Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:00:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549028.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_SRR1549028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:00:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,695,625
Mapped reads	7,680,270 / 88.32%
Unmapped reads	1,015,355 / 11.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	335,051 / 3.85%
Duplication rate	3.07%
Clipped reads	637,828 / 7.34%

2.2. ACGT Content

Number/percentage of A's	86,137,685 / 28.37%
Number/percentage of C's	64,790,328 / 21.34%
Number/percentage of T's	87,416,198 / 28.79%
Number/percentage of G's	65,276,100 / 21.5%
Number/percentage of N's	3,229 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0981
Standard Deviation	0.9714

2.4. Mapping Quality

Mean Mapping Quality	38.31

2.5. Mismatches and indels

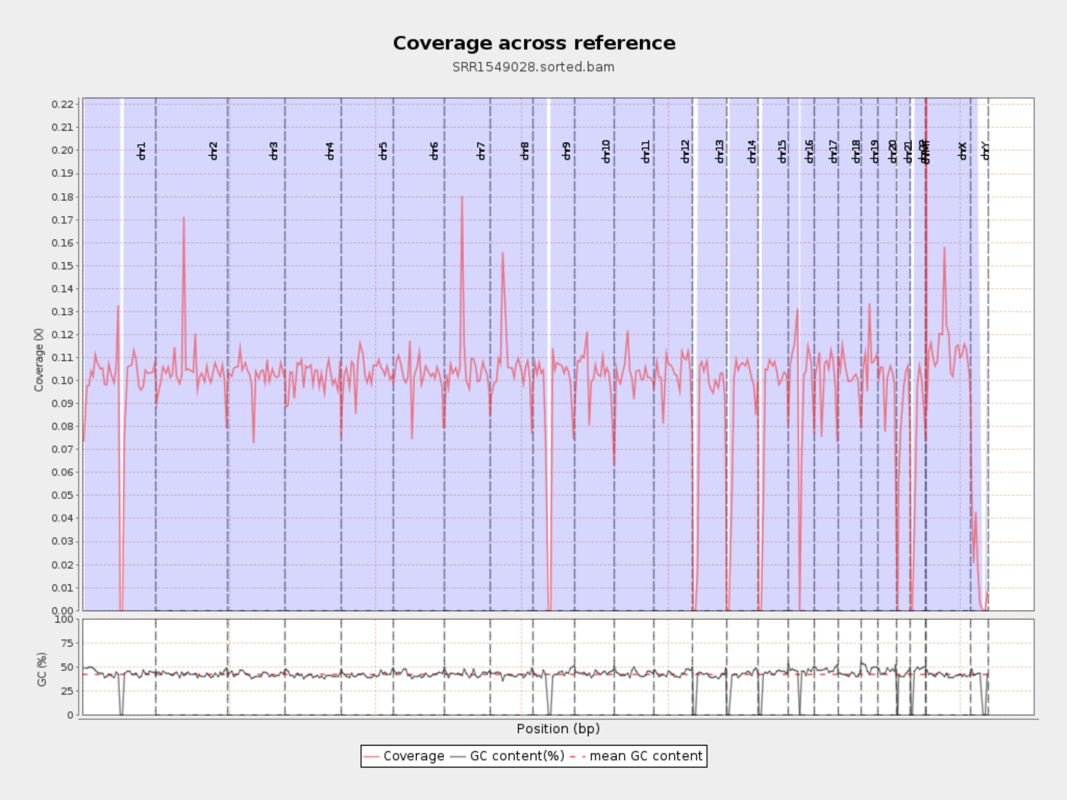
General error rate	0.31%
Mismatches	927,248
Insertions	10,578
Mapped reads with at least one insertion	0.14%
Deletions	23,372
Mapped reads with at least one deletion	0.3%
Homopolymer indels	38.71%

2.6. Chromosome stats

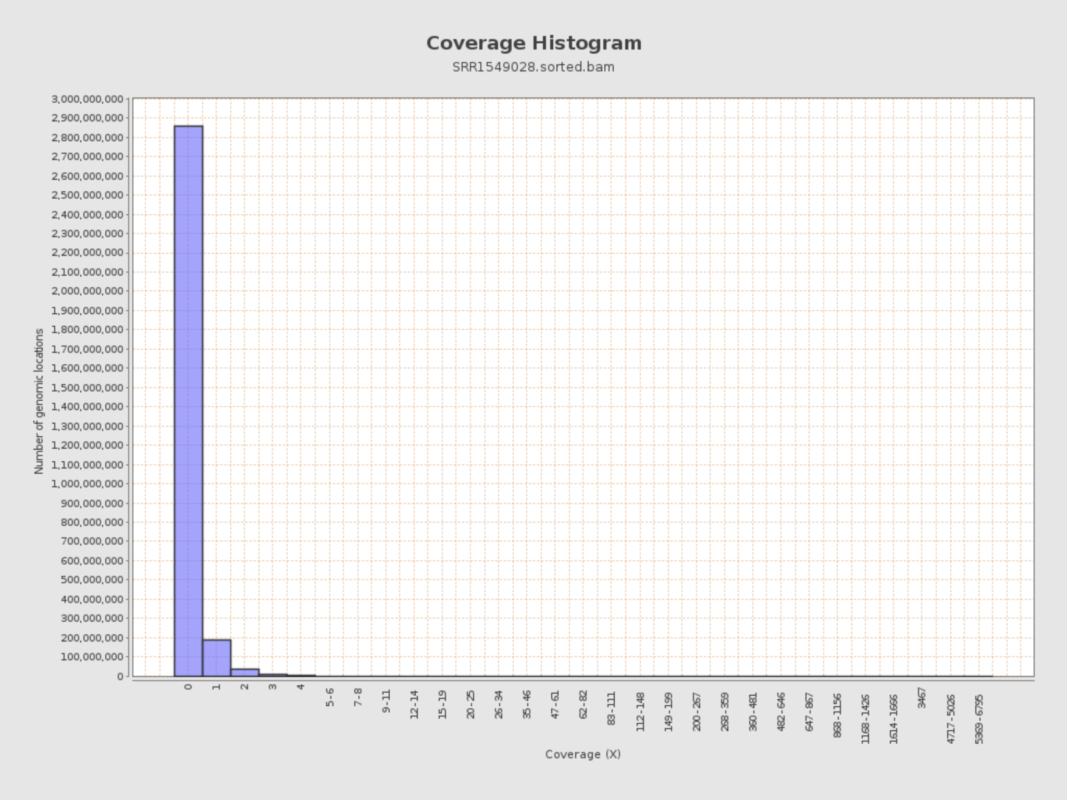
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23996359	0.0963	1.0034
chr2	243199373	25494604	0.1048	0.7448
chr3	198022430	20353789	0.1028	0.3948
chr4	191154276	19430301	0.1016	0.4063
chr5	180915260	18678434	0.1032	0.4059
chr6	171115067	17541115	0.1025	0.4439
chr7	159138663	17002471	0.1068	1.0351
chr8	146364022	15667280	0.107	3.3164

chr9	141213431	12797655	0.0906	0.7862
chr10	135534747	13910929	0.1026	0.5284
chr11	135006516	13801887	0.1022	0.8408
chr12	133851895	13885037	0.1037	0.4238
chr13	115169878	9658833	0.0839	0.351
chr14	107349540	9272570	0.0864	0.494
chr15	102531392	8683601	0.0847	0.3584
chr16	90354753	8556128	0.0947	0.4437
chr17	81195210	8312879	0.1024	0.4489
chr18	78077248	8058430	0.1032	1.4146
chr19	59128983	6447738	0.109	1.0273
chr20	63025520	6170961	0.0979	0.4111
chr21	48129895	3821782	0.0794	0.4359
chr22	51304566	3465596	0.0675	0.3556
chrMT	16571	13624	0.8222	1.2621
chrX	155270560	17632285	0.1136	0.5589
chrY	59373566	999139	0.0168	0.202

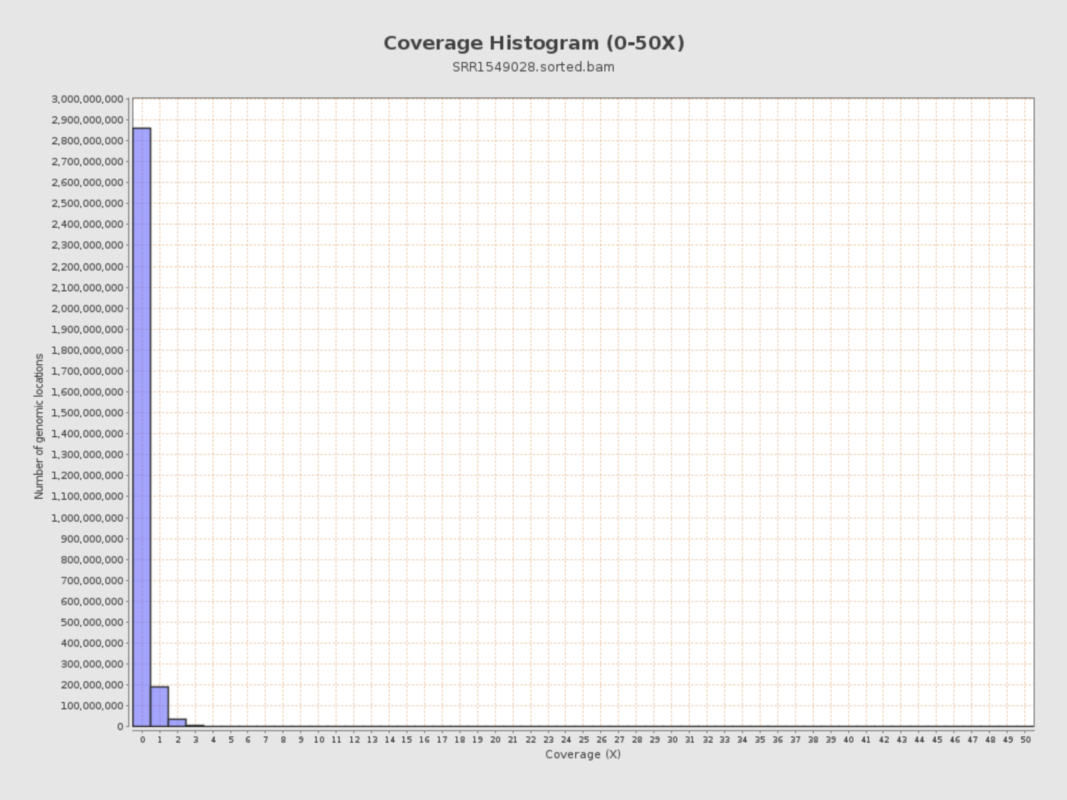
3. Results : Coverage across reference



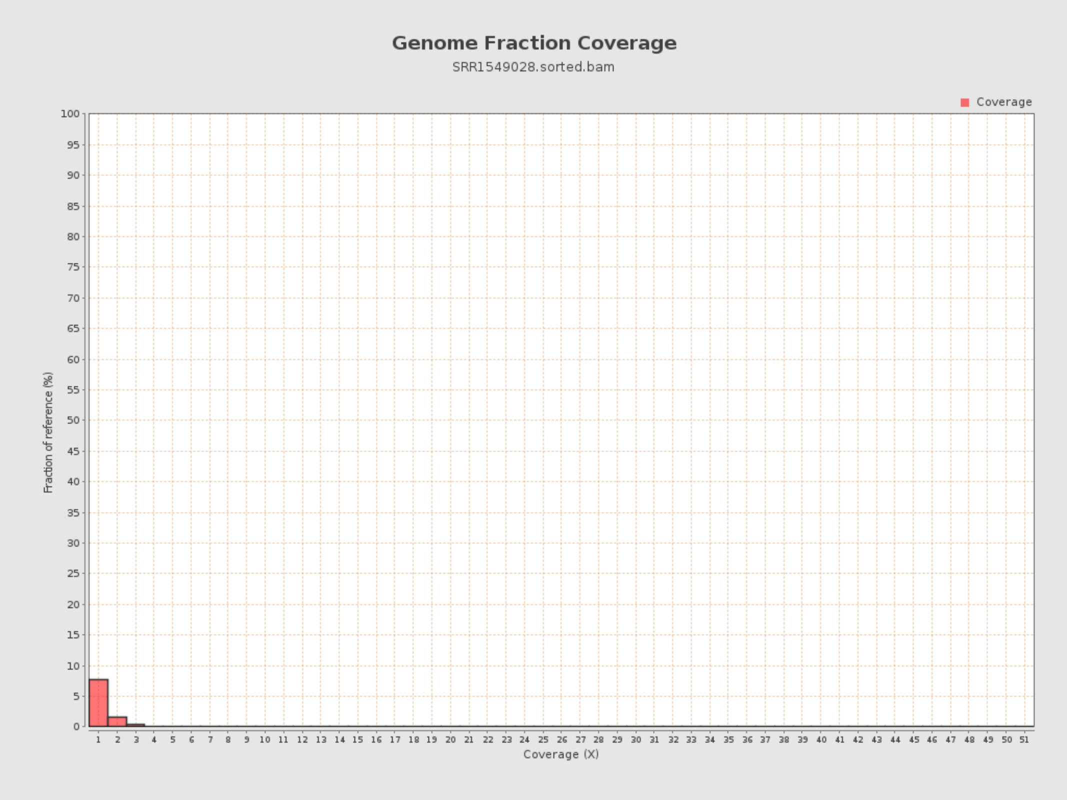
4. Results : Coverage Histogram



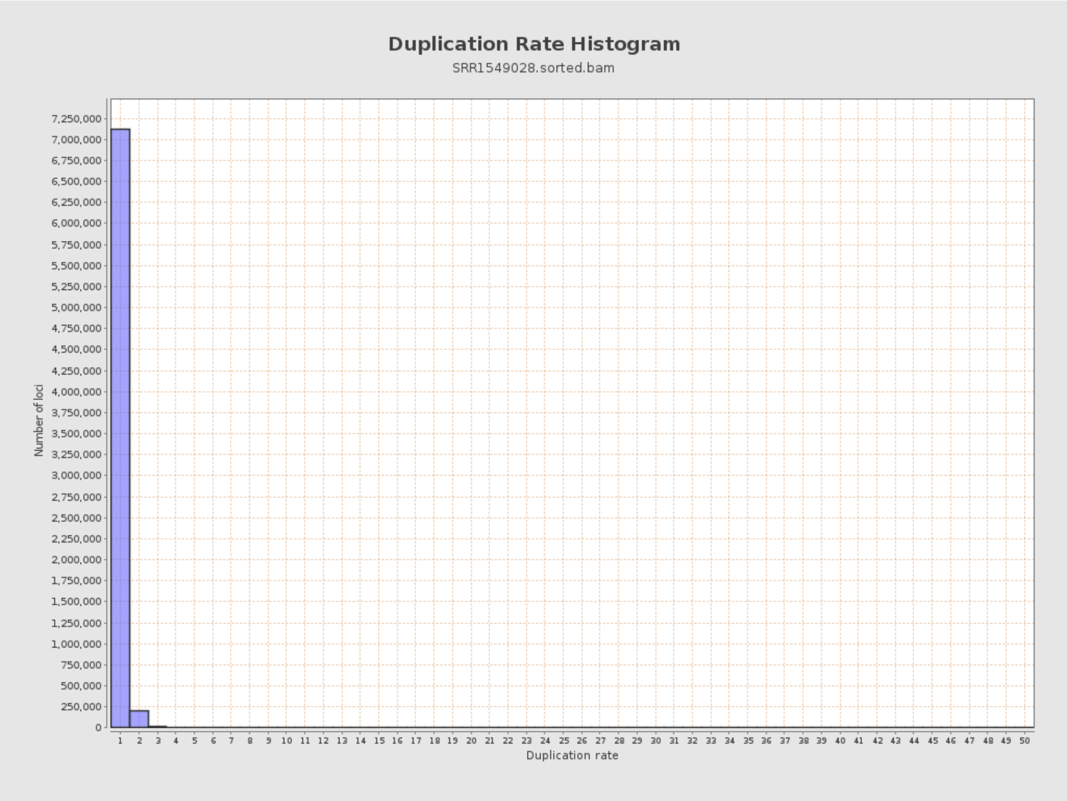
5. Results : Coverage Histogram (0-50X)



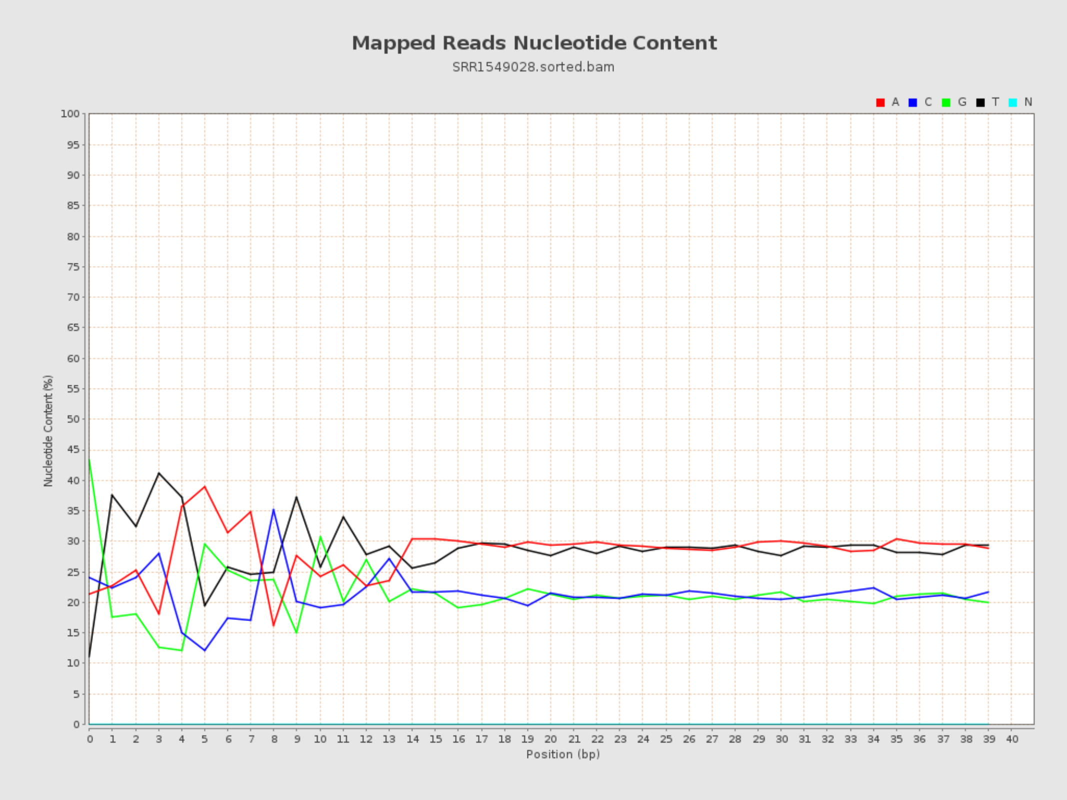
6. Results : Genome Fraction Coverage



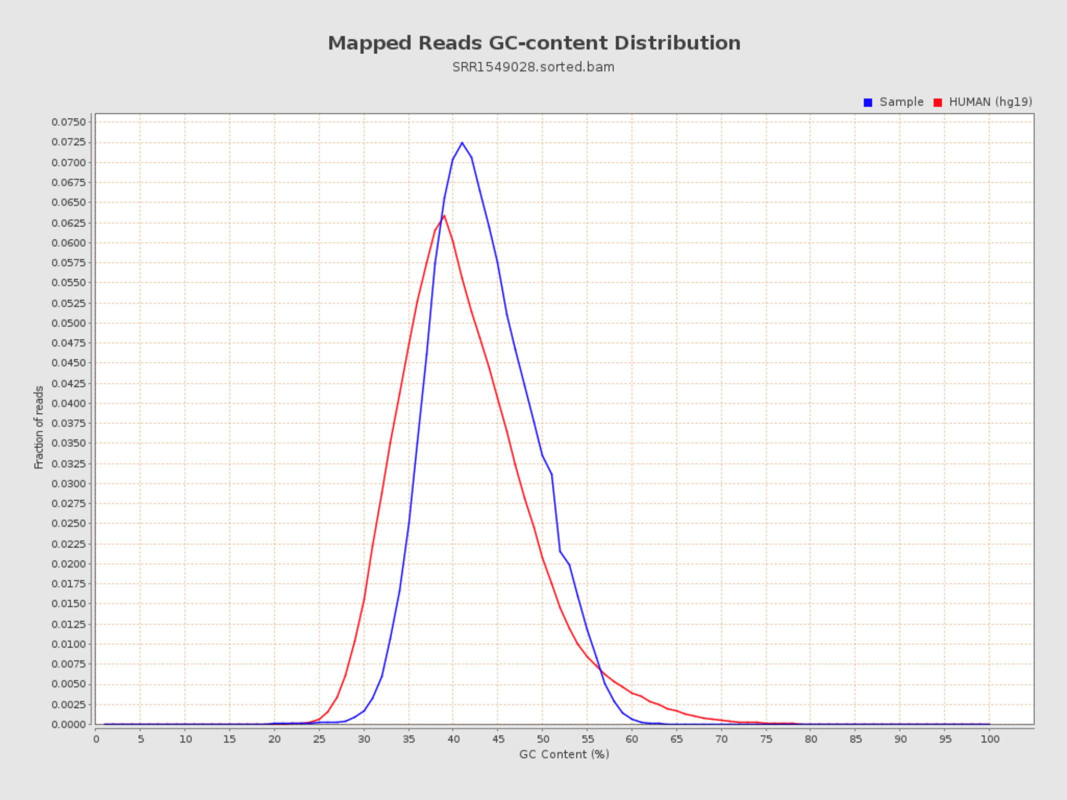
7. Results : Duplication Rate Histogram



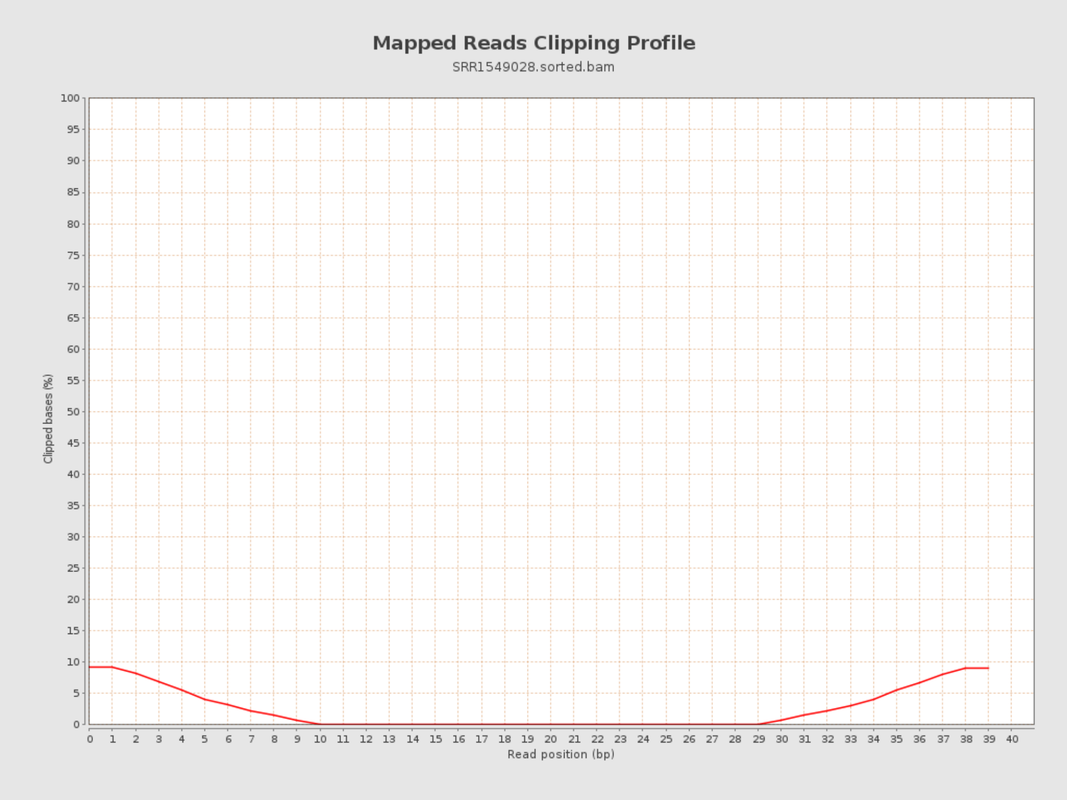
8. Results : Mapped Reads Nucleotide Content



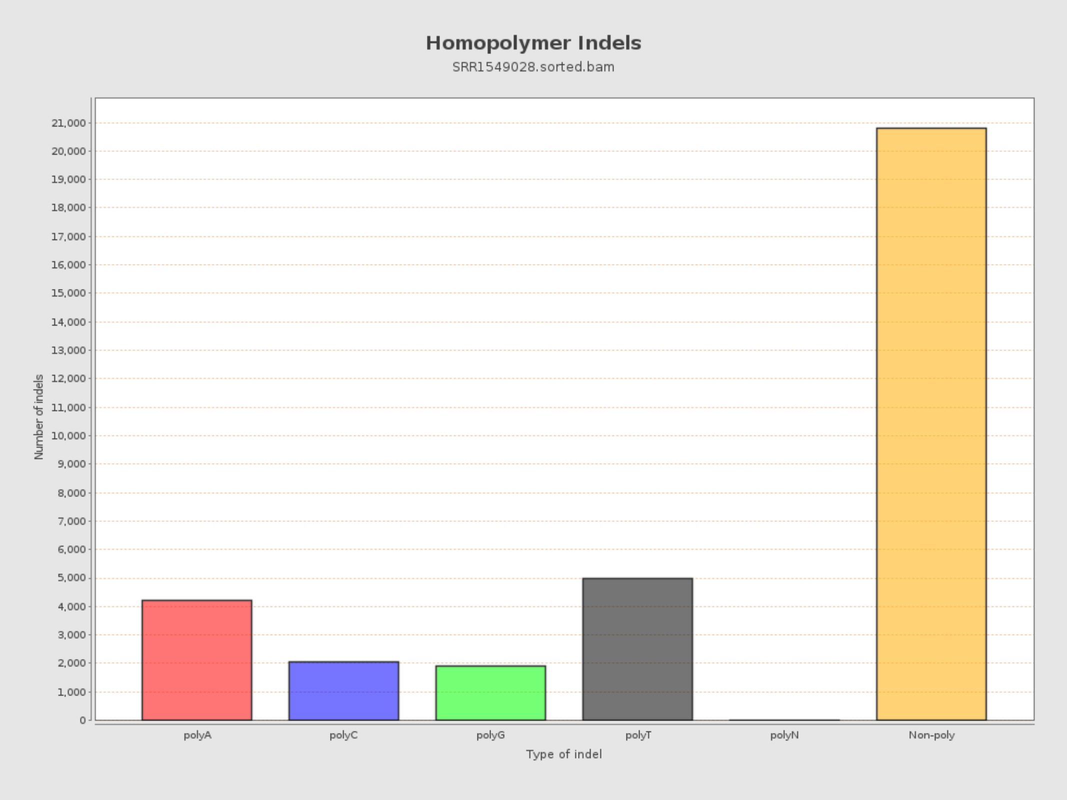
9. Results : Mapped Reads GC-content Distribution



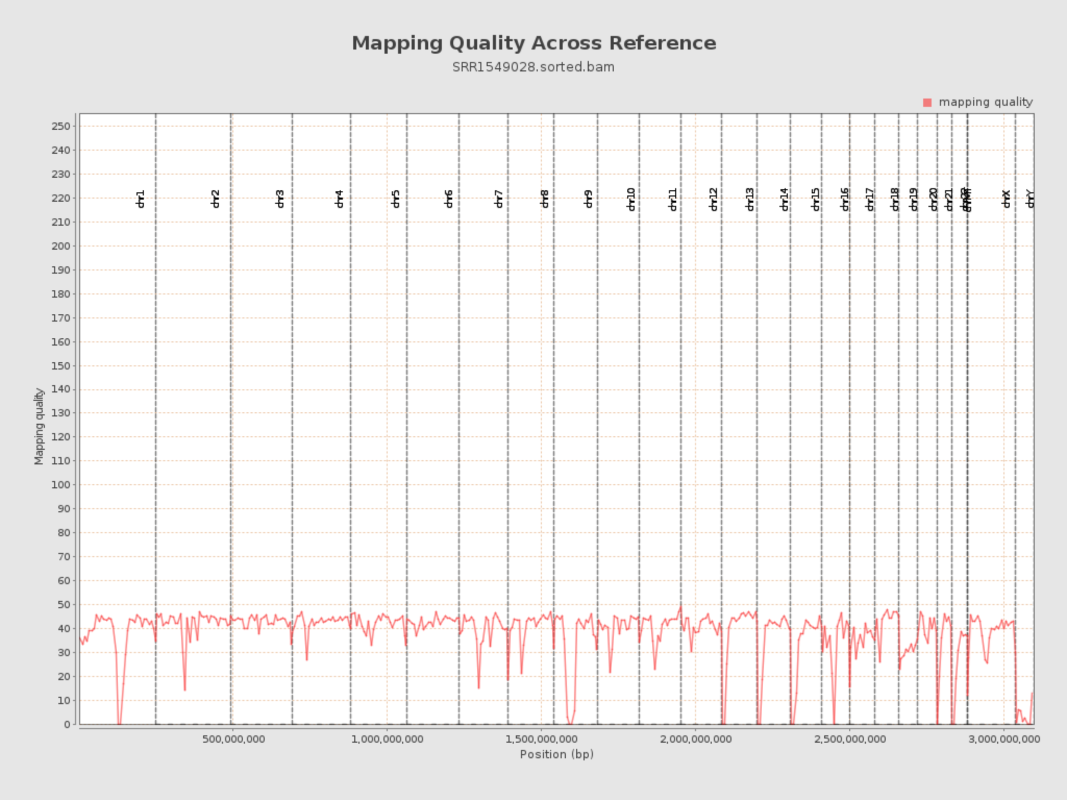
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram