Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:57:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818916.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_SRR1818916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818916.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:57:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,298,204
Mapped reads	3,232,620 / 98.01%
Unmapped reads	65,584 / 1.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,324 / 1.37%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	992,735 / 30.1%
Duplication rate	25.68%
Clipped reads	3,266,681 / 99.04%

2.2. ACGT Content

Number/percentage of A's	84,894,843 / 28.37%
Number/percentage of C's	65,958,265 / 22.05%
Number/percentage of T's	85,714,451 / 28.65%
Number/percentage of G's	62,618,741 / 20.93%
Number/percentage of N's	4,152 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0967

Standard Deviation	1.1692

2.4. Mapping Quality

Mean Mapping Quality	49.28

2.5. Mismatches and indels

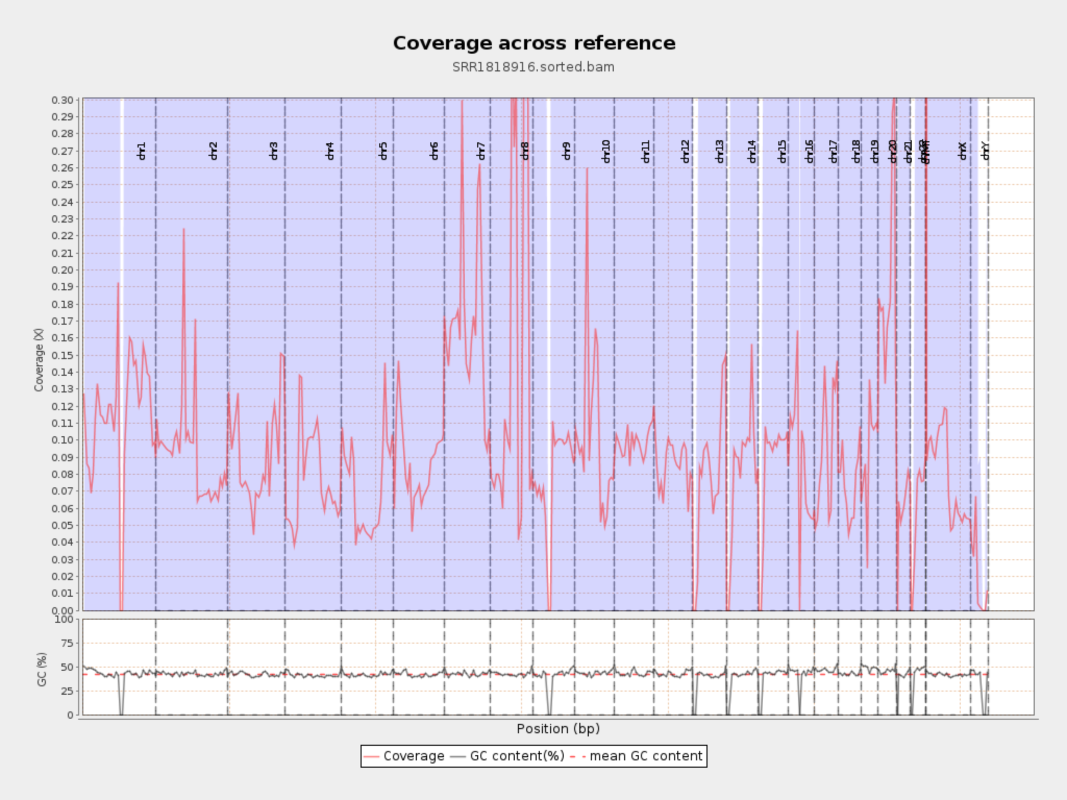
General error rate	0.64%
Mismatches	1,820,550
Insertions	40,830
Mapped reads with at least one insertion	1.22%
Deletions	94,966
Mapped reads with at least one deletion	2.87%
Homopolymer indels	42.13%

2.6. Chromosome stats

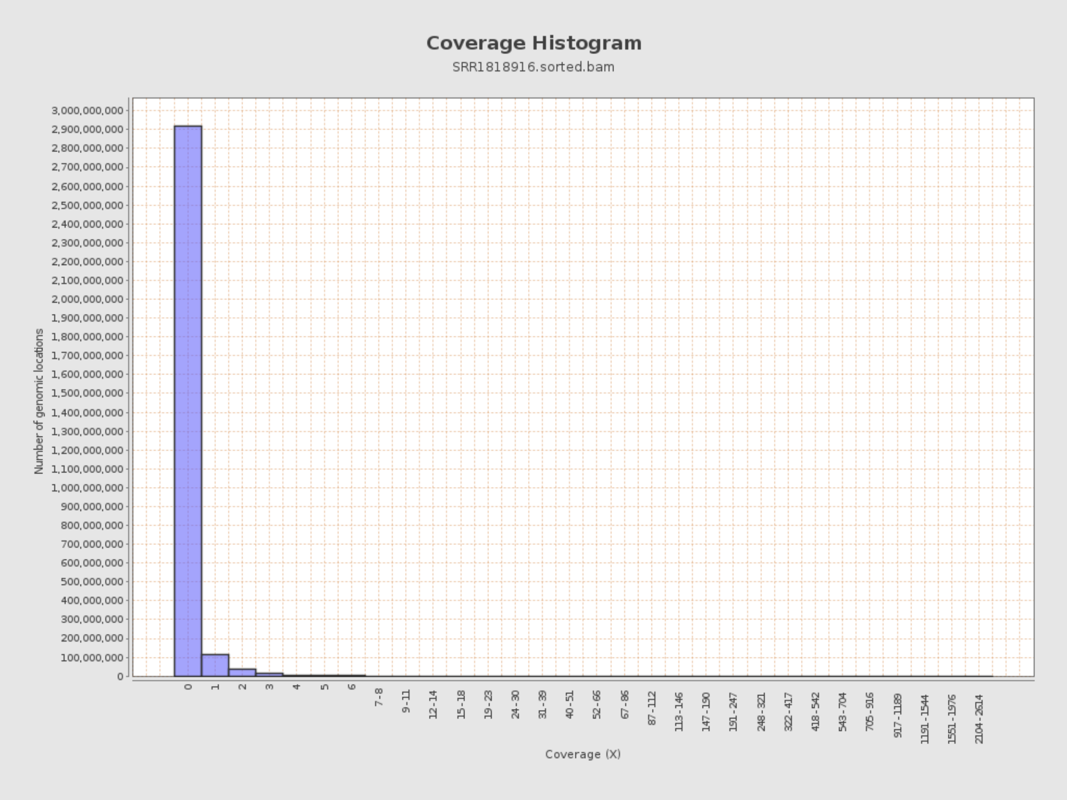
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28522550	0.1144	1.9009
chr2	243199373	22629771	0.0931	1.5541
chr3	198022430	18333120	0.0926	0.4678
chr4	191154276	14859638	0.0777	0.6355
chr5	180915260	13158544	0.0727	0.4422
chr6	171115067	14699257	0.0859	0.5146
chr7	159138663	26807288	0.1685	2.6787

chr8	146364022	25908661	0.177	0.917
chr9	141213431	11019960	0.078	0.9734
chr10	135534747	14003337	0.1033	1.5848
chr11	135006516	13255600	0.0982	0.6693
chr12	133851895	11556443	0.0863	0.4554
chr13	115169878	9054484	0.0786	0.4255
chr14	107349540	8809991	0.0821	0.4982
chr15	102531392	8334060	0.0813	0.4374
chr16	90354753	7654842	0.0847	1.0814
chr17	81195210	7538892	0.0928	0.6883
chr18	78077248	5784716	0.0741	1.1884
chr19	59128983	5417364	0.0916	1.7011
chr20	63025520	12609545	0.2001	0.7791
chr21	48129895	2923581	0.0607	0.5181
chr22	51304566	2813789	0.0548	0.413
chrMT	16571	350983	21.1806	13.7552
chrX	155270560	12220329	0.0787	0.576
chrY	59373566	1109098	0.0187	1.282

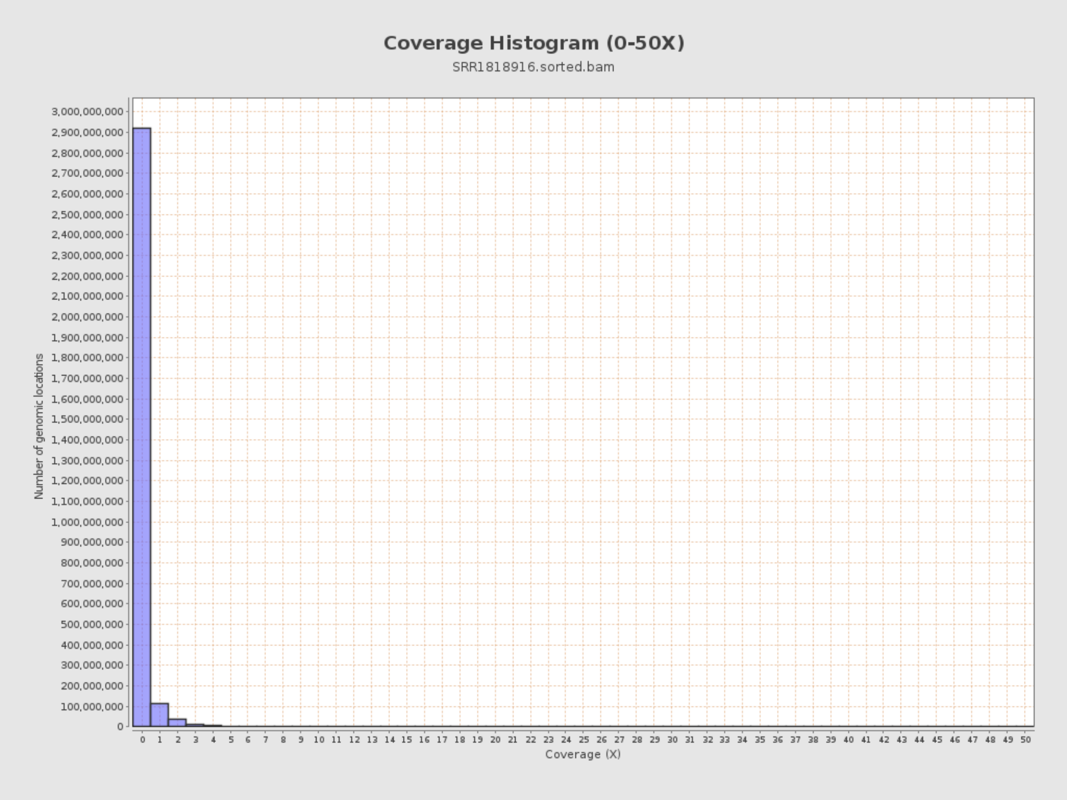
3. Results : Coverage across reference



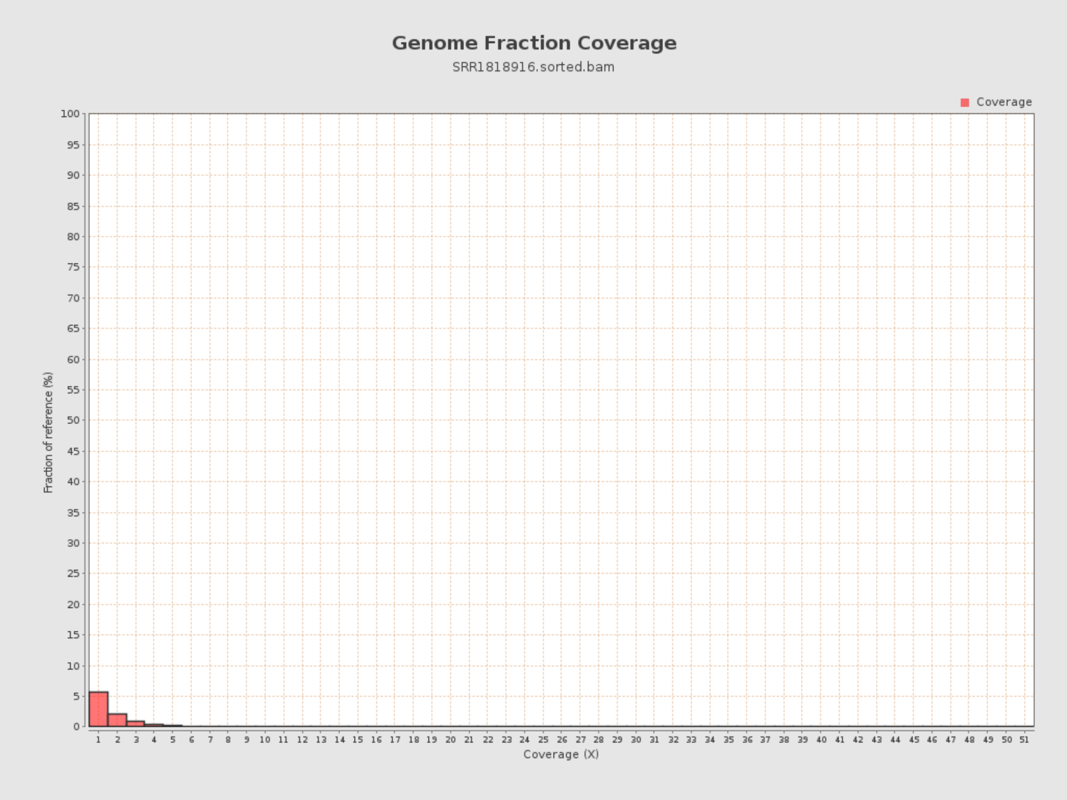
4. Results : Coverage Histogram



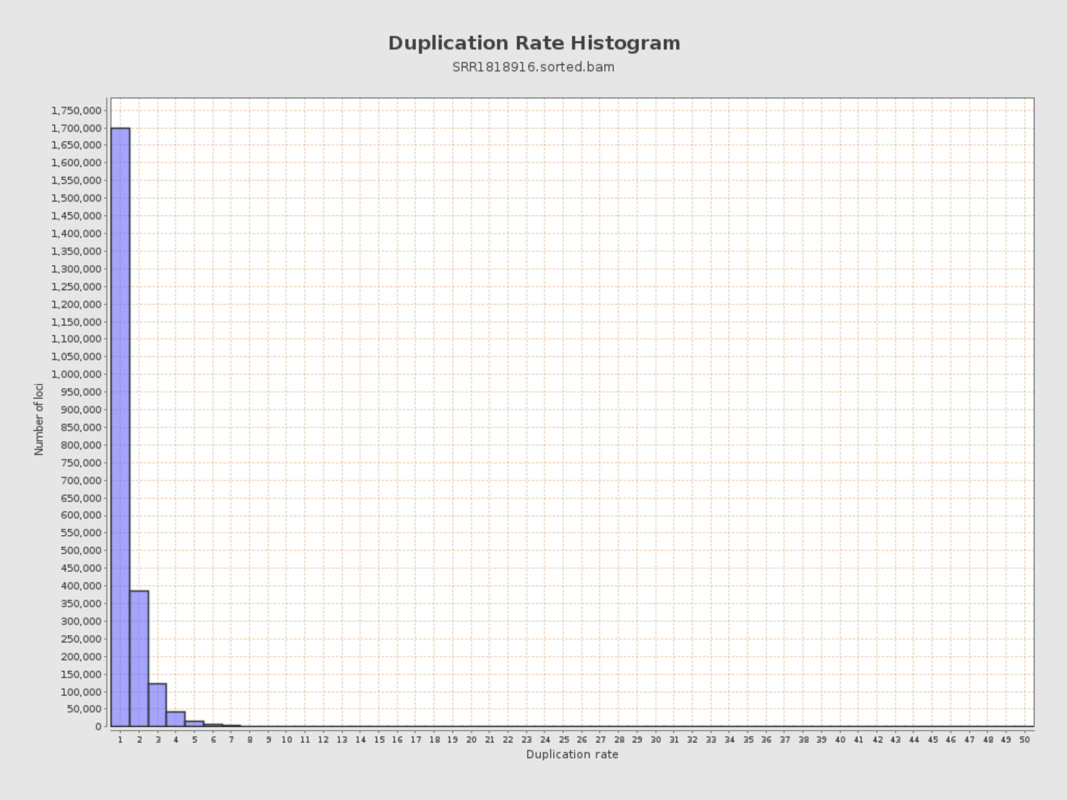
5. Results : Coverage Histogram (0-50X)



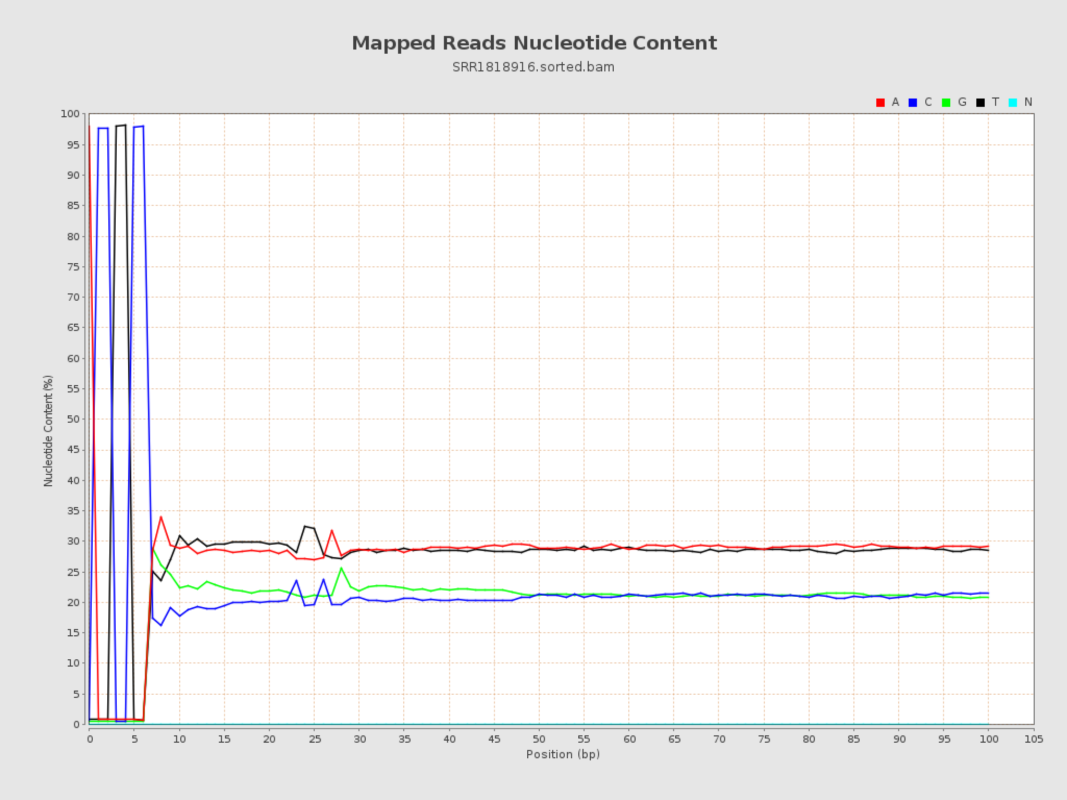
6. Results : Genome Fraction Coverage



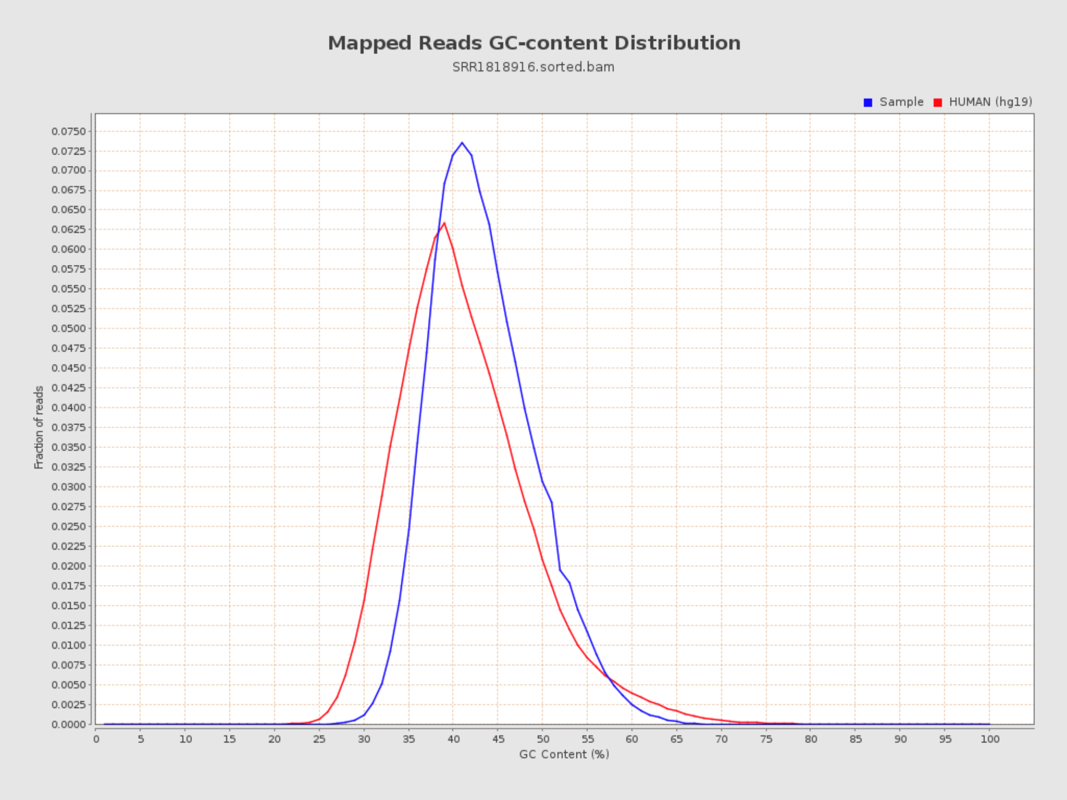
7. Results : Duplication Rate Histogram



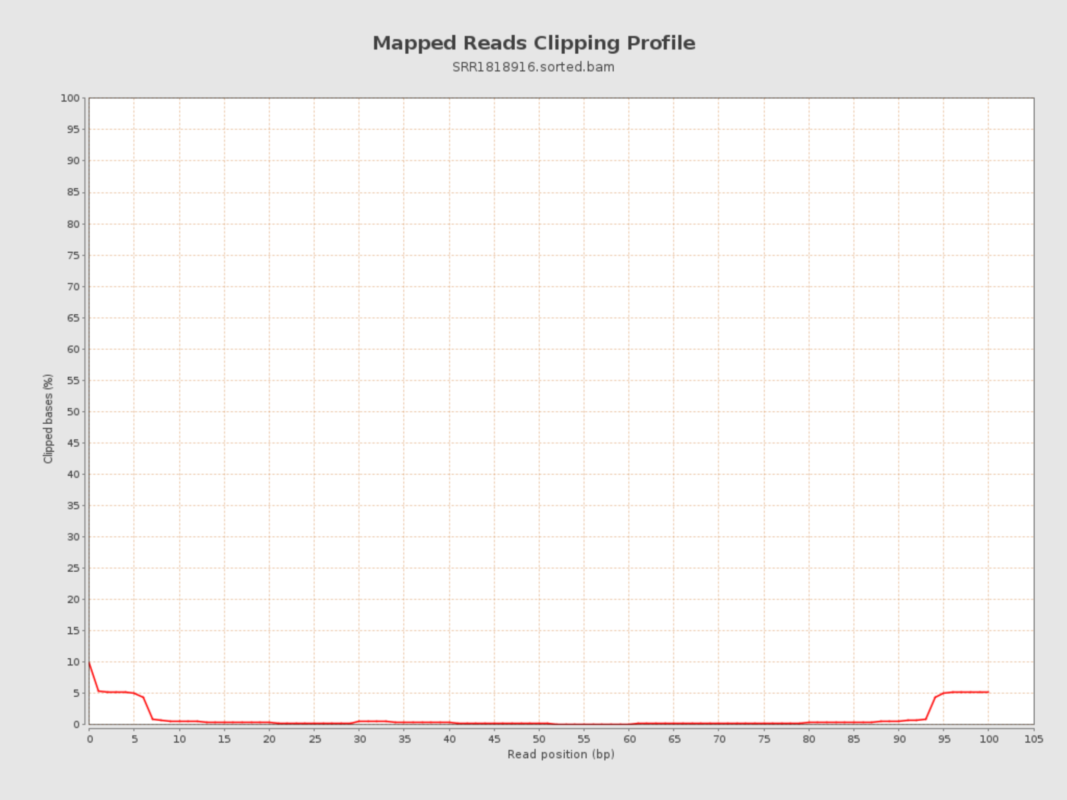
8. Results : Mapped Reads Nucleotide Content



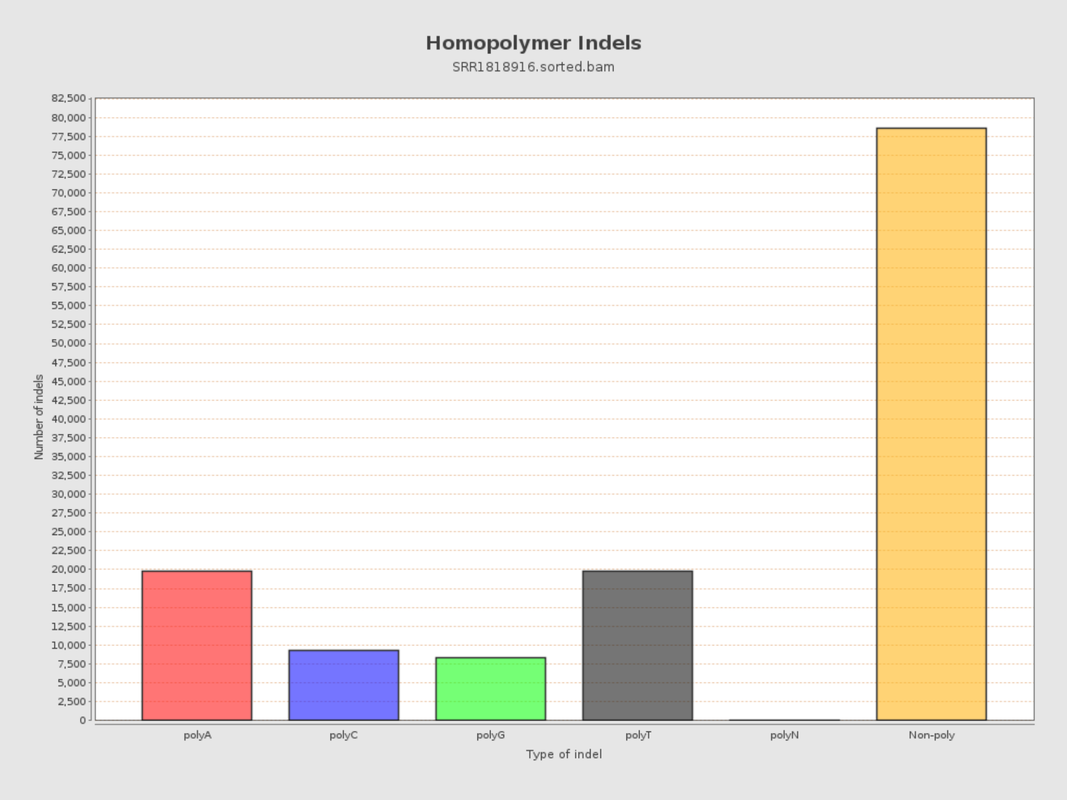
9. Results : Mapped Reads GC-content Distribution



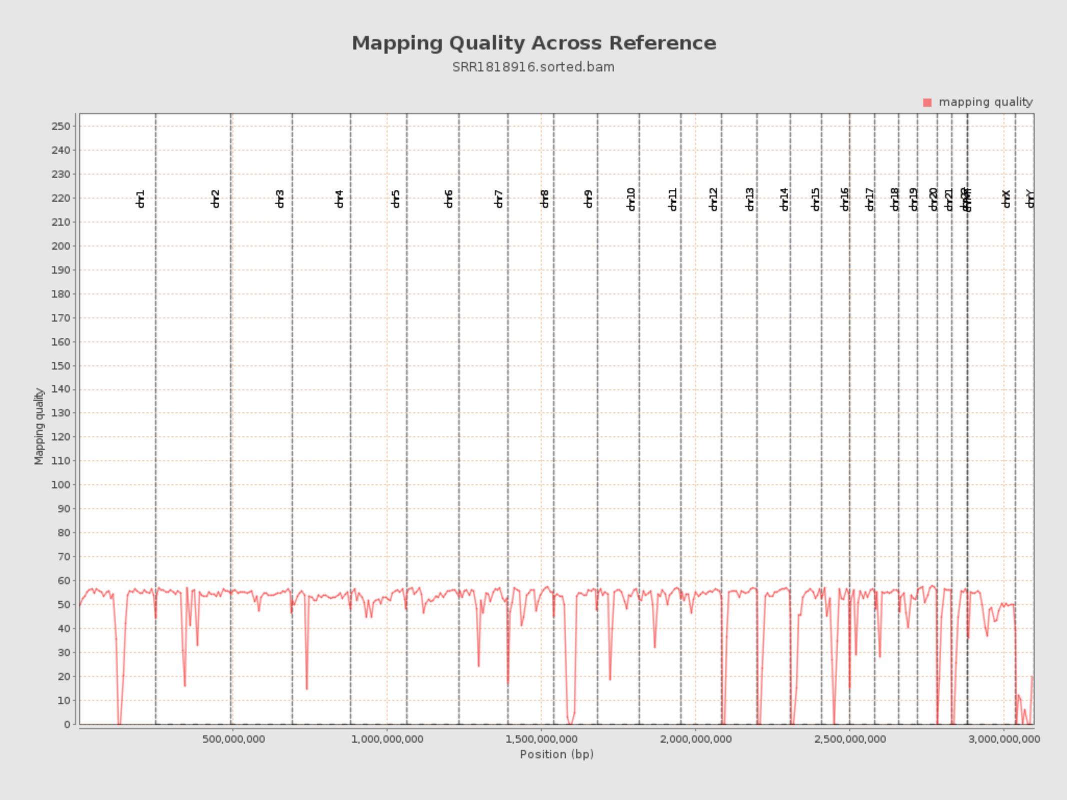
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram