Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:58:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819013.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_SRR1819013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:58:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,046,867
Mapped reads	1,995,911 / 97.51%
Unmapped reads	50,956 / 2.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,157 / 1.47%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	851,192 / 41.59%
Duplication rate	36.12%
Clipped reads	1,997,775 / 97.6%

2.2. ACGT Content

Number/percentage of A's	51,872,760 / 28.09%
Number/percentage of C's	38,783,994 / 21%
Number/percentage of T's	53,301,109 / 28.86%
Number/percentage of G's	40,722,942 / 22.05%
Number/percentage of N's	8,609 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0597

Standard Deviation	0.7005

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

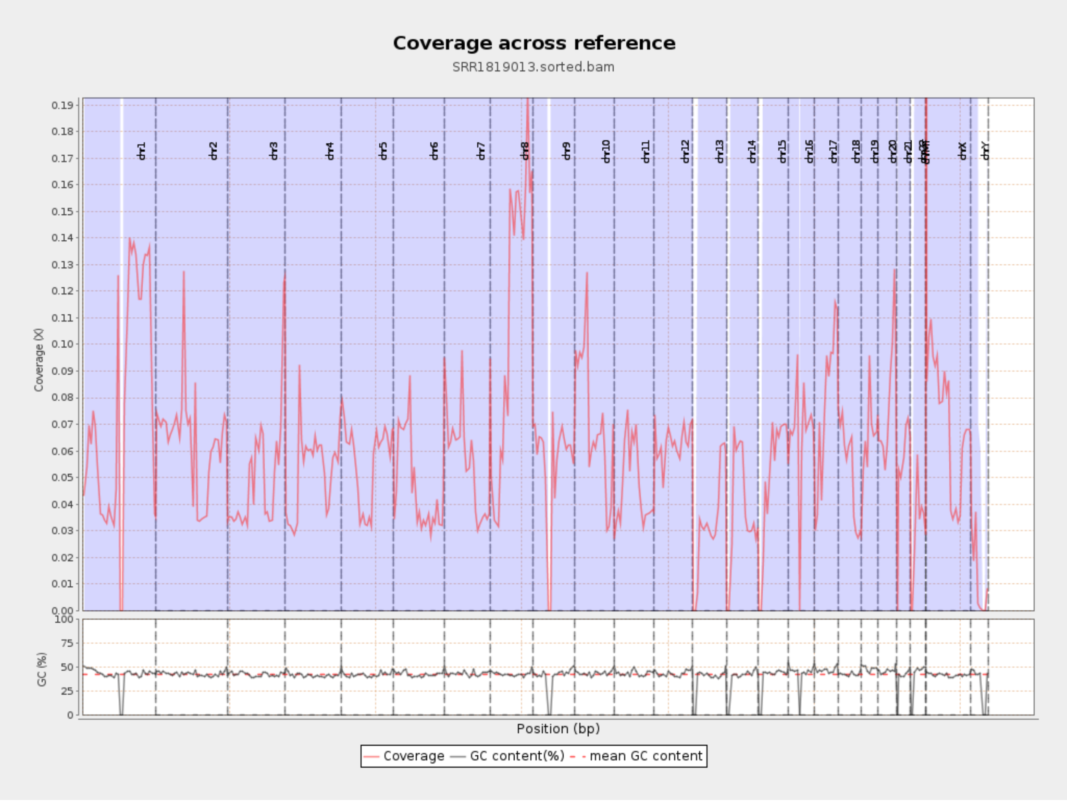
General error rate	0.67%
Mismatches	1,171,293
Insertions	29,844
Mapped reads with at least one insertion	1.46%
Deletions	59,059
Mapped reads with at least one deletion	2.9%
Homopolymer indels	41.53%

2.6. Chromosome stats

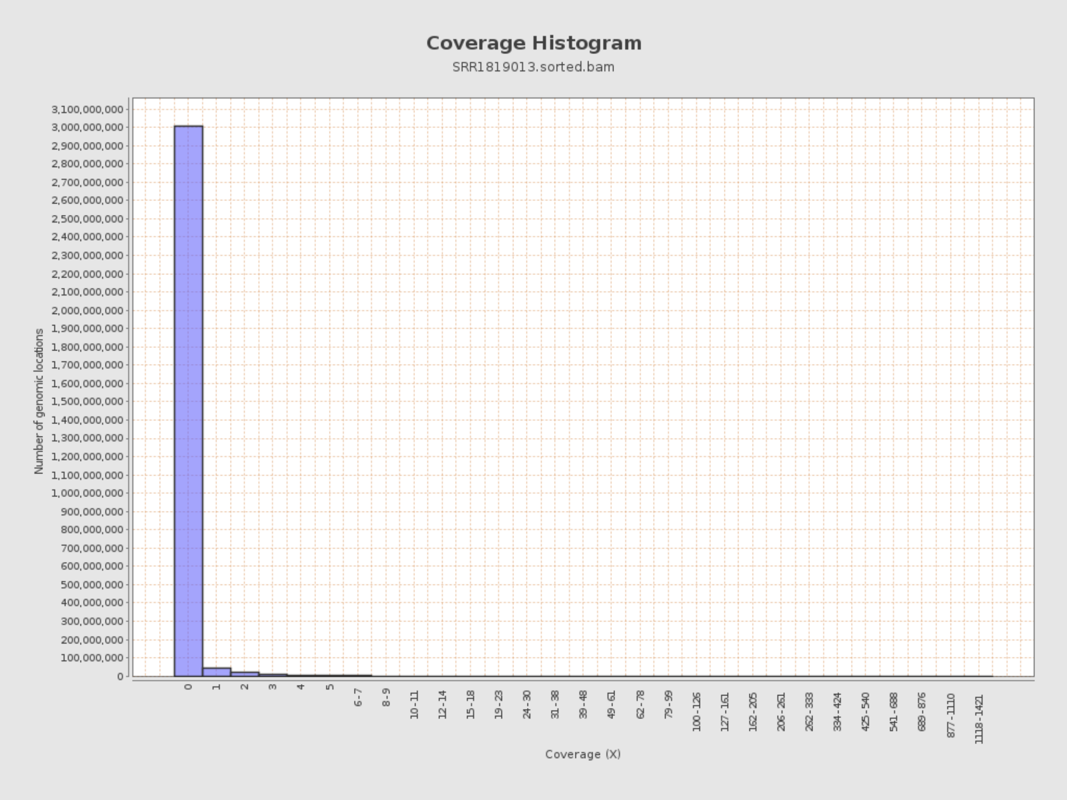
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19092980	0.0766	1.3039
chr2	243199373	15547678	0.0639	0.8966
chr3	198022430	9805499	0.0495	0.3952
chr4	191154276	10077256	0.0527	0.472
chr5	180915260	10161637	0.0562	0.4365
chr6	171115067	7970365	0.0466	0.4803
chr7	159138663	8928154	0.0561	0.7886

chr8	146364022	16551087	0.1131	0.6988
chr9	141213431	7737254	0.0548	0.645
chr10	135534747	9633312	0.0711	0.8244
chr11	135006516	6339811	0.047	0.4707
chr12	133851895	8436689	0.063	0.4625
chr13	115169878	3803842	0.033	0.3275
chr14	107349540	4117465	0.0384	0.3704
chr15	102531392	5014070	0.0489	0.3972
chr16	90354753	5899809	0.0653	0.6991
chr17	81195210	6248195	0.077	0.5618
chr18	78077248	4142249	0.0531	0.7686
chr19	59128983	3866908	0.0654	1.2172
chr20	63025520	5017433	0.0796	0.5411
chr21	48129895	2667303	0.0554	0.4625
chr22	51304566	1517466	0.0296	0.3725
chrMT	16571	404433	24.4061	17.1126
chrX	155270560	11130147	0.0717	0.5693
chrY	59373566	687762	0.0116	0.6347

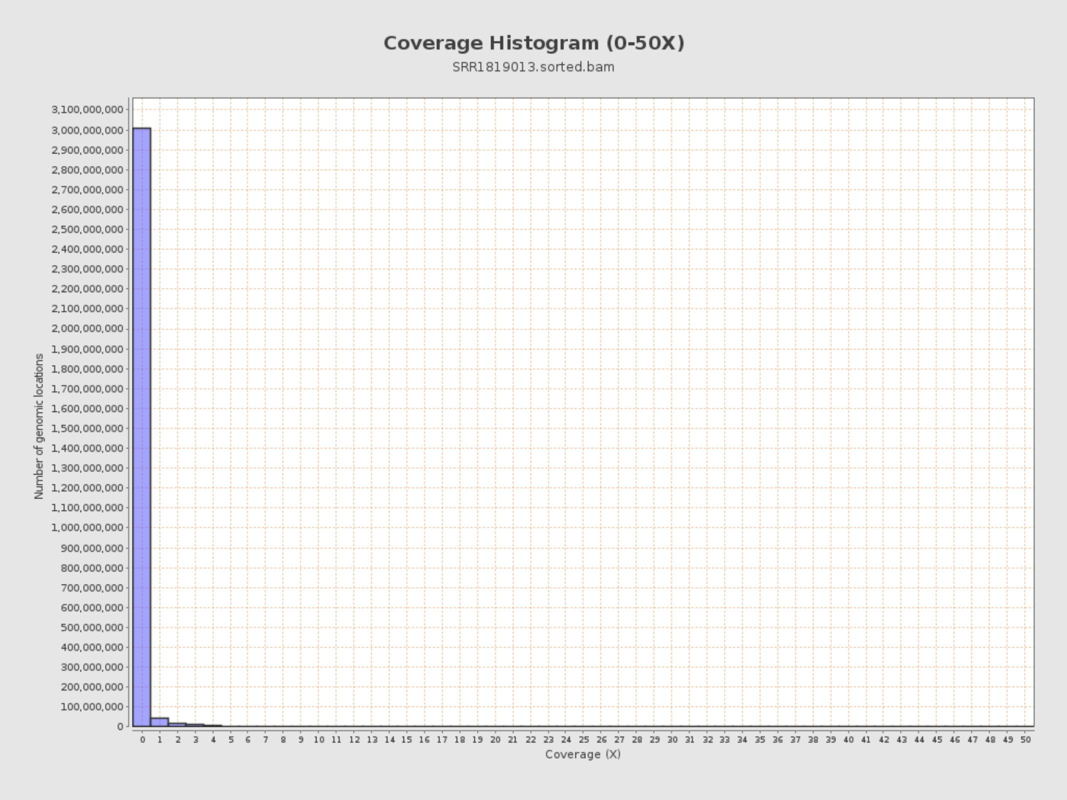
3. Results : Coverage across reference



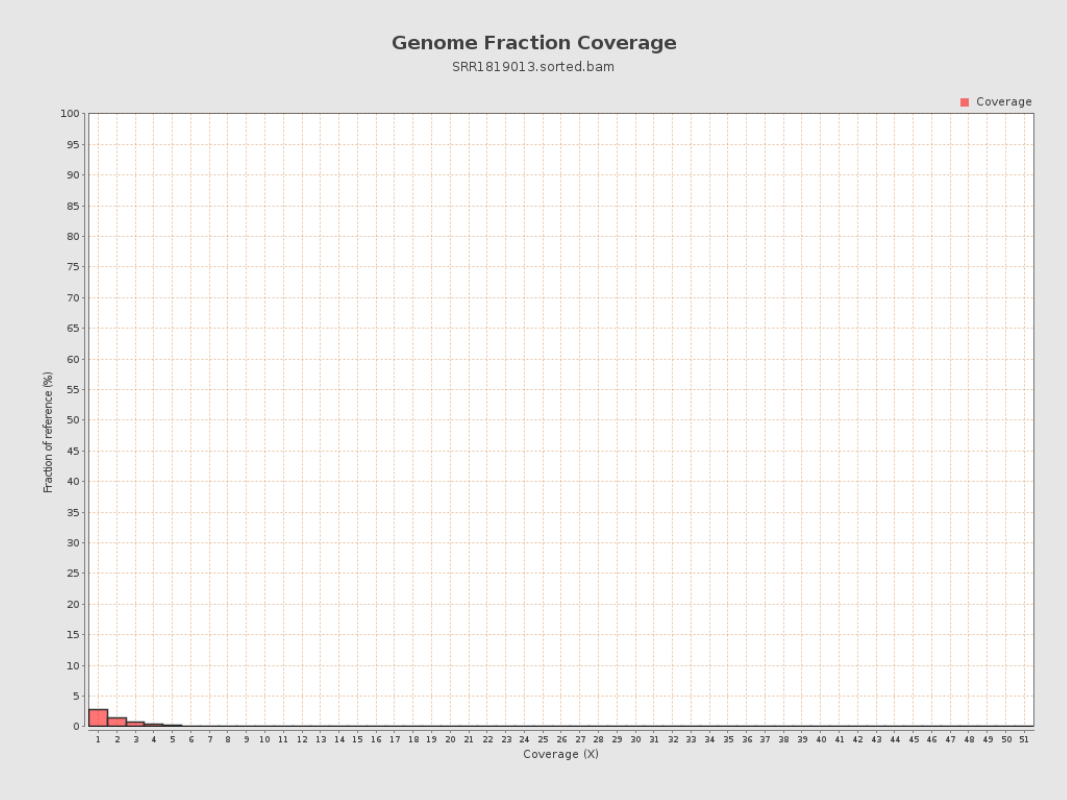
4. Results : Coverage Histogram



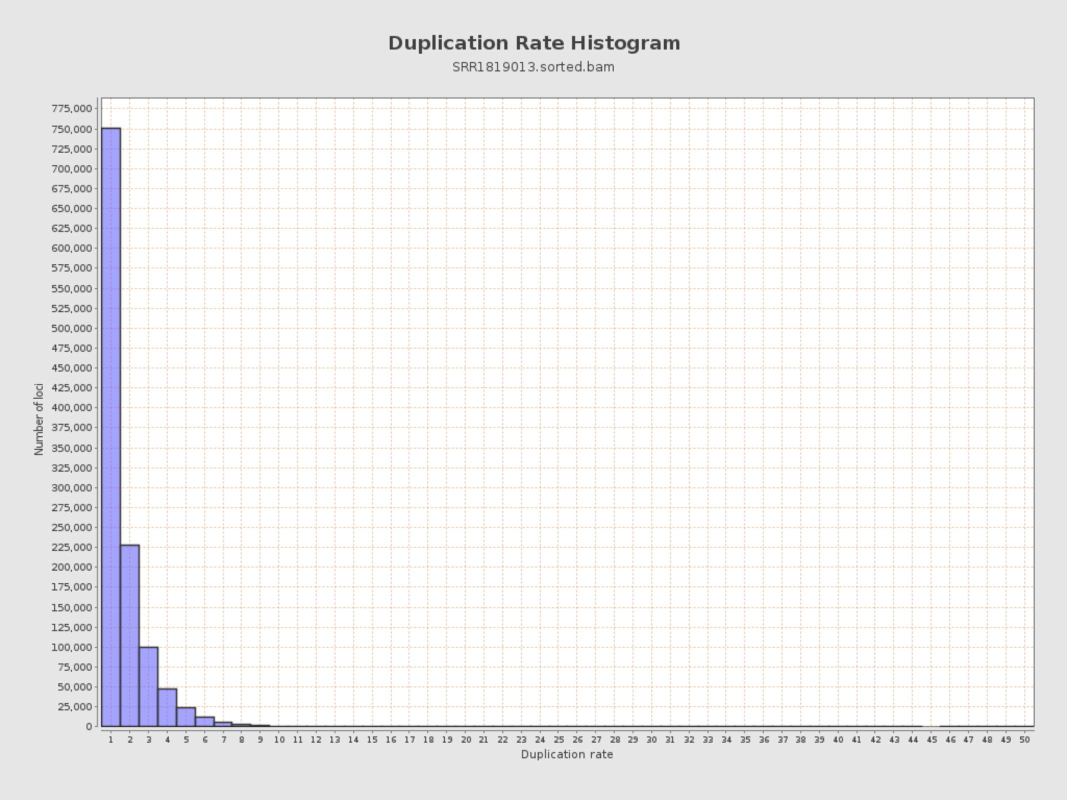
5. Results : Coverage Histogram (0-50X)



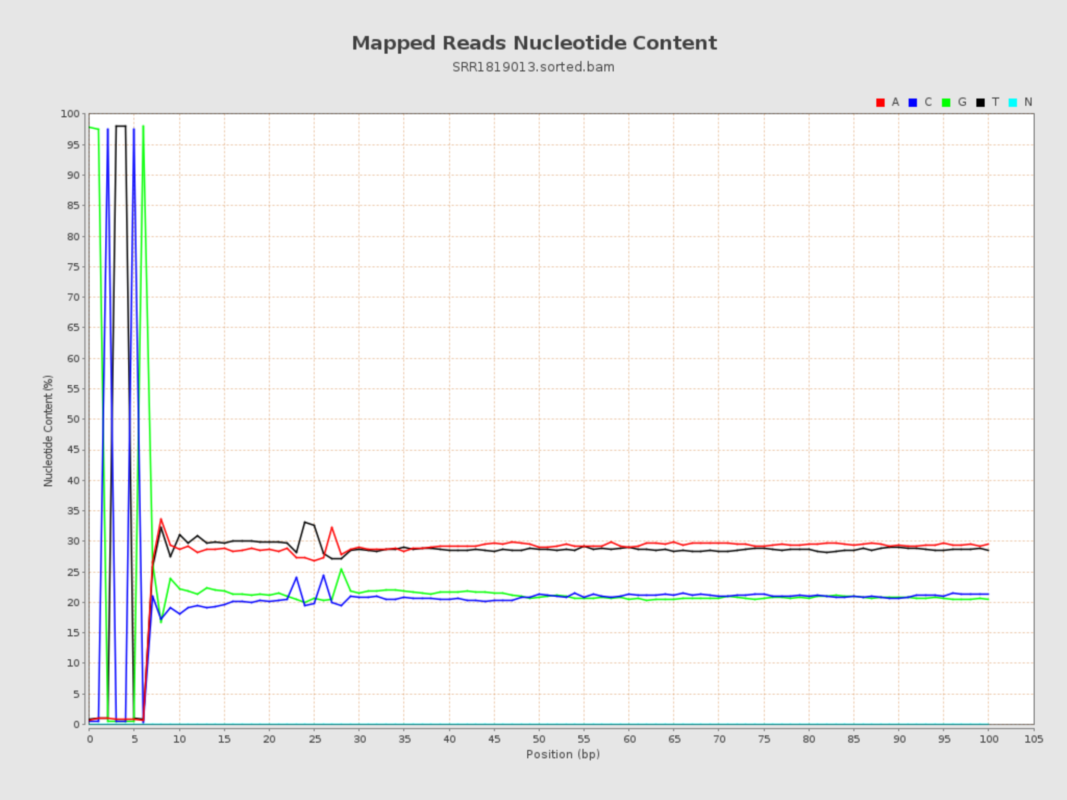
6. Results : Genome Fraction Coverage



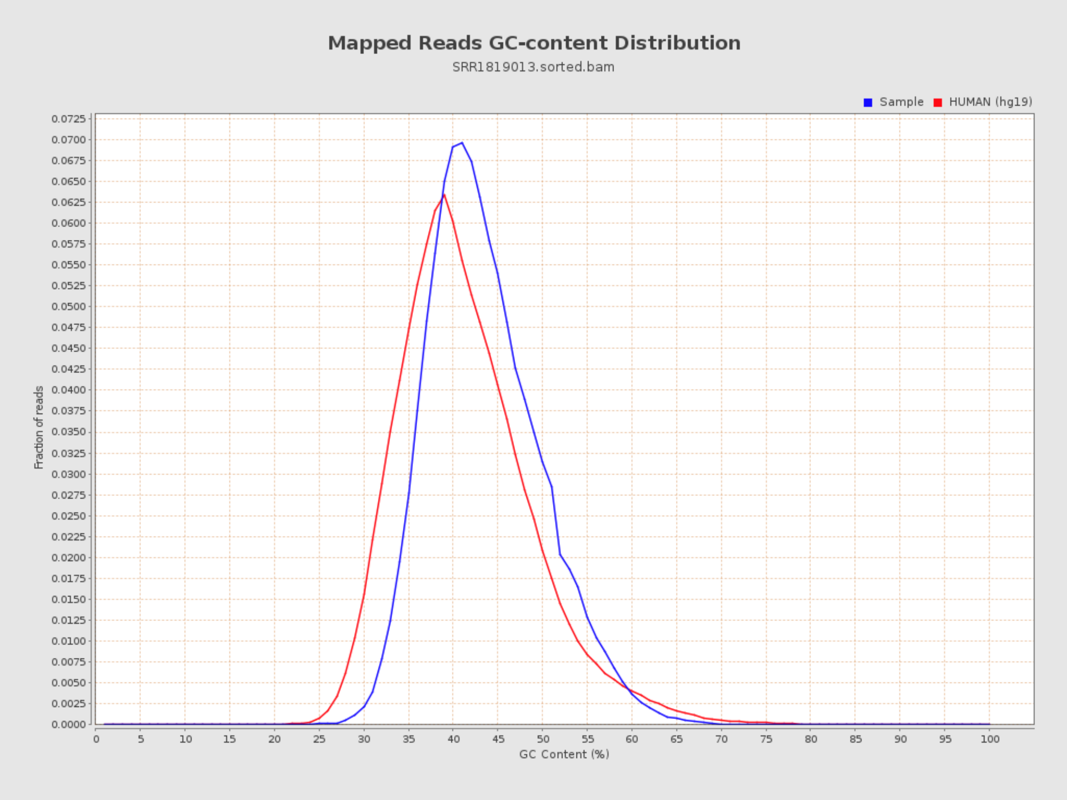
7. Results : Duplication Rate Histogram



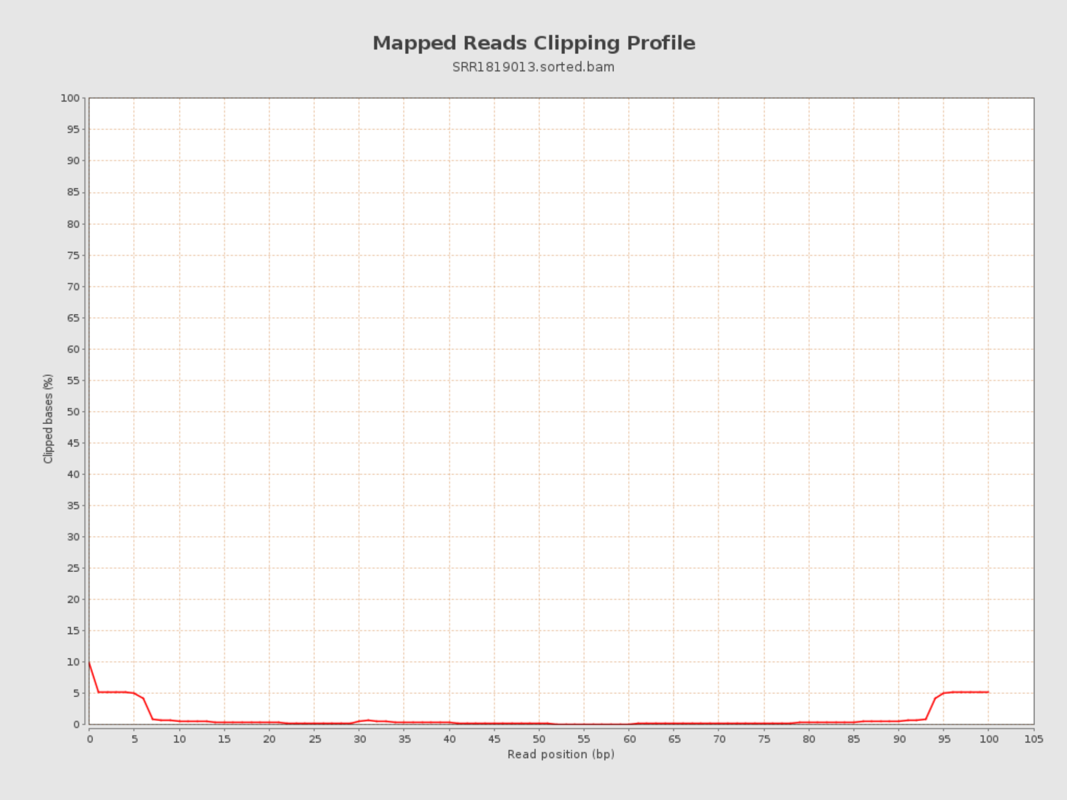
8. Results : Mapped Reads Nucleotide Content



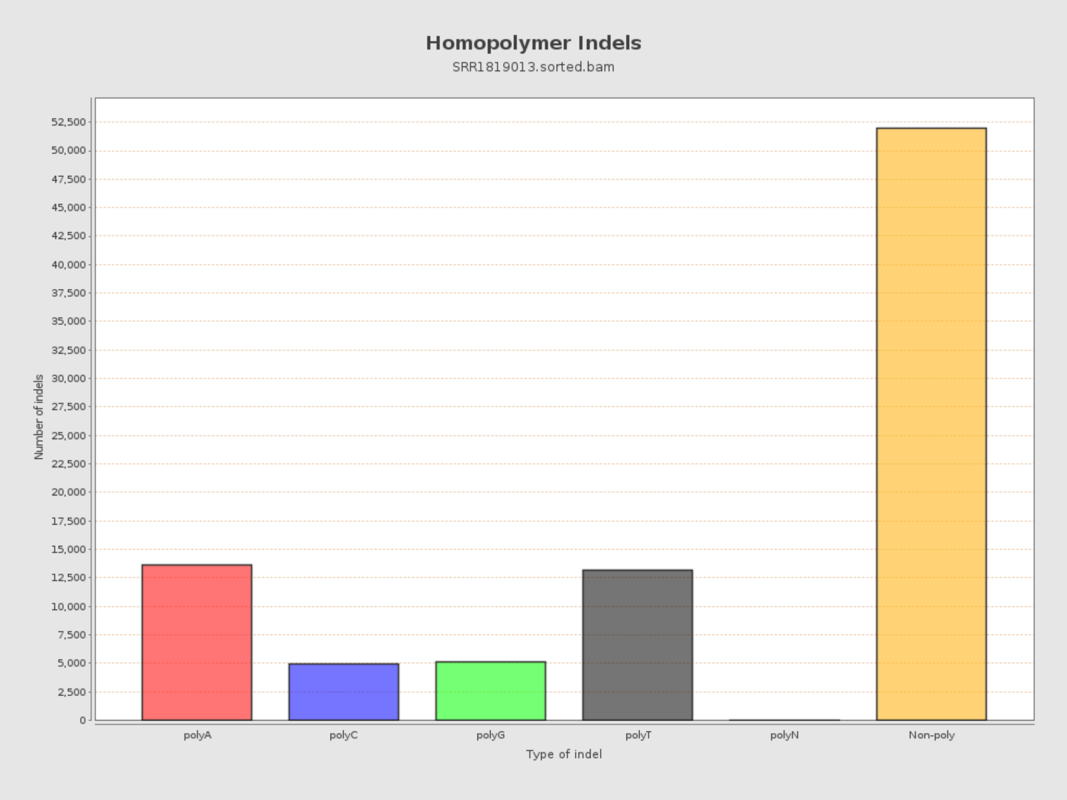
9. Results : Mapped Reads GC-content Distribution



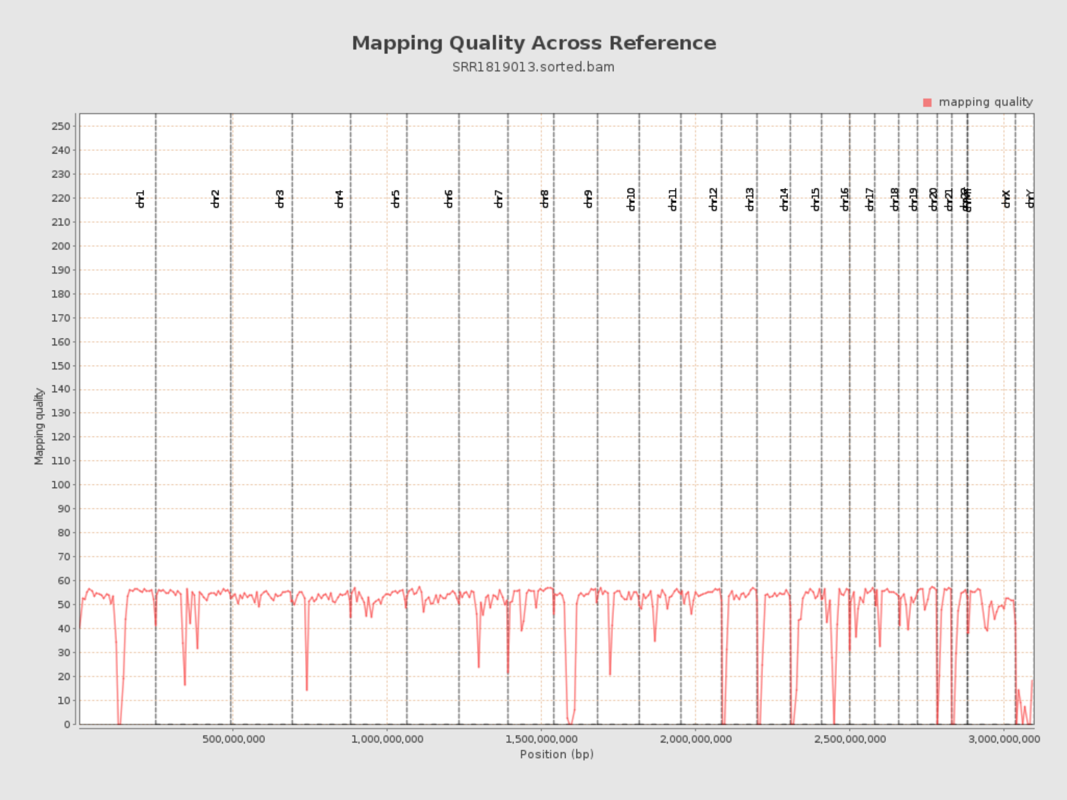
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram