Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:41:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818992.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_SRR1818992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818992.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:41:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,075,549
Mapped reads	2,046,447 / 98.6%
Unmapped reads	29,102 / 1.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,968 / 1.4%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	929,388 / 44.78%
Duplication rate	37.68%
Clipped reads	2,068,287 / 99.65%

2.2. ACGT Content

Number/percentage of A's	53,233,567 / 28.1%
Number/percentage of C's	39,762,581 / 20.99%
Number/percentage of T's	54,189,734 / 28.61%
Number/percentage of G's	42,241,528 / 22.3%
Number/percentage of N's	9,184 / 0%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0612

Standard Deviation	0.7063

2.4. Mapping Quality

Mean Mapping Quality	49.14

2.5. Mismatches and indels

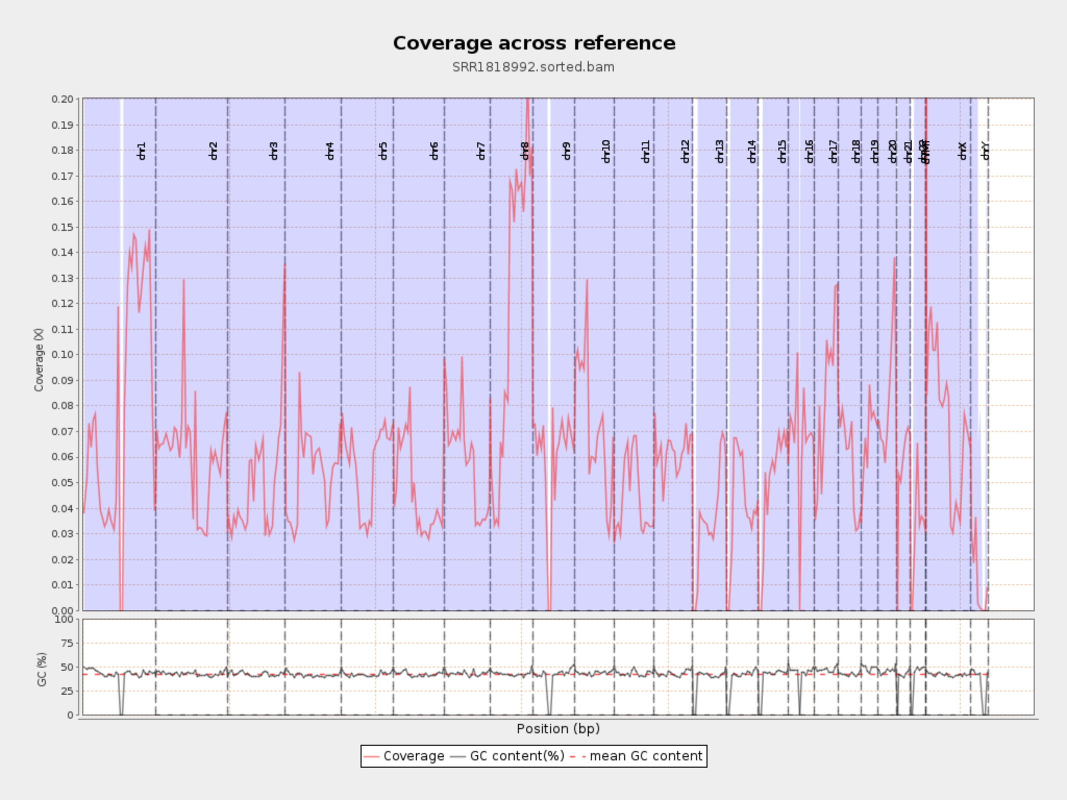
General error rate	0.64%
Mismatches	1,154,705
Insertions	25,360
Mapped reads with at least one insertion	1.21%
Deletions	59,672
Mapped reads with at least one deletion	2.85%
Homopolymer indels	42.75%

2.6. Chromosome stats

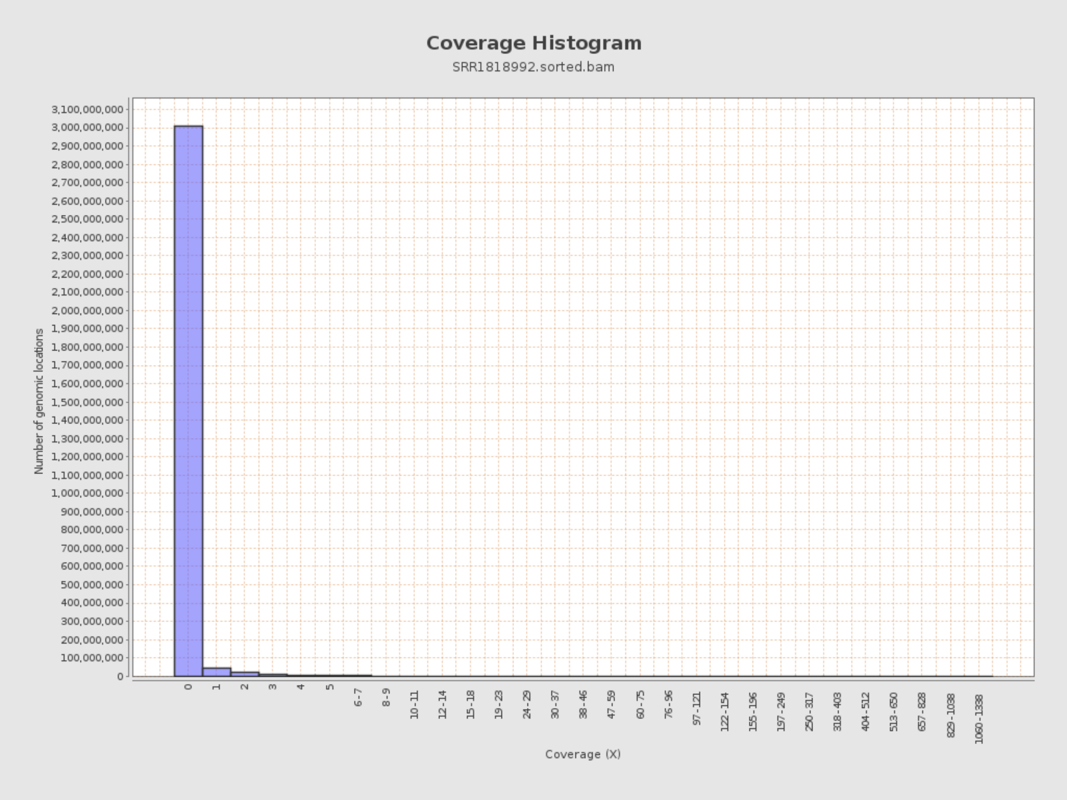
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19691199	0.079	1.2268
chr2	243199373	14886734	0.0612	0.9245
chr3	198022430	9822537	0.0496	0.4176
chr4	191154276	10258718	0.0537	0.4915
chr5	180915260	10428455	0.0576	0.4644
chr6	171115067	7903316	0.0462	0.4923
chr7	159138663	9382713	0.059	0.8085

chr8	146364022	17894299	0.1223	0.7303
chr9	141213431	8304627	0.0588	0.6966
chr10	135534747	9737528	0.0718	0.8421
chr11	135006516	5957136	0.0441	0.4773
chr12	133851895	8343177	0.0623	0.4783
chr13	115169878	4160604	0.0361	0.3515
chr14	107349540	4439771	0.0414	0.3977
chr15	102531392	4870484	0.0475	0.4187
chr16	90354753	5967645	0.066	0.7993
chr17	81195210	6783665	0.0835	0.6244
chr18	78077248	4548210	0.0583	0.8292
chr19	59128983	4044646	0.0684	1.1337
chr20	63025520	5451208	0.0865	0.6034
chr21	48129895	2712821	0.0564	0.4872
chr22	51304566	1548936	0.0302	0.3662
chrMT	16571	142596	8.6052	7.5817
chrX	155270560	11583173	0.0746	0.6015
chrY	59373566	683215	0.0115	0.6245

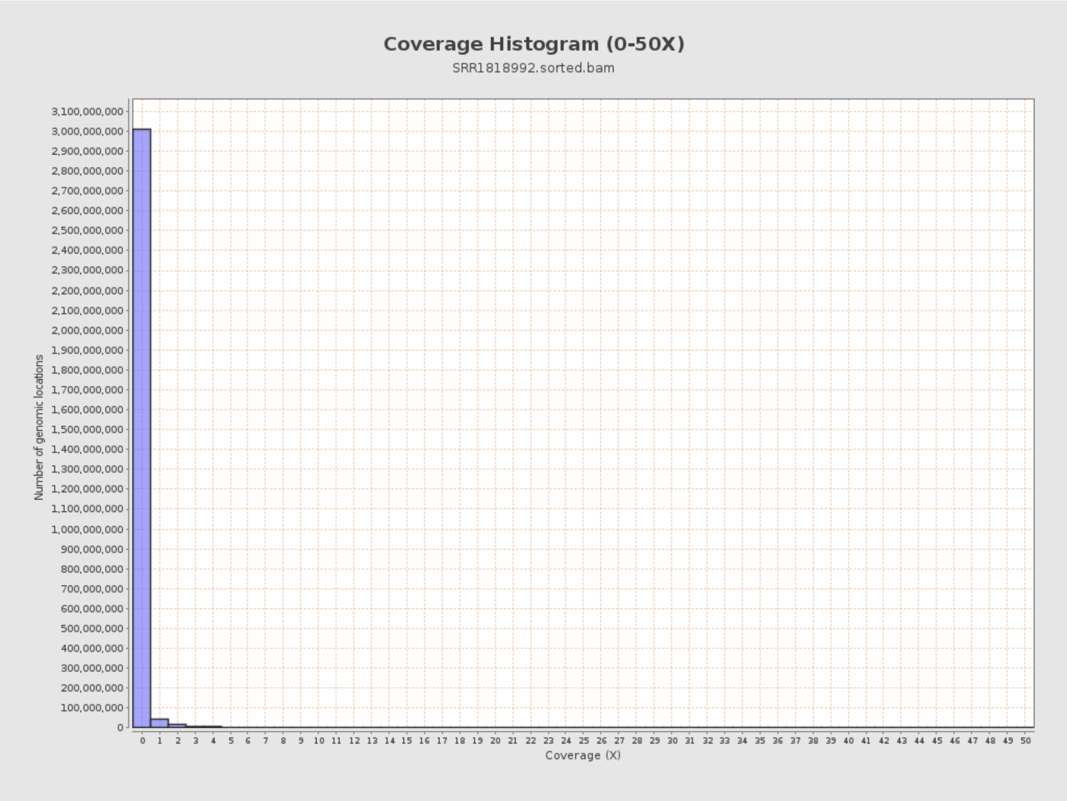
3. Results : Coverage across reference



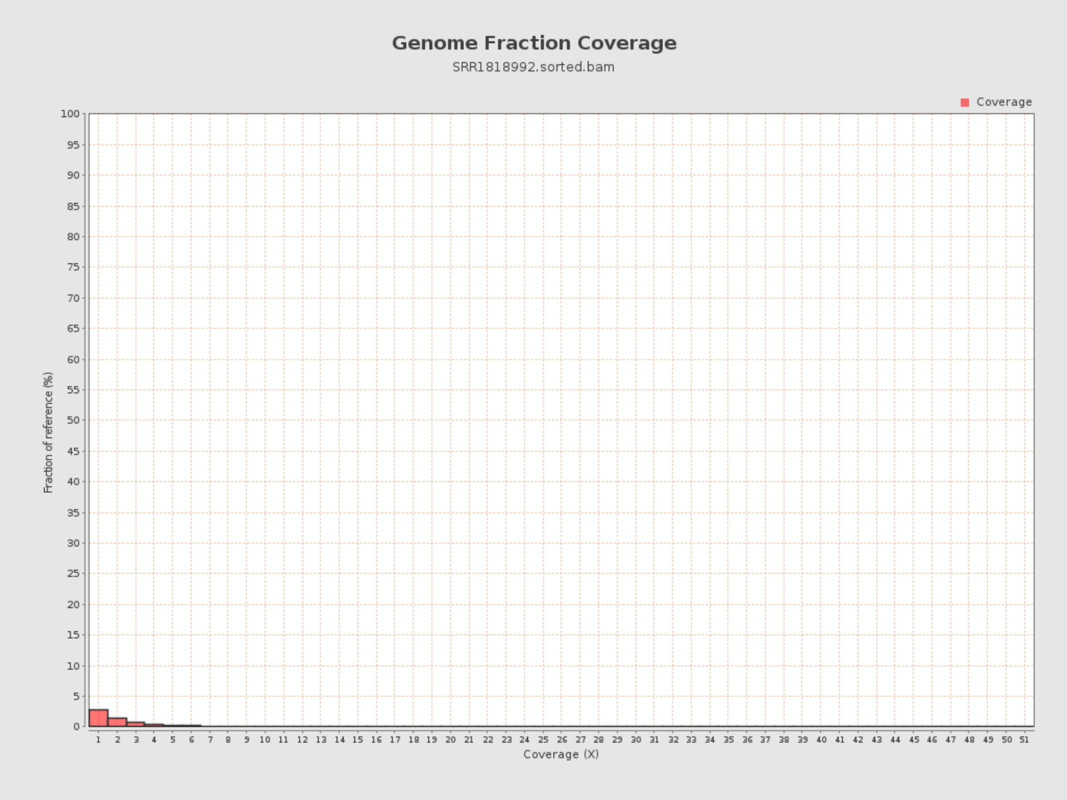
4. Results : Coverage Histogram



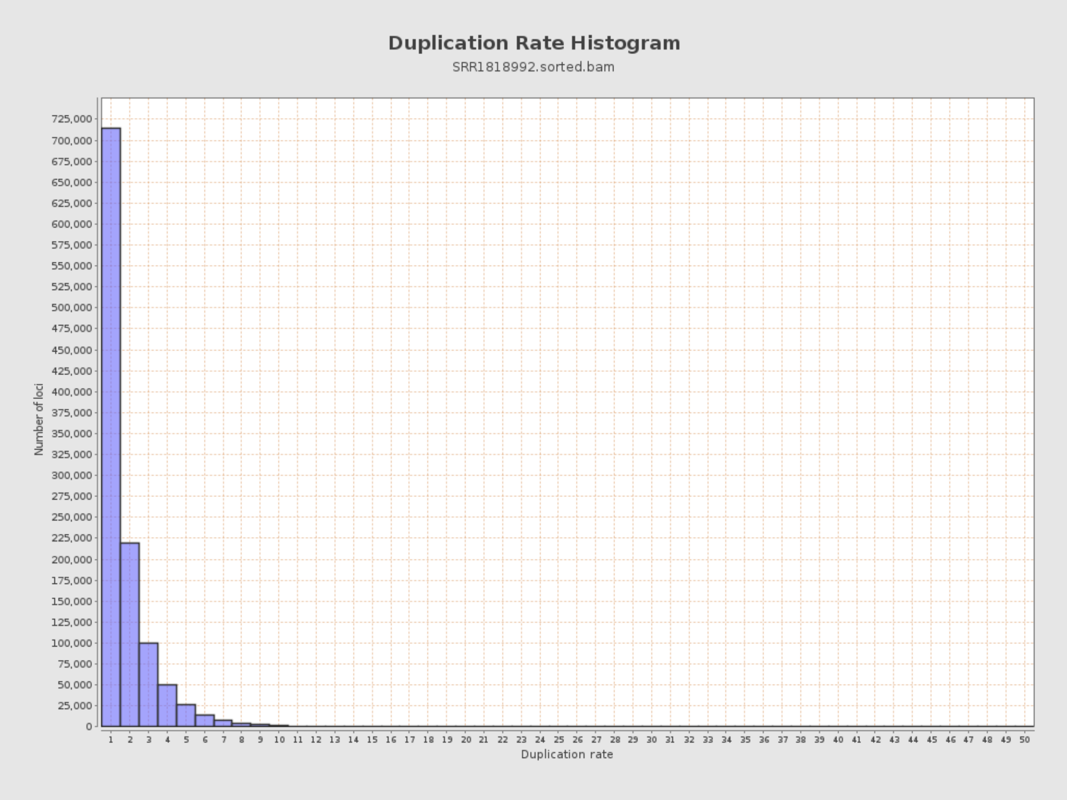
5. Results : Coverage Histogram (0-50X)



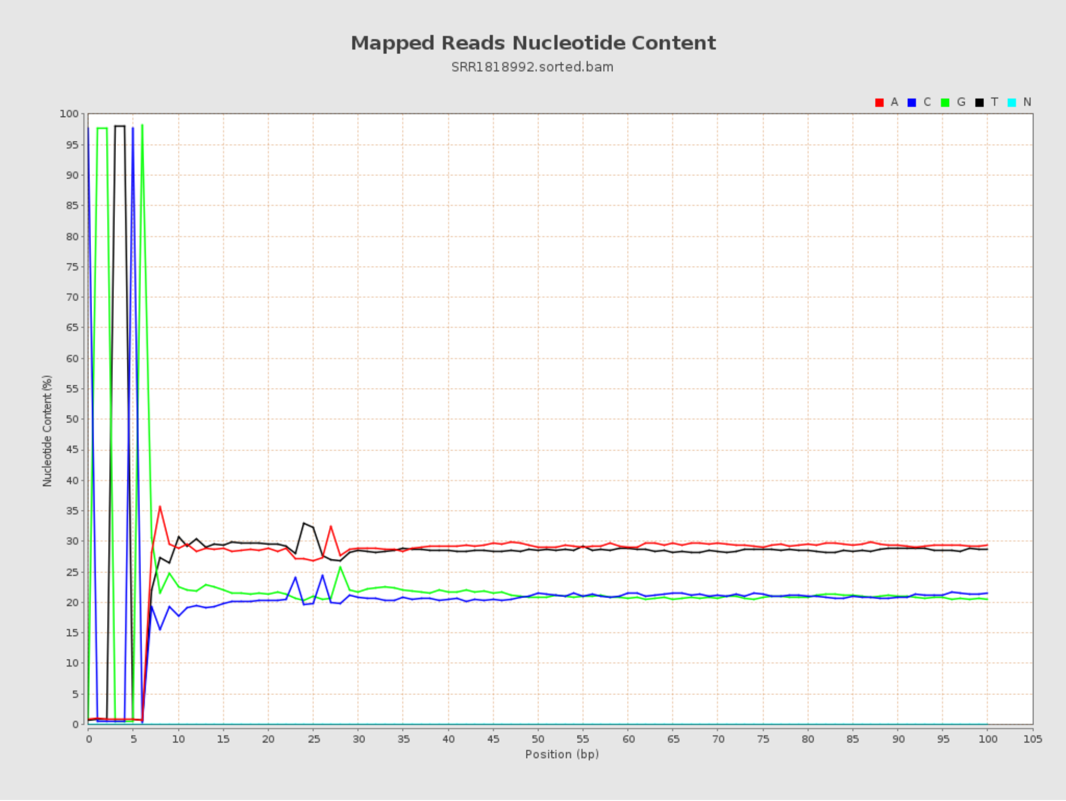
6. Results : Genome Fraction Coverage



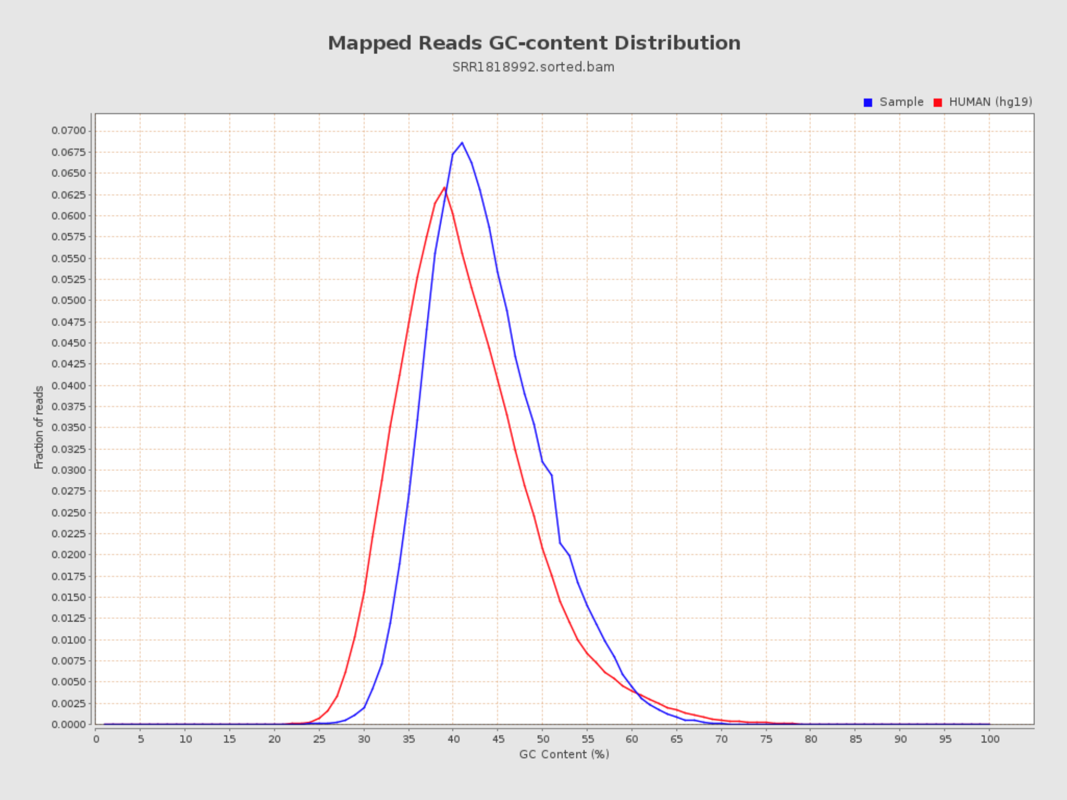
7. Results : Duplication Rate Histogram



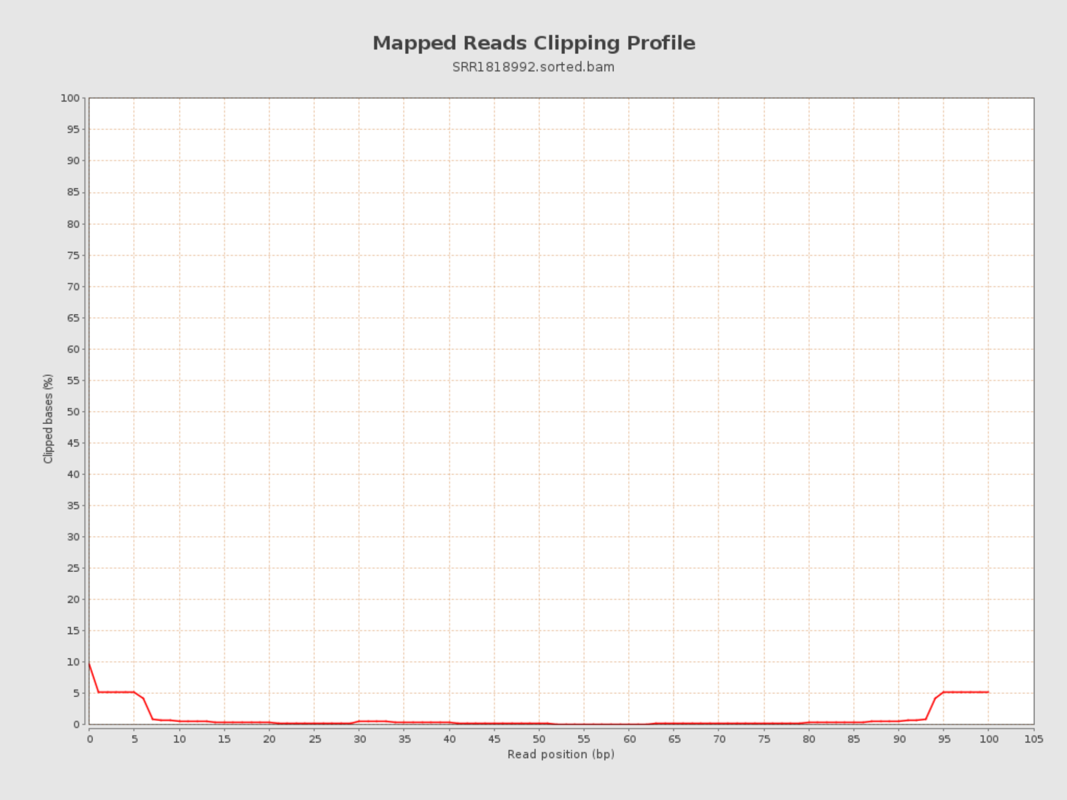
8. Results : Mapped Reads Nucleotide Content



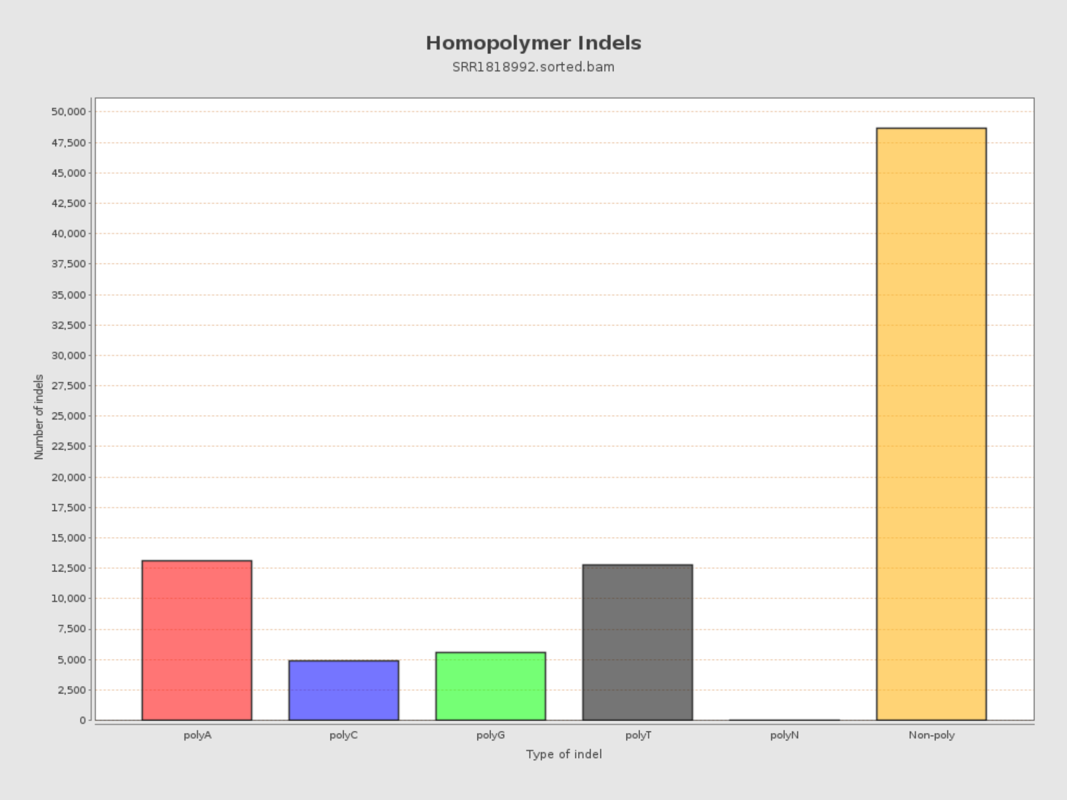
9. Results : Mapped Reads GC-content Distribution



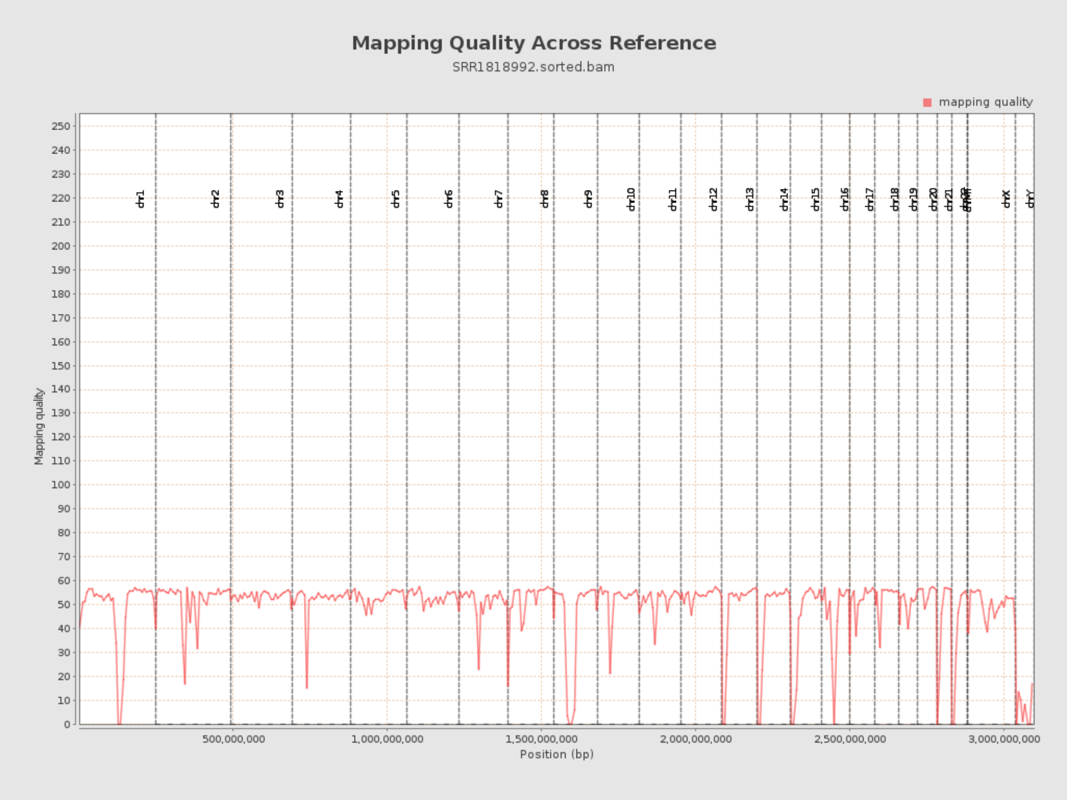
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram