Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:40:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548929.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_SRR1548929 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548929.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:40:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548929.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,872,336
Mapped reads	9,472,293 / 87.12%
Unmapped reads	1,400,043 / 12.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	392,148 / 3.61%
Duplication rate	2.82%
Clipped reads	770,885 / 7.09%

2.2. ACGT Content

Number/percentage of A's	110,844,830 / 29.59%
Number/percentage of C's	76,215,753 / 20.34%
Number/percentage of T's	111,519,809 / 29.77%
Number/percentage of G's	76,053,115 / 20.3%
Number/percentage of N's	3,308 / 0%
GC Percentage	40.64%

2.3. Coverage

Mean	0.121
Standard Deviation	1.3209

2.4. Mapping Quality

Mean Mapping Quality	40.65

2.5. Mismatches and indels

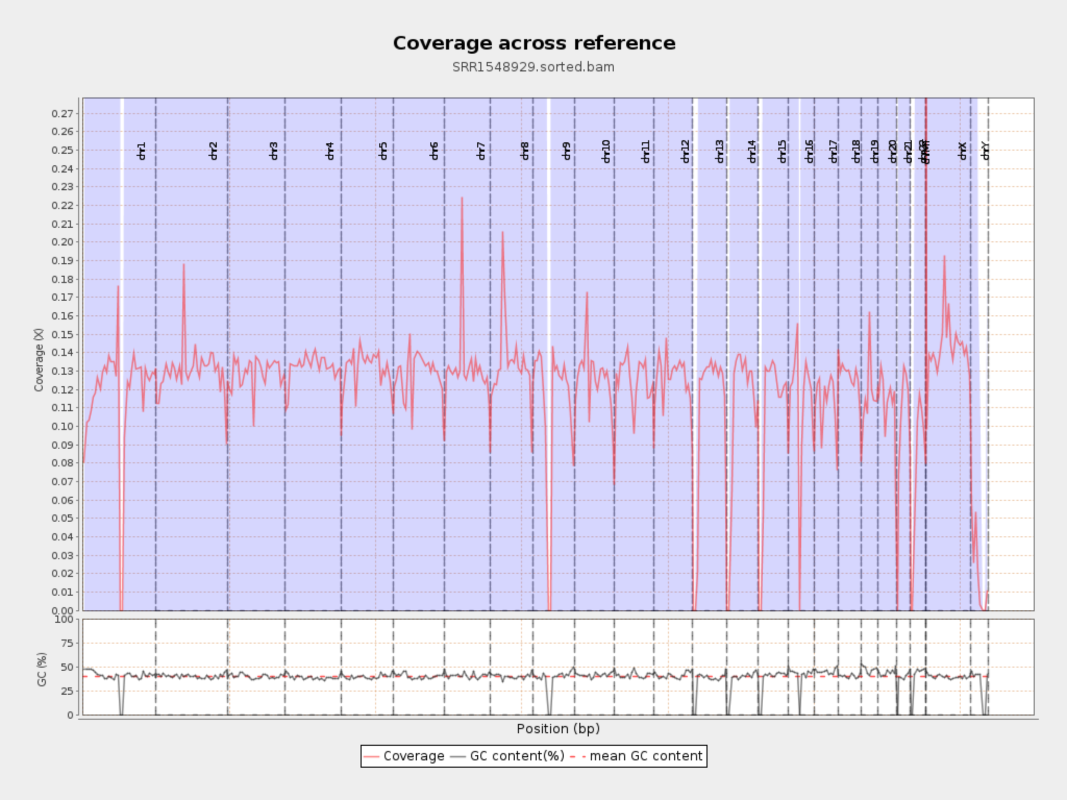
General error rate	0.3%
Mismatches	1,110,533
Insertions	13,003
Mapped reads with at least one insertion	0.14%
Deletions	30,722
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.38%

2.6. Chromosome stats

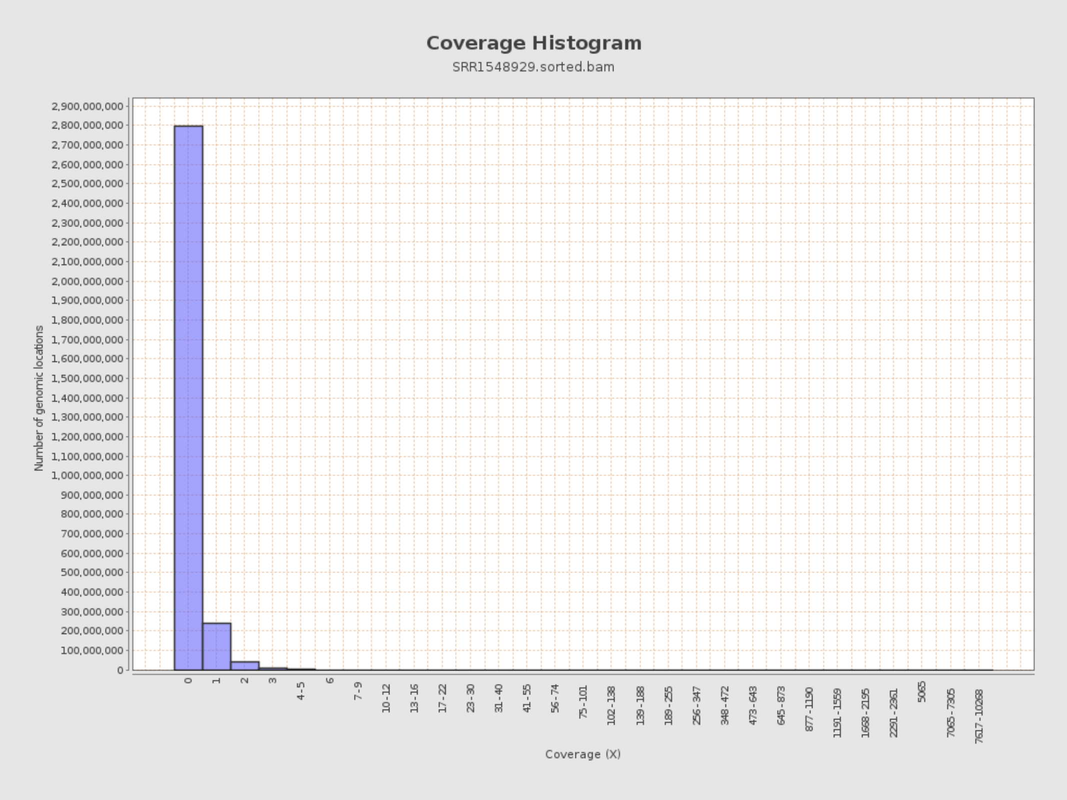
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29127763	0.1169	1.4026
chr2	243199373	31754728	0.1306	0.7825
chr3	198022430	25613742	0.1293	0.4382
chr4	191154276	25312345	0.1324	0.4618
chr5	180915260	23699476	0.131	0.4512
chr6	171115067	22054079	0.1289	0.5083
chr7	159138663	21036249	0.1322	1.2309
chr8	146364022	19732601	0.1348	4.9701

chr9	141213431	15675680	0.111	0.7764
chr10	135534747	17270792	0.1274	0.6675
chr11	135006516	16851710	0.1248	0.8471
chr12	133851895	16999061	0.127	0.4652
chr13	115169878	12302944	0.1068	0.3875
chr14	107349540	11516584	0.1073	0.5301
chr15	102531392	10498564	0.1024	0.3886
chr16	90354753	9916748	0.1098	0.4799
chr17	81195210	9295184	0.1145	0.4724
chr18	78077248	9987807	0.1279	1.4908
chr19	59128983	6952836	0.1176	1.3321
chr20	63025520	7206388	0.1143	0.4359
chr21	48129895	4755386	0.0988	0.4577
chr22	51304566	3793746	0.0739	0.3923
chrMT	16571	9413	0.568	0.9213
chrX	155270560	22132275	0.1425	0.6183
chrY	59373566	1180771	0.0199	0.2477

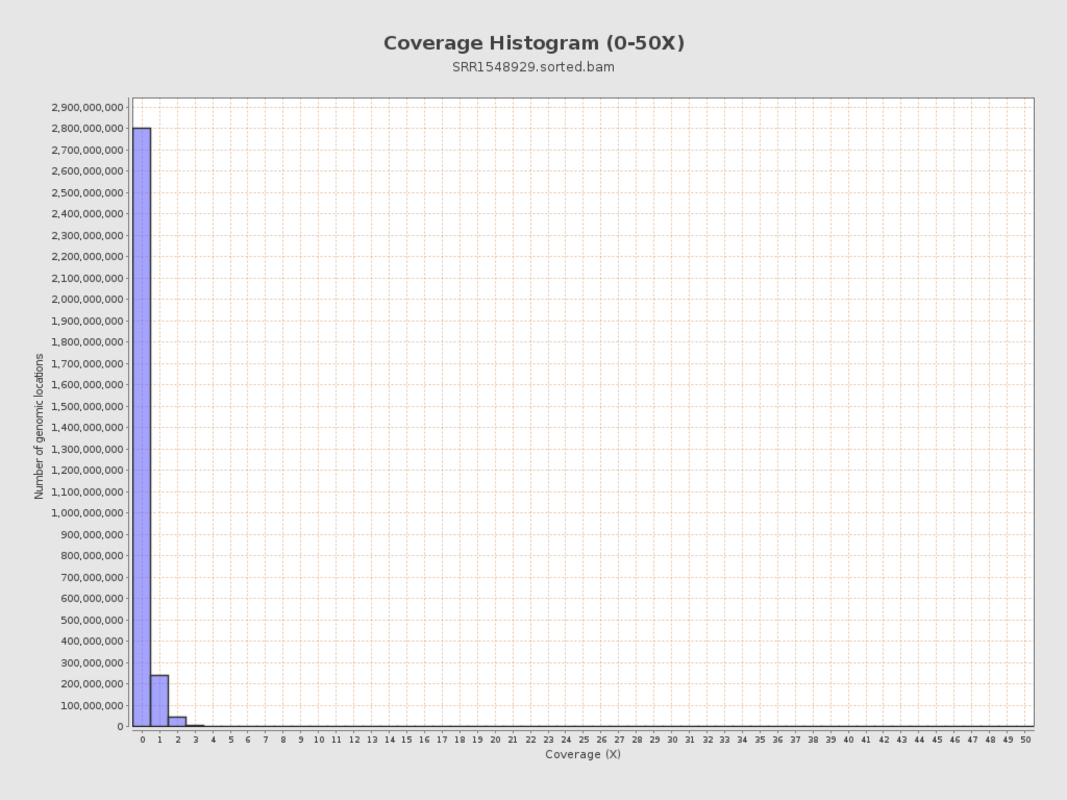
3. Results : Coverage across reference



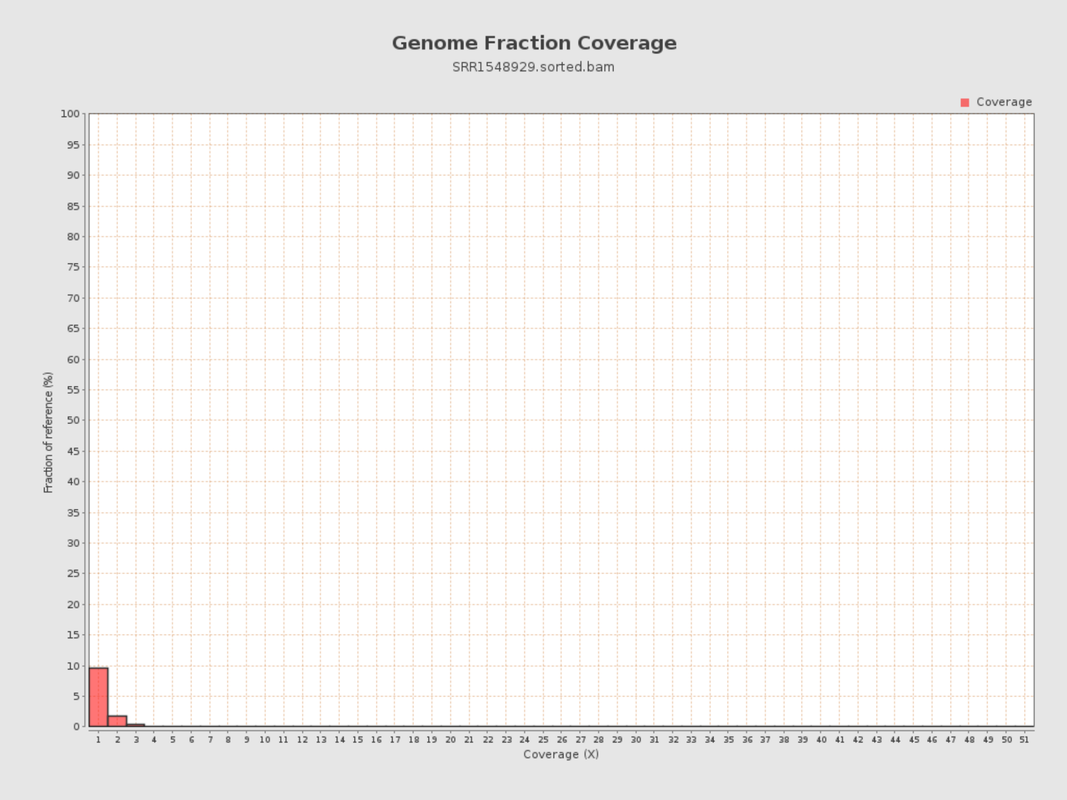
4. Results : Coverage Histogram



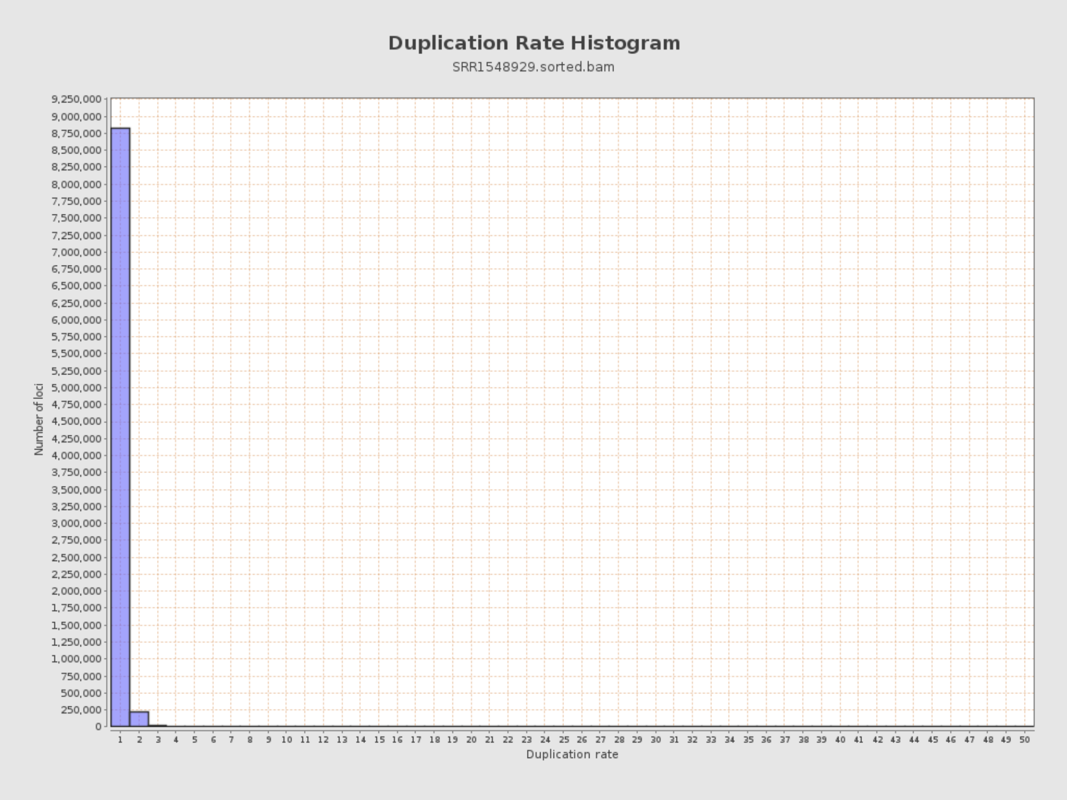
5. Results : Coverage Histogram (0-50X)



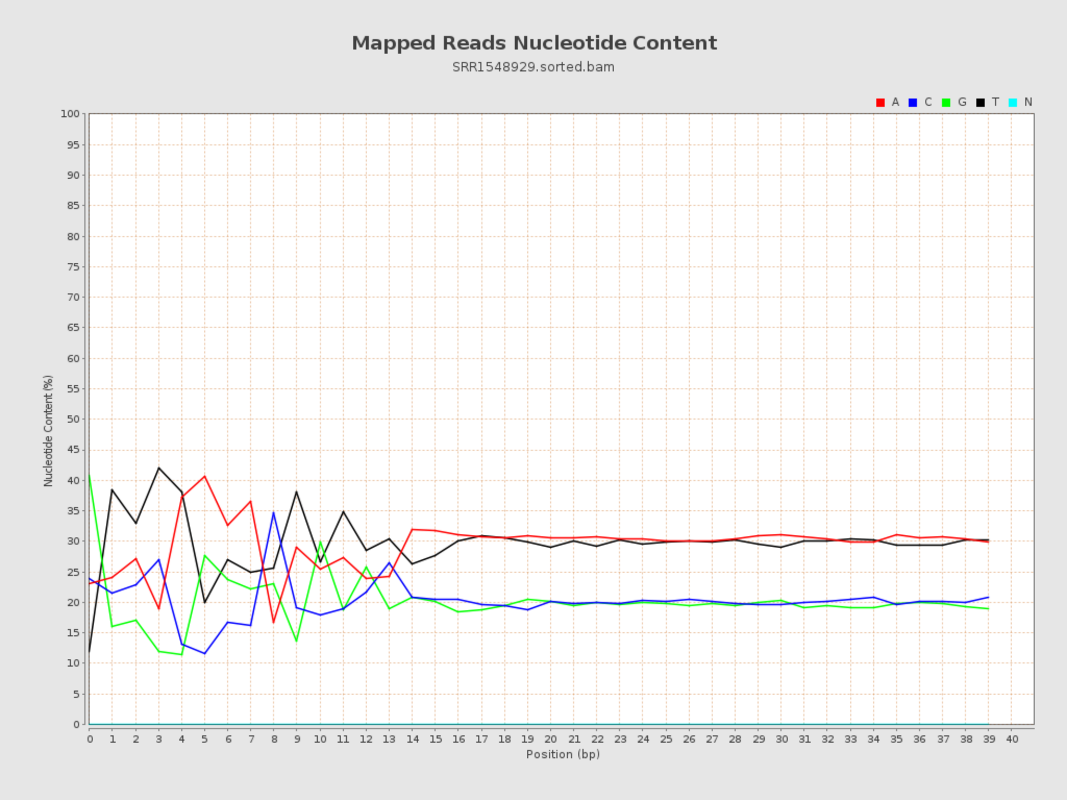
6. Results : Genome Fraction Coverage



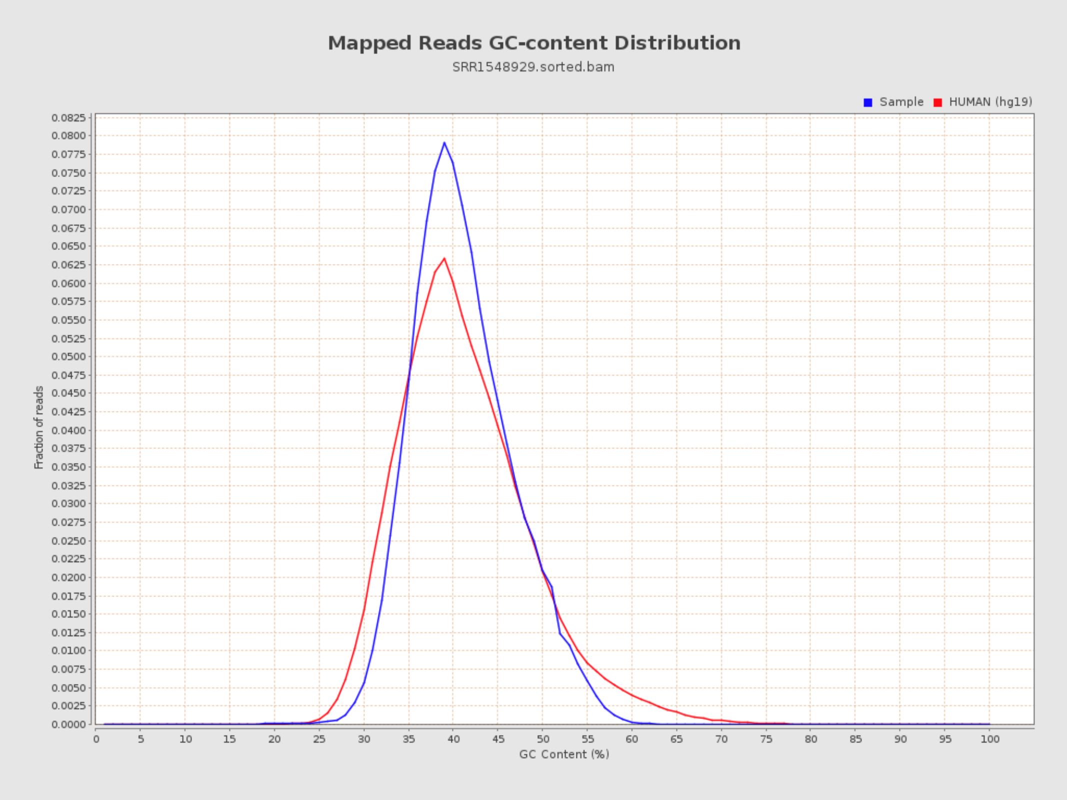
7. Results : Duplication Rate Histogram



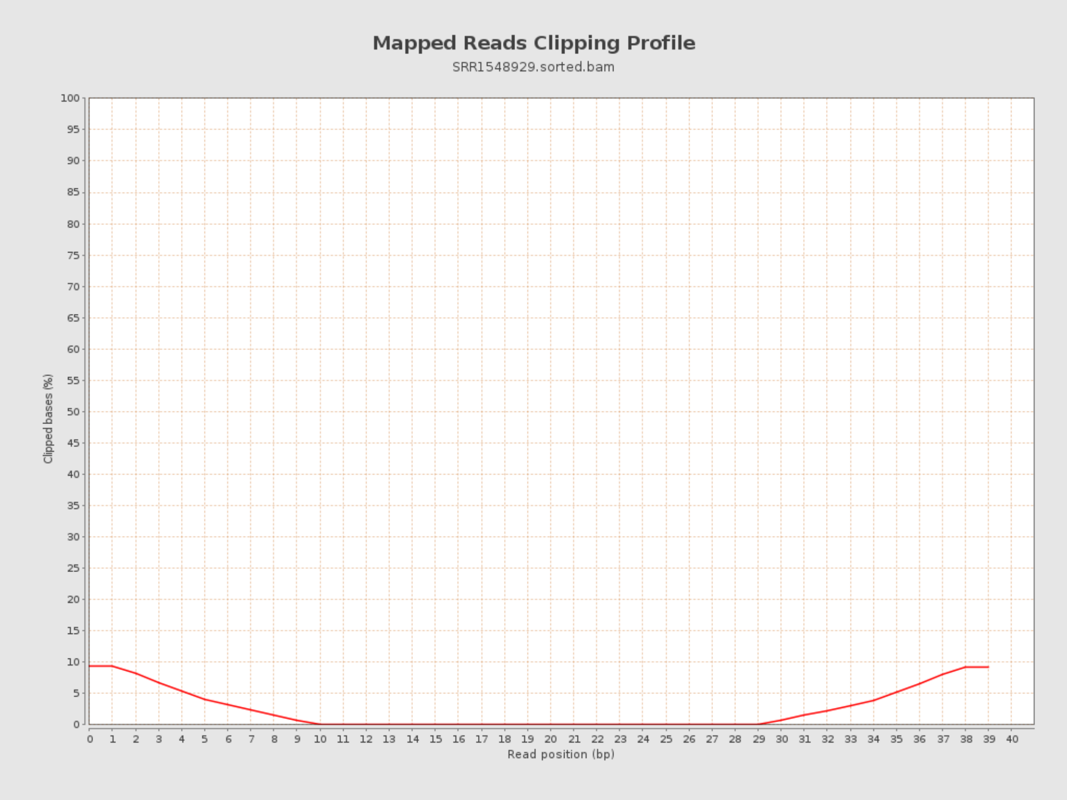
8. Results : Mapped Reads Nucleotide Content



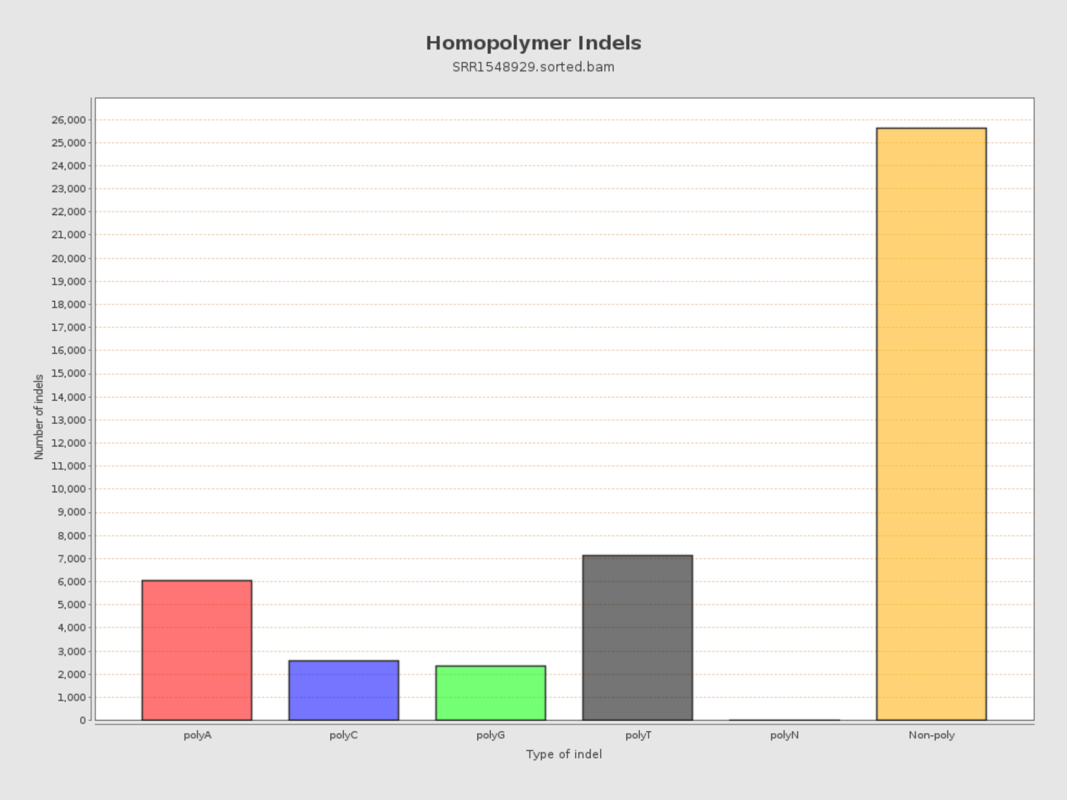
9. Results : Mapped Reads GC-content Distribution



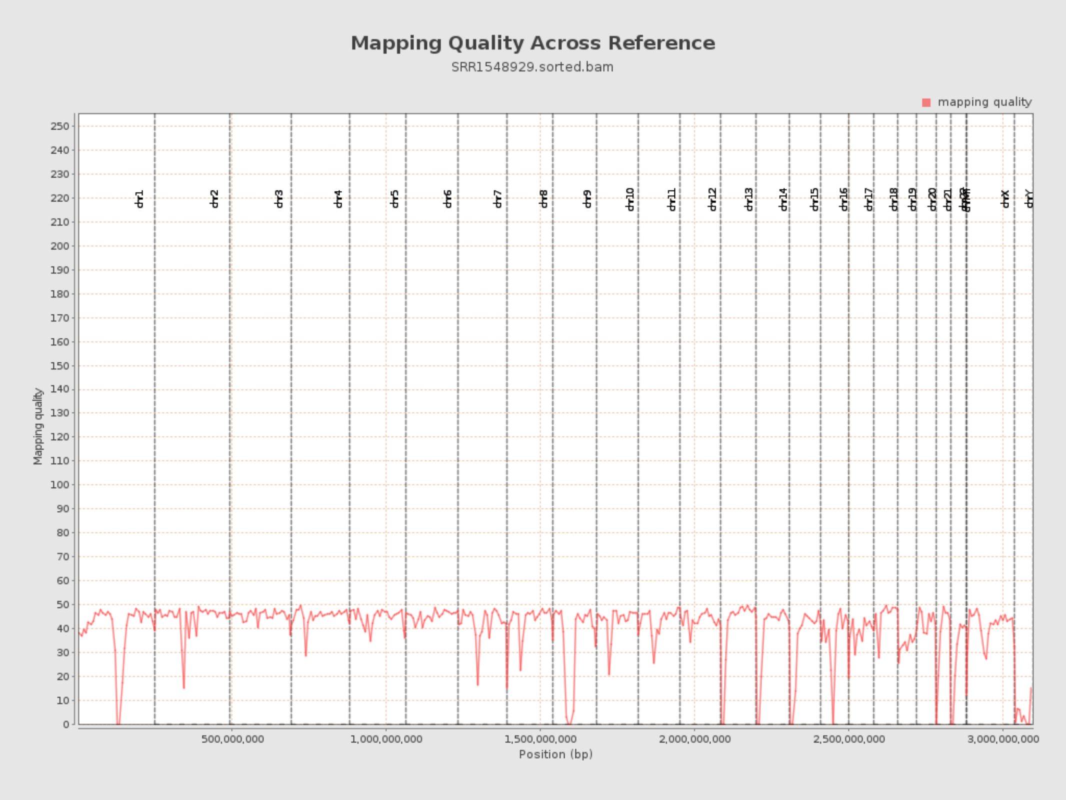
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram