Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:19:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506329.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_SRR1506329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:19:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,909,341
Mapped reads	4,496,998 / 65.09%
Unmapped reads	2,412,343 / 34.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	59,865 / 0.87%
Read min/max/mean length	30 / 94 / 94.31
Duplicated reads (estimated)	783,647 / 11.34%
Duplication rate	12.91%
Clipped reads	2,917,868 / 42.23%

2.2. ACGT Content

Number/percentage of A's	99,088,488 / 28.16%
Number/percentage of C's	63,391,703 / 18.01%
Number/percentage of T's	97,230,021 / 27.63%
Number/percentage of G's	92,140,011 / 26.18%
Number/percentage of N's	77,480 / 0.02%
GC Percentage	44.19%

2.3. Coverage

Mean	0.1137

Standard Deviation	0.7521

2.4. Mapping Quality

Mean Mapping Quality	47.12

2.5. Mismatches and indels

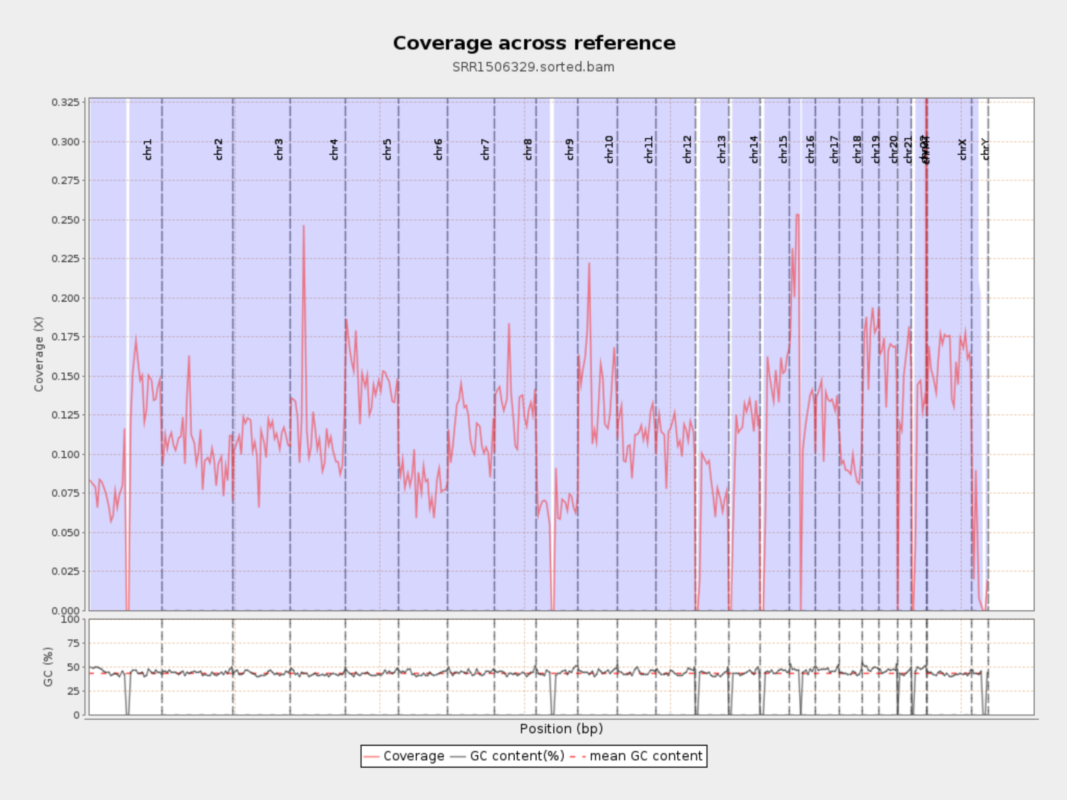
General error rate	0.81%
Mismatches	2,789,717
Insertions	28,696
Mapped reads with at least one insertion	0.62%
Deletions	73,764
Mapped reads with at least one deletion	1.61%
Homopolymer indels	43.51%

2.6. Chromosome stats

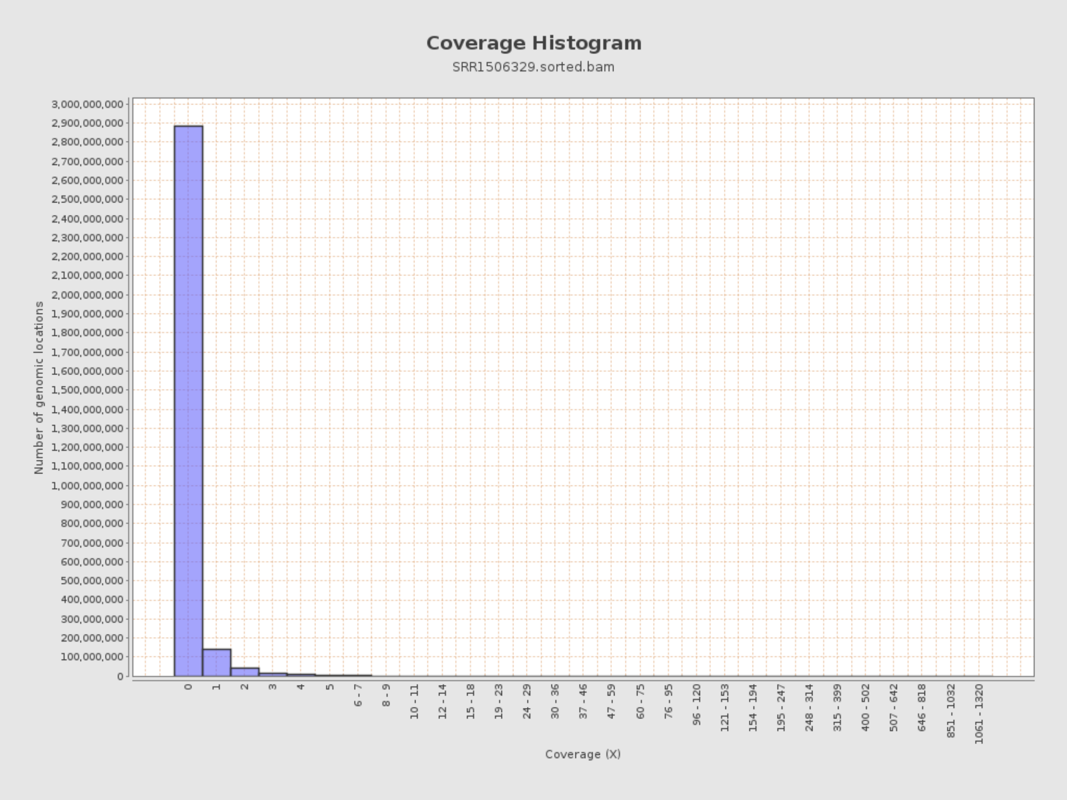
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25210159	0.1011	1.049
chr2	243199373	25252078	0.1038	0.8217
chr3	198022430	21573228	0.1089	0.5149
chr4	191154276	21943538	0.1148	0.7389
chr5	180915260	26721466	0.1477	0.6154
chr6	171115067	13959959	0.0816	0.4776
chr7	159138663	18168000	0.1142	0.8108

chr8	146364022	19378047	0.1324	1.1258
chr9	141213431	8506501	0.0602	0.6573
chr10	135534747	19662870	0.1451	0.8665
chr11	135006516	15128750	0.1121	0.7504
chr12	133851895	15015140	0.1122	0.5465
chr13	115169878	7727566	0.0671	0.4015
chr14	107349540	11054346	0.103	0.5366
chr15	102531392	12584877	0.1227	0.5713
chr16	90354753	14066085	0.1557	0.7822
chr17	81195210	10725205	0.1321	0.6605
chr18	78077248	7138405	0.0914	0.8958
chr19	59128983	10367425	0.1753	0.9876
chr20	63025520	10260022	0.1628	0.6908
chr21	48129895	6471390	0.1345	0.7216
chr22	51304566	4885726	0.0952	0.5133
chrMT	16571	97738	5.8981	5.4243
chrX	155270560	24797280	0.1597	0.6846
chrY	59373566	1380869	0.0233	0.8198

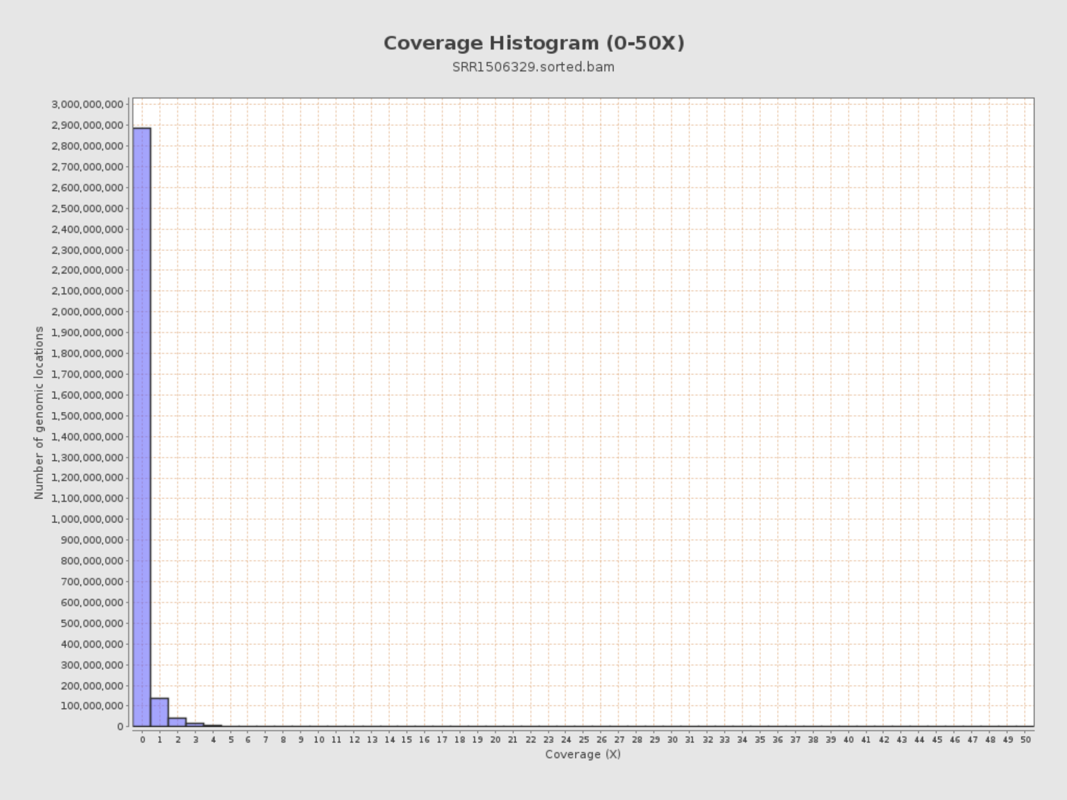
3. Results : Coverage across reference



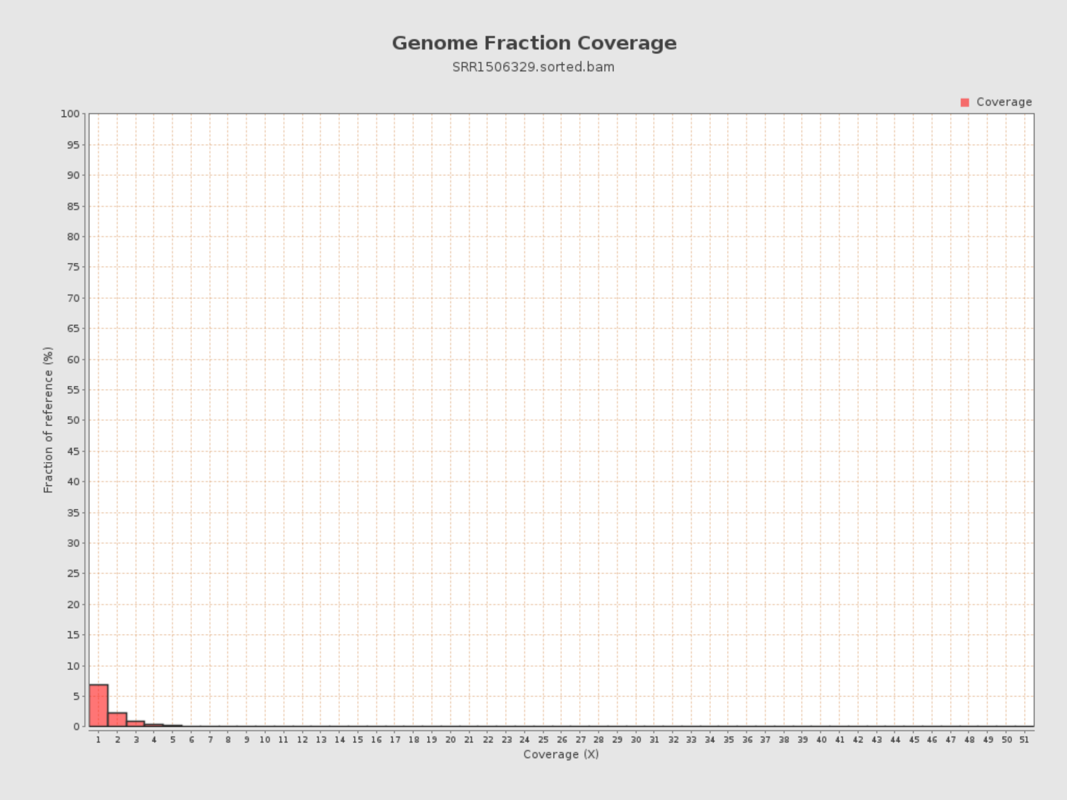
4. Results : Coverage Histogram



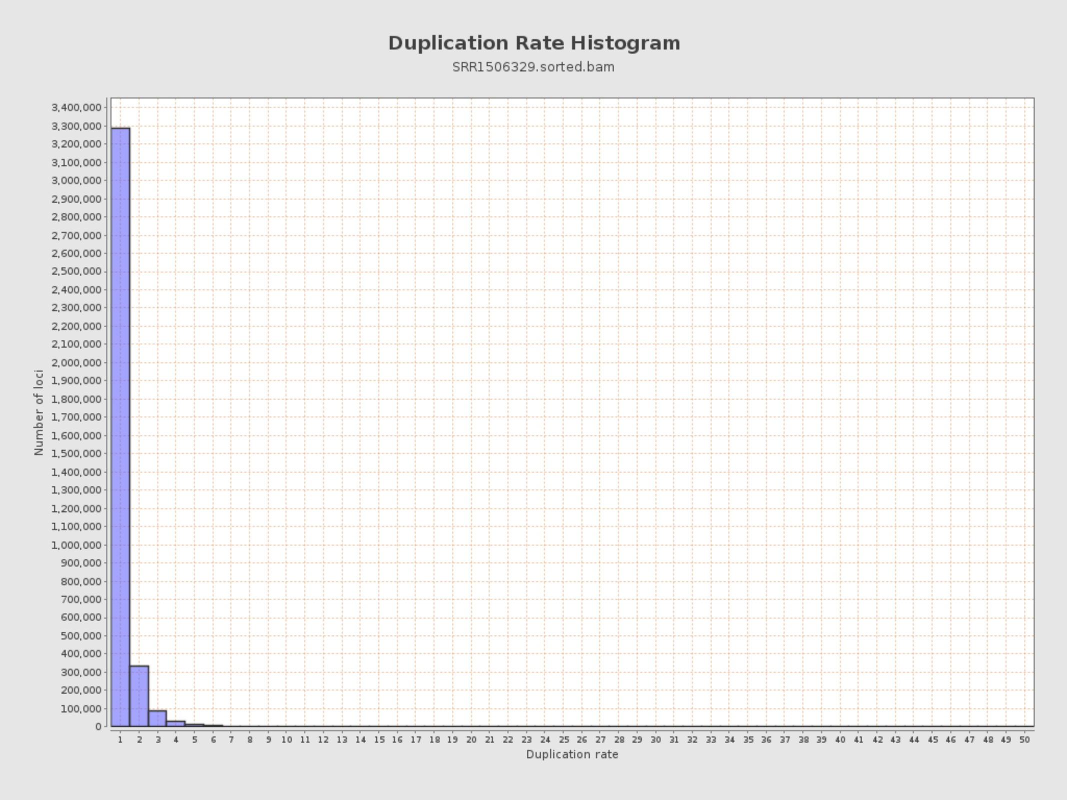
5. Results : Coverage Histogram (0-50X)



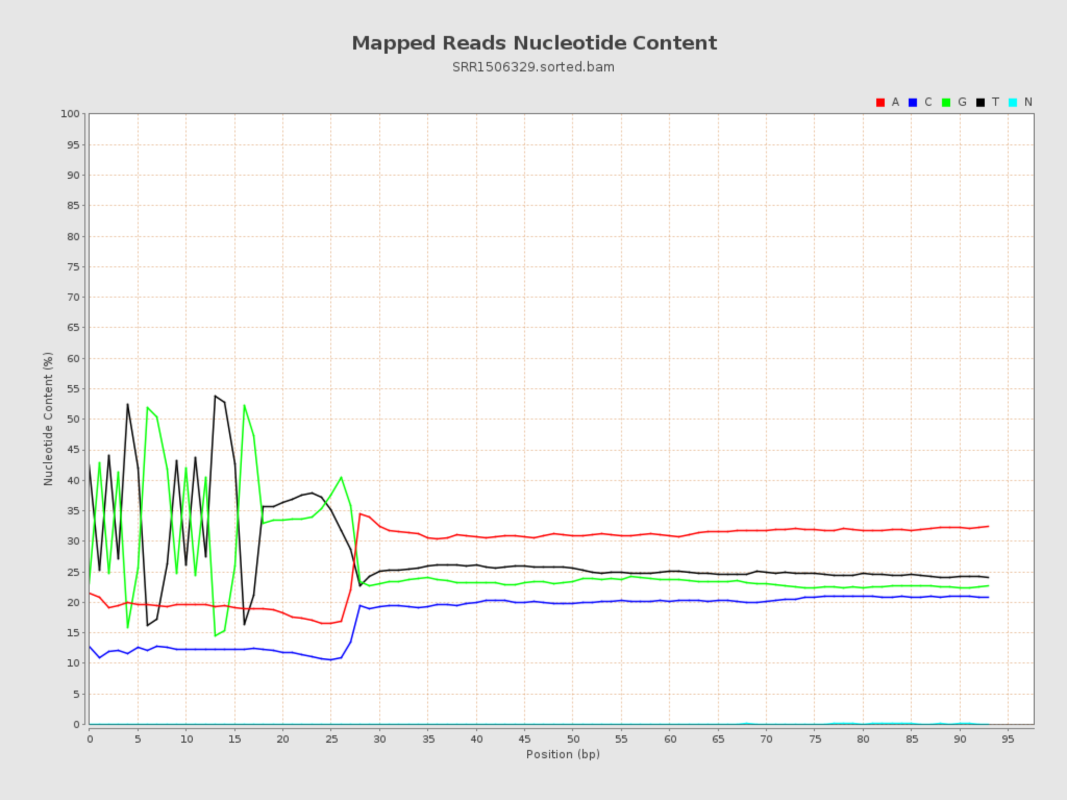
6. Results : Genome Fraction Coverage



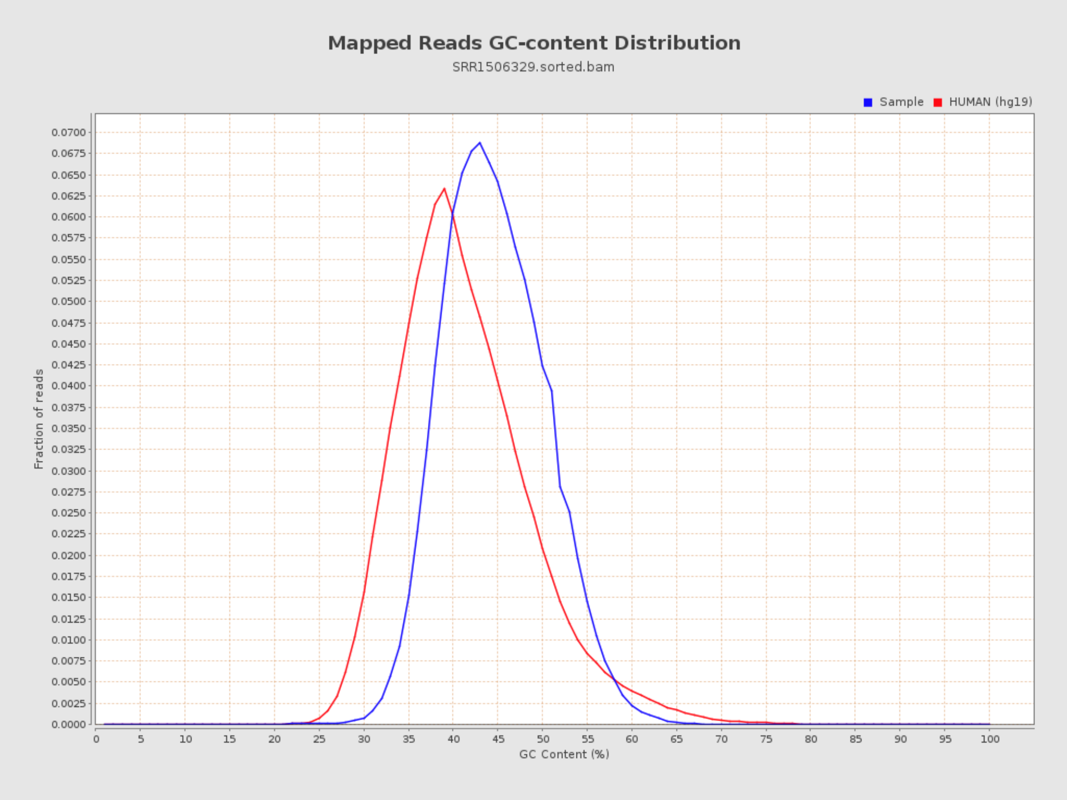
7. Results : Duplication Rate Histogram



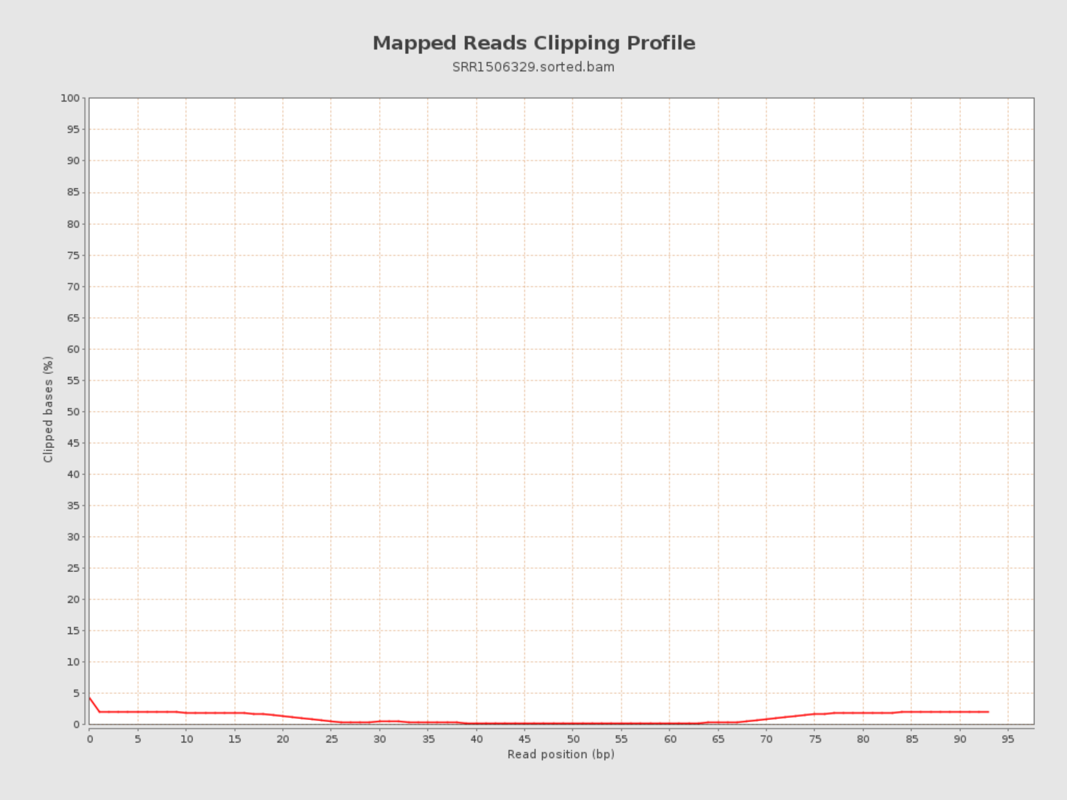
8. Results : Mapped Reads Nucleotide Content



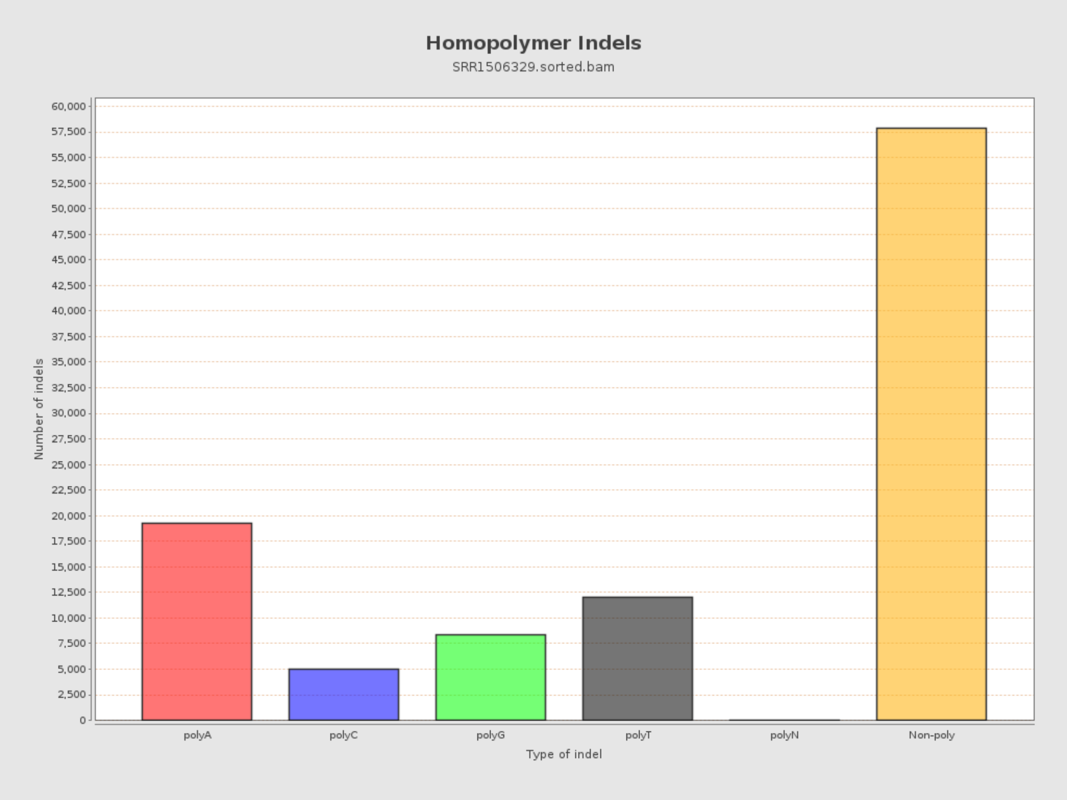
9. Results : Mapped Reads GC-content Distribution



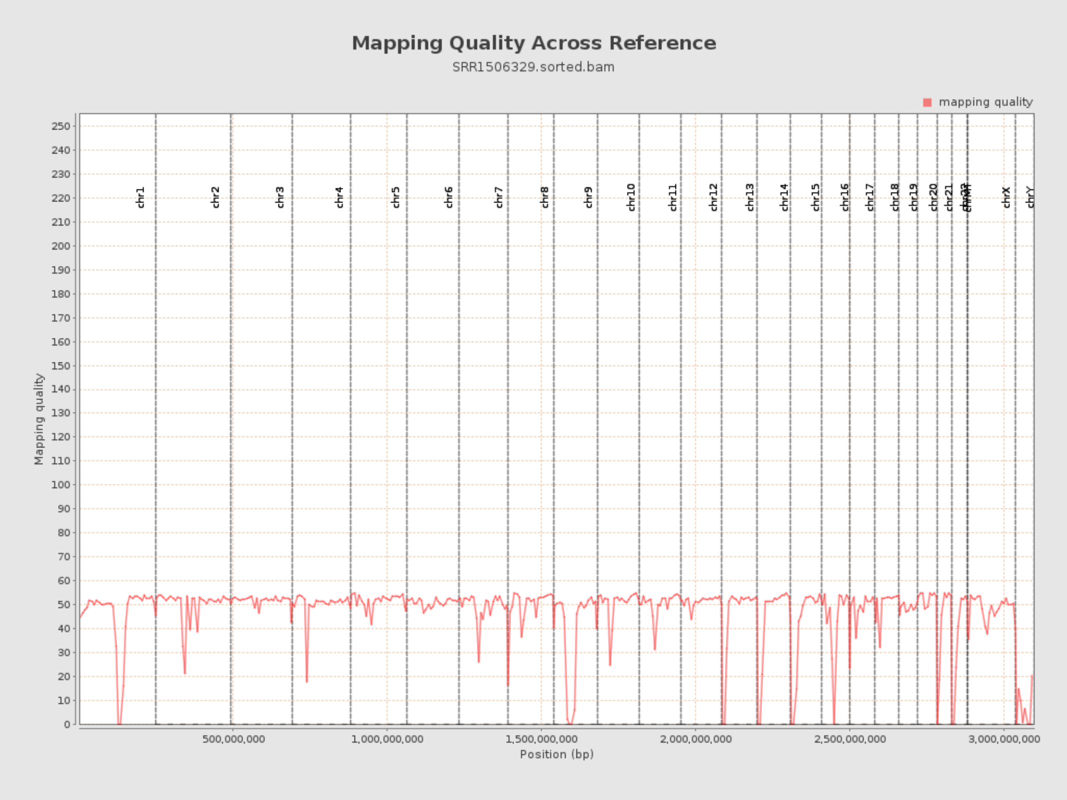
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram