Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:54:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818888.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_SRR1818888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818888.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:54:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,607,692
Mapped reads	1,586,111 / 98.66%
Unmapped reads	21,581 / 1.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,421 / 1.33%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	278,064 / 17.3%
Duplication rate	14.59%
Clipped reads	1,574,239 / 97.92%

2.2. ACGT Content

Number/percentage of A's	41,881,888 / 28.47%
Number/percentage of C's	30,089,955 / 20.46%
Number/percentage of T's	41,609,905 / 28.29%
Number/percentage of G's	33,513,430 / 22.78%
Number/percentage of N's	2,095 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0475

Standard Deviation	0.5914

2.4. Mapping Quality

Mean Mapping Quality	49.29

2.5. Mismatches and indels

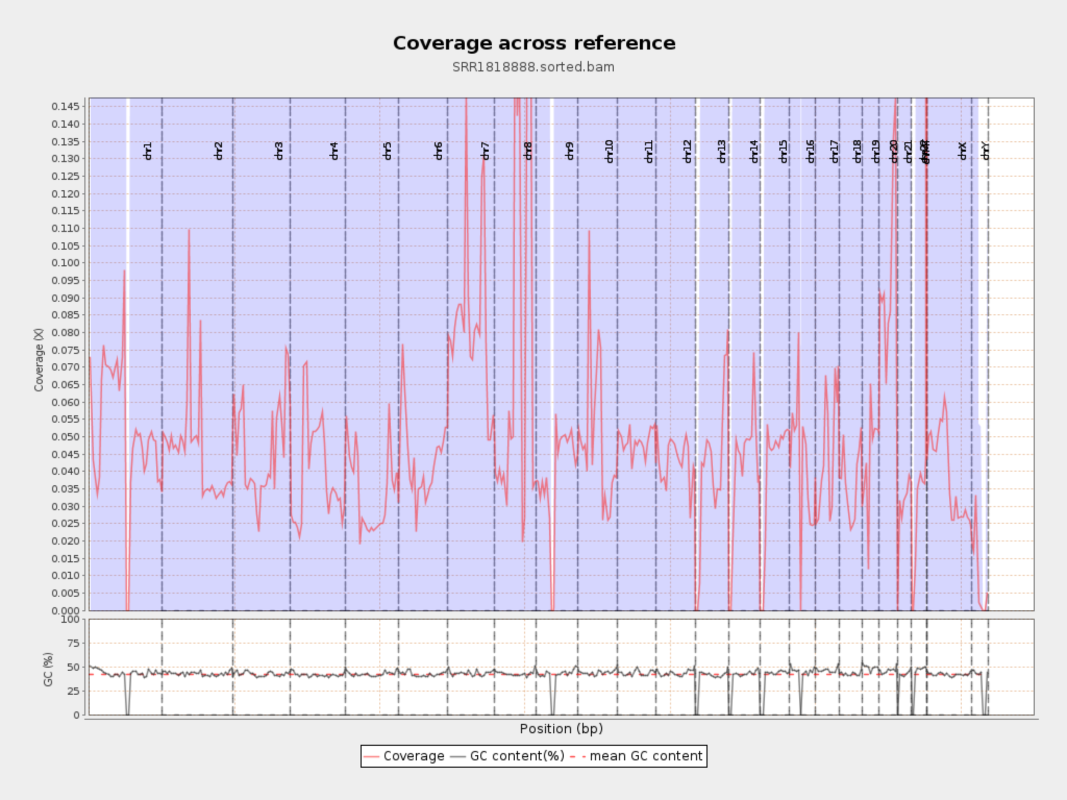
General error rate	0.66%
Mismatches	914,434
Insertions	23,818
Mapped reads with at least one insertion	1.46%
Deletions	46,941
Mapped reads with at least one deletion	2.89%
Homopolymer indels	39.1%

2.6. Chromosome stats

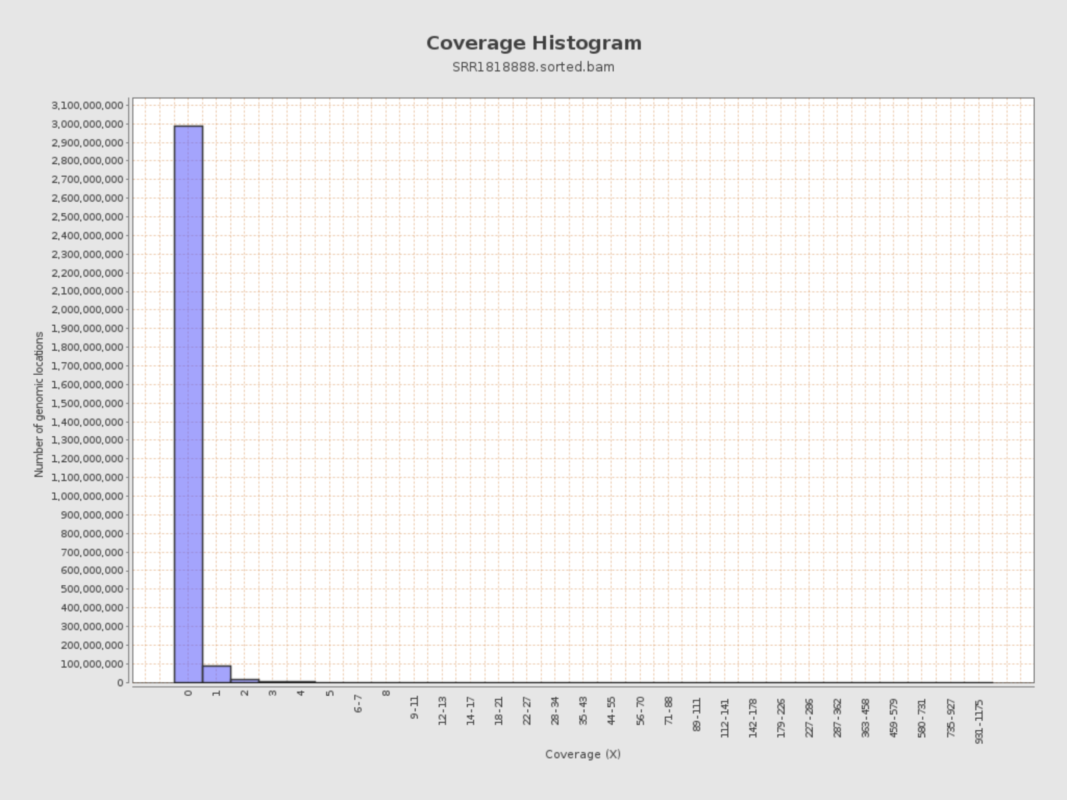
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12911579	0.0518	0.8959
chr2	243199373	11167188	0.0459	0.7947
chr3	198022430	9253903	0.0467	0.2716
chr4	191154276	7488702	0.0392	0.3479
chr5	180915260	6115479	0.0338	0.2493
chr6	171115067	7387643	0.0432	0.29
chr7	159138663	13424219	0.0844	1.402

chr8	146364022	12996258	0.0888	0.4989
chr9	141213431	5458375	0.0387	0.4907
chr10	135534747	6769464	0.0499	0.6806
chr11	135006516	6572406	0.0487	0.3606
chr12	133851895	5822926	0.0435	0.2687
chr13	115169878	4592795	0.0399	0.2506
chr14	107349540	4374999	0.0408	0.2816
chr15	102531392	4105905	0.04	0.2582
chr16	90354753	3692360	0.0409	0.578
chr17	81195210	3693405	0.0455	0.3629
chr18	78077248	2858556	0.0366	0.5689
chr19	59128983	2592913	0.0439	0.7835
chr20	63025520	6139234	0.0974	0.4283
chr21	48129895	1441188	0.0299	0.274
chr22	51304566	1332539	0.026	0.2227
chrMT	16571	303975	18.3438	11.2672
chrX	155270560	6145645	0.0396	0.3115
chrY	59373566	548119	0.0092	0.6647

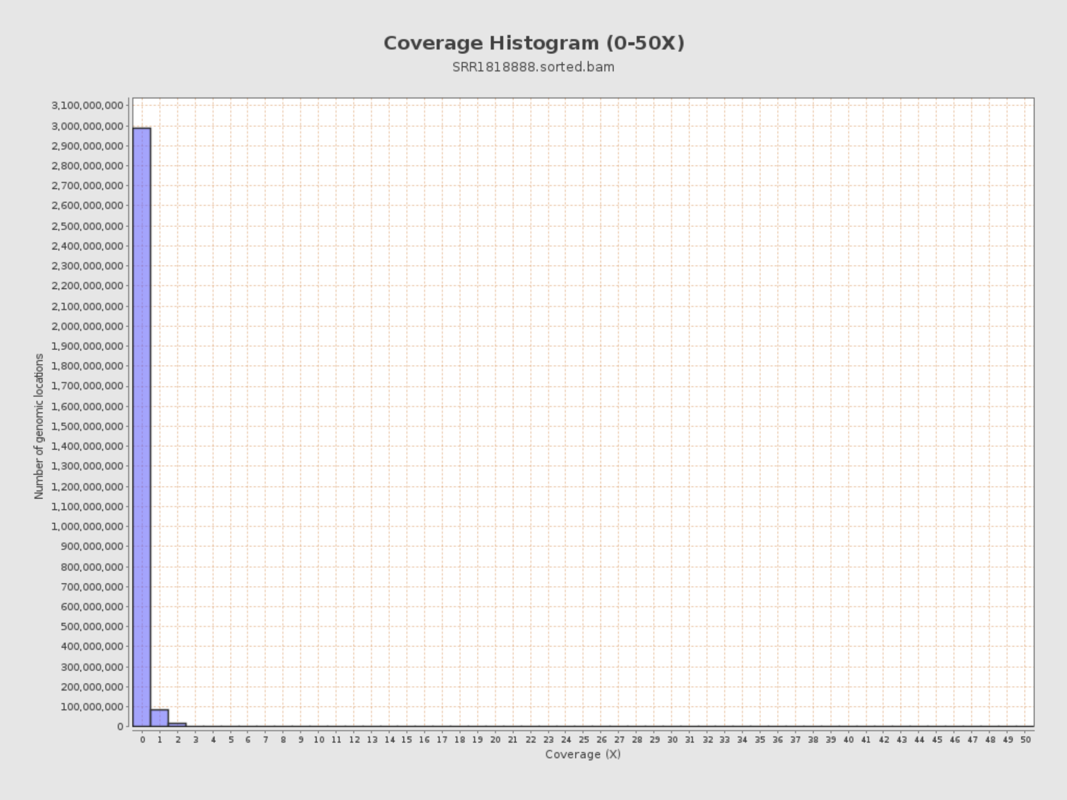
3. Results : Coverage across reference



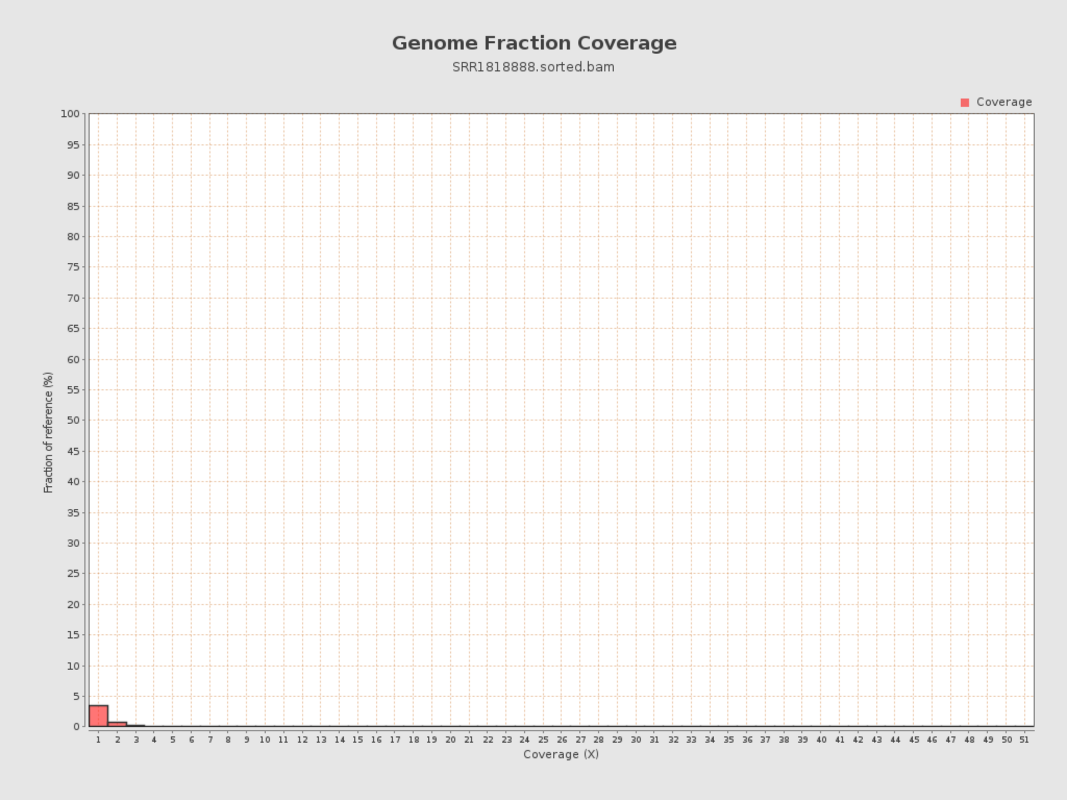
4. Results : Coverage Histogram



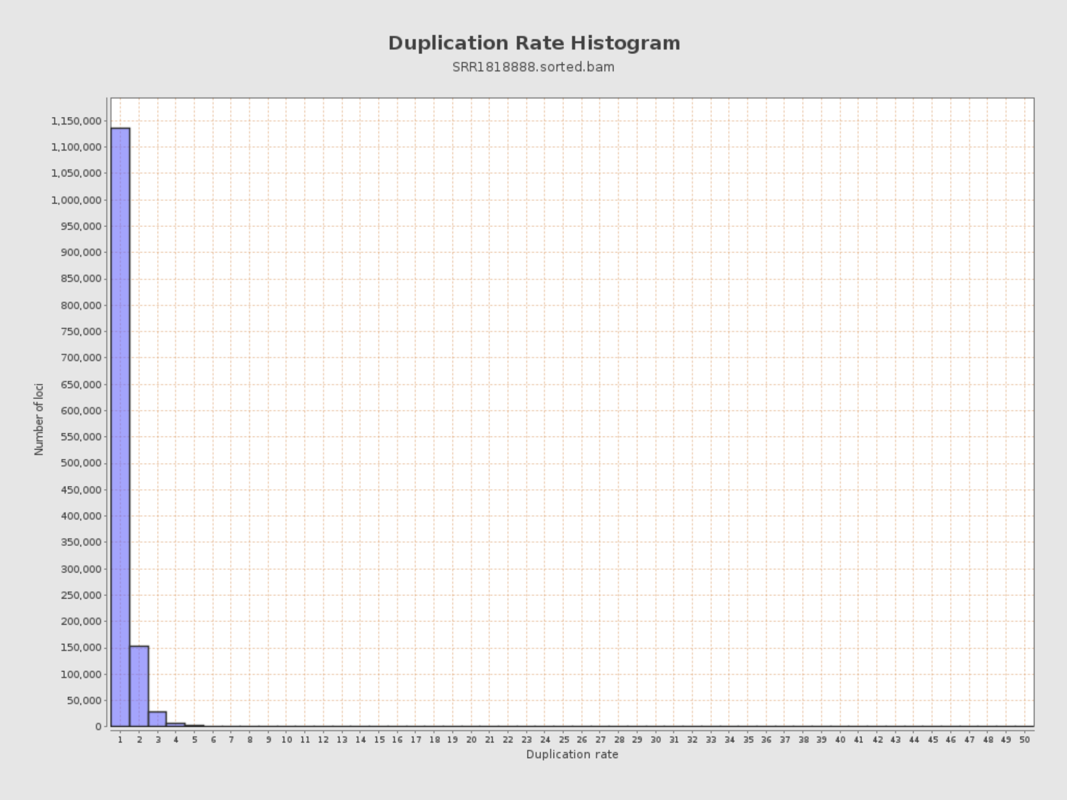
5. Results : Coverage Histogram (0-50X)



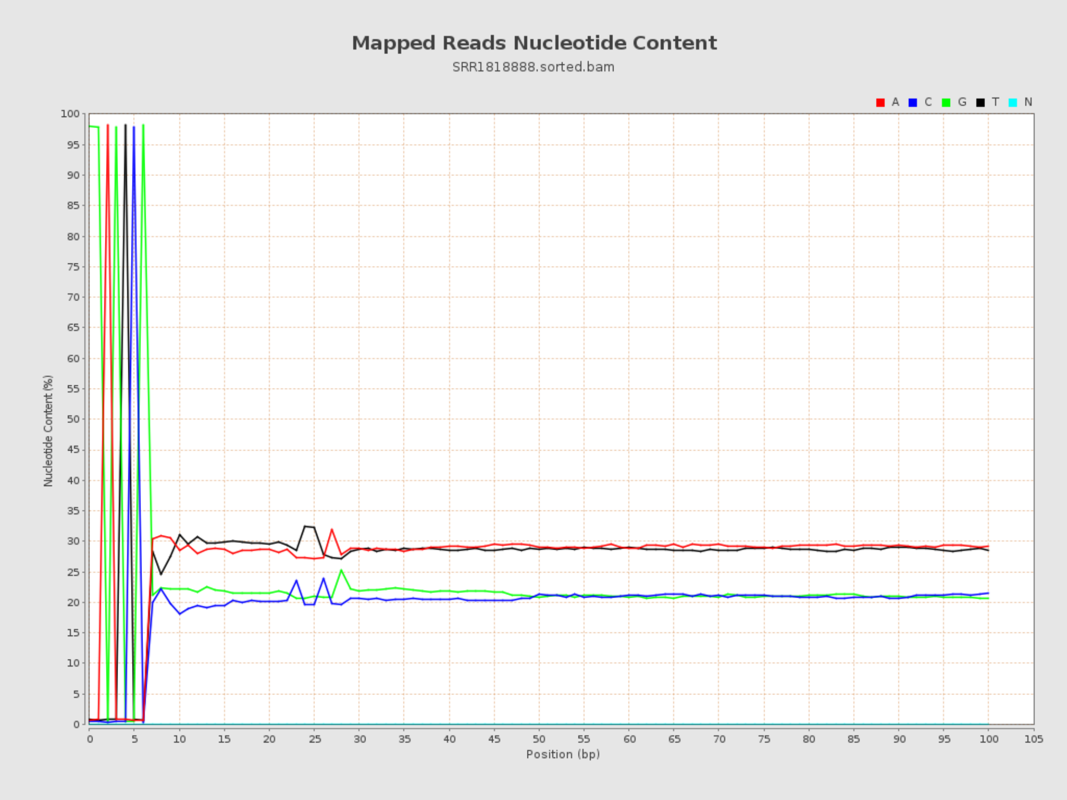
6. Results : Genome Fraction Coverage



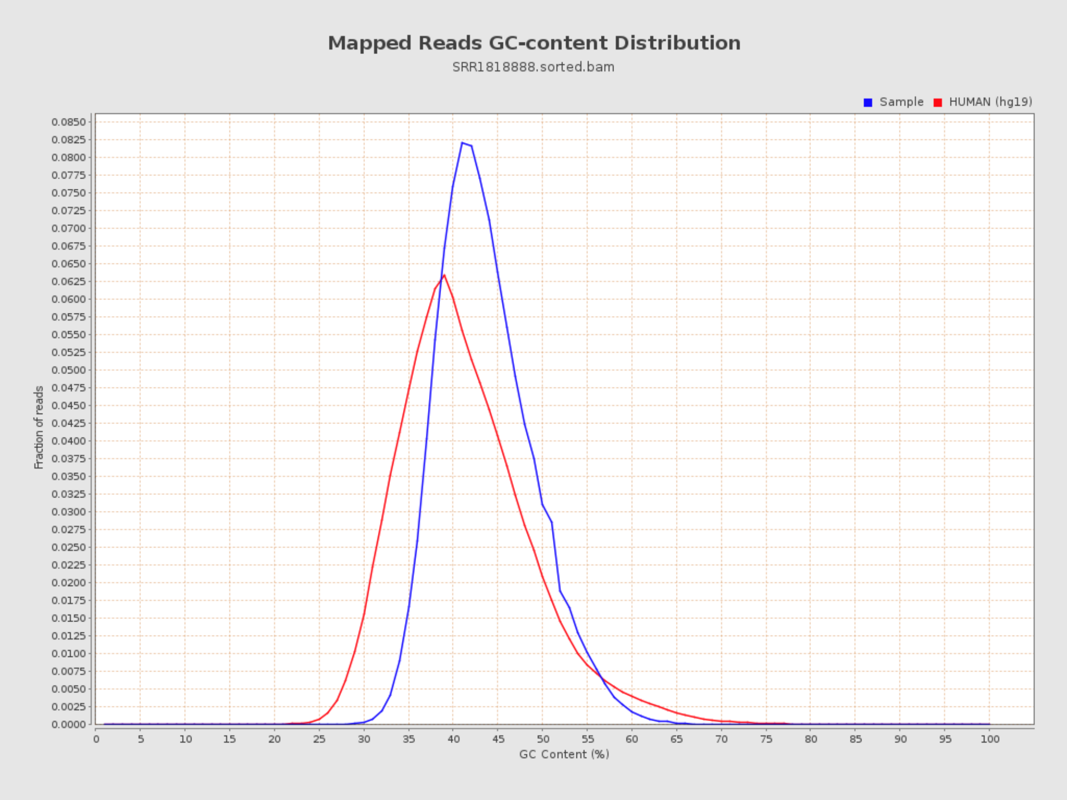
7. Results : Duplication Rate Histogram



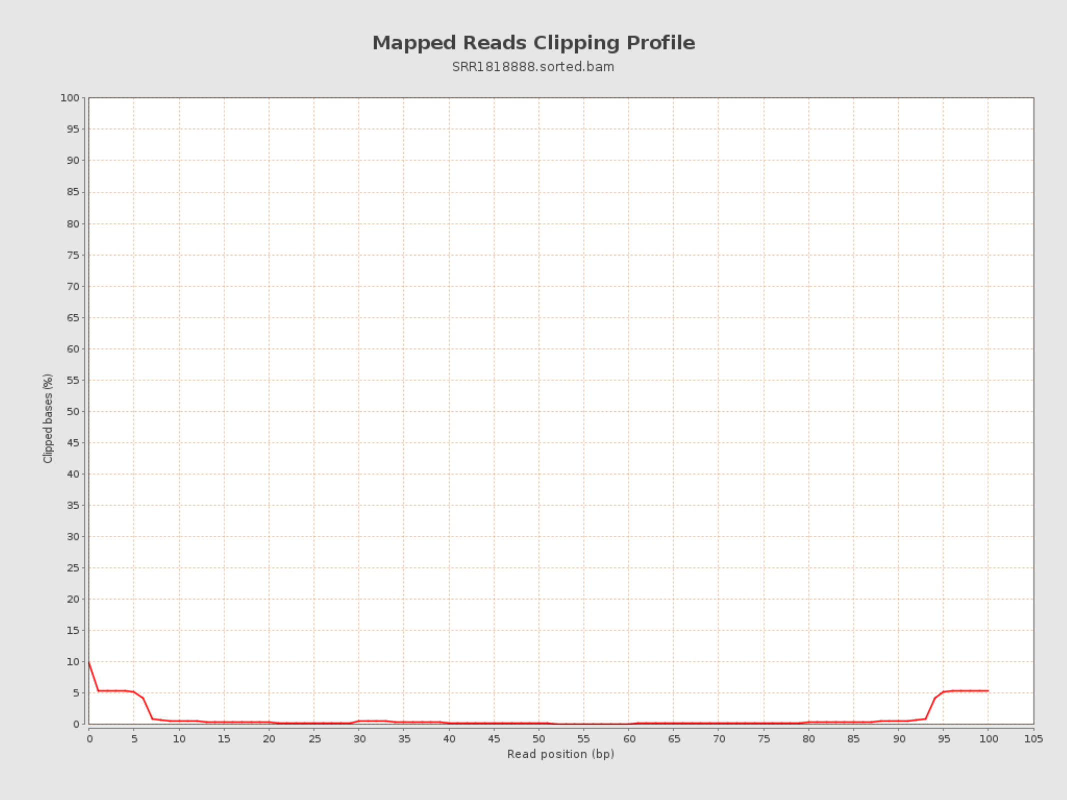
8. Results : Mapped Reads Nucleotide Content



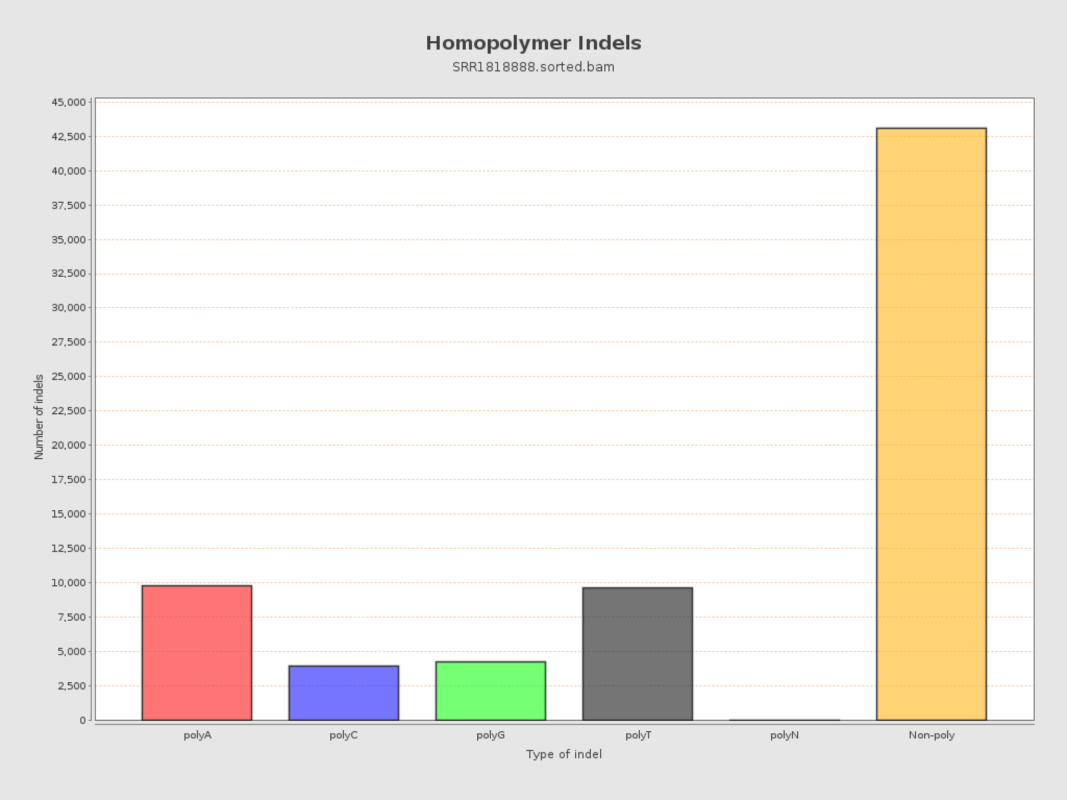
9. Results : Mapped Reads GC-content Distribution



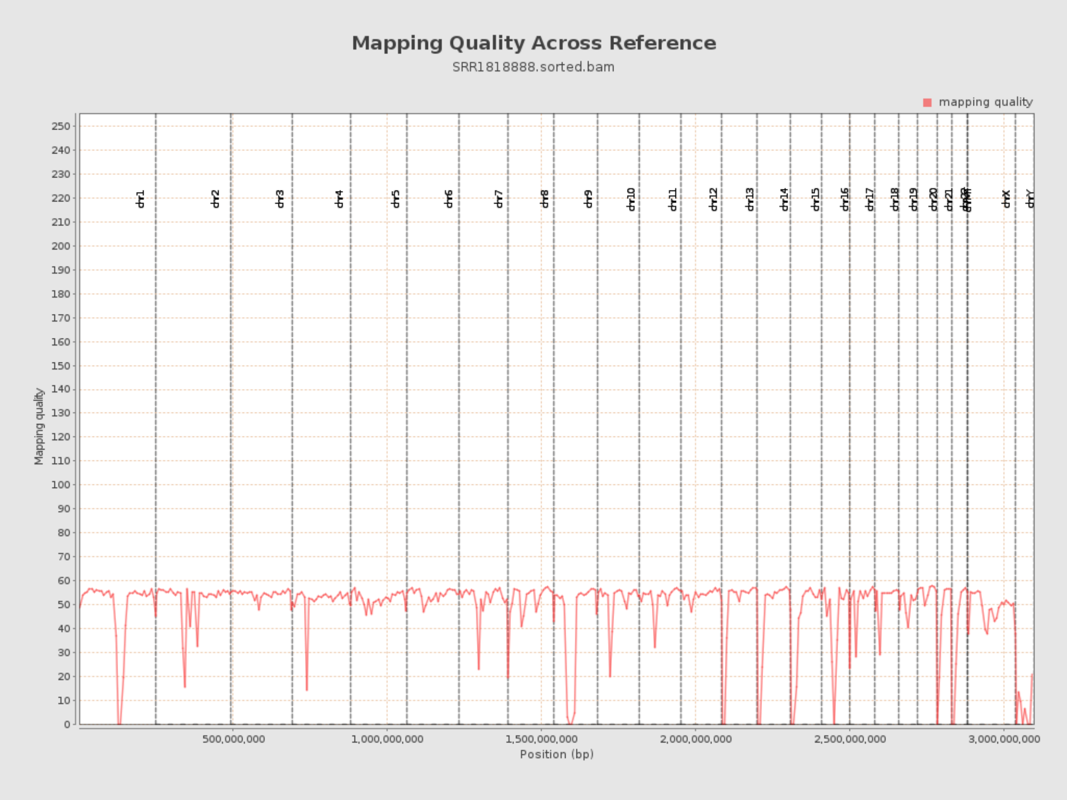
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram