Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 18:54:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163157.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_SRR1163157 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163157.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 18:54:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	84,207,346
Mapped reads	81,901,699 / 97.26%
Unmapped reads	2,305,647 / 2.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	391,154 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	45,466,432 / 53.99%
Duplication rate	43.96%
Clipped reads	11,753,975 / 13.96%

2.2. ACGT Content

Number/percentage of A's	1,945,391,811 / 24.36%
Number/percentage of C's	2,040,713,923 / 25.56%
Number/percentage of T's	1,938,694,088 / 24.28%
Number/percentage of G's	2,046,553,880 / 25.63%
Number/percentage of N's	13,236,896 / 0.17%
GC Percentage	51.19%

2.3. Coverage

Mean	2.5795

Standard Deviation	32.8959

2.4. Mapping Quality

Mean Mapping Quality	49.18

2.5. Mismatches and indels

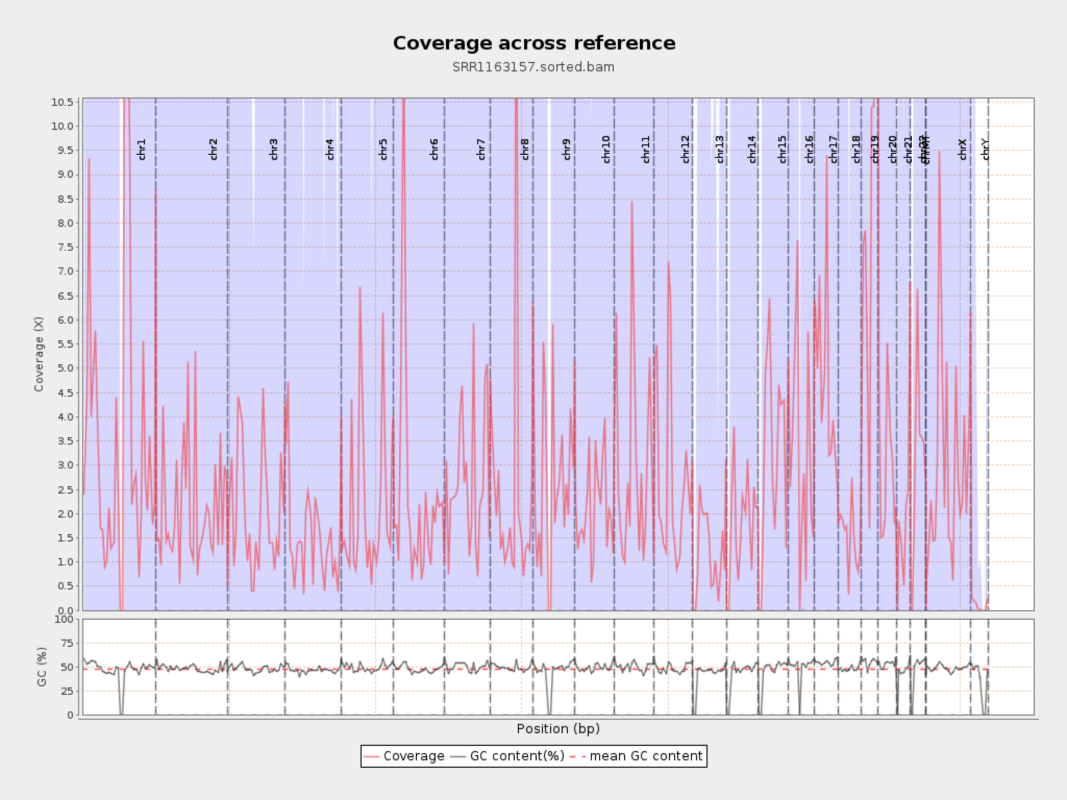
General error rate	0.65%
Mismatches	51,069,747
Insertions	529,278
Mapped reads with at least one insertion	0.64%
Deletions	372,637
Mapped reads with at least one deletion	0.45%
Homopolymer indels	43.59%

2.6. Chromosome stats

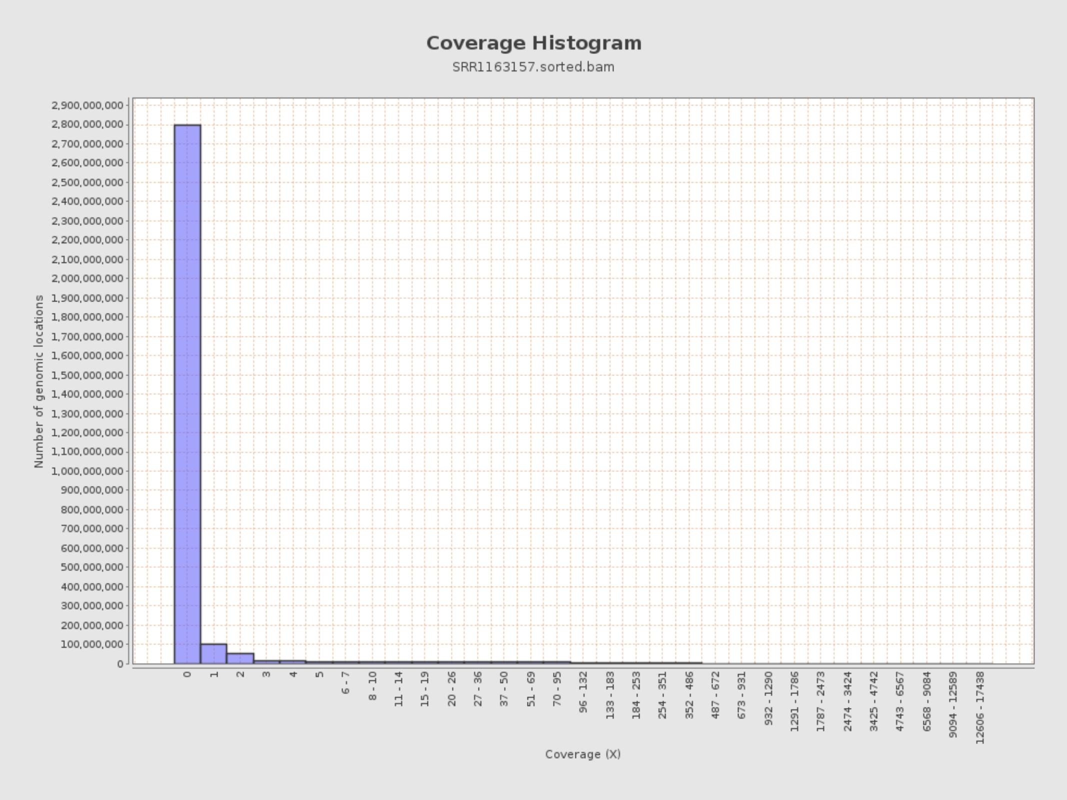
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	902173024	3.6195	40.7312
chr2	243199373	516949587	2.1256	23.7256
chr3	198022430	410237820	2.0717	23.4754
chr4	191154276	289668699	1.5154	22.3876
chr5	180915260	400102740	2.2115	37.0515
chr6	171115067	403801032	2.3598	27.9305
chr7	159138663	428058087	2.6898	35.7598

chr8	146364022	363788344	2.4855	50.0128
chr9	141213431	358400158	2.538	30.8291
chr10	135534747	288143718	2.126	22.3674
chr11	135006516	413238728	3.0609	33.8547
chr12	133851895	380535238	2.843	30.7766
chr13	115169878	134778420	1.1703	15.5159
chr14	107349540	191102337	1.7802	21.1253
chr15	102531392	323191503	3.1521	32.0349
chr16	90354753	286896028	3.1752	29.955
chr17	81195210	395388895	4.8696	43.0719
chr18	78077248	118697665	1.5203	17.6509
chr19	59128983	478129828	8.0862	58.7409
chr20	63025520	181268393	2.8761	30.0173
chr21	48129895	98984554	2.0566	39.9905
chr22	51304566	155459422	3.0301	28.7139
chrMT	16571	562	0.0339	0.2063
chrX	155270560	459961130	2.9623	46.4935
chrY	59373566	6508221	0.1096	7.3846

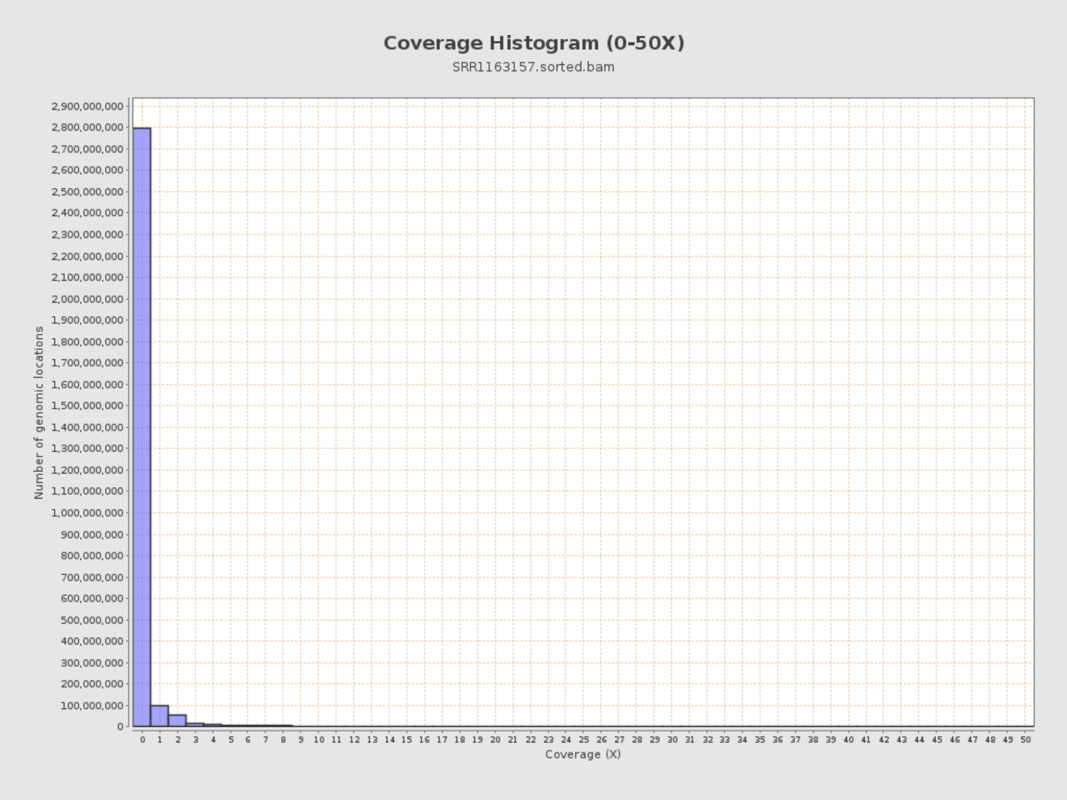
3. Results : Coverage across reference



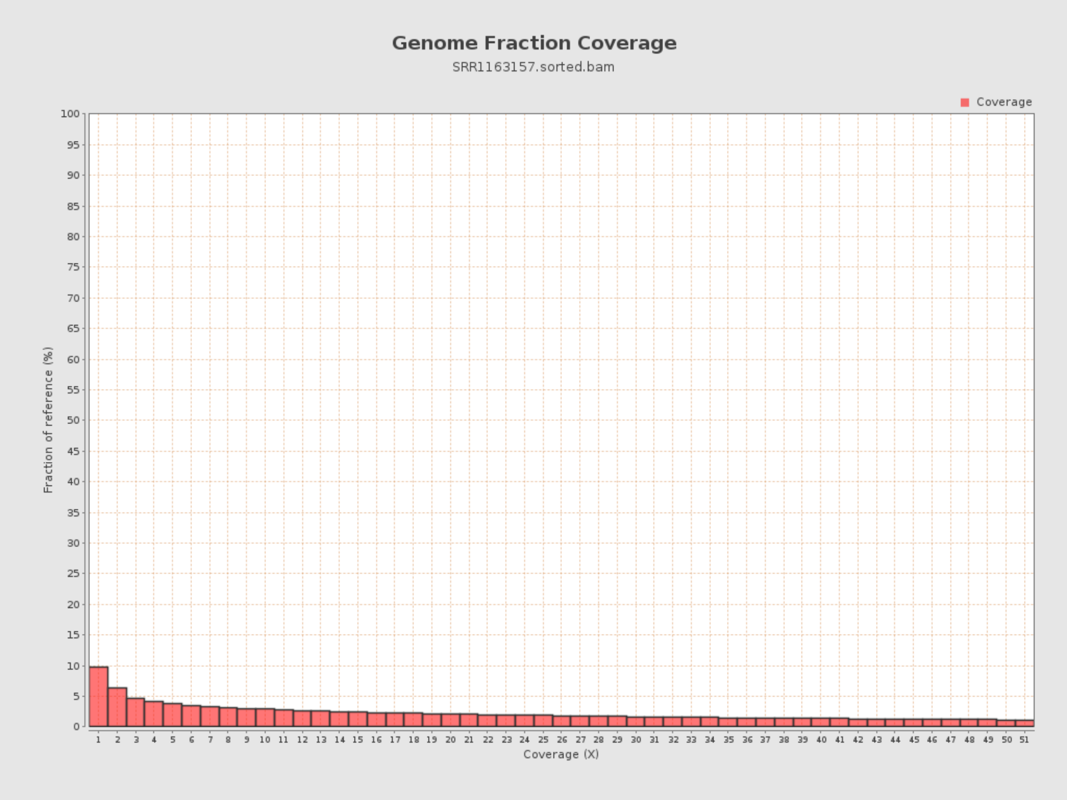
4. Results : Coverage Histogram



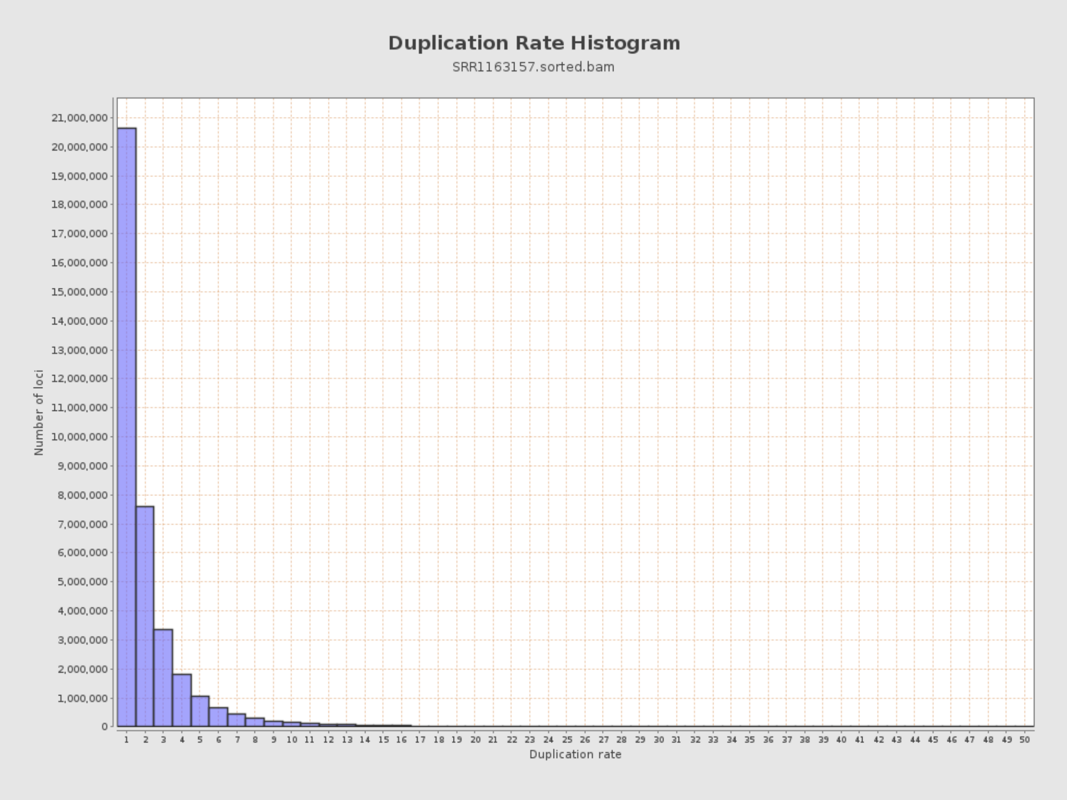
5. Results : Coverage Histogram (0-50X)



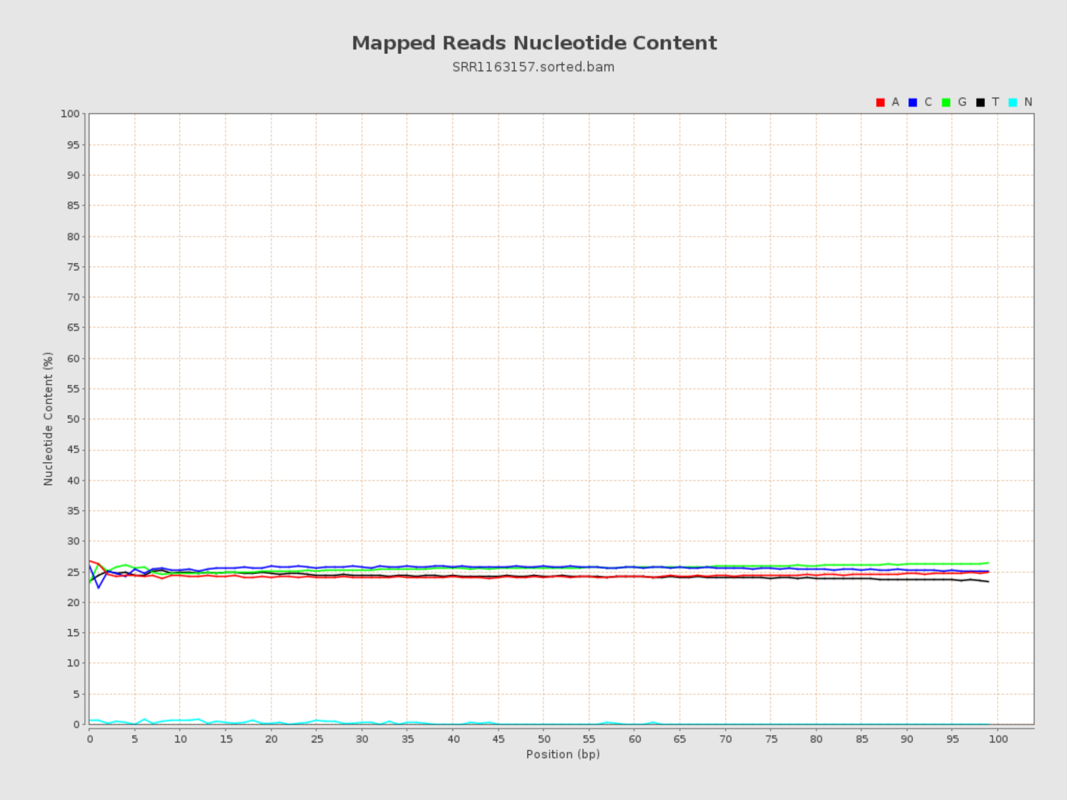
6. Results : Genome Fraction Coverage



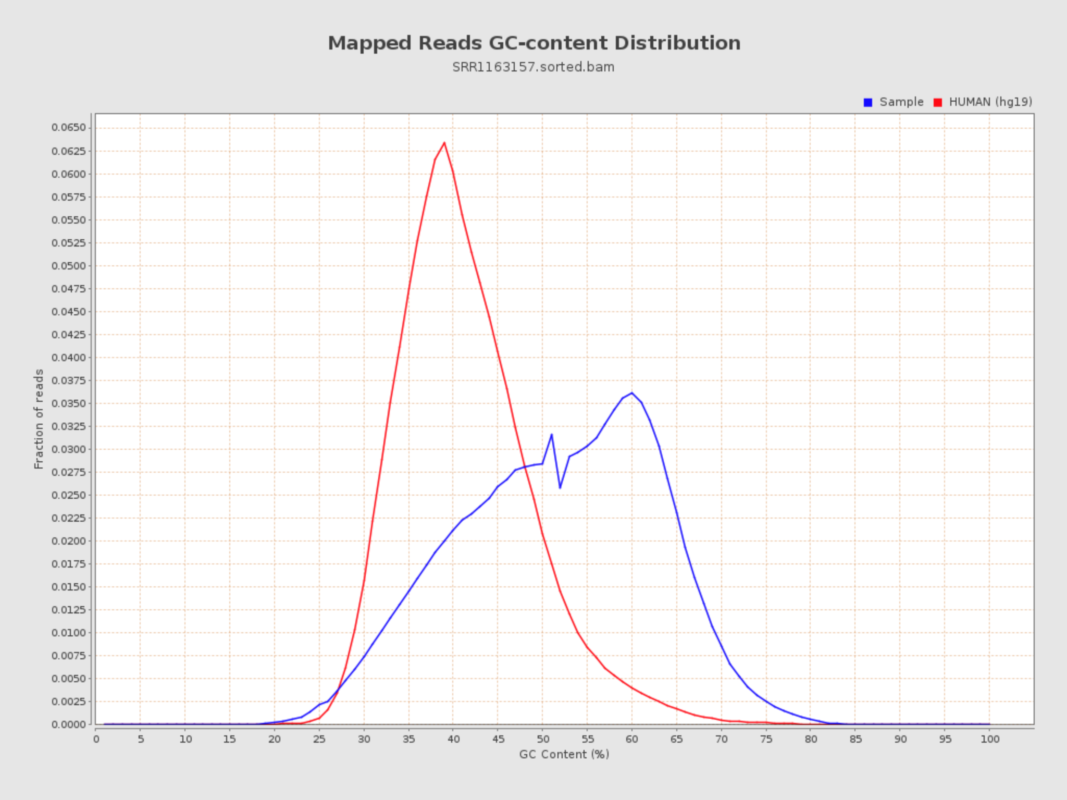
7. Results : Duplication Rate Histogram



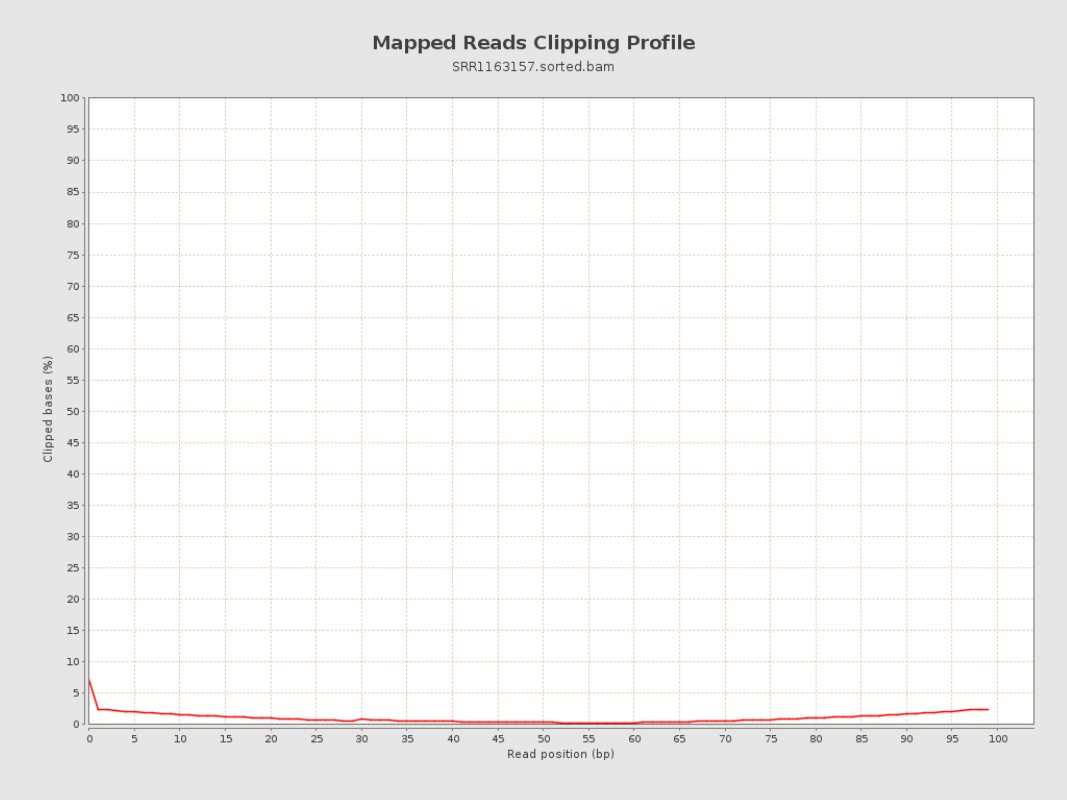
8. Results : Mapped Reads Nucleotide Content



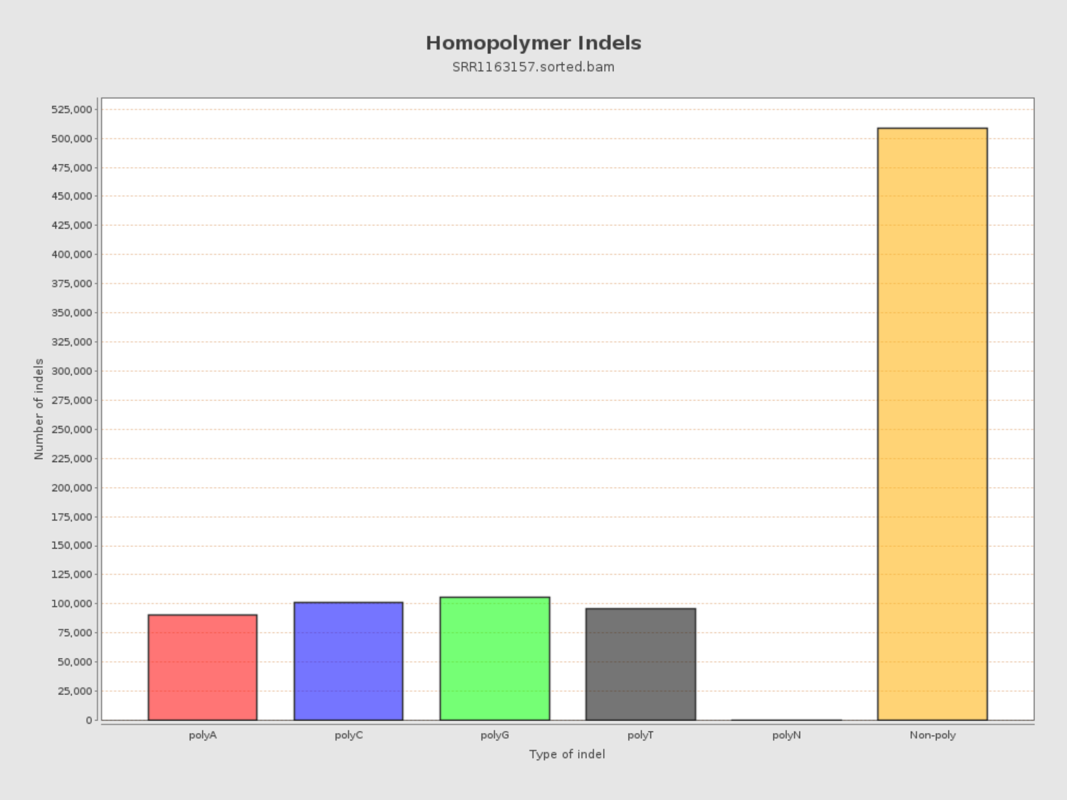
9. Results : Mapped Reads GC-content Distribution



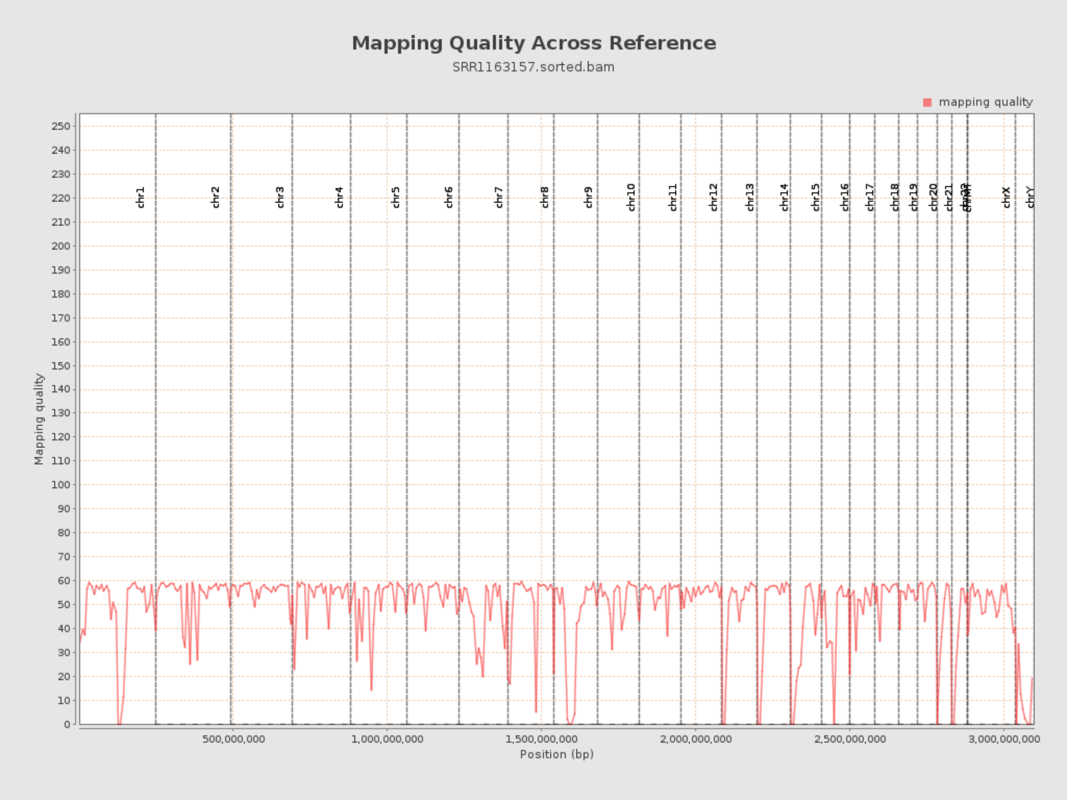
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram