Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 22:13:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163160.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_SRR1163160 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163160.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 22:13:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	82,517,320
Mapped reads	81,422,545 / 98.67%
Unmapped reads	1,094,775 / 1.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	932,231 / 1.13%
Read min/max/mean length	30 / 100 / 100.47
Duplicated reads (estimated)	45,328,885 / 54.93%
Duplication rate	50.04%
Clipped reads	4,925,098 / 5.97%

2.2. ACGT Content

Number/percentage of A's	2,125,063,904 / 26.24%
Number/percentage of C's	1,922,672,498 / 23.74%
Number/percentage of T's	2,148,416,964 / 26.53%
Number/percentage of G's	1,895,991,456 / 23.41%
Number/percentage of N's	6,124,107 / 0.08%
GC Percentage	47.15%

2.3. Coverage

Mean	2.6164

Standard Deviation	24.6938

2.4. Mapping Quality

Mean Mapping Quality	49.29

2.5. Mismatches and indels

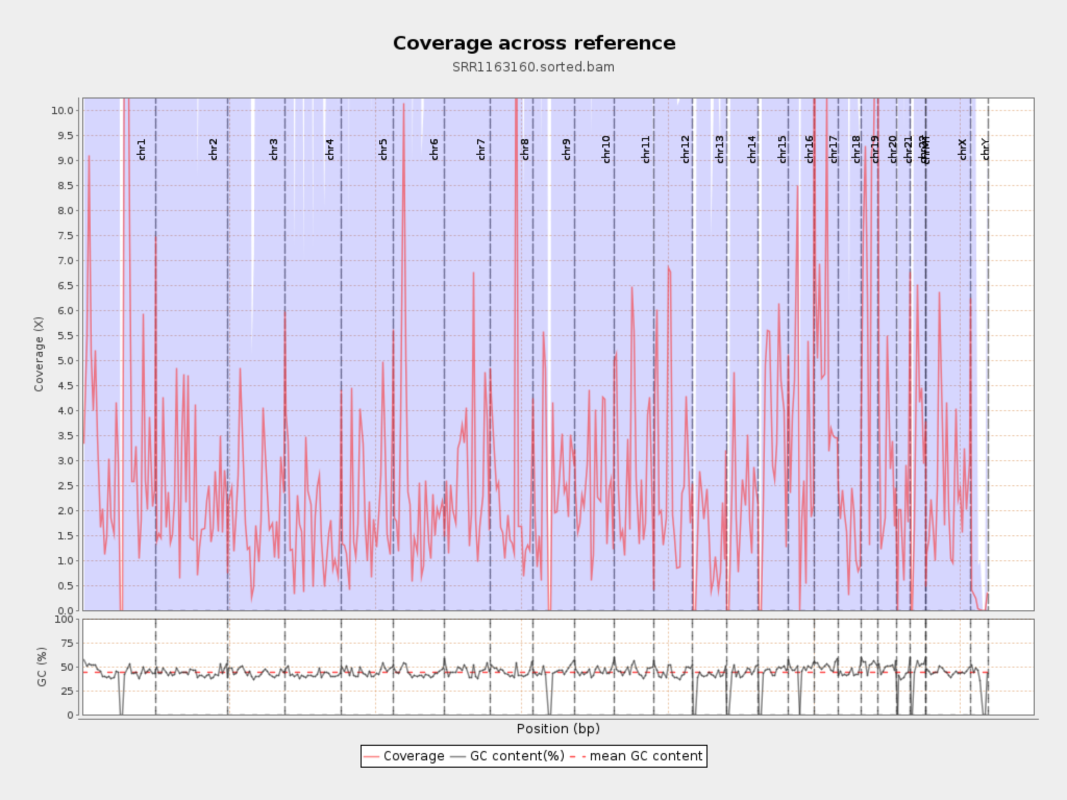
General error rate	0.7%
Mismatches	55,342,174
Insertions	577,967
Mapped reads with at least one insertion	0.7%
Deletions	640,349
Mapped reads with at least one deletion	0.78%
Homopolymer indels	46.52%

2.6. Chromosome stats

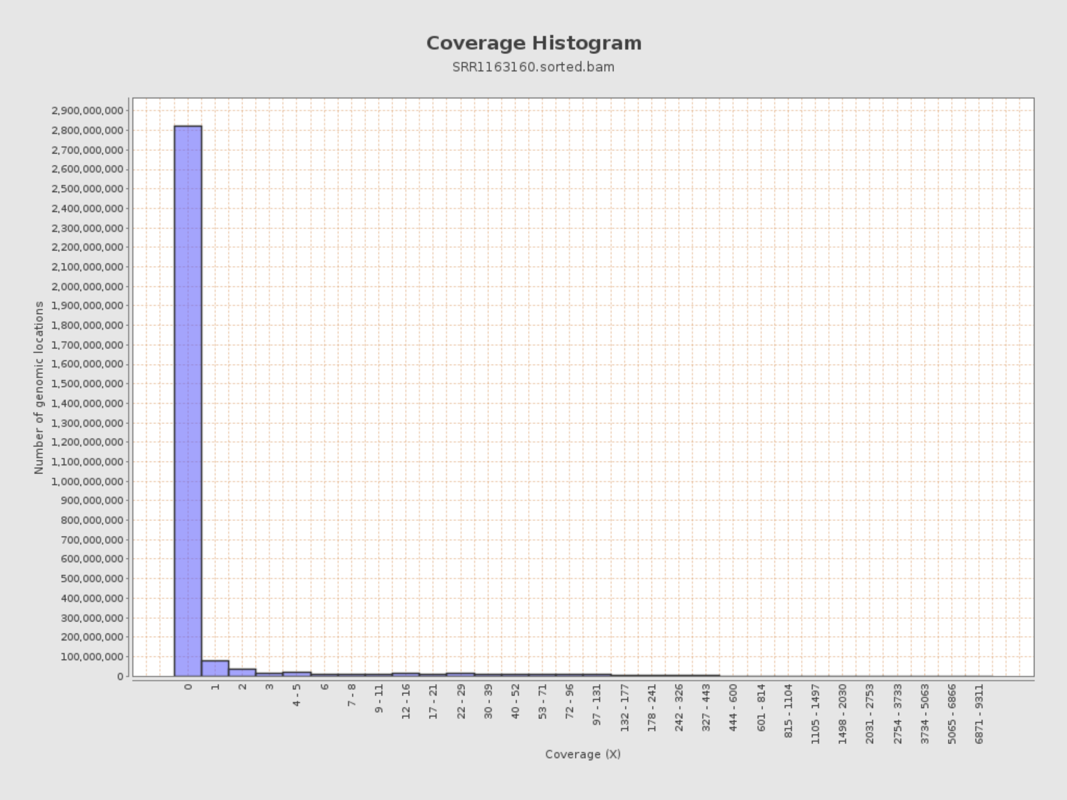
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	938645019	3.7659	30.7457
chr2	243199373	554176843	2.2787	20.6211
chr3	198022430	403698577	2.0387	17.3944
chr4	191154276	319847724	1.6732	19.2619
chr5	180915260	388232745	2.1459	28.1757
chr6	171115067	393676796	2.3007	20.4095
chr7	159138663	430309341	2.704	24.4562

chr8	146364022	362635811	2.4776	38.9672
chr9	141213431	337069696	2.387	20.9187
chr10	135534747	332141597	2.4506	20.4896
chr11	135006516	389012795	2.8814	21.55
chr12	133851895	392297651	2.9308	22.607
chr13	115169878	151902548	1.3189	15.559
chr14	107349540	219144133	2.0414	17.3072
chr15	102531392	341788605	3.3335	25.9549
chr16	90354753	290807677	3.2185	23.1258
chr17	81195210	415765507	5.1206	34.6713
chr18	78077248	123879899	1.5866	15.5763
chr19	59128983	479783427	8.1142	46.8939
chr20	63025520	171876374	2.7271	21.716
chr21	48129895	105554710	2.1931	34.1496
chr22	51304566	160474343	3.1279	24.7504
chrMT	16571	7899	0.4767	1.0414
chrX	155270560	387283527	2.4942	22.7312
chrY	59373566	9561766	0.161	13.2585

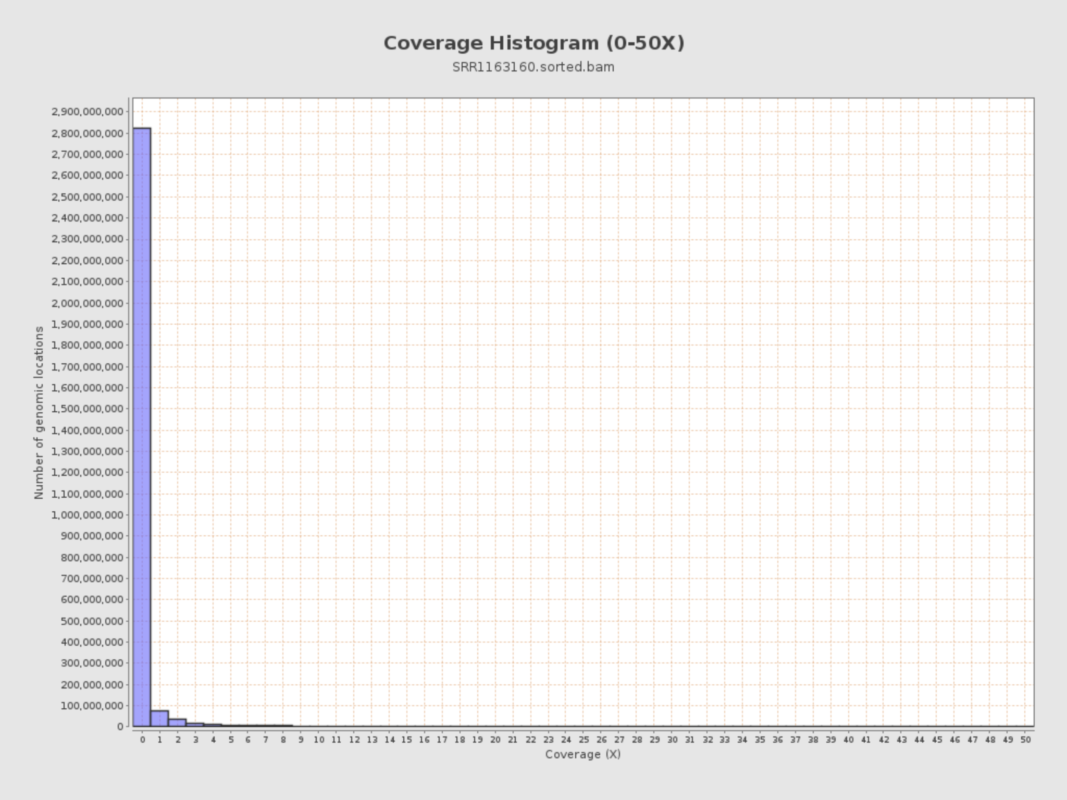
3. Results : Coverage across reference



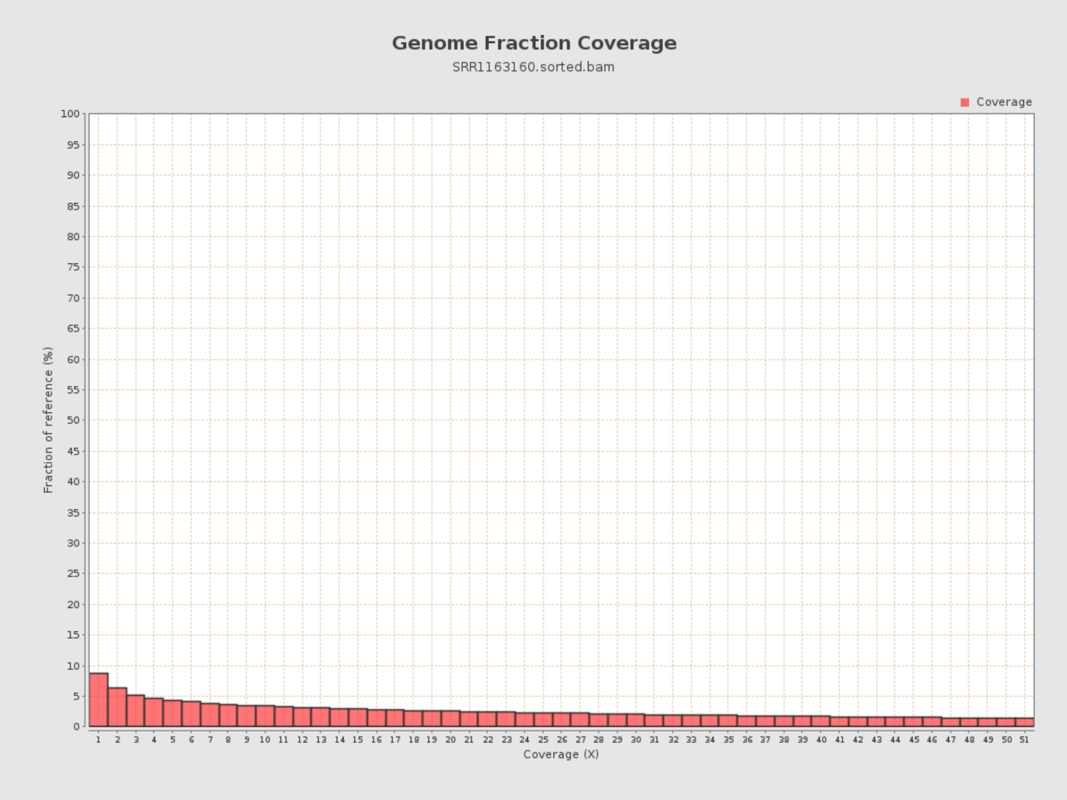
4. Results : Coverage Histogram



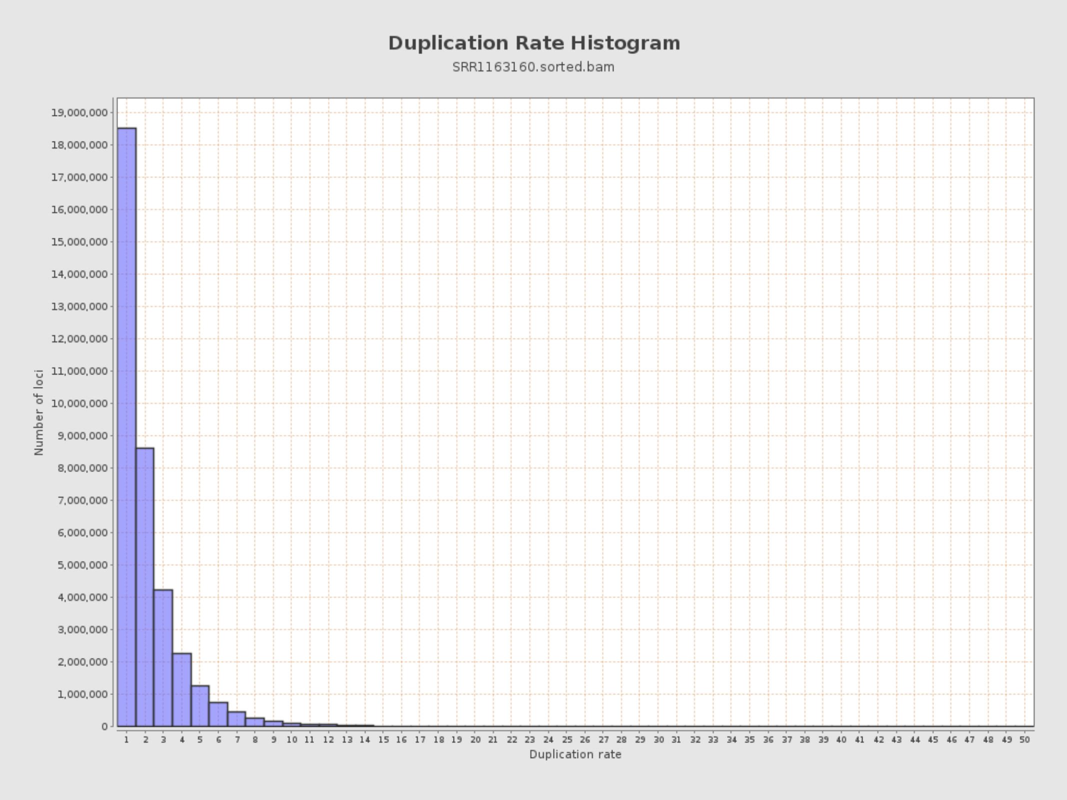
5. Results : Coverage Histogram (0-50X)



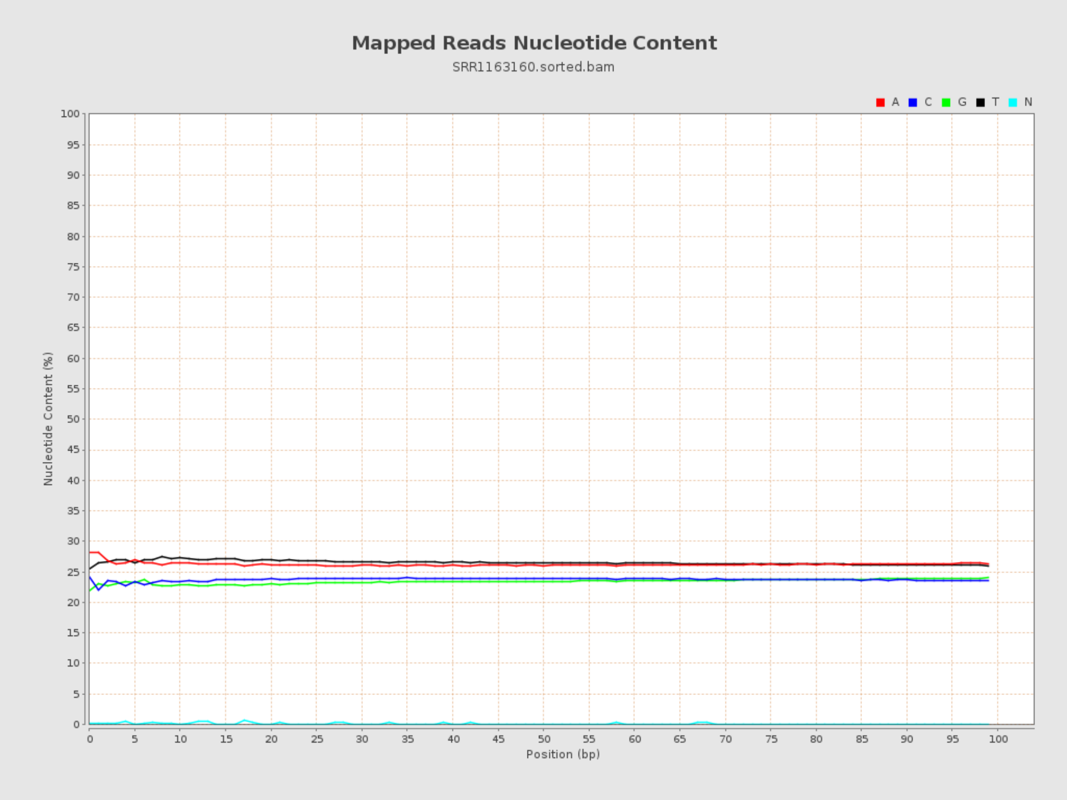
6. Results : Genome Fraction Coverage



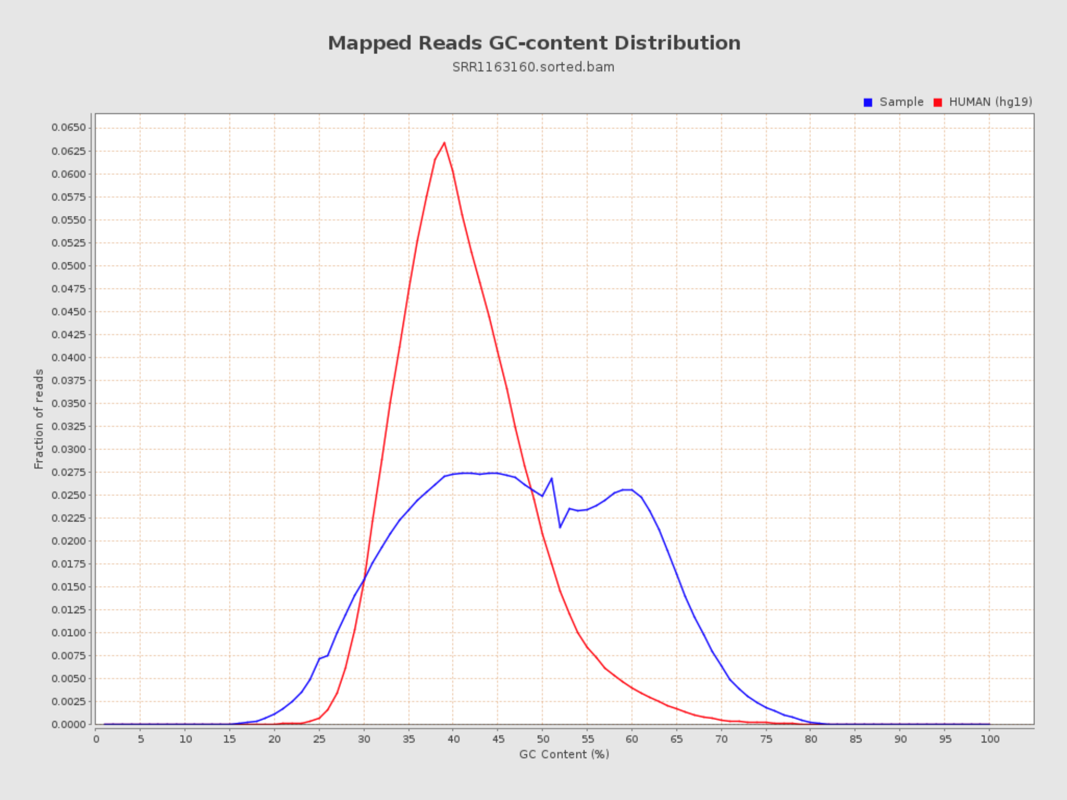
7. Results : Duplication Rate Histogram



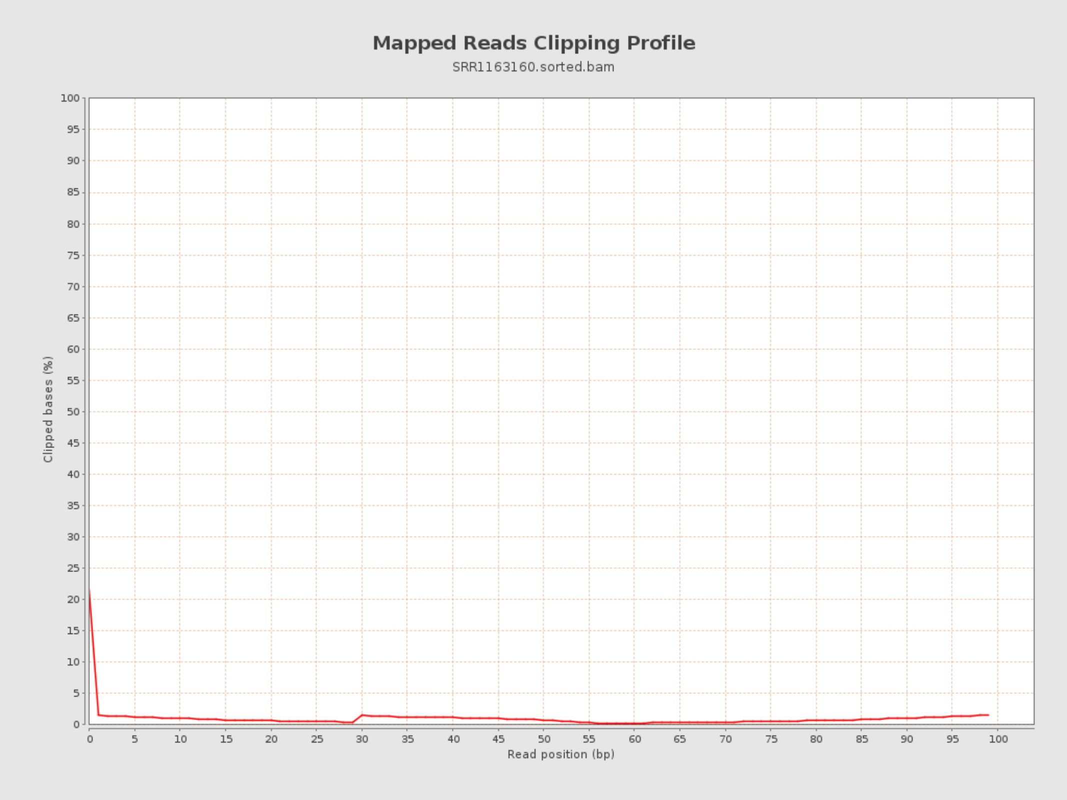
8. Results : Mapped Reads Nucleotide Content



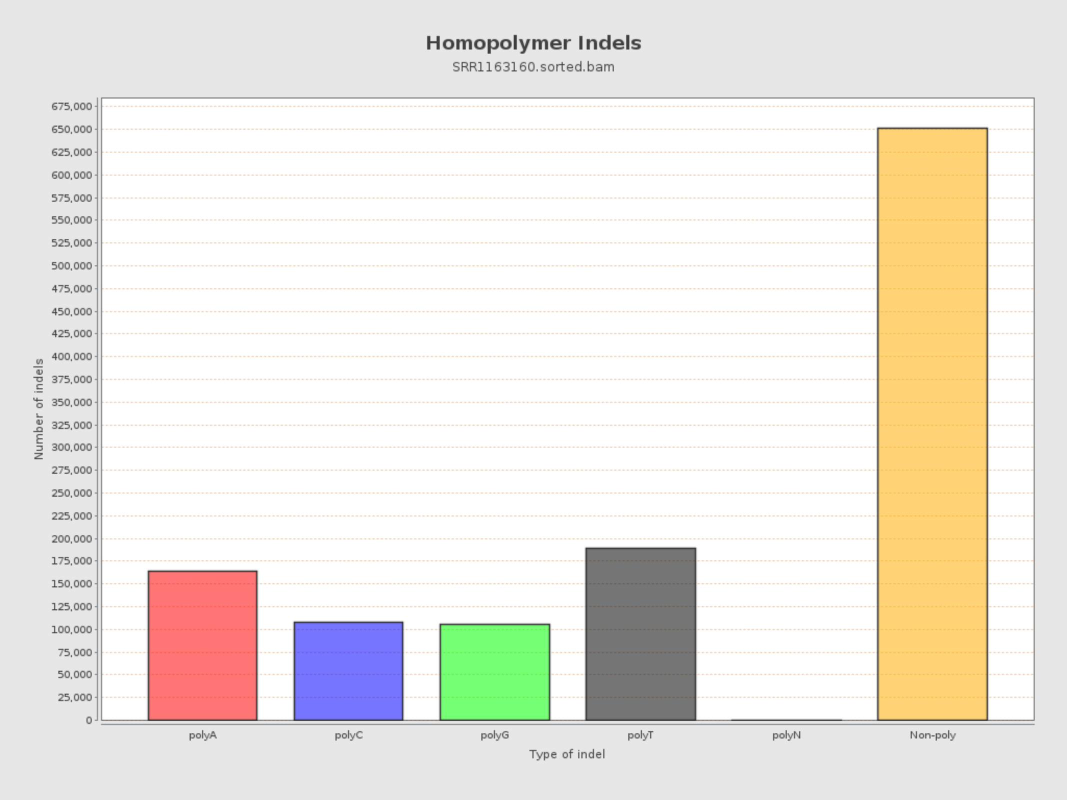
9. Results : Mapped Reads GC-content Distribution



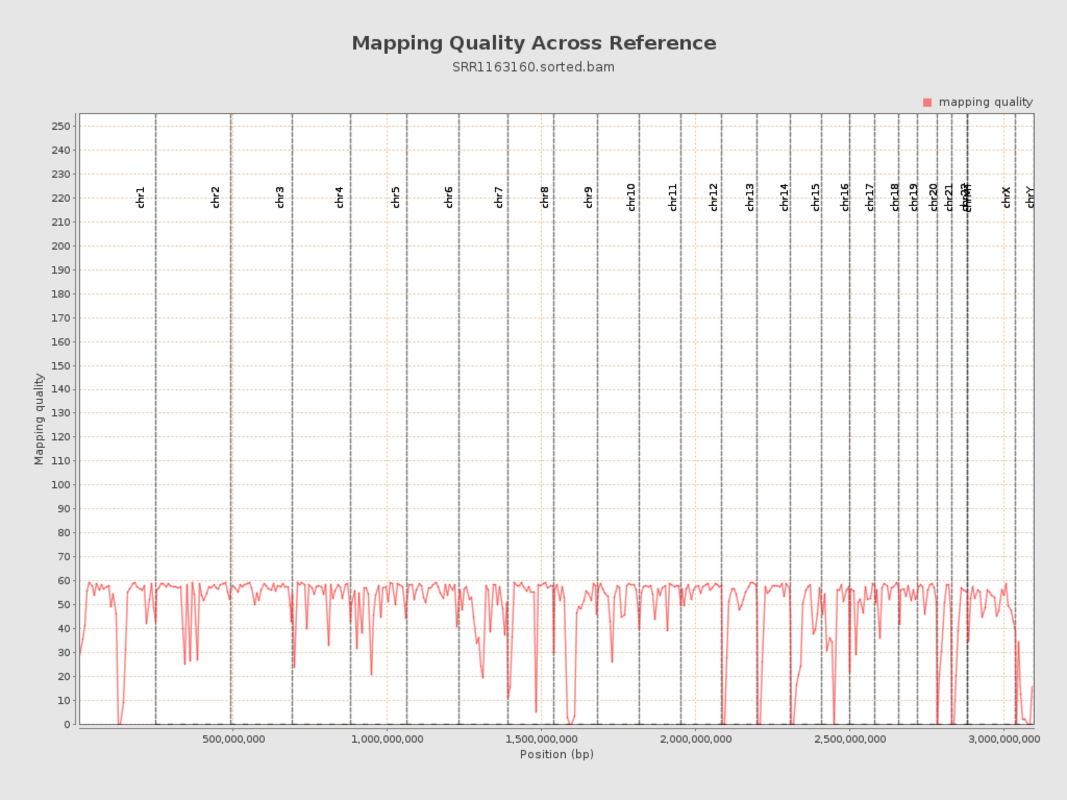
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram