Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:35:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818912.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_SRR1818912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818912.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:35:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818912.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,219,798
Mapped reads	2,112,015 / 95.14%
Unmapped reads	107,783 / 4.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,503 / 1.37%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	552,248 / 24.88%
Duplication rate	21.9%
Clipped reads	2,110,492 / 95.08%

2.2. ACGT Content

Number/percentage of A's	56,025,997 / 28.61%
Number/percentage of C's	38,914,999 / 19.87%
Number/percentage of T's	56,387,719 / 28.8%
Number/percentage of G's	44,472,035 / 22.71%
Number/percentage of N's	2,832 / 0%
GC Percentage	42.59%

2.3. Coverage

Mean	0.0633

Standard Deviation	0.7836

2.4. Mapping Quality

Mean Mapping Quality	49.28

2.5. Mismatches and indels

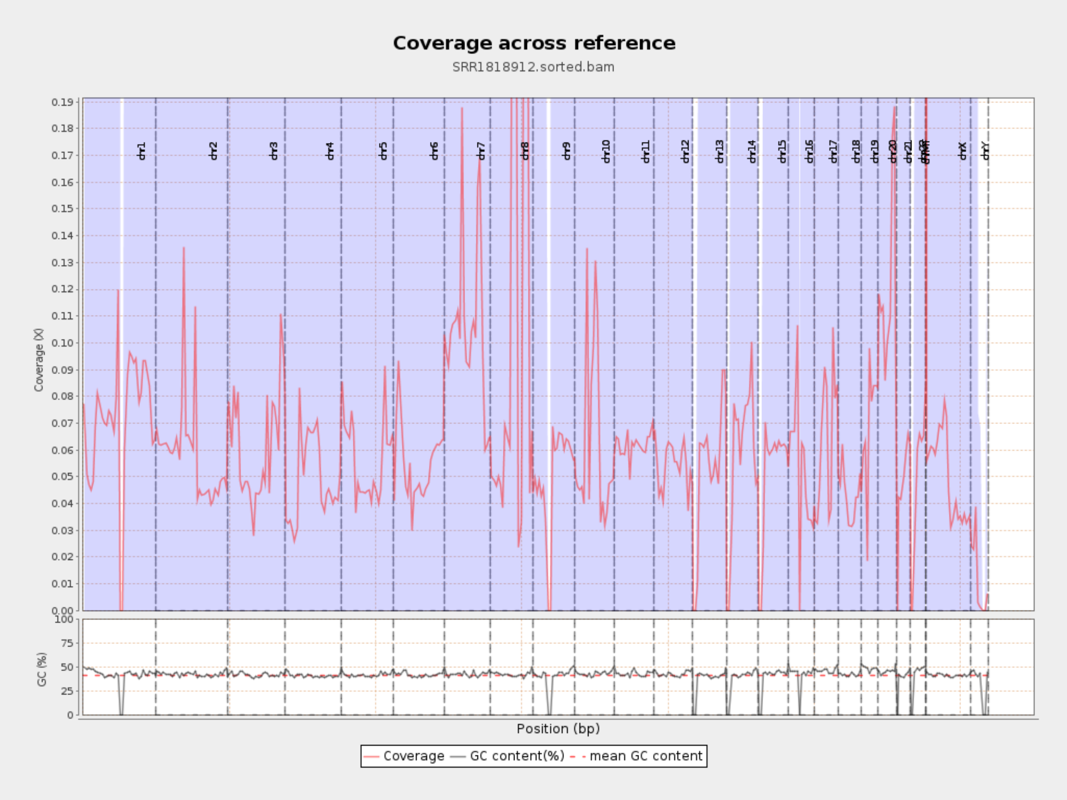
General error rate	0.64%
Mismatches	1,193,889
Insertions	26,698
Mapped reads with at least one insertion	1.23%
Deletions	64,465
Mapped reads with at least one deletion	2.98%
Homopolymer indels	41.83%

2.6. Chromosome stats

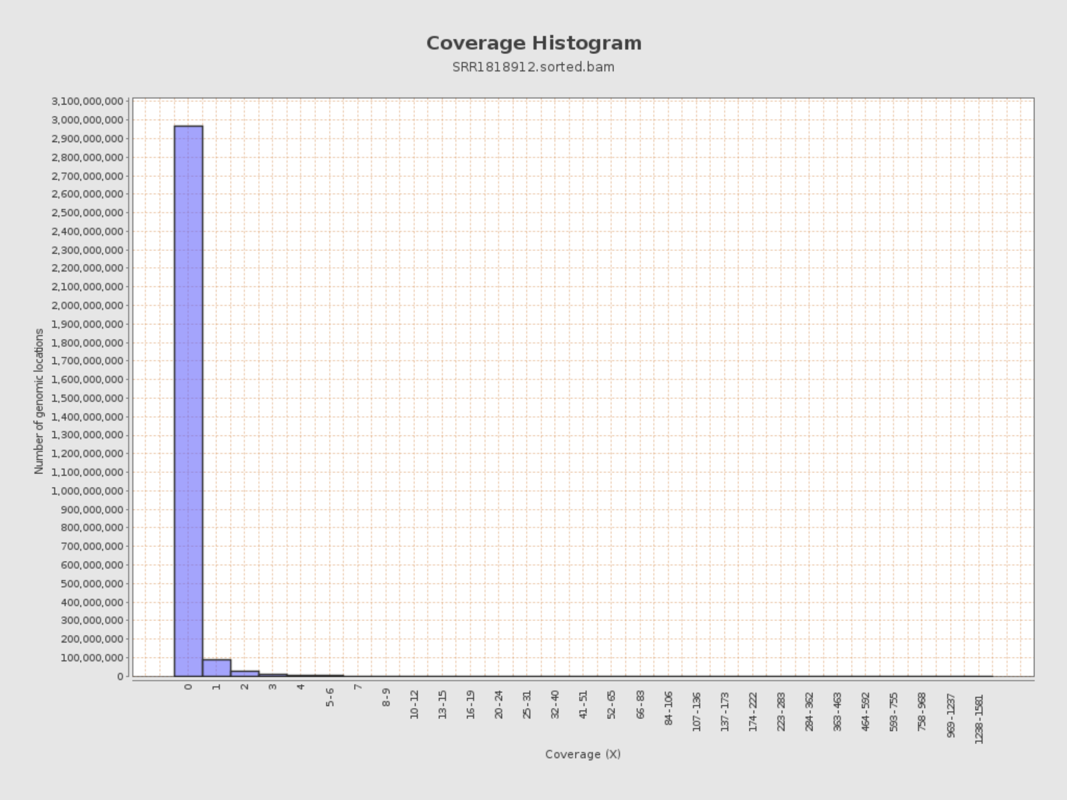
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17824109	0.0715	1.2357
chr2	243199373	14324234	0.0589	1.0907
chr3	198022430	12129264	0.0613	0.3521
chr4	191154276	9450243	0.0494	0.4317
chr5	180915260	10256962	0.0567	0.3607
chr6	171115067	9375704	0.0548	0.3651
chr7	159138663	16890400	0.1061	1.7685

chr8	146364022	18463565	0.1261	0.6585
chr9	141213431	6993861	0.0495	0.6203
chr10	135534747	8458023	0.0624	0.9344
chr11	135006516	8335118	0.0617	0.44
chr12	133851895	7307946	0.0546	0.3348
chr13	115169878	6087360	0.0529	0.3211
chr14	107349540	6374190	0.0594	0.3839
chr15	102531392	5146743	0.0502	0.3144
chr16	90354753	4697377	0.052	0.7998
chr17	81195210	5068799	0.0624	0.4585
chr18	78077248	3367871	0.0431	0.719
chr19	59128983	4058737	0.0686	1.1356
chr20	63025520	7848986	0.1245	0.5469
chr21	48129895	2306726	0.0479	0.3837
chr22	51304566	2324599	0.0453	0.3329
chrMT	16571	437416	26.3965	16.2086
chrX	155270560	7718016	0.0497	0.3962
chrY	59373566	682355	0.0115	0.8893

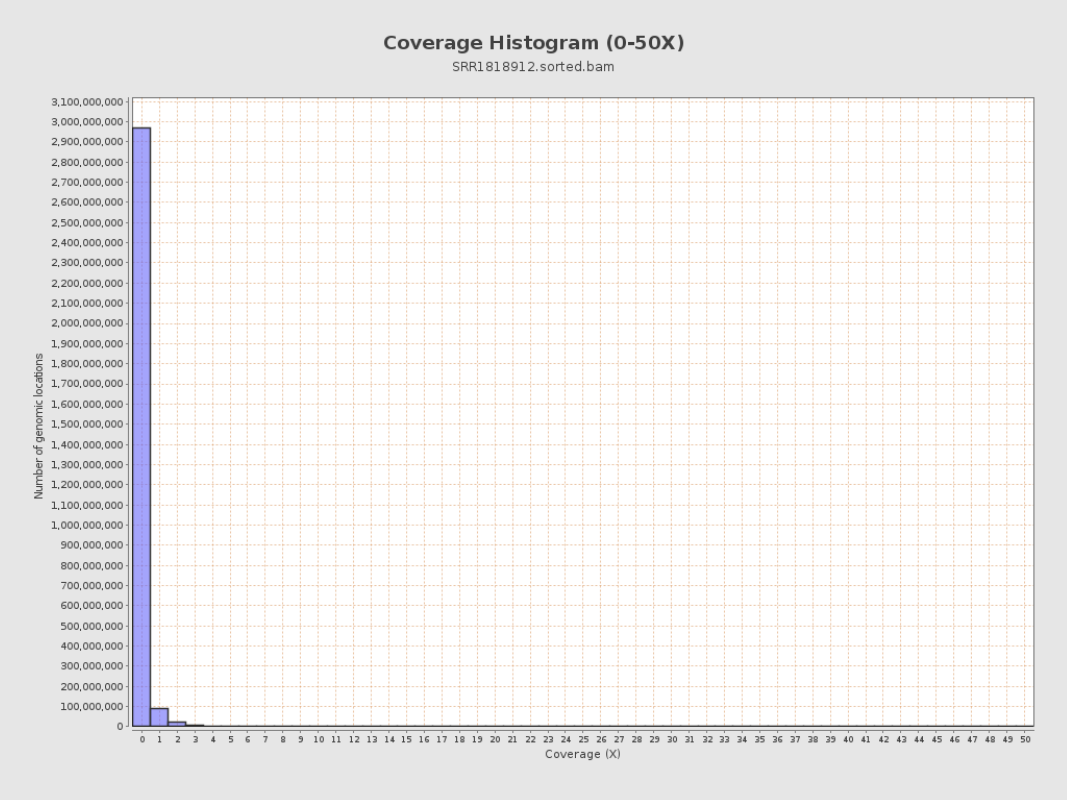
3. Results : Coverage across reference



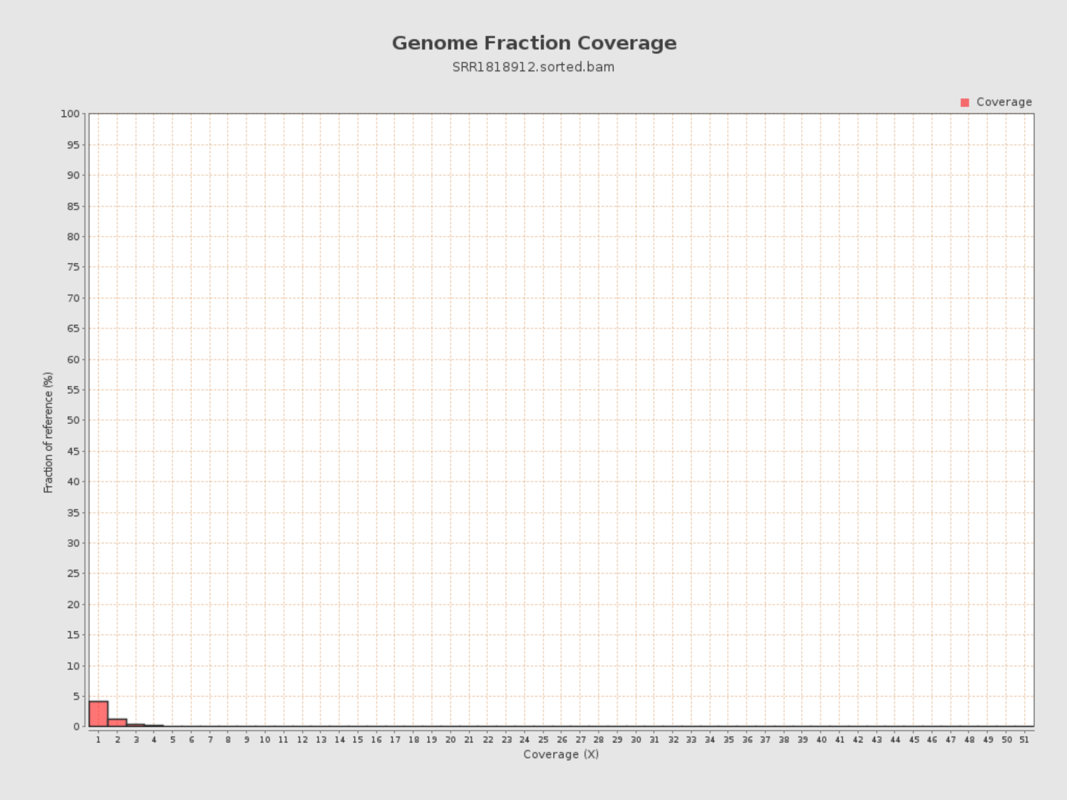
4. Results : Coverage Histogram



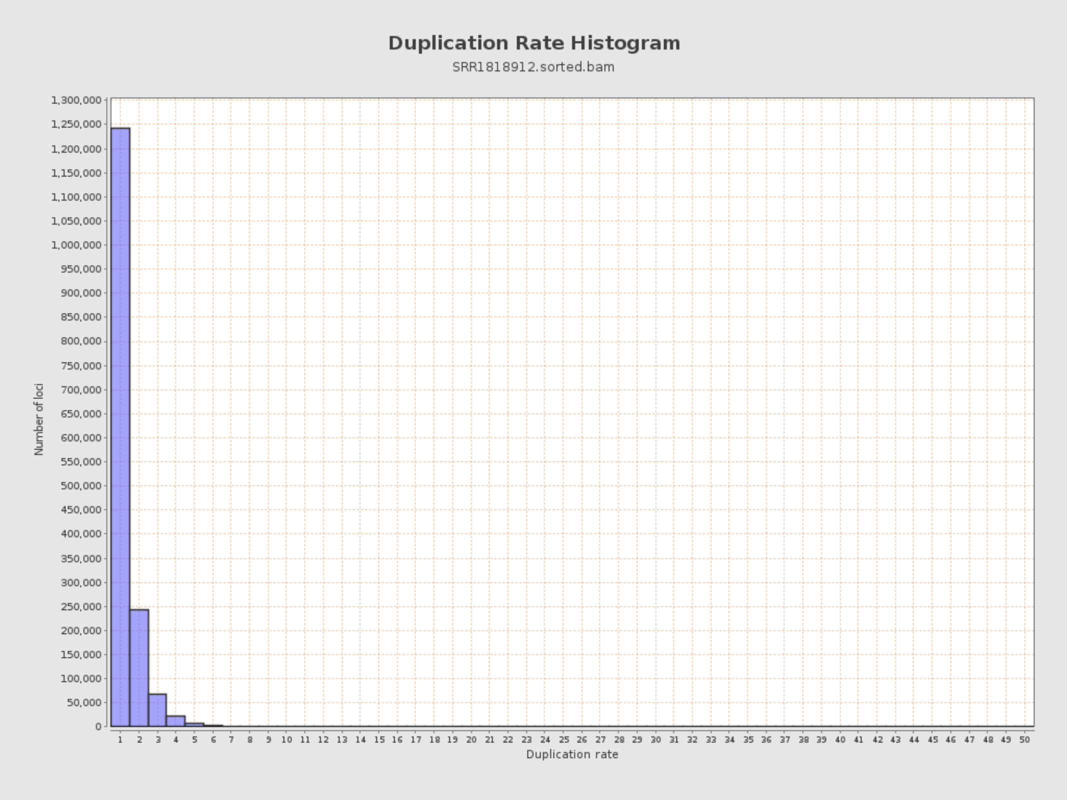
5. Results : Coverage Histogram (0-50X)



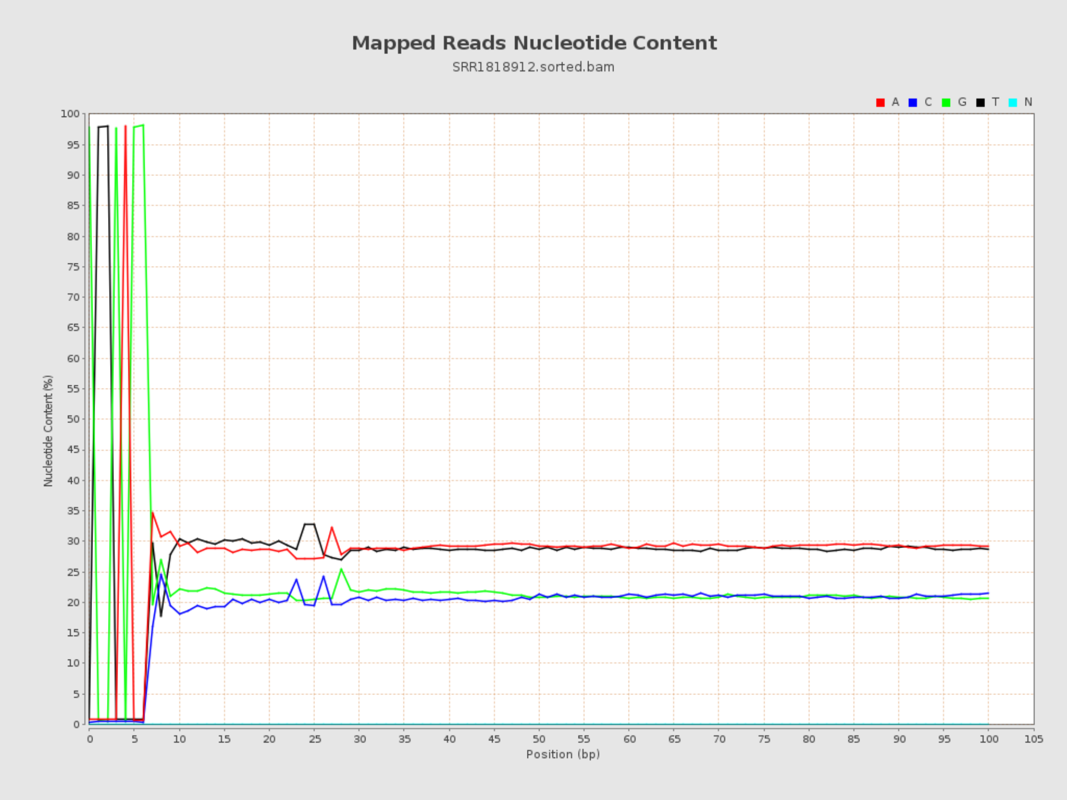
6. Results : Genome Fraction Coverage



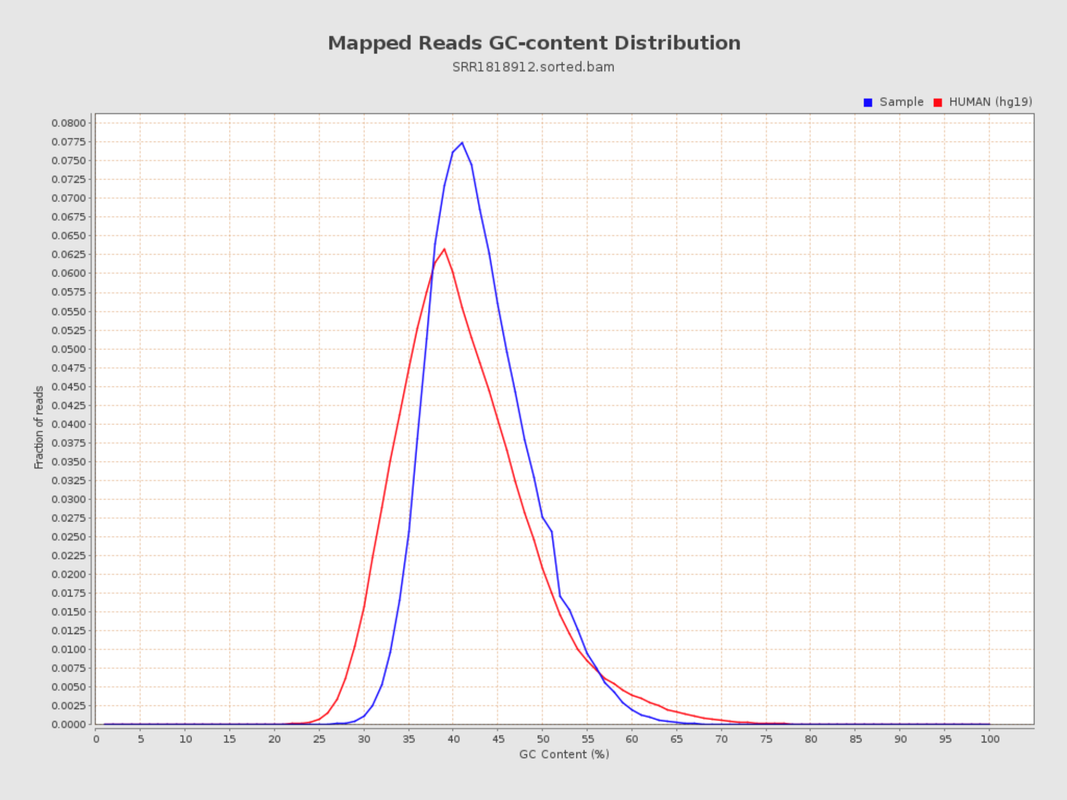
7. Results : Duplication Rate Histogram



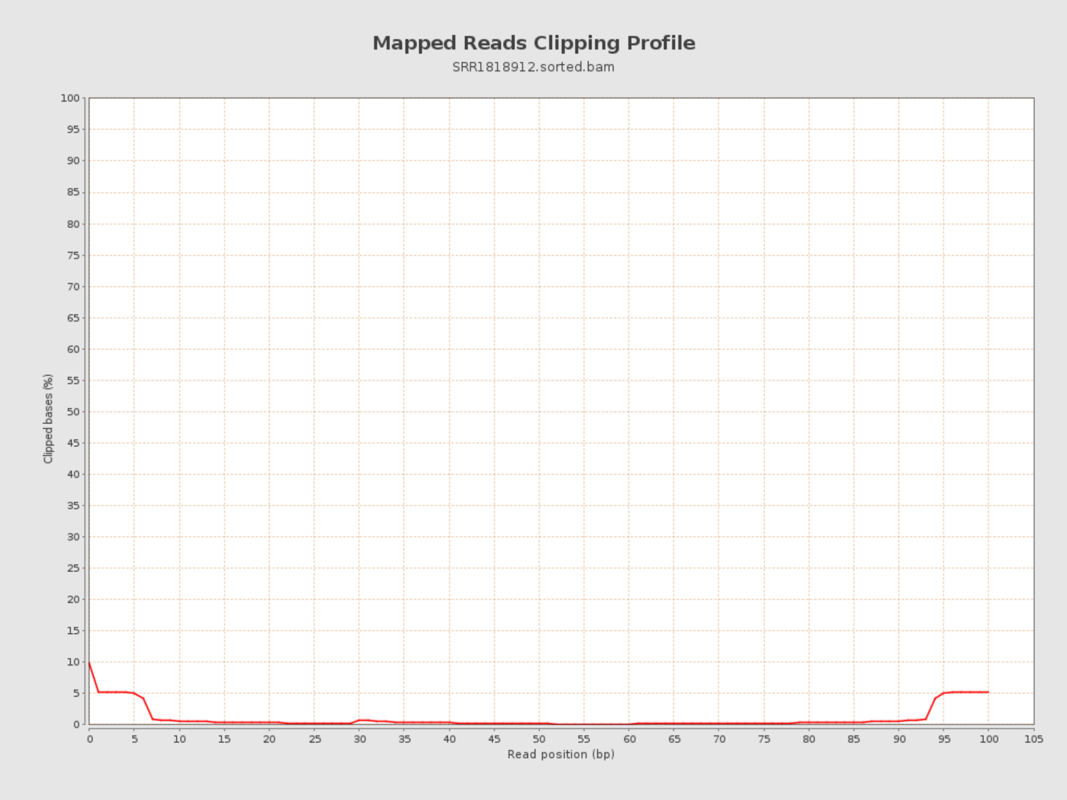
8. Results : Mapped Reads Nucleotide Content



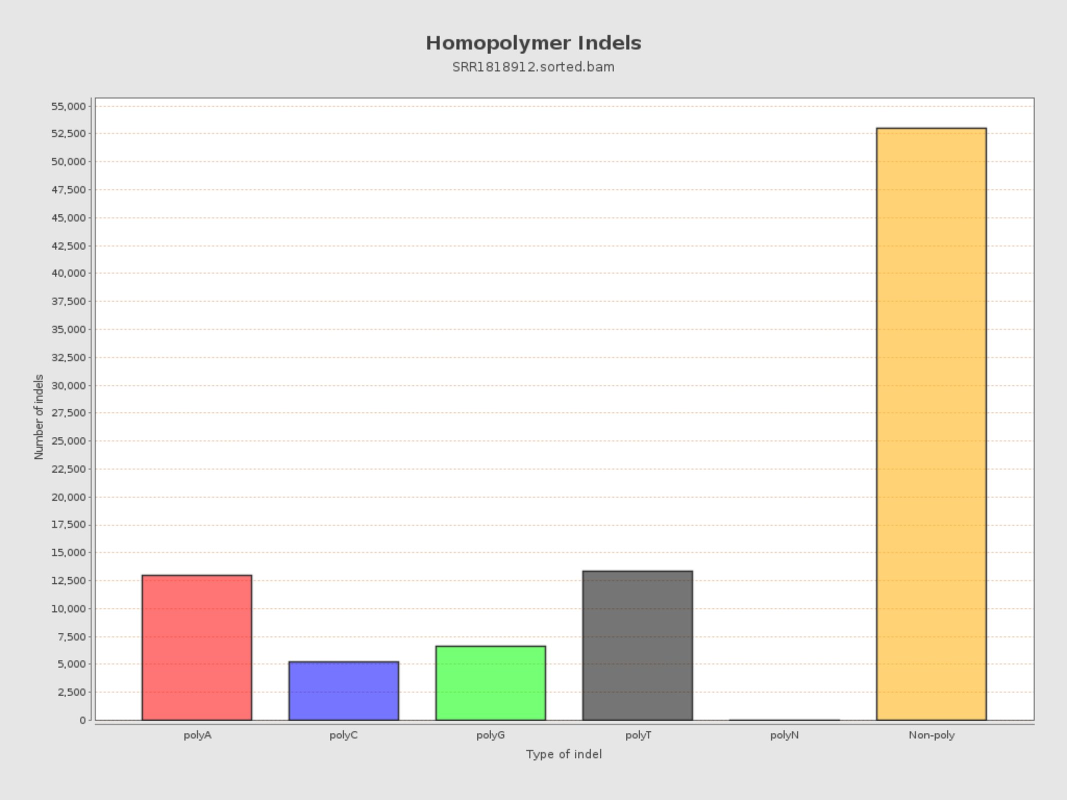
9. Results : Mapped Reads GC-content Distribution



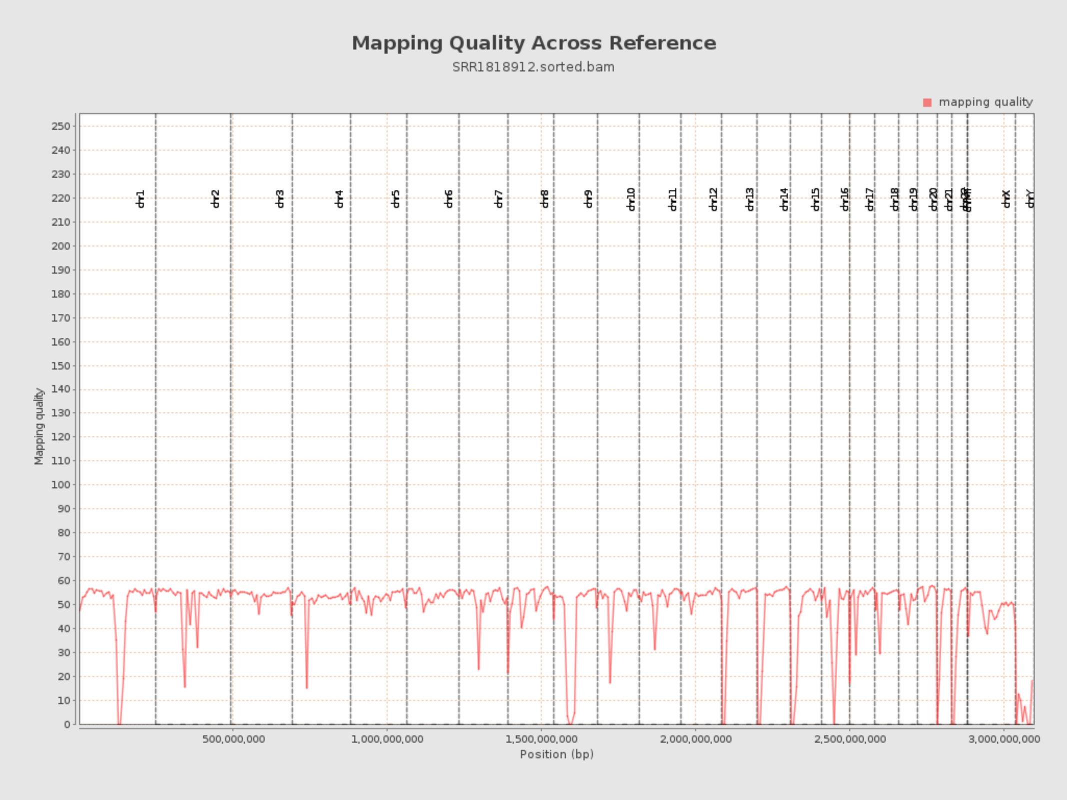
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram