Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:06:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506327.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_SRR1506327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506327.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:06:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,798,316
Mapped reads	5,000,044 / 73.55%
Unmapped reads	1,798,272 / 26.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	71,895 / 1.06%
Read min/max/mean length	30 / 94 / 94.38
Duplicated reads (estimated)	771,566 / 11.35%
Duplication rate	10.24%
Clipped reads	2,805,465 / 41.27%

2.2. ACGT Content

Number/percentage of A's	112,861,589 / 28.05%
Number/percentage of C's	75,344,344 / 18.73%
Number/percentage of T's	110,712,833 / 27.52%
Number/percentage of G's	103,347,210 / 25.69%
Number/percentage of N's	92,810 / 0.02%
GC Percentage	44.41%

2.3. Coverage

Mean	0.13

Standard Deviation	0.9638

2.4. Mapping Quality

Mean Mapping Quality	47.66

2.5. Mismatches and indels

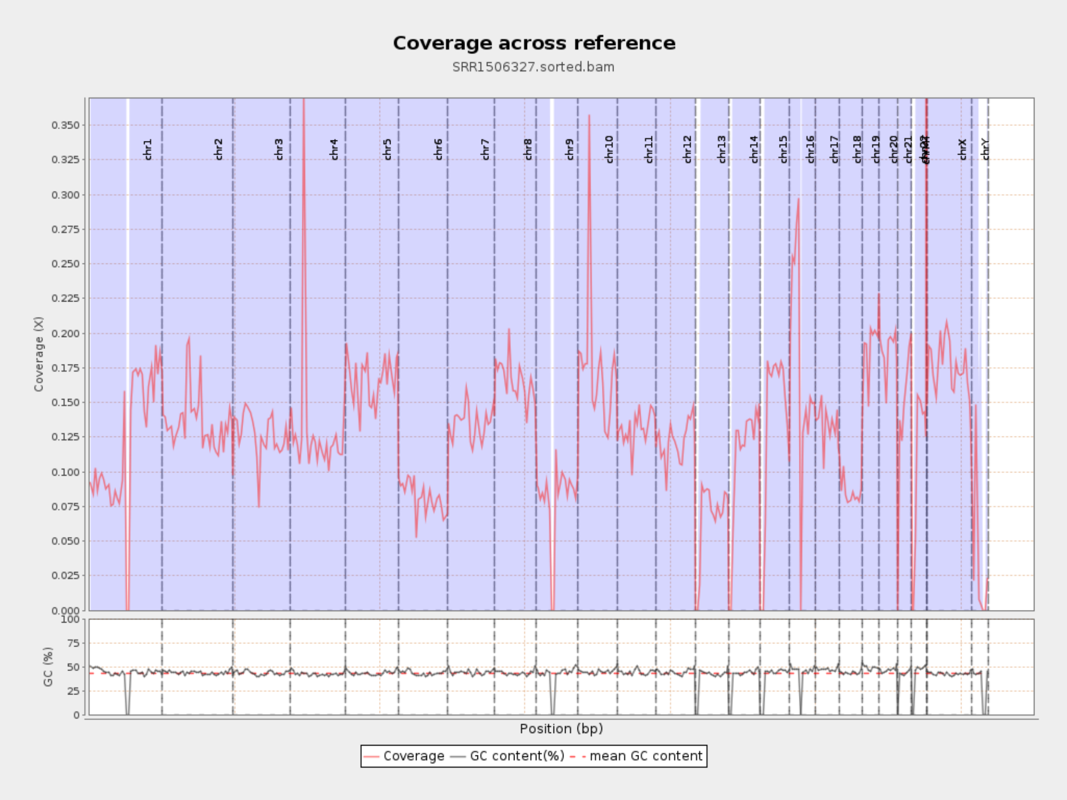
General error rate	0.76%
Mismatches	2,965,358
Insertions	36,520
Mapped reads with at least one insertion	0.71%
Deletions	89,937
Mapped reads with at least one deletion	1.76%
Homopolymer indels	42.31%

2.6. Chromosome stats

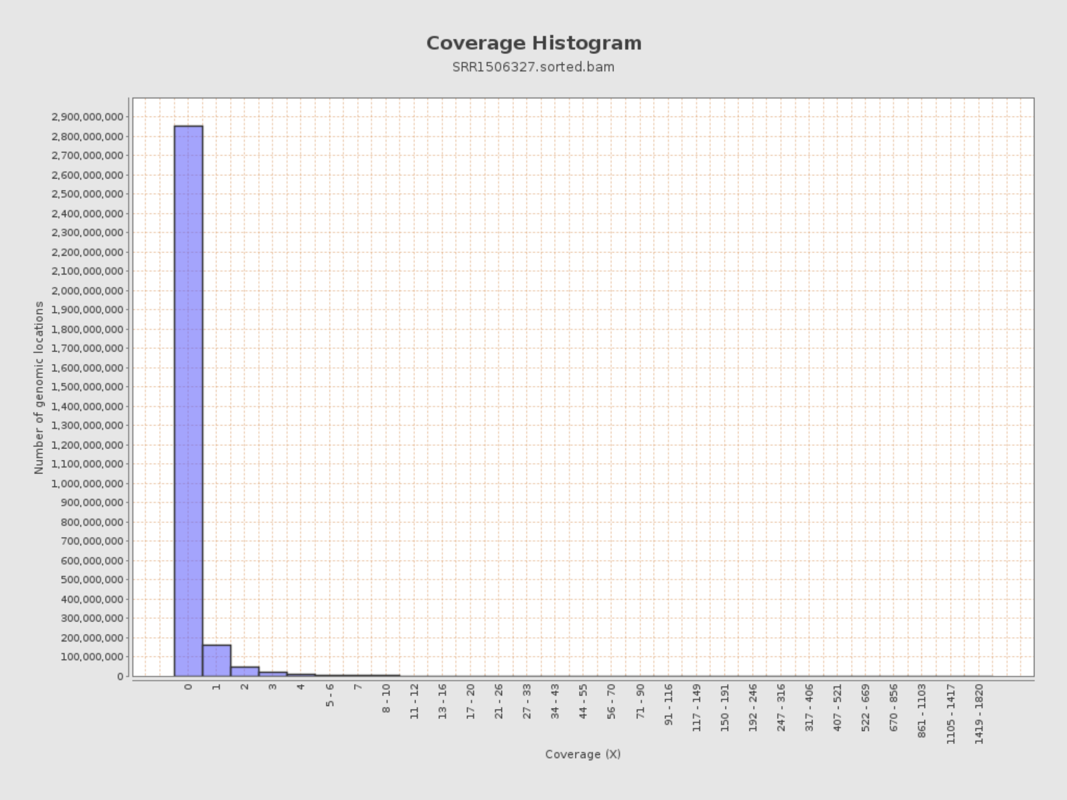
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29662395	0.119	1.5592
chr2	243199373	33188967	0.1365	1.039
chr3	198022430	25066644	0.1266	0.5605
chr4	191154276	24769525	0.1296	1.0972
chr5	180915260	29937660	0.1655	0.6435
chr6	171115067	13917690	0.0813	0.4666
chr7	159138663	21458308	0.1348	1.0111

chr8	146364022	24292744	0.166	1.1551
chr9	141213431	11157678	0.079	0.7989
chr10	135534747	23804926	0.1756	1.5025
chr11	135006516	17762875	0.1316	0.8331
chr12	133851895	16363062	0.1222	0.5589
chr13	115169878	7579337	0.0658	0.3968
chr14	107349540	11687334	0.1089	0.5568
chr15	102531392	13850006	0.1351	0.5945
chr16	90354753	15998691	0.1771	0.9322
chr17	81195210	10885330	0.1341	0.6837
chr18	78077248	6692904	0.0857	1.1334
chr19	59128983	11204170	0.1895	1.2802
chr20	63025520	11802106	0.1873	0.7795
chr21	48129895	6938793	0.1442	0.9486
chr22	51304566	5215815	0.1017	0.5538
chrMT	16571	60384	3.644	3.2797
chrX	155270560	27309491	0.1759	0.7157
chrY	59373566	1943780	0.0327	1.4838

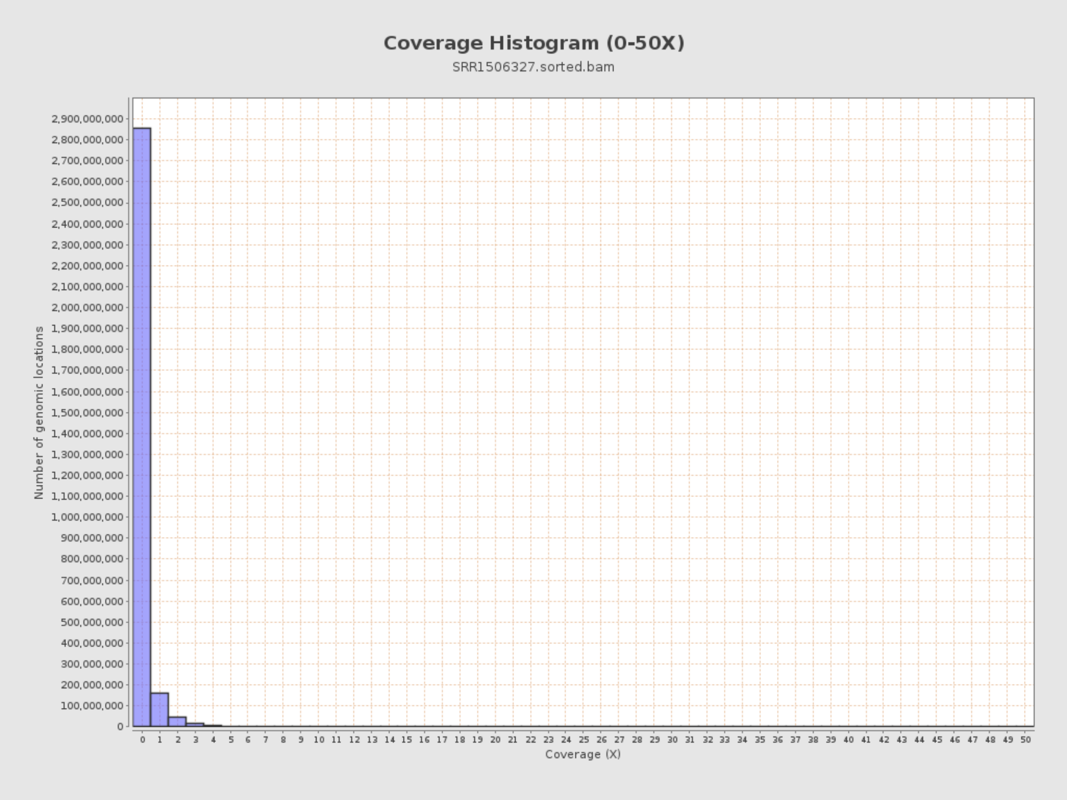
3. Results : Coverage across reference



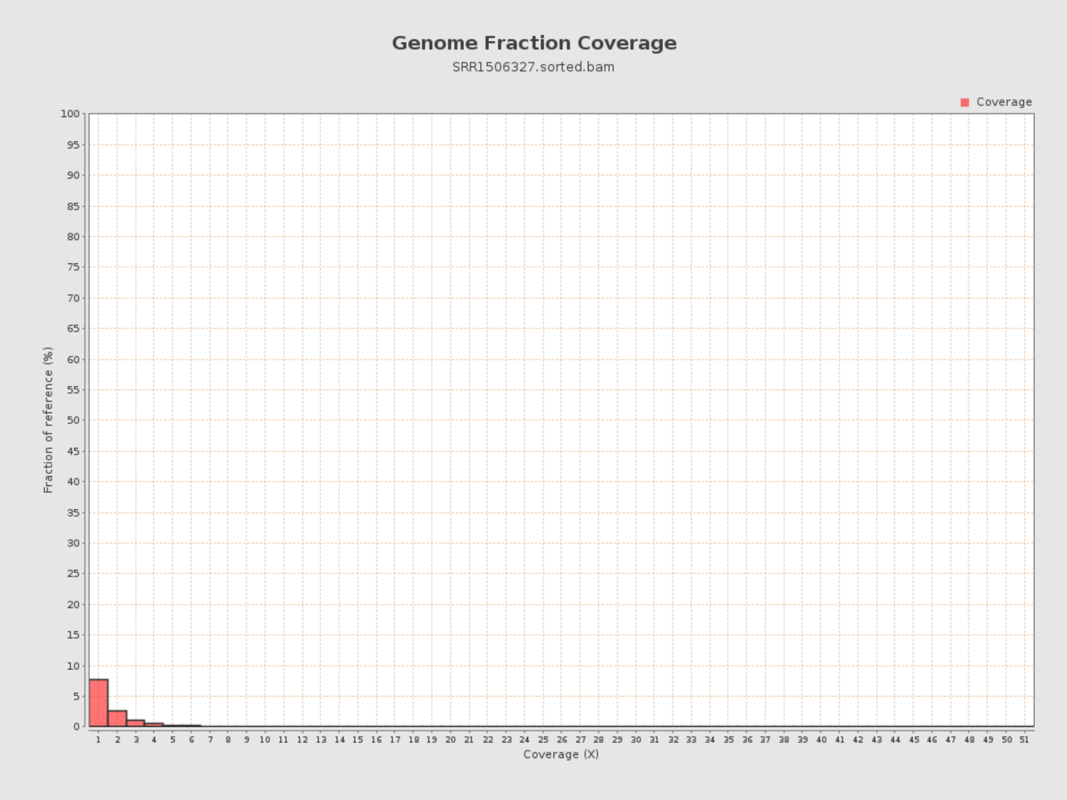
4. Results : Coverage Histogram



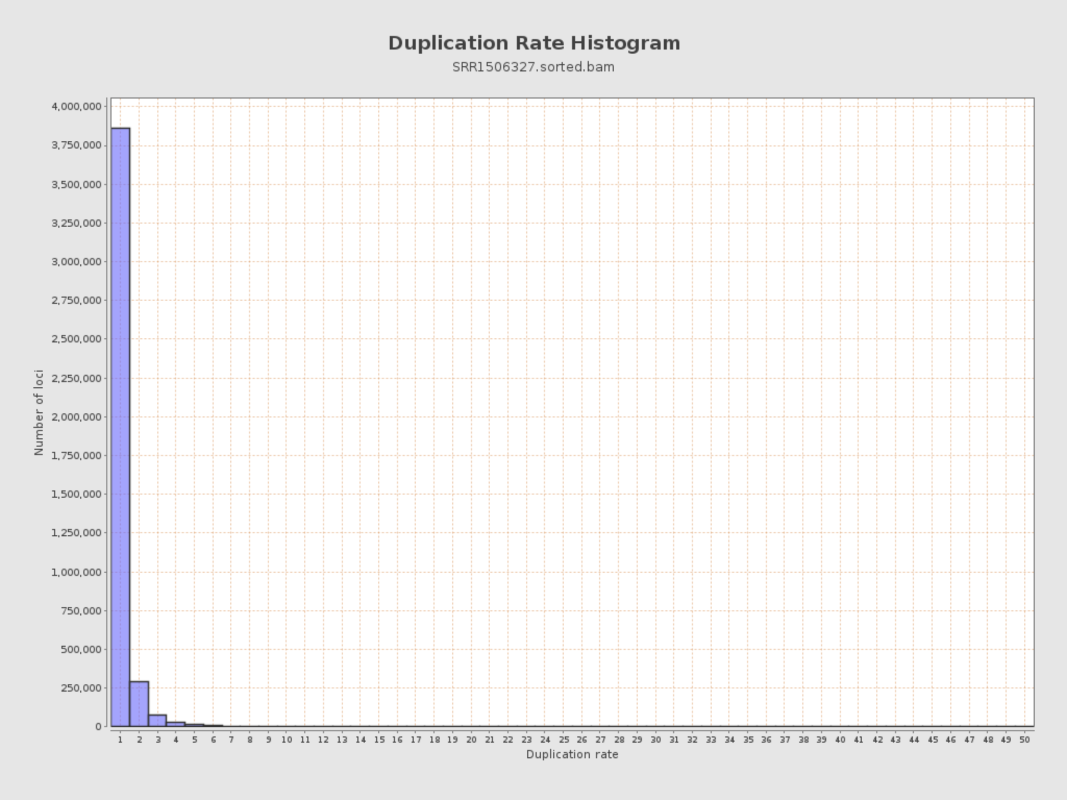
5. Results : Coverage Histogram (0-50X)



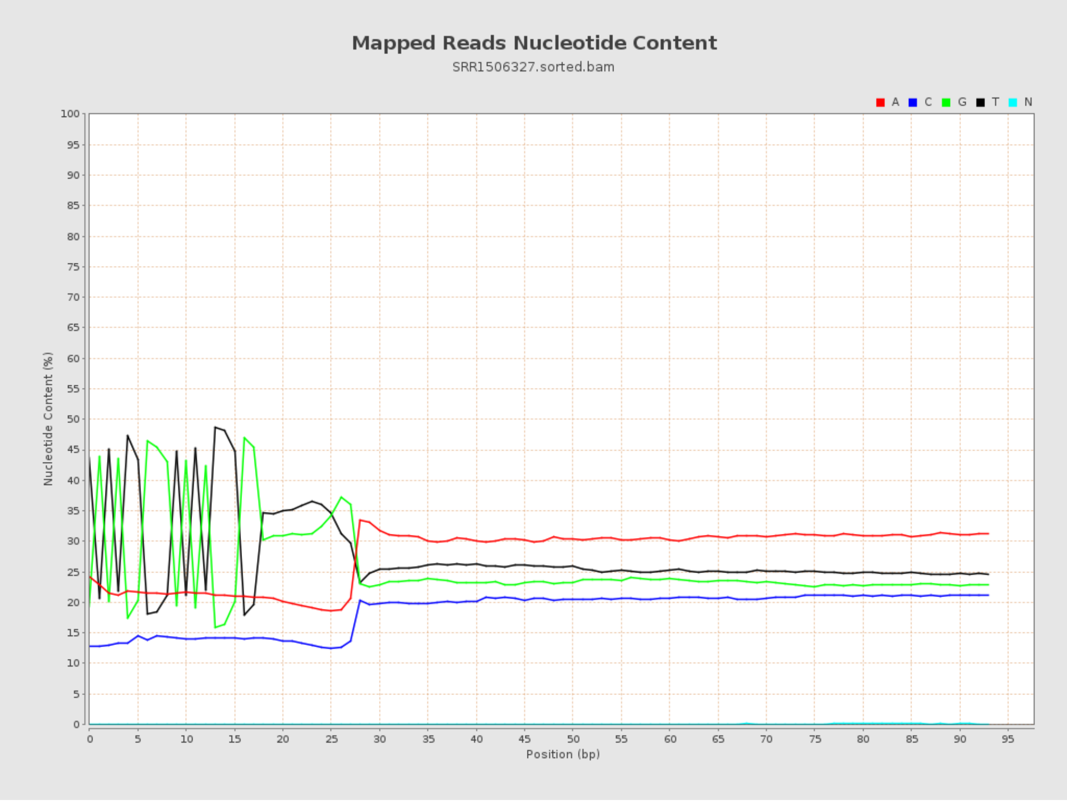
6. Results : Genome Fraction Coverage



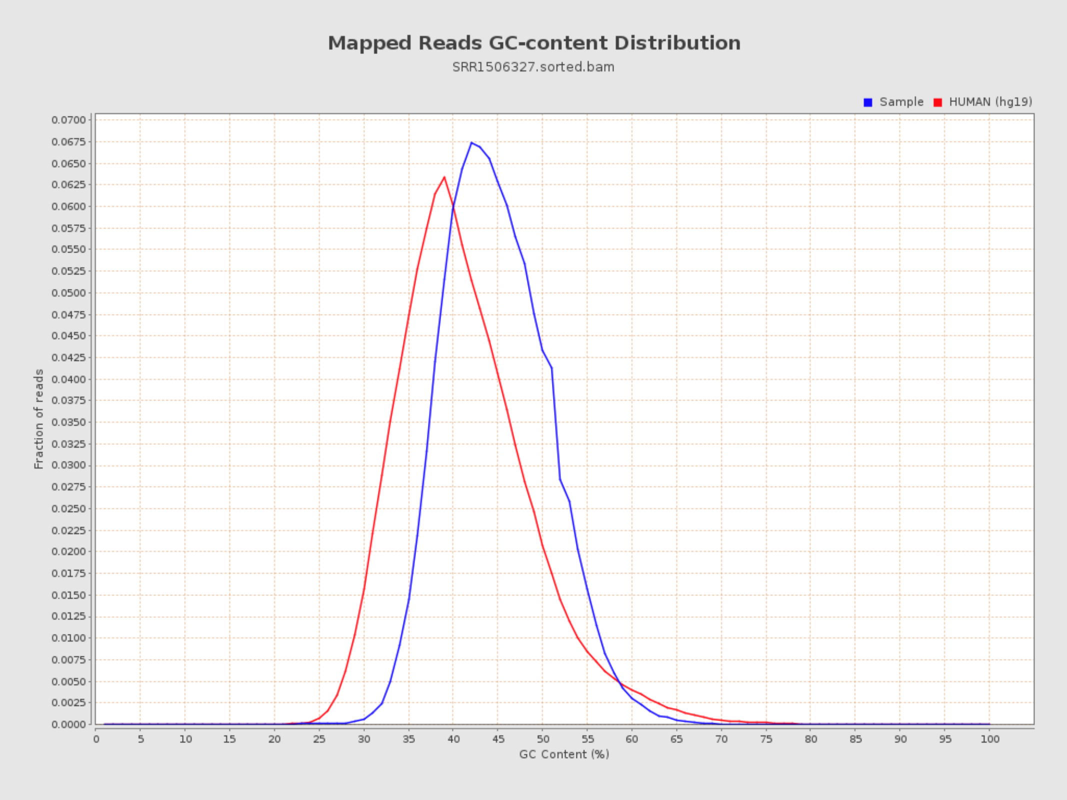
7. Results : Duplication Rate Histogram



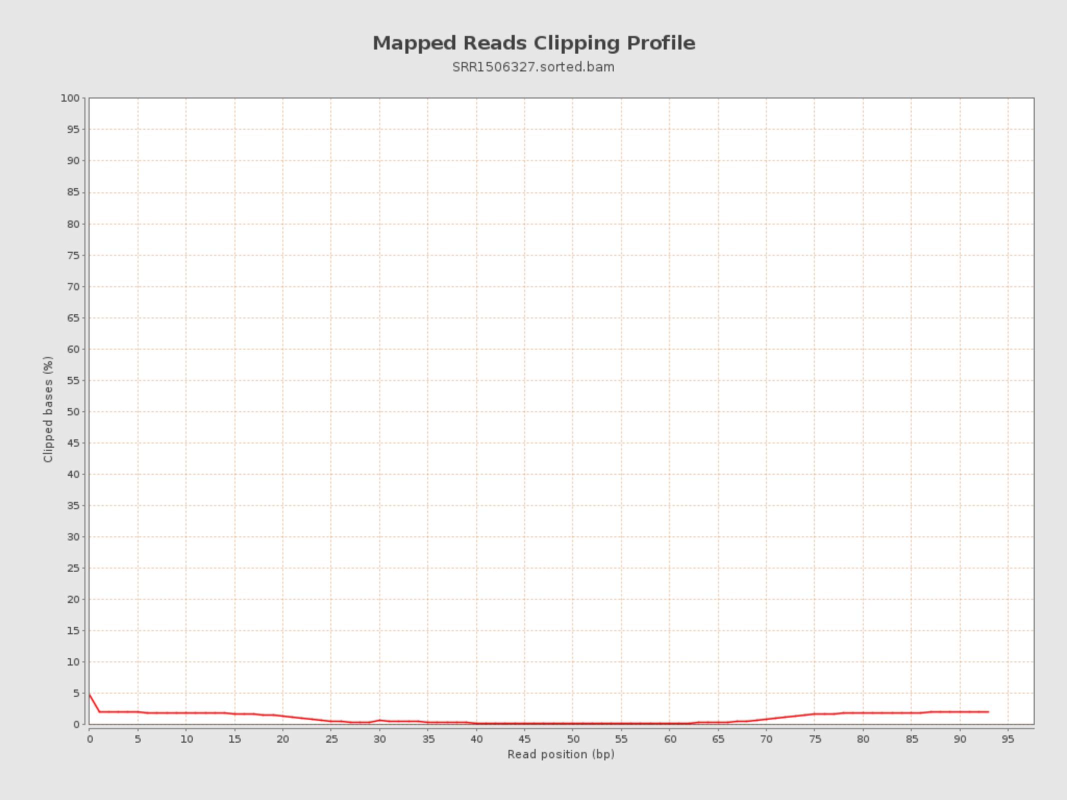
8. Results : Mapped Reads Nucleotide Content



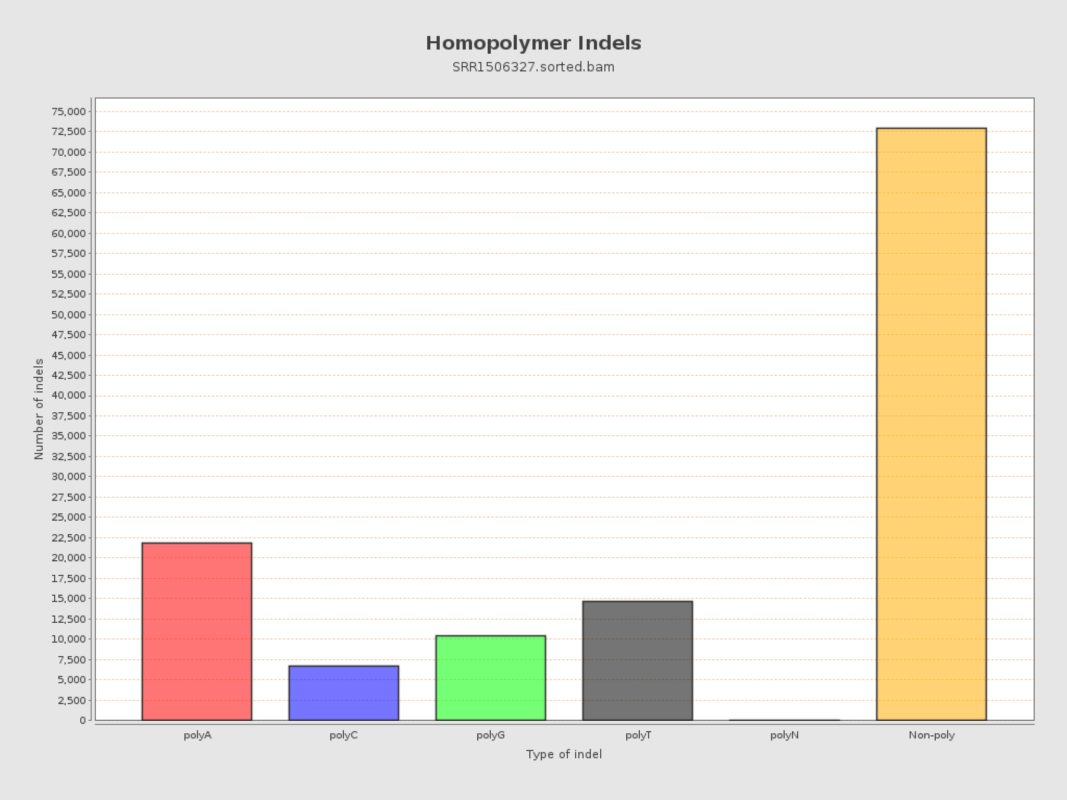
9. Results : Mapped Reads GC-content Distribution



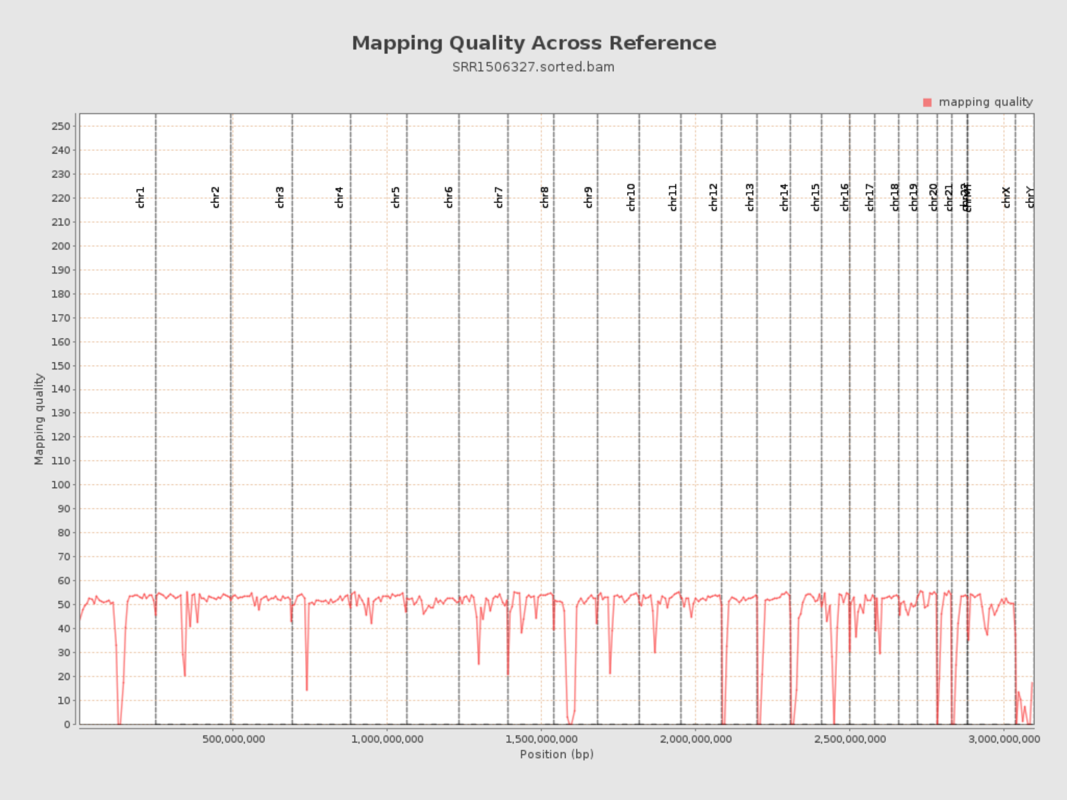
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram