Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 08:46:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163091.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_SRR1163091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 08:46:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	83,375,384
Mapped reads	82,241,733 / 98.64%
Unmapped reads	1,133,651 / 1.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	349,099 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	49,657,643 / 59.56%
Duplication rate	48.45%
Clipped reads	21,692,324 / 26.02%

2.2. ACGT Content

Number/percentage of A's	1,858,753,045 / 24.08%
Number/percentage of C's	2,001,058,071 / 25.92%
Number/percentage of T's	1,839,027,384 / 23.82%
Number/percentage of G's	2,020,096,832 / 26.17%
Number/percentage of N's	300,737 / 0%
GC Percentage	52.09%

2.3. Coverage

Mean	2.4938

Standard Deviation	33.855

2.4. Mapping Quality

Mean Mapping Quality	48.84

2.5. Mismatches and indels

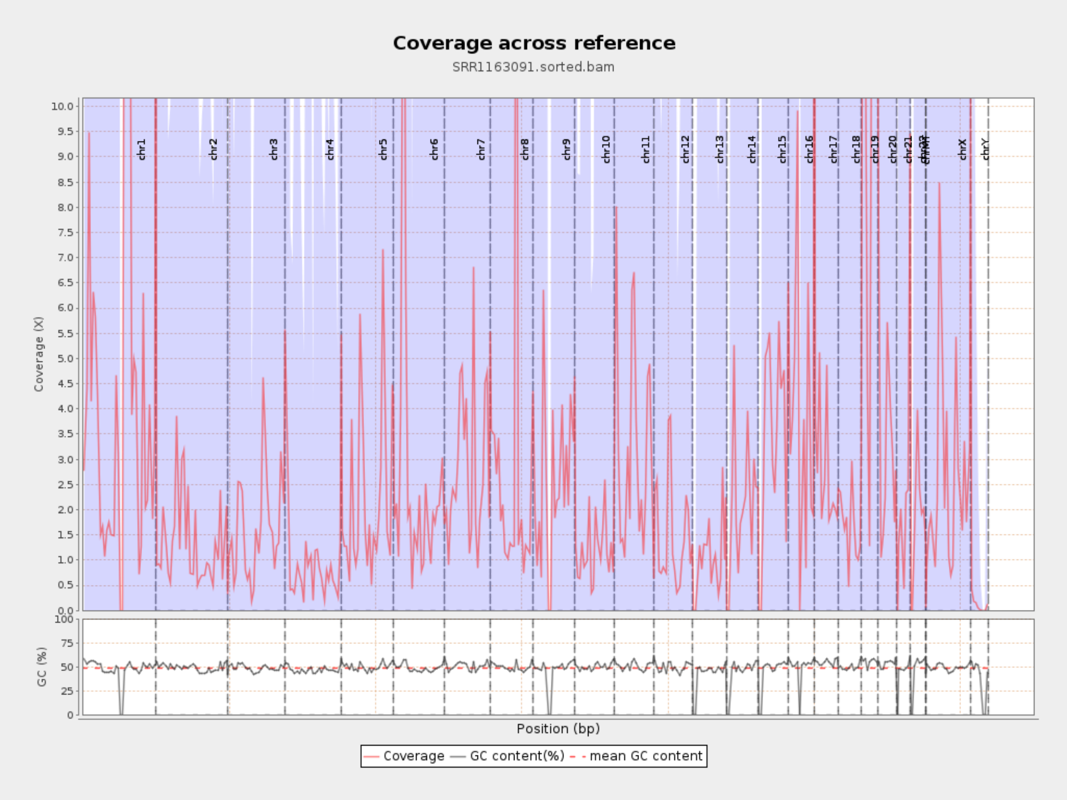
General error rate	0.37%
Mismatches	27,958,069
Insertions	473,455
Mapped reads with at least one insertion	0.57%
Deletions	395,220
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.31%

2.6. Chromosome stats

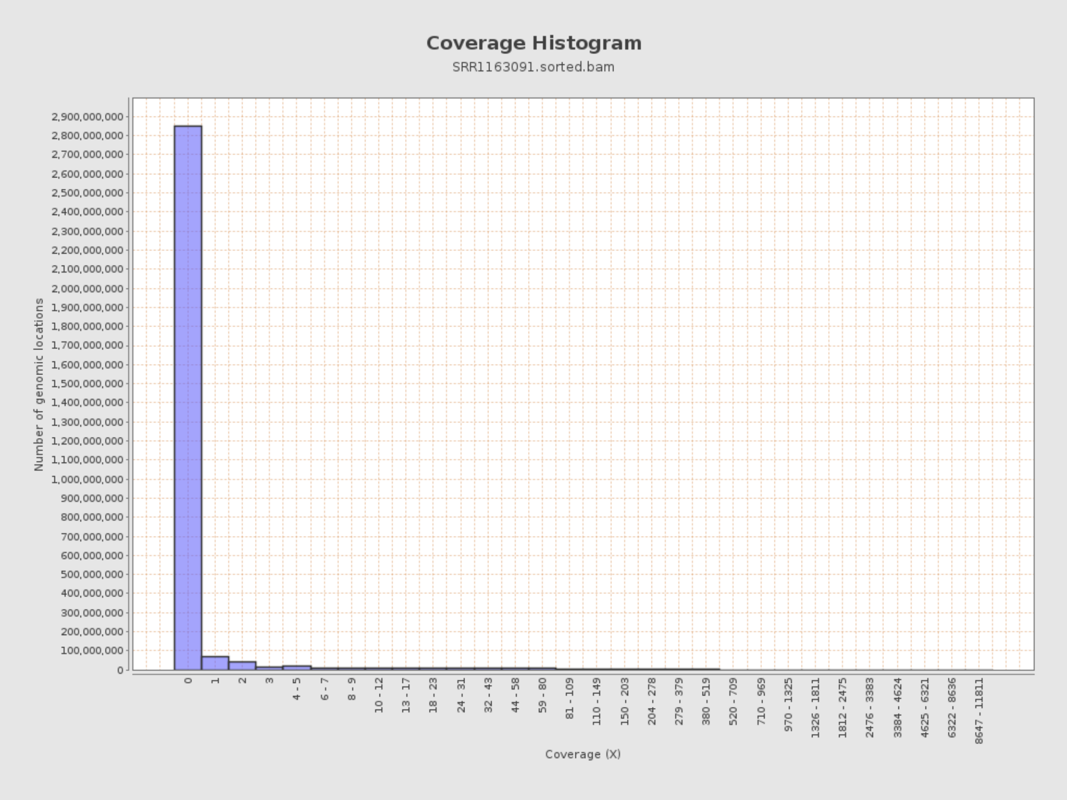
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1164335560	4.6713	49.3099
chr2	243199373	326170720	1.3412	17.6293
chr3	198022430	327533152	1.654	21.6731
chr4	191154276	171608997	0.8978	15.7706
chr5	180915260	414088391	2.2889	34.2997
chr6	171115067	457436609	2.6733	34.0406
chr7	159138663	449895479	2.8271	35.0503

chr8	146364022	416120827	2.8431	61.4869
chr9	141213431	352870479	2.4988	28.1782
chr10	135534747	162800644	1.2012	14.8314
chr11	135006516	436786317	3.2353	34.929
chr12	133851895	203711158	1.5219	19.064
chr13	115169878	116986030	1.0158	17.7098
chr14	107349540	225991938	2.1052	24.5486
chr15	102531392	344115463	3.3562	31.1228
chr16	90354753	339203565	3.7541	35.0637
chr17	81195210	229201380	2.8228	32.2816
chr18	78077248	131533607	1.6847	20.4648
chr19	59128983	618972007	10.4682	77.1965
chr20	63025520	197459891	3.133	36.1215
chr21	48129895	112081590	2.3287	54.5664
chr22	51304566	93541422	1.8233	19.8583
chrMT	16571	896	0.0541	0.3036
chrX	155270560	421330386	2.7135	33.5253
chrY	59373566	6334683	0.1067	6.1008

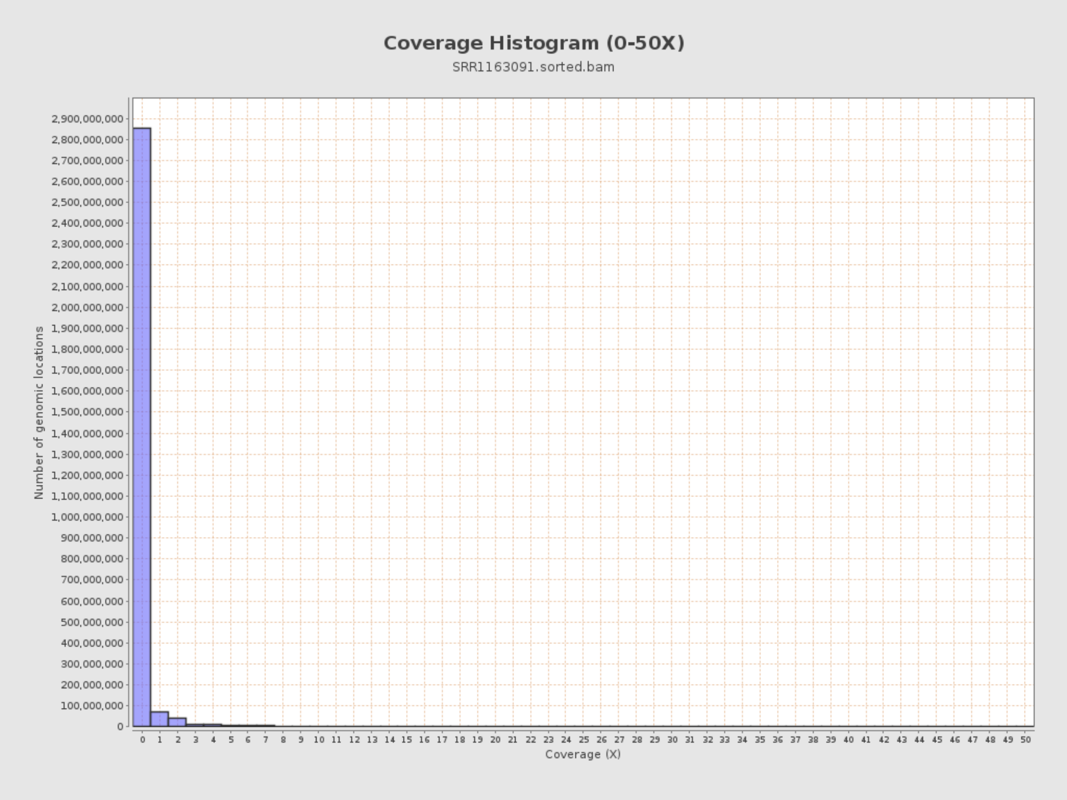
3. Results : Coverage across reference



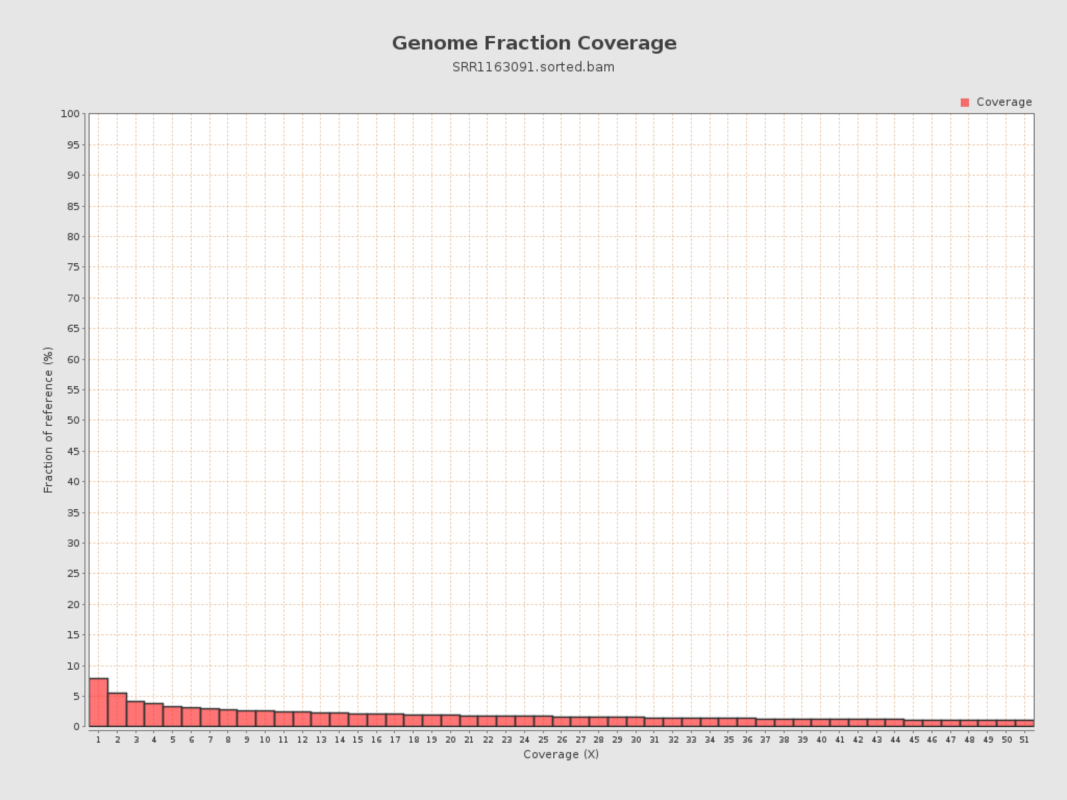
4. Results : Coverage Histogram



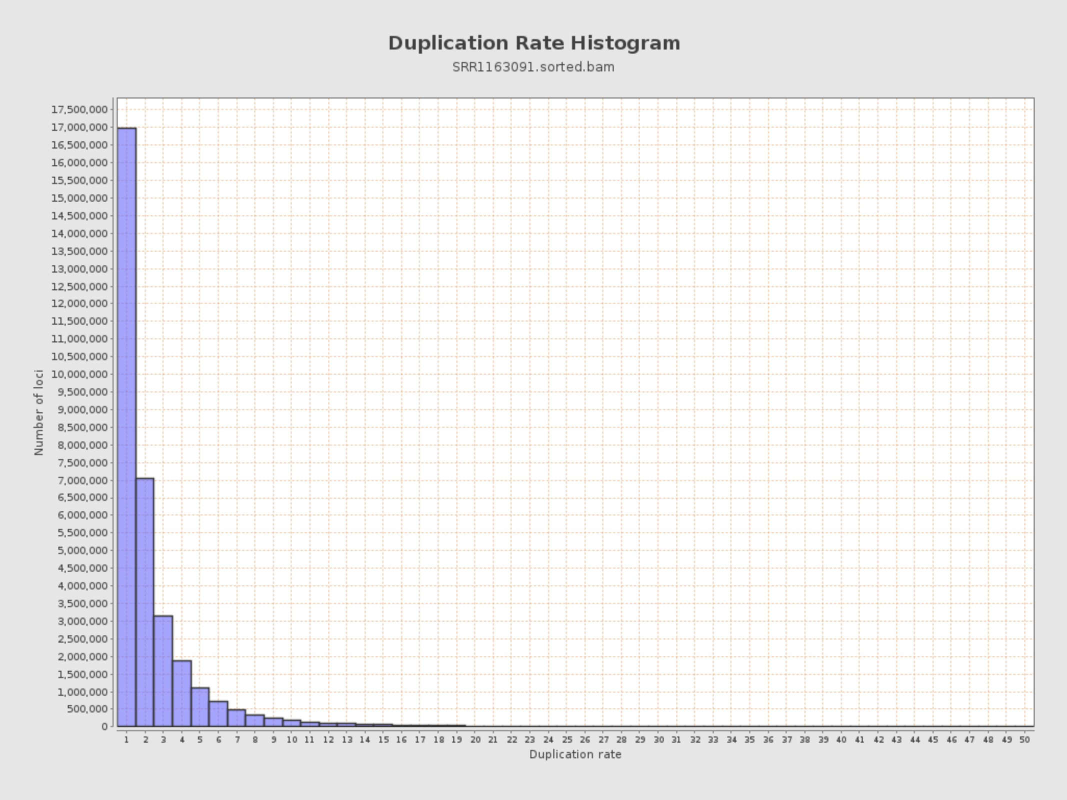
5. Results : Coverage Histogram (0-50X)



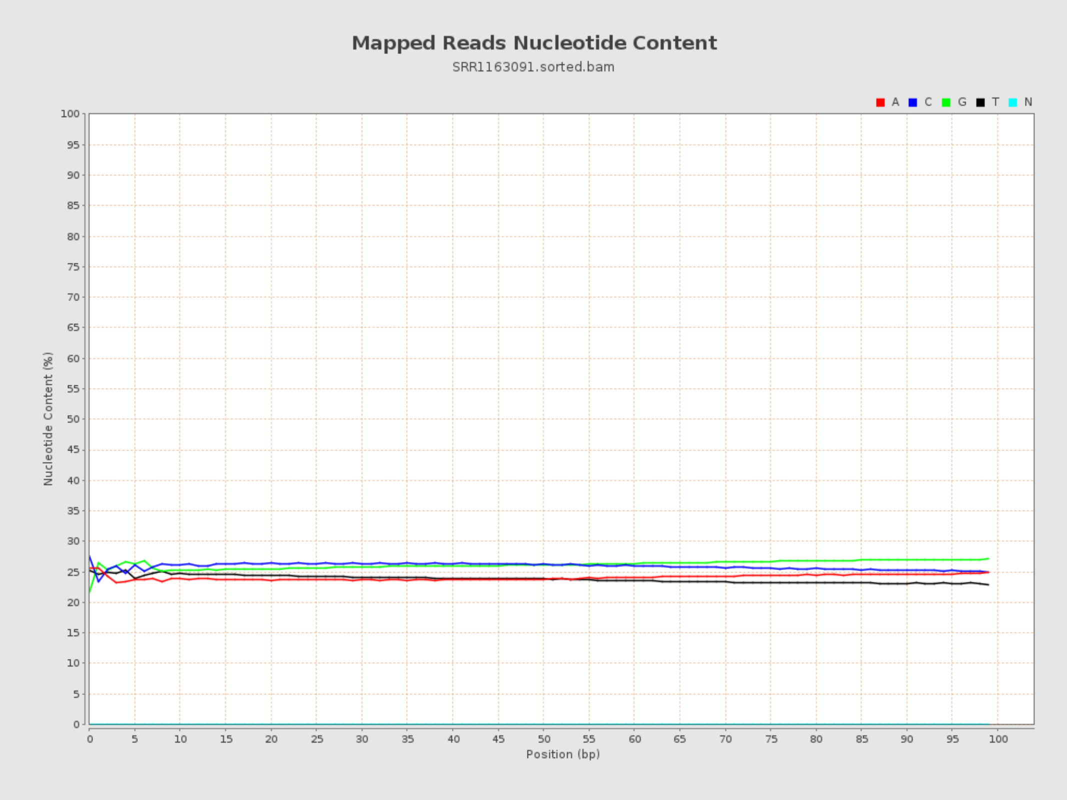
6. Results : Genome Fraction Coverage



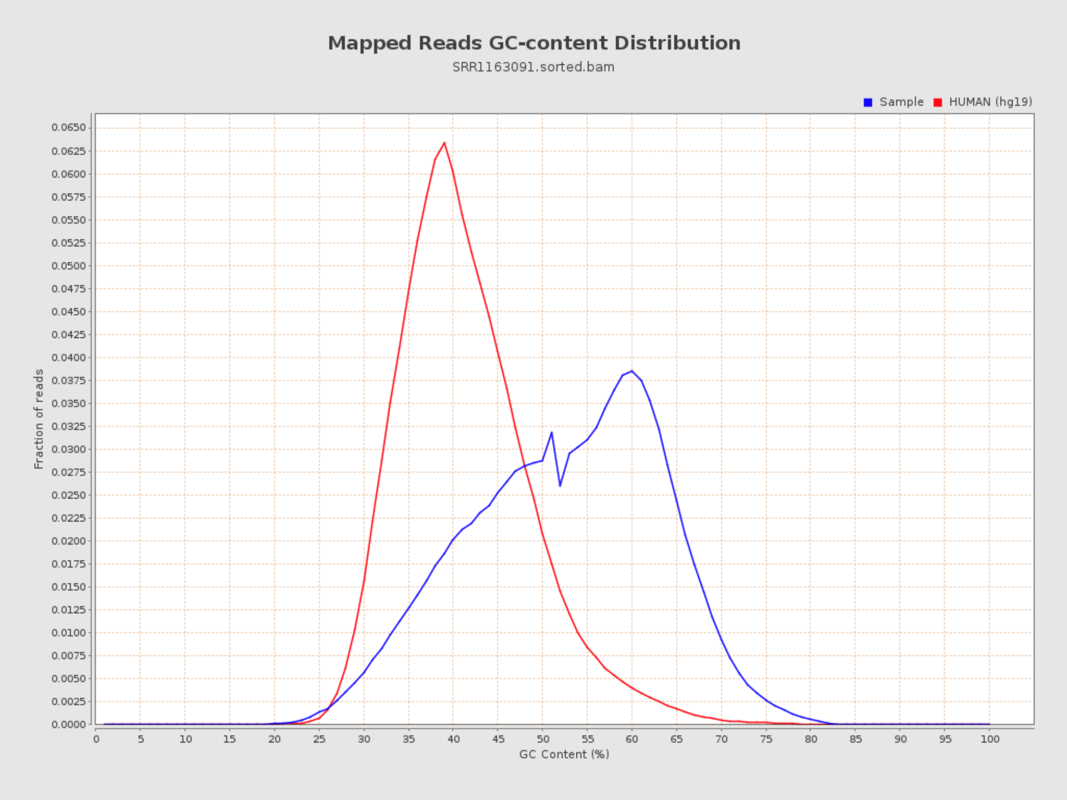
7. Results : Duplication Rate Histogram



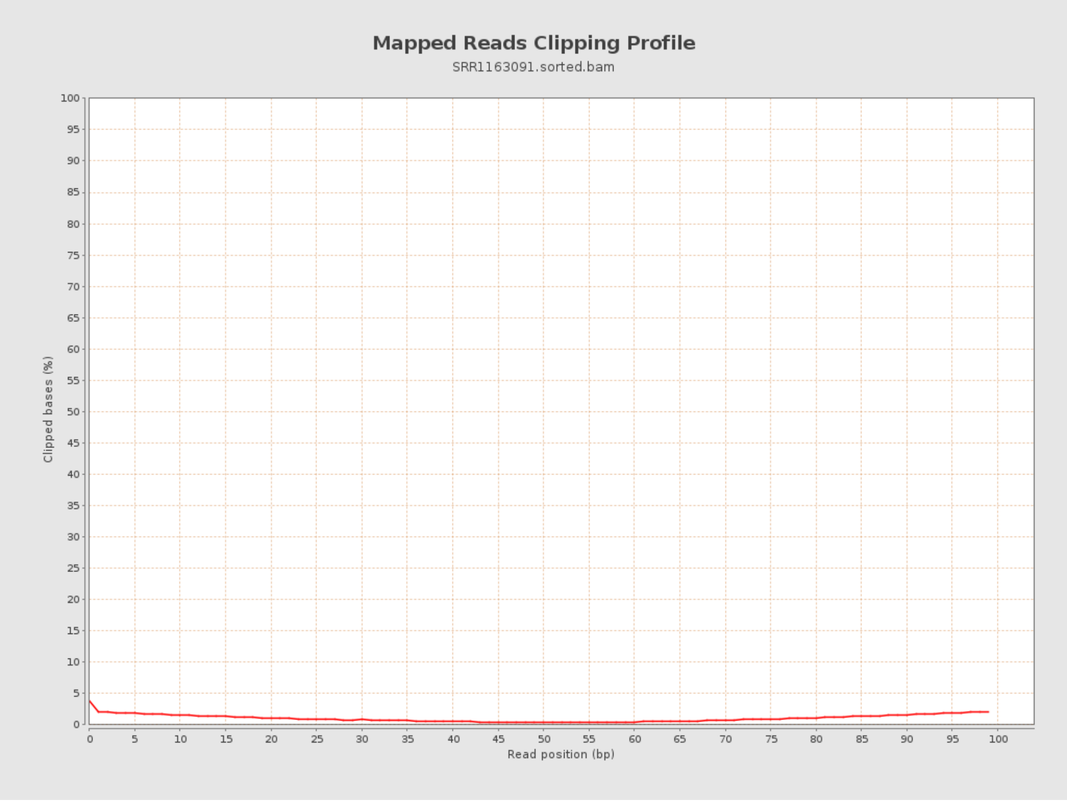
8. Results : Mapped Reads Nucleotide Content



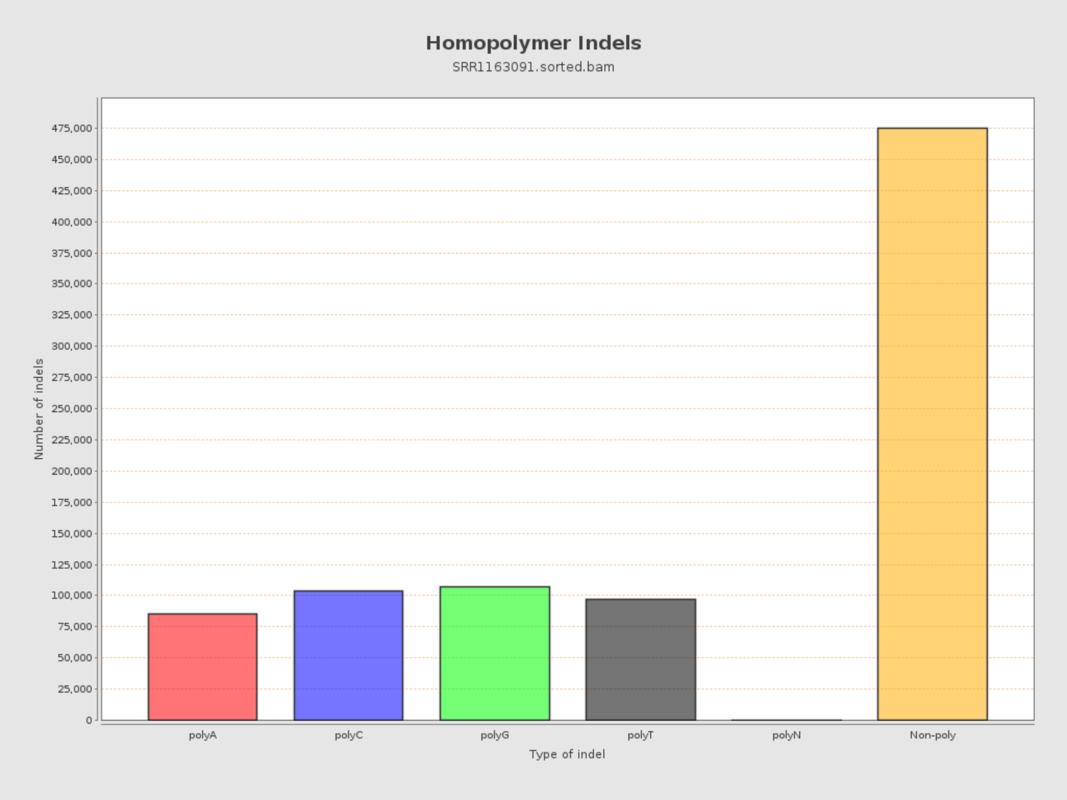
9. Results : Mapped Reads GC-content Distribution



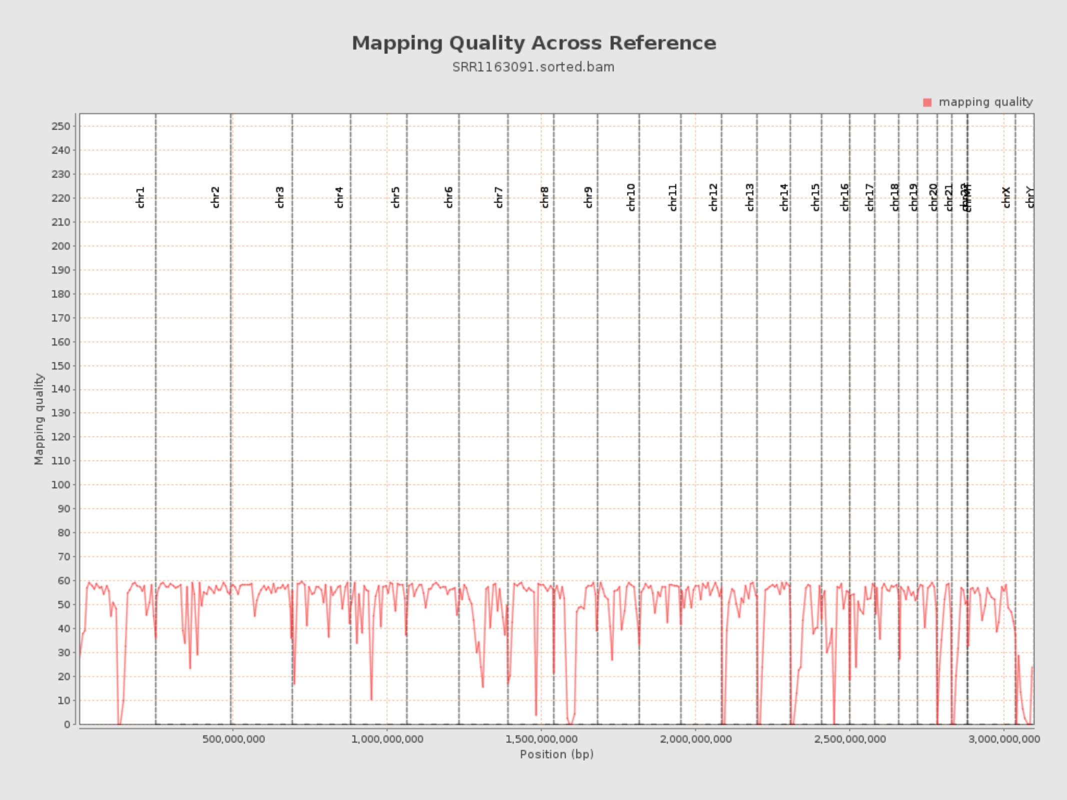
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram