Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 03:26:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506330.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_SRR1506330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506330.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 03:26:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,345,009
Mapped reads	5,400,227 / 73.52%
Unmapped reads	1,944,782 / 26.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	94,347 / 1.28%
Read min/max/mean length	30 / 94 / 94.46
Duplicated reads (estimated)	592,969 / 8.07%
Duplication rate	7.79%
Clipped reads	3,901,893 / 53.12%

2.2. ACGT Content

Number/percentage of A's	113,619,835 / 27.87%
Number/percentage of C's	73,685,113 / 18.07%
Number/percentage of T's	114,384,820 / 28.06%
Number/percentage of G's	105,889,201 / 25.97%
Number/percentage of N's	96,653 / 0.02%
GC Percentage	44.05%

2.3. Coverage

Mean	0.1318

Standard Deviation	0.845

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

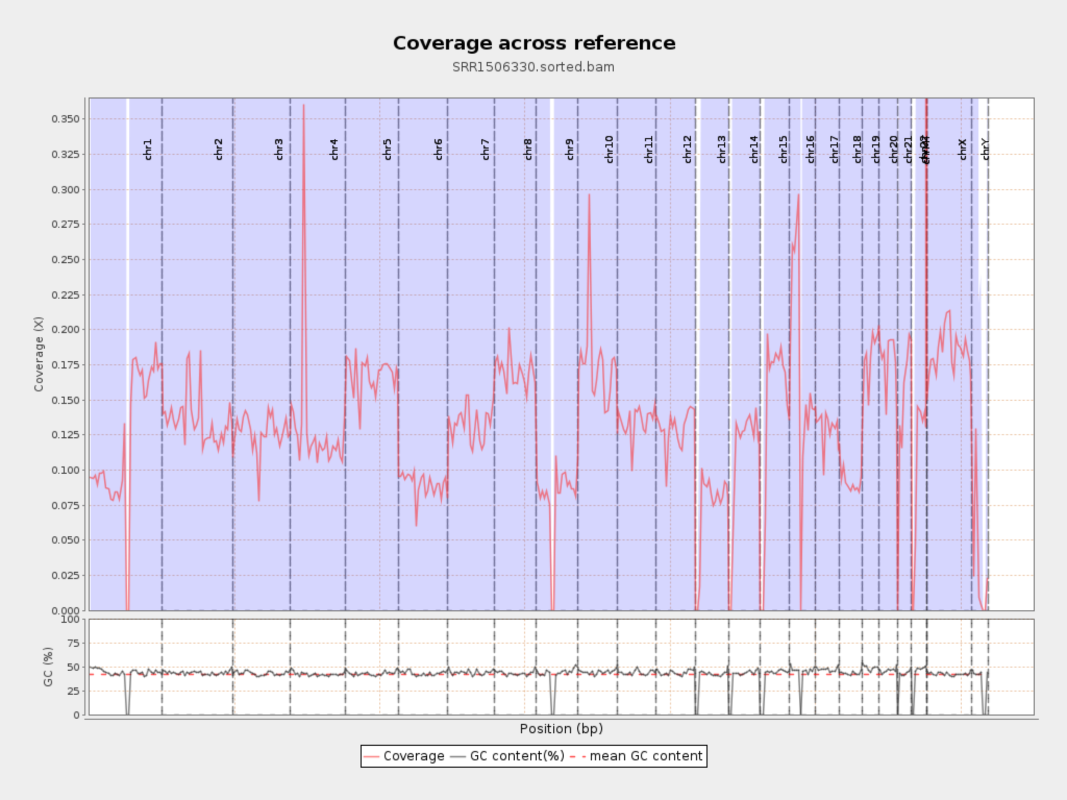
General error rate	0.77%
Mismatches	3,035,855
Insertions	37,263
Mapped reads with at least one insertion	0.67%
Deletions	88,298
Mapped reads with at least one deletion	1.6%
Homopolymer indels	42.42%

2.6. Chromosome stats

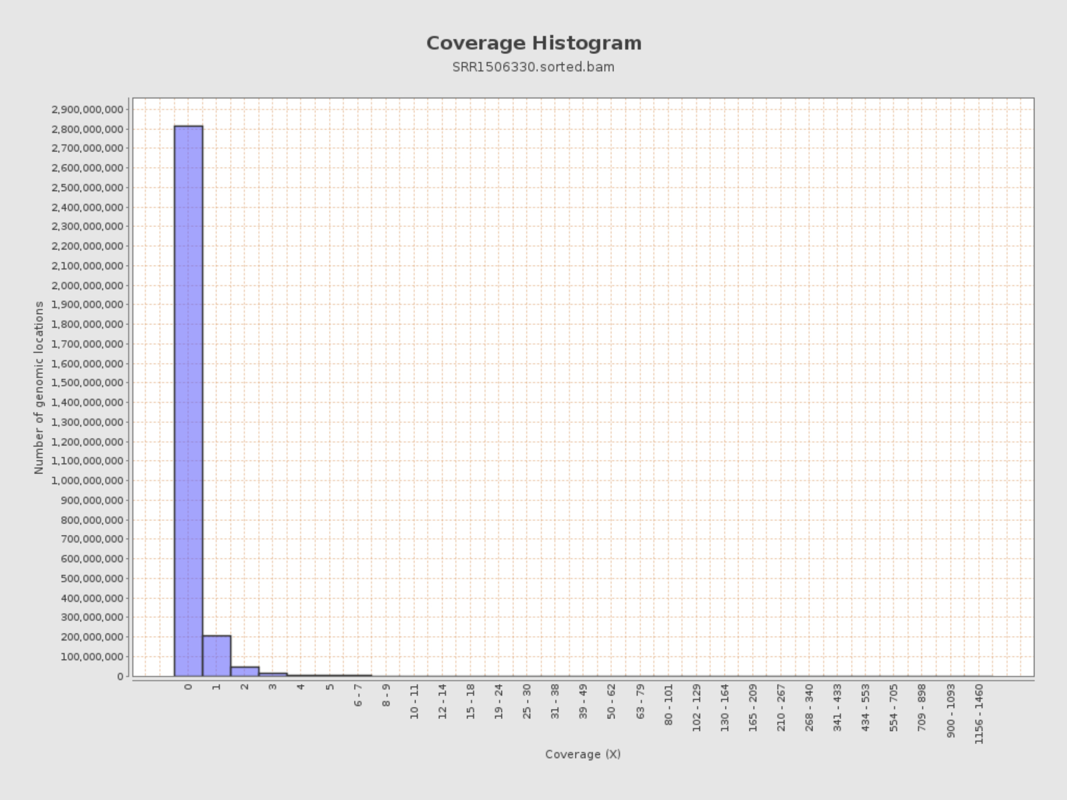
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30027173	0.1205	1.1821
chr2	243199373	33060024	0.1359	0.969
chr3	198022430	25082939	0.1267	0.4892
chr4	191154276	24720900	0.1293	1.016
chr5	180915260	30326222	0.1676	0.5805
chr6	171115067	15387759	0.0899	0.4527
chr7	159138663	21113590	0.1327	0.8939

chr8	146364022	24967026	0.1706	1.2114
chr9	141213431	11037738	0.0782	0.6432
chr10	135534747	23963820	0.1768	1.2139
chr11	135006516	18182487	0.1347	0.7483
chr12	133851895	17362963	0.1297	0.5189
chr13	115169878	8278037	0.0719	0.3623
chr14	107349540	11686901	0.1089	0.5179
chr15	102531392	14536895	0.1418	0.553
chr16	90354753	15791646	0.1748	0.8301
chr17	81195210	10538445	0.1298	0.5779
chr18	78077248	7154383	0.0916	1.087
chr19	59128983	10654032	0.1802	1.0057
chr20	63025520	11247438	0.1785	0.7006
chr21	48129895	7017832	0.1458	0.8937
chr22	51304566	4982033	0.0971	0.4622
chrMT	16571	162062	9.7799	7.3568
chrX	155270560	28722901	0.185	0.6866
chrY	59373566	1853847	0.0312	1.3309

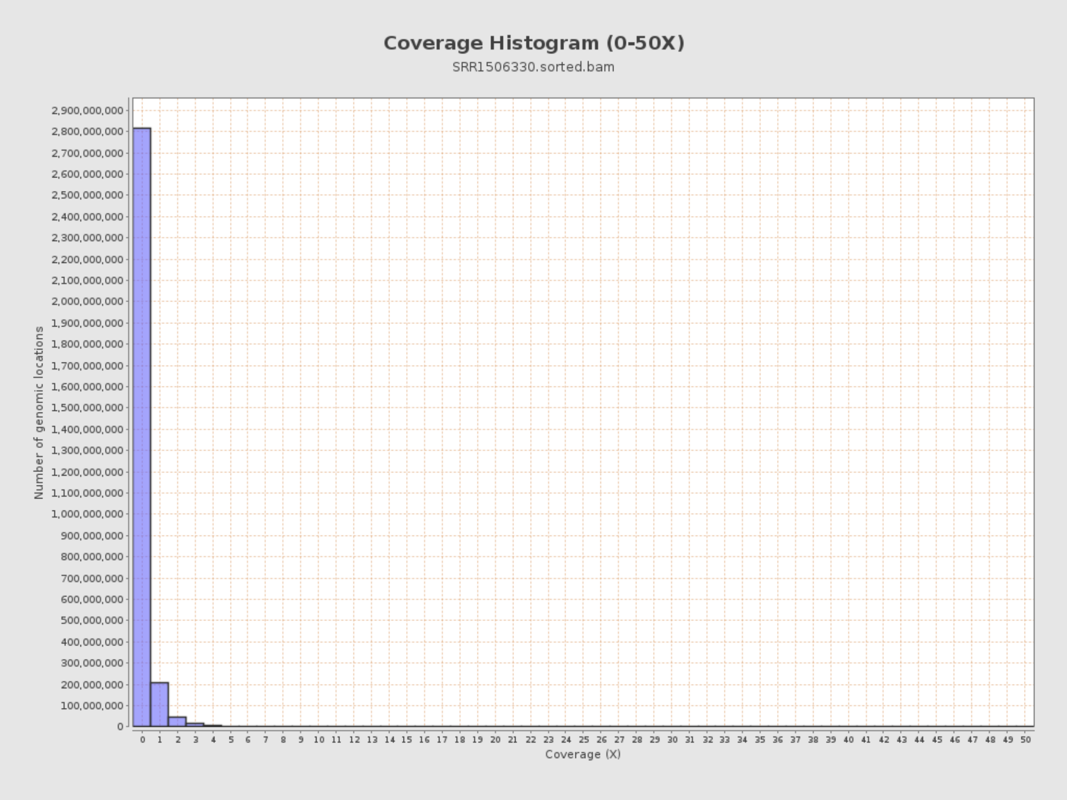
3. Results : Coverage across reference



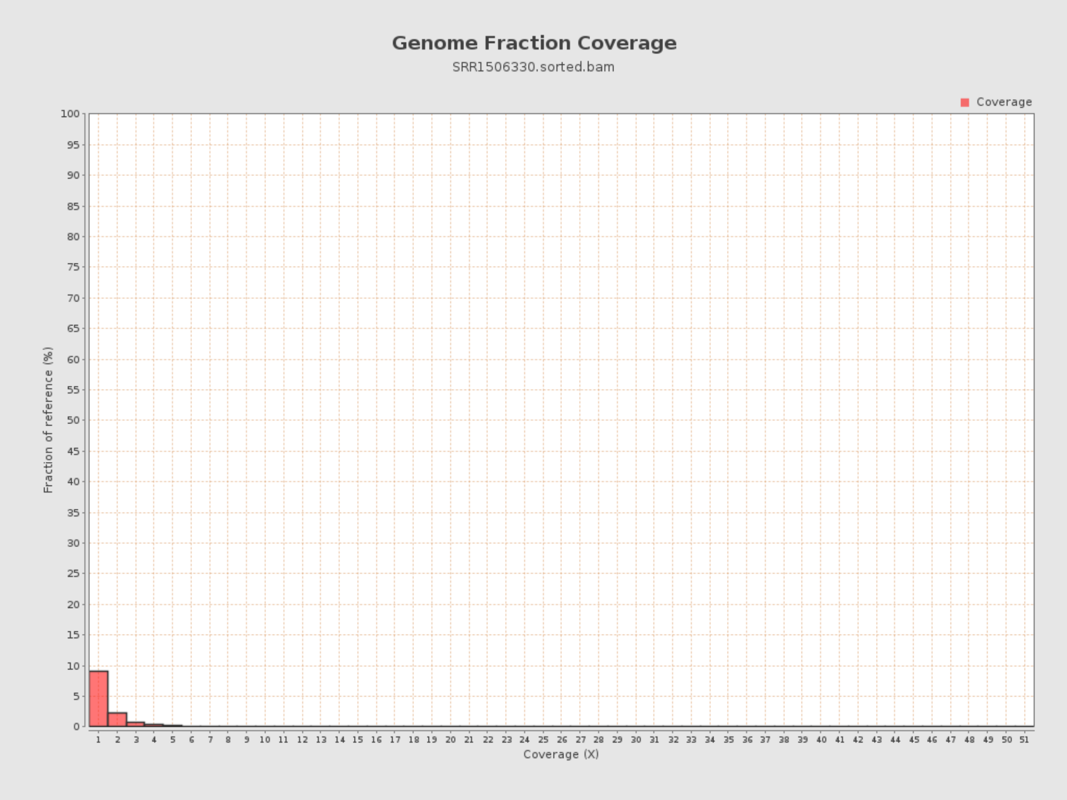
4. Results : Coverage Histogram



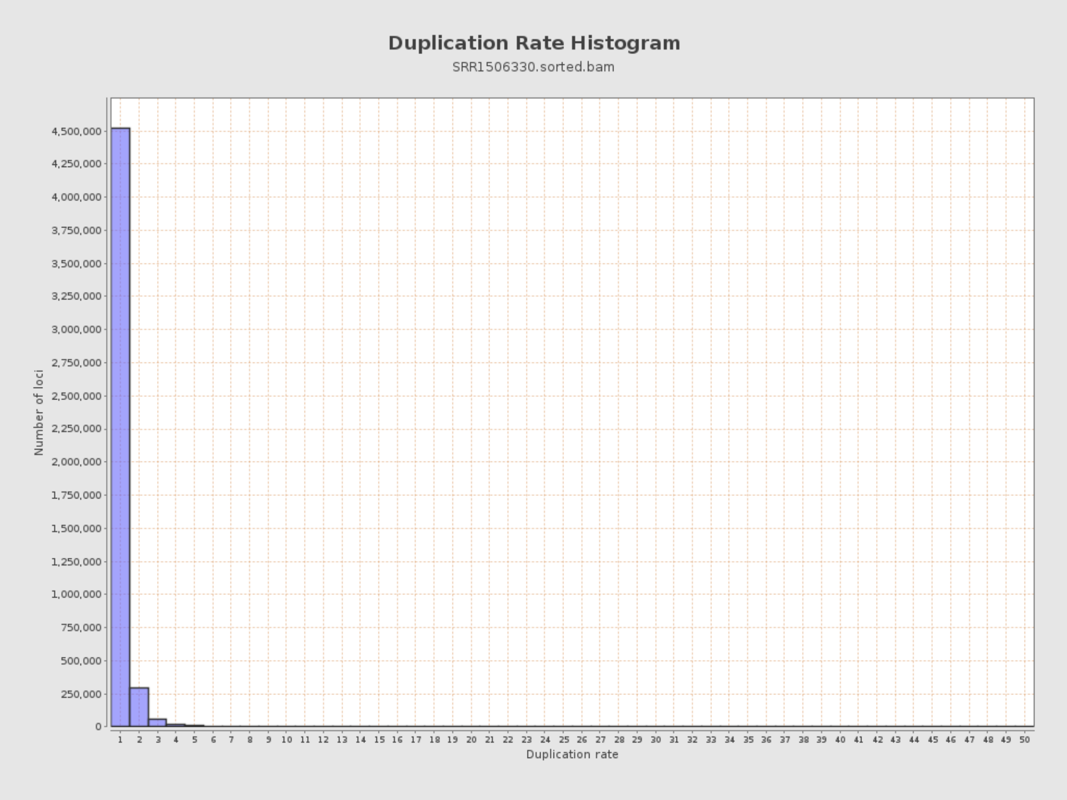
5. Results : Coverage Histogram (0-50X)



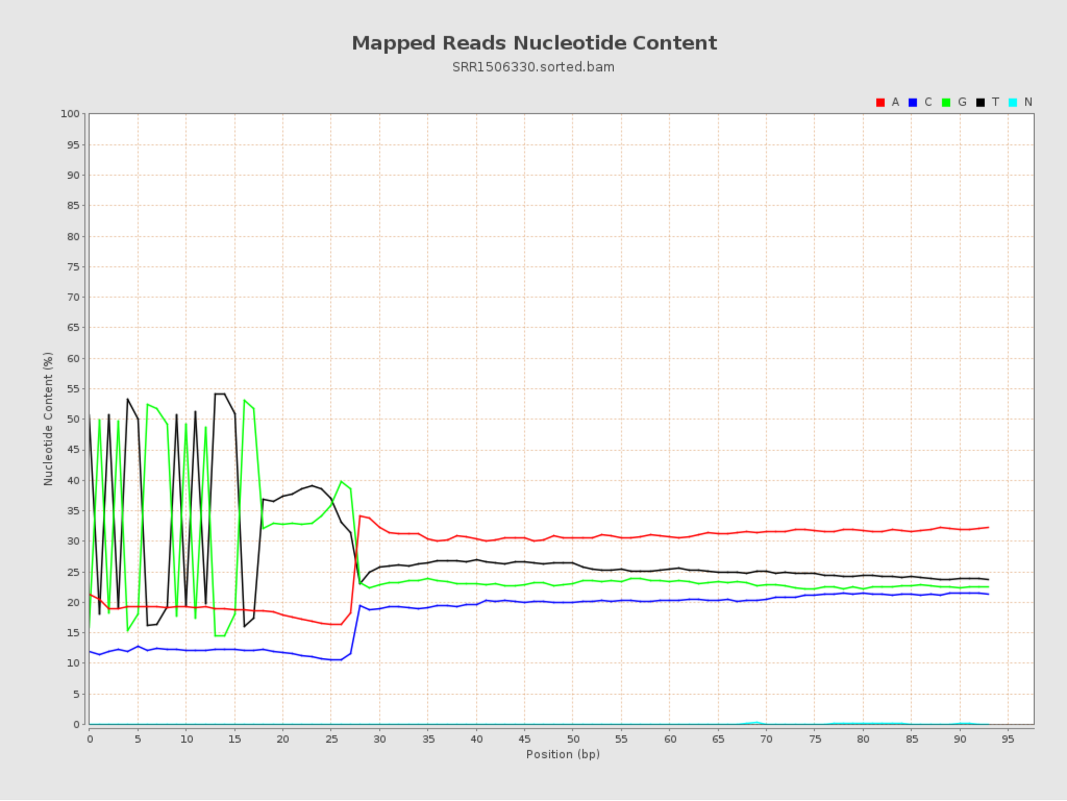
6. Results : Genome Fraction Coverage



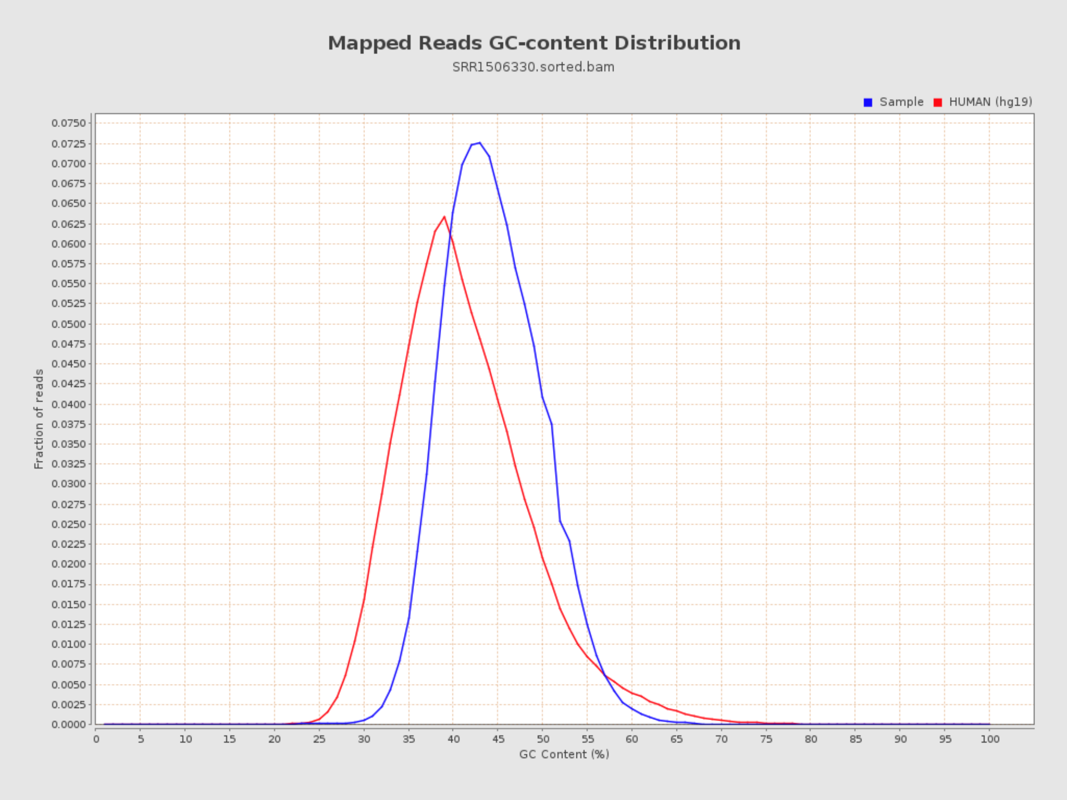
7. Results : Duplication Rate Histogram



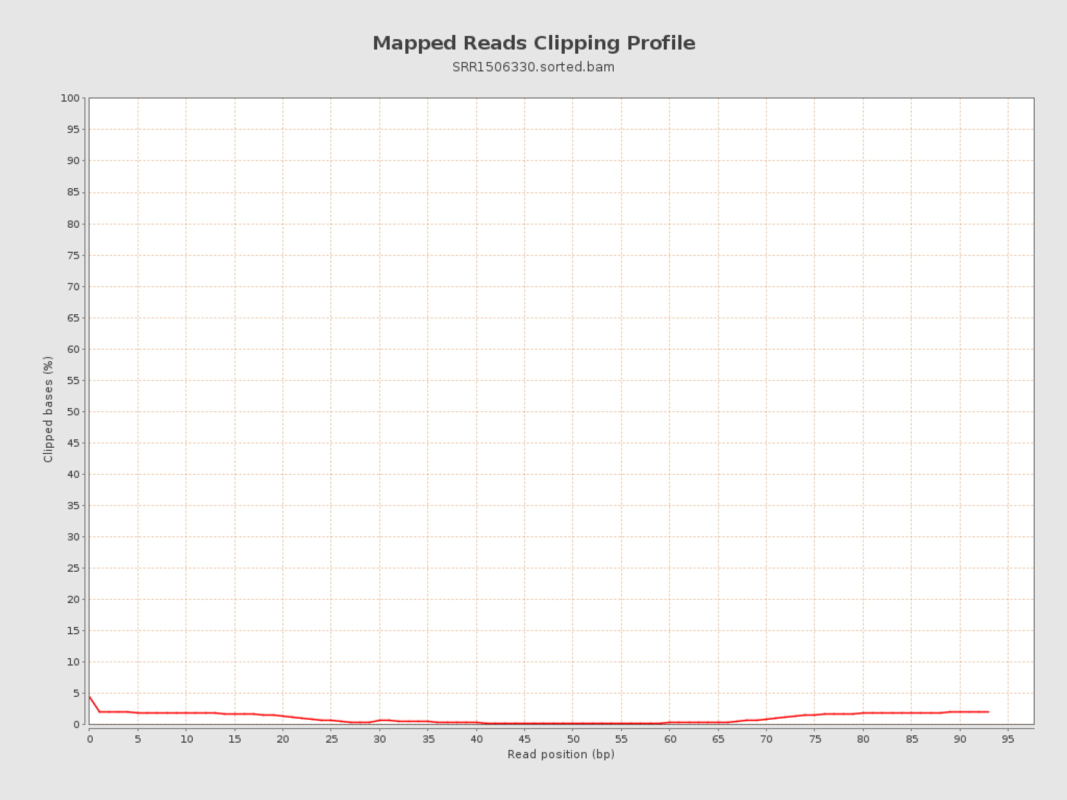
8. Results : Mapped Reads Nucleotide Content



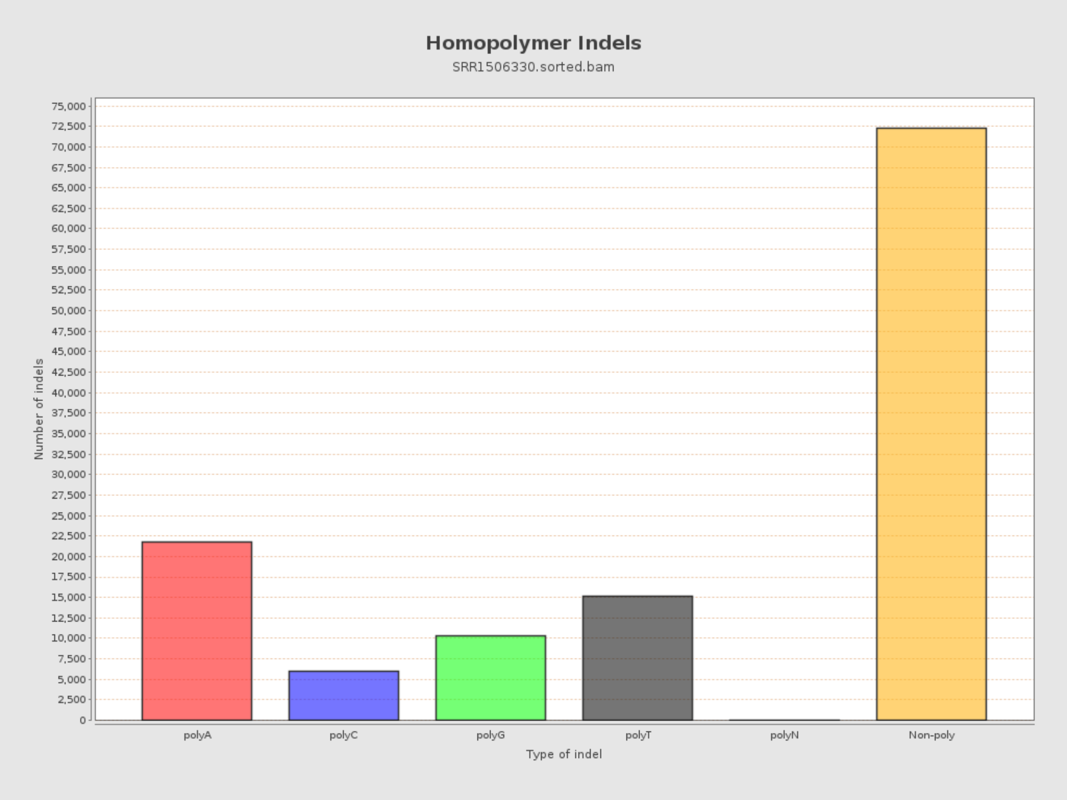
9. Results : Mapped Reads GC-content Distribution



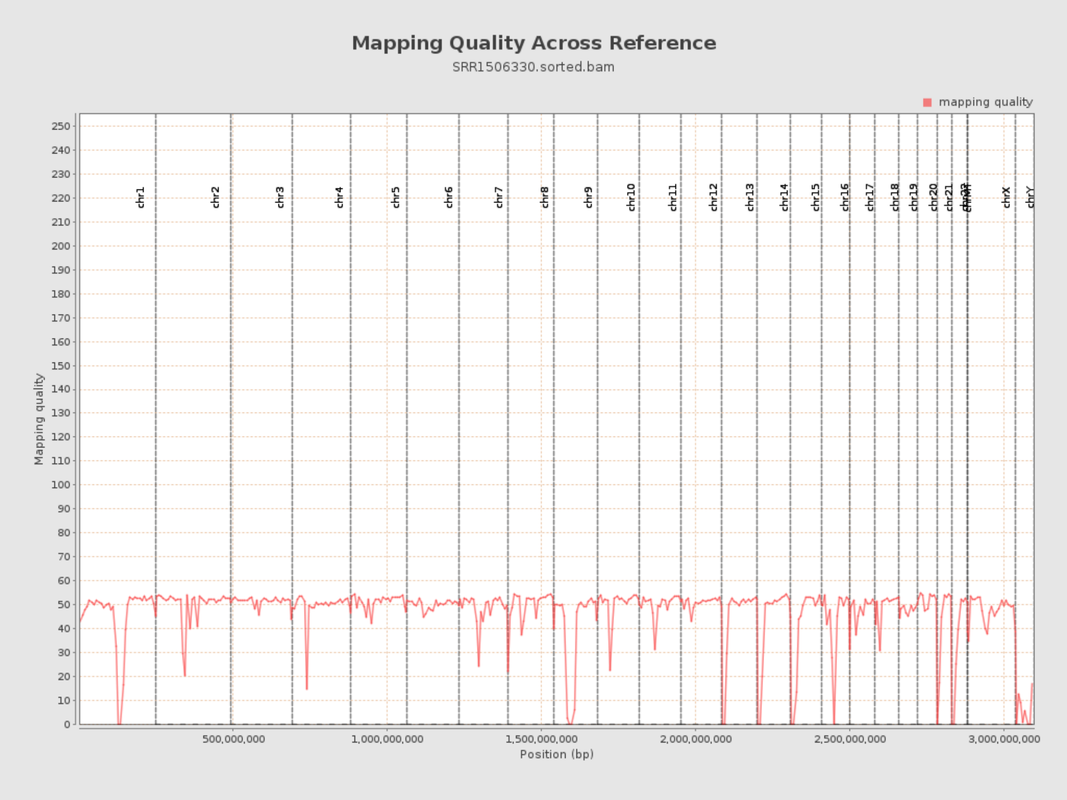
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram