Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:56:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818982.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_SRR1818982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:56:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,375,765
Mapped reads	1,356,451 / 98.6%
Unmapped reads	19,314 / 1.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,300 / 1.33%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	516,612 / 37.55%
Duplication rate	32.24%
Clipped reads	1,367,301 / 99.38%

2.2. ACGT Content

Number/percentage of A's	36,433,707 / 29.01%
Number/percentage of C's	28,217,824 / 22.47%
Number/percentage of T's	34,510,919 / 27.48%
Number/percentage of G's	26,403,354 / 21.03%
Number/percentage of N's	6,339 / 0.01%
GC Percentage	43.5%

2.3. Coverage

Mean	0.0406

Standard Deviation	0.5102

2.4. Mapping Quality

Mean Mapping Quality	49.21

2.5. Mismatches and indels

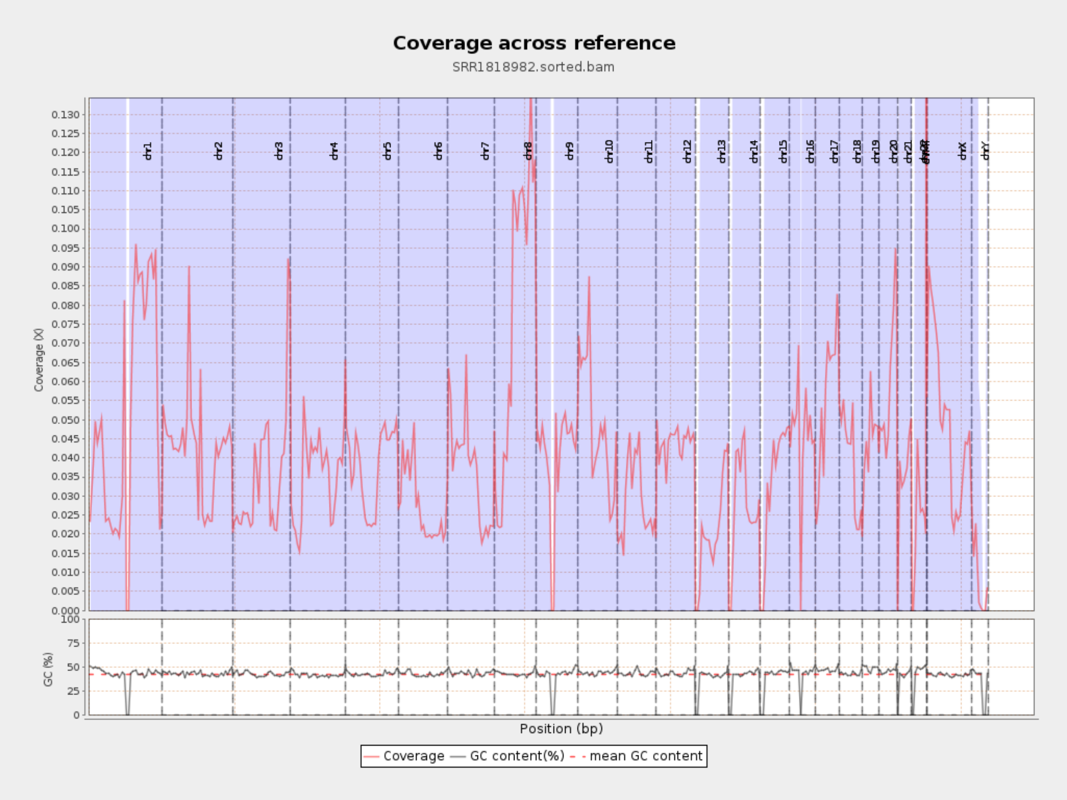
General error rate	0.67%
Mismatches	793,735
Insertions	18,794
Mapped reads with at least one insertion	1.34%
Deletions	39,310
Mapped reads with at least one deletion	2.83%
Homopolymer indels	41.6%

2.6. Chromosome stats

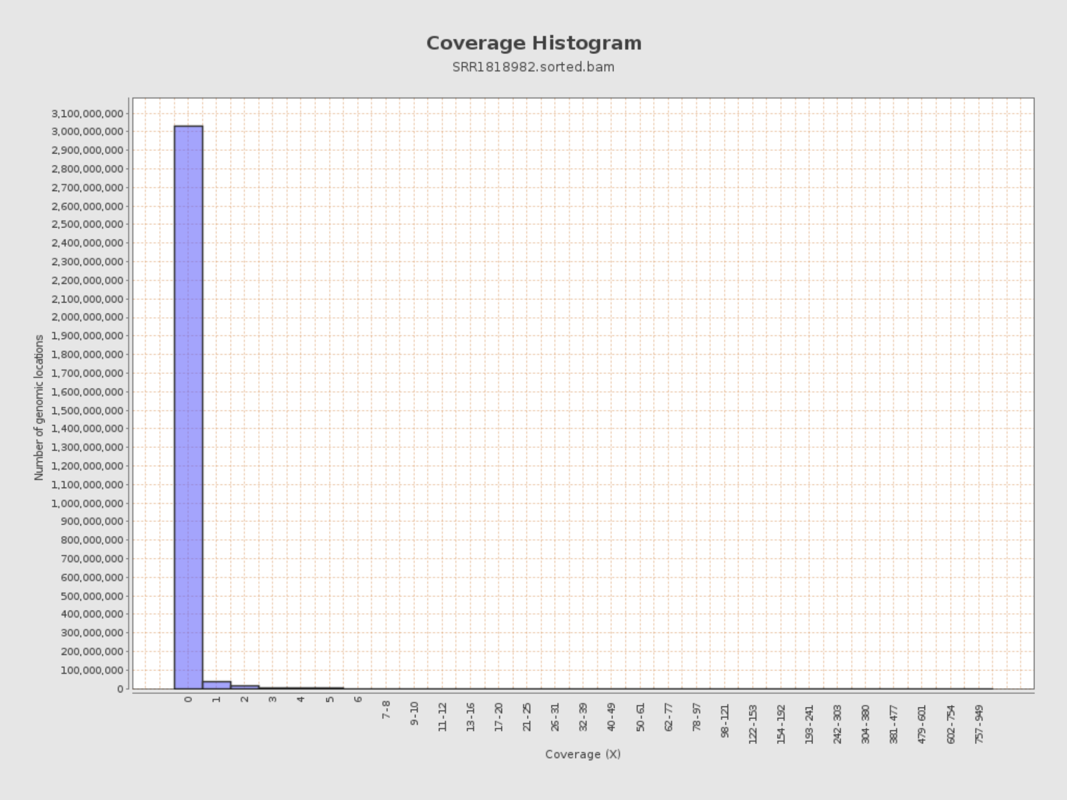
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12642112	0.0507	0.894
chr2	243199373	10425818	0.0429	0.6986
chr3	198022430	6841486	0.0345	0.3081
chr4	191154276	6715833	0.0351	0.3477
chr5	180915260	6905412	0.0382	0.3365
chr6	171115067	4714519	0.0276	0.3106
chr7	159138663	5859431	0.0368	0.5636

chr8	146364022	11586895	0.0792	0.5095
chr9	141213431	5578143	0.0395	0.4787
chr10	135534747	6624289	0.0489	0.6326
chr11	135006516	3948361	0.0292	0.3217
chr12	133851895	5903606	0.0441	0.3565
chr13	115169878	2352526	0.0204	0.2355
chr14	107349540	2903694	0.027	0.2818
chr15	102531392	3387247	0.033	0.3019
chr16	90354753	4120468	0.0456	0.5814
chr17	81195210	4588480	0.0565	0.4429
chr18	78077248	3114888	0.0399	0.5303
chr19	59128983	2646334	0.0448	0.9017
chr20	63025520	3796961	0.0602	0.4354
chr21	48129895	1705451	0.0354	0.3558
chr22	51304566	1097248	0.0214	0.2632
chrMT	16571	10379	0.6263	1.1546
chrX	155270560	7719716	0.0497	0.4073
chrY	59373566	455991	0.0077	0.49

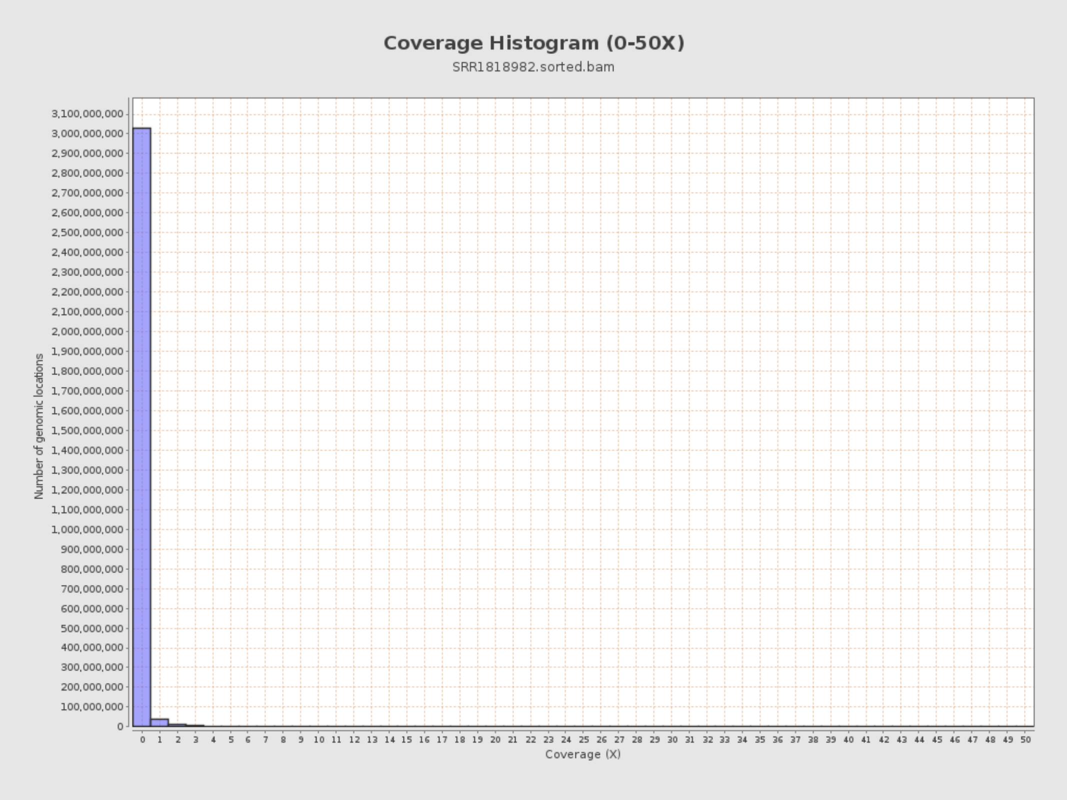
3. Results : Coverage across reference



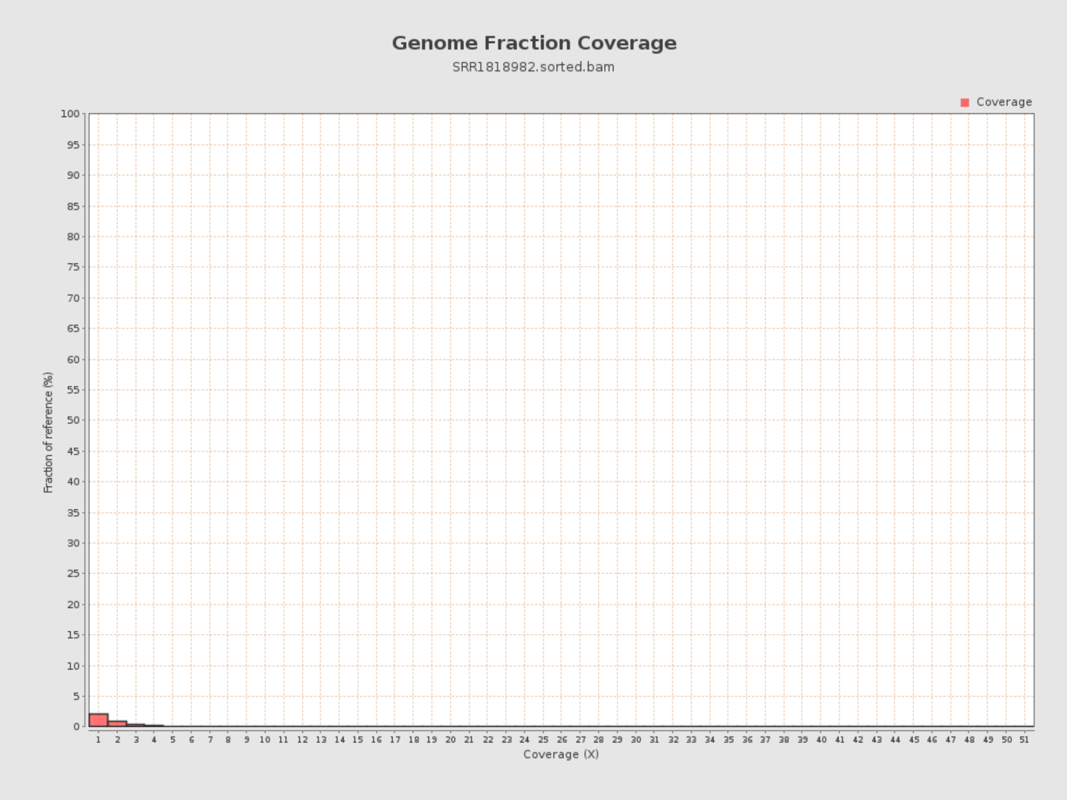
4. Results : Coverage Histogram



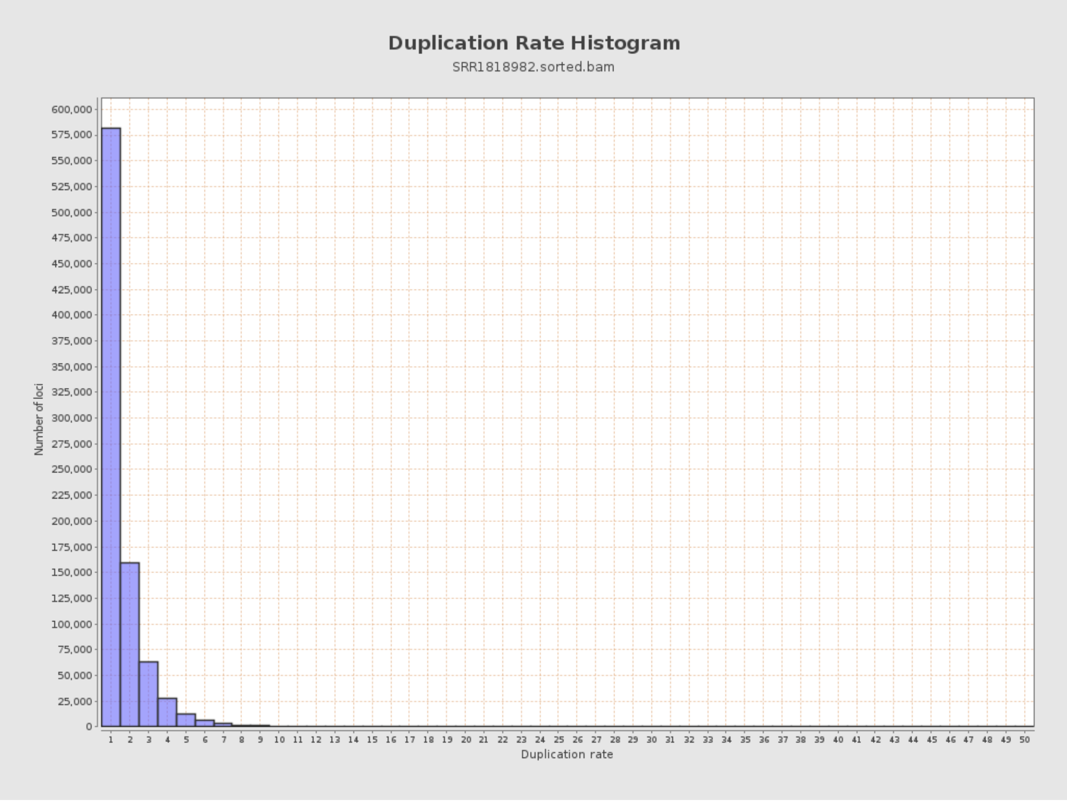
5. Results : Coverage Histogram (0-50X)



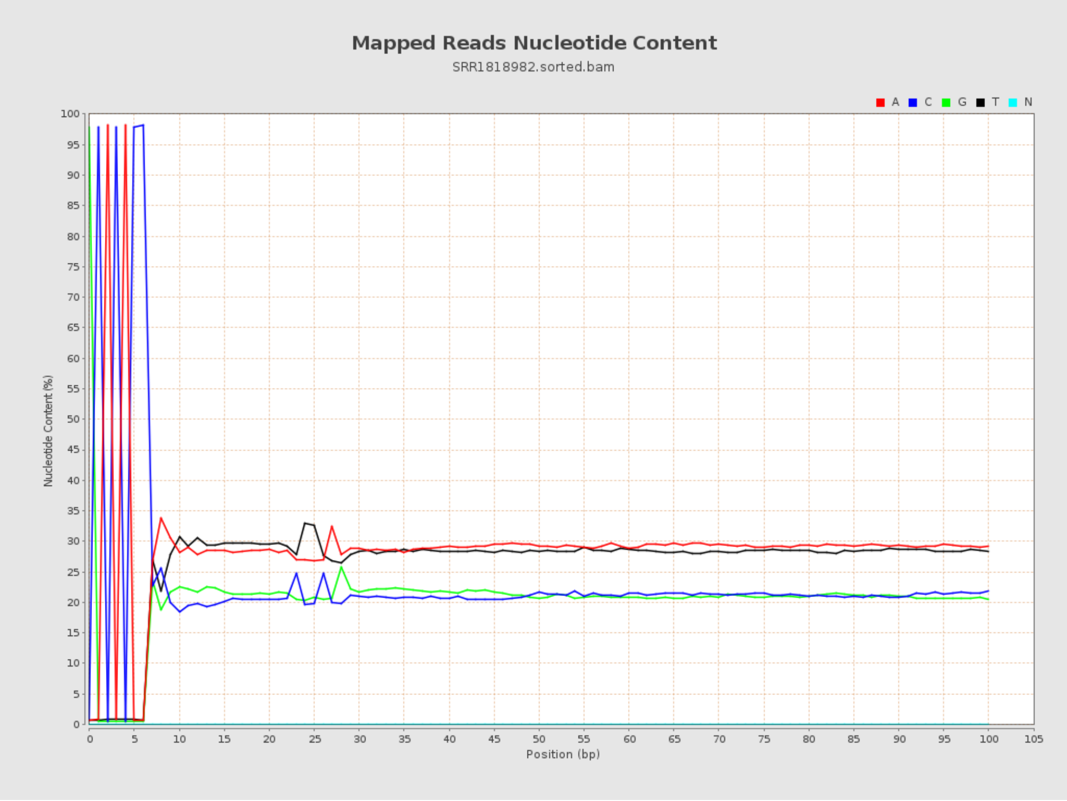
6. Results : Genome Fraction Coverage



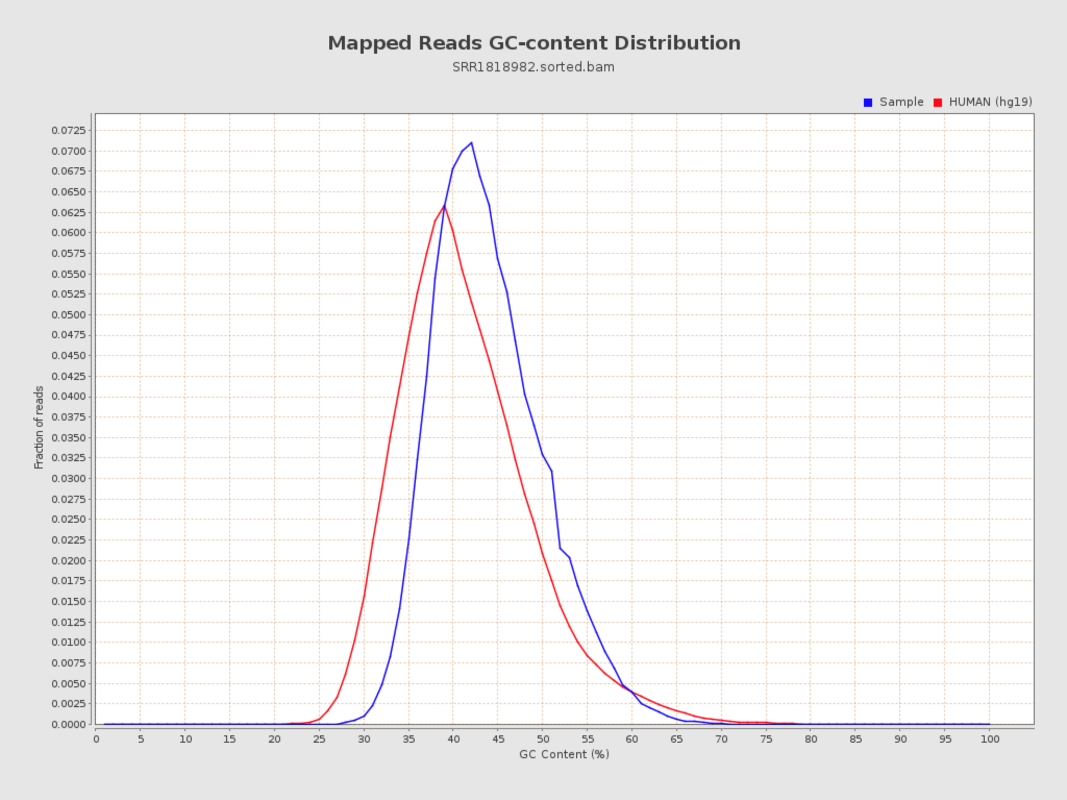
7. Results : Duplication Rate Histogram



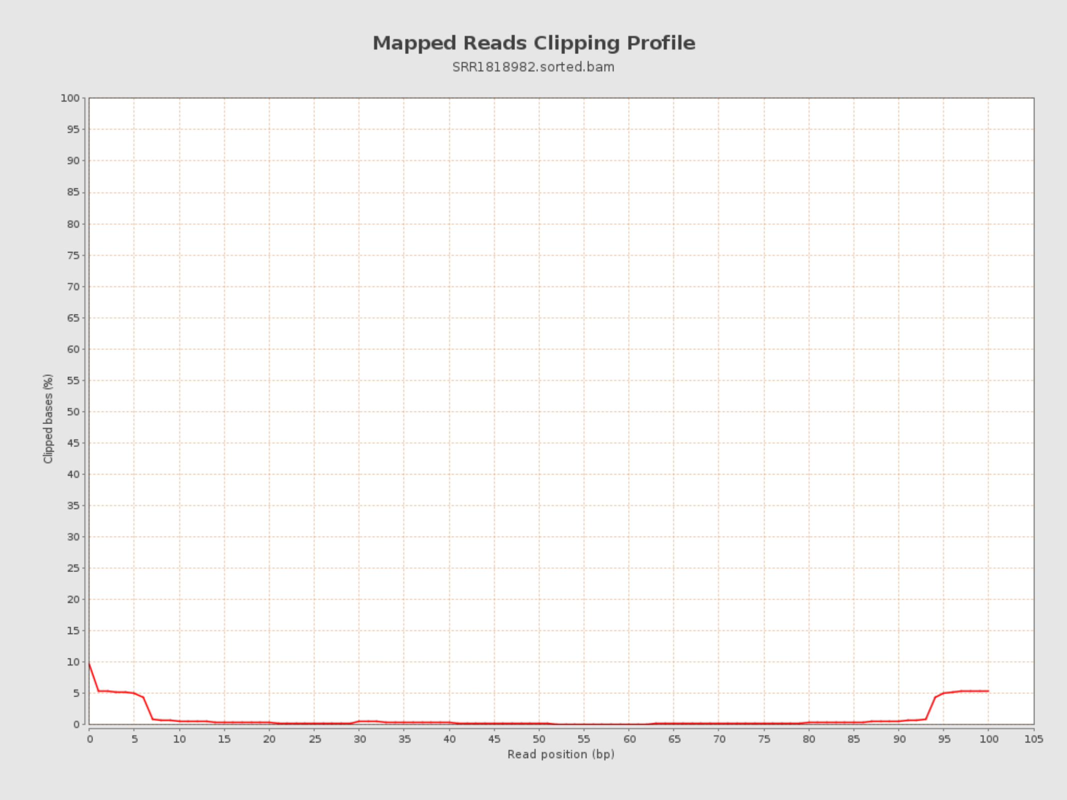
8. Results : Mapped Reads Nucleotide Content



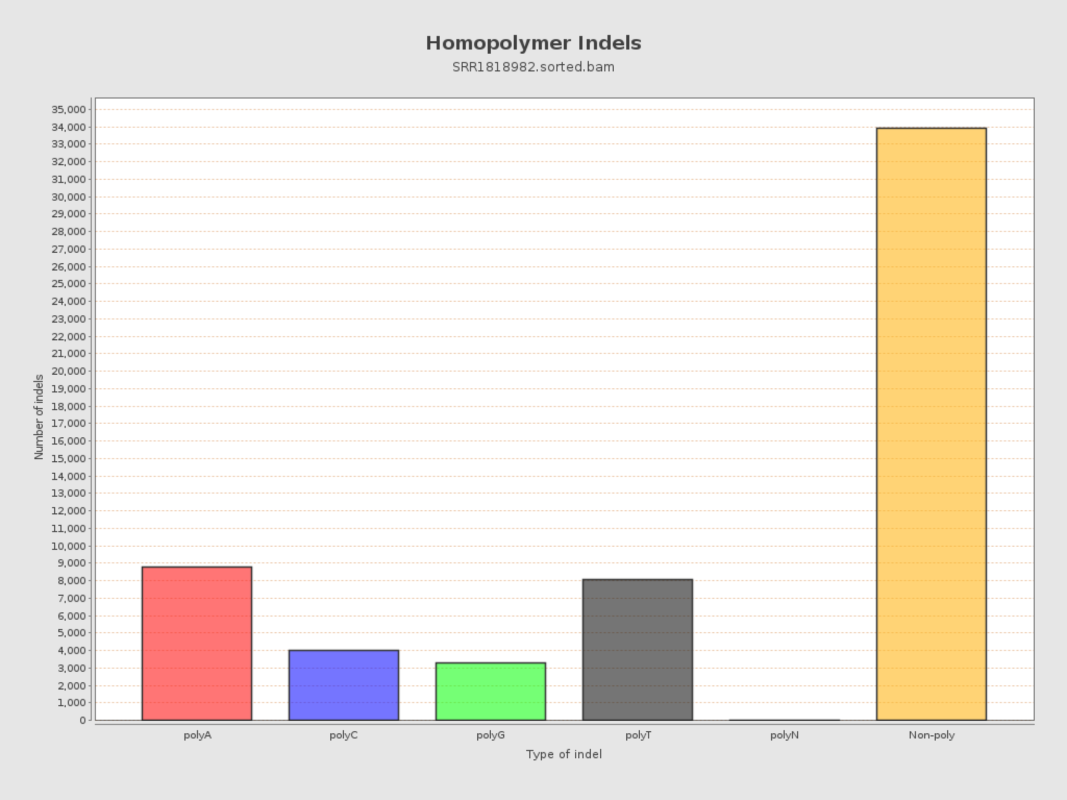
9. Results : Mapped Reads GC-content Distribution



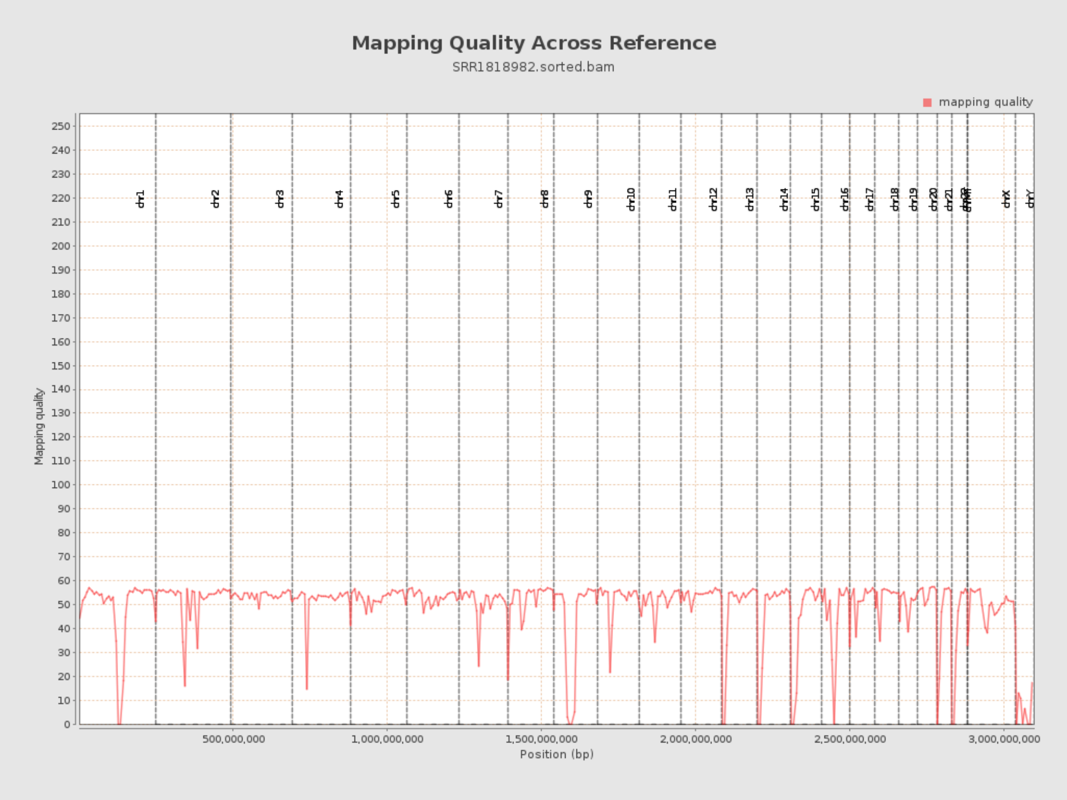
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram