Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:51:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818954.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_SRR1818954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:51:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,185,609
Mapped reads	2,136,117 / 97.74%
Unmapped reads	49,492 / 2.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,038 / 1.37%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	934,045 / 42.74%
Duplication rate	36.64%
Clipped reads	2,137,263 / 97.79%

2.2. ACGT Content

Number/percentage of A's	55,755,795 / 28.19%
Number/percentage of C's	41,145,218 / 20.81%
Number/percentage of T's	57,435,803 / 29.04%
Number/percentage of G's	43,419,566 / 21.96%
Number/percentage of N's	7,982 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0639

Standard Deviation	0.7015

2.4. Mapping Quality

Mean Mapping Quality	49.24

2.5. Mismatches and indels

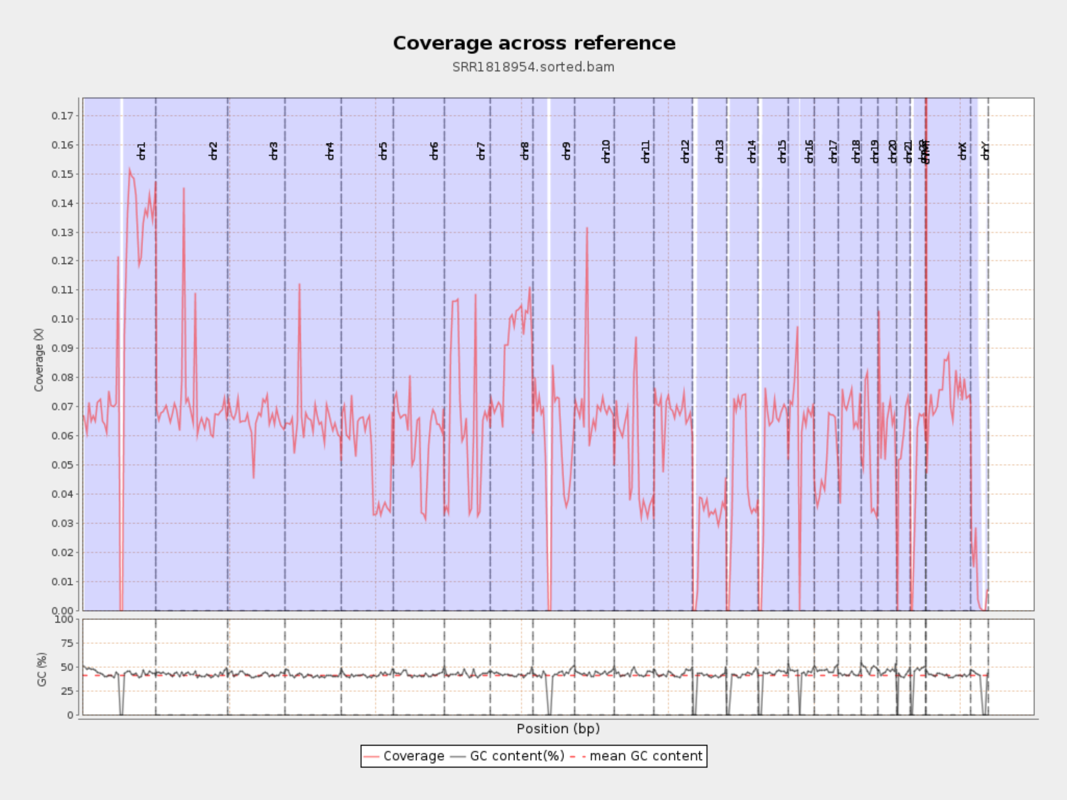
General error rate	0.67%
Mismatches	1,267,312
Insertions	27,391
Mapped reads with at least one insertion	1.26%
Deletions	60,455
Mapped reads with at least one deletion	2.78%
Homopolymer indels	42.4%

2.6. Chromosome stats

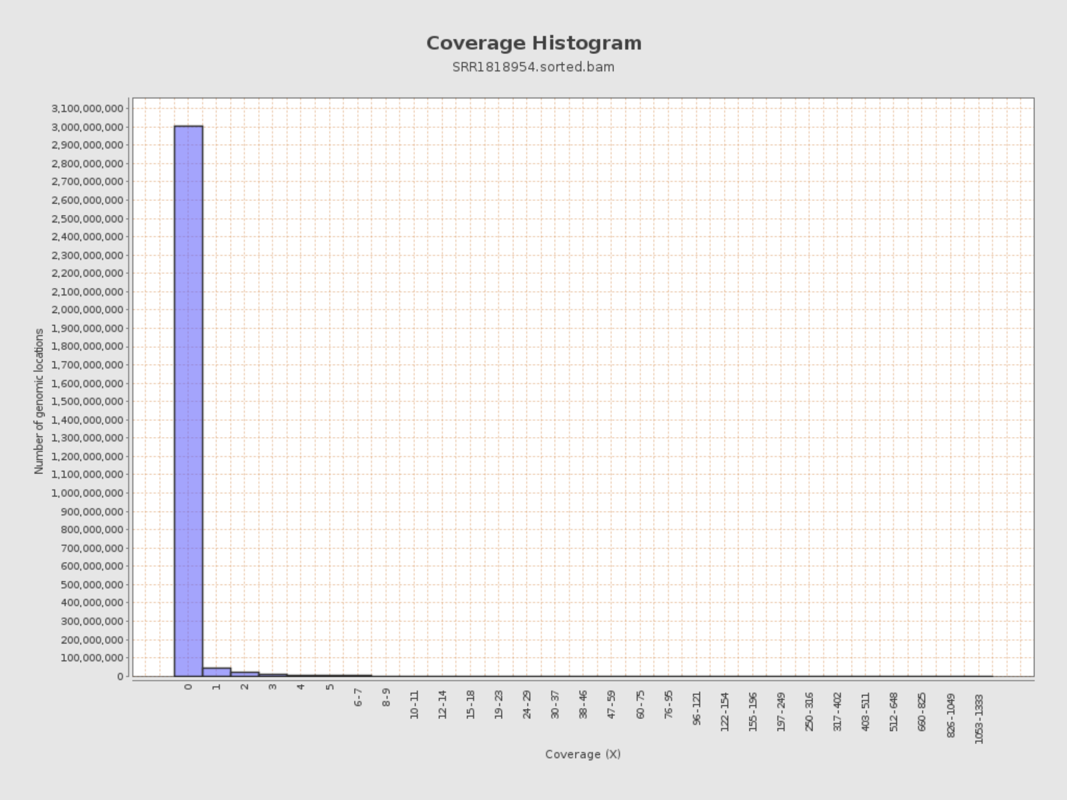
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23654319	0.0949	1.2621
chr2	243199373	17262728	0.071	0.8934
chr3	198022430	13086479	0.0661	0.4806
chr4	191154276	12620754	0.066	0.5335
chr5	180915260	9742592	0.0539	0.4411
chr6	171115067	10411536	0.0608	0.4913
chr7	159138663	10225769	0.0643	0.5976

chr8	146364022	13186125	0.0901	0.6551
chr9	141213431	7752593	0.0549	0.8041
chr10	135534747	9612747	0.0709	0.8774
chr11	135006516	7094496	0.0525	0.4943
chr12	133851895	9164562	0.0685	0.4976
chr13	115169878	3389669	0.0294	0.317
chr14	107349540	5038684	0.0469	0.4435
chr15	102531392	5681542	0.0554	0.4429
chr16	90354753	5831407	0.0645	0.6519
chr17	81195210	4253486	0.0524	0.4518
chr18	78077248	5110875	0.0655	1.0085
chr19	59128983	3100304	0.0524	1.0902
chr20	63025520	4189865	0.0665	0.5118
chr21	48129895	2709088	0.0563	0.4926
chr22	51304566	2351090	0.0458	0.4299
chrMT	16571	346140	20.8883	13.3375
chrX	155270560	11505682	0.0741	0.6057
chrY	59373566	550117	0.0093	0.4336

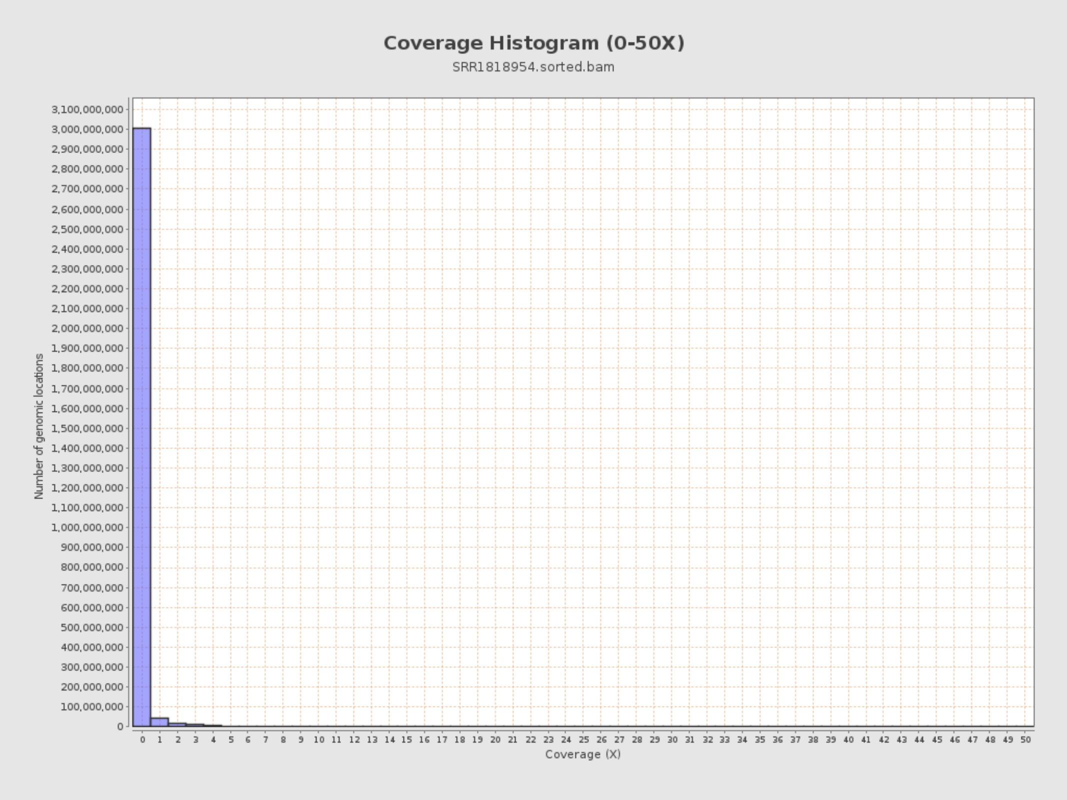
3. Results : Coverage across reference



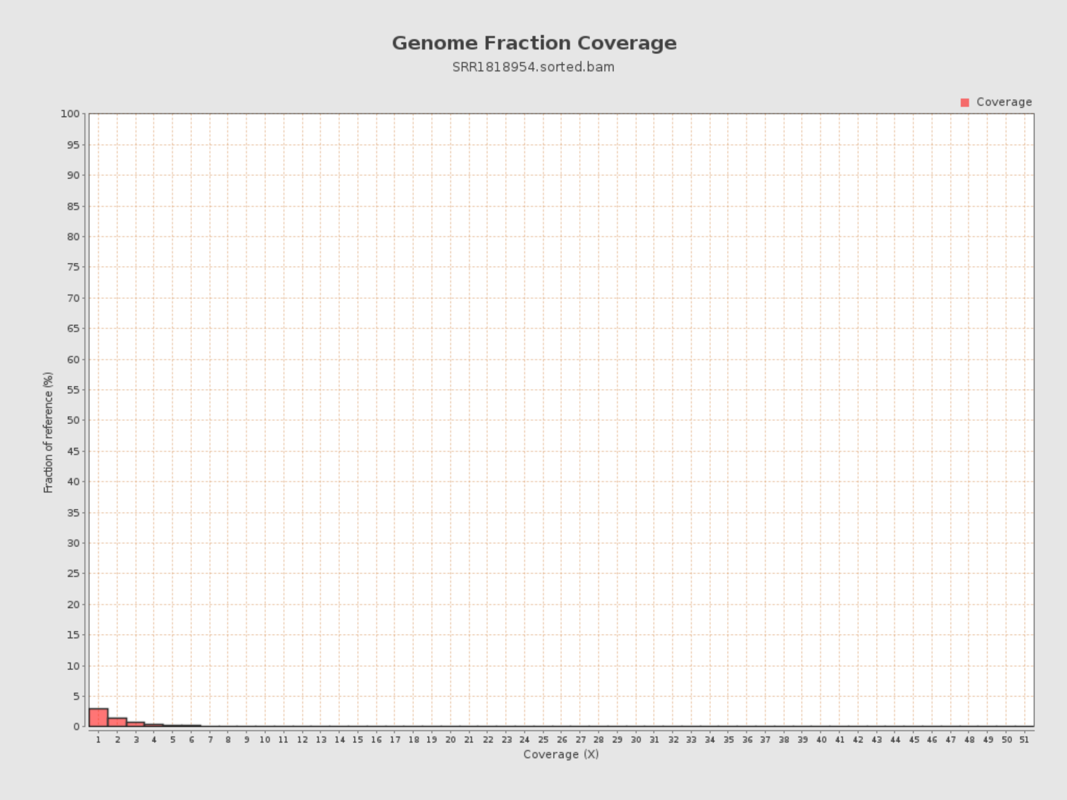
4. Results : Coverage Histogram



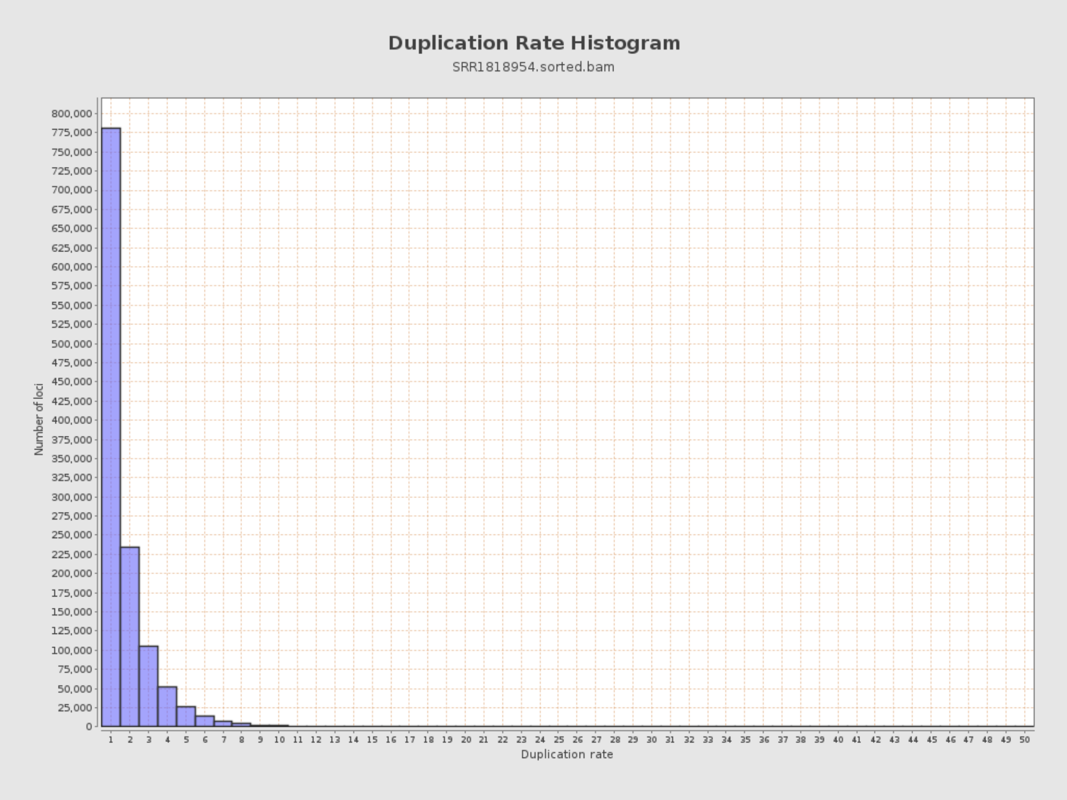
5. Results : Coverage Histogram (0-50X)



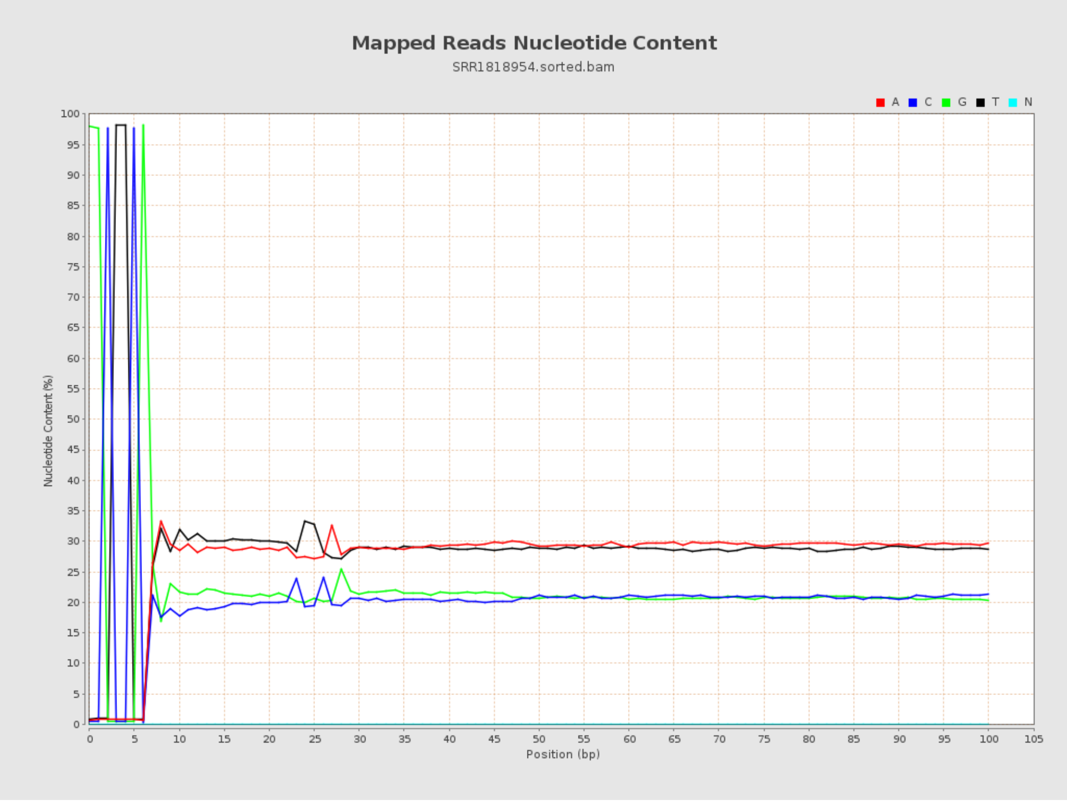
6. Results : Genome Fraction Coverage



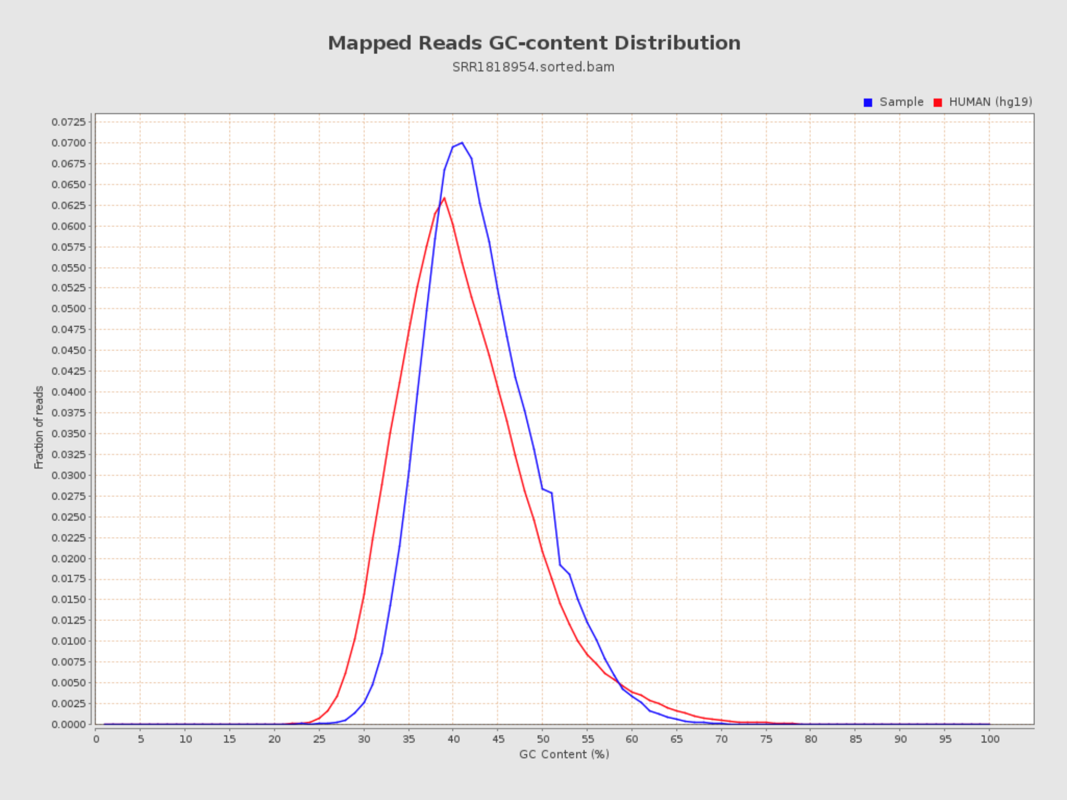
7. Results : Duplication Rate Histogram



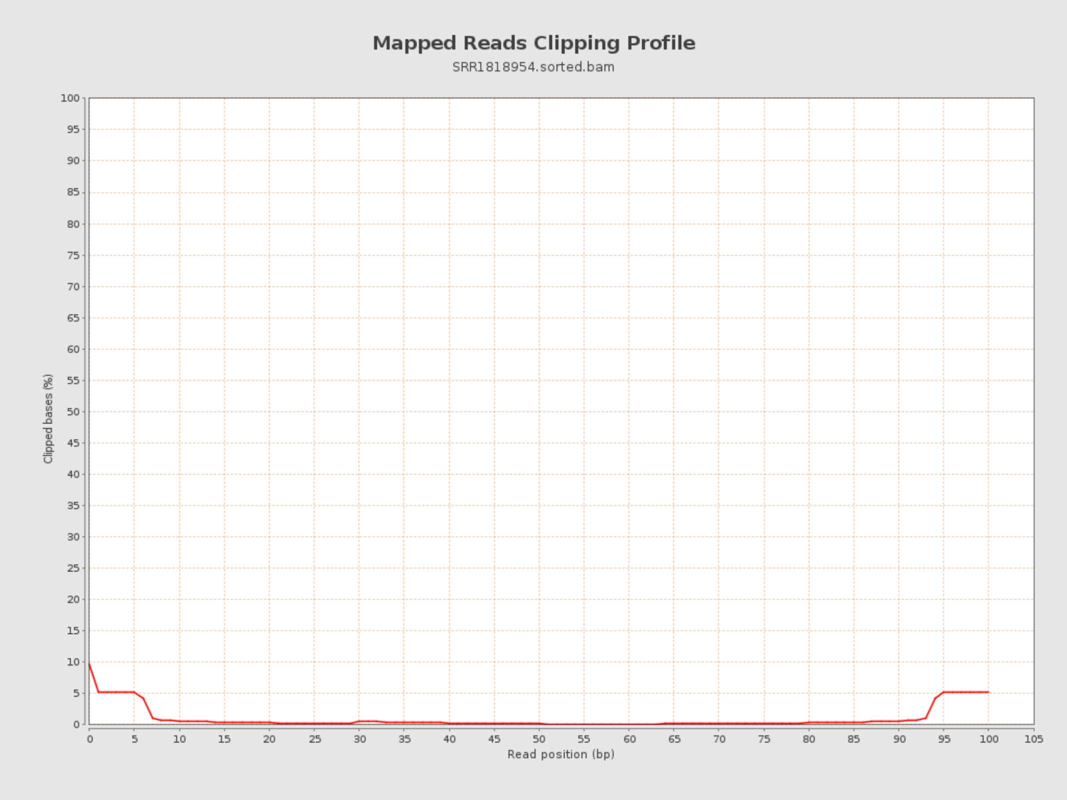
8. Results : Mapped Reads Nucleotide Content



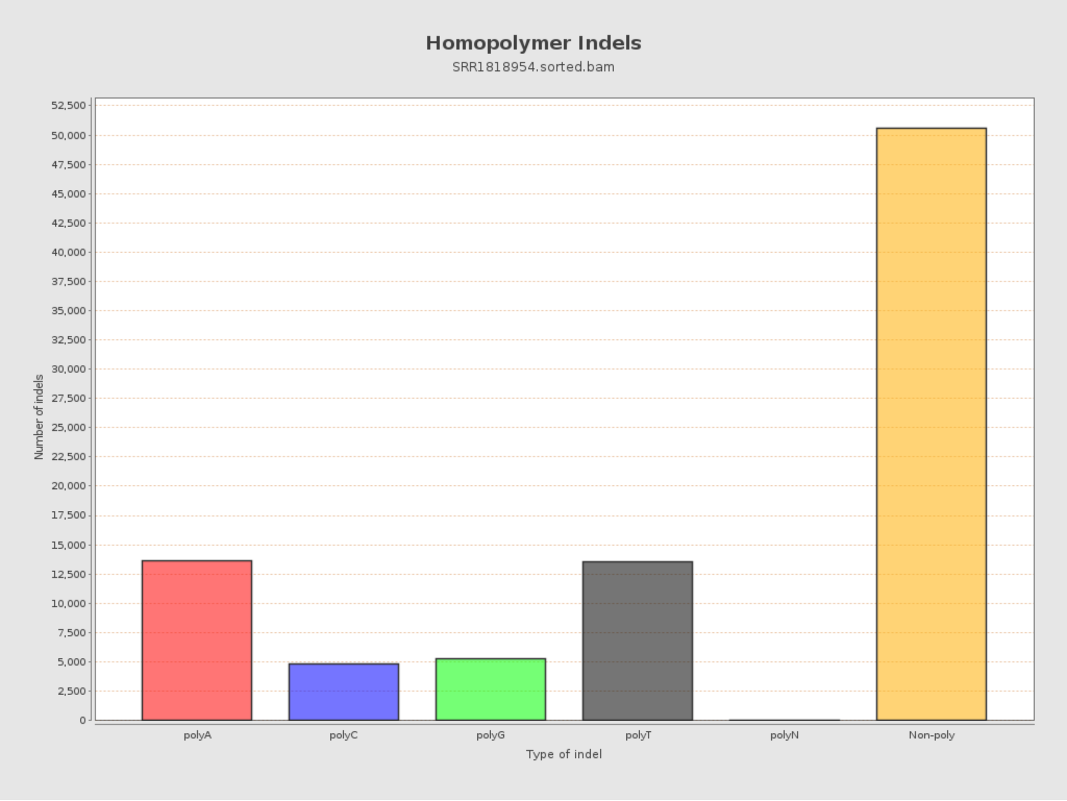
9. Results : Mapped Reads GC-content Distribution



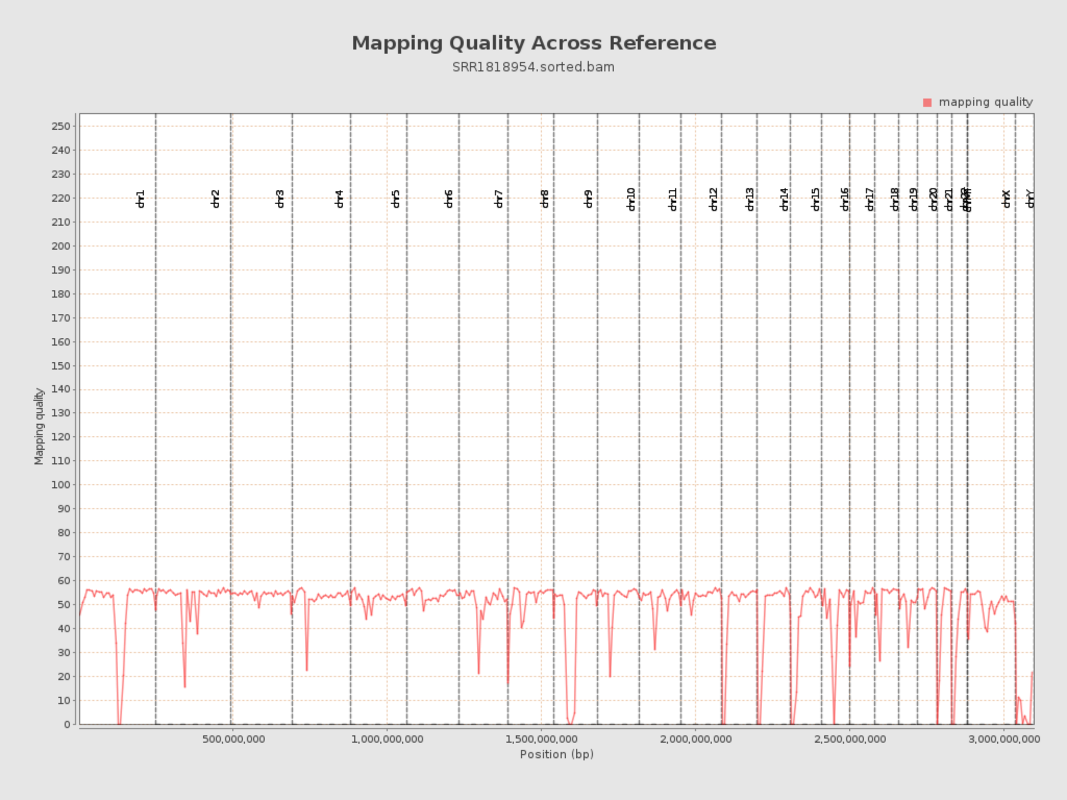
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram