Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:04:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818917.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_SRR1818917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:04:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,500,363
Mapped reads	2,408,446 / 96.32%
Unmapped reads	91,917 / 3.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,077 / 1.48%
Read min/max/mean length	30 / 101 / 101.57
Duplicated reads (estimated)	660,236 / 26.41%
Duplication rate	22.75%
Clipped reads	2,395,065 / 95.79%

2.2. ACGT Content

Number/percentage of A's	65,029,968 / 29.14%
Number/percentage of C's	44,217,094 / 19.81%
Number/percentage of T's	64,537,855 / 28.92%
Number/percentage of G's	49,400,403 / 22.13%
Number/percentage of N's	2,991 / 0%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0721

Standard Deviation	0.8979

2.4. Mapping Quality

Mean Mapping Quality	49.29

2.5. Mismatches and indels

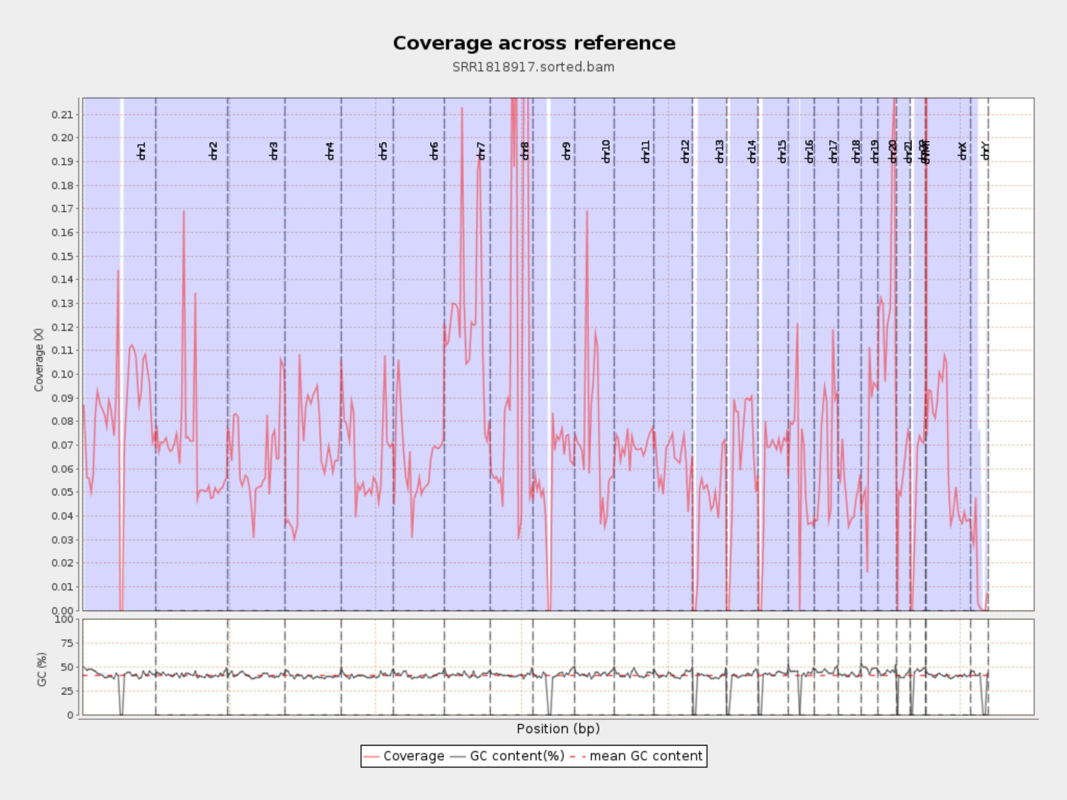
General error rate	0.67%
Mismatches	1,411,584
Insertions	36,229
Mapped reads with at least one insertion	1.46%
Deletions	74,276
Mapped reads with at least one deletion	3.01%
Homopolymer indels	40.87%

2.6. Chromosome stats

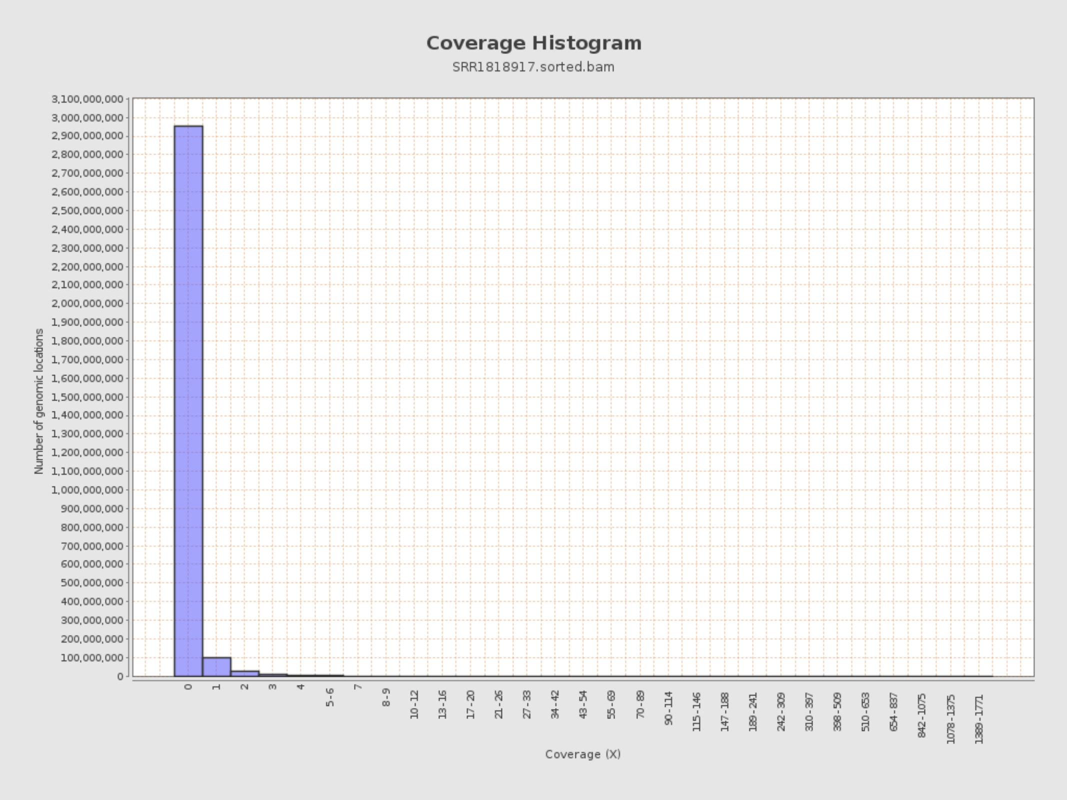
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20577888	0.0826	1.436
chr2	243199373	16484906	0.0678	1.328
chr3	198022430	12919395	0.0652	0.3698
chr4	191154276	12965952	0.0678	0.5249
chr5	180915260	11878132	0.0657	0.4
chr6	171115067	10768778	0.0629	0.4064
chr7	159138663	19750704	0.1241	1.995

chr8	146364022	19073290	0.1303	0.6708
chr9	141213431	7989461	0.0566	0.7582
chr10	135534747	9925220	0.0732	1.0967
chr11	135006516	9420719	0.0698	0.4953
chr12	133851895	8510509	0.0636	0.3763
chr13	115169878	5132125	0.0446	0.3002
chr14	107349540	7028873	0.0655	0.4126
chr15	102531392	5950527	0.058	0.3447
chr16	90354753	5441424	0.0602	0.887
chr17	81195210	5629991	0.0693	0.5314
chr18	78077248	3908209	0.0501	0.843
chr19	59128983	4251659	0.0719	1.1867
chr20	63025520	8962733	0.1422	0.607
chr21	48129895	2702718	0.0562	0.4306
chr22	51304566	2598070	0.0506	0.3585
chrMT	16571	289161	17.4498	10.9215
chrX	155270560	10322906	0.0665	0.473
chrY	59373566	849888	0.0143	1.0418

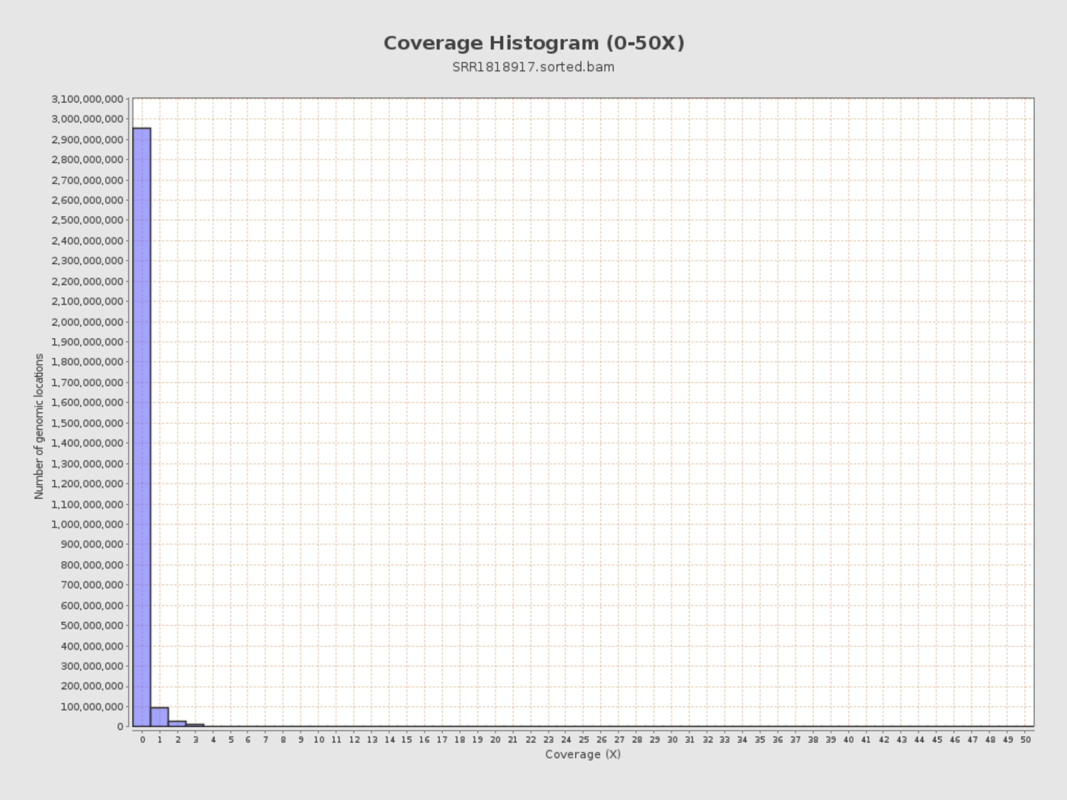
3. Results : Coverage across reference



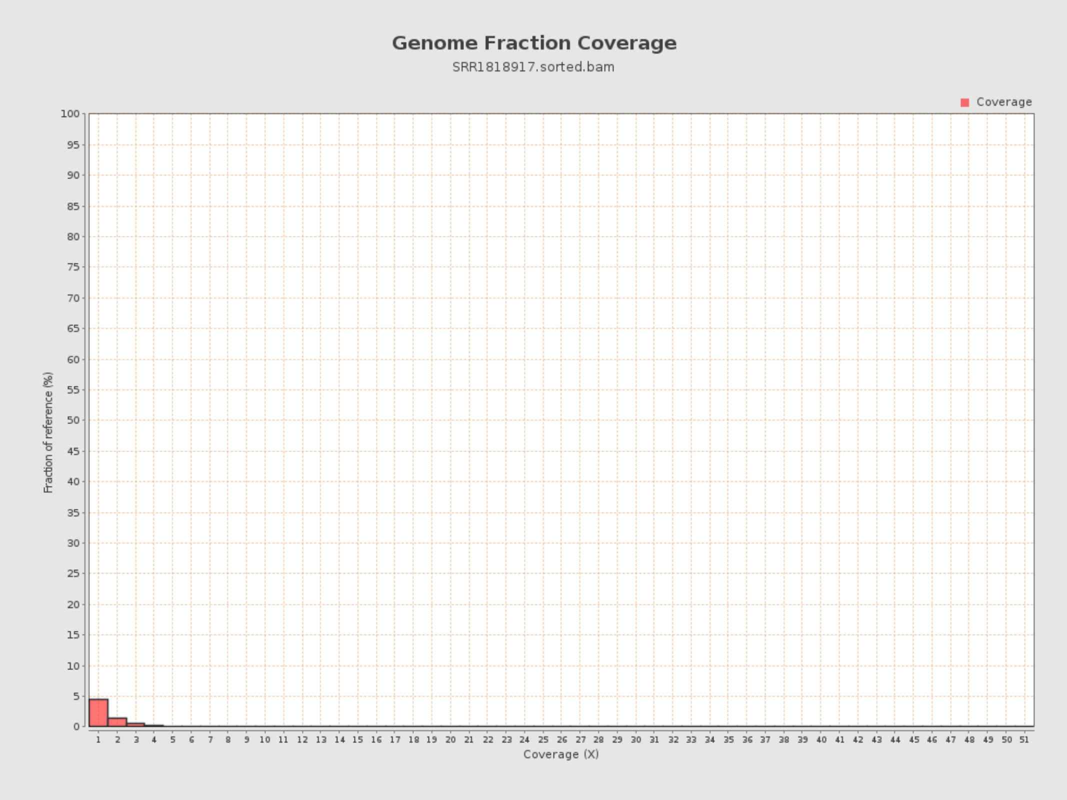
4. Results : Coverage Histogram



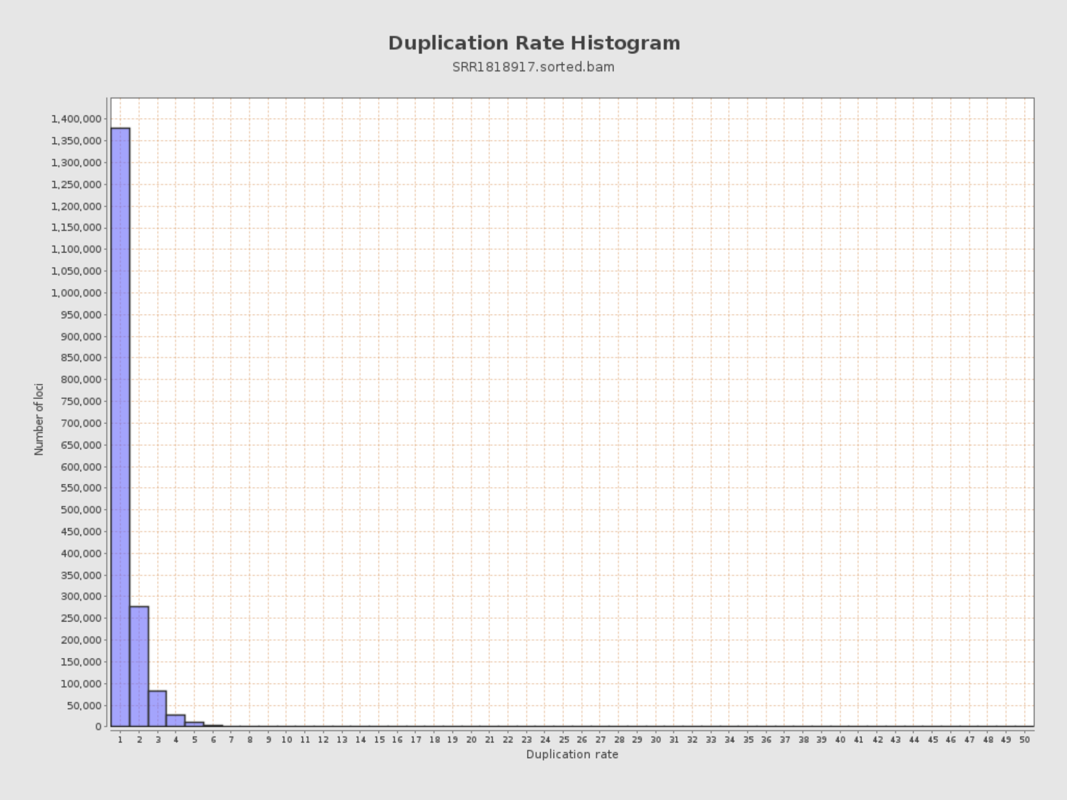
5. Results : Coverage Histogram (0-50X)



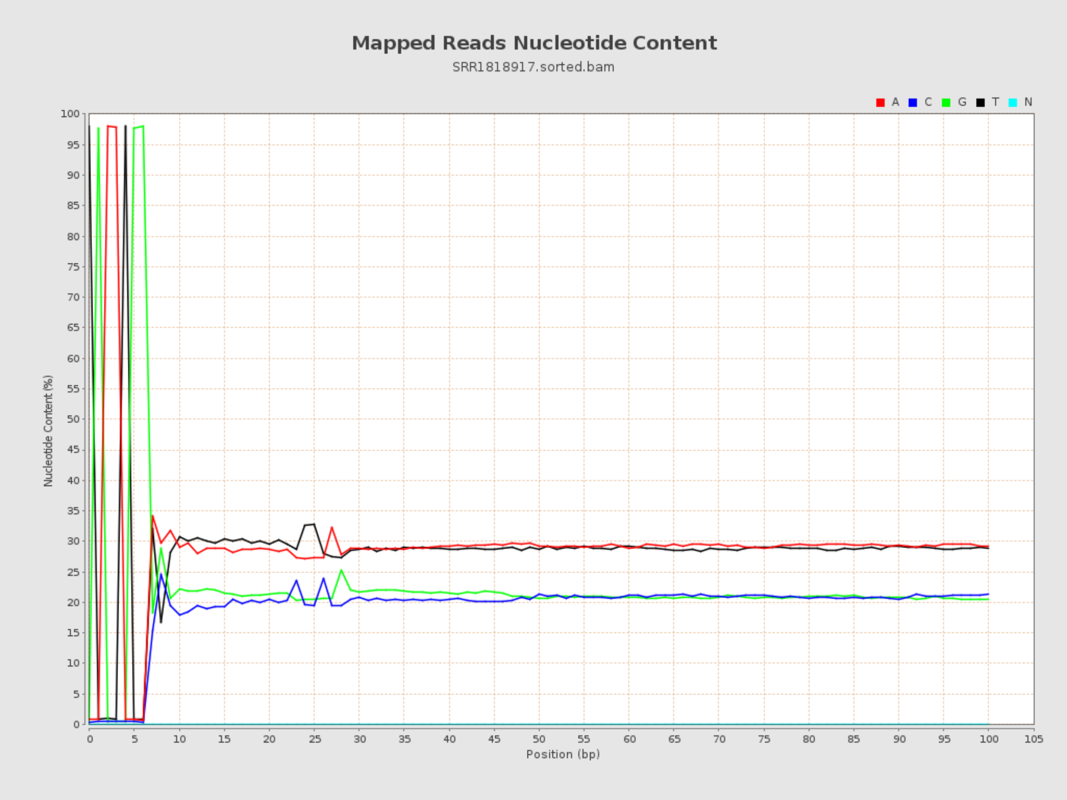
6. Results : Genome Fraction Coverage



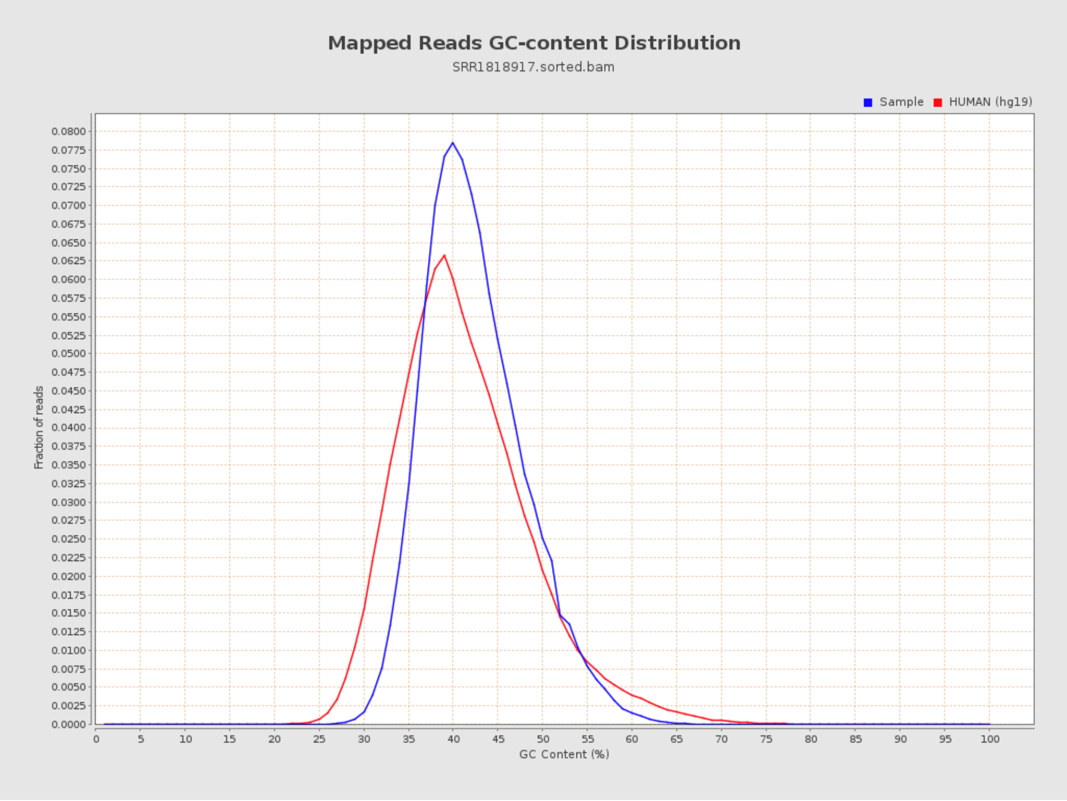
7. Results : Duplication Rate Histogram



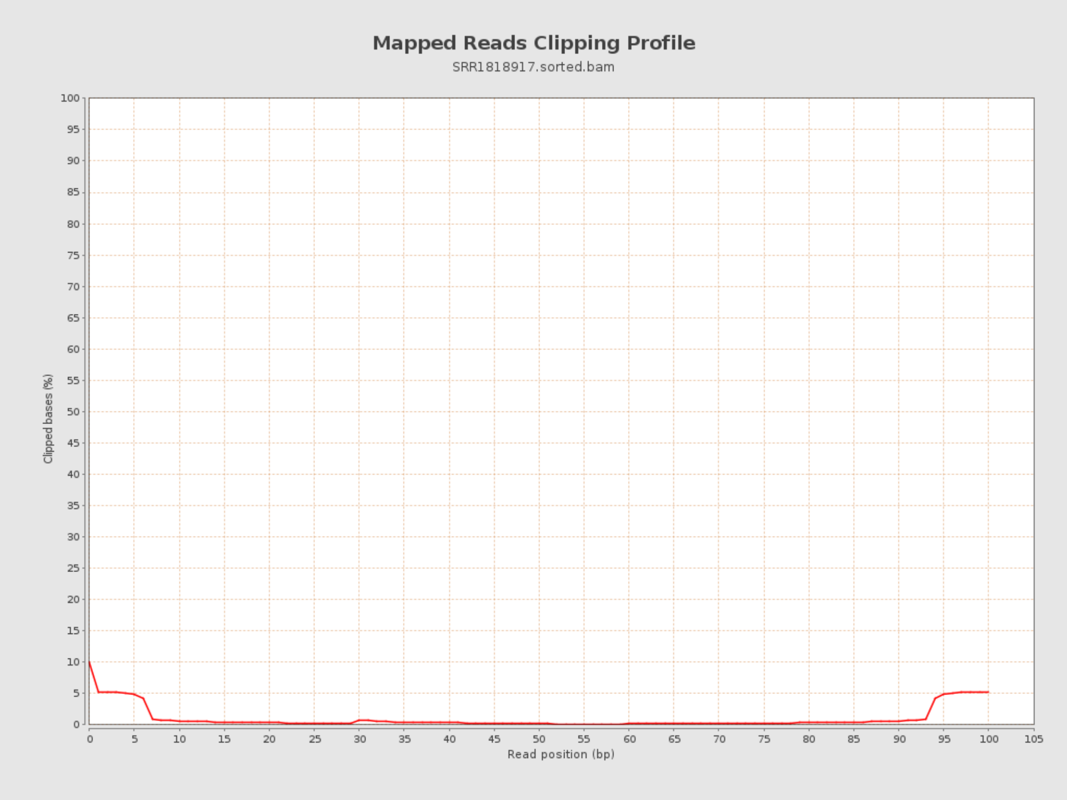
8. Results : Mapped Reads Nucleotide Content



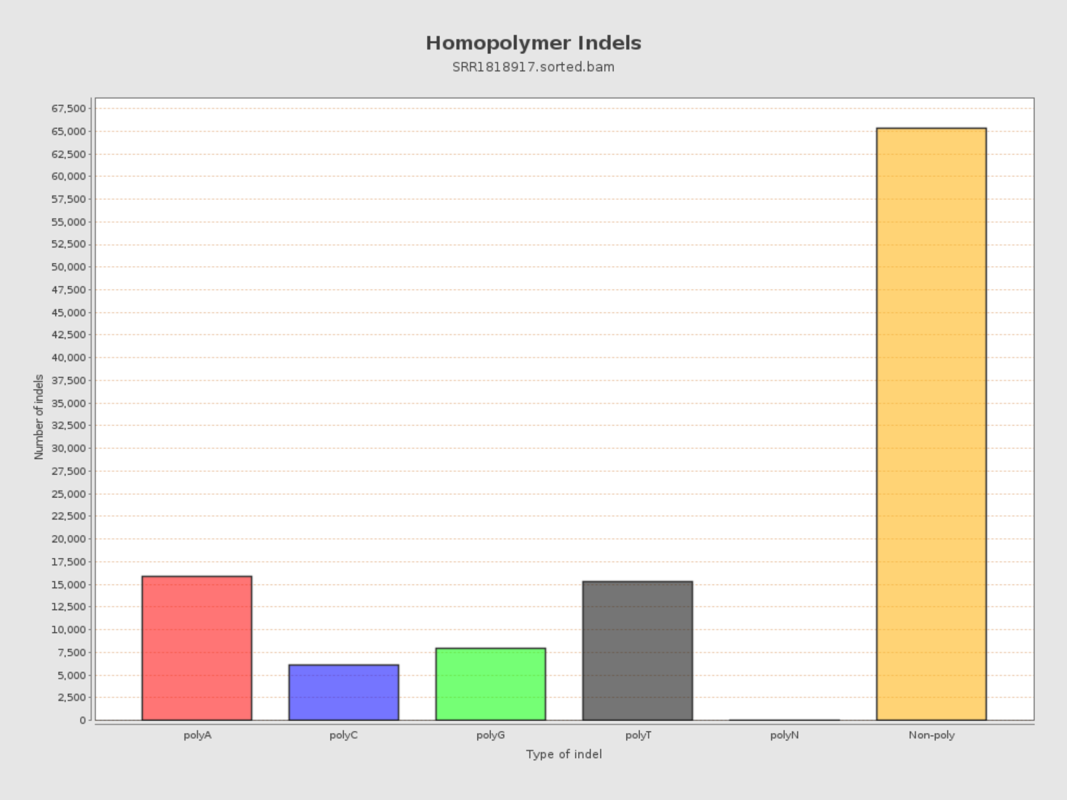
9. Results : Mapped Reads GC-content Distribution



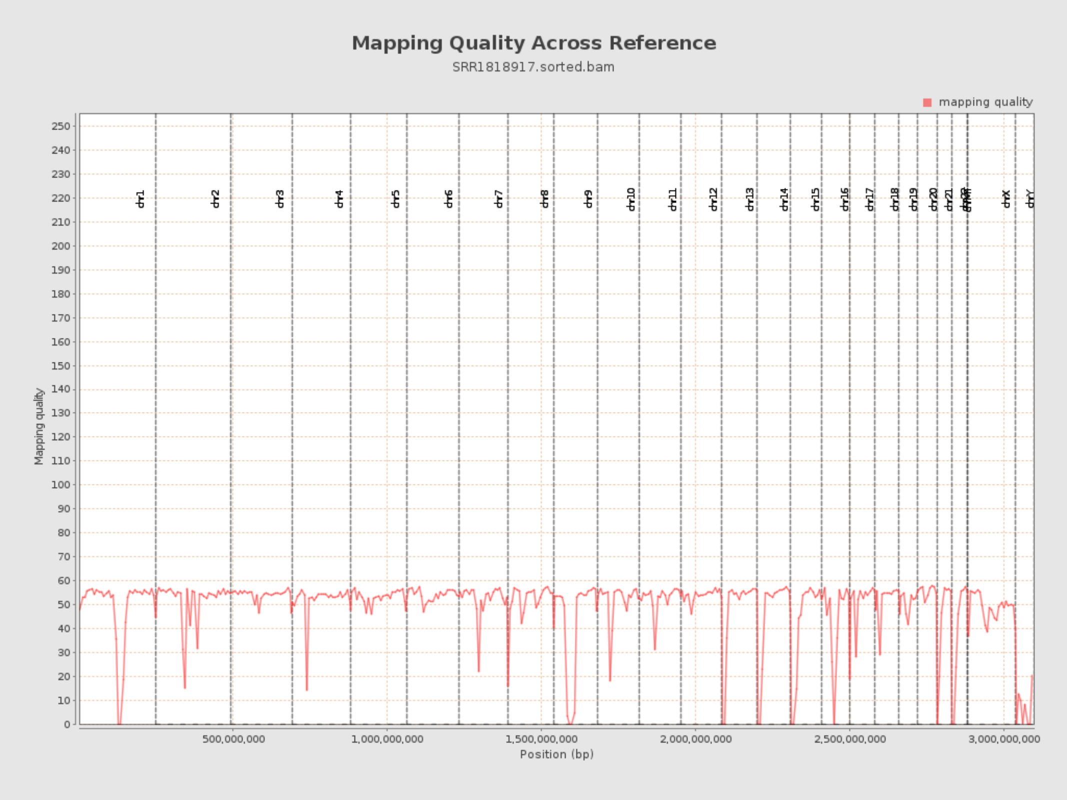
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram