Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:27:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818938.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_SRR1818938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818938.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:27:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	227,134
Mapped reads	221,622 / 97.57%
Unmapped reads	5,512 / 2.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,011 / 1.33%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	22,576 / 9.94%
Duplication rate	9.05%
Clipped reads	223,711 / 98.49%

2.2. ACGT Content

Number/percentage of A's	5,895,688 / 28.73%
Number/percentage of C's	4,534,271 / 22.1%
Number/percentage of T's	5,765,299 / 28.1%
Number/percentage of G's	4,323,356 / 21.07%
Number/percentage of N's	985 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0066

Standard Deviation	0.107

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

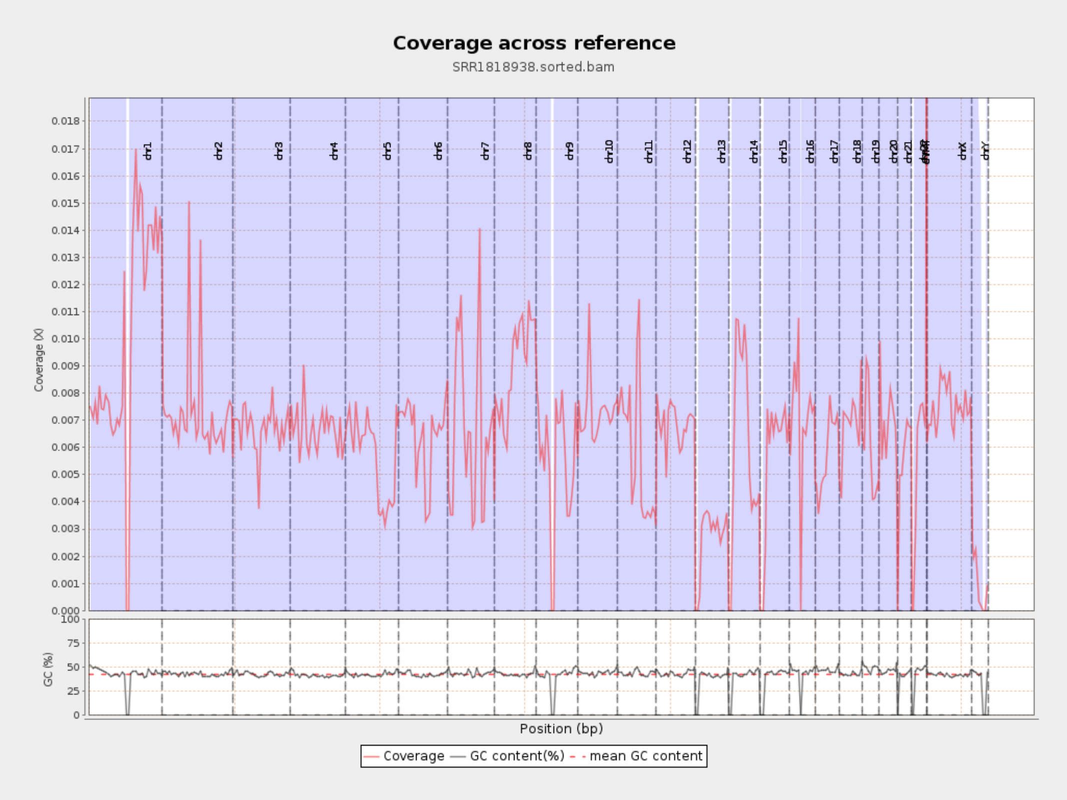
General error rate	0.66%
Mismatches	128,553
Insertions	2,625
Mapped reads with at least one insertion	1.15%
Deletions	6,123
Mapped reads with at least one deletion	2.72%
Homopolymer indels	43.23%

2.6. Chromosome stats

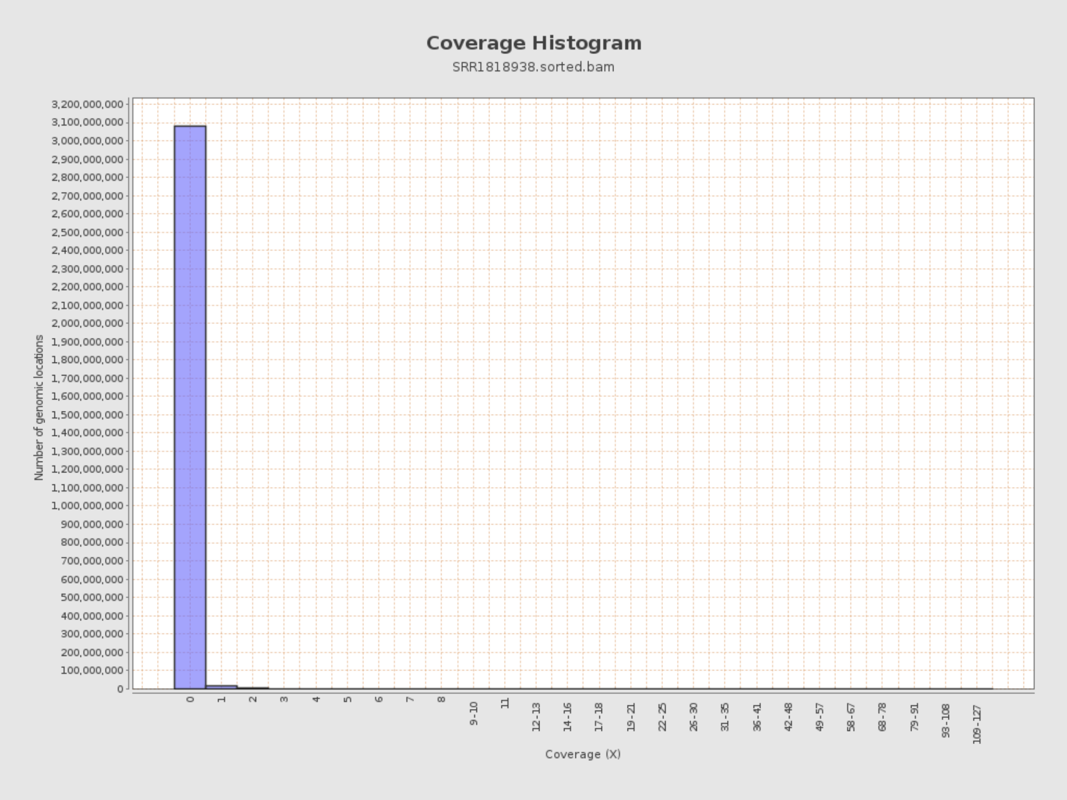
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2462013	0.0099	0.1531
chr2	243199373	1775289	0.0073	0.1428
chr3	198022430	1324582	0.0067	0.0921
chr4	191154276	1270555	0.0066	0.0935
chr5	180915260	1028347	0.0057	0.0858
chr6	171115067	1104694	0.0065	0.0926
chr7	159138663	1049871	0.0066	0.0964

chr8	146364022	1322954	0.009	0.1106
chr9	141213431	754520	0.0053	0.1011
chr10	135534747	988891	0.0073	0.1151
chr11	135006516	803301	0.006	0.0902
chr12	133851895	920414	0.0069	0.0937
chr13	115169878	306989	0.0027	0.0579
chr14	107349540	660281	0.0062	0.0907
chr15	102531392	567528	0.0055	0.0842
chr16	90354753	638856	0.0071	0.1232
chr17	81195210	476478	0.0059	0.0882
chr18	78077248	531144	0.0068	0.1284
chr19	59128983	360696	0.0061	0.1429
chr20	63025520	439796	0.007	0.0966
chr21	48129895	262221	0.0054	0.0845
chr22	51304566	257921	0.005	0.0833
chrMT	16571	566	0.0342	0.2357
chrX	155270560	1166344	0.0075	0.1035
chrY	59373566	56296	0.0009	0.0676

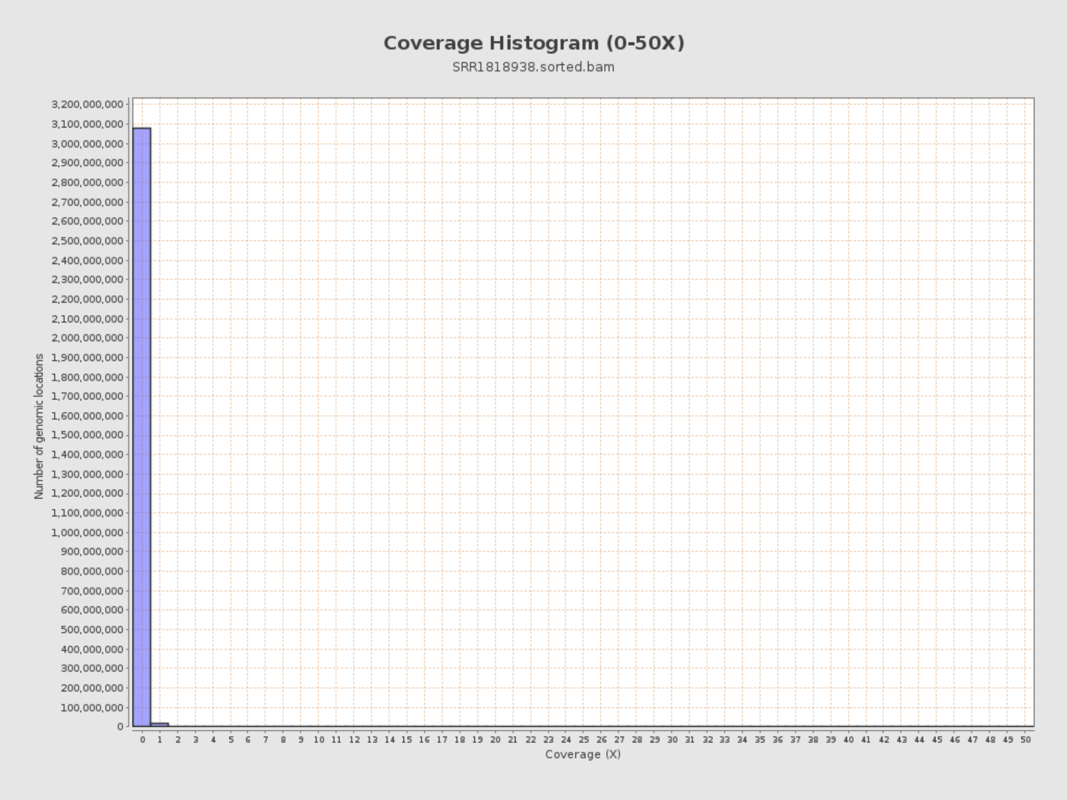
3. Results : Coverage across reference



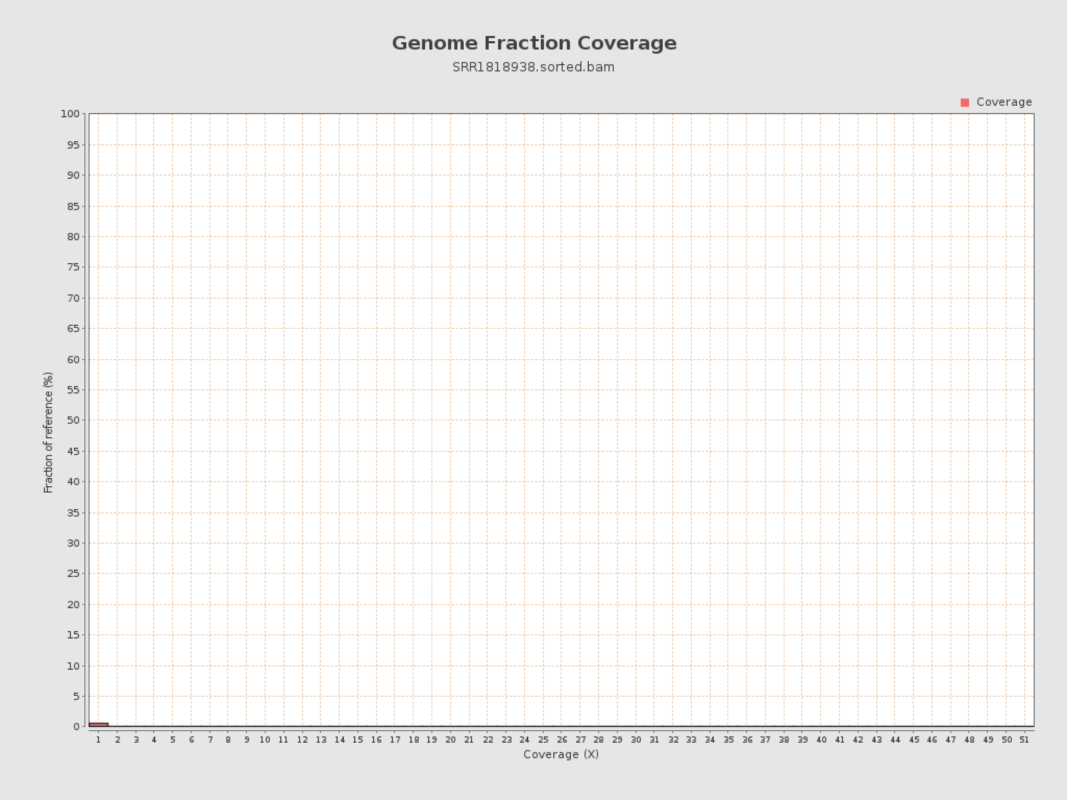
4. Results : Coverage Histogram



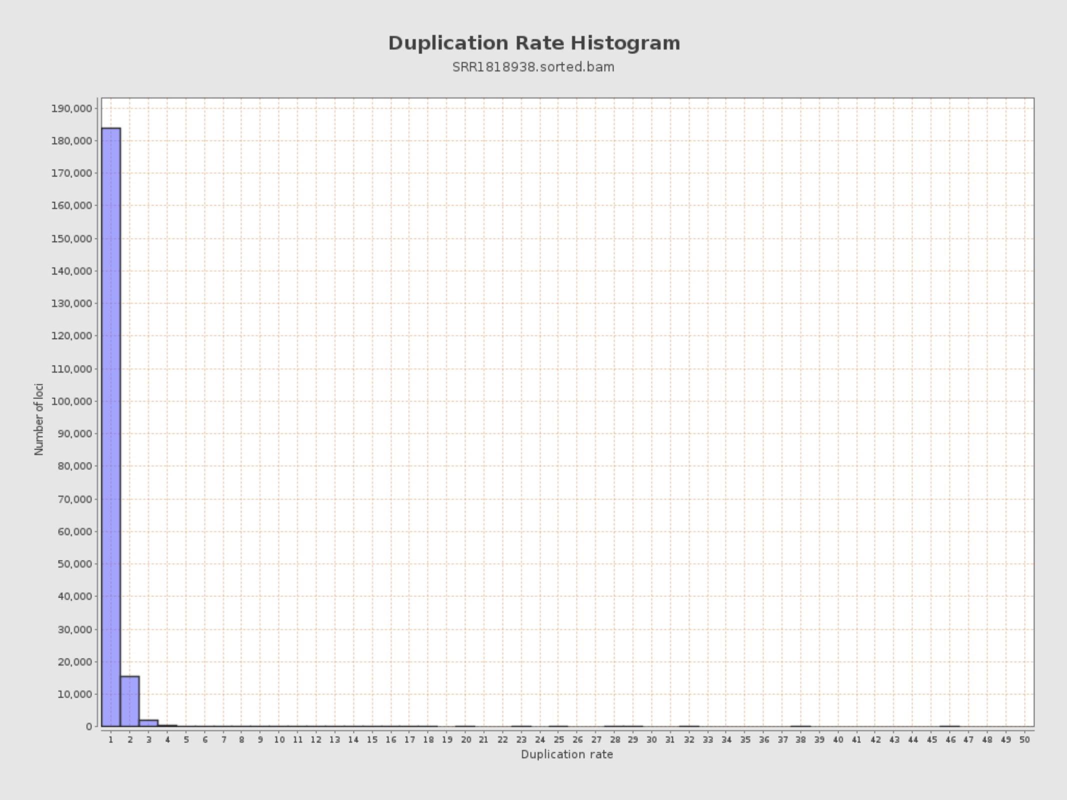
5. Results : Coverage Histogram (0-50X)



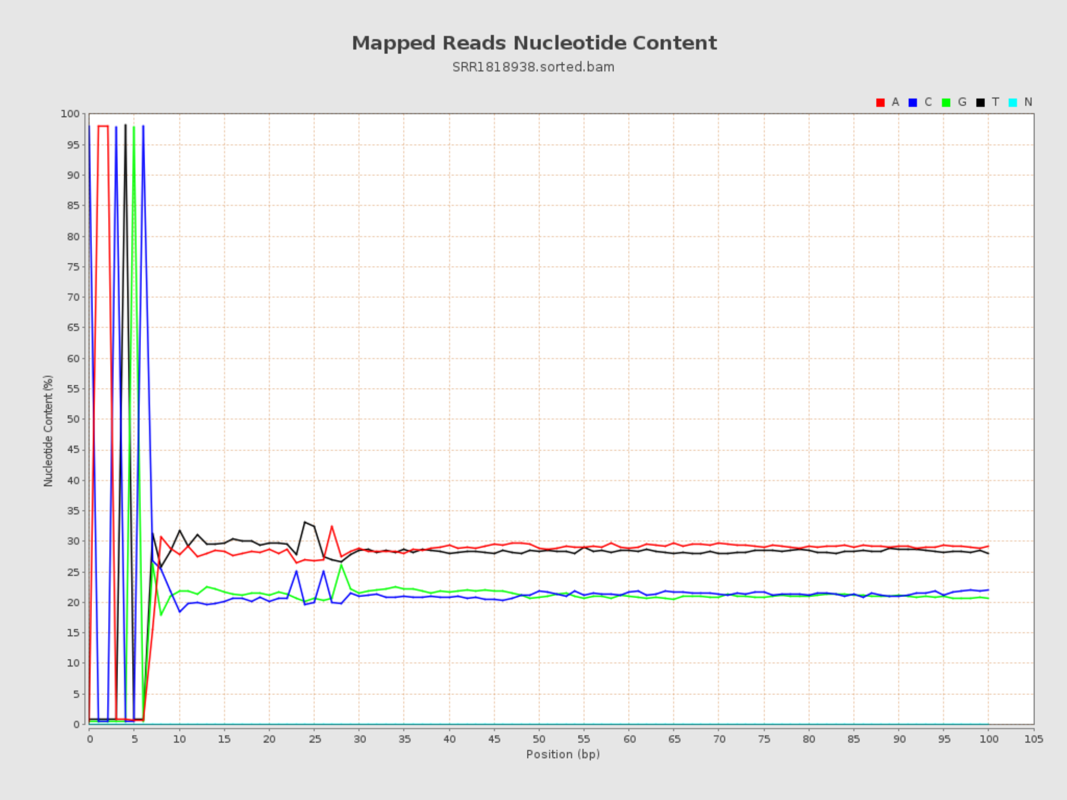
6. Results : Genome Fraction Coverage



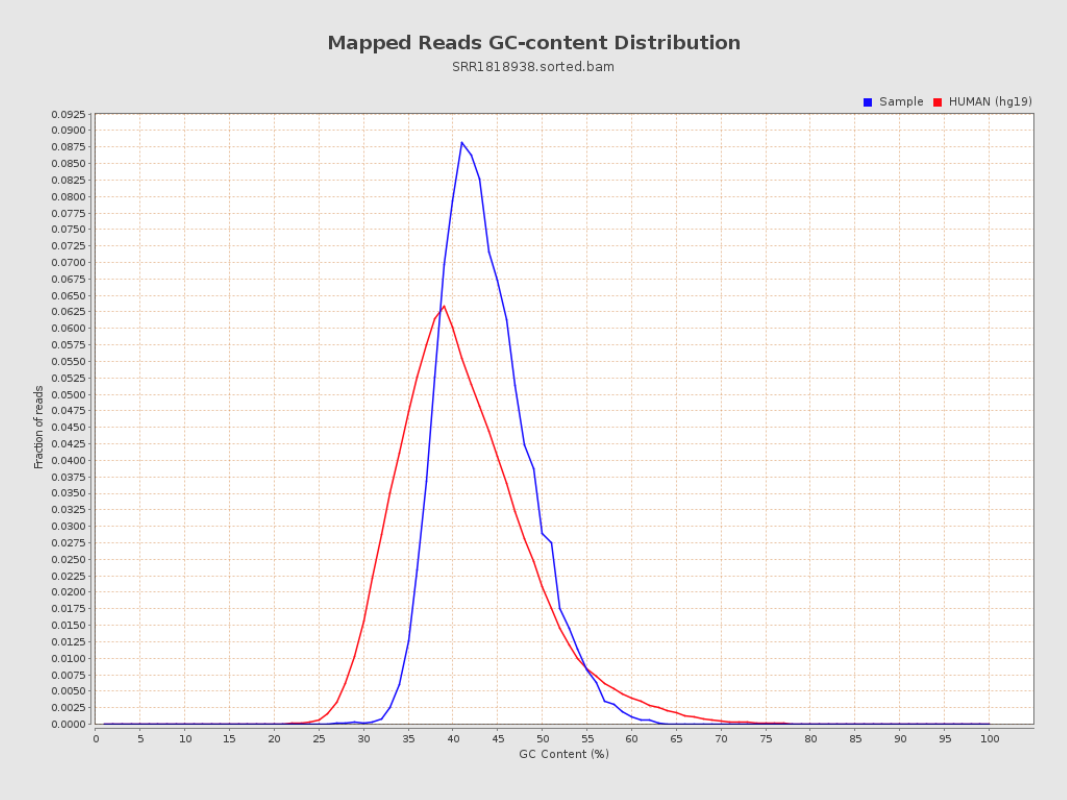
7. Results : Duplication Rate Histogram



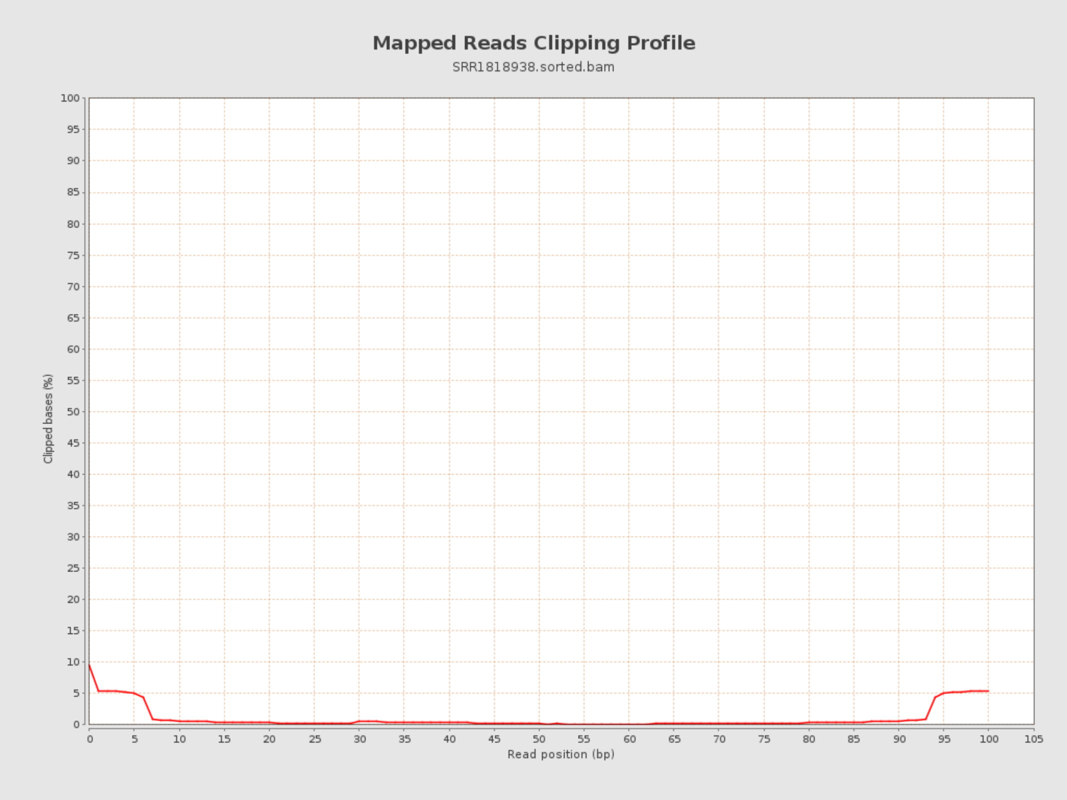
8. Results : Mapped Reads Nucleotide Content



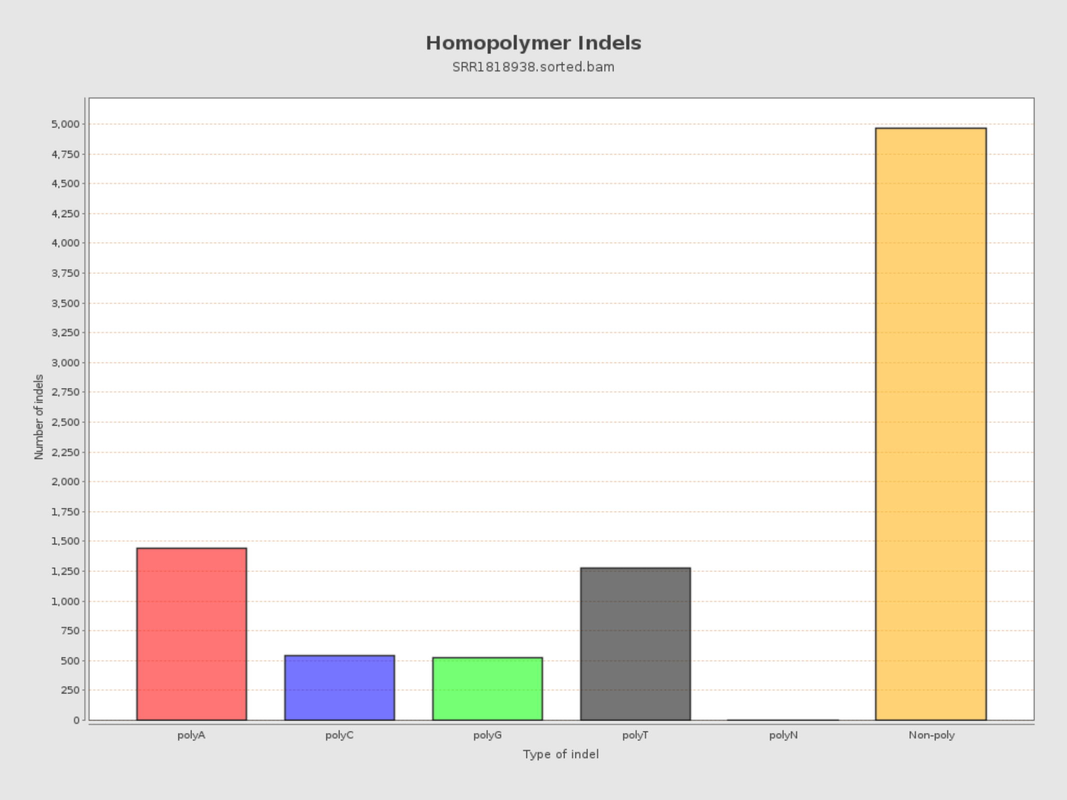
9. Results : Mapped Reads GC-content Distribution



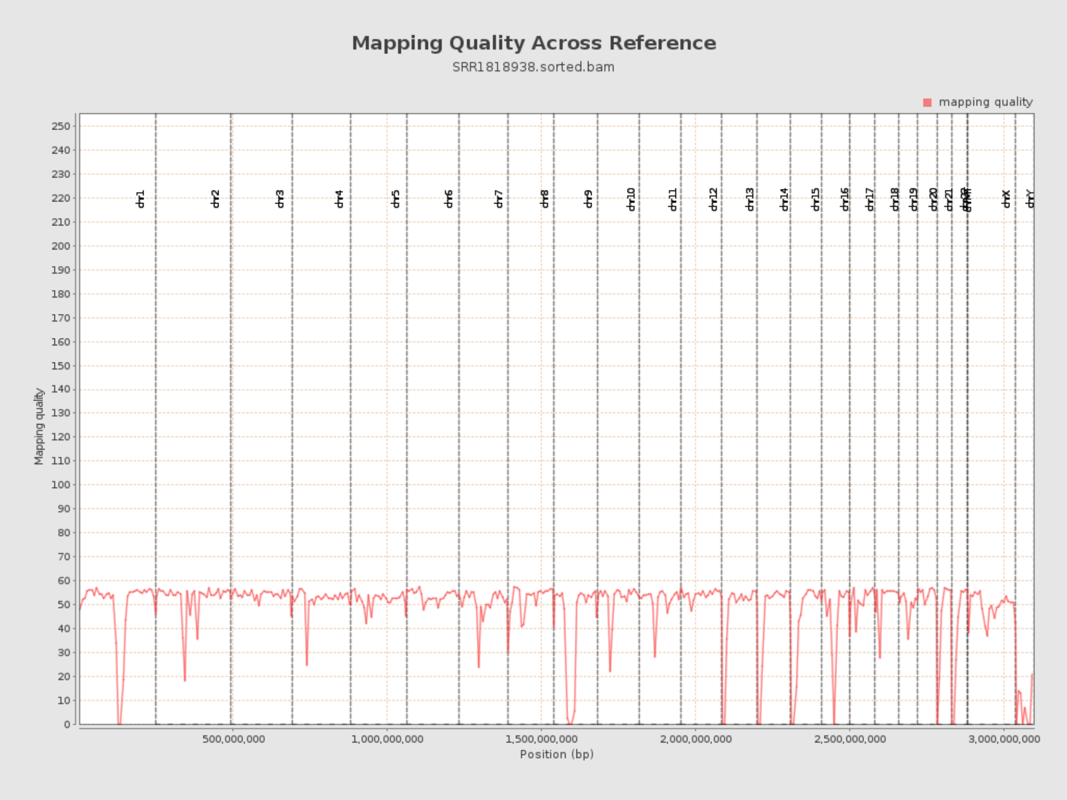
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram