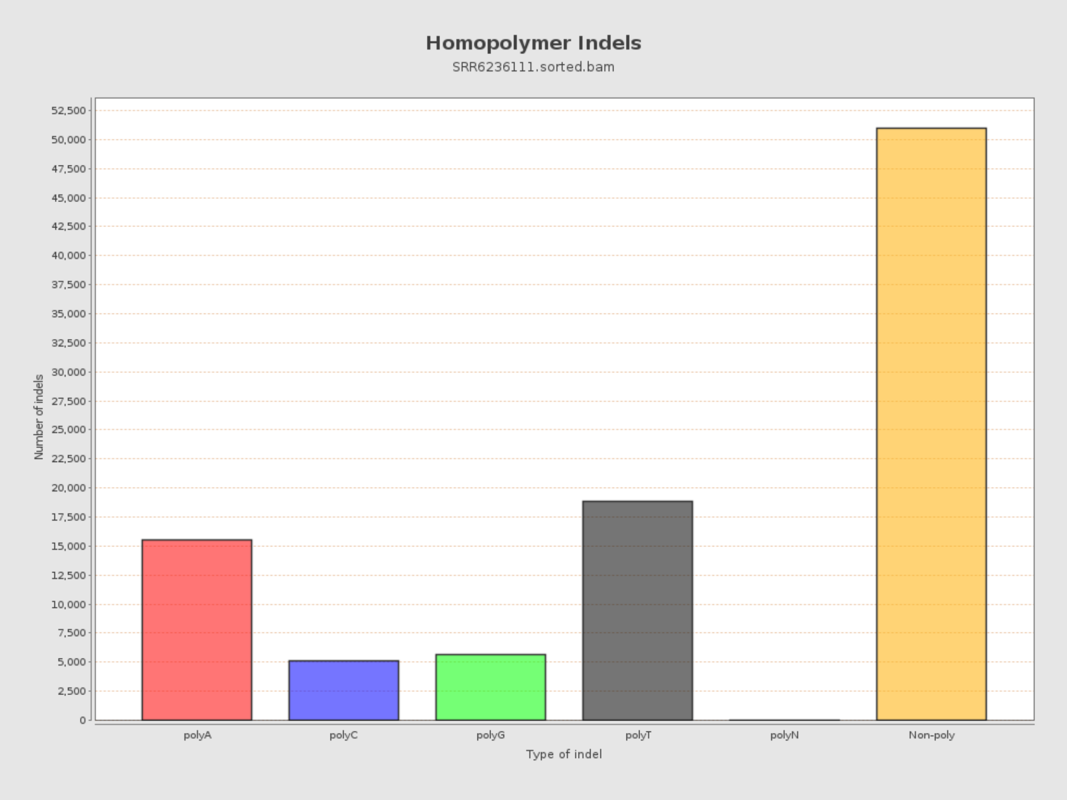
9. Results : Mapped Reads GC-content Distribution



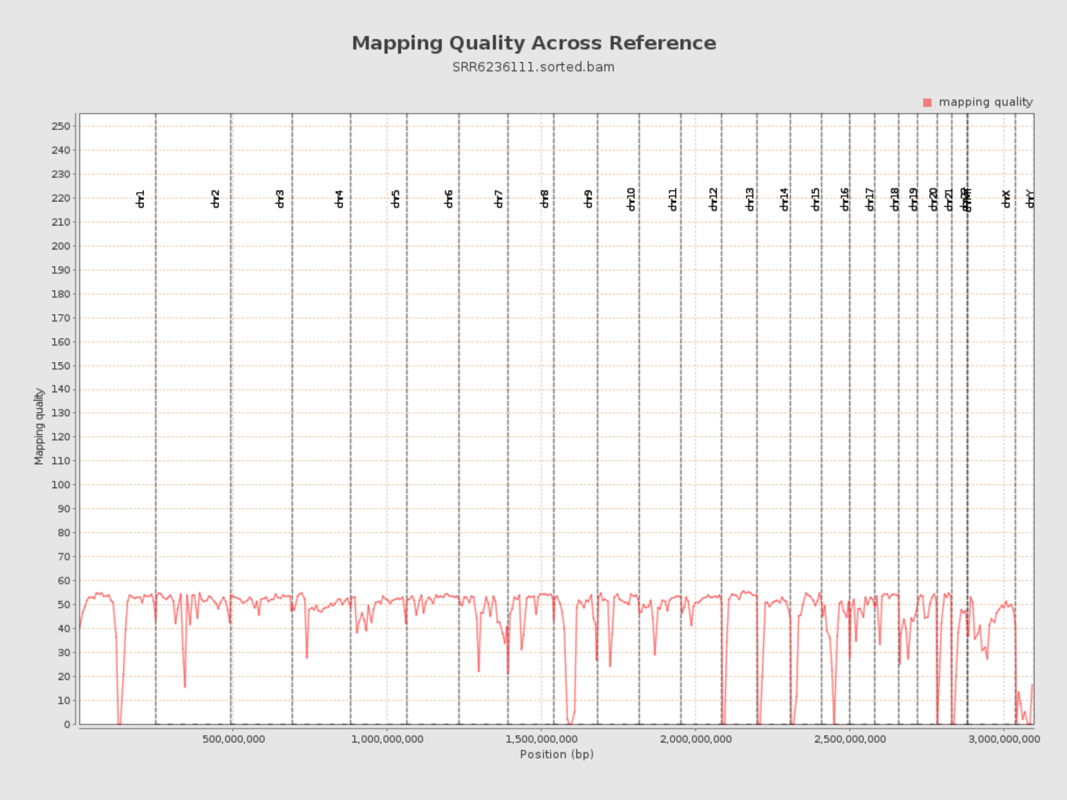
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram