Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:54:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082441.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_SRR3082441 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082441.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:54:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082441.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,998,024
Mapped reads	2,740,969 / 91.43%
Unmapped reads	257,055 / 8.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,090 / 0.9%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	107,757 / 3.59%
Duplication rate	2.91%
Clipped reads	1,097,566 / 36.61%

2.2. ACGT Content

Number/percentage of A's	53,250,241 / 28.47%
Number/percentage of C's	35,247,968 / 18.85%
Number/percentage of T's	58,099,871 / 31.07%
Number/percentage of G's	40,406,768 / 21.61%
Number/percentage of N's	3,899 / 0%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.5063

2.4. Mapping Quality

Mean Mapping Quality	46.66

2.5. Mismatches and indels

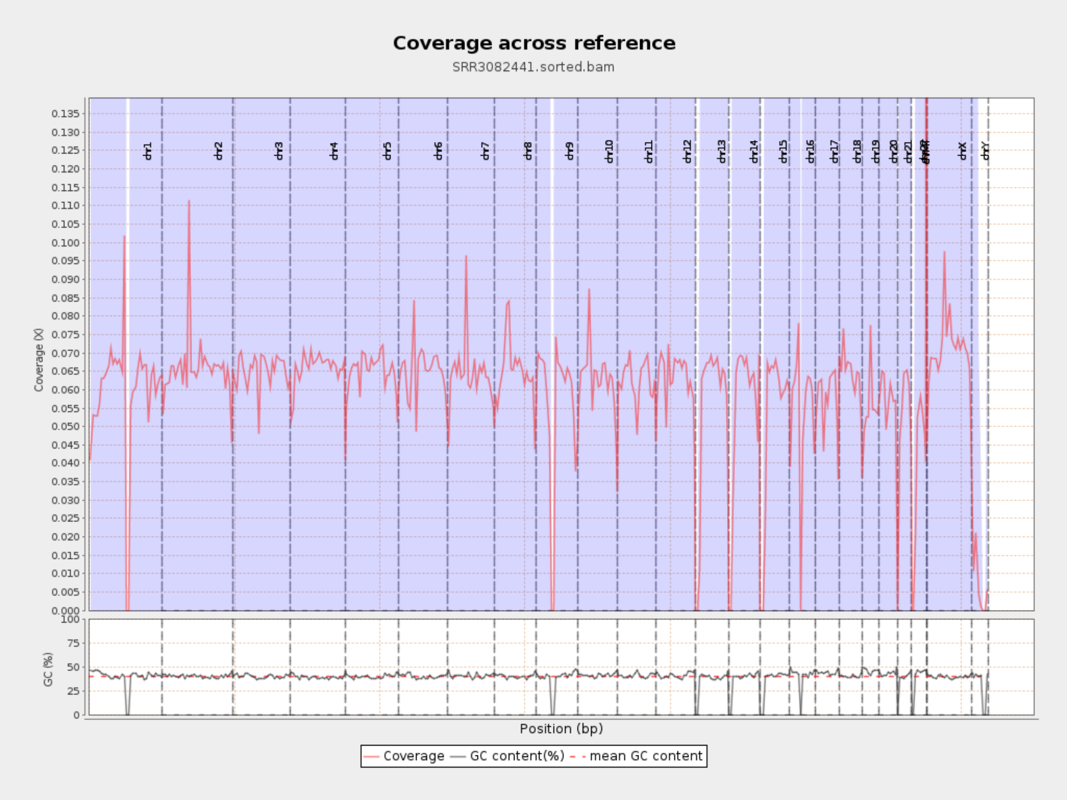
General error rate	0.83%
Mismatches	1,532,471
Insertions	14,746
Mapped reads with at least one insertion	0.53%
Deletions	41,622
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.56%

2.6. Chromosome stats

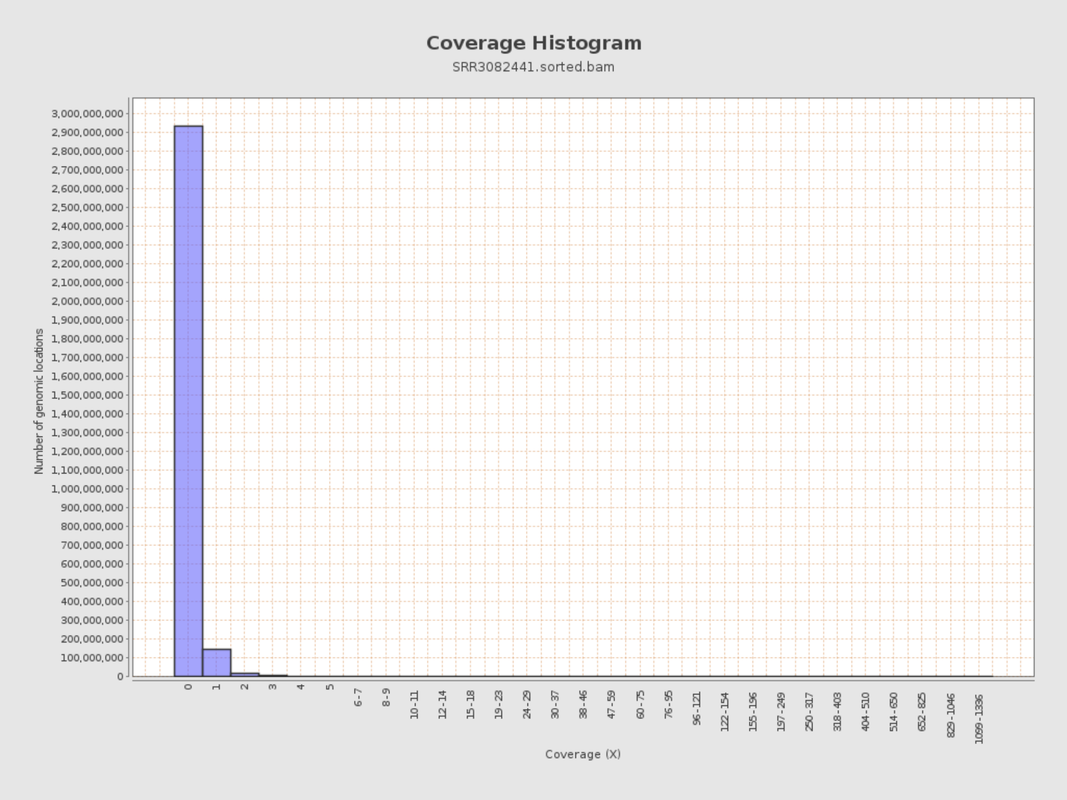
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14789073	0.0593	0.9581
chr2	243199373	16075045	0.0661	0.5863
chr3	198022430	12913890	0.0652	0.2848
chr4	191154276	12621032	0.066	0.2999
chr5	180915260	11803586	0.0652	0.2887
chr6	171115067	11147644	0.0651	0.3526
chr7	159138663	10316145	0.0648	0.6318

chr8	146364022	9492633	0.0649	0.861
chr9	141213431	7861511	0.0557	0.4438
chr10	135534747	8623081	0.0636	0.437
chr11	135006516	8391040	0.0622	0.4065
chr12	133851895	8530550	0.0637	0.289
chr13	115169878	6229303	0.0541	0.2602
chr14	107349540	5706596	0.0532	0.2827
chr15	102531392	5275642	0.0515	0.26
chr16	90354753	4871977	0.0539	0.3008
chr17	81195210	4625239	0.057	0.302
chr18	78077248	5082842	0.0651	0.8412
chr19	59128983	3277605	0.0554	0.6782
chr20	63025520	3606087	0.0572	0.2754
chr21	48129895	2470911	0.0513	0.2744
chr22	51304566	1871953	0.0365	0.2118
chrMT	16571	15445	0.932	1.1737
chrX	155270560	11031931	0.071	0.3436
chrY	59373566	445299	0.0075	0.1572

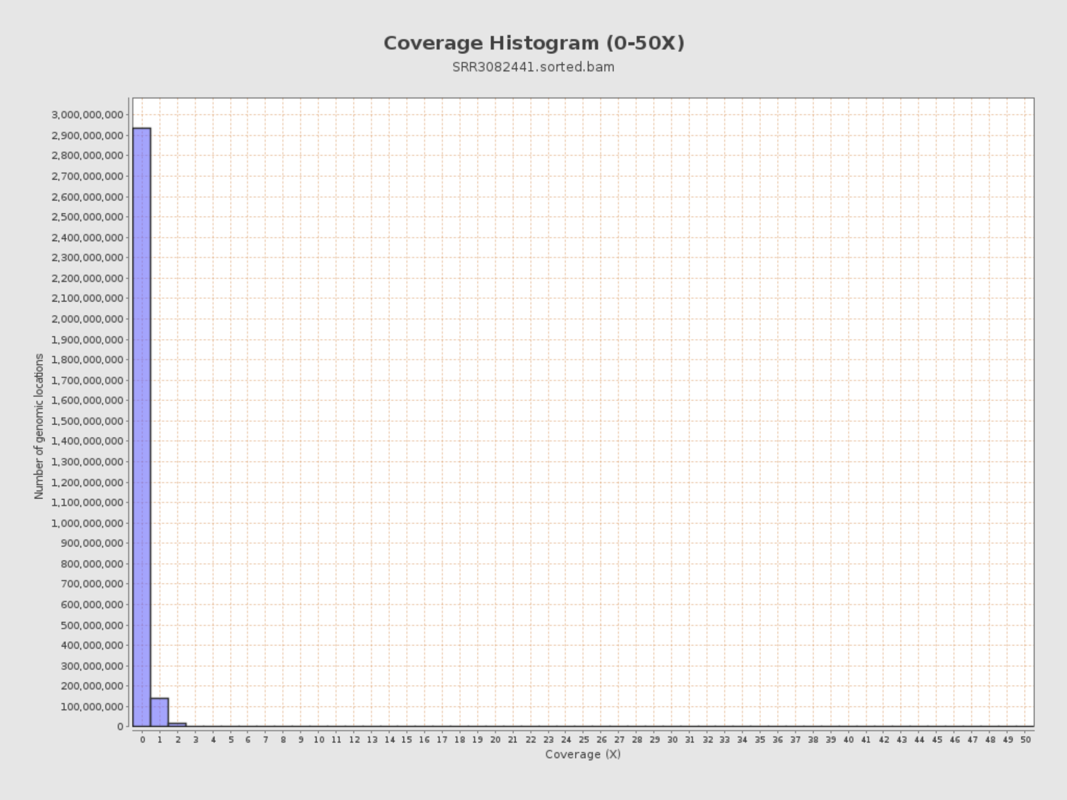
3. Results : Coverage across reference



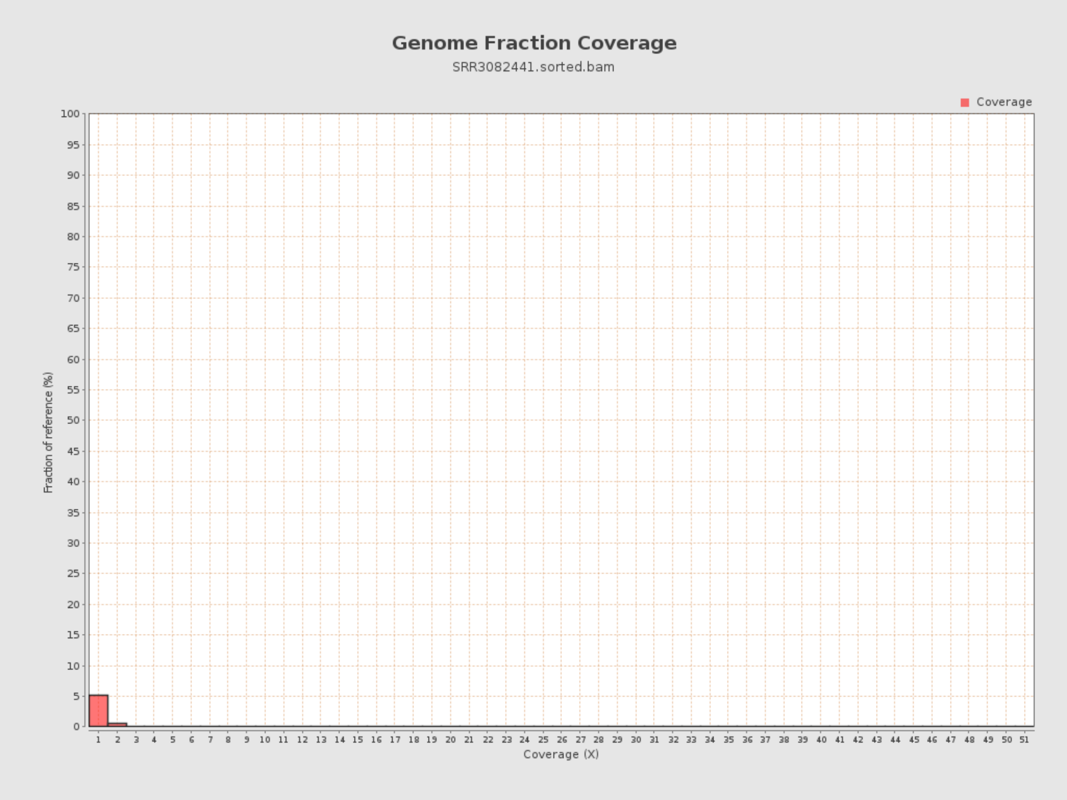
4. Results : Coverage Histogram



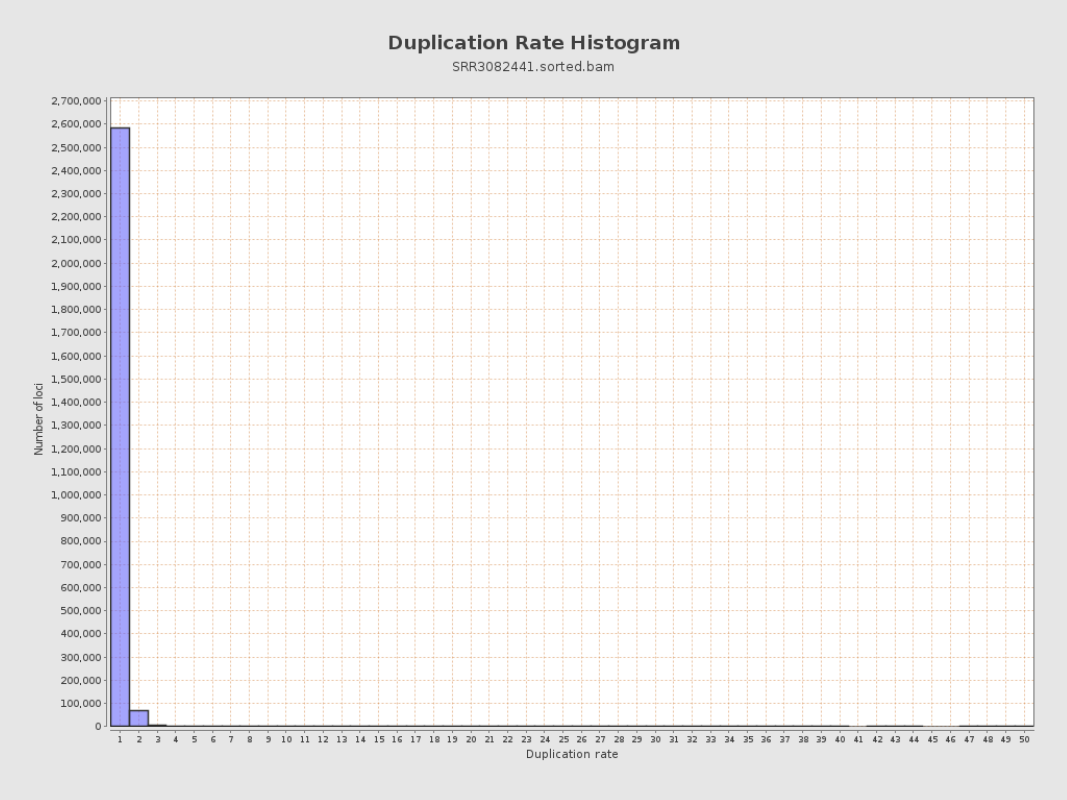
5. Results : Coverage Histogram (0-50X)



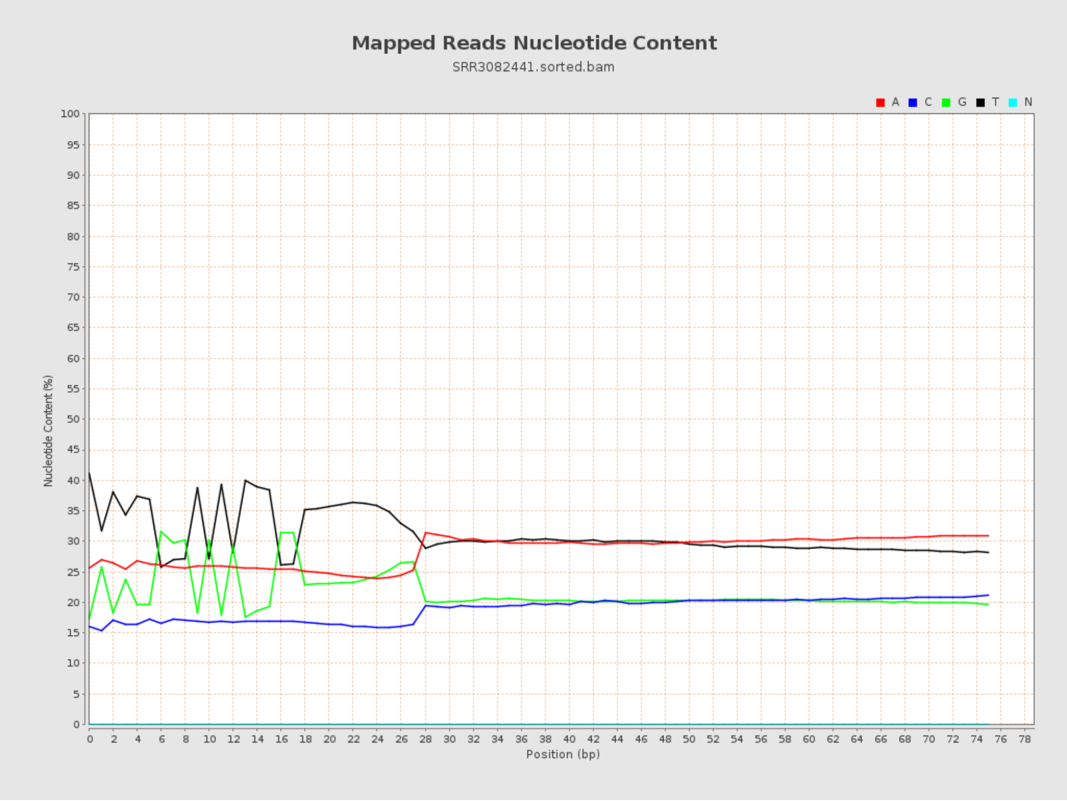
6. Results : Genome Fraction Coverage



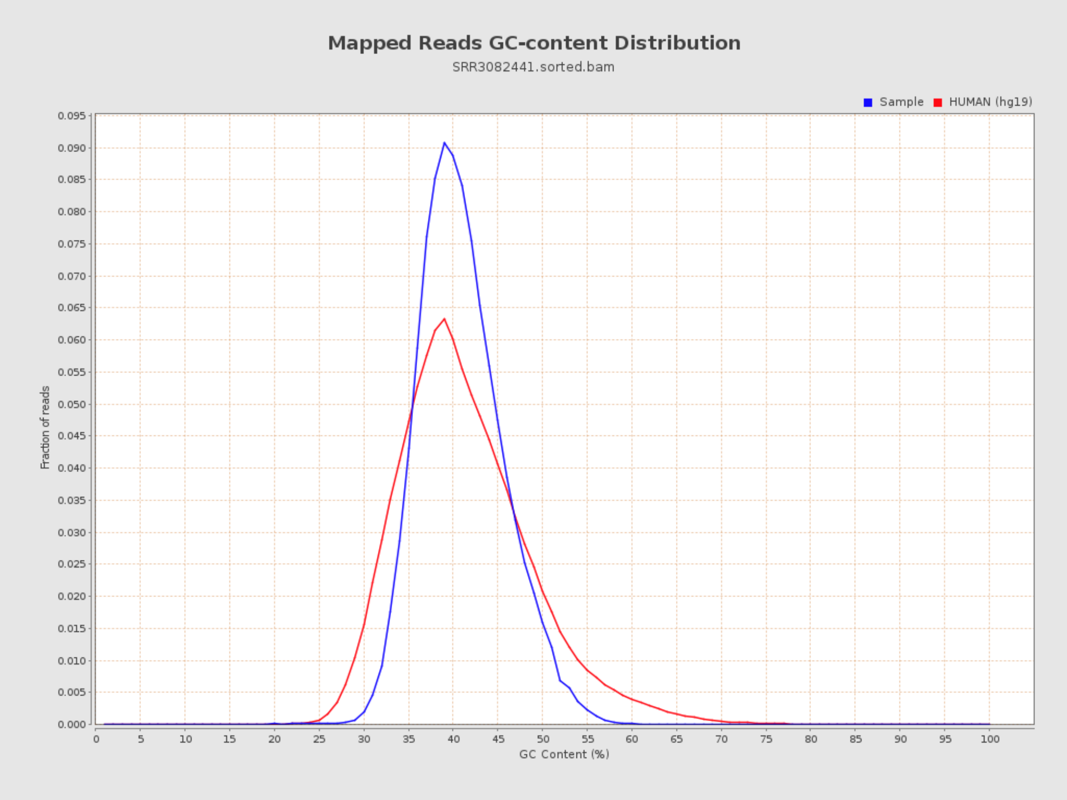
7. Results : Duplication Rate Histogram



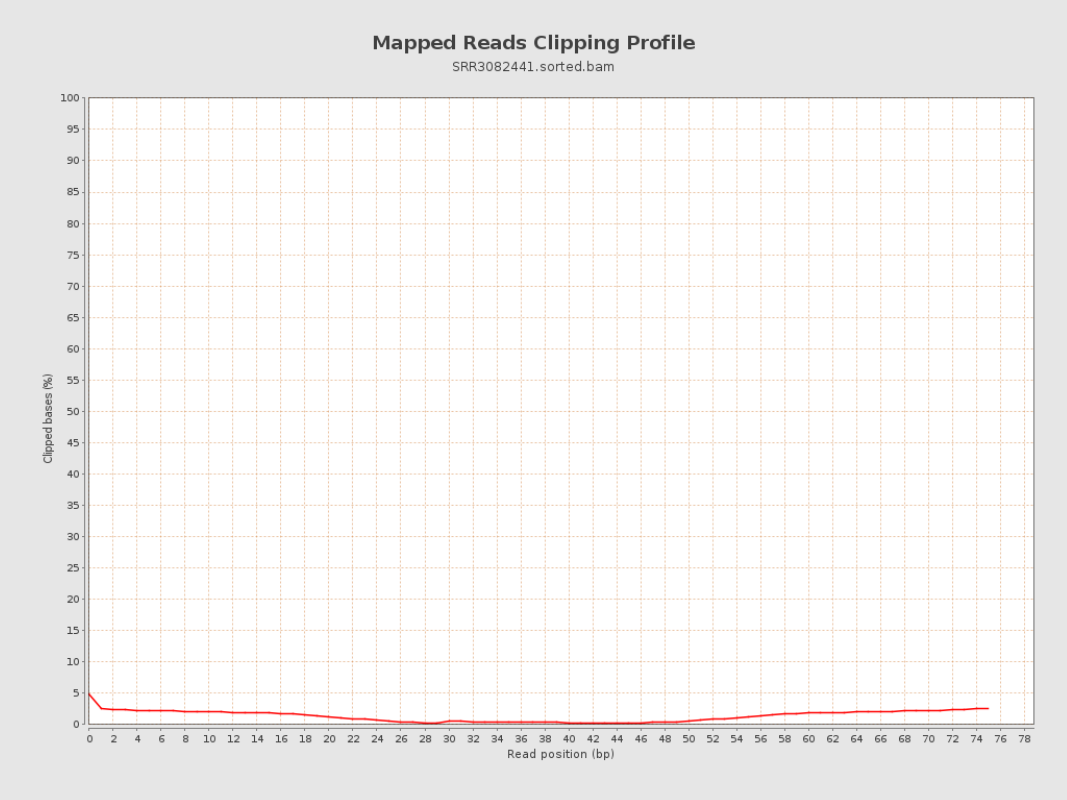
8. Results : Mapped Reads Nucleotide Content



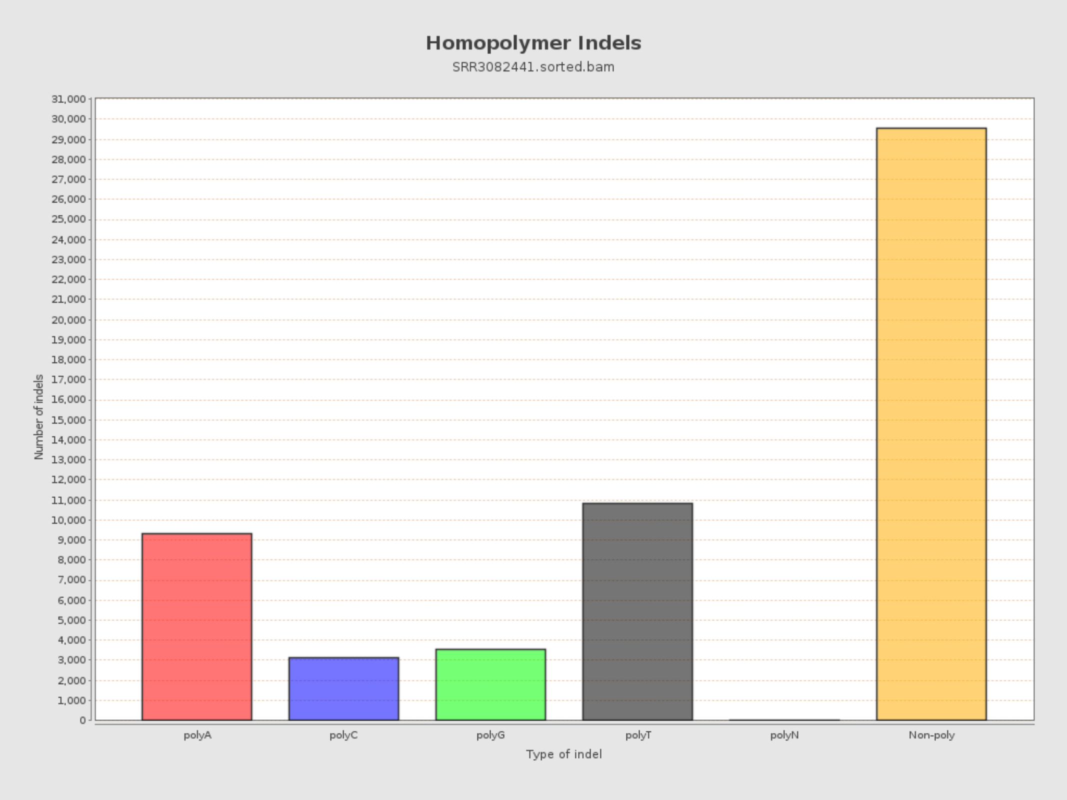
9. Results : Mapped Reads GC-content Distribution



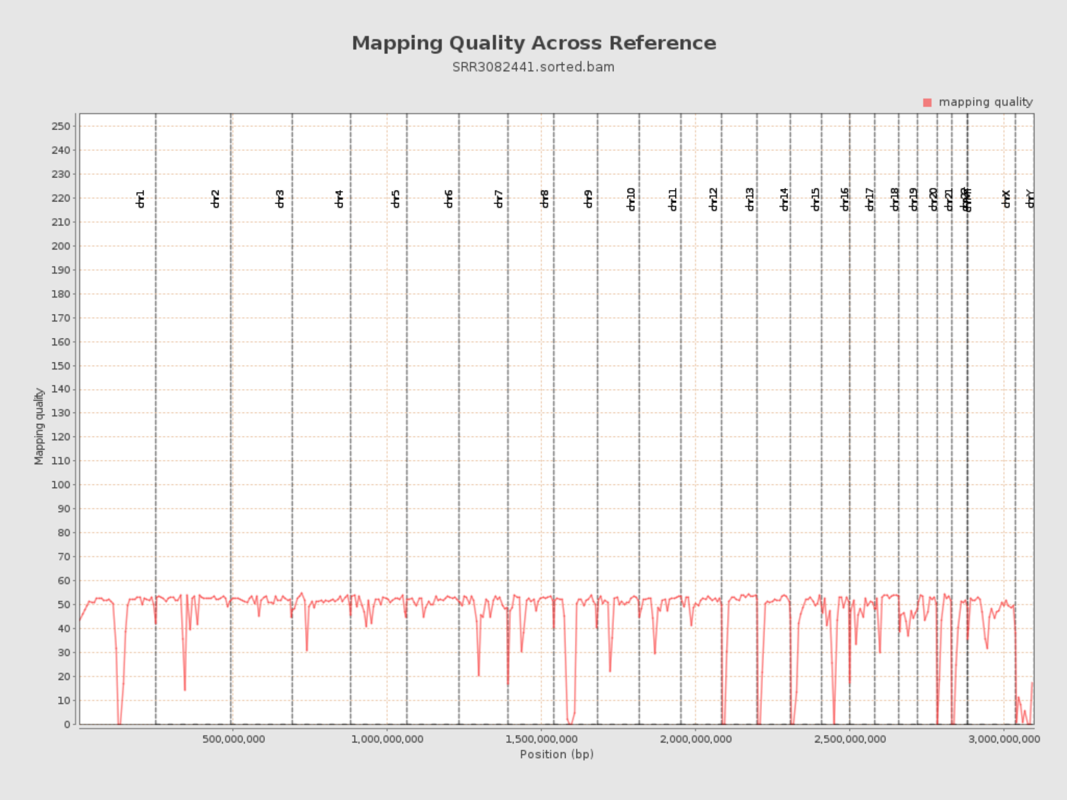
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram