Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:26:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818937.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_SRR1818937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818937.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:26:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	597,333
Mapped reads	586,741 / 98.23%
Unmapped reads	10,592 / 1.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,234 / 1.04%
Read min/max/mean length	30 / 101 / 101.4
Duplicated reads (estimated)	124,344 / 20.82%
Duplication rate	18.63%
Clipped reads	590,056 / 98.78%

2.2. ACGT Content

Number/percentage of A's	15,377,442 / 28.23%
Number/percentage of C's	11,470,929 / 21.06%
Number/percentage of T's	14,958,422 / 27.46%
Number/percentage of G's	12,659,055 / 23.24%
Number/percentage of N's	2,374 / 0%
GC Percentage	44.3%

2.3. Coverage

Mean	0.0176

Standard Deviation	0.227

2.4. Mapping Quality

Mean Mapping Quality	49.27

2.5. Mismatches and indels

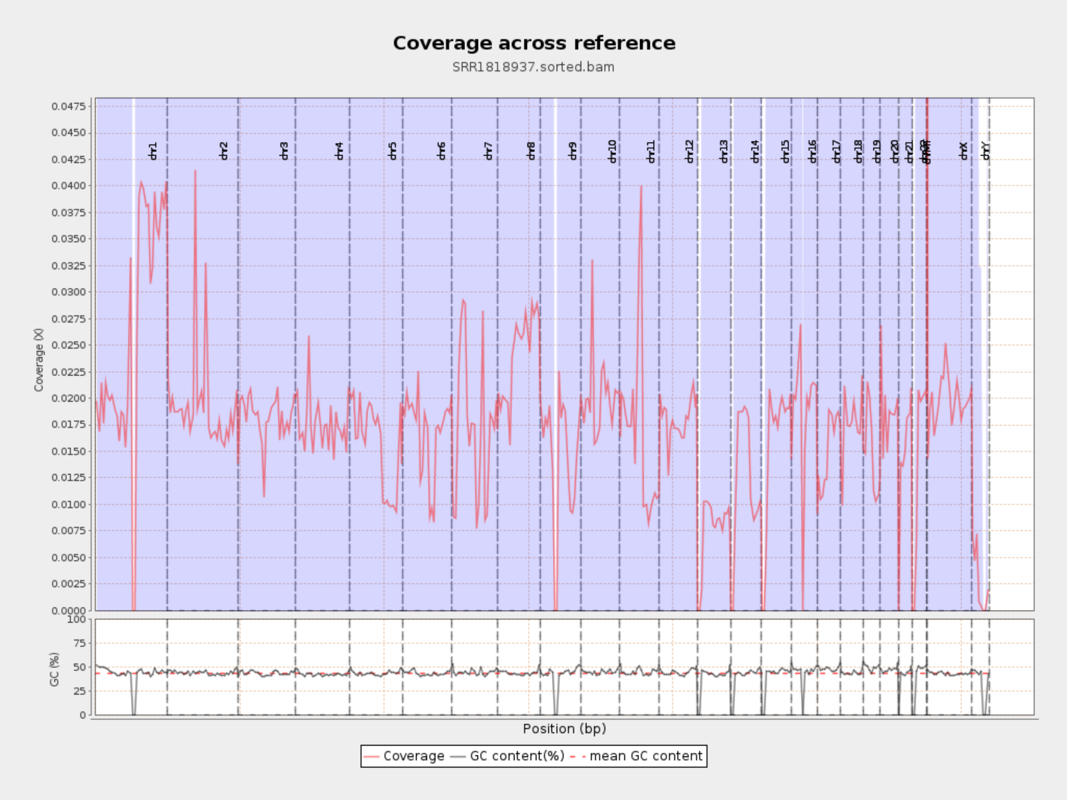
General error rate	0.65%
Mismatches	341,704
Insertions	6,075
Mapped reads with at least one insertion	1.01%
Deletions	16,127
Mapped reads with at least one deletion	2.69%
Homopolymer indels	43.32%

2.6. Chromosome stats

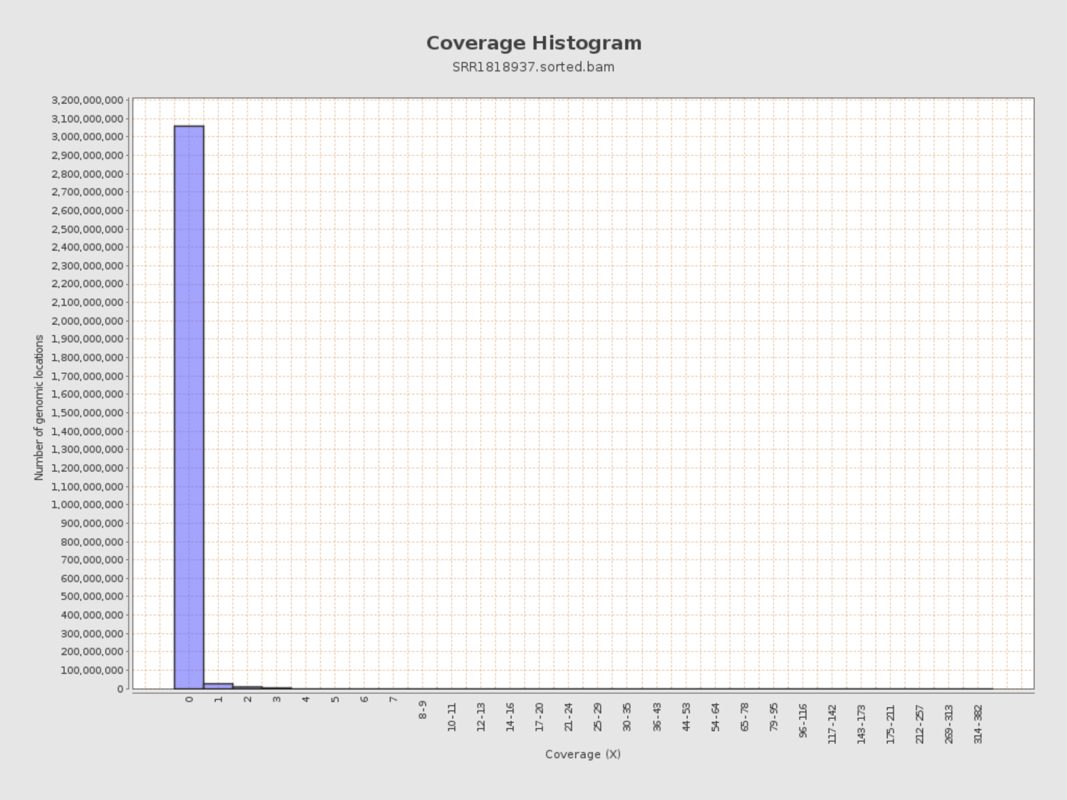
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6471187	0.026	0.3616
chr2	243199373	4707844	0.0194	0.3005
chr3	198022430	3608601	0.0182	0.1787
chr4	191154276	3368999	0.0176	0.1809
chr5	180915260	2820651	0.0156	0.1679
chr6	171115067	2880361	0.0168	0.1767
chr7	159138663	2743975	0.0172	0.1987

chr8	146364022	3548302	0.0242	0.2233
chr9	141213431	2019131	0.0143	0.2393
chr10	135534747	2743578	0.0202	0.2644
chr11	135006516	2328735	0.0172	0.1922
chr12	133851895	2411651	0.018	0.1824
chr13	115169878	872449	0.0076	0.1141
chr14	107349540	1313365	0.0122	0.1574
chr15	102531392	1574519	0.0154	0.1636
chr16	90354753	1680103	0.0186	0.2395
chr17	81195210	1229436	0.0151	0.173
chr18	78077248	1351732	0.0173	0.3047
chr19	59128983	893041	0.0151	0.3024
chr20	63025520	1179347	0.0187	0.1871
chr21	48129895	714521	0.0148	0.1758
chr22	51304566	716678	0.014	0.1698
chrMT	16571	93692	5.654	4.4651
chrX	155270560	3071504	0.0198	0.209
chrY	59373566	154386	0.0026	0.1485

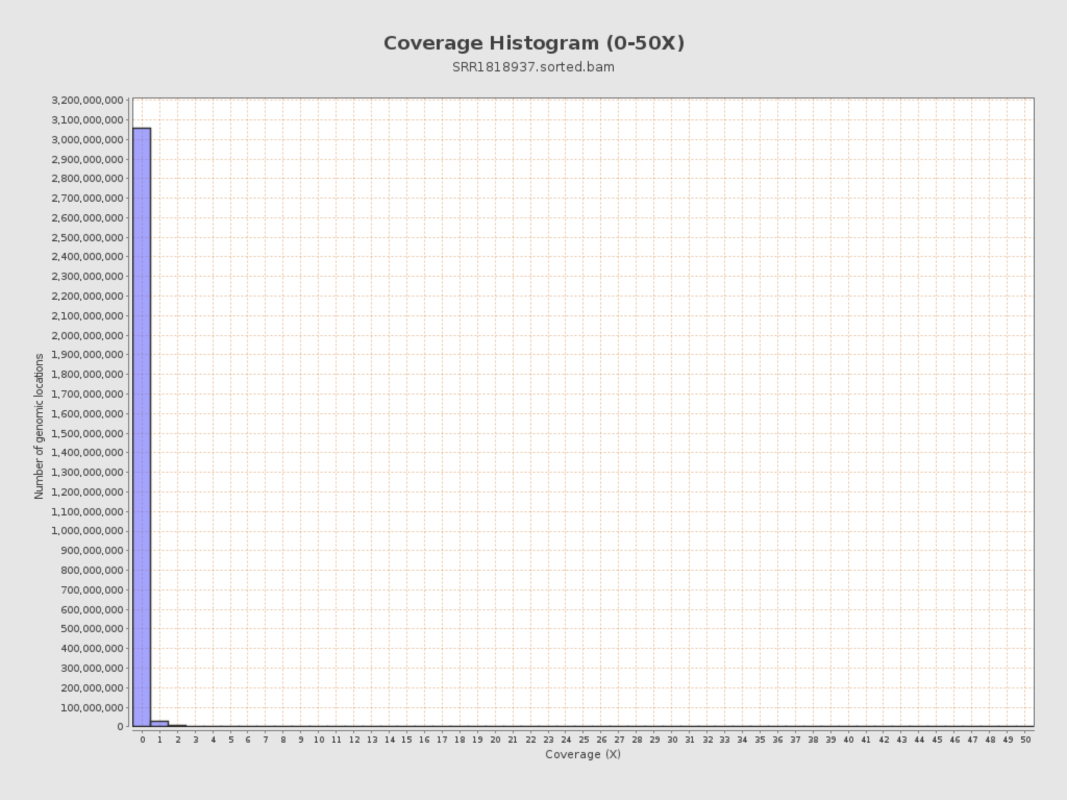
3. Results : Coverage across reference



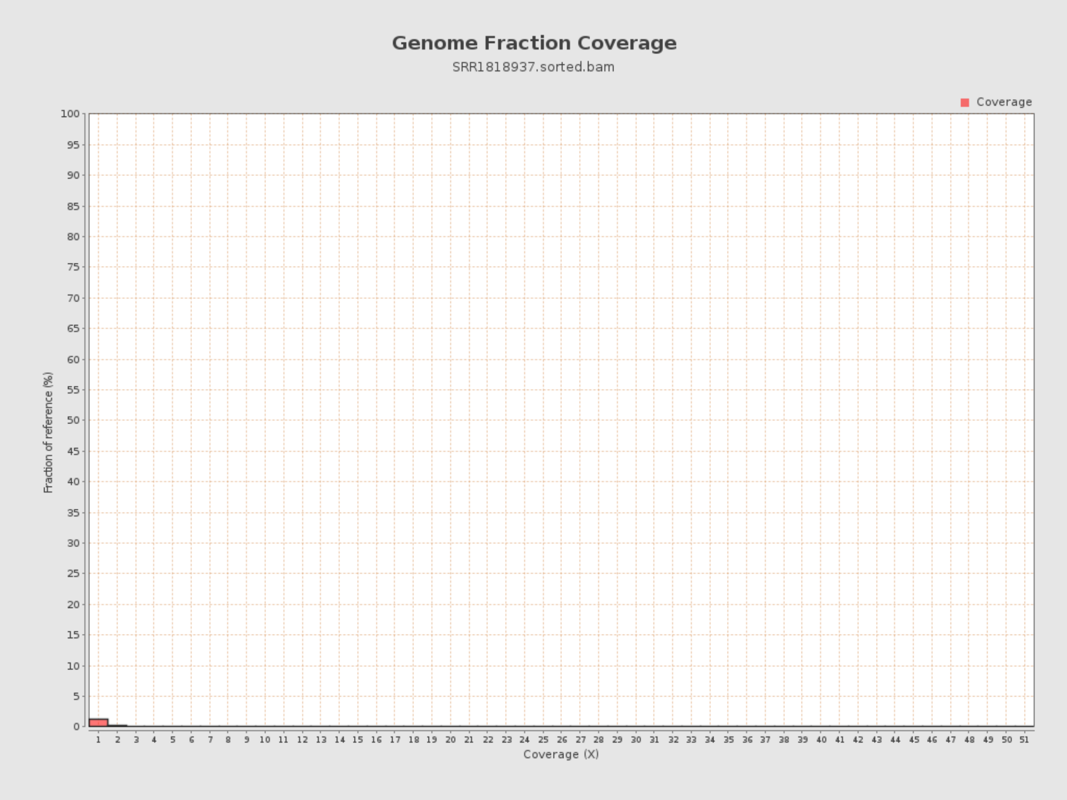
4. Results : Coverage Histogram



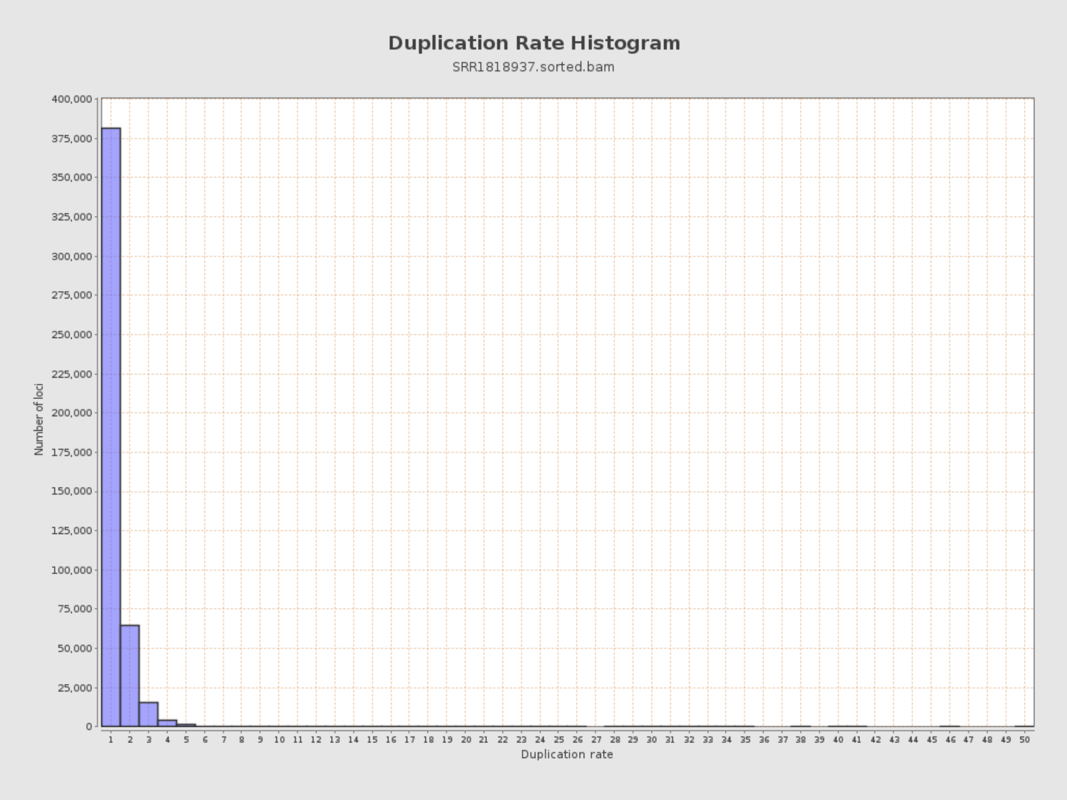
5. Results : Coverage Histogram (0-50X)



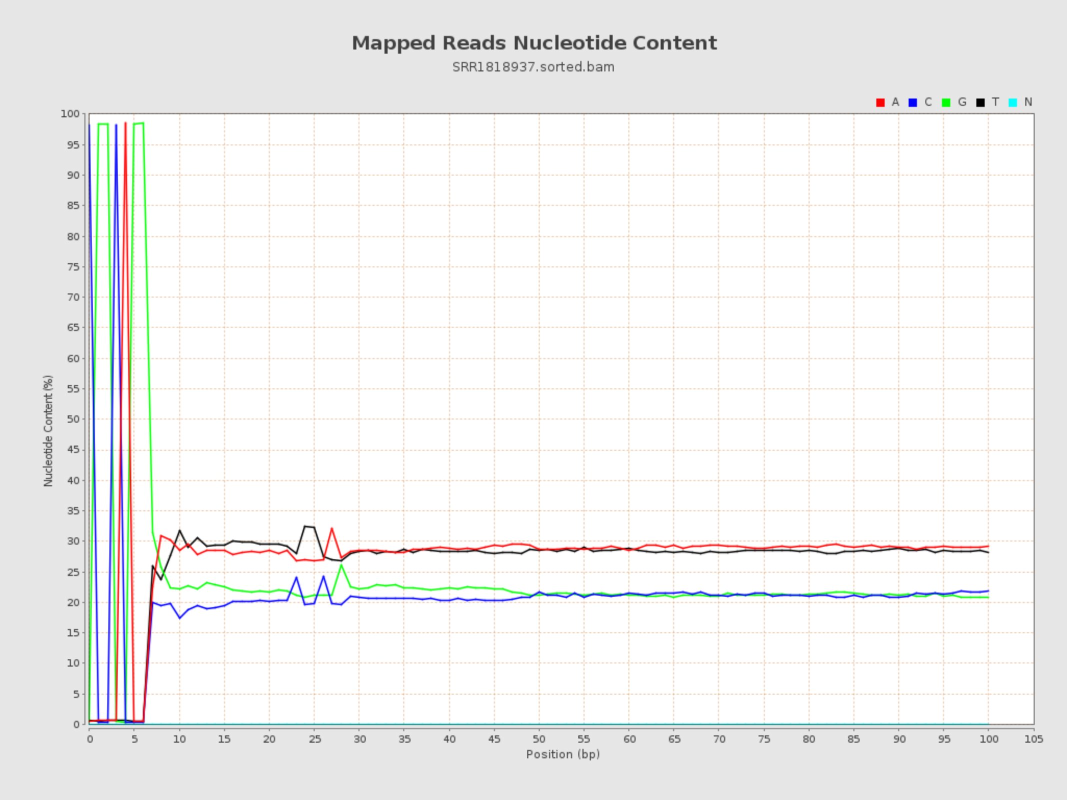
6. Results : Genome Fraction Coverage



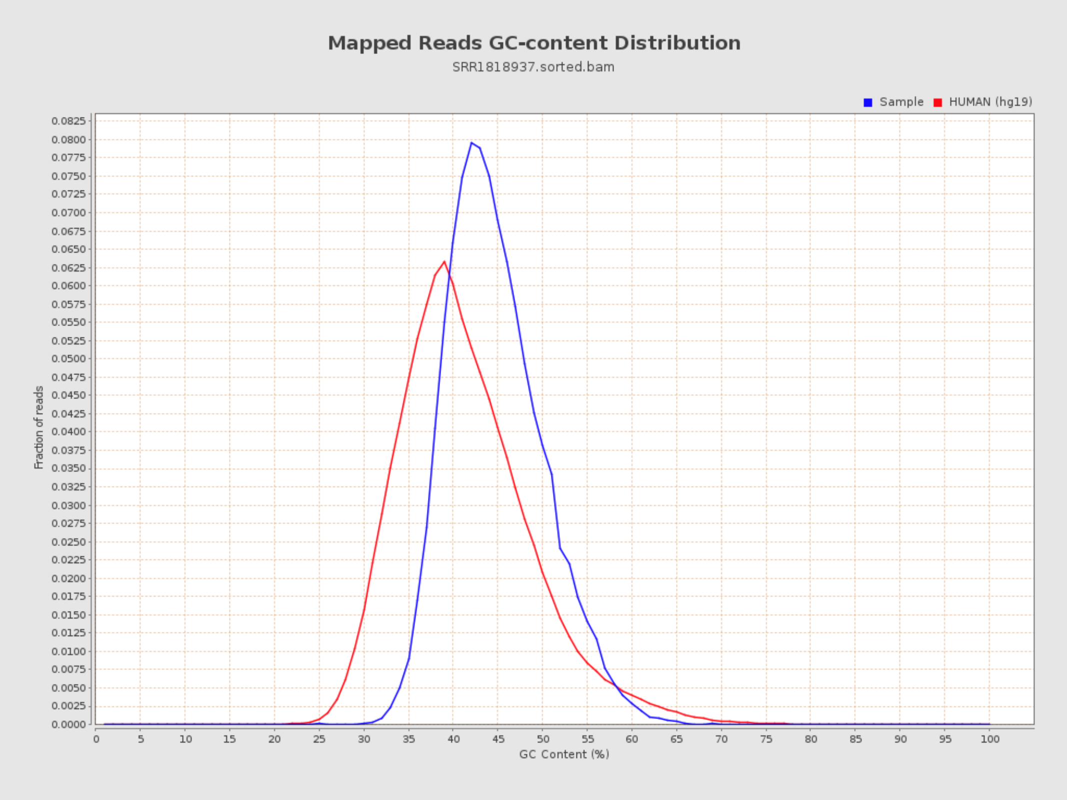
7. Results : Duplication Rate Histogram



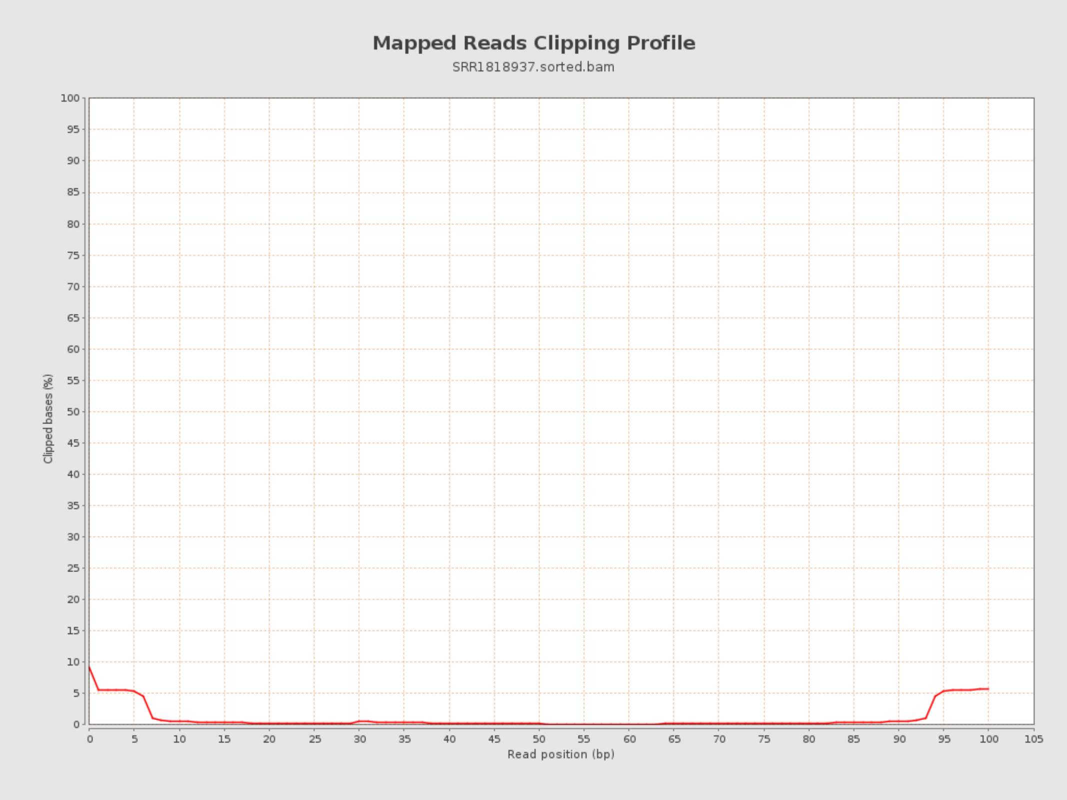
8. Results : Mapped Reads Nucleotide Content



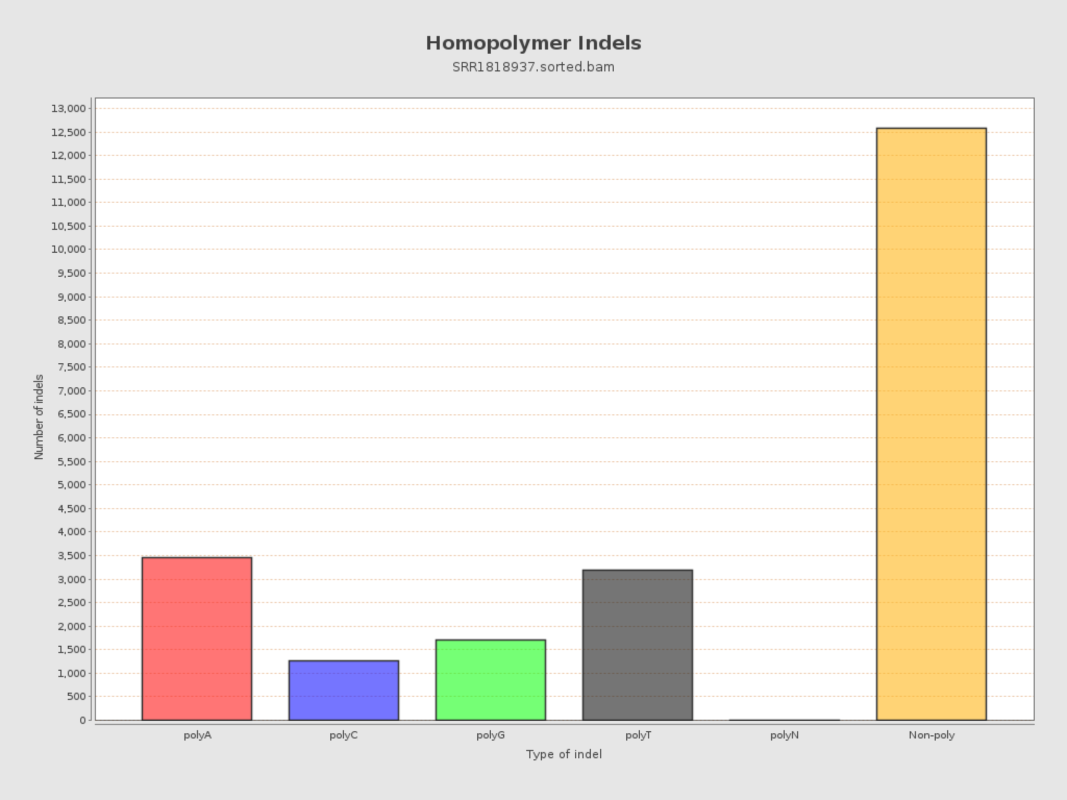
9. Results : Mapped Reads GC-content Distribution



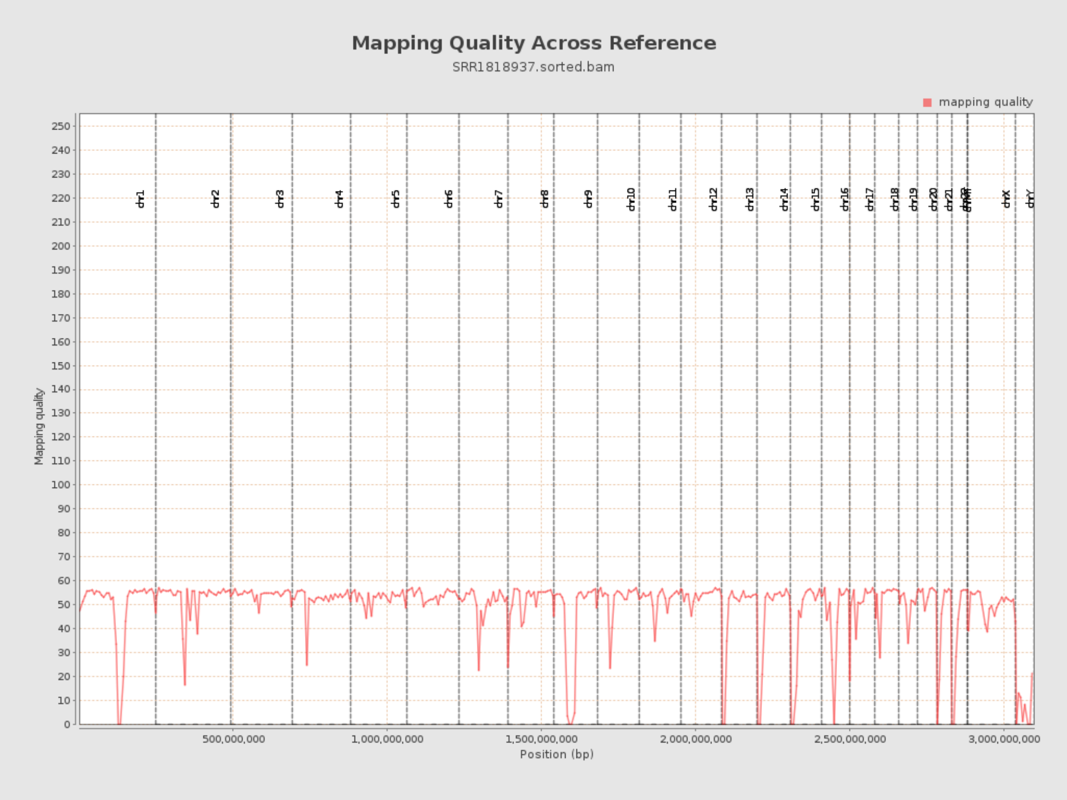
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram