Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 03:41:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085137.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_SRR3085137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 03:41:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,633,344
Mapped reads	2,392,302 / 90.85%
Unmapped reads	241,042 / 9.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,917 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	89,982 / 3.42%
Duplication rate	2.99%
Clipped reads	1,003,877 / 38.12%

2.2. ACGT Content

Number/percentage of A's	45,620,755 / 28.22%
Number/percentage of C's	29,930,792 / 18.51%
Number/percentage of T's	50,880,440 / 31.47%
Number/percentage of G's	35,212,555 / 21.78%
Number/percentage of N's	31,737 / 0.02%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0522

Standard Deviation	0.3889

2.4. Mapping Quality

Mean Mapping Quality	46.68

2.5. Mismatches and indels

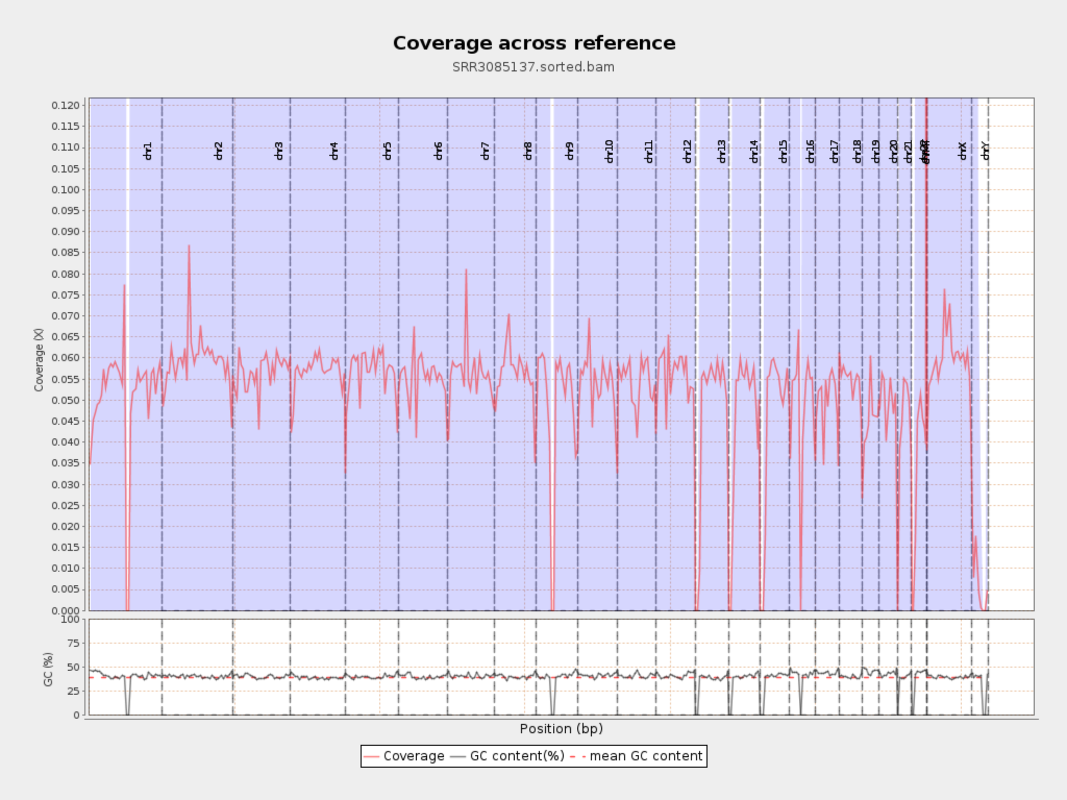
General error rate	0.86%
Mismatches	1,363,762
Insertions	12,488
Mapped reads with at least one insertion	0.52%
Deletions	35,613
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.67%

2.6. Chromosome stats

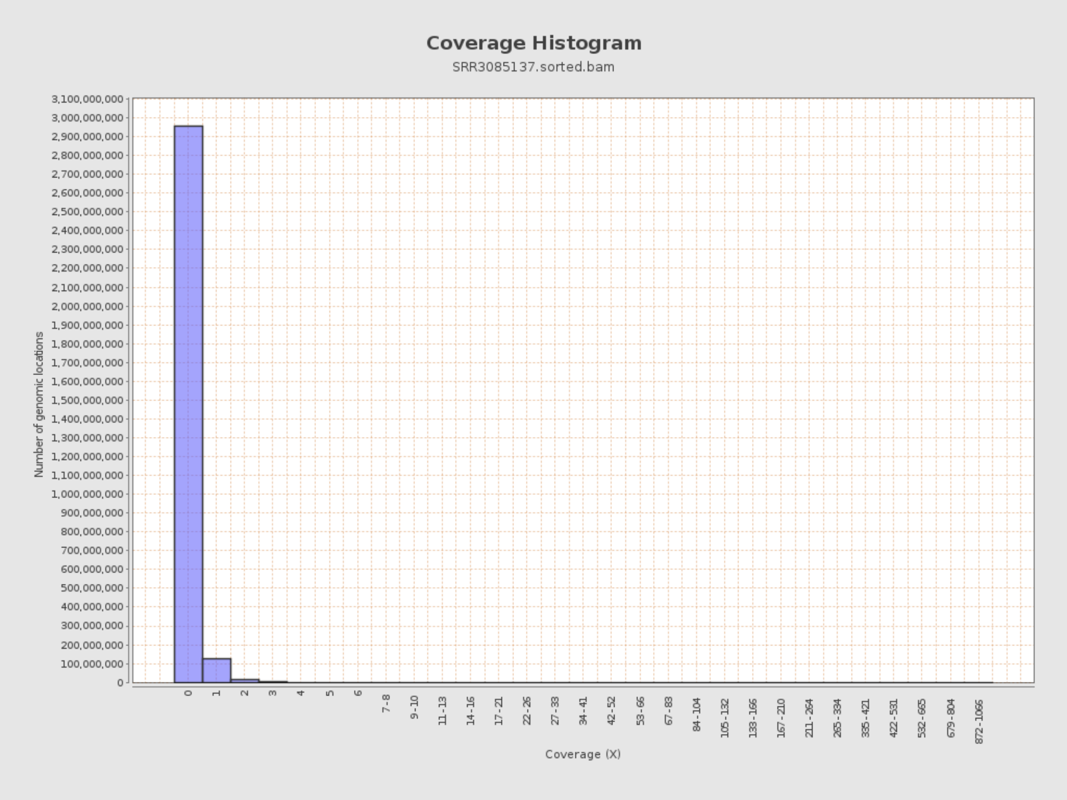
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12645179	0.0507	0.6159
chr2	243199373	14526687	0.0597	0.472
chr3	198022430	11212910	0.0566	0.2648
chr4	191154276	10847306	0.0567	0.2733
chr5	180915260	10307437	0.057	0.2667
chr6	171115067	9441431	0.0552	0.2974
chr7	159138663	9036160	0.0568	0.496

chr8	146364022	8224053	0.0562	0.6846
chr9	141213431	6830886	0.0484	0.348
chr10	135534747	7397019	0.0546	0.3576
chr11	135006516	7293446	0.054	0.3401
chr12	133851895	7478373	0.0559	0.2676
chr13	115169878	5315286	0.0462	0.242
chr14	107349540	4822396	0.0449	0.2511
chr15	102531392	4570971	0.0446	0.2395
chr16	90354753	4355445	0.0482	0.2636
chr17	81195210	4018993	0.0495	0.2702
chr18	78077248	4297603	0.055	0.5906
chr19	59128983	2692661	0.0455	0.4754
chr20	63025520	3095067	0.0491	0.2522
chr21	48129895	2051046	0.0426	0.2442
chr22	51304566	1644937	0.0321	0.1986
chrMT	16571	13247	0.7994	0.9277
chrX	155270560	9248403	0.0596	0.2961
chrY	59373566	366862	0.0062	0.1246

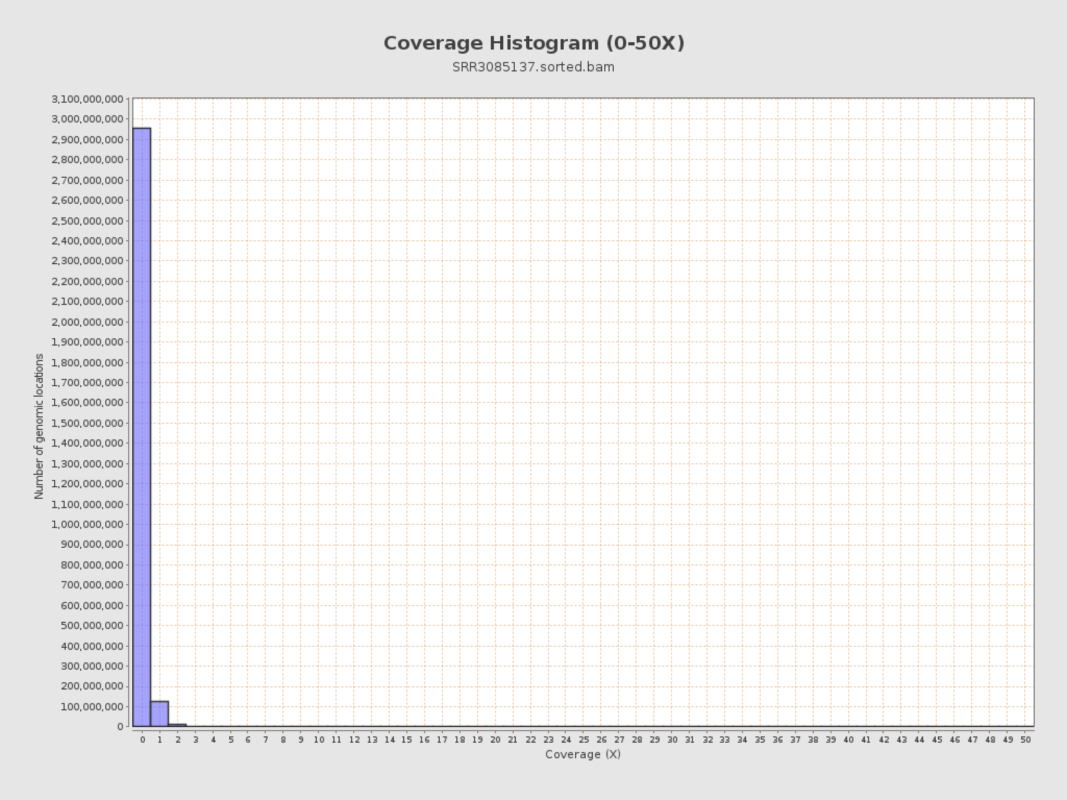
3. Results : Coverage across reference



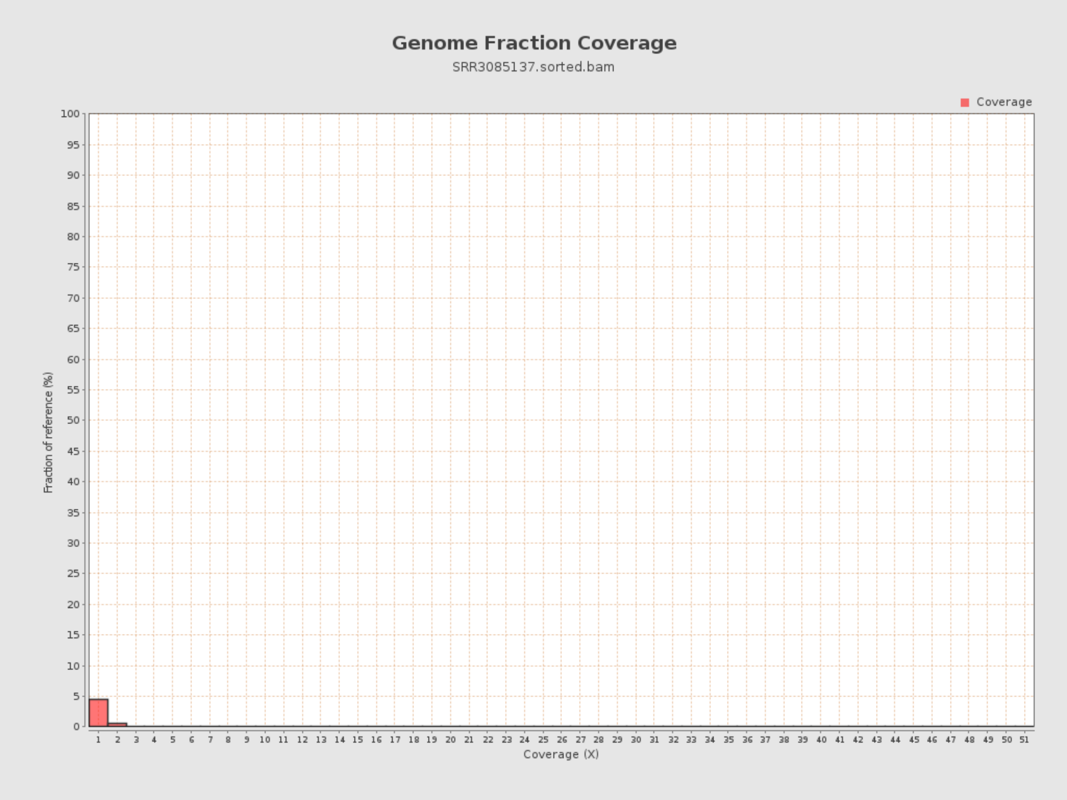
4. Results : Coverage Histogram



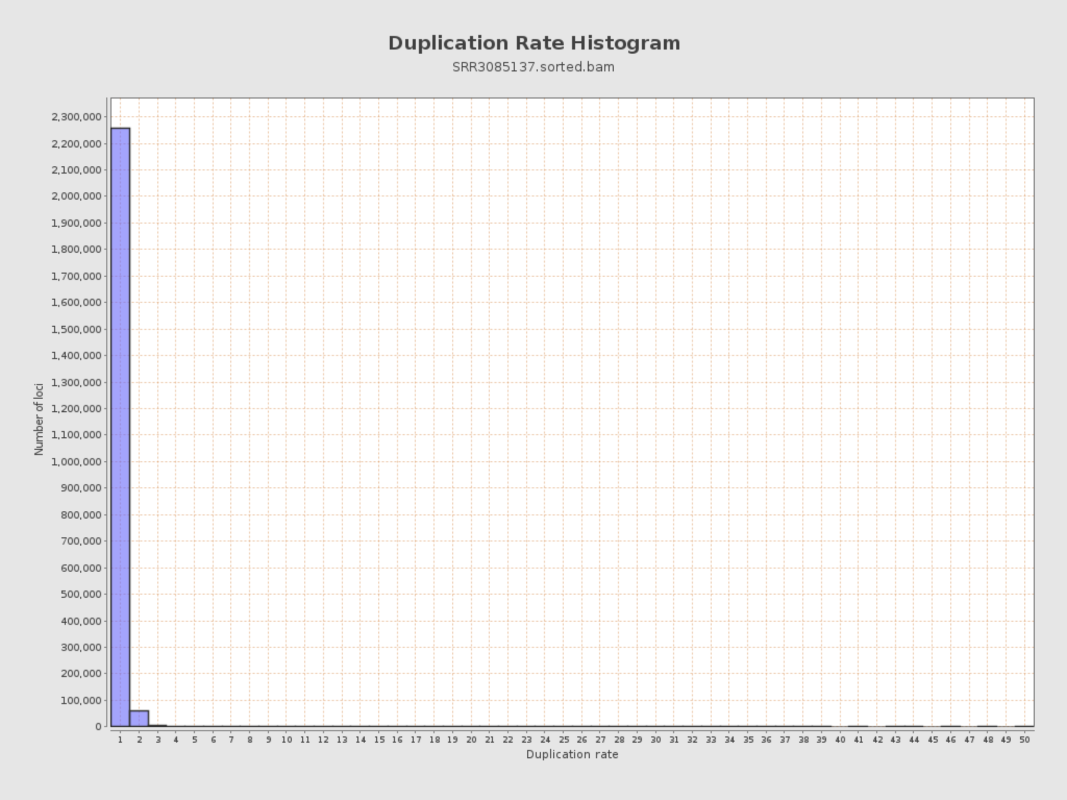
5. Results : Coverage Histogram (0-50X)



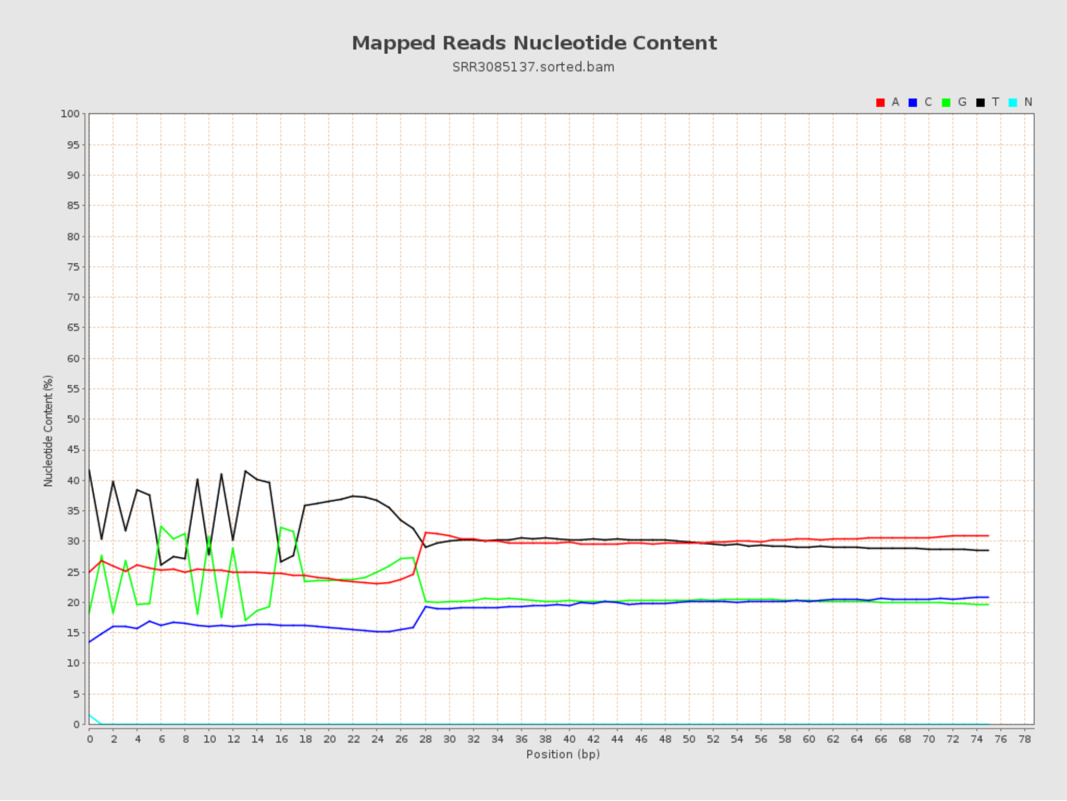
6. Results : Genome Fraction Coverage



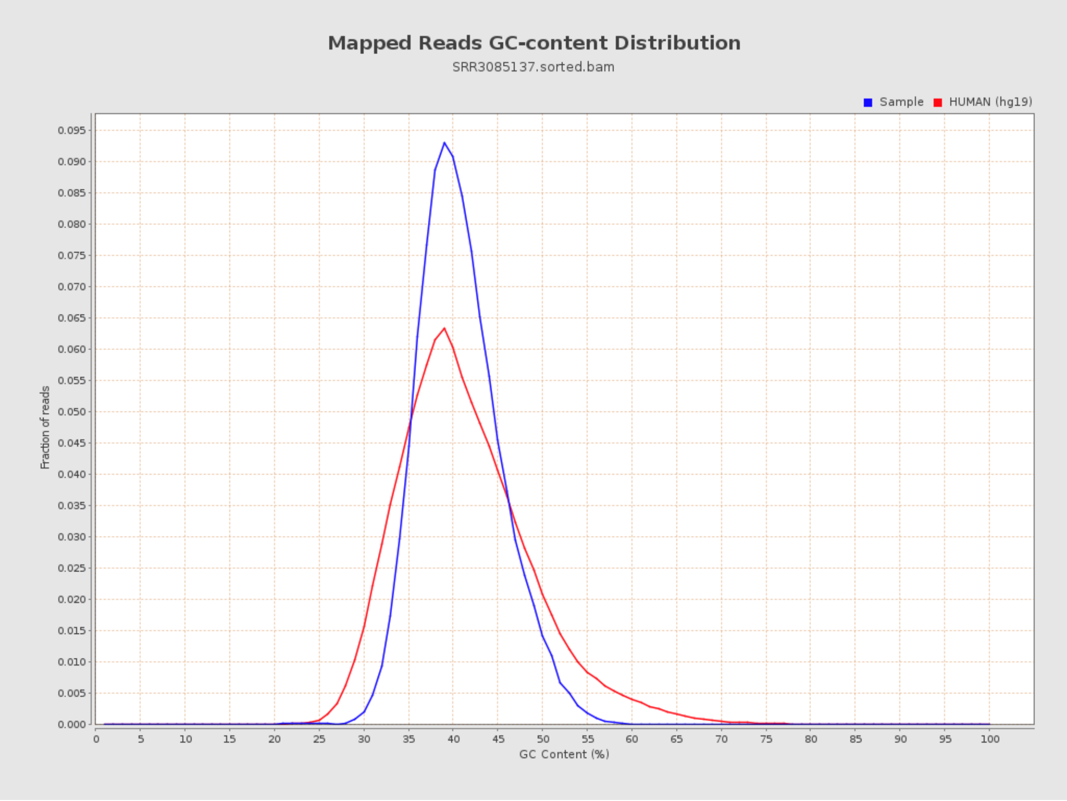
7. Results : Duplication Rate Histogram



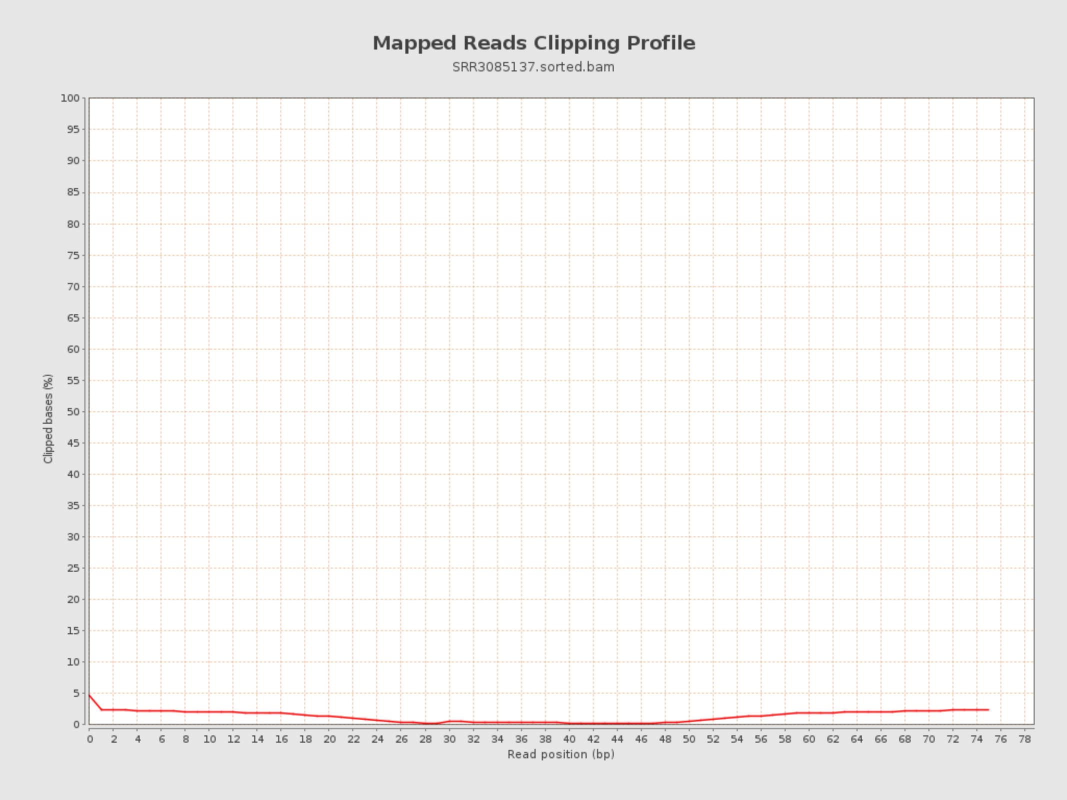
8. Results : Mapped Reads Nucleotide Content



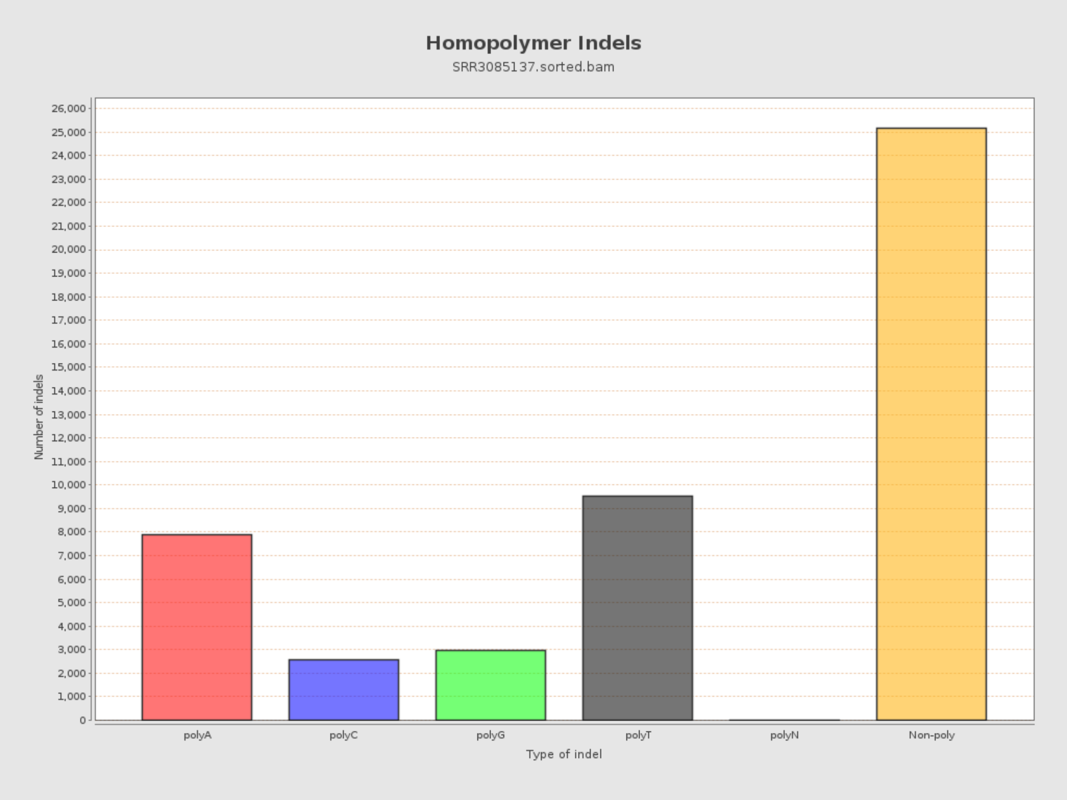
9. Results : Mapped Reads GC-content Distribution



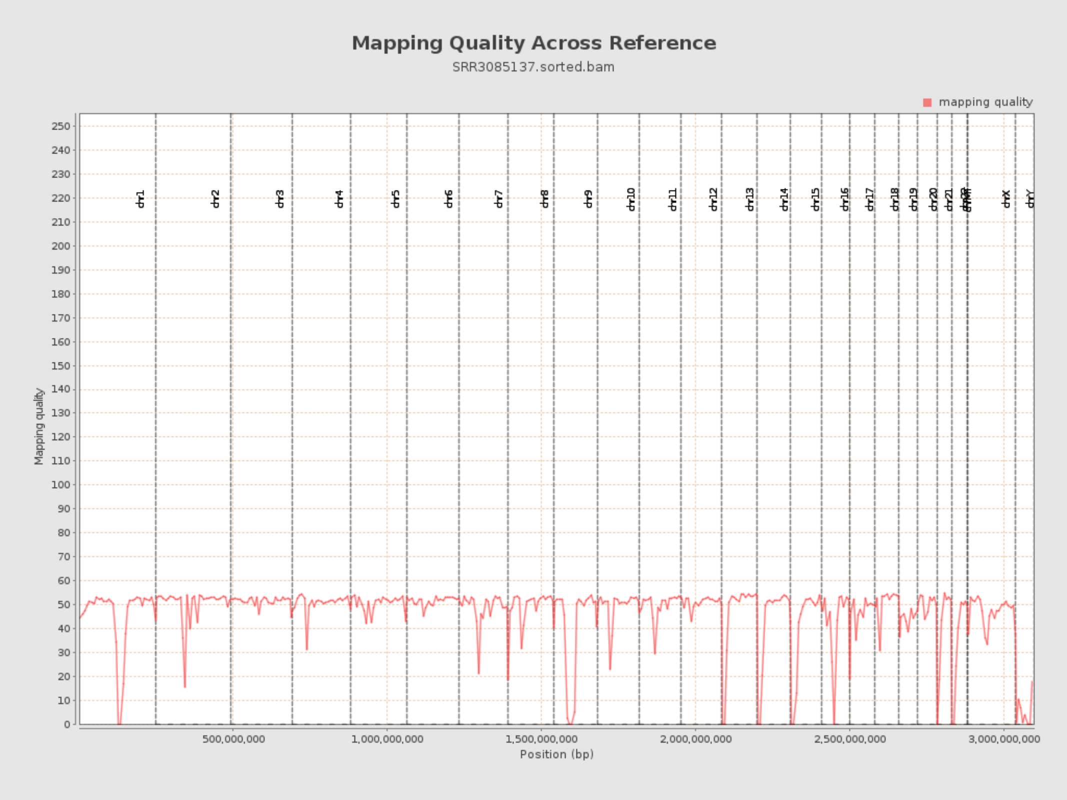
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram