Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 00:17:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548916.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_SRR1548916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548916.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 00:17:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,513,729
Mapped reads	6,595,325 / 87.78%
Unmapped reads	918,404 / 12.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	214,088 / 2.85%
Duplication rate	2.19%
Clipped reads	522,088 / 6.95%

2.2. ACGT Content

Number/percentage of A's	76,238,812 / 29.22%
Number/percentage of C's	54,039,165 / 20.71%
Number/percentage of T's	76,644,737 / 29.37%
Number/percentage of G's	54,001,202 / 20.7%
Number/percentage of N's	2,635 / 0%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0843
Standard Deviation	0.9639

2.4. Mapping Quality

Mean Mapping Quality	40.18

2.5. Mismatches and indels

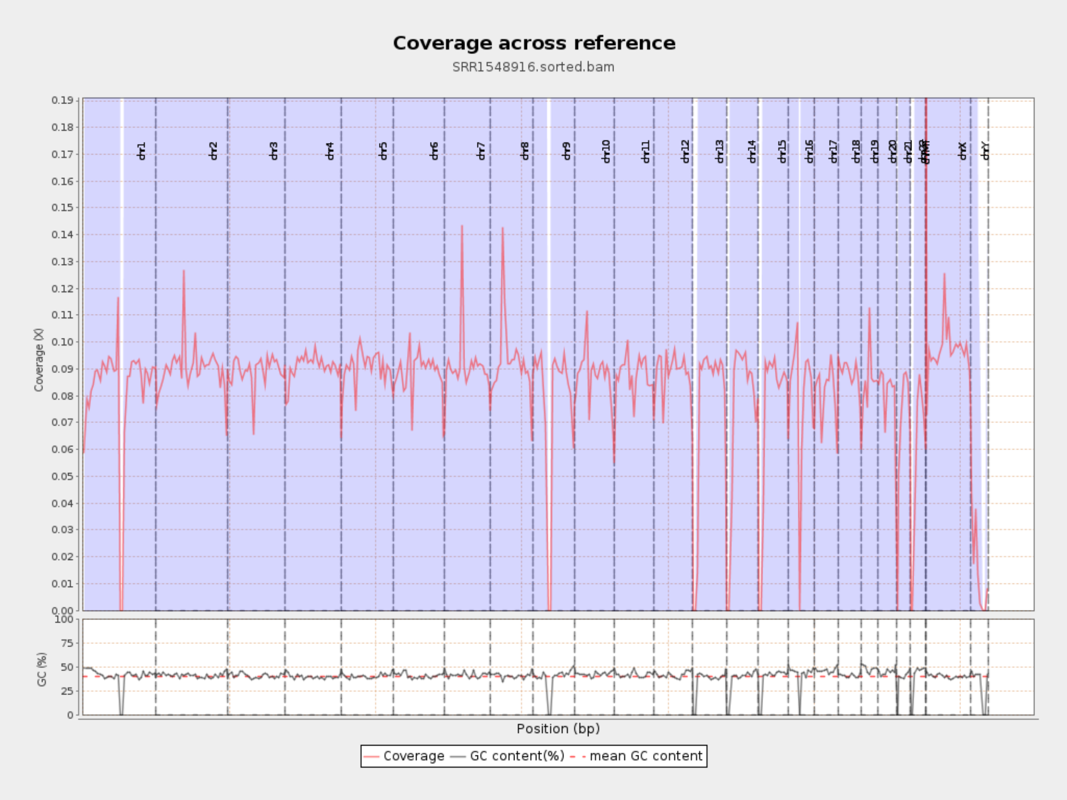
General error rate	0.29%
Mismatches	755,553
Insertions	8,868
Mapped reads with at least one insertion	0.13%
Deletions	21,559
Mapped reads with at least one deletion	0.33%
Homopolymer indels	40.79%

2.6. Chromosome stats

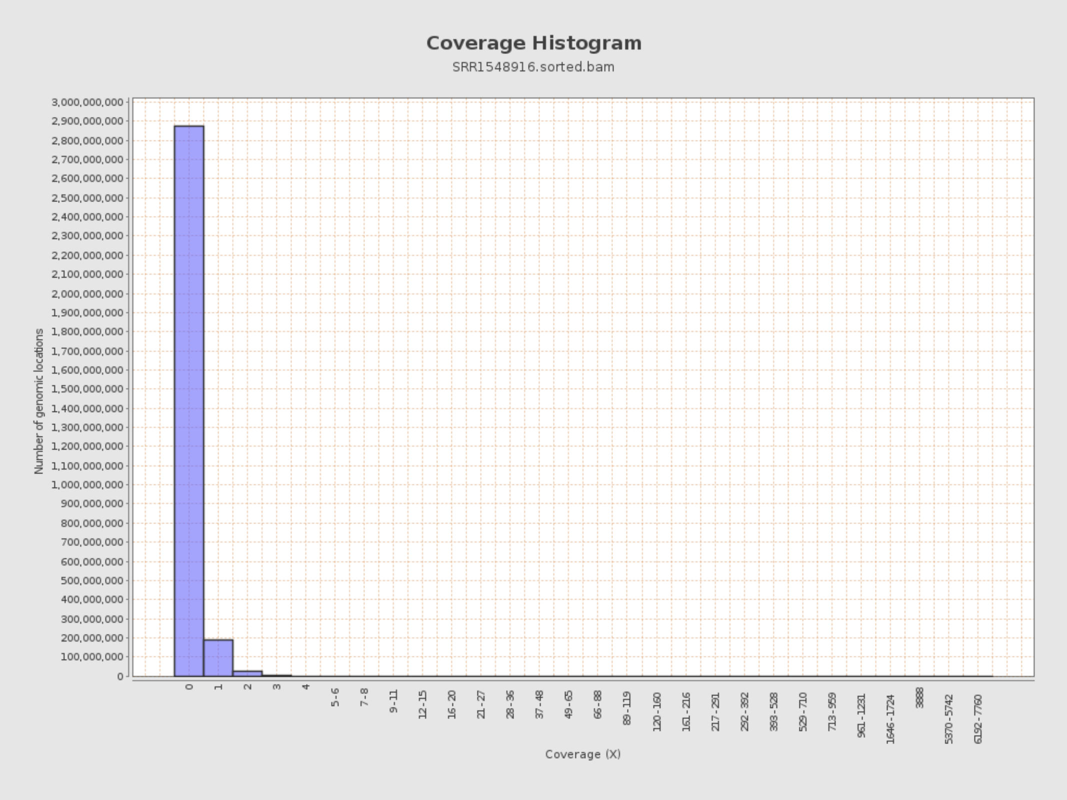
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20445038	0.082	0.9345
chr2	243199373	22009027	0.0905	0.5252
chr3	198022430	17707105	0.0894	0.3414
chr4	191154276	17386946	0.091	0.3576
chr5	180915260	16343123	0.0903	0.3512
chr6	171115067	15283081	0.0893	0.3825
chr7	159138663	14581997	0.0916	0.7647
chr8	146364022	13612182	0.093	3.748

chr9	141213431	10920157	0.0773	0.5111
chr10	135534747	11939008	0.0881	0.4605
chr11	135006516	11838426	0.0877	0.5417
chr12	133851895	11915418	0.089	0.3551
chr13	115169878	8648895	0.0751	0.3086
chr14	107349540	8004091	0.0746	0.3733
chr15	102531392	7417811	0.0723	0.3071
chr16	90354753	7027217	0.0778	0.3593
chr17	81195210	6682989	0.0823	0.3569
chr18	78077248	6926026	0.0887	0.9505
chr19	59128983	5076184	0.0858	0.8866
chr20	63025520	5142998	0.0816	0.3413
chr21	48129895	3287409	0.0683	0.3375
chr22	51304566	2829059	0.0551	0.3154
chrMT	16571	8477	0.5116	0.9148
chrX	155270560	15083761	0.0971	0.439
chrY	59373566	838437	0.0141	0.1861

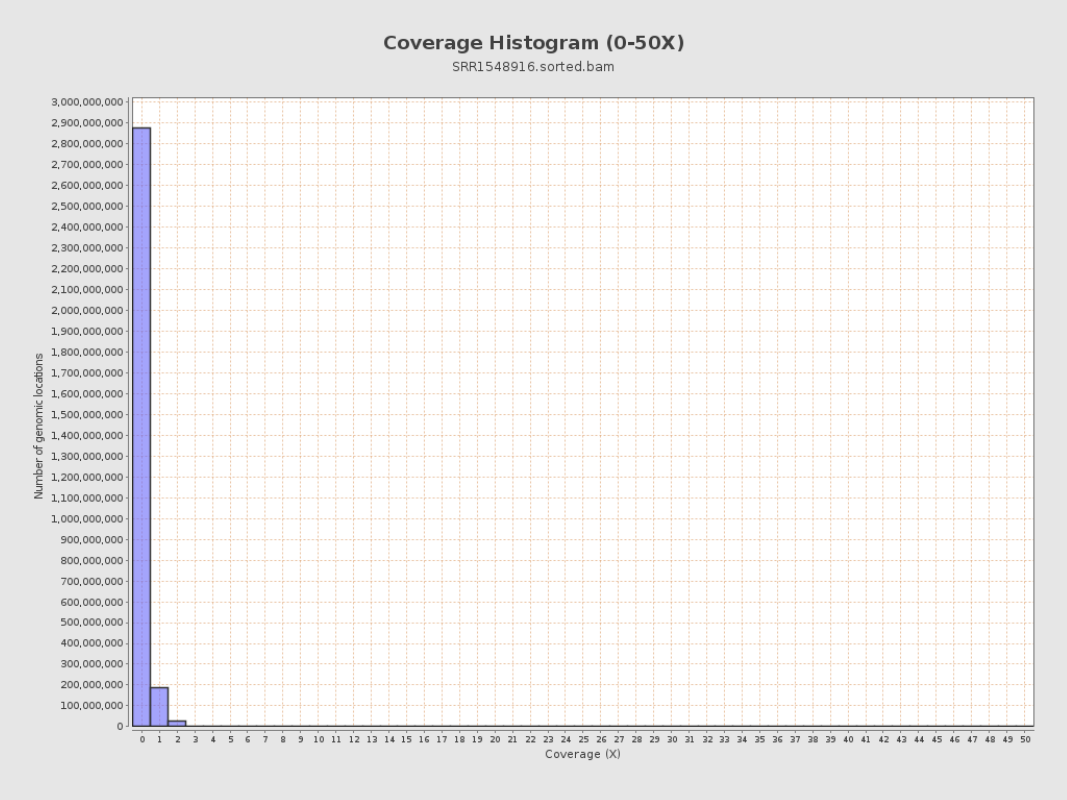
3. Results : Coverage across reference



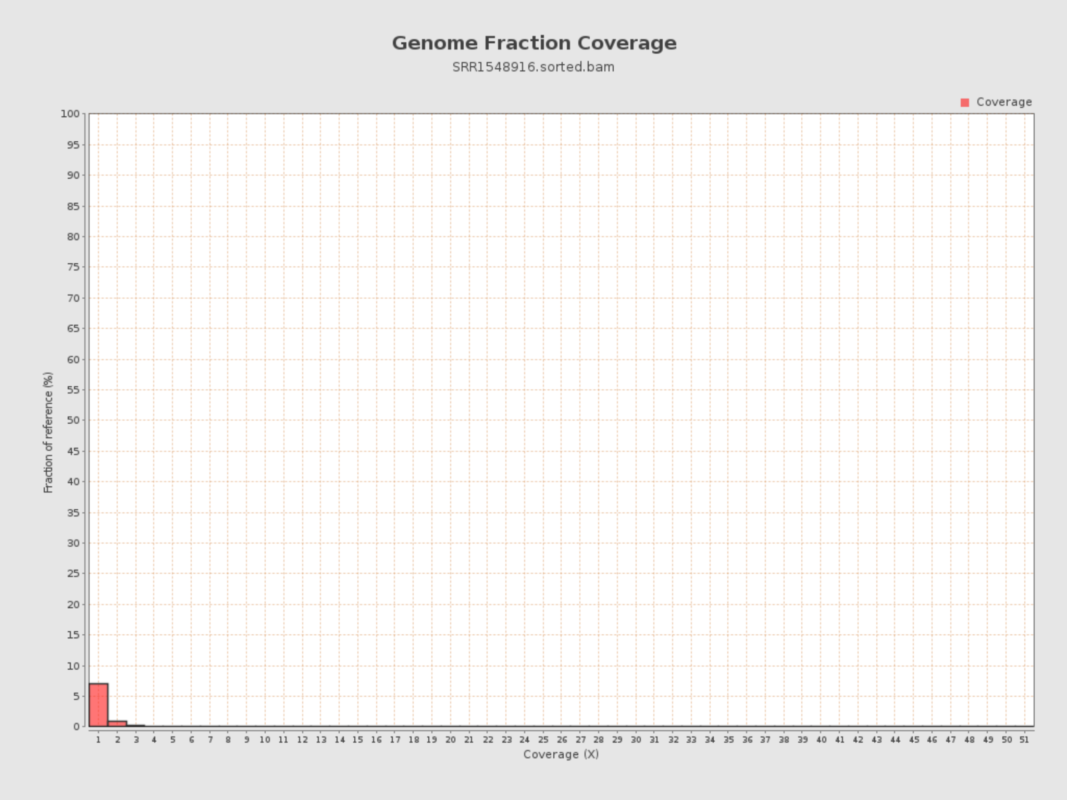
4. Results : Coverage Histogram



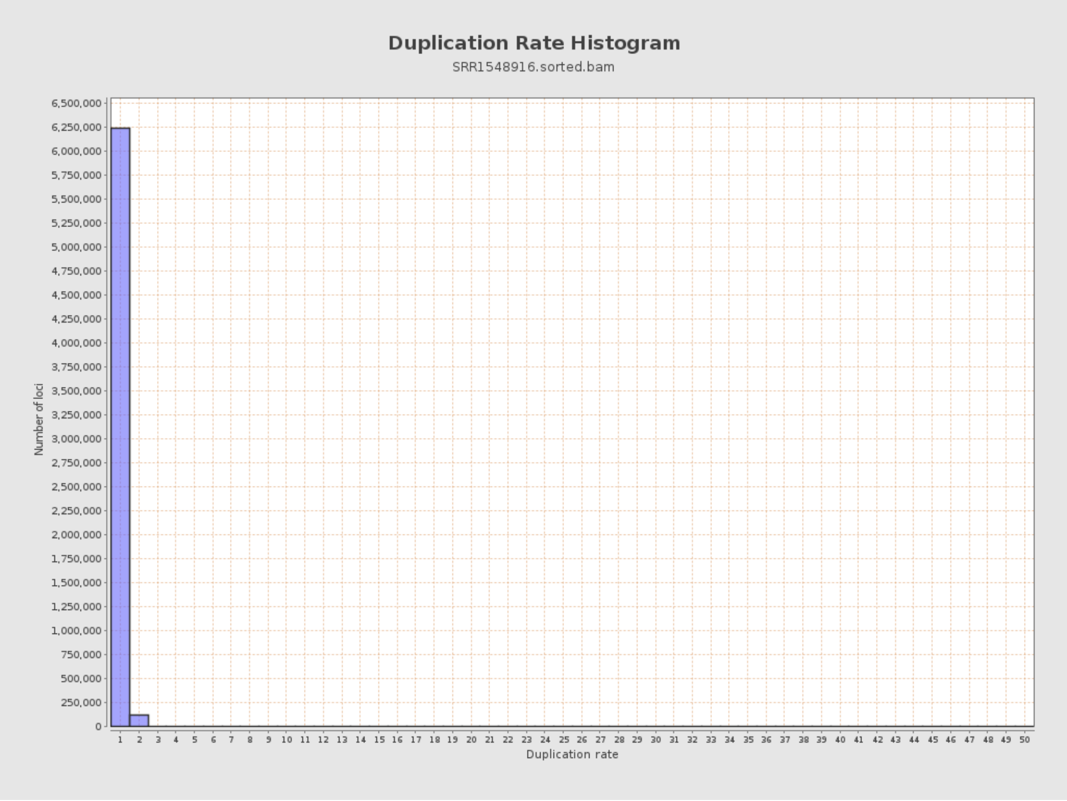
5. Results : Coverage Histogram (0-50X)



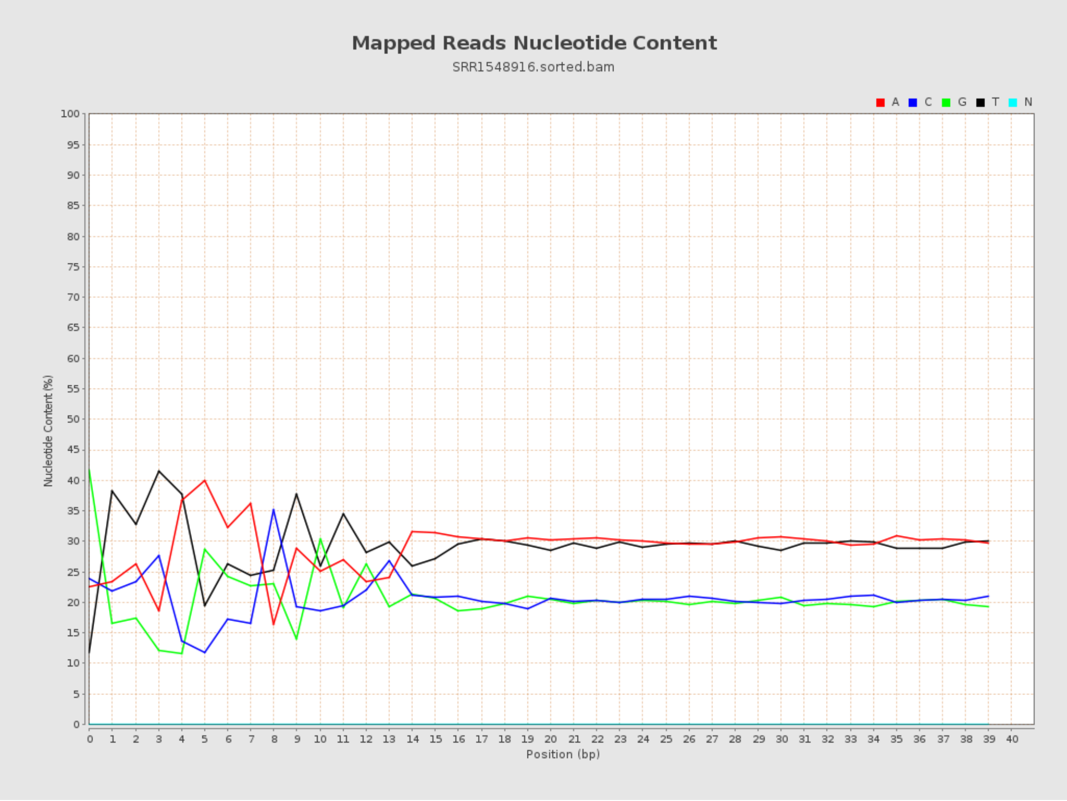
6. Results : Genome Fraction Coverage



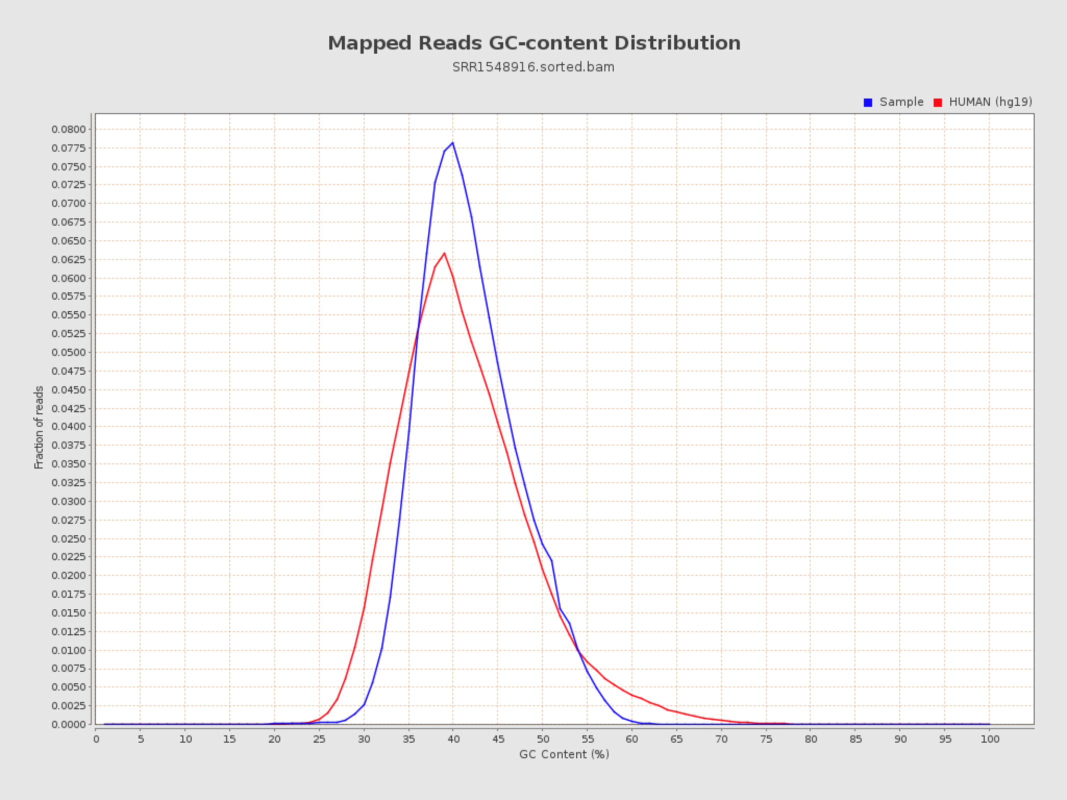
7. Results : Duplication Rate Histogram



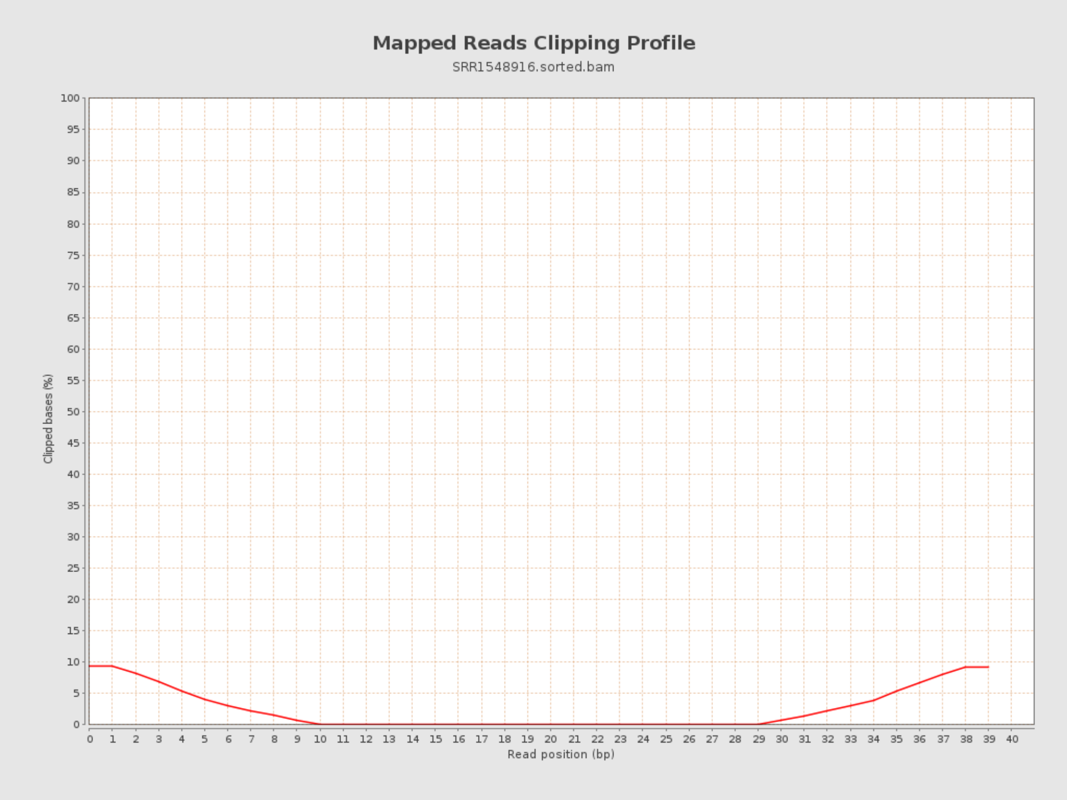
8. Results : Mapped Reads Nucleotide Content



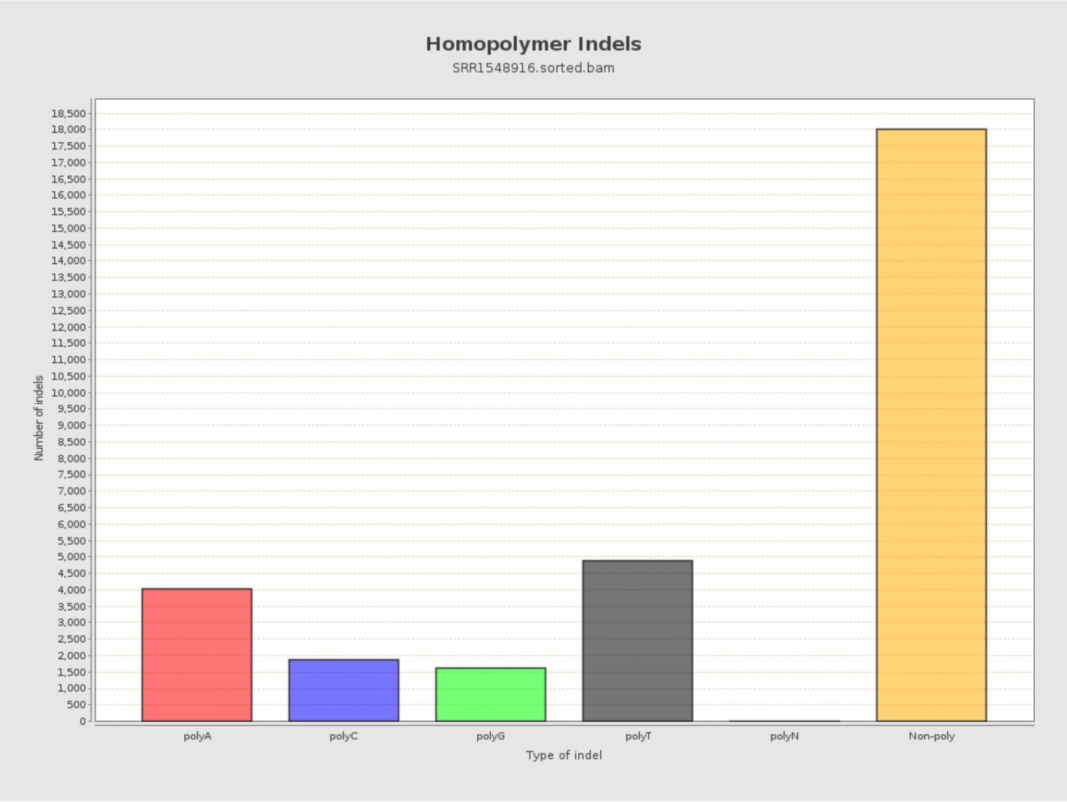
9. Results : Mapped Reads GC-content Distribution



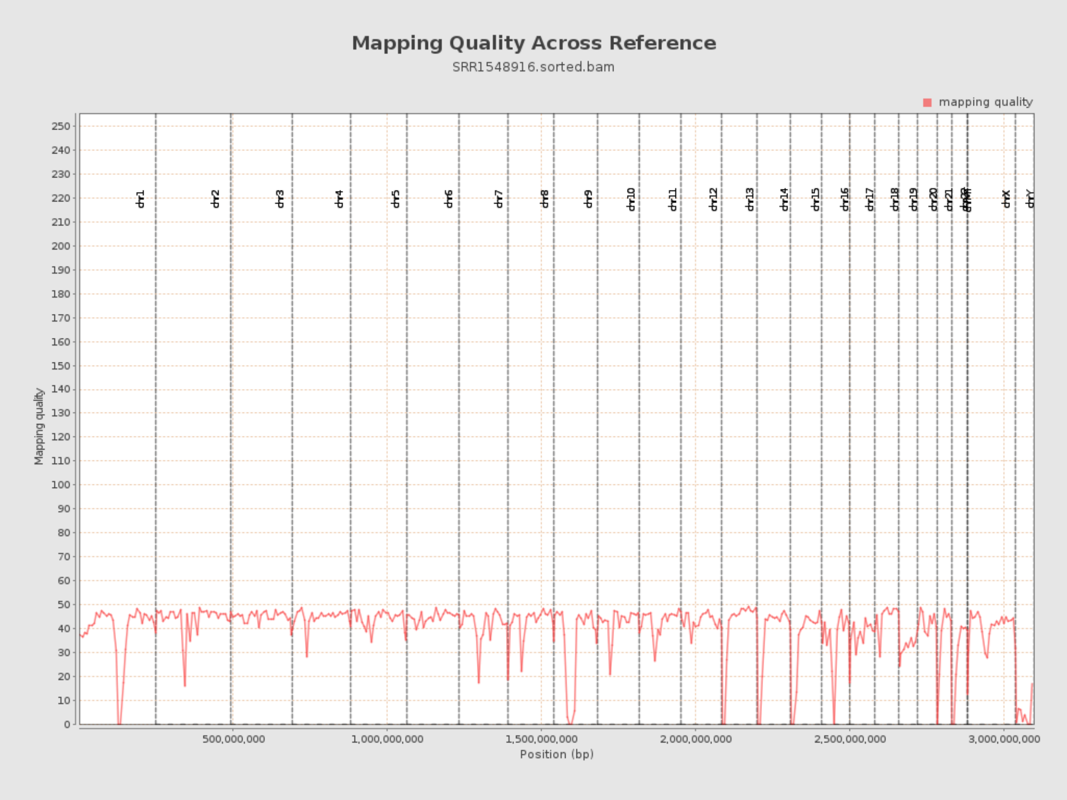
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram