Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 22:28:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163019.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_SRR1163019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 22:28:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	93,316,692
Mapped reads	91,393,240 / 97.94%
Unmapped reads	1,923,452 / 2.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	547,071 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	51,444,545 / 55.13%
Duplication rate	45.35%
Clipped reads	12,789,429 / 13.71%

2.2. ACGT Content

Number/percentage of A's	2,136,456,633 / 23.98%
Number/percentage of C's	2,320,052,552 / 26.04%
Number/percentage of T's	2,129,833,645 / 23.9%
Number/percentage of G's	2,322,079,583 / 26.06%
Number/percentage of N's	2,031,205 / 0.02%
GC Percentage	52.1%

2.3. Coverage

Mean	2.8787

Standard Deviation	34.933

2.4. Mapping Quality

Mean Mapping Quality	49.04

2.5. Mismatches and indels

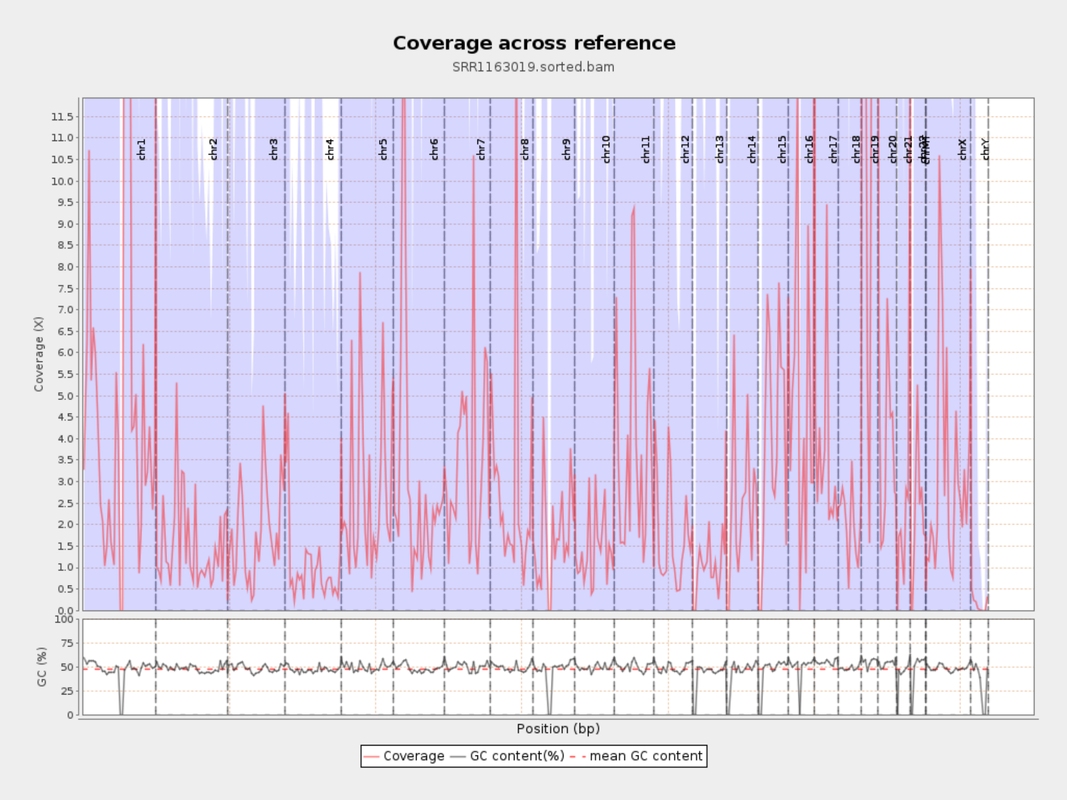
General error rate	0.45%
Mismatches	38,943,193
Insertions	623,666
Mapped reads with at least one insertion	0.67%
Deletions	512,002
Mapped reads with at least one deletion	0.55%
Homopolymer indels	46.38%

2.6. Chromosome stats

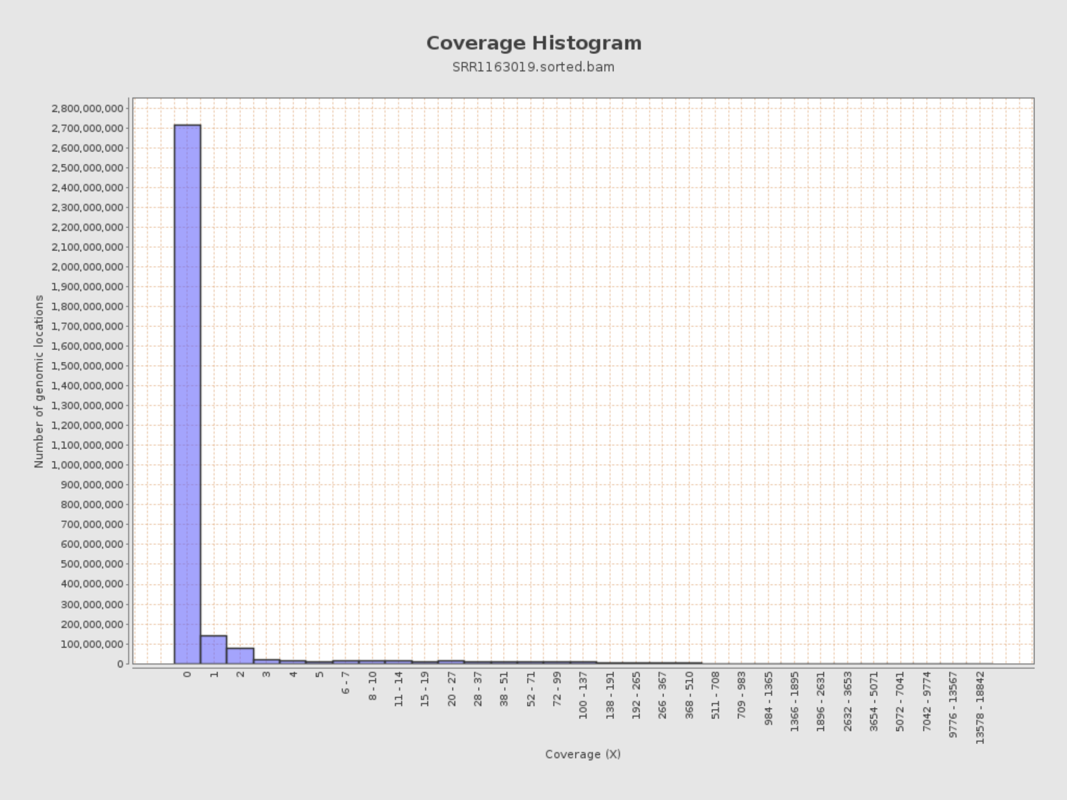
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1312060877	5.264	47.9895
chr2	243199373	368111686	1.5136	16.4088
chr3	198022430	363458813	1.8354	18.8542
chr4	191154276	192610842	1.0076	17.0774
chr5	180915260	506899829	2.8019	49.7514
chr6	171115067	508854353	2.9738	30.2567
chr7	159138663	555089745	3.4881	36.4464

chr8	146364022	421686722	2.8811	45.2228
chr9	141213431	233993749	1.657	18.2034
chr10	135534747	195786890	1.4446	14.4473
chr11	135006516	513093640	3.8005	32.421
chr12	133851895	242066197	1.8085	17.7452
chr13	115169878	123661645	1.0737	13.989
chr14	107349540	262393868	2.4443	23.6234
chr15	102531392	398414874	3.8858	31.9324
chr16	90354753	419595838	4.6439	35.955
chr17	81195210	292580754	3.6034	30.168
chr18	78077248	157020981	2.0111	23.0333
chr19	59128983	865898026	14.6442	108.8178
chr20	63025520	236007468	3.7446	31.8512
chr21	48129895	134205553	2.7884	67.2785
chr22	51304566	111801480	2.1792	19.91
chrMT	16571	7590	0.458	0.9127
chrX	155270560	487217883	3.1379	35.7036
chrY	59373566	9070319	0.1528	9.3986

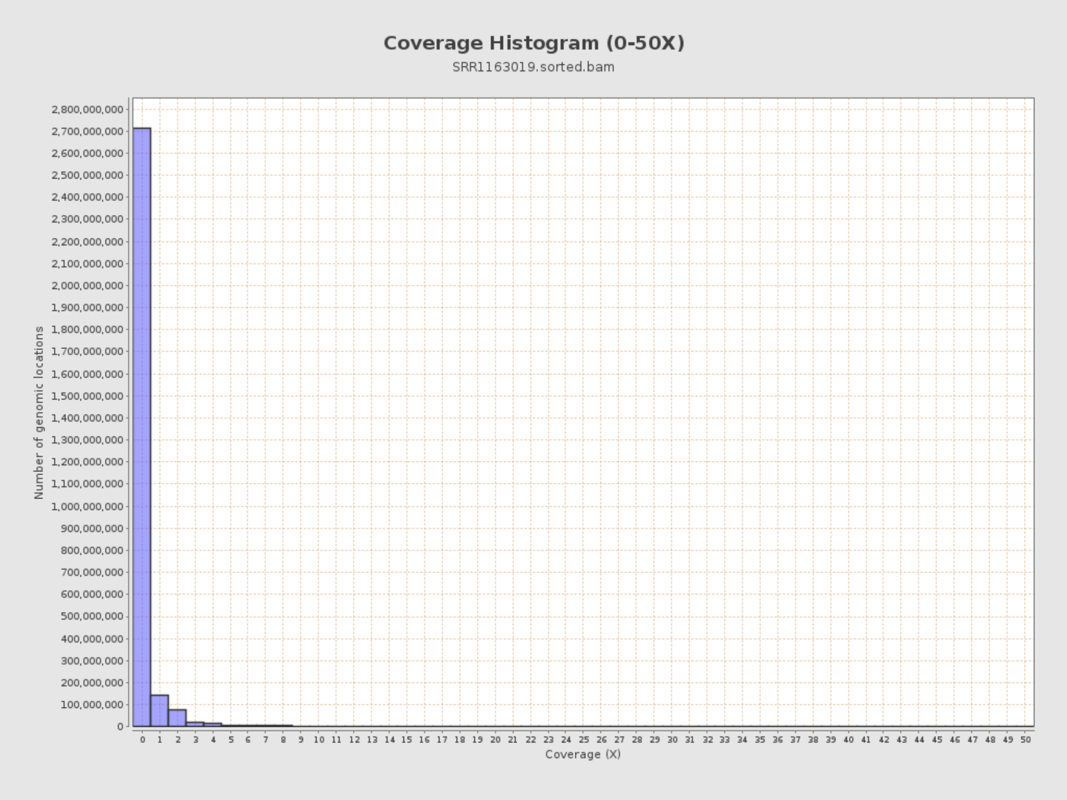
3. Results : Coverage across reference



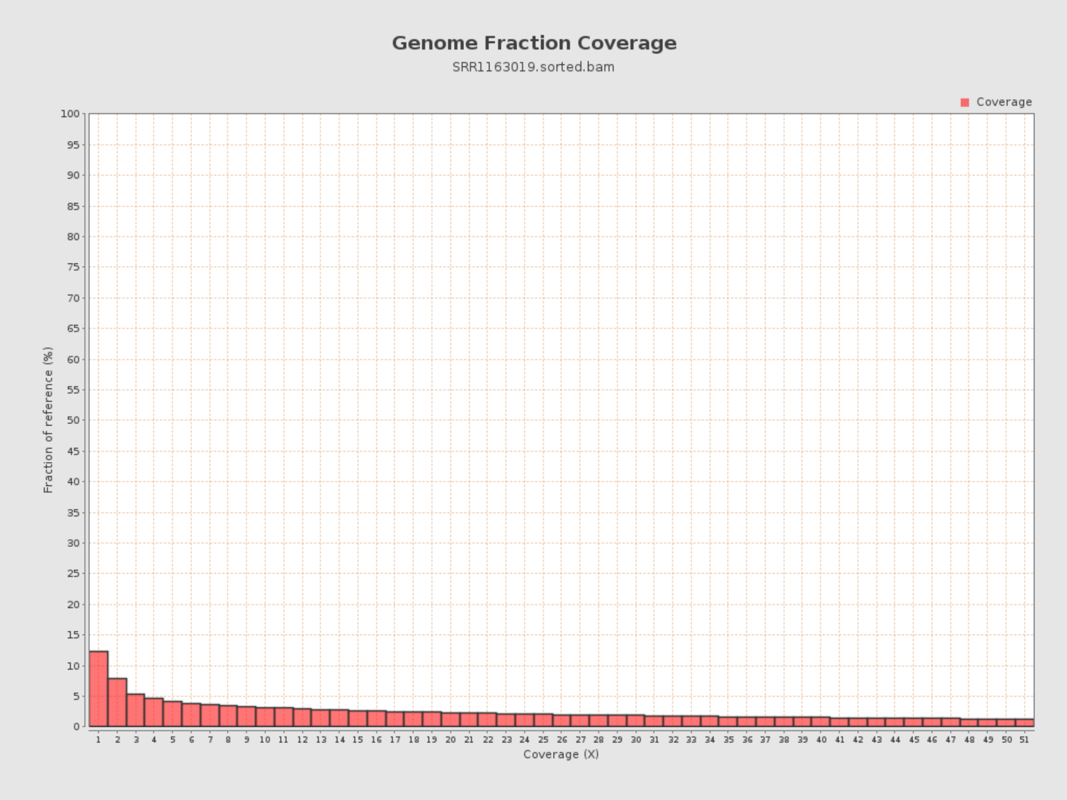
4. Results : Coverage Histogram



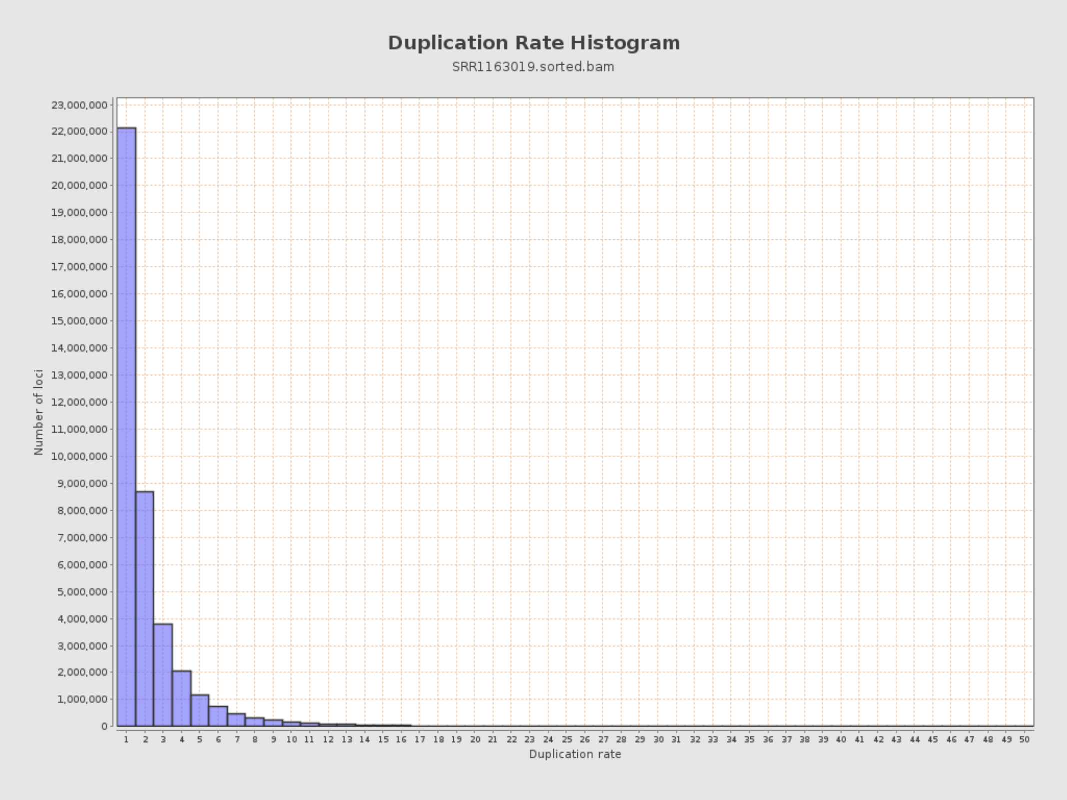
5. Results : Coverage Histogram (0-50X)



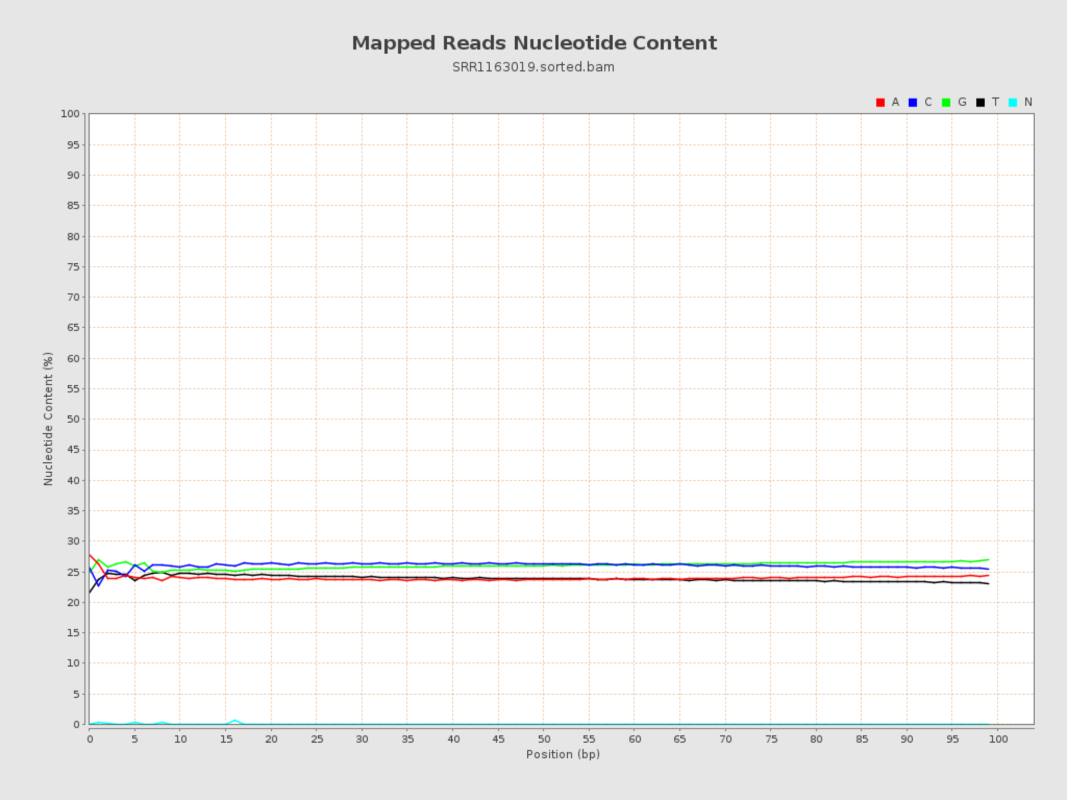
6. Results : Genome Fraction Coverage



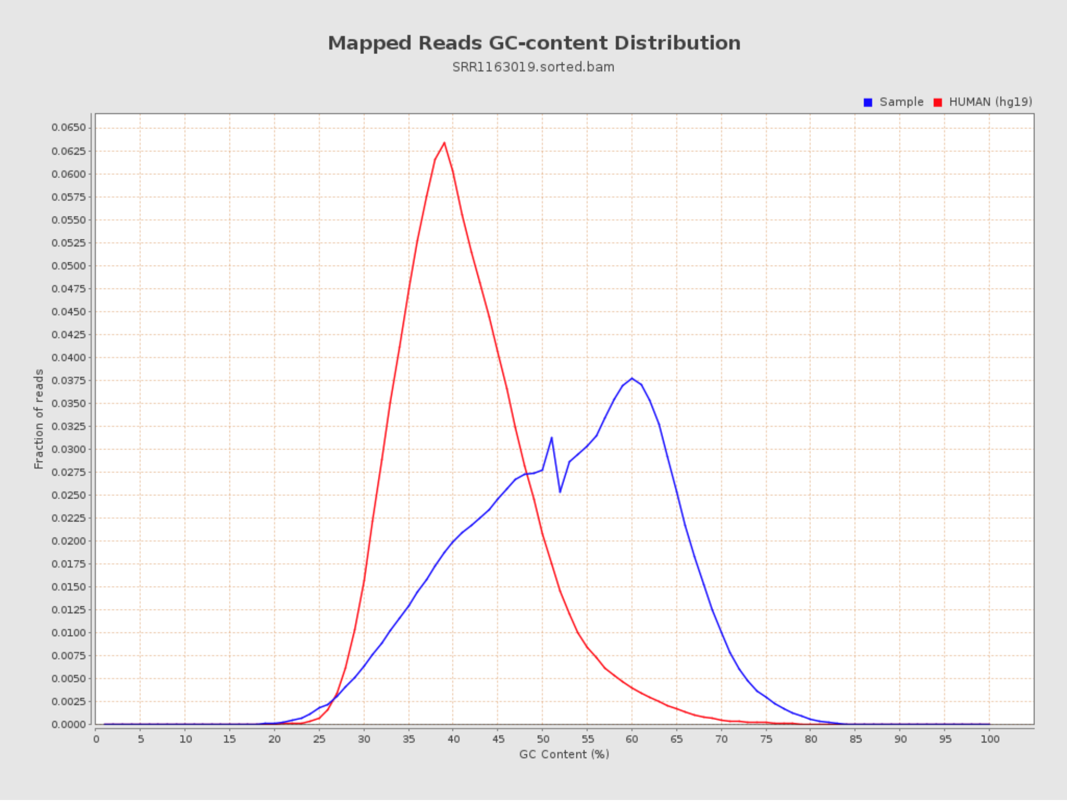
7. Results : Duplication Rate Histogram



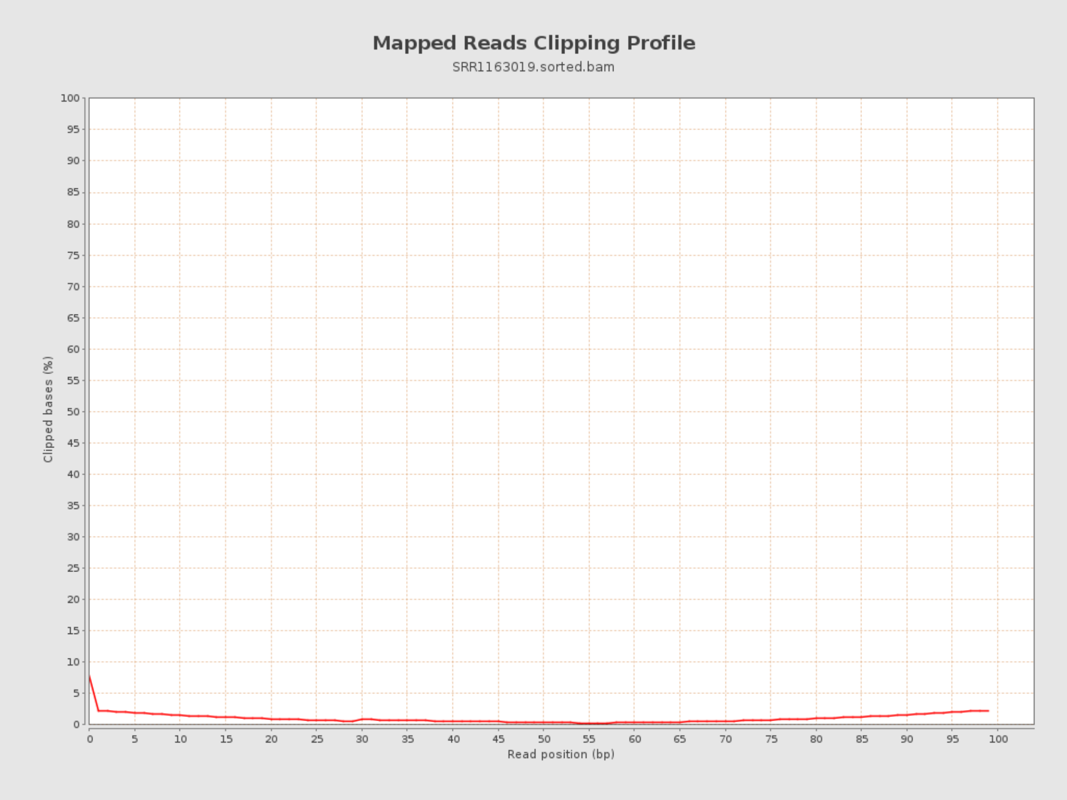
8. Results : Mapped Reads Nucleotide Content



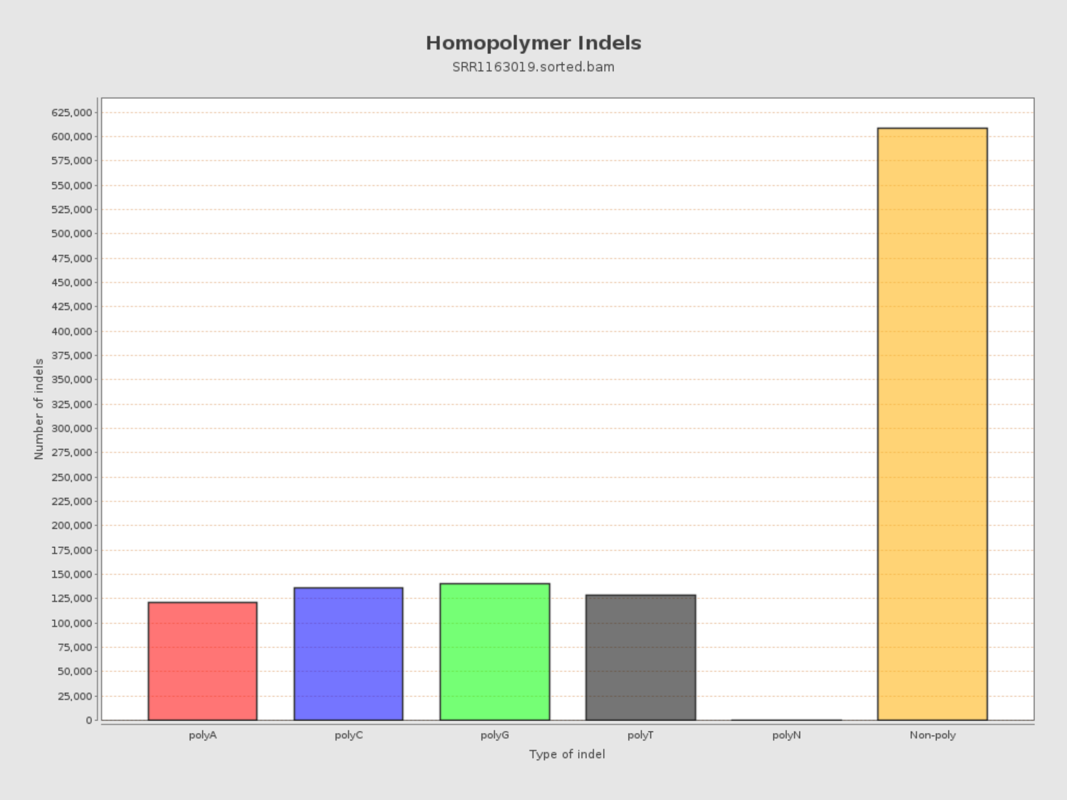
9. Results : Mapped Reads GC-content Distribution



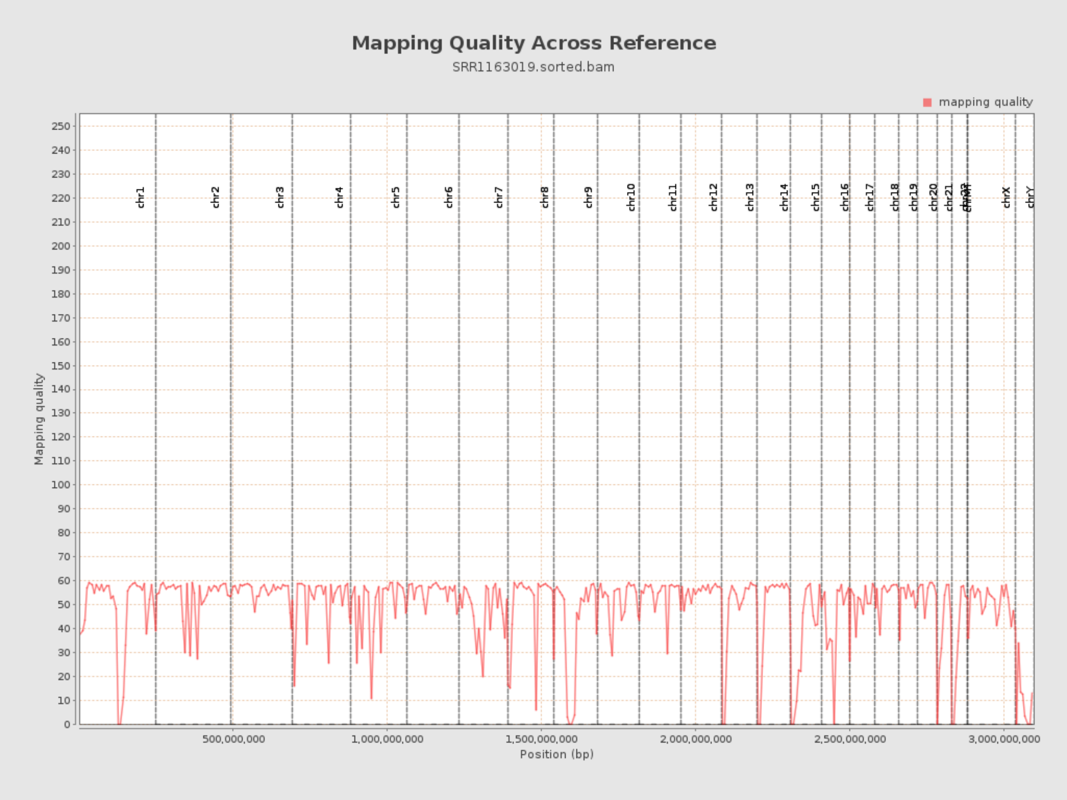
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram