Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:55:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818929.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_SRR1818929 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818929.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:55:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818929.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,990,213
Mapped reads	2,951,426 / 98.7%
Unmapped reads	38,787 / 1.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,079 / 1.34%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	1,598,518 / 53.46%
Duplication rate	45.06%
Clipped reads	2,963,092 / 99.09%

2.2. ACGT Content

Number/percentage of A's	78,914,725 / 28.86%
Number/percentage of C's	56,794,174 / 20.77%
Number/percentage of T's	79,250,959 / 28.98%
Number/percentage of G's	58,460,314 / 21.38%
Number/percentage of N's	11,595 / 0%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0884

Standard Deviation	0.9158

2.4. Mapping Quality

Mean Mapping Quality	49.23

2.5. Mismatches and indels

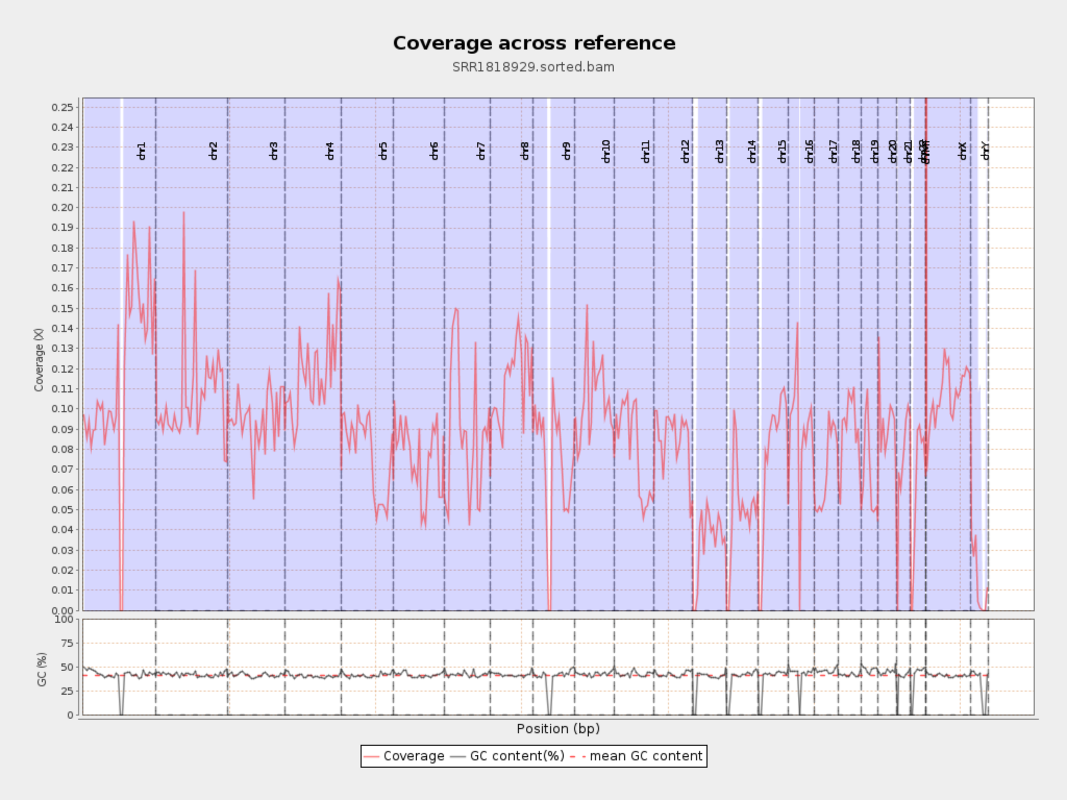
General error rate	0.65%
Mismatches	1,686,449
Insertions	36,709
Mapped reads with at least one insertion	1.21%
Deletions	84,645
Mapped reads with at least one deletion	2.81%
Homopolymer indels	43.21%

2.6. Chromosome stats

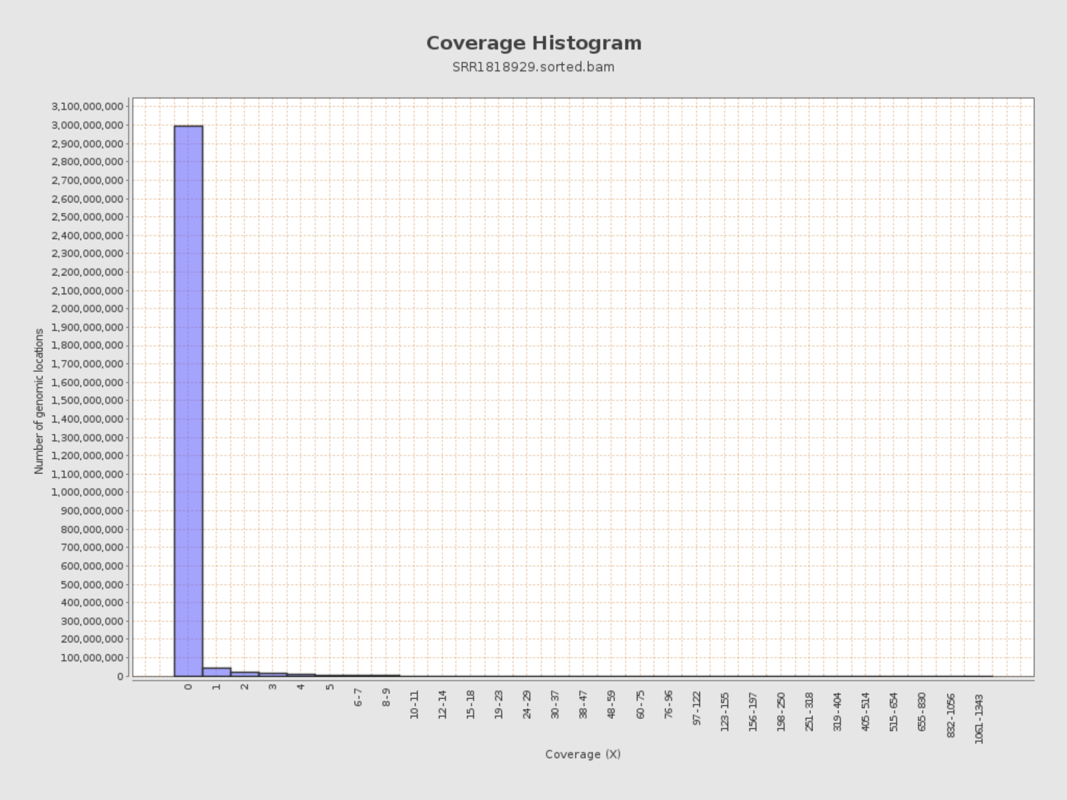
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29025598	0.1165	1.3601
chr2	243199373	25919114	0.1066	1.3831
chr3	198022430	18834122	0.0951	0.6648
chr4	191154276	22703600	0.1188	0.7893
chr5	180915260	14101920	0.0779	0.6183
chr6	171115067	13067854	0.0764	0.6308
chr7	159138663	14095997	0.0886	0.8164

chr8	146364022	16655717	0.1138	0.8352
chr9	141213431	10207265	0.0723	1.0226
chr10	135534747	14124227	0.1042	1.0729
chr11	135006516	10687863	0.0792	0.6976
chr12	133851895	11552871	0.0863	0.64
chr13	115169878	3960213	0.0344	0.3925
chr14	107349540	5335679	0.0497	0.5366
chr15	102531392	7795490	0.076	0.5944
chr16	90354753	7777716	0.0861	1.0192
chr17	81195210	5711052	0.0703	0.6399
chr18	78077248	6975051	0.0893	1.2477
chr19	59128983	4077105	0.069	1.147
chr20	63025520	5916806	0.0939	0.7004
chr21	48129895	3612103	0.075	0.6592
chr22	51304566	3095970	0.0603	0.5517
chrMT	16571	906446	54.7007	35.248
chrX	155270560	16625016	0.1071	0.8417
chrY	59373566	822040	0.0138	0.7497

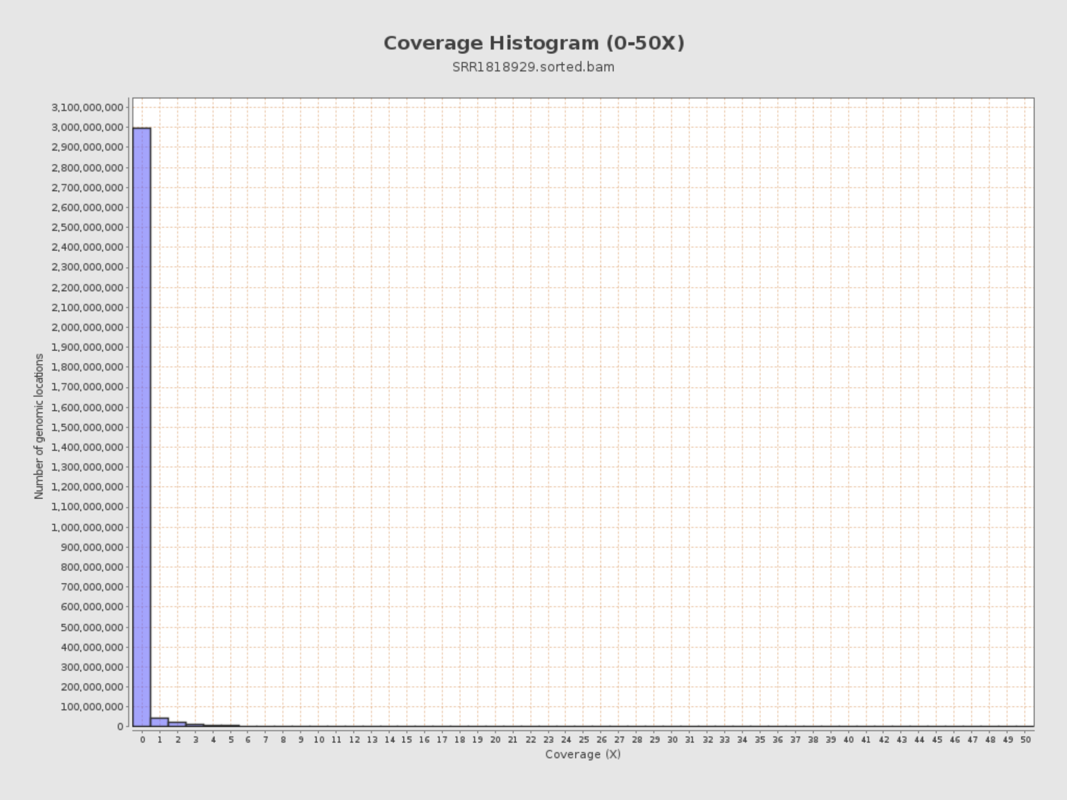
3. Results : Coverage across reference



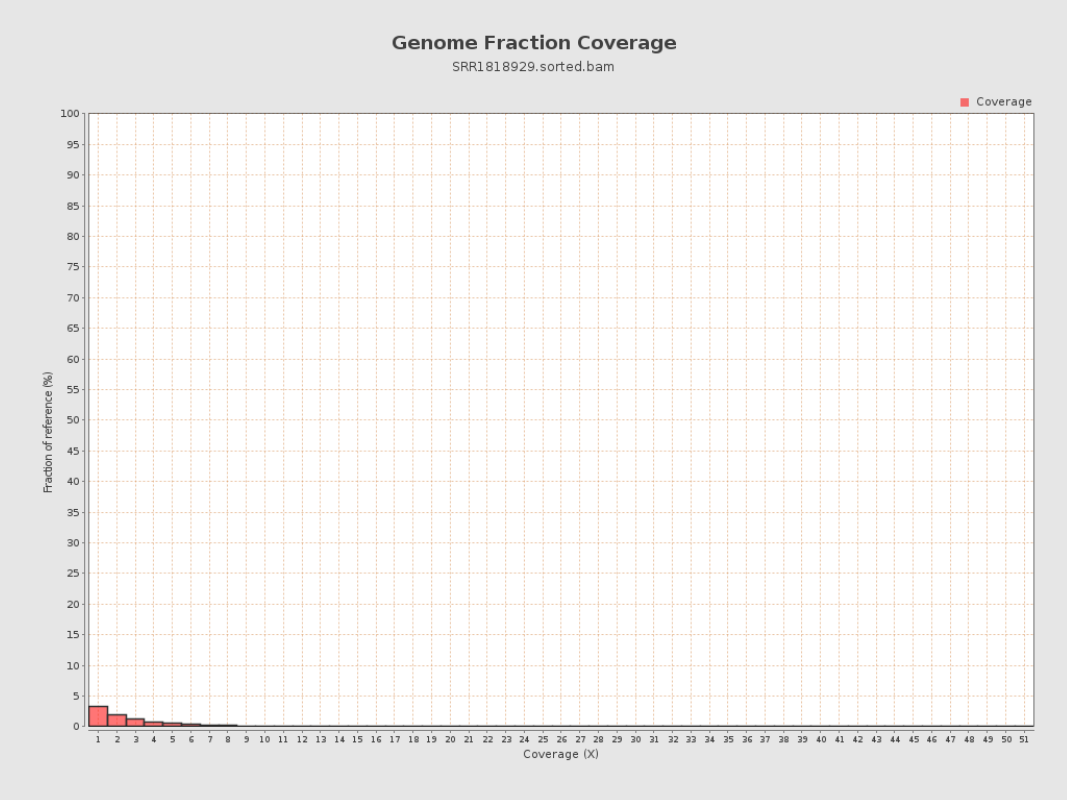
4. Results : Coverage Histogram



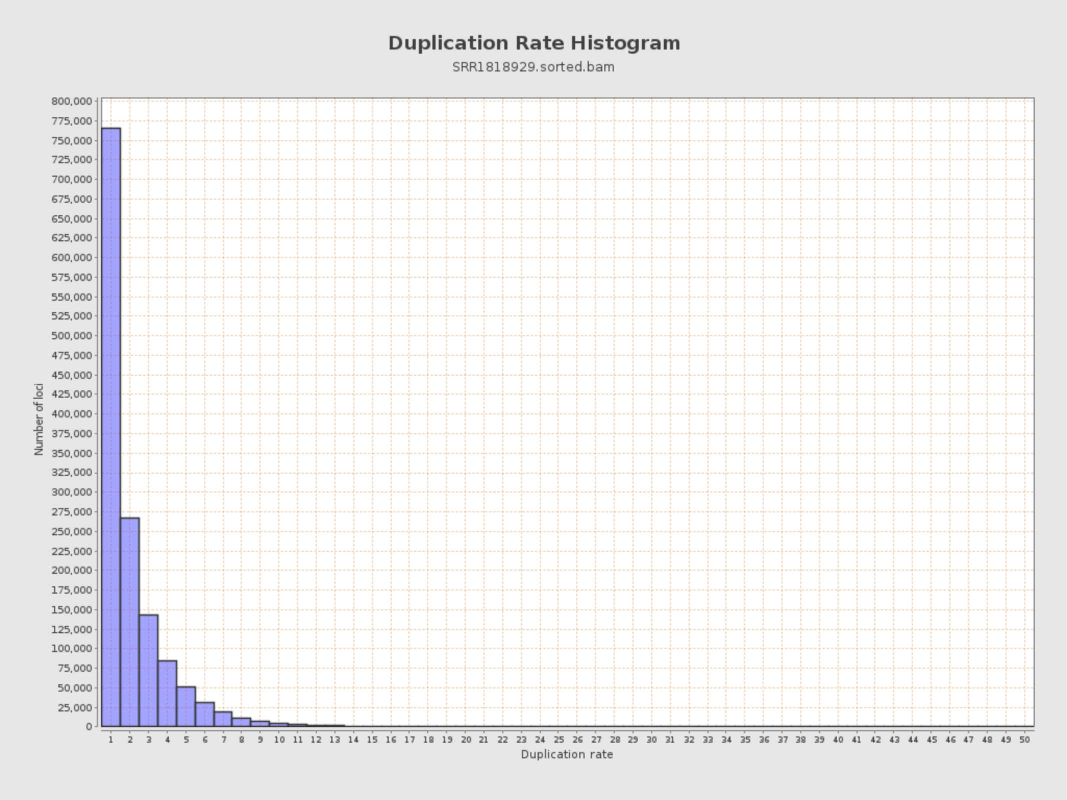
5. Results : Coverage Histogram (0-50X)



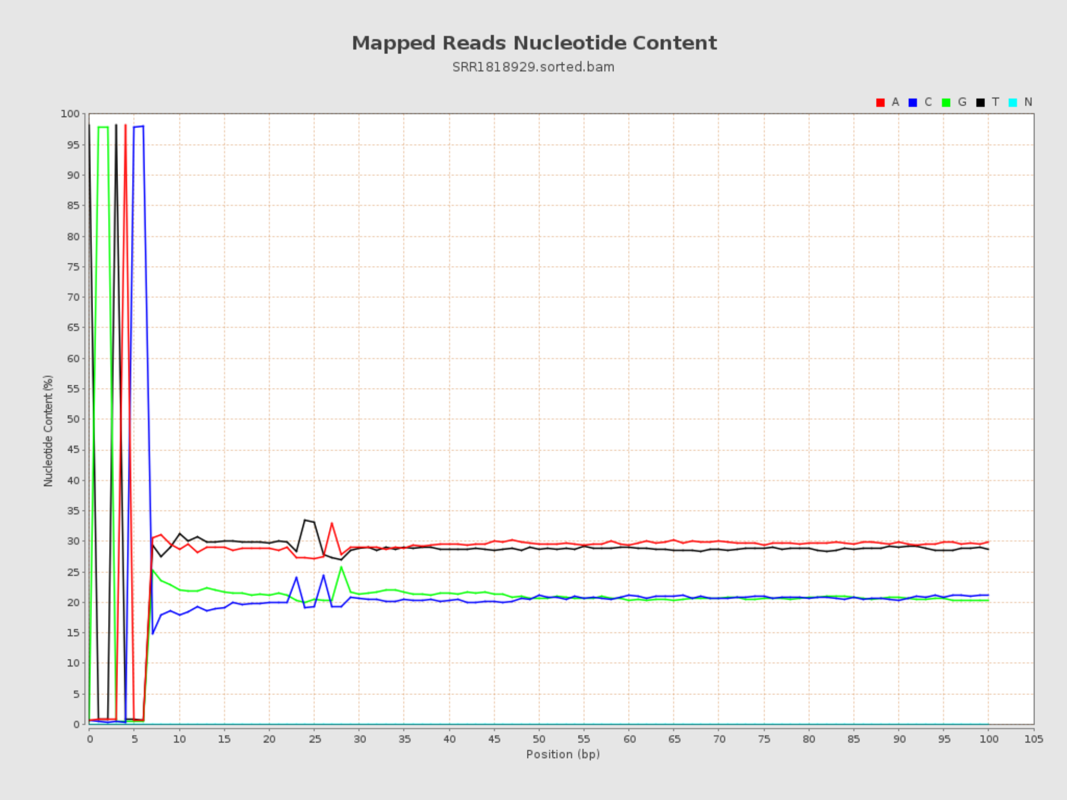
6. Results : Genome Fraction Coverage



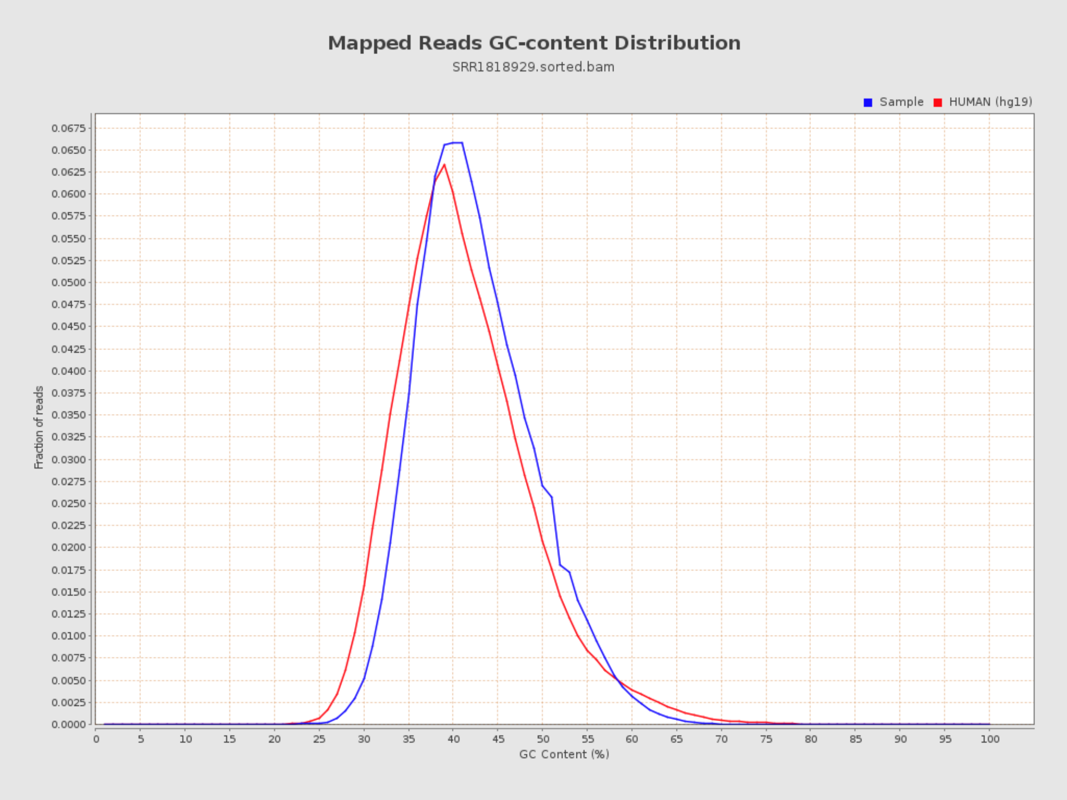
7. Results : Duplication Rate Histogram



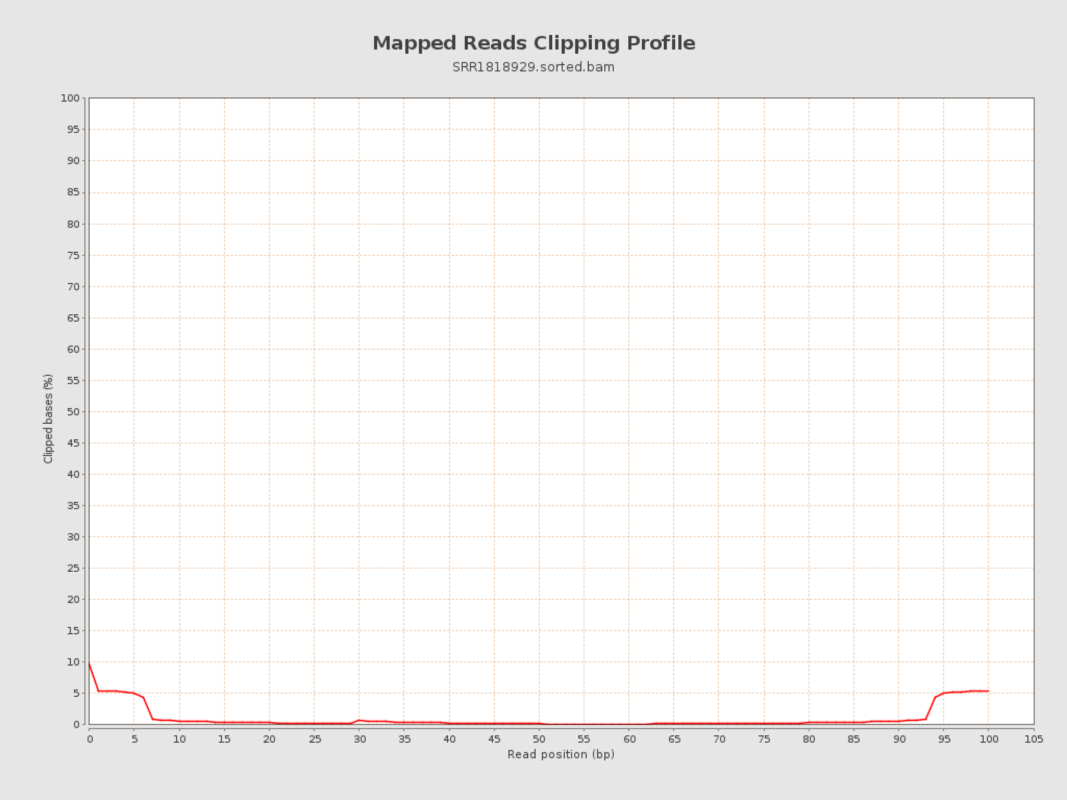
8. Results : Mapped Reads Nucleotide Content



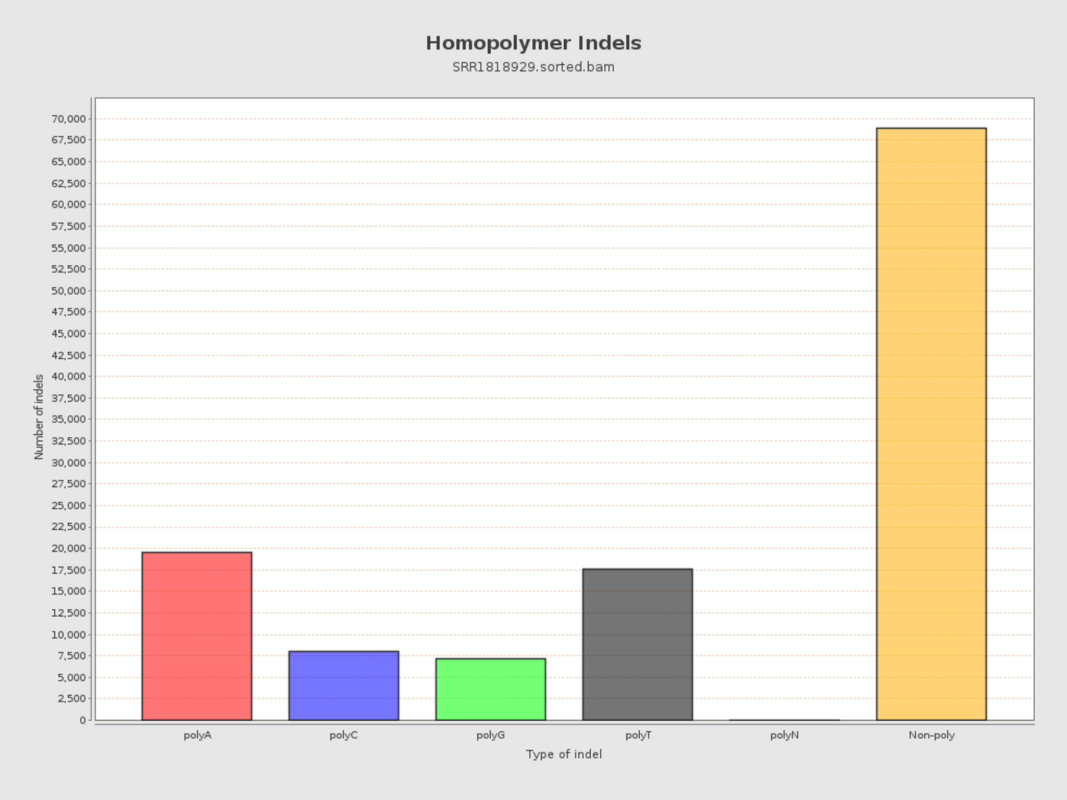
9. Results : Mapped Reads GC-content Distribution



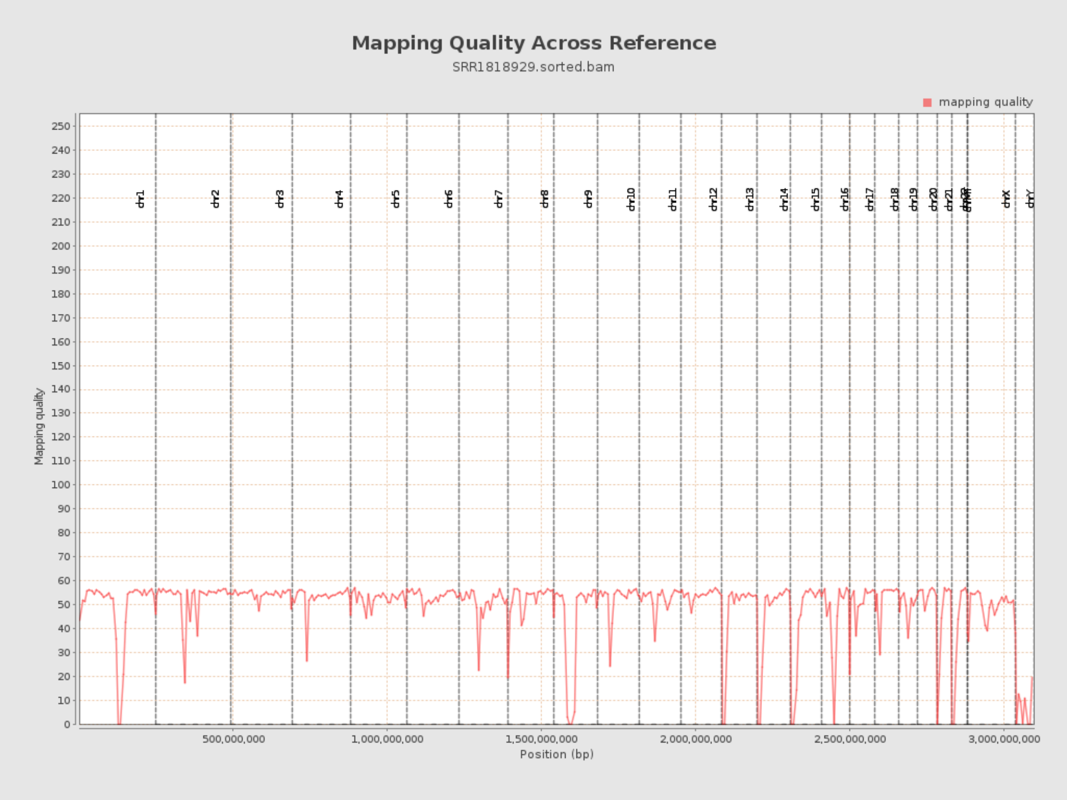
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram