Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:11:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549015.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_SRR1549015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:11:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,730,820
Mapped reads	6,756,445 / 87.4%
Unmapped reads	974,375 / 12.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	238,676 / 3.09%
Duplication rate	2.48%
Clipped reads	529,236 / 6.85%

2.2. ACGT Content

Number/percentage of A's	77,942,629 / 29.16%
Number/percentage of C's	55,737,752 / 20.85%
Number/percentage of T's	78,252,868 / 29.28%
Number/percentage of G's	55,351,797 / 20.71%
Number/percentage of N's	8,895 / 0%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0864
Standard Deviation	0.8899

2.4. Mapping Quality

Mean Mapping Quality	41.3

2.5. Mismatches and indels

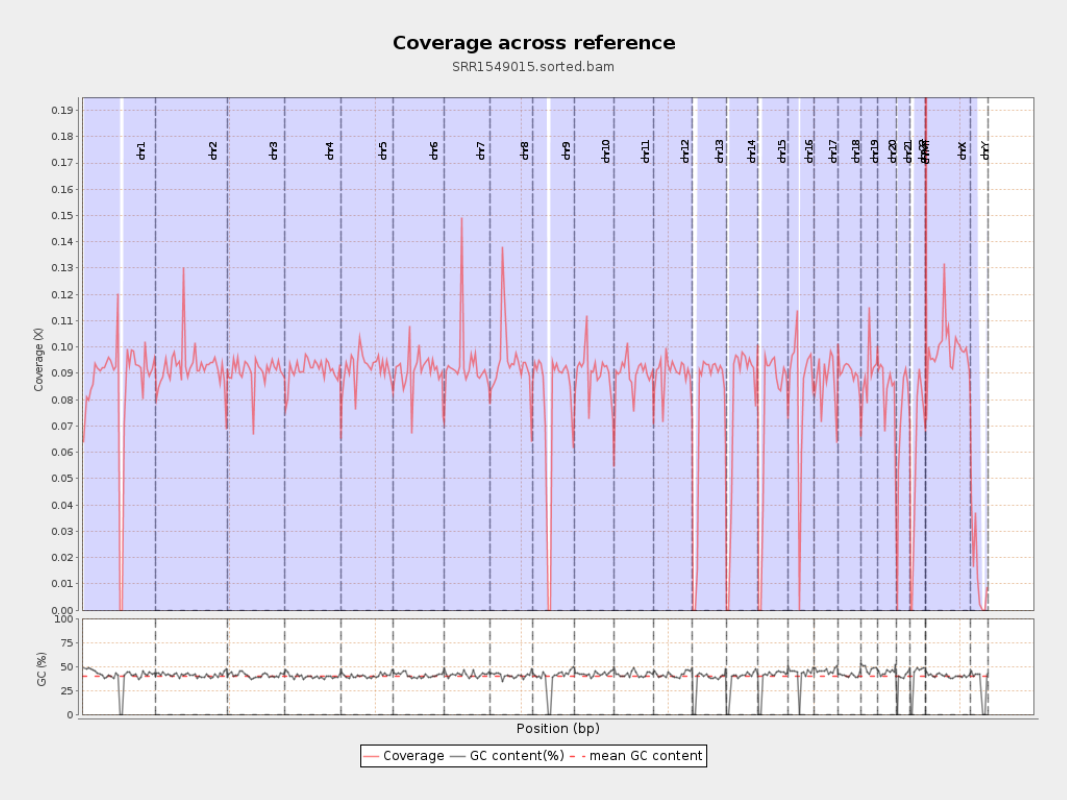
General error rate	0.27%
Mismatches	711,520
Insertions	8,729
Mapped reads with at least one insertion	0.13%
Deletions	21,926
Mapped reads with at least one deletion	0.32%
Homopolymer indels	41.12%

2.6. Chromosome stats

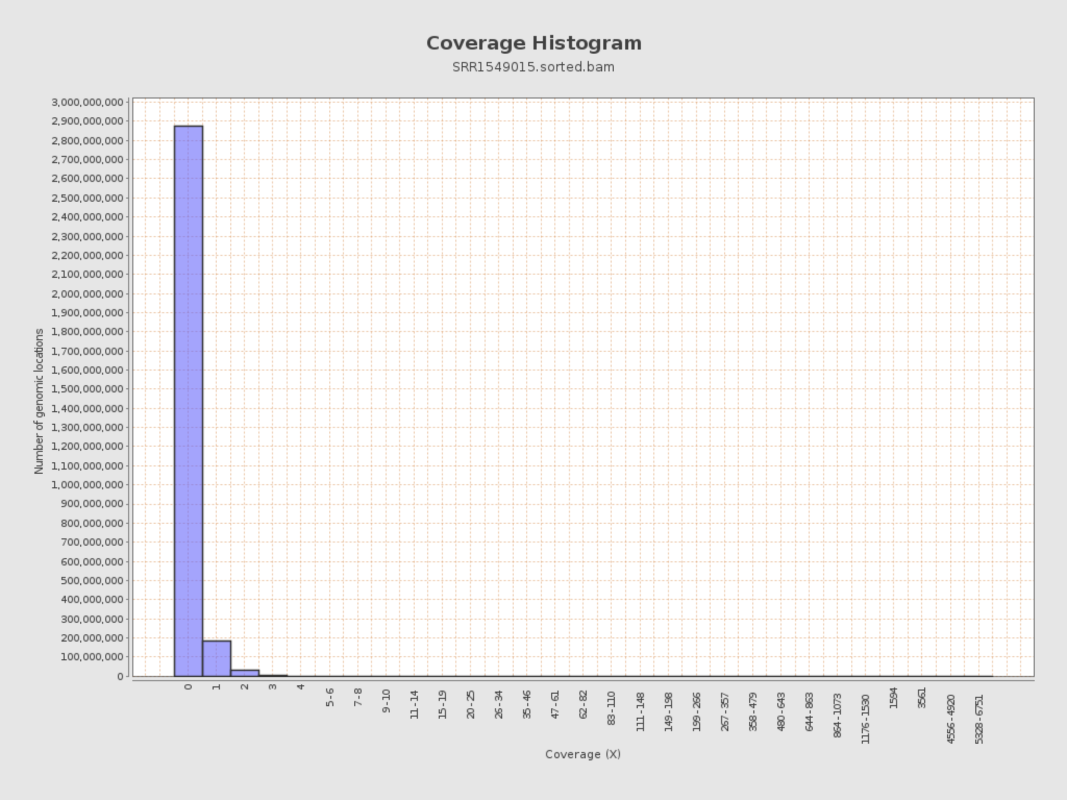
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21307685	0.0855	0.9733
chr2	243199373	22484318	0.0925	0.5475
chr3	198022430	17985018	0.0908	0.3526
chr4	191154276	17462522	0.0914	0.3618
chr5	180915260	16613130	0.0918	0.3622
chr6	171115067	15585256	0.0911	0.4038
chr7	159138663	14864367	0.0934	0.7857
chr8	146364022	13831252	0.0945	3.275

chr9	141213431	11120684	0.0788	0.5297
chr10	135534747	12245527	0.0903	0.4784
chr11	135006516	12102170	0.0896	0.5777
chr12	133851895	12088438	0.0903	0.3693
chr13	115169878	8742313	0.0759	0.3185
chr14	107349540	8364445	0.0779	0.4079
chr15	102531392	7607146	0.0742	0.3157
chr16	90354753	7481749	0.0828	0.371
chr17	81195210	7111762	0.0876	0.3761
chr18	78077248	7076195	0.0906	0.9533
chr19	59128983	5364558	0.0907	0.9142
chr20	63025520	5329641	0.0846	0.3574
chr21	48129895	3378284	0.0702	0.3542
chr22	51304566	2962991	0.0578	0.3319
chrMT	16571	22732	1.3718	1.7388
chrX	155270560	15374447	0.099	0.4588
chrY	59373566	816209	0.0137	0.1921

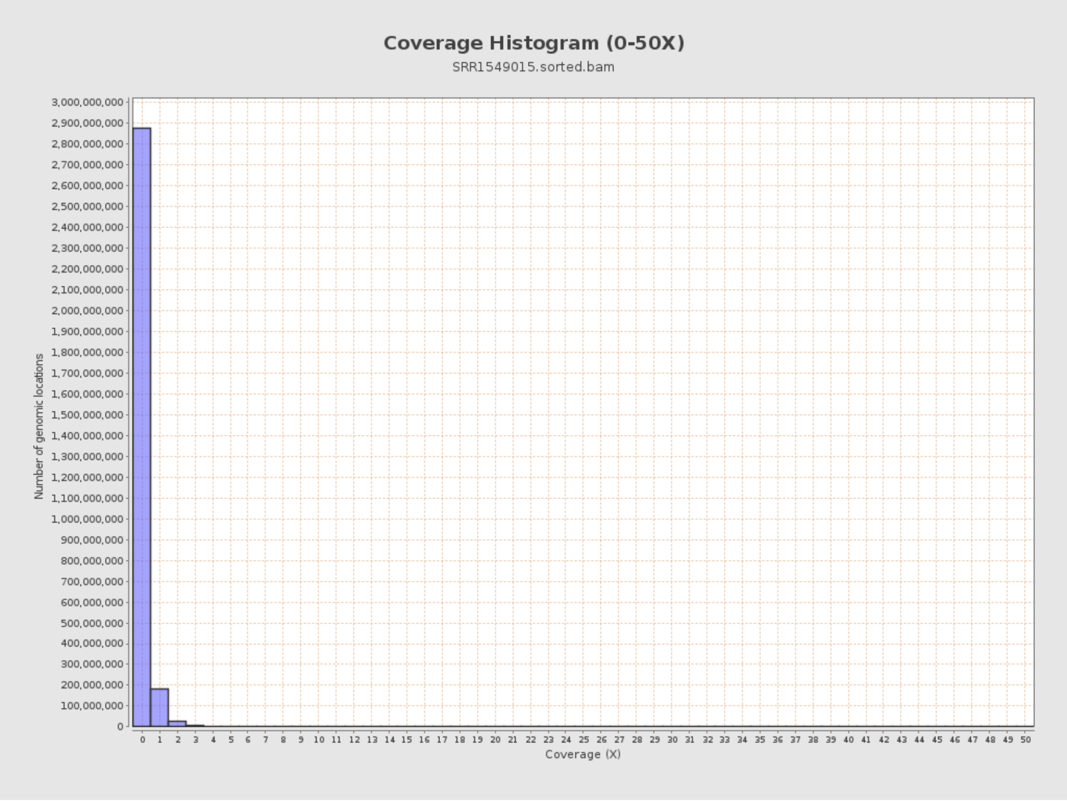
3. Results : Coverage across reference



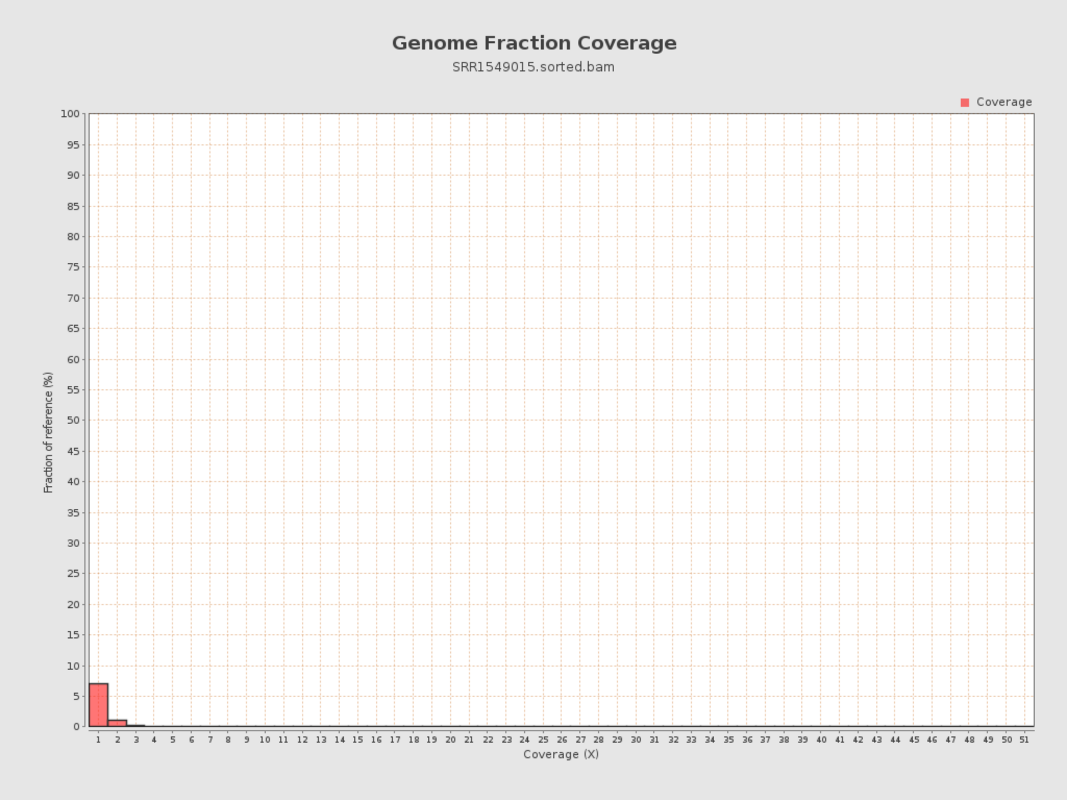
4. Results : Coverage Histogram



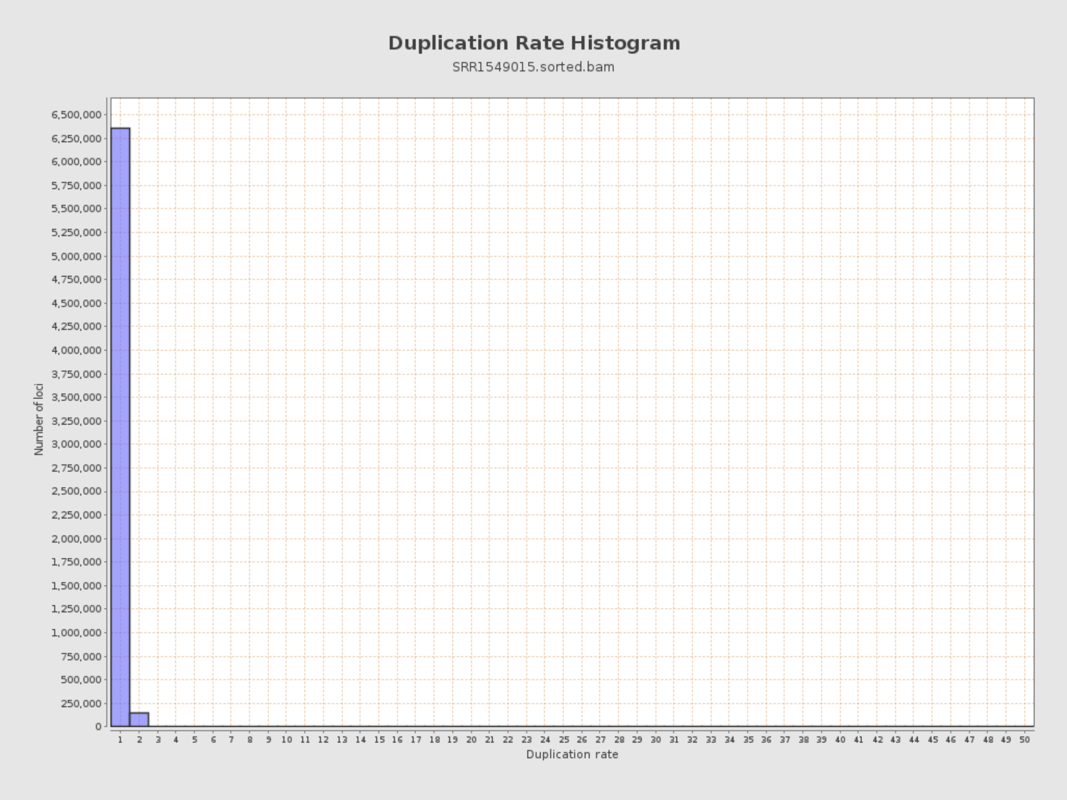
5. Results : Coverage Histogram (0-50X)



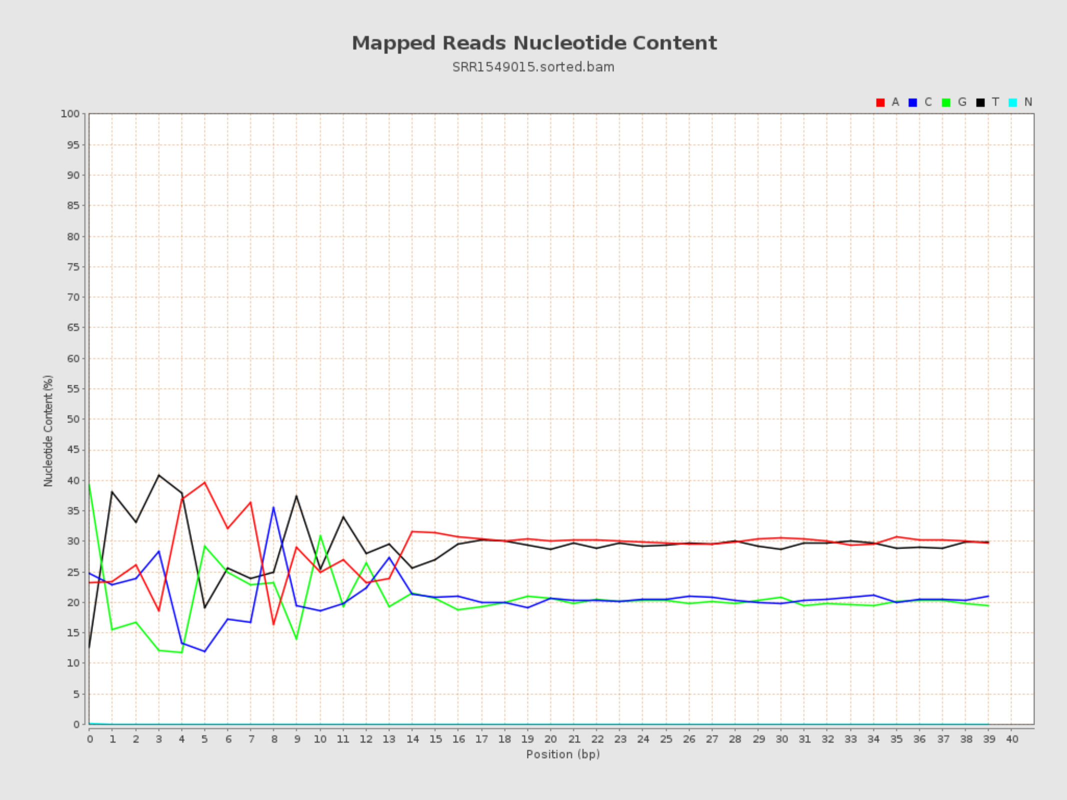
6. Results : Genome Fraction Coverage



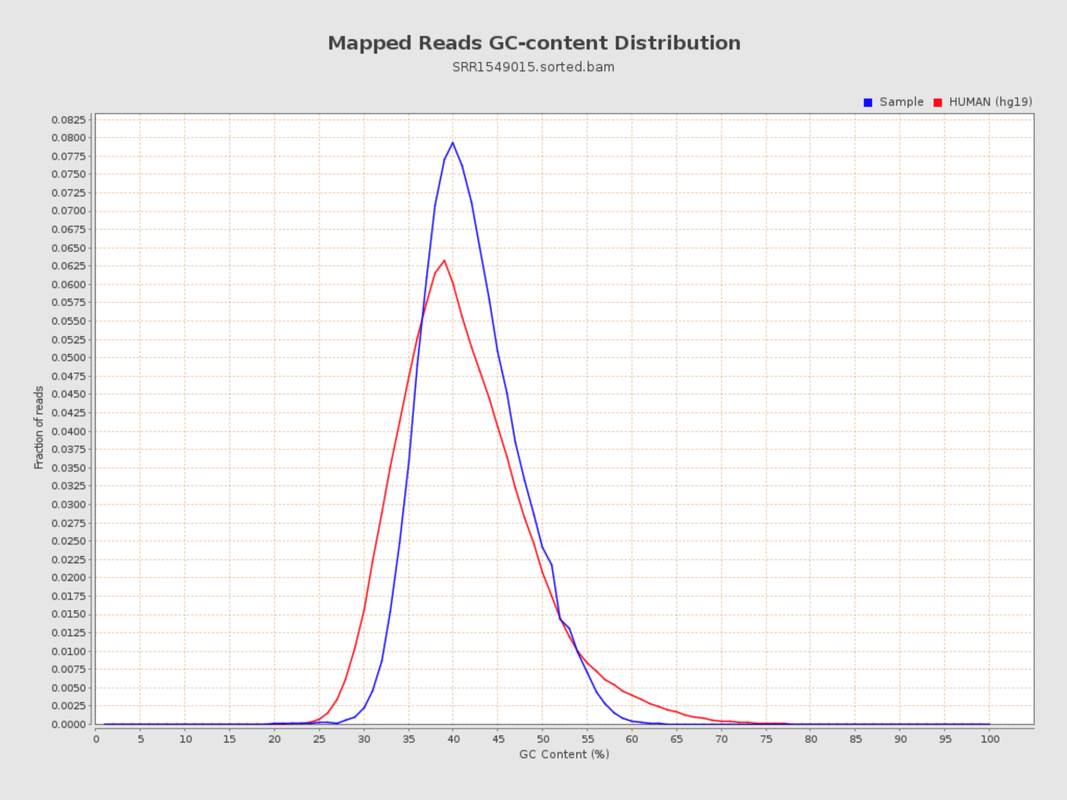
7. Results : Duplication Rate Histogram



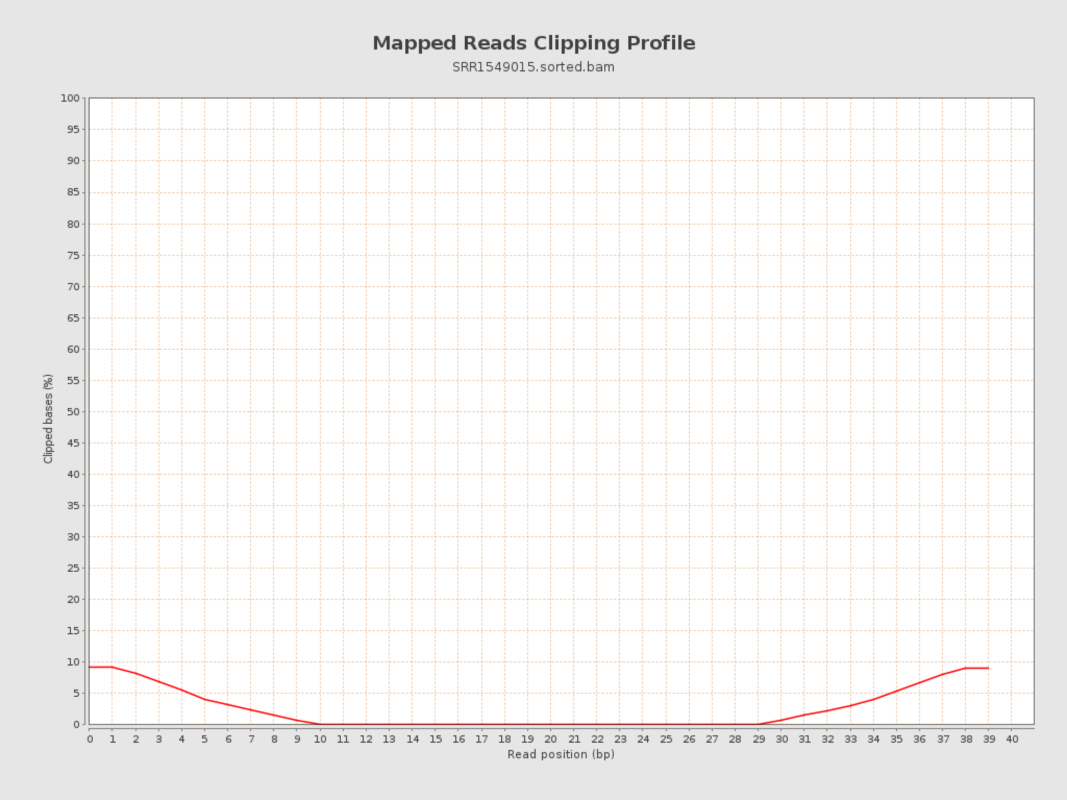
8. Results : Mapped Reads Nucleotide Content



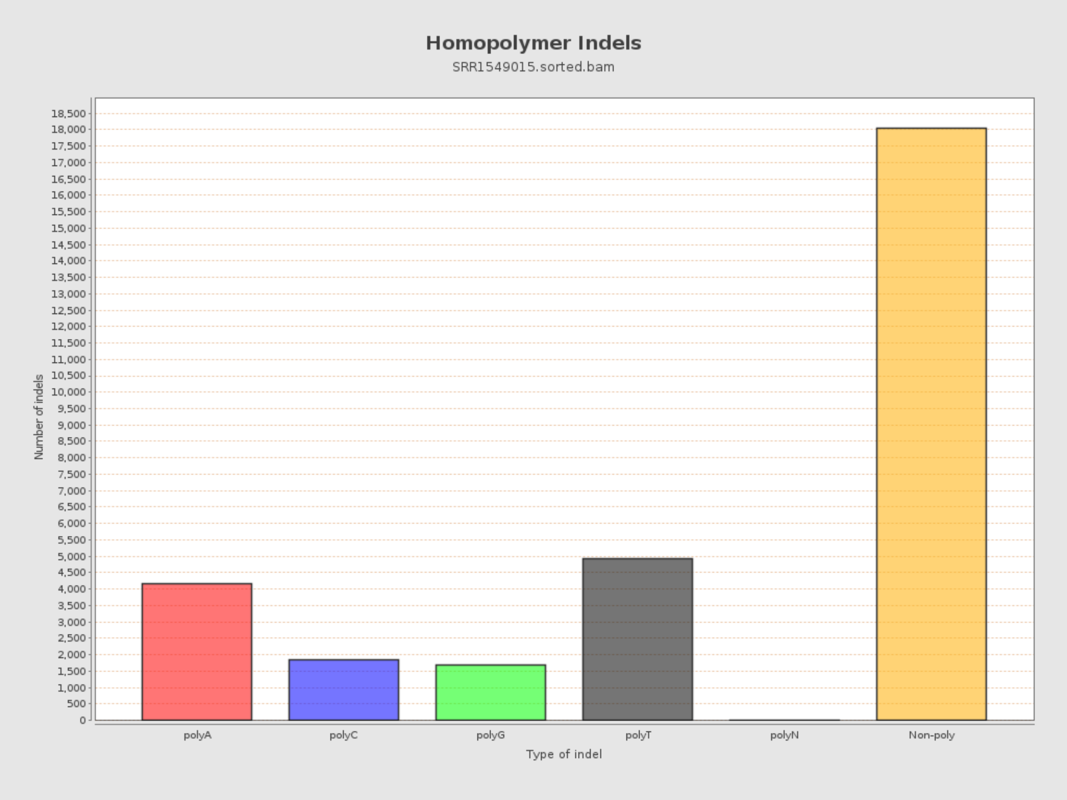
9. Results : Mapped Reads GC-content Distribution



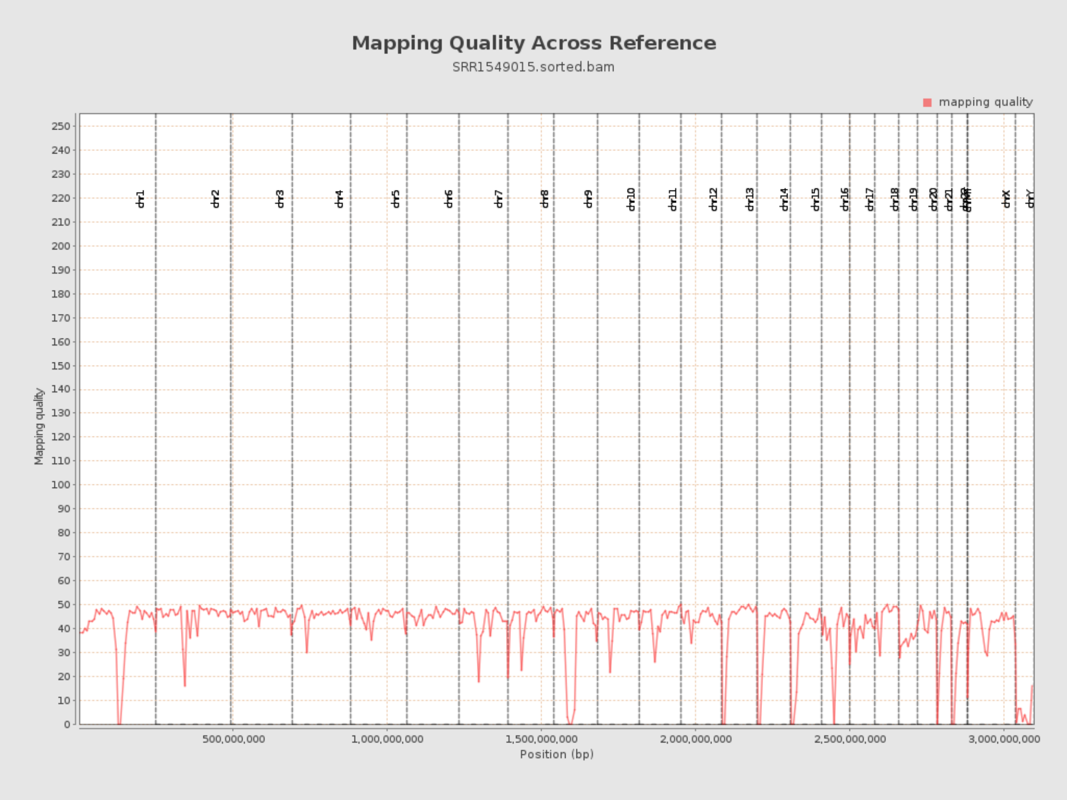
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram