Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:44:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818927.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_SRR1818927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818927.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:44:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,057,787
Mapped reads	2,993,676 / 97.9%
Unmapped reads	64,111 / 2.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,289 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	1,578,516 / 51.62%
Duplication rate	43.66%
Clipped reads	3,005,975 / 98.31%

2.2. ACGT Content

Number/percentage of A's	78,061,650 / 28.15%
Number/percentage of C's	59,352,980 / 21.4%
Number/percentage of T's	82,152,627 / 29.62%
Number/percentage of G's	57,764,540 / 20.83%
Number/percentage of N's	12,528 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0896

Standard Deviation	0.8951

2.4. Mapping Quality

Mean Mapping Quality	49.18

2.5. Mismatches and indels

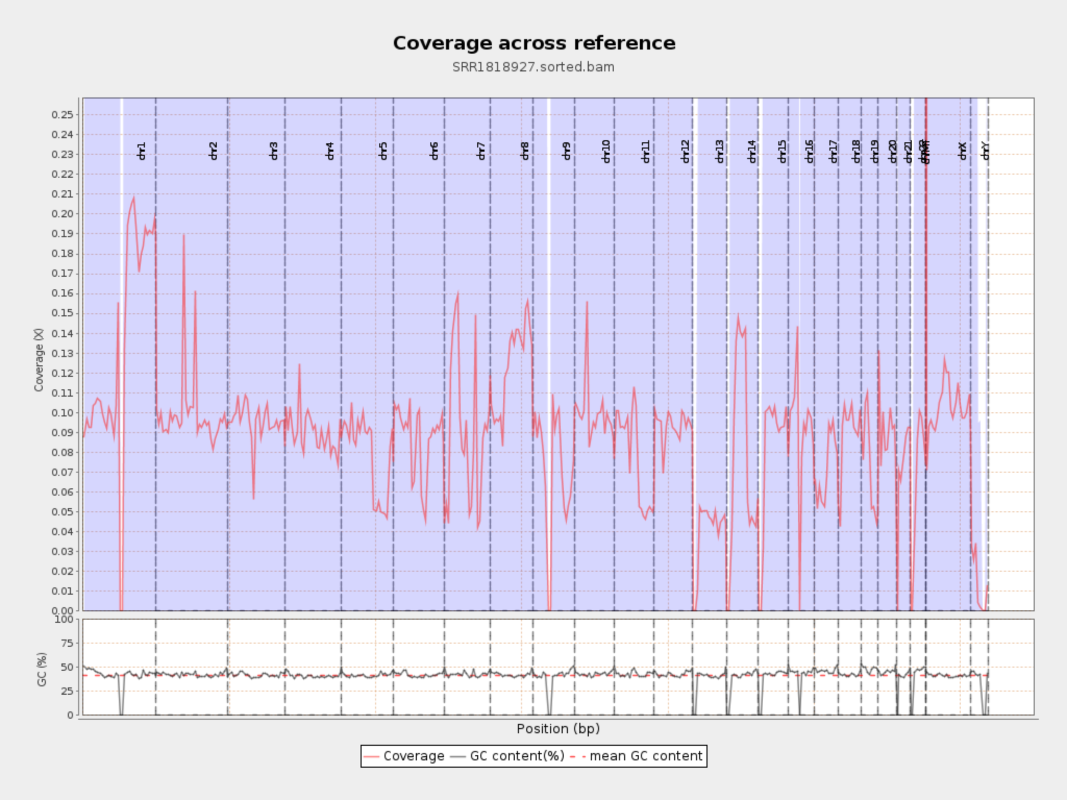
General error rate	0.66%
Mismatches	1,751,152
Insertions	37,891
Mapped reads with at least one insertion	1.23%
Deletions	85,584
Mapped reads with at least one deletion	2.81%
Homopolymer indels	42%

2.6. Chromosome stats

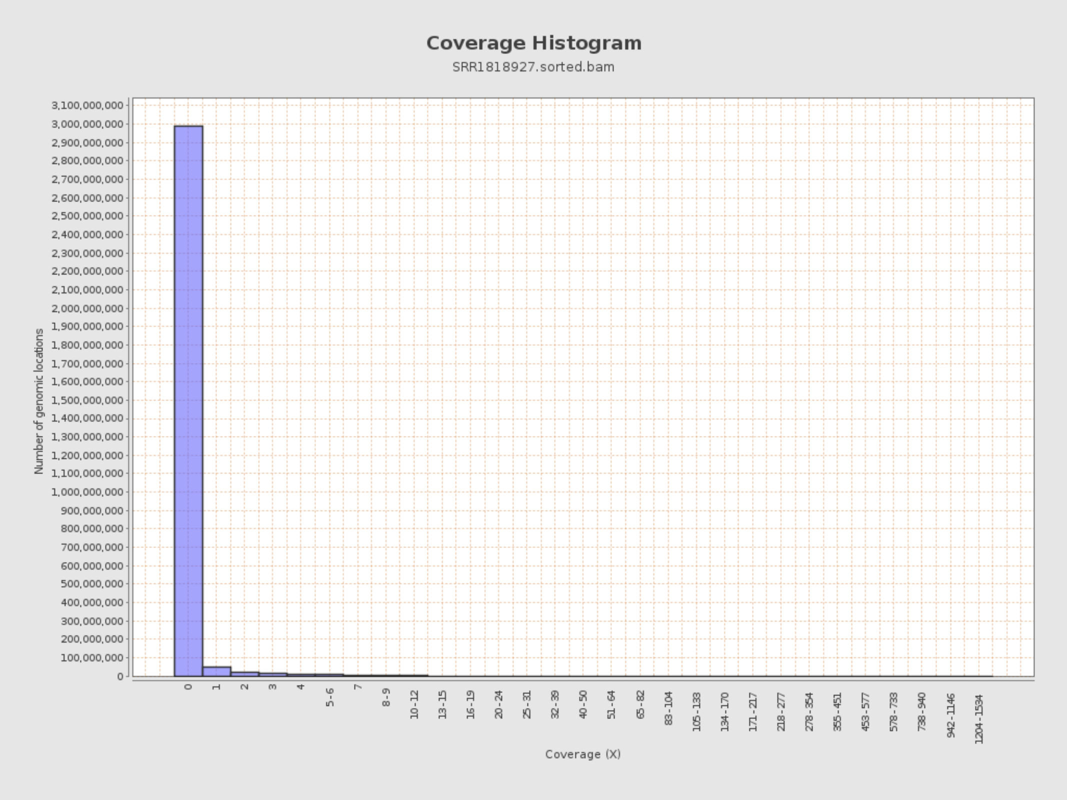
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33267321	0.1335	1.4887
chr2	243199373	24329108	0.1	1.2734
chr3	198022430	18862608	0.0953	0.6446
chr4	191154276	17263318	0.0903	0.6843
chr5	180915260	14281332	0.0789	0.5952
chr6	171115067	14834932	0.0867	0.6684
chr7	159138663	14248555	0.0895	0.8257

chr8	146364022	18169251	0.1241	0.8627
chr9	141213431	10011356	0.0709	0.9531
chr10	135534747	13504063	0.0996	1.0691
chr11	135006516	10403310	0.0771	0.6787
chr12	133851895	12524599	0.0936	0.656
chr13	115169878	4551027	0.0395	0.4091
chr14	107349540	8385198	0.0781	0.6529
chr15	102531392	8081795	0.0788	0.5946
chr16	90354753	8136899	0.0901	0.9191
chr17	81195210	5885664	0.0725	0.6289
chr18	78077248	6932371	0.0888	1.1738
chr19	59128983	4406586	0.0745	1.2437
chr20	63025520	5811146	0.0922	0.6823
chr21	48129895	3517163	0.0731	0.6207
chr22	51304566	3284245	0.064	0.5792
chrMT	16571	88586	5.3458	5.9344
chrX	155270560	15941845	0.1027	0.7708
chrY	59373566	773487	0.013	0.7326

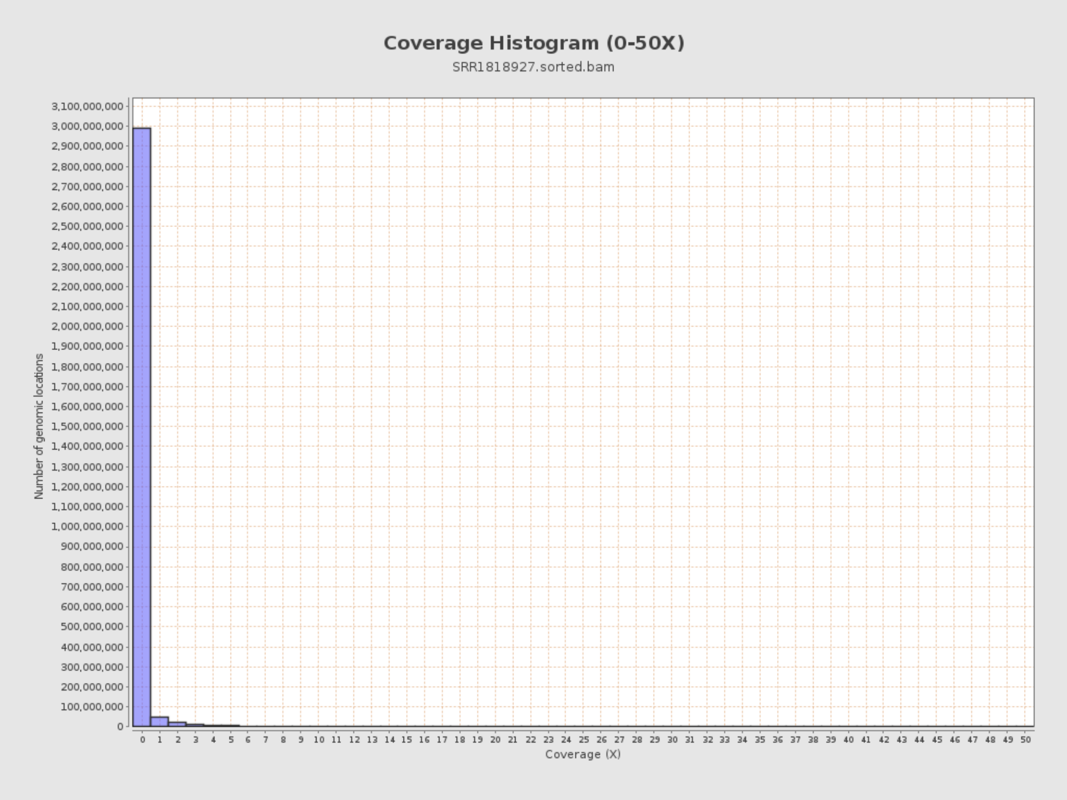
3. Results : Coverage across reference



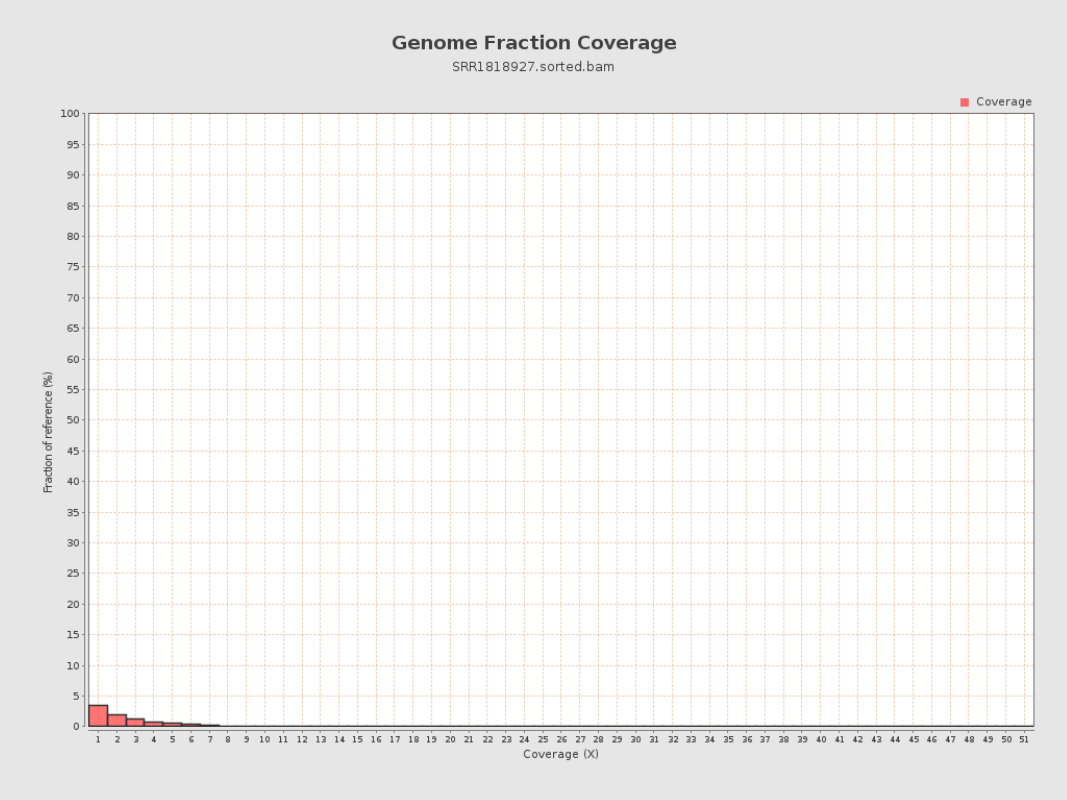
4. Results : Coverage Histogram



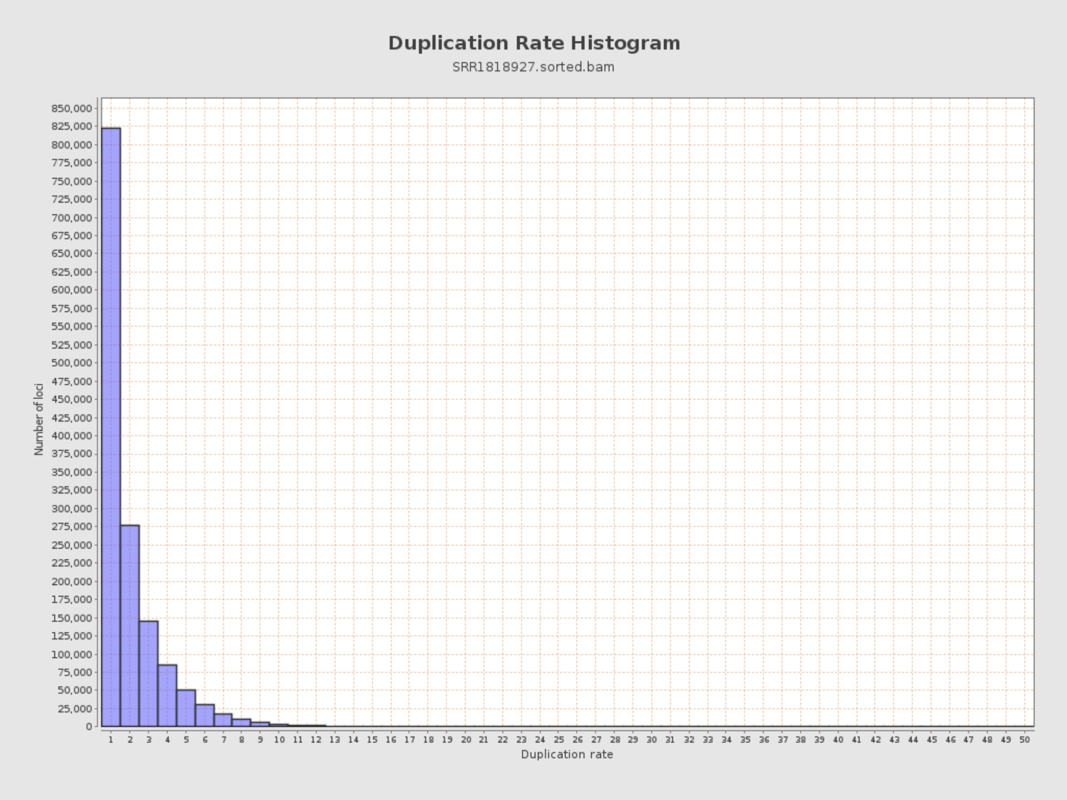
5. Results : Coverage Histogram (0-50X)



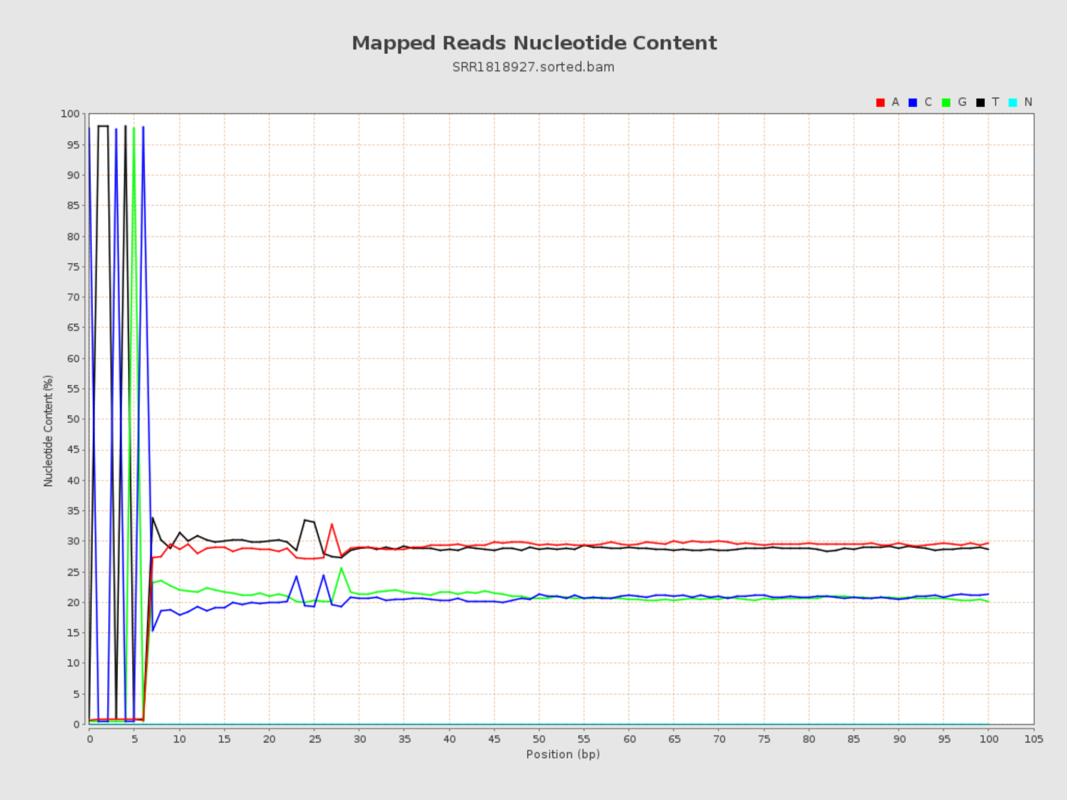
6. Results : Genome Fraction Coverage



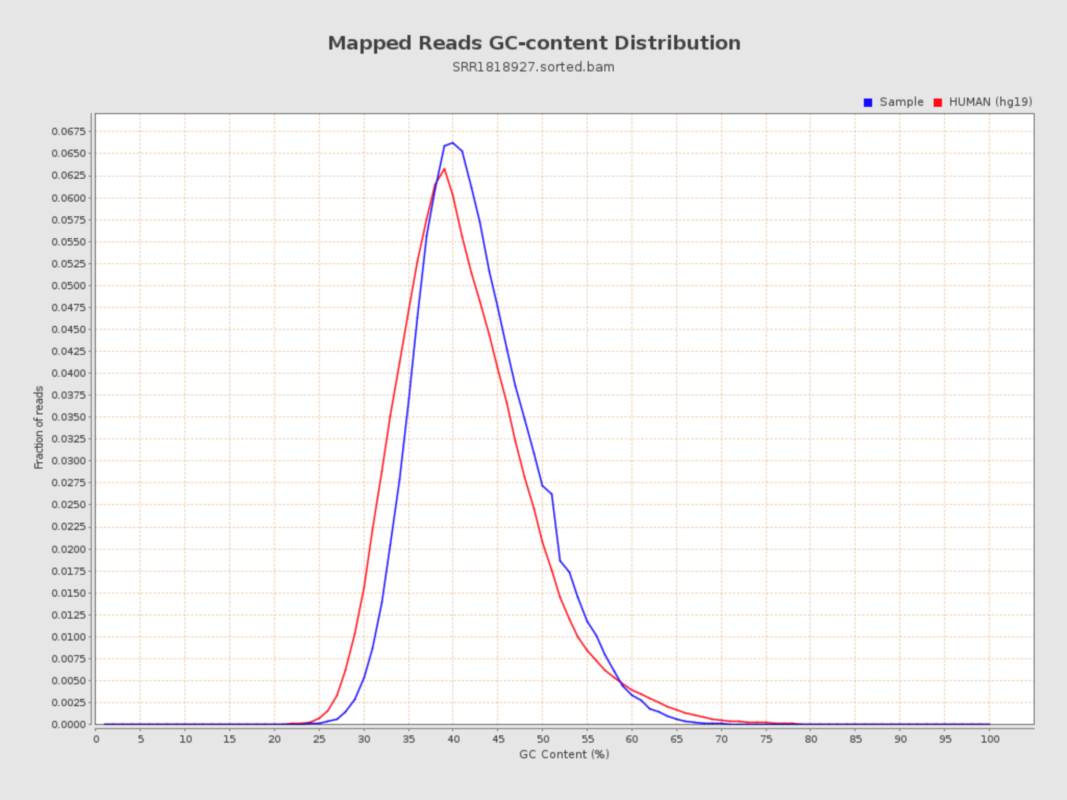
7. Results : Duplication Rate Histogram



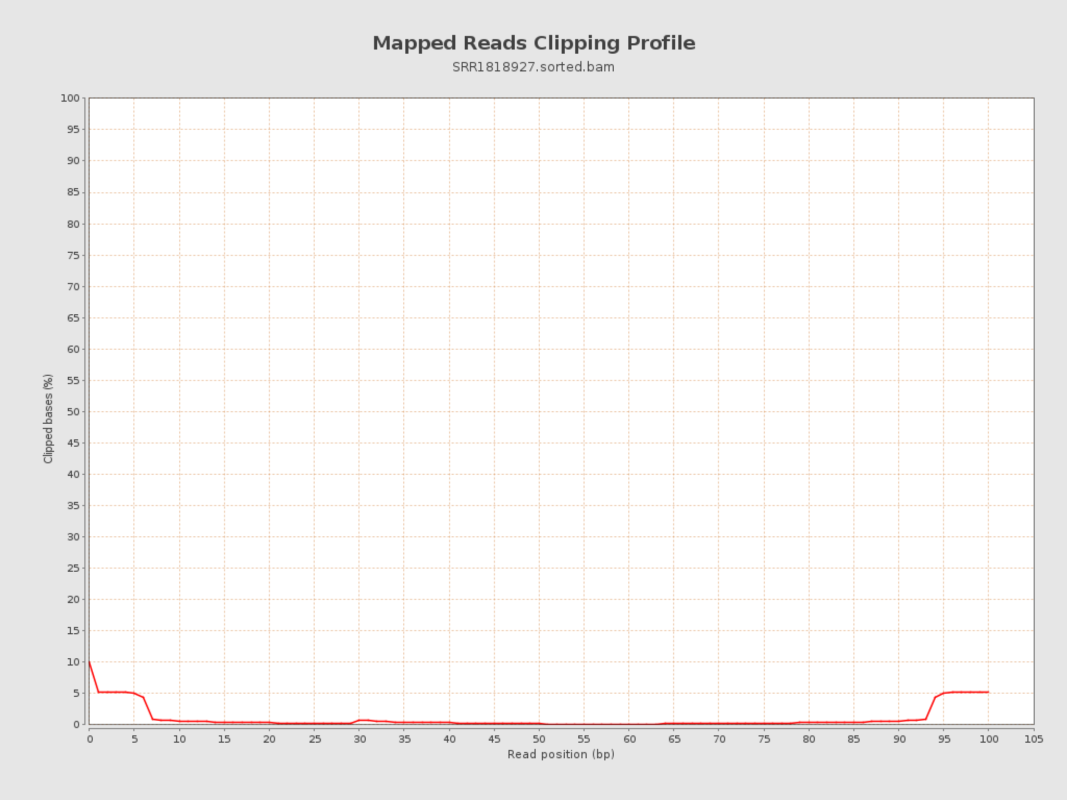
8. Results : Mapped Reads Nucleotide Content



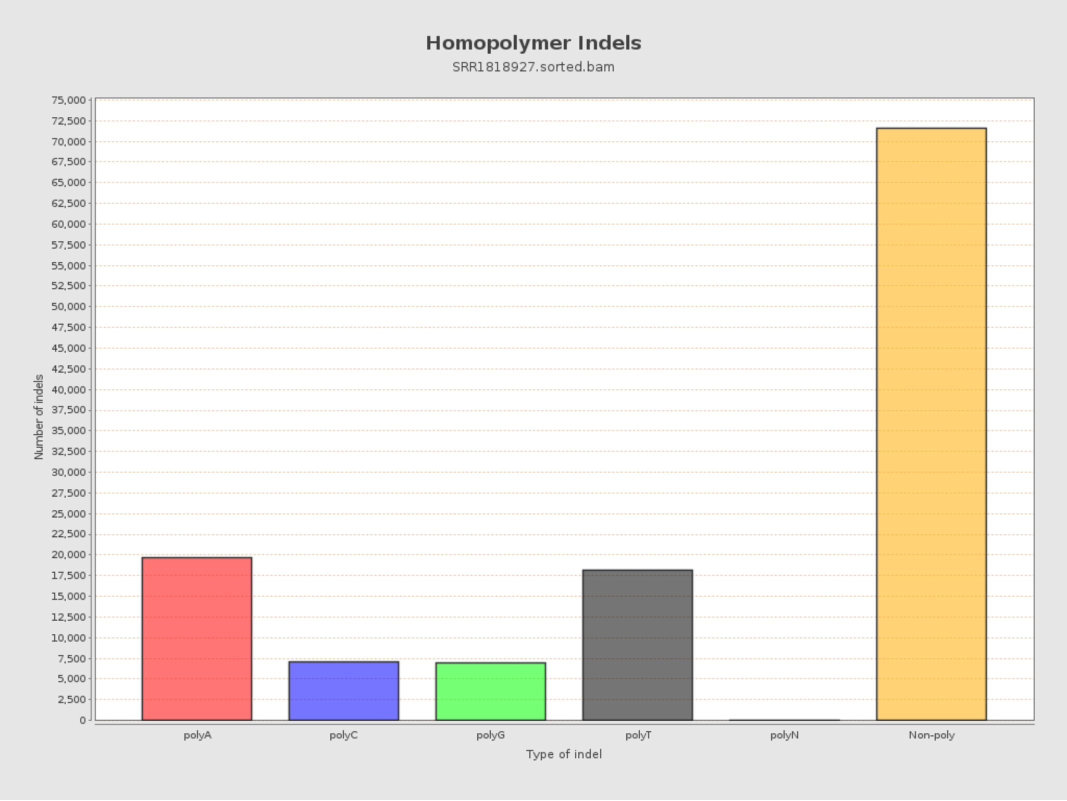
9. Results : Mapped Reads GC-content Distribution



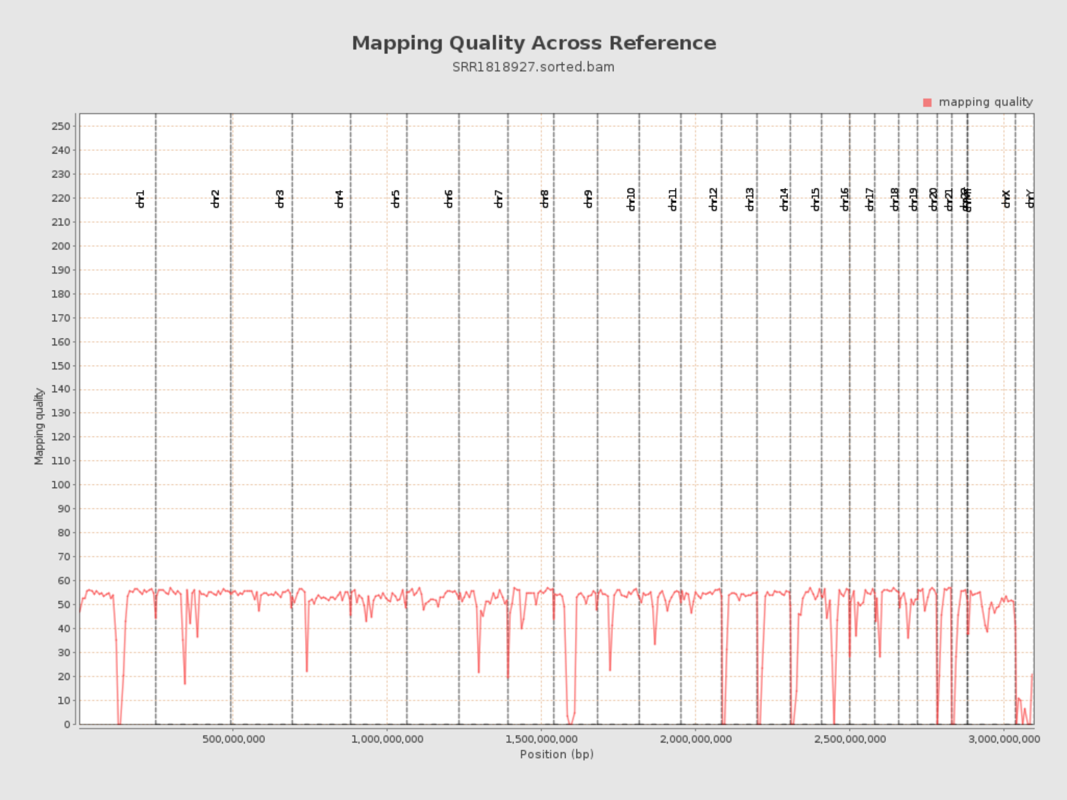
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram