Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 02:58:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163043.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_SRR1163043 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163043.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 02:58:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163043.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	81,266,328
Mapped reads	79,422,387 / 97.73%
Unmapped reads	1,843,941 / 2.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	402,636 / 0.5%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	44,210,020 / 54.4%
Duplication rate	45.56%
Clipped reads	20,446,390 / 25.16%

2.2. ACGT Content

Number/percentage of A's	1,794,097,456 / 23.92%
Number/percentage of C's	1,957,615,797 / 26.1%
Number/percentage of T's	1,767,321,503 / 23.56%
Number/percentage of G's	1,977,541,313 / 26.37%
Number/percentage of N's	3,704,387 / 0.05%
GC Percentage	52.47%

2.3. Coverage

Mean	2.4231

Standard Deviation	29.0813

2.4. Mapping Quality

Mean Mapping Quality	49.01

2.5. Mismatches and indels

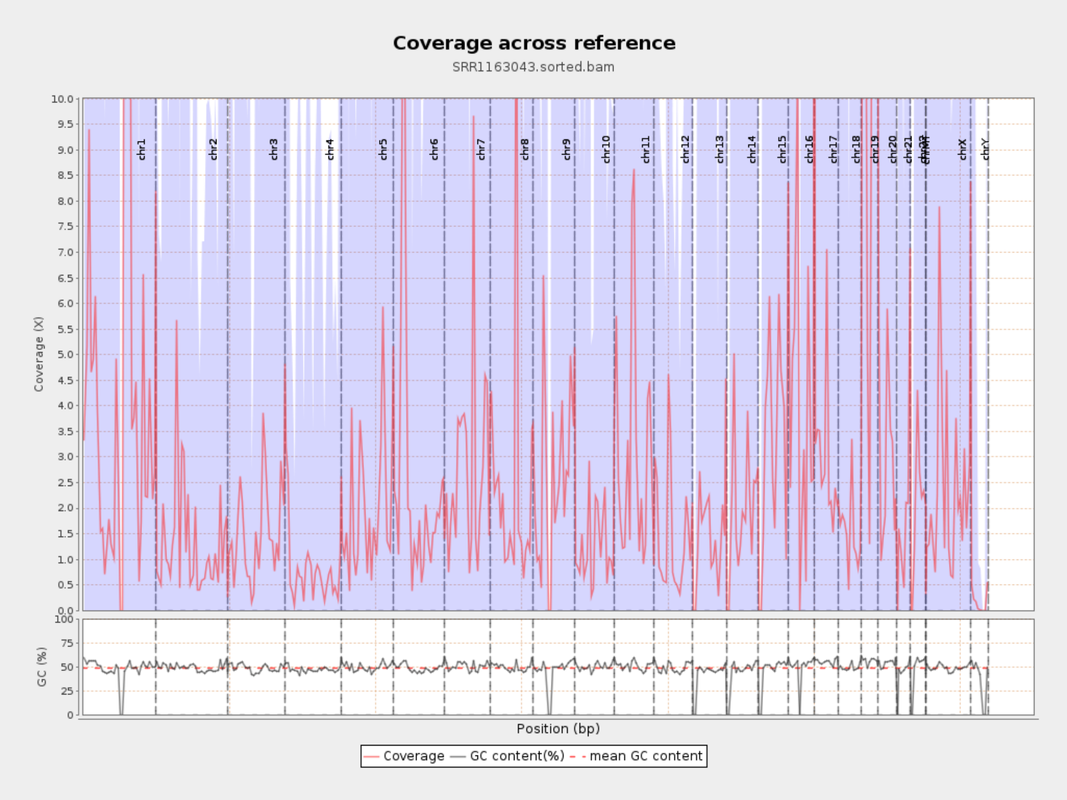
General error rate	0.54%
Mismatches	39,482,670
Insertions	467,995
Mapped reads with at least one insertion	0.58%
Deletions	408,985
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.95%

2.6. Chromosome stats

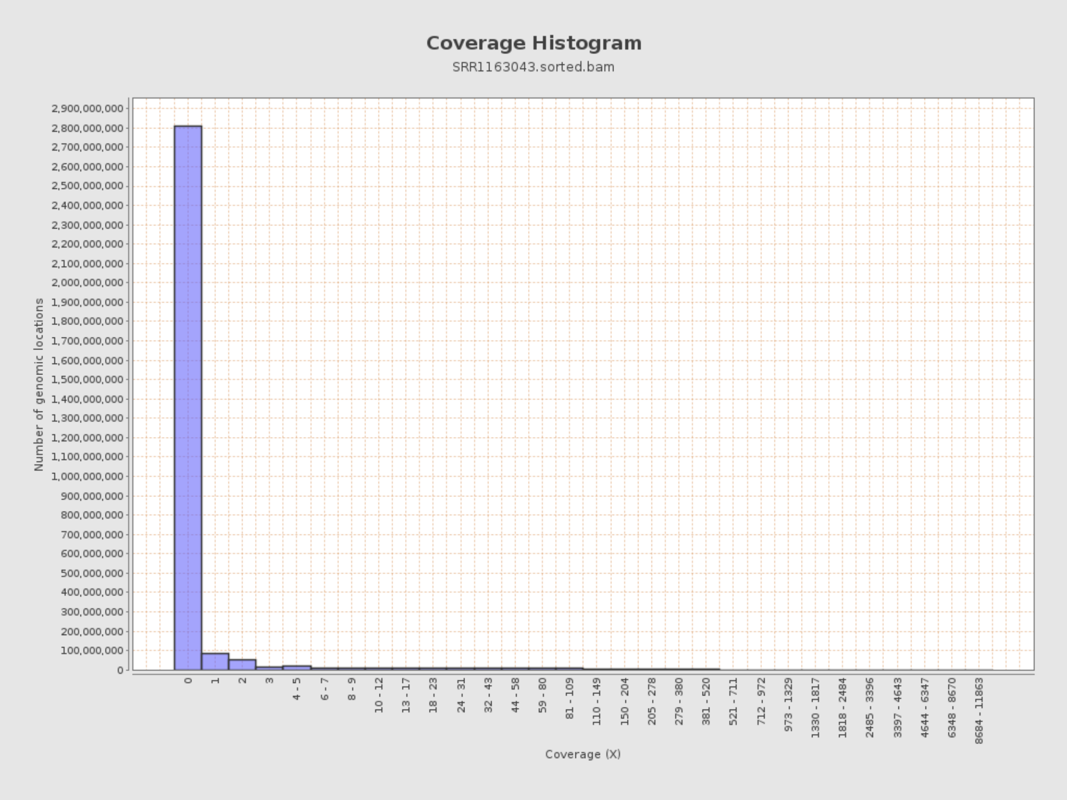
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1128115552	4.526	44.6165
chr2	243199373	319136623	1.3122	15.9092
chr3	198022430	296195161	1.4958	15.9443
chr4	191154276	145281266	0.76	11.2126
chr5	180915260	369411381	2.0419	30.2794
chr6	171115067	431418465	2.5212	26.9222
chr7	159138663	440571913	2.7685	31.2371

chr8	146364022	358943872	2.4524	45.3638
chr9	141213431	355575385	2.518	25.7966
chr10	135534747	168136691	1.2405	13.4213
chr11	135006516	422879799	3.1323	28.7963
chr12	133851895	200420227	1.4973	16.1507
chr13	115169878	162932549	1.4147	17.041
chr14	107349540	210397994	1.9599	19.1801
chr15	102531392	320719951	3.128	26.5026
chr16	90354753	364917072	4.0387	34.3467
chr17	81195210	244393891	3.01	24.3603
chr18	78077248	119363838	1.5288	19.4526
chr19	59128983	686093685	11.6033	82.5384
chr20	63025520	181208893	2.8752	26.0875
chr21	48129895	92312785	1.918	30.2515
chr22	51304566	102622251	2.0003	18.9855
chrMT	16571	5207	0.3142	0.7197
chrX	155270560	369952529	2.3826	28.2321
chrY	59373566	10179952	0.1715	8.9283

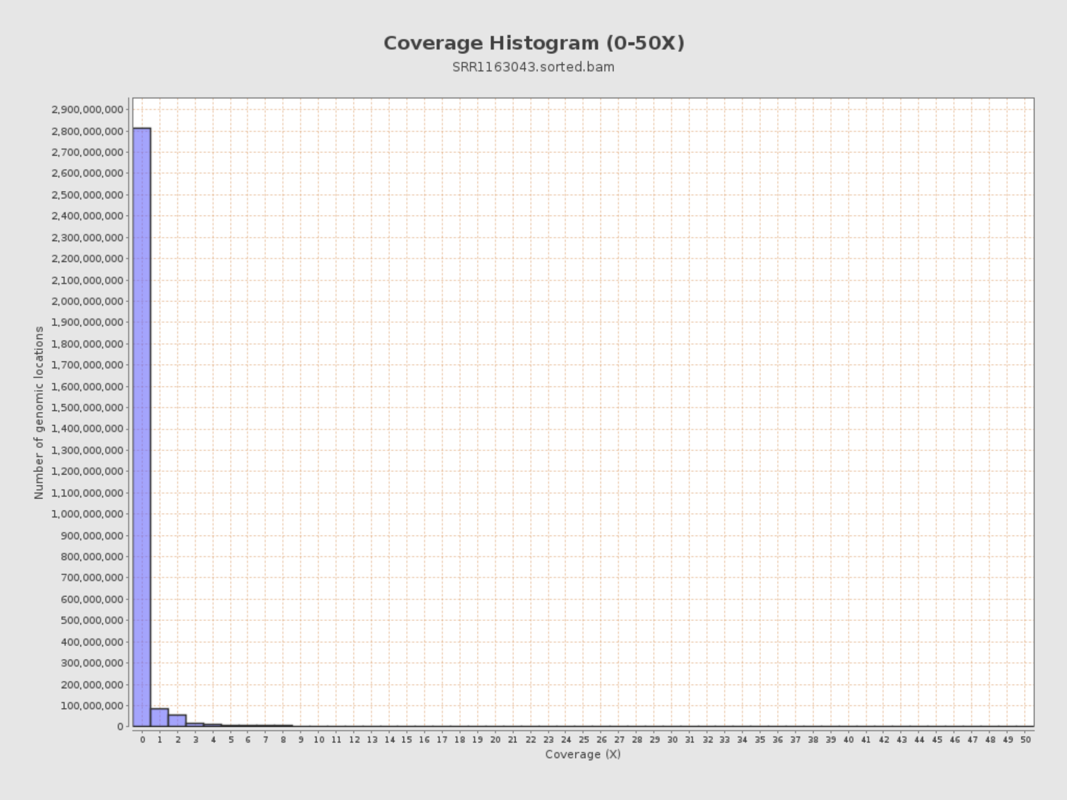
3. Results : Coverage across reference



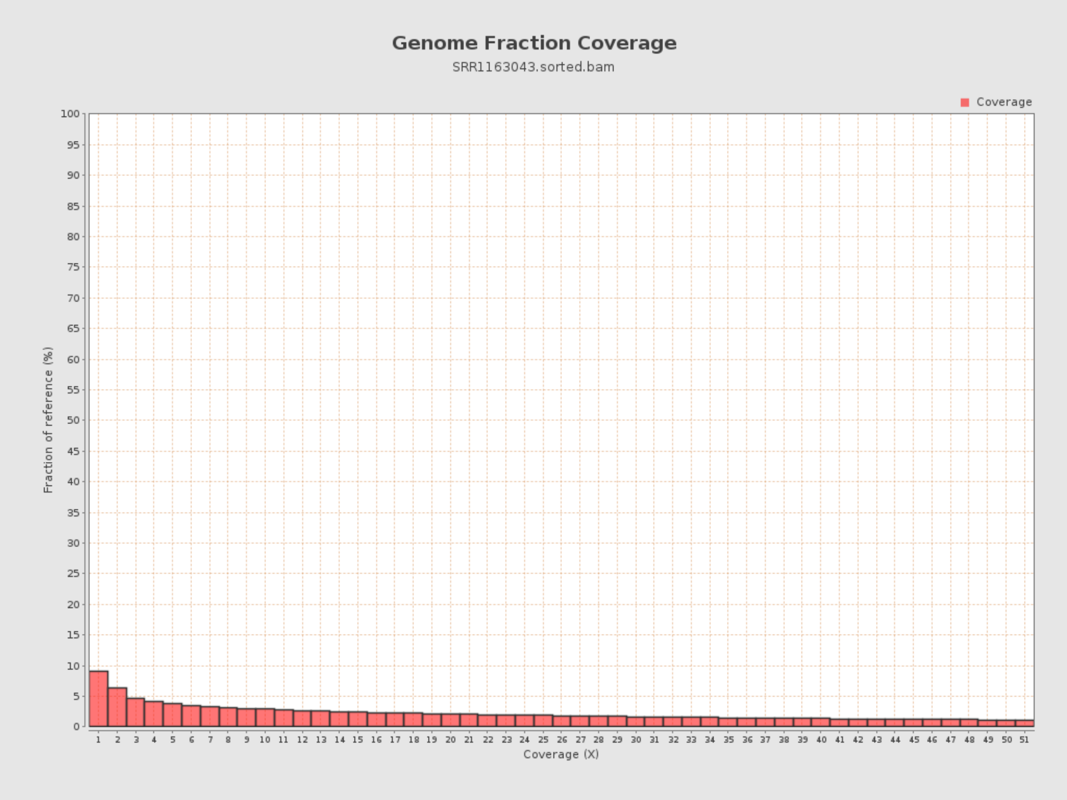
4. Results : Coverage Histogram



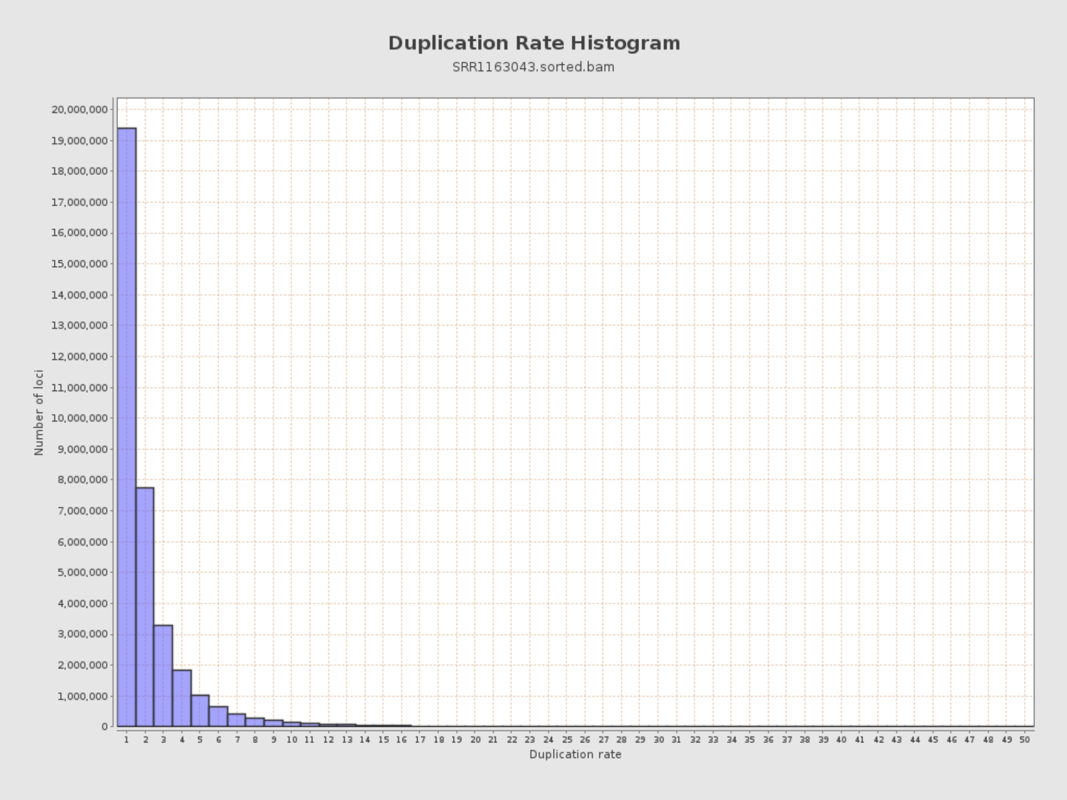
5. Results : Coverage Histogram (0-50X)



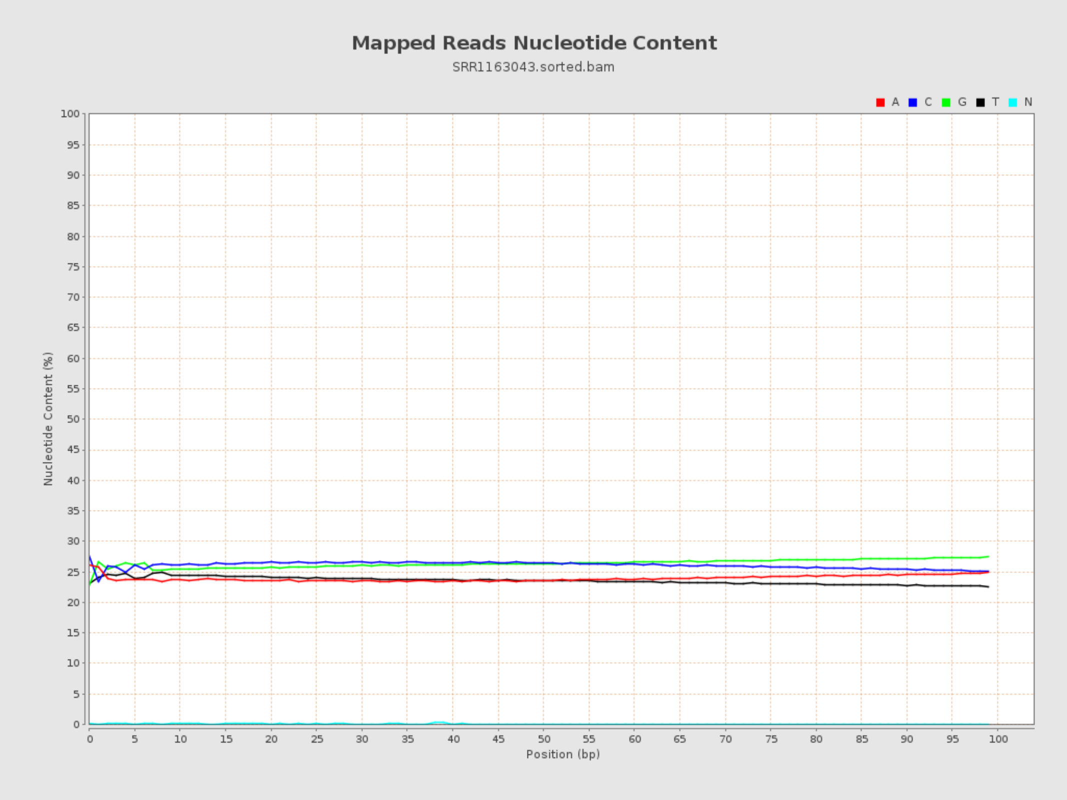
6. Results : Genome Fraction Coverage



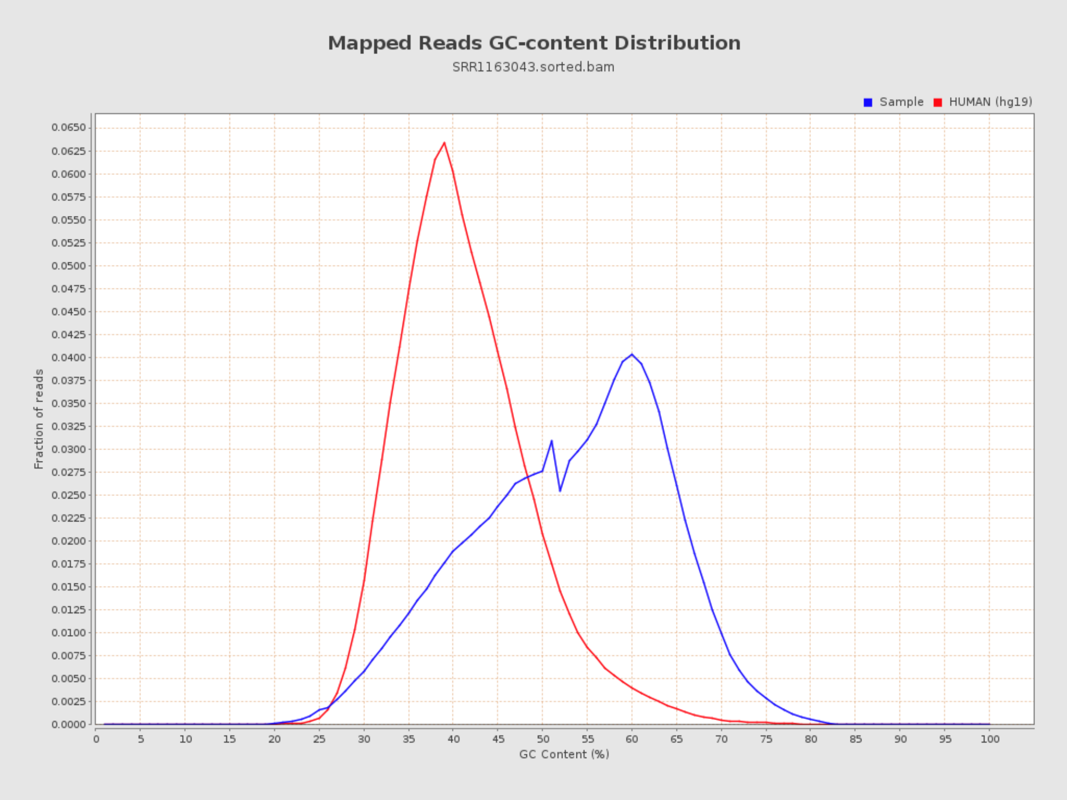
7. Results : Duplication Rate Histogram



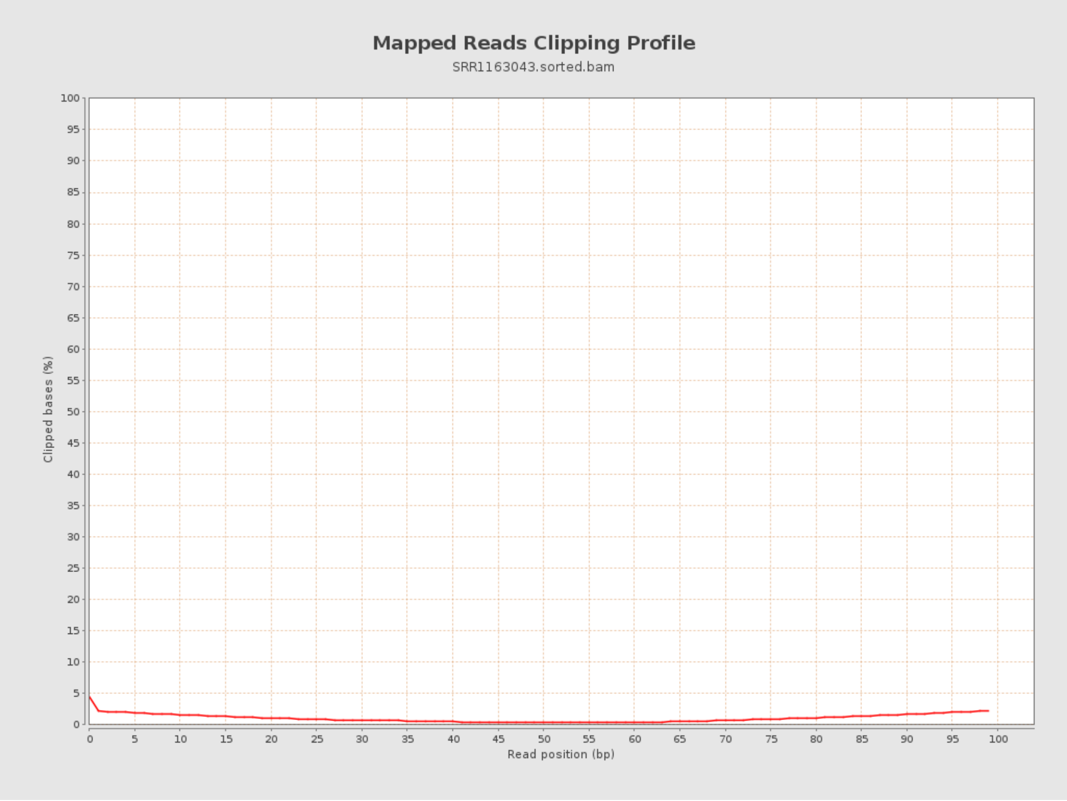
8. Results : Mapped Reads Nucleotide Content



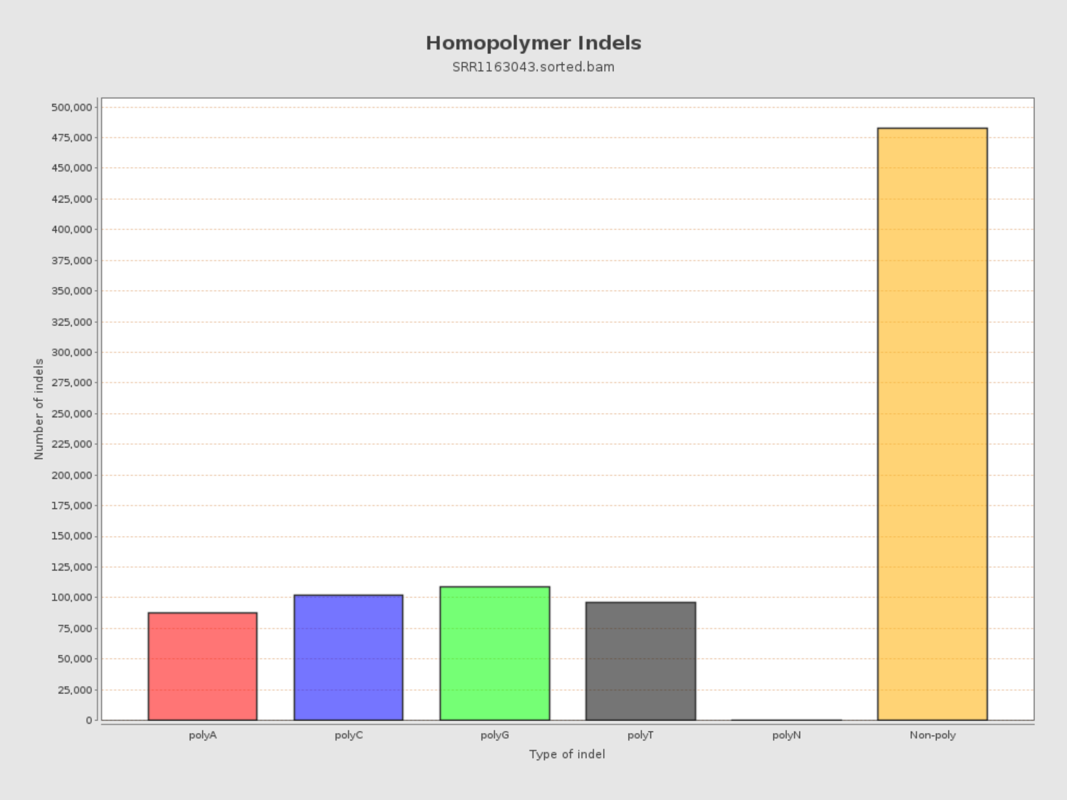
9. Results : Mapped Reads GC-content Distribution



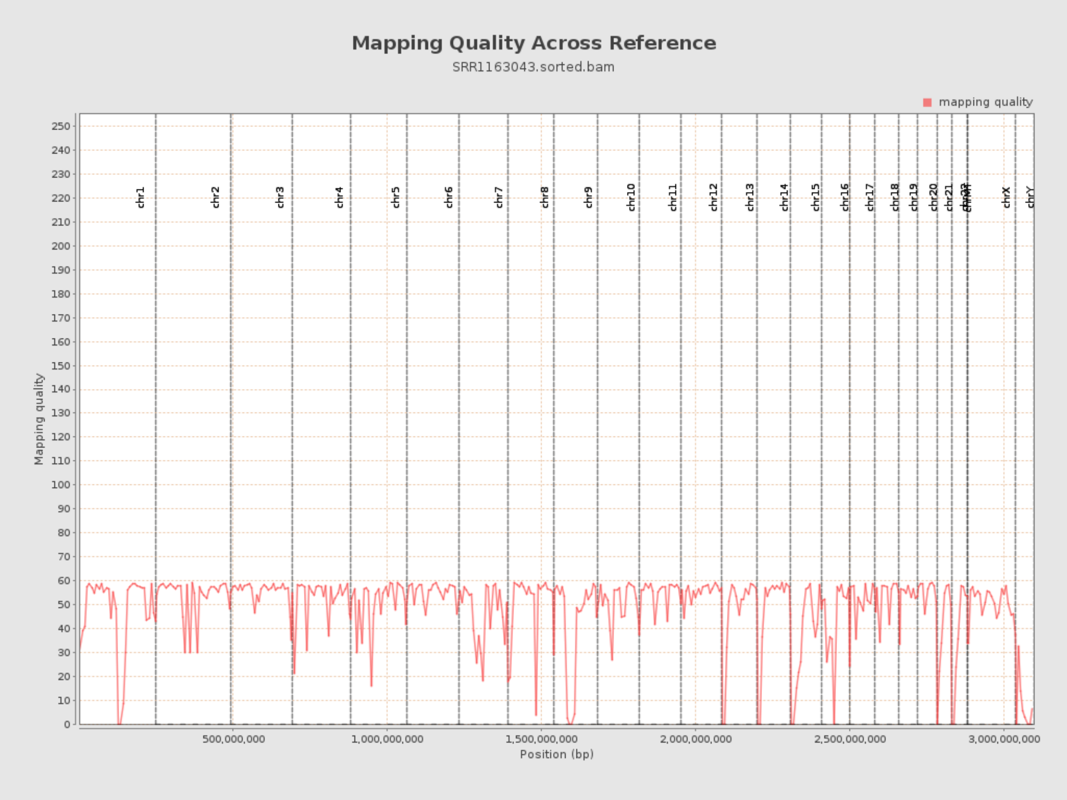
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram