Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 04:40:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163070.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_SRR1163070 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163070.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 04:40:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163070.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	92,258,792
Mapped reads	90,975,423 / 98.61%
Unmapped reads	1,283,369 / 1.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	617,375 / 0.67%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	52,362,443 / 56.76%
Duplication rate	45.23%
Clipped reads	11,239,285 / 12.18%

2.2. ACGT Content

Number/percentage of A's	2,174,720,458 / 24.42%
Number/percentage of C's	2,278,506,963 / 25.59%
Number/percentage of T's	2,158,129,699 / 24.23%
Number/percentage of G's	2,293,336,411 / 25.75%
Number/percentage of N's	643,491 / 0.01%
GC Percentage	51.34%

2.3. Coverage

Mean	2.8771

Standard Deviation	37.1961

2.4. Mapping Quality

Mean Mapping Quality	48.95

2.5. Mismatches and indels

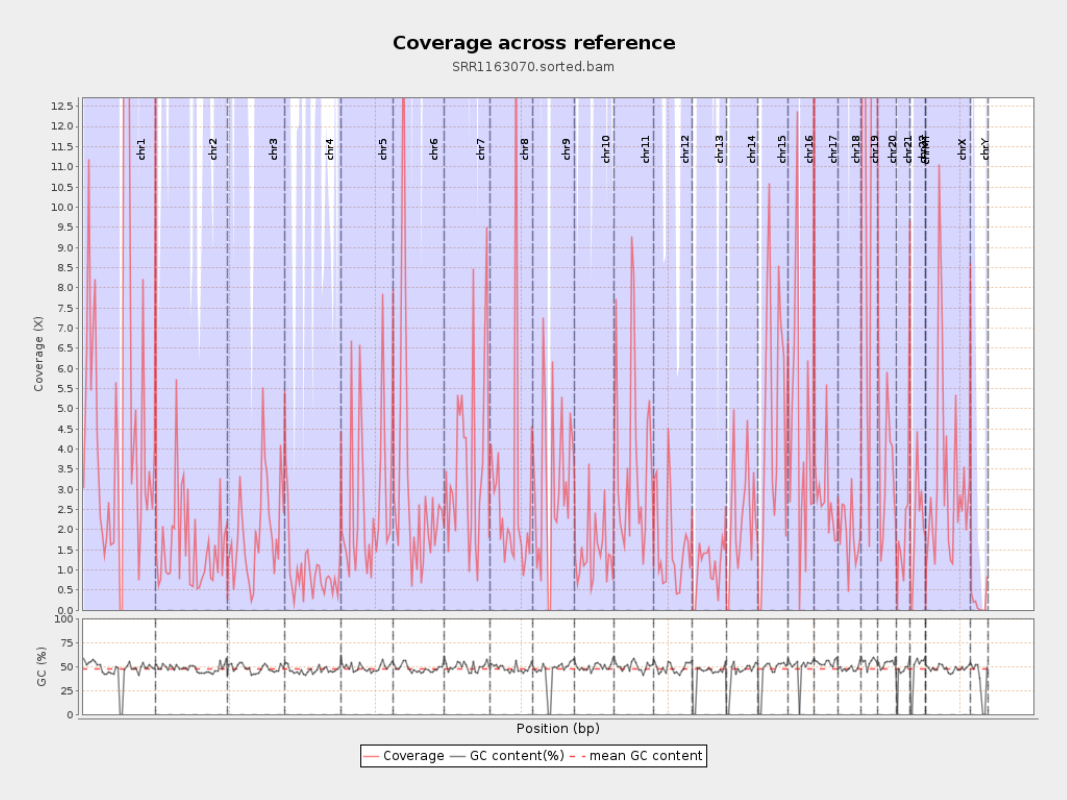
General error rate	0.39%
Mismatches	33,387,482
Insertions	605,686
Mapped reads with at least one insertion	0.66%
Deletions	534,185
Mapped reads with at least one deletion	0.58%
Homopolymer indels	46.58%

2.6. Chromosome stats

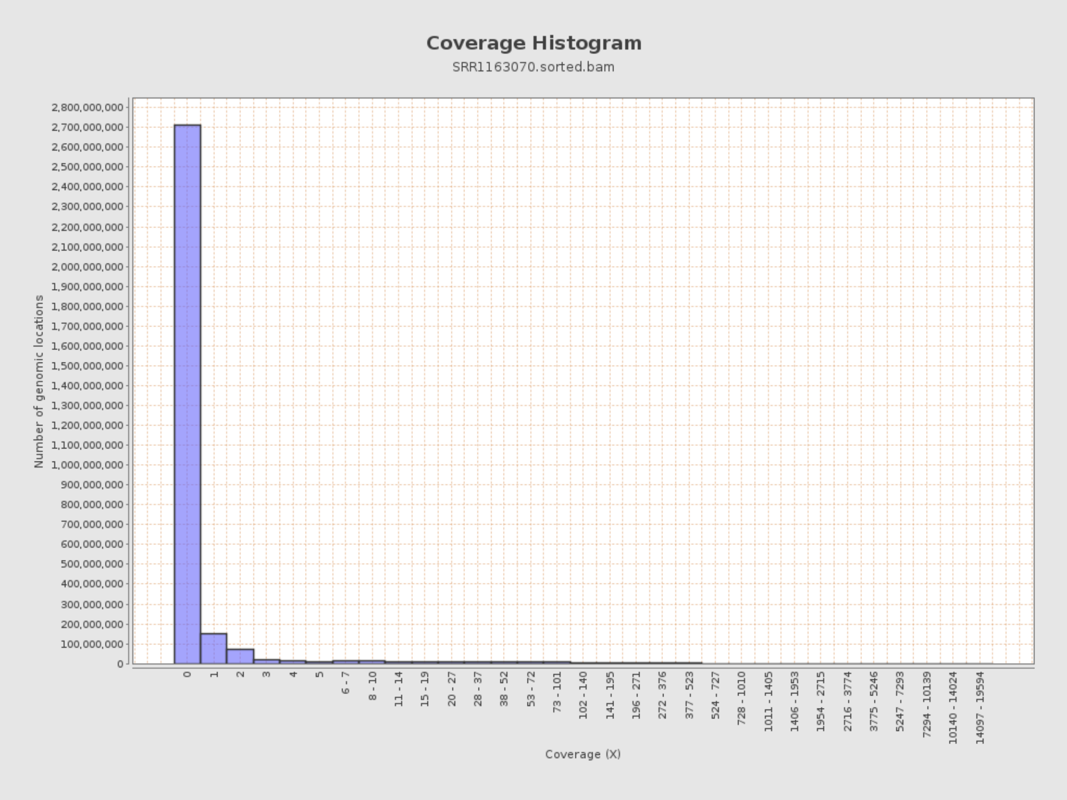
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1274282549	5.1125	50.9217
chr2	243199373	383355601	1.5763	19.4978
chr3	198022430	386982912	1.9542	21.9764
chr4	191154276	184903951	0.9673	15.1608
chr5	180915260	500296302	2.7654	48.6173
chr6	171115067	507061788	2.9633	33.9308
chr7	159138663	591361724	3.716	61.8722

chr8	146364022	421940498	2.8828	47.265
chr9	141213431	428070168	3.0314	35.2823
chr10	135534747	197398388	1.4564	16.2369
chr11	135006516	505611224	3.7451	34.3907
chr12	133851895	225837637	1.6872	20.037
chr13	115169878	126567870	1.099	15.077
chr14	107349540	248362925	2.3136	23.3154
chr15	102531392	465774083	4.5427	45.5048
chr16	90354753	392394332	4.3428	37.2323
chr17	81195210	229830272	2.8306	26.0841
chr18	78077248	148439792	1.9012	20.0278
chr19	59128983	727287732	12.3	87.0264
chr20	63025520	219956062	3.49	31.7741
chr21	48129895	117293232	2.437	44.6644
chr22	51304566	107411674	2.0936	25.4729
chrMT	16571	242	0.0146	0.12
chrX	155270560	503757626	3.2444	40.4437
chrY	59373566	12335068	0.2078	9.7704

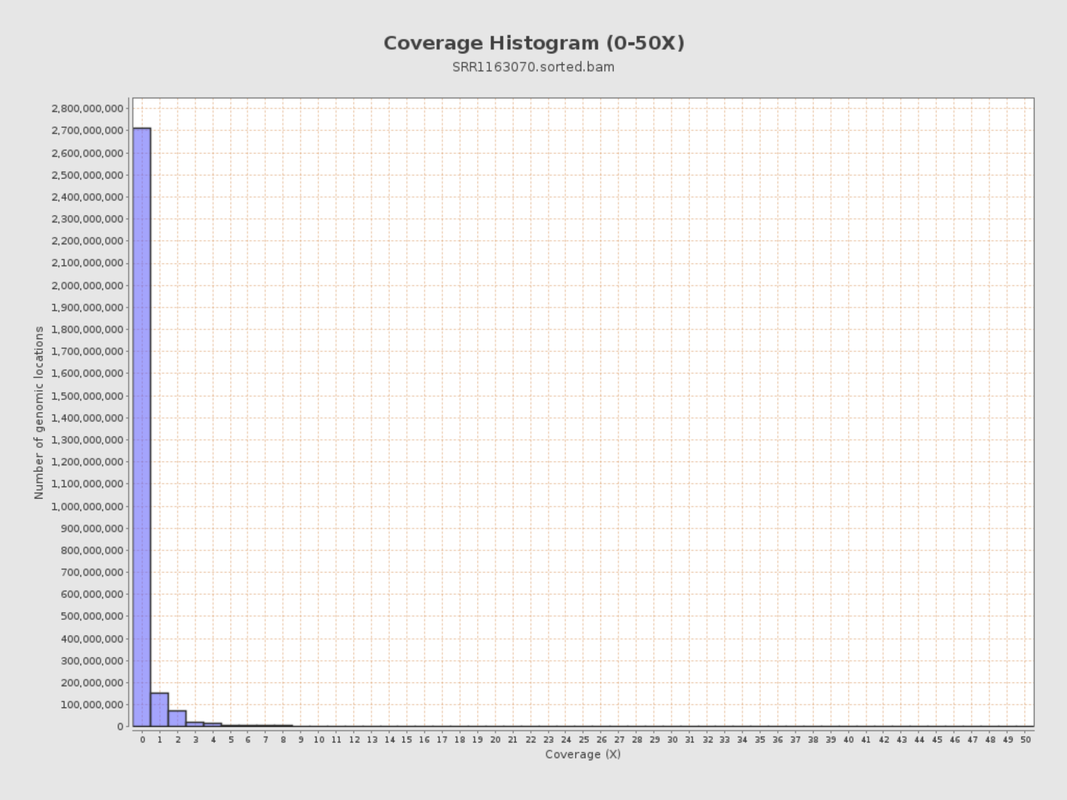
3. Results : Coverage across reference



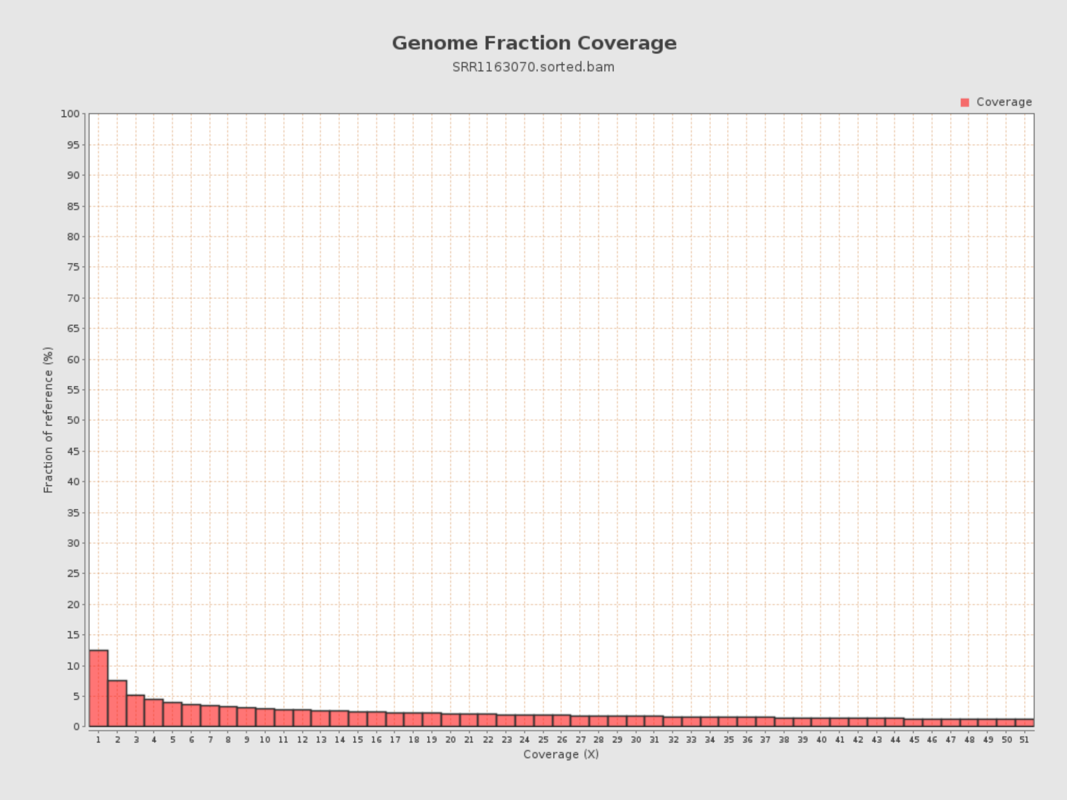
4. Results : Coverage Histogram



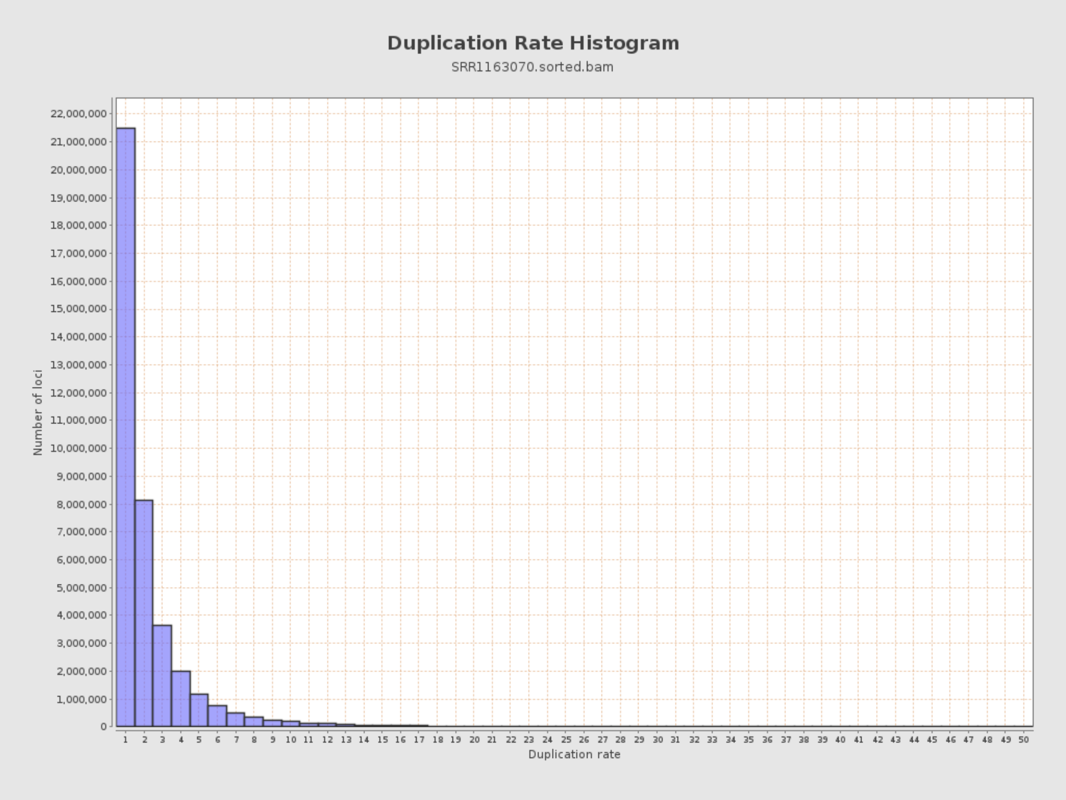
5. Results : Coverage Histogram (0-50X)



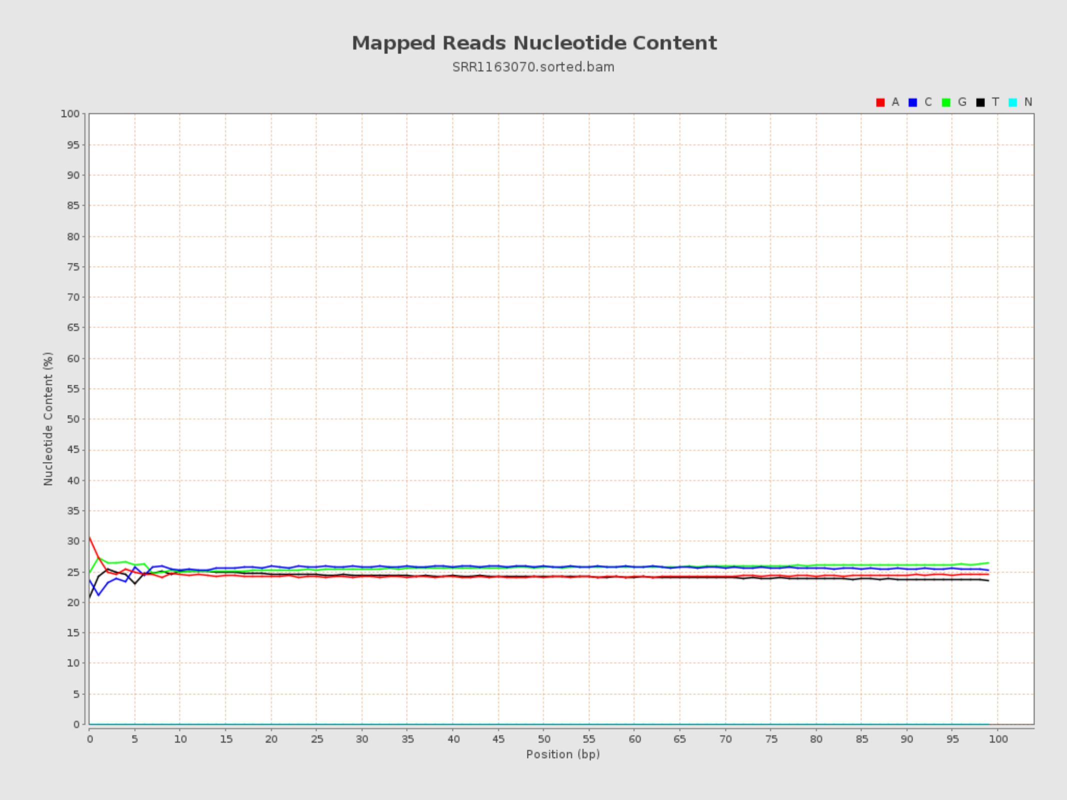
6. Results : Genome Fraction Coverage



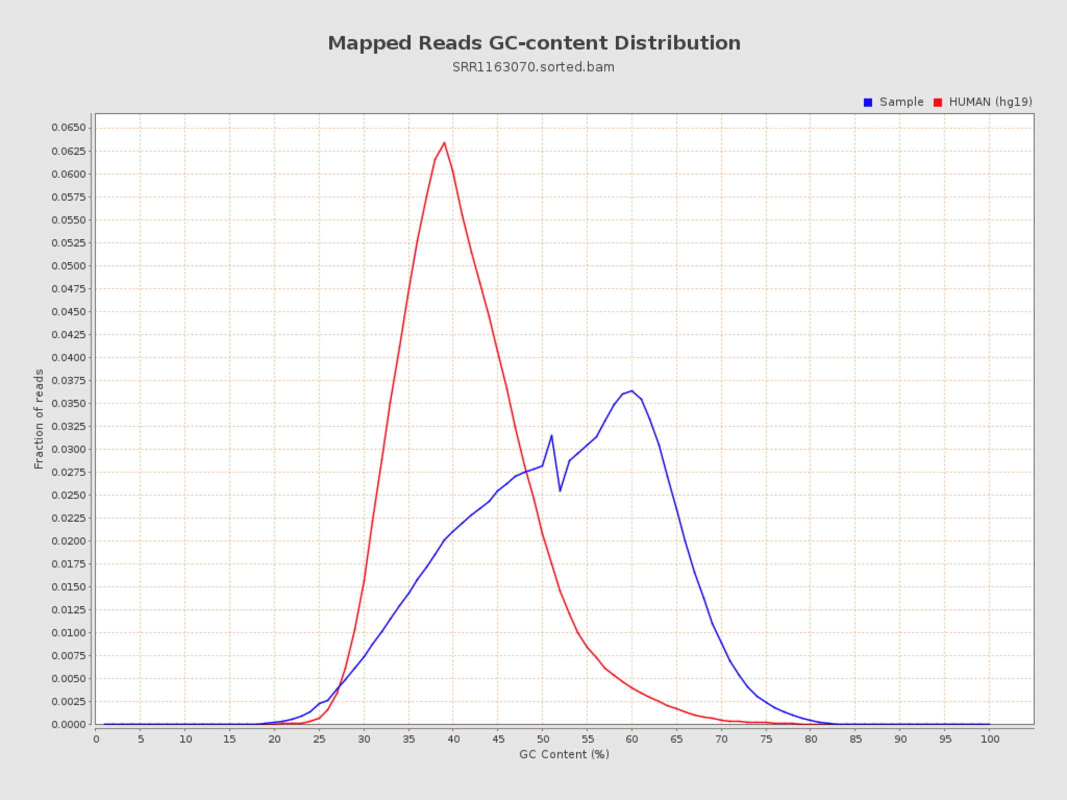
7. Results : Duplication Rate Histogram



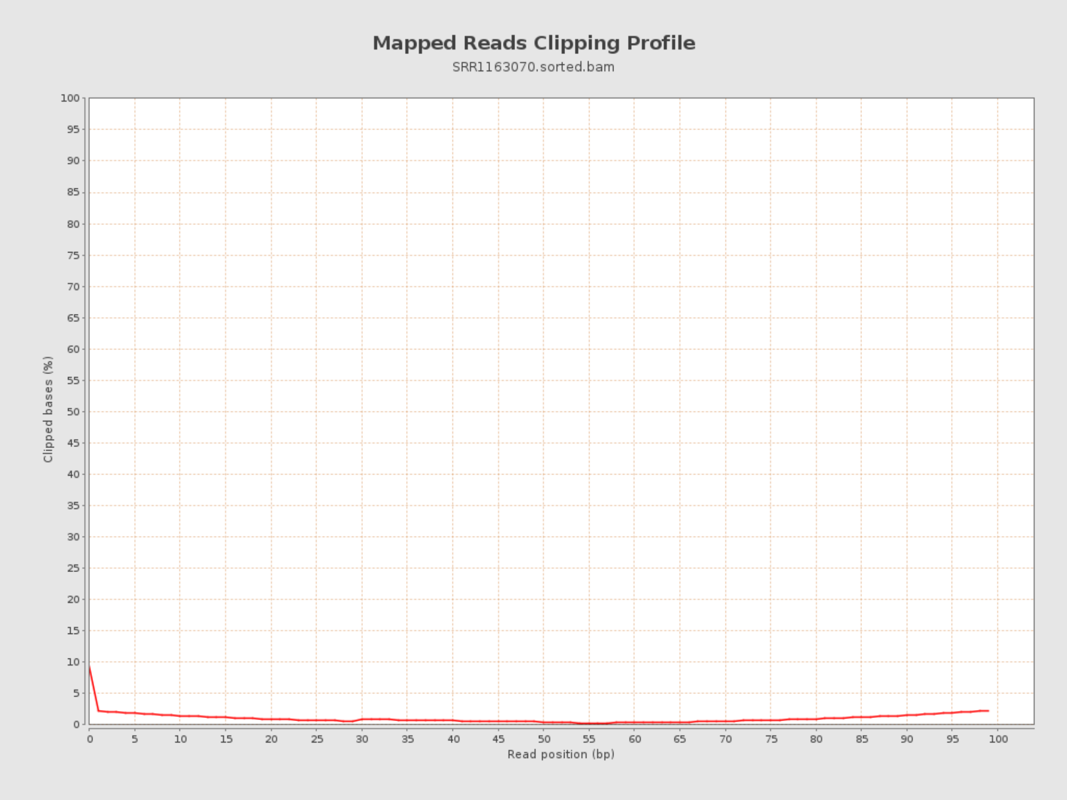
8. Results : Mapped Reads Nucleotide Content



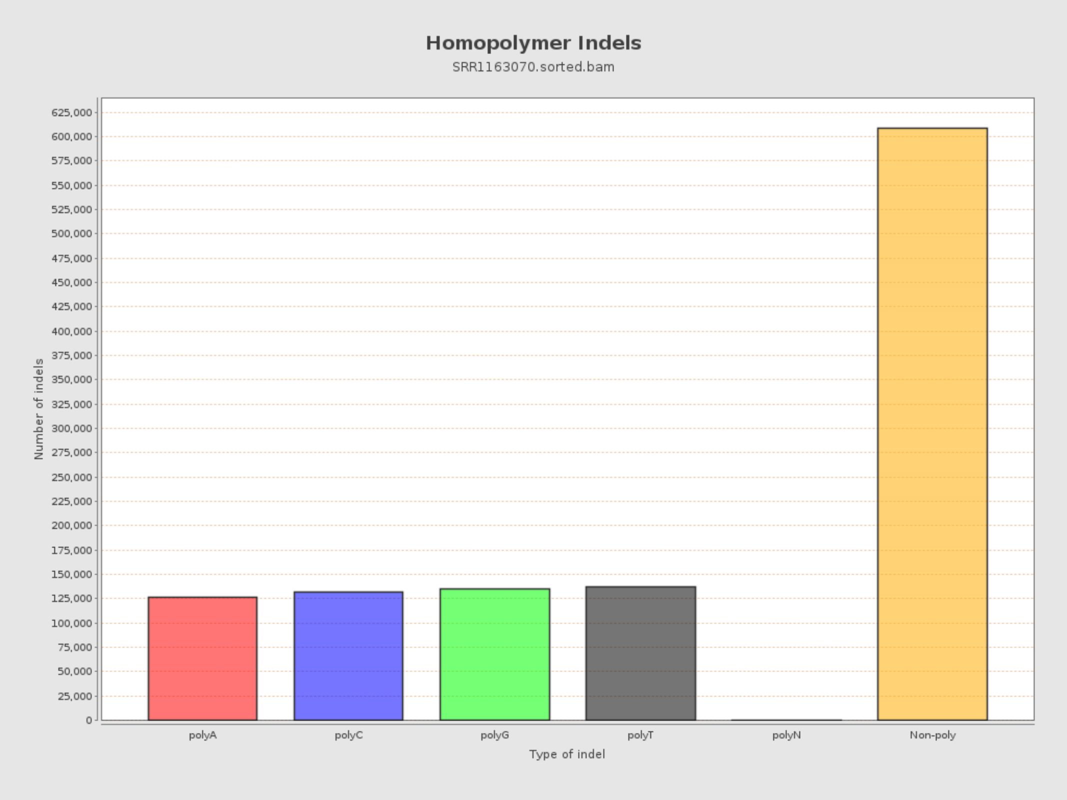
9. Results : Mapped Reads GC-content Distribution



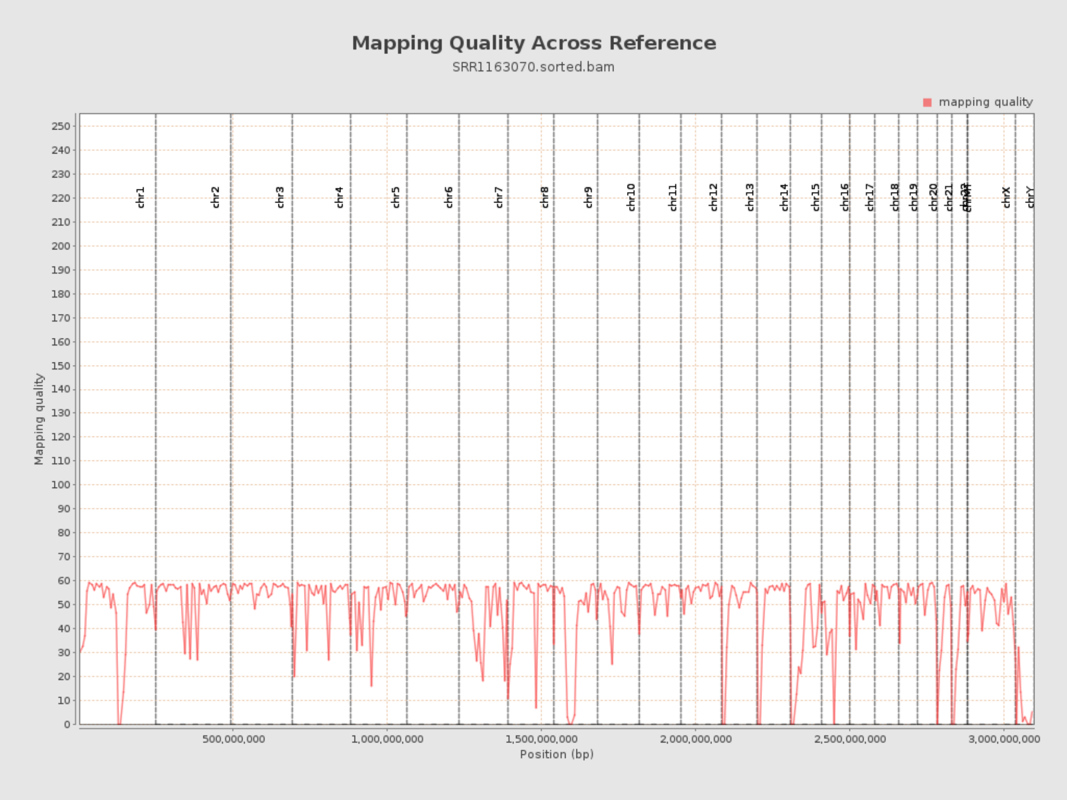
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram