Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 05:03:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506343.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_SRR1506343 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506343.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 05:03:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506343.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,964,400
Mapped reads	5,300,942 / 76.11%
Unmapped reads	1,663,458 / 23.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	88,141 / 1.27%
Read min/max/mean length	30 / 94 / 94.46
Duplicated reads (estimated)	688,580 / 9.89%
Duplication rate	9.8%
Clipped reads	3,414,164 / 49.02%

2.2. ACGT Content

Number/percentage of A's	119,020,241 / 28.83%
Number/percentage of C's	76,297,687 / 18.48%
Number/percentage of T's	113,775,794 / 27.56%
Number/percentage of G's	103,622,103 / 25.1%
Number/percentage of N's	103,455 / 0.03%
GC Percentage	43.58%

2.3. Coverage

Mean	0.1334

Standard Deviation	0.8304

2.4. Mapping Quality

Mean Mapping Quality	47.34

2.5. Mismatches and indels

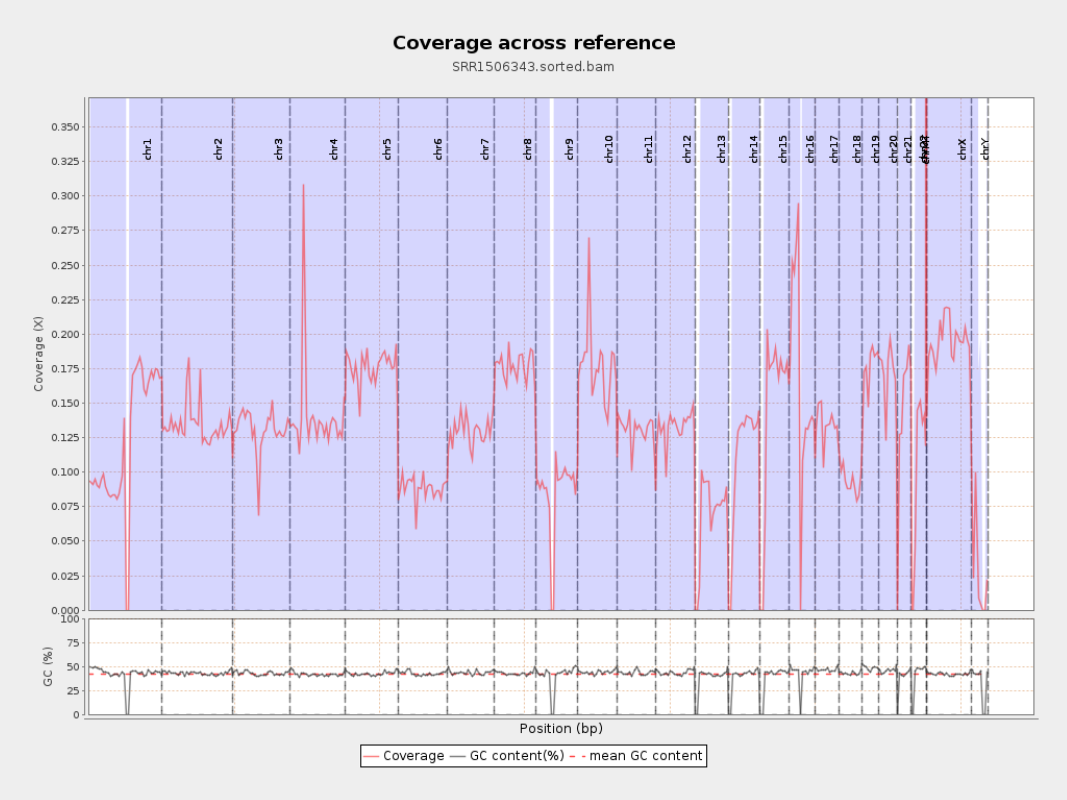
General error rate	0.75%
Mismatches	2,996,175
Insertions	37,212
Mapped reads with at least one insertion	0.68%
Deletions	87,799
Mapped reads with at least one deletion	1.62%
Homopolymer indels	43.98%

2.6. Chromosome stats

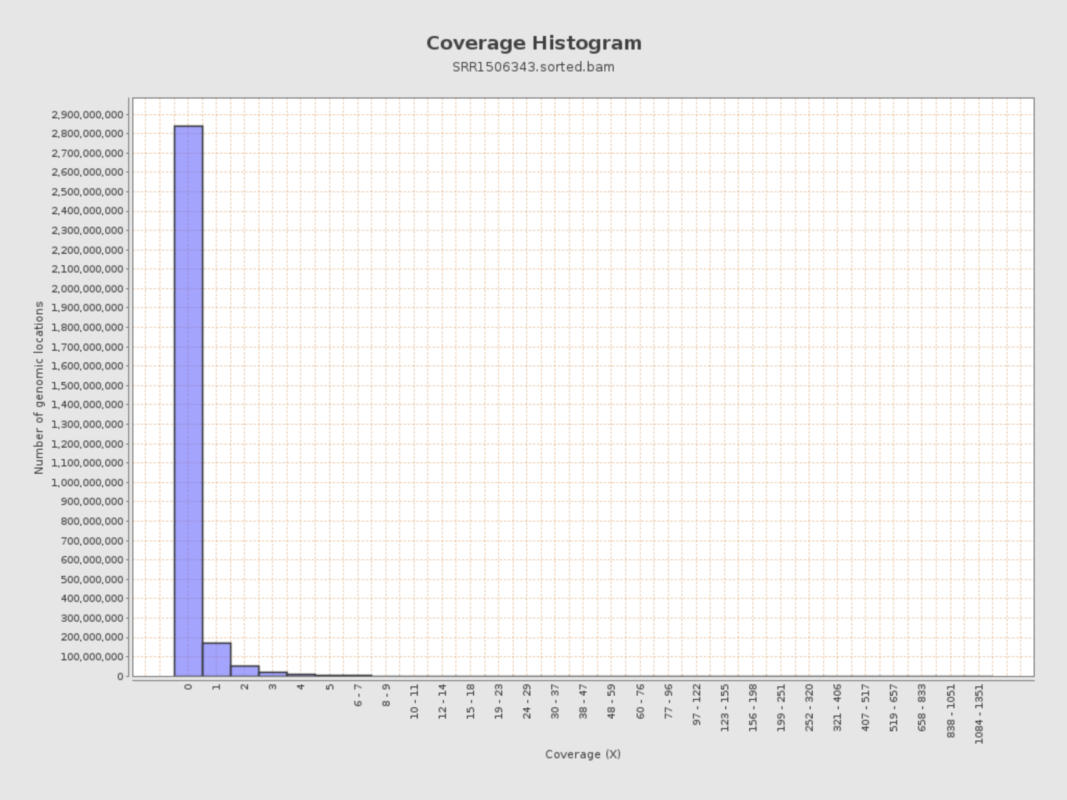
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29992704	0.1203	1.1786
chr2	243199373	32859309	0.1351	0.9238
chr3	198022430	25785069	0.1302	0.5381
chr4	191154276	26707552	0.1397	0.9058
chr5	180915260	31884012	0.1762	0.6453
chr6	171115067	15144899	0.0885	0.471
chr7	159138663	20659760	0.1298	0.9213

chr8	146364022	25911104	0.177	1.1994
chr9	141213431	11825164	0.0837	0.7196
chr10	135534747	24102449	0.1778	1.0716
chr11	135006516	17567254	0.1301	0.7674
chr12	133851895	17765931	0.1327	0.5549
chr13	115169878	7850138	0.0682	0.3847
chr14	107349540	11872540	0.1106	0.5469
chr15	102531392	14928081	0.1456	0.6007
chr16	90354753	15180408	0.168	0.8509
chr17	81195210	10876608	0.134	0.6309
chr18	78077248	7294982	0.0934	1.131
chr19	59128983	10357632	0.1752	1.0196
chr20	63025520	10694406	0.1697	0.694
chr21	48129895	6996478	0.1454	0.8183
chr22	51304566	5024989	0.0979	0.492
chrMT	16571	47668	2.8766	2.5524
chrX	155270560	30110970	0.1939	0.7404
chrY	59373566	1557950	0.0262	0.9064

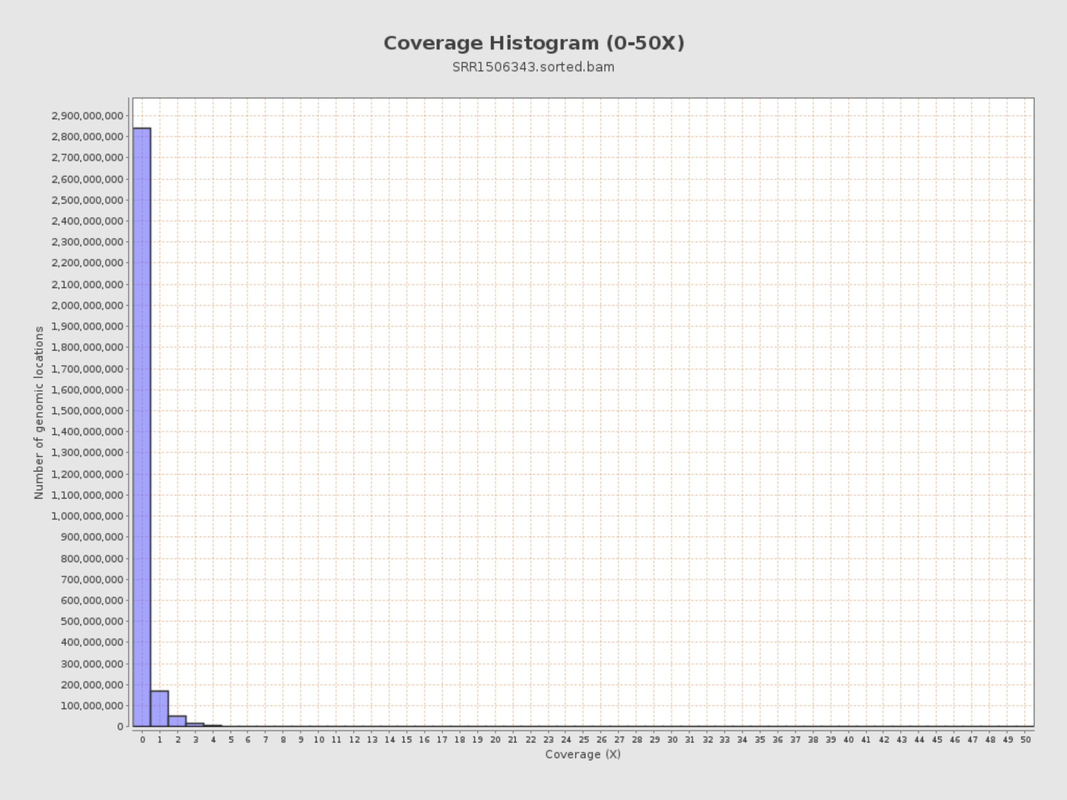
3. Results : Coverage across reference



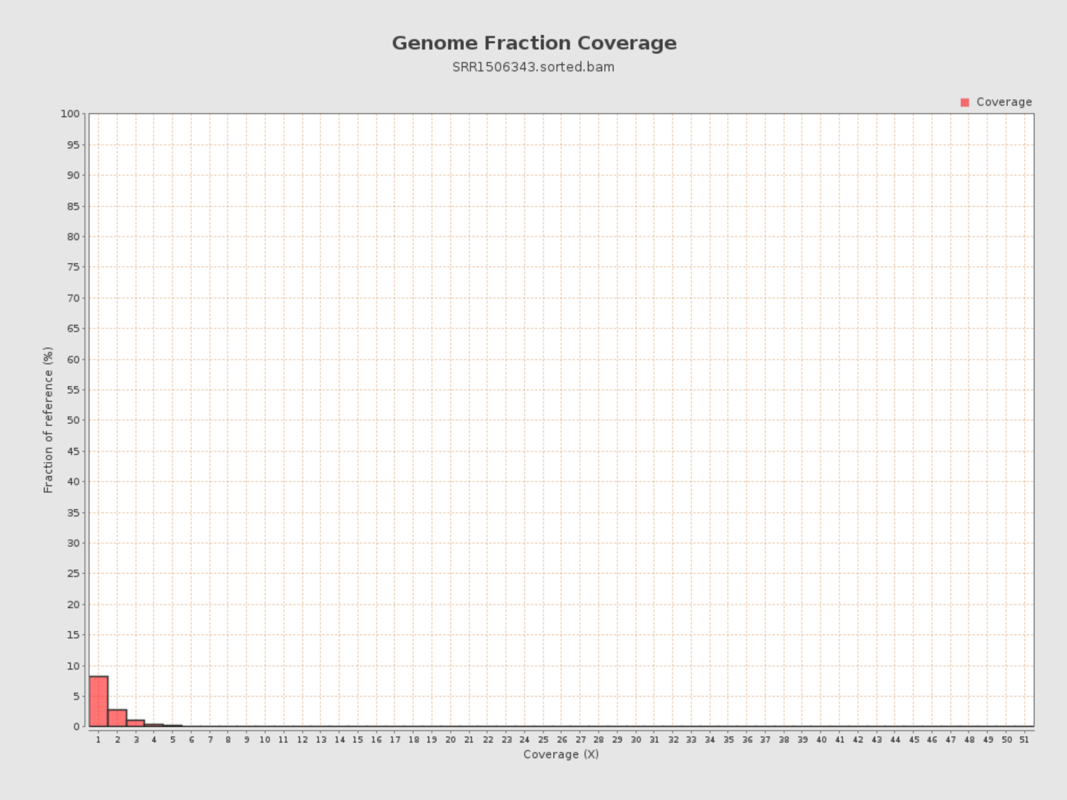
4. Results : Coverage Histogram



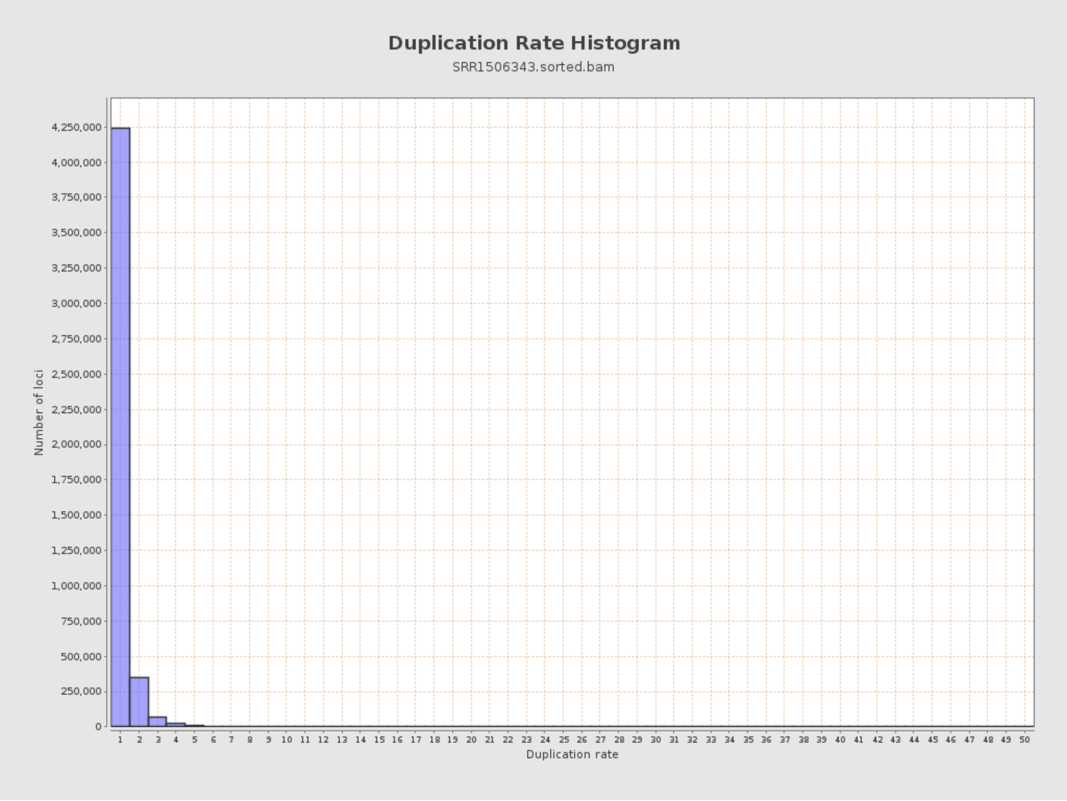
5. Results : Coverage Histogram (0-50X)



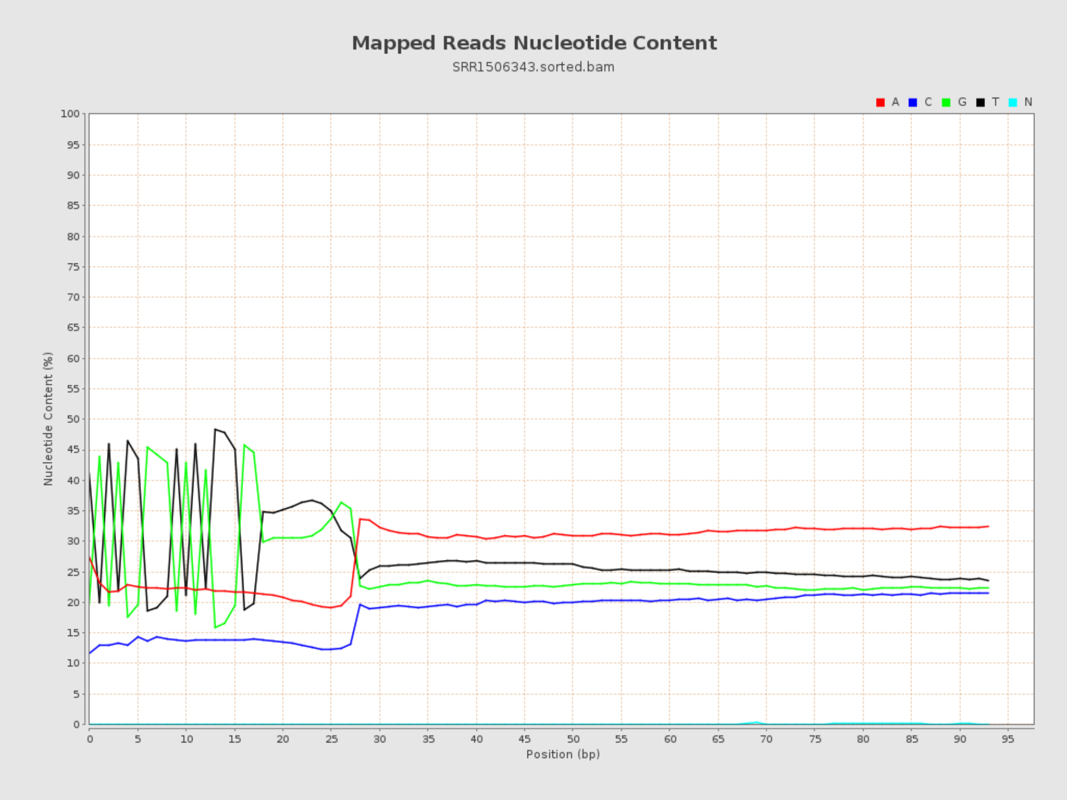
6. Results : Genome Fraction Coverage



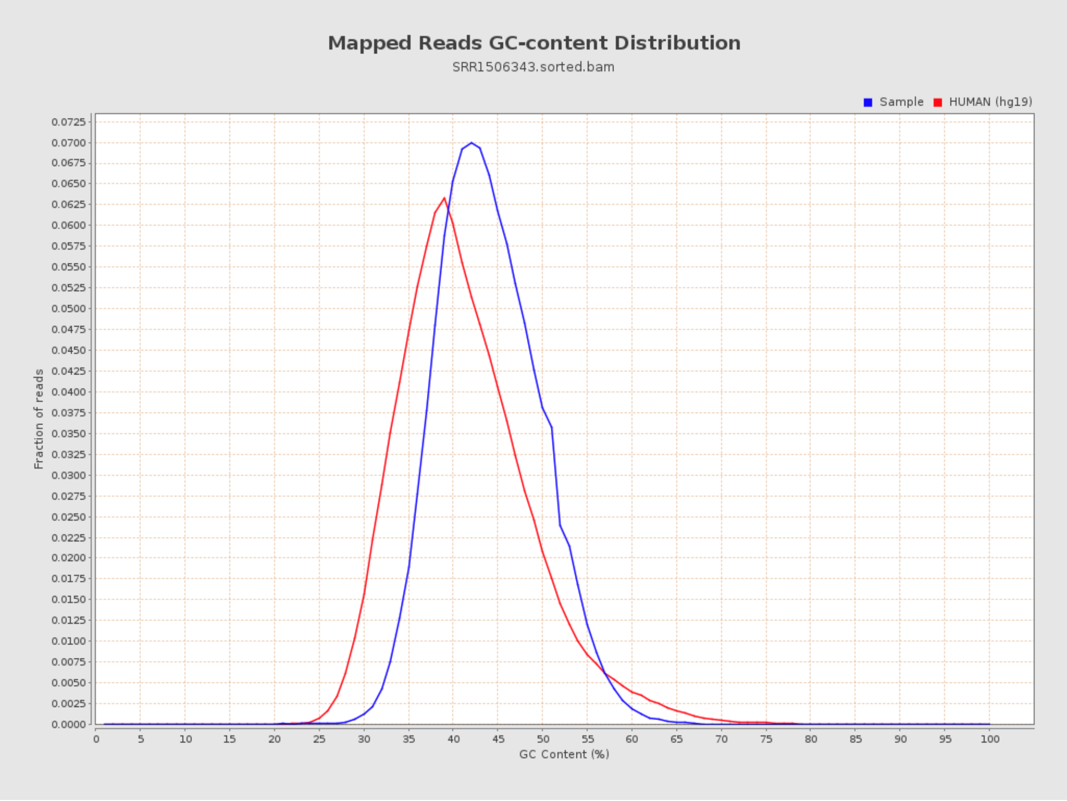
7. Results : Duplication Rate Histogram



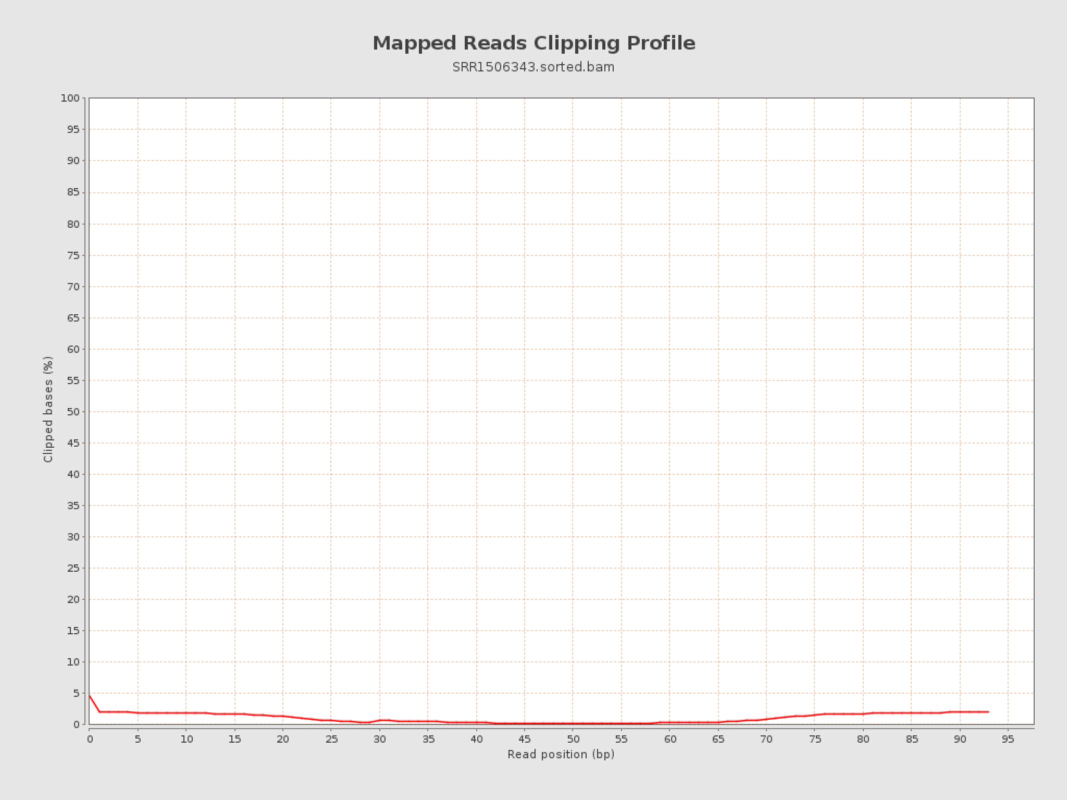
8. Results : Mapped Reads Nucleotide Content



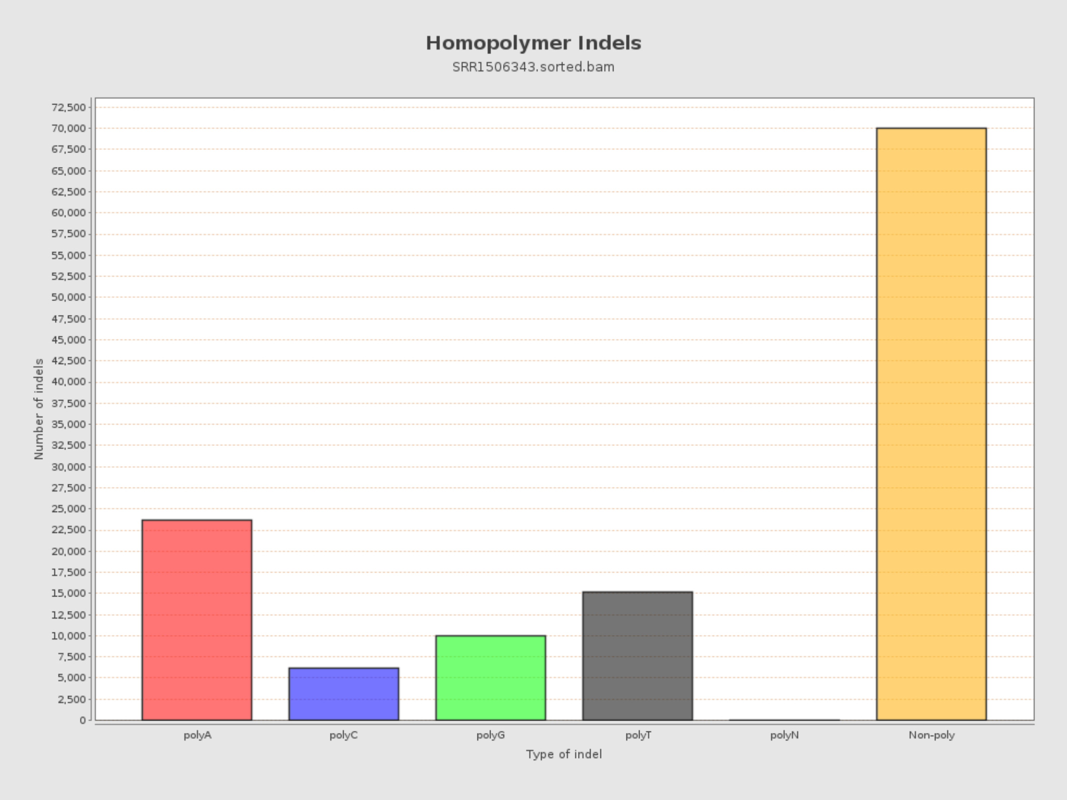
9. Results : Mapped Reads GC-content Distribution



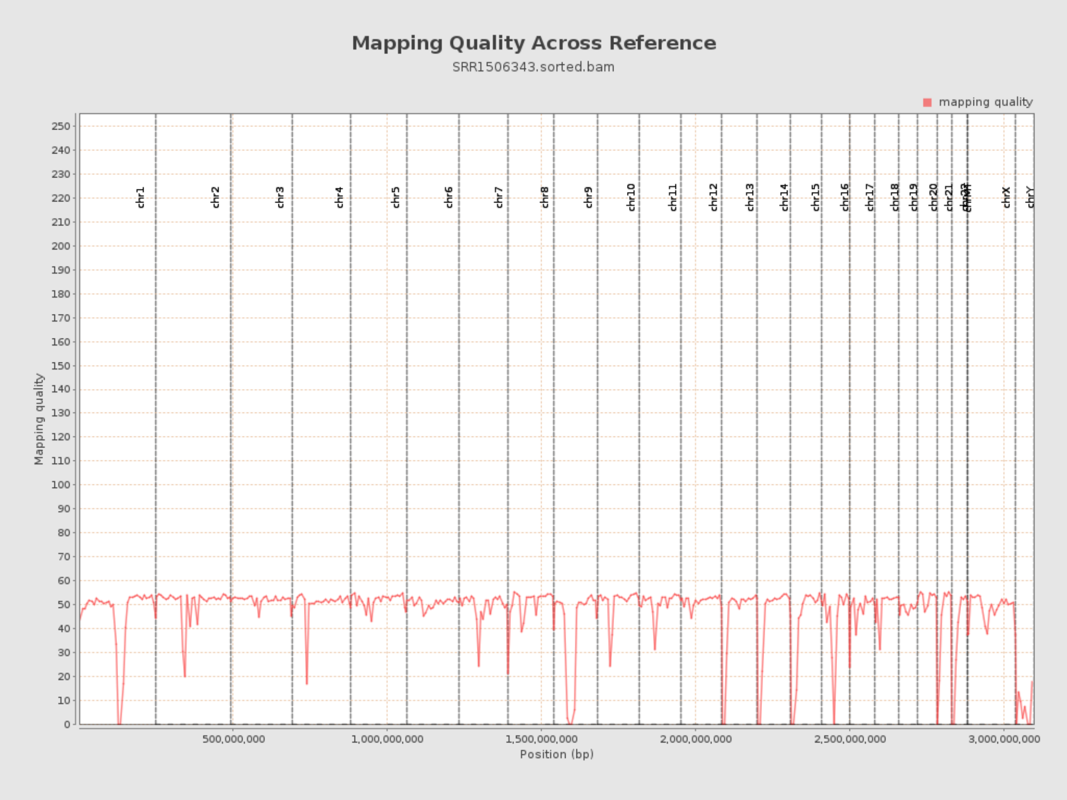
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram