

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:09:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548922.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_SRR1548922 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548922.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:09:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,632,633
Mapped reads	6,675,684 / 87.46%
Unmapped reads	956,949 / 12.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	205,079 / 2.69%
Duplication rate	2.13%
Clipped reads	440,217 / 5.77%

2.2. ACGT Content

Number/percentage of A's	78,589,758 / 29.71%
Number/percentage of C's	53,670,904 / 20.29%
Number/percentage of T's	78,733,584 / 29.76%
Number/percentage of G's	53,531,238 / 20.24%
Number/percentage of N's	2,475 / 0%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0855
Standard Deviation	0.9317

2.4. Mapping Quality

Mean Mapping Quality	42.54
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2.5. Mismatches and indels

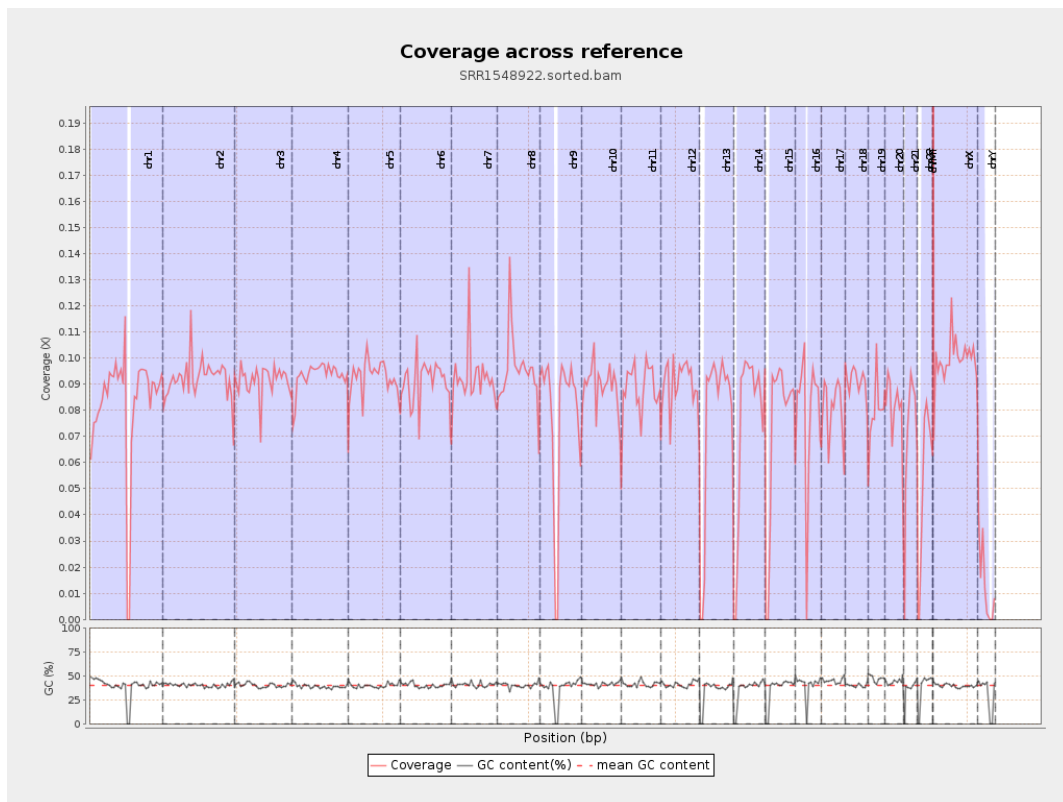
General error rate	0.27%
Mismatches	705,044
Insertions	7,834
Mapped reads with at least one insertion	0.12%
Deletions	21,276
Mapped reads with at least one deletion	0.32%
Homopolymer indels	42.4%

2.6. Chromosome stats

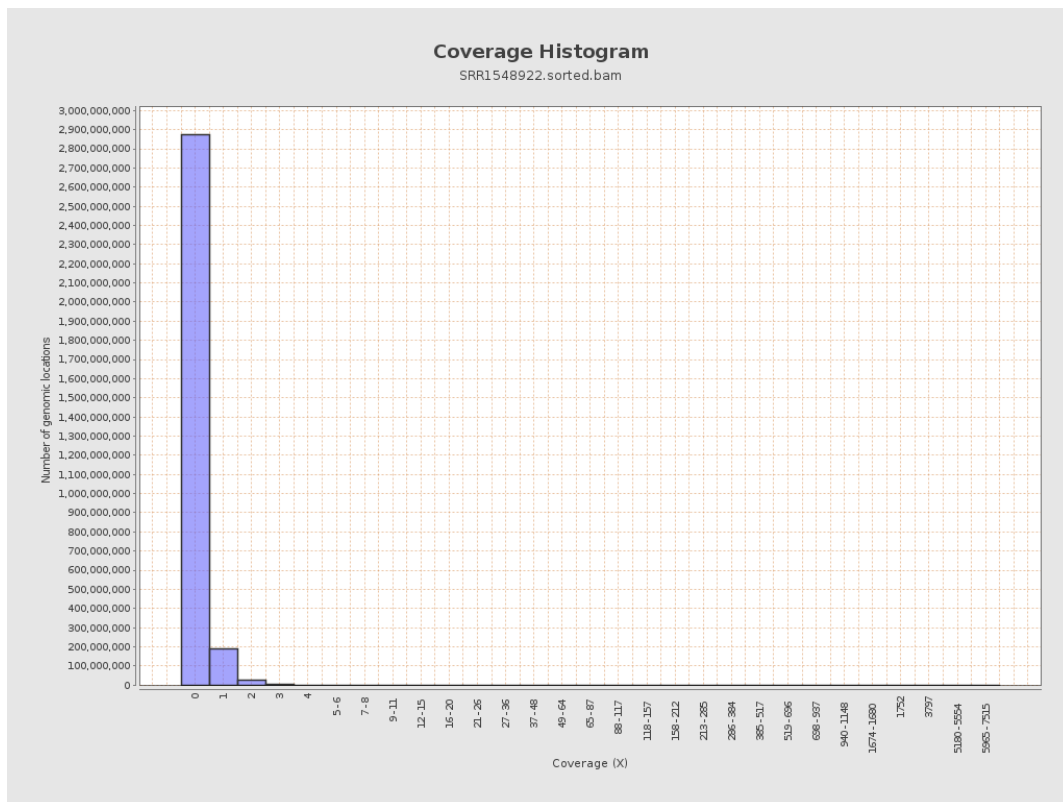
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20633449	0.0828	0.8898
chr2	243199373	22425800	0.0922	0.4971
chr3	198022430	18110462	0.0915	0.3483
chr4	191154276	17835063	0.0933	0.3607
chr5	180915260	16718060	0.0924	0.3562
chr6	171115067	15599788	0.0912	0.3881
chr7	159138663	14682676	0.0923	0.6977
chr8	146364022	13939120	0.0952	3.639

chr9	141213431	11079855	0.0785	0.4749
chr10	135534747	12108206	0.0893	0.4457
chr11	135006516	11963613	0.0886	0.5325
chr12	133851895	12092845	0.0903	0.36
chr13	115169878	8787858	0.0763	0.3152
chr14	107349540	8186952	0.0763	0.3747
chr15	102531392	7448456	0.0726	0.3083
chr16	90354753	6993058	0.0774	0.3489
chr17	81195210	6578022	0.081	0.3523
chr18	78077248	7136203	0.0914	0.8655
chr19	59128983	4755751	0.0804	0.7936
chr20	63025520	5150451	0.0817	0.3368
chr21	48129895	3373448	0.0701	0.3365
chr22	51304566	2729060	0.0532	0.294
chrMT	16571	9731	0.5872	0.9296
chrX	155270560	15441611	0.0994	0.4352
chrY	59373566	776602	0.0131	0.1788

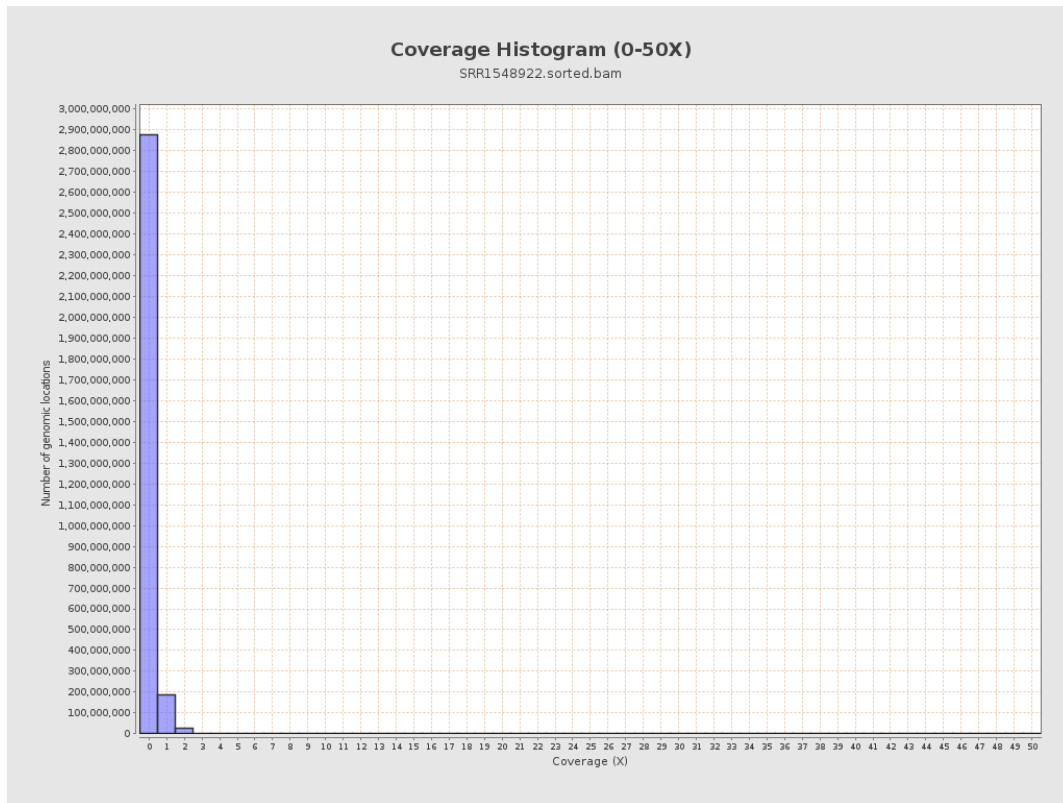
3. Results : Coverage across reference



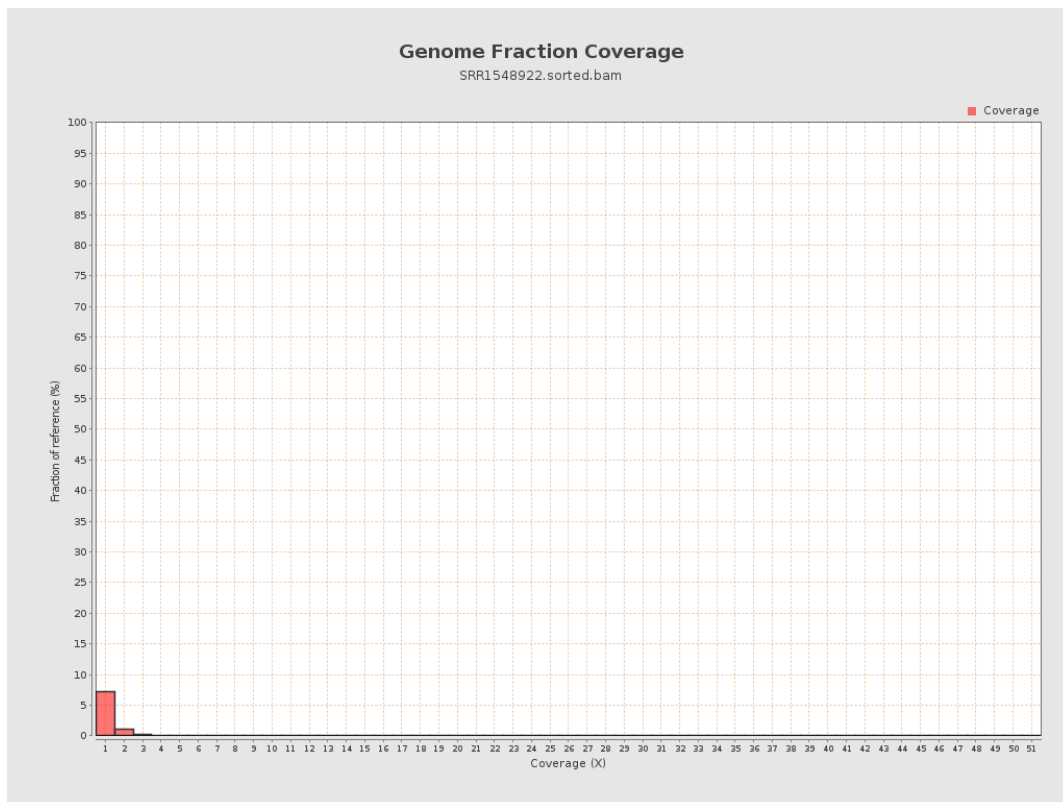
4. Results : Coverage Histogram



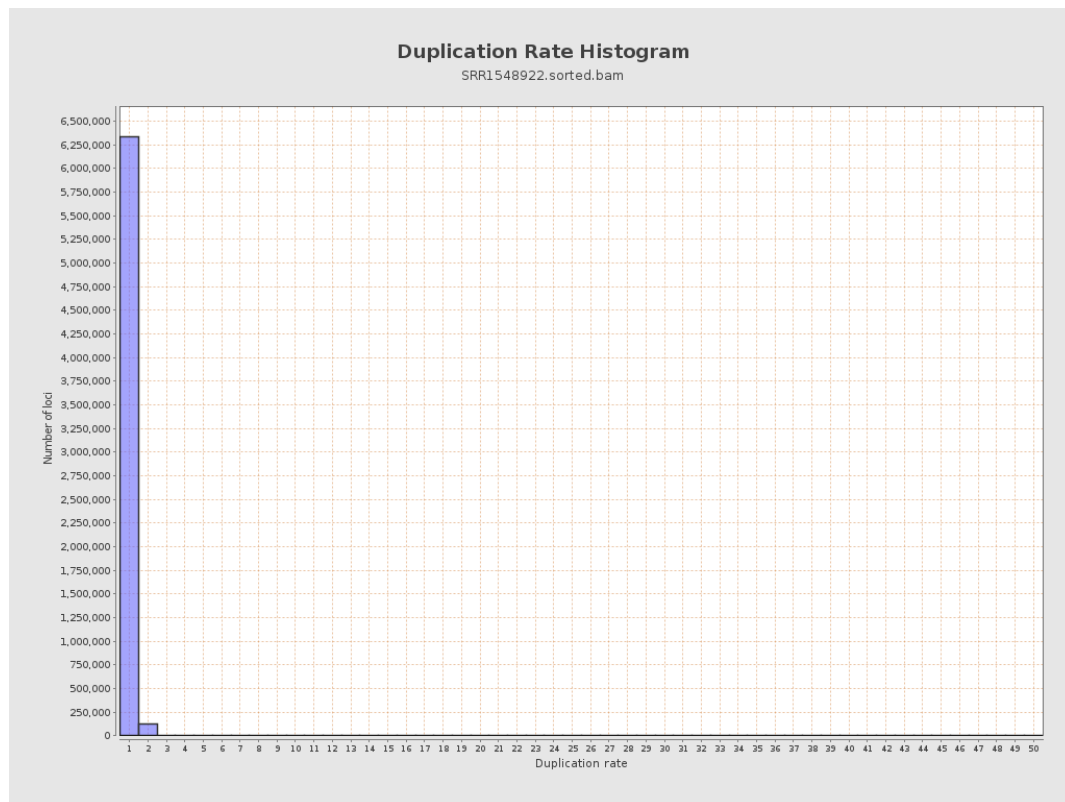
5. Results : Coverage Histogram (0-50X)



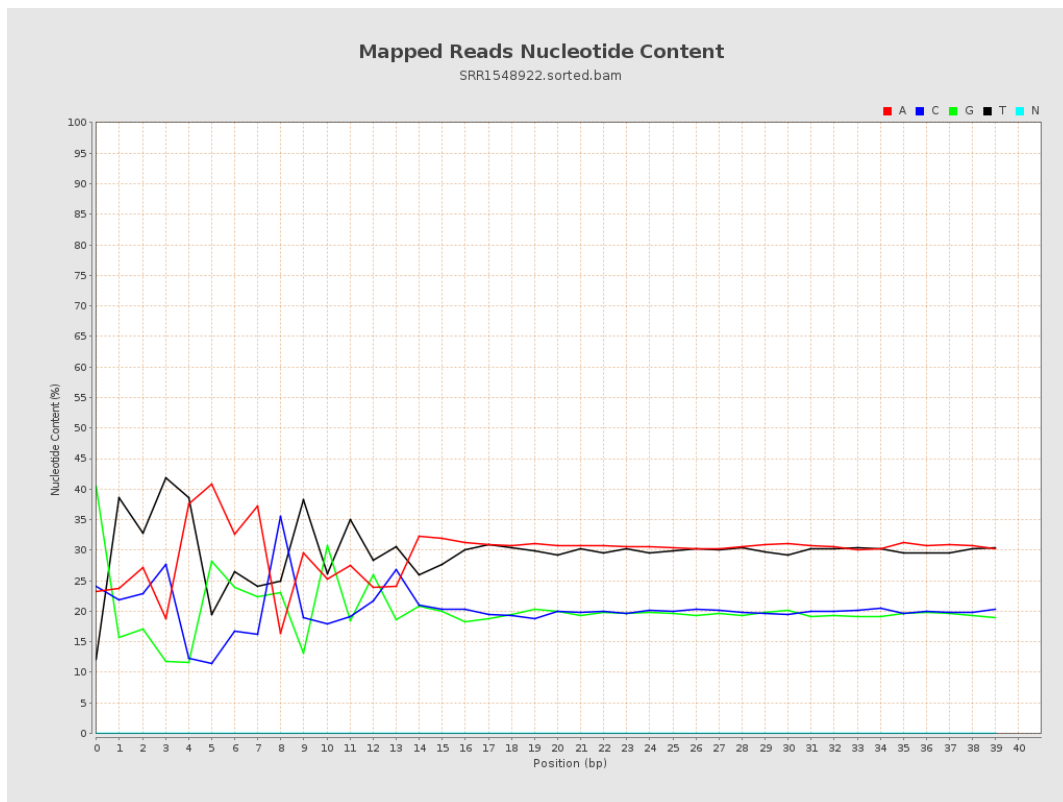
6. Results : Genome Fraction Coverage



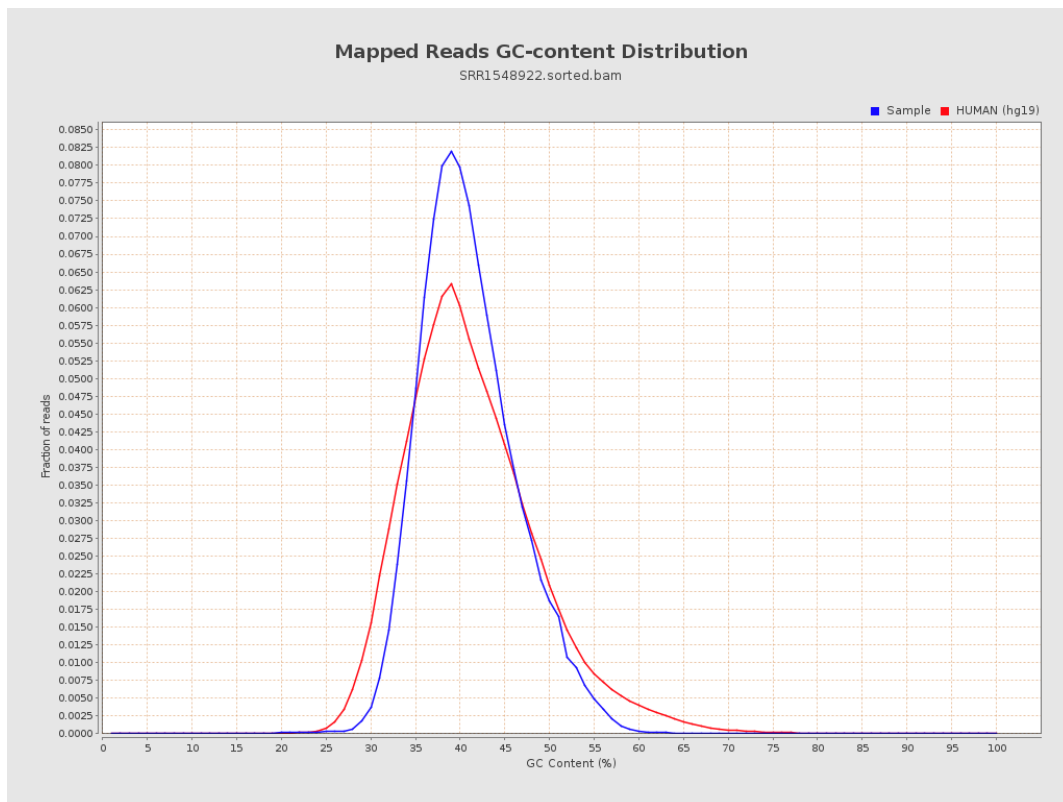
7. Results : Duplication Rate Histogram



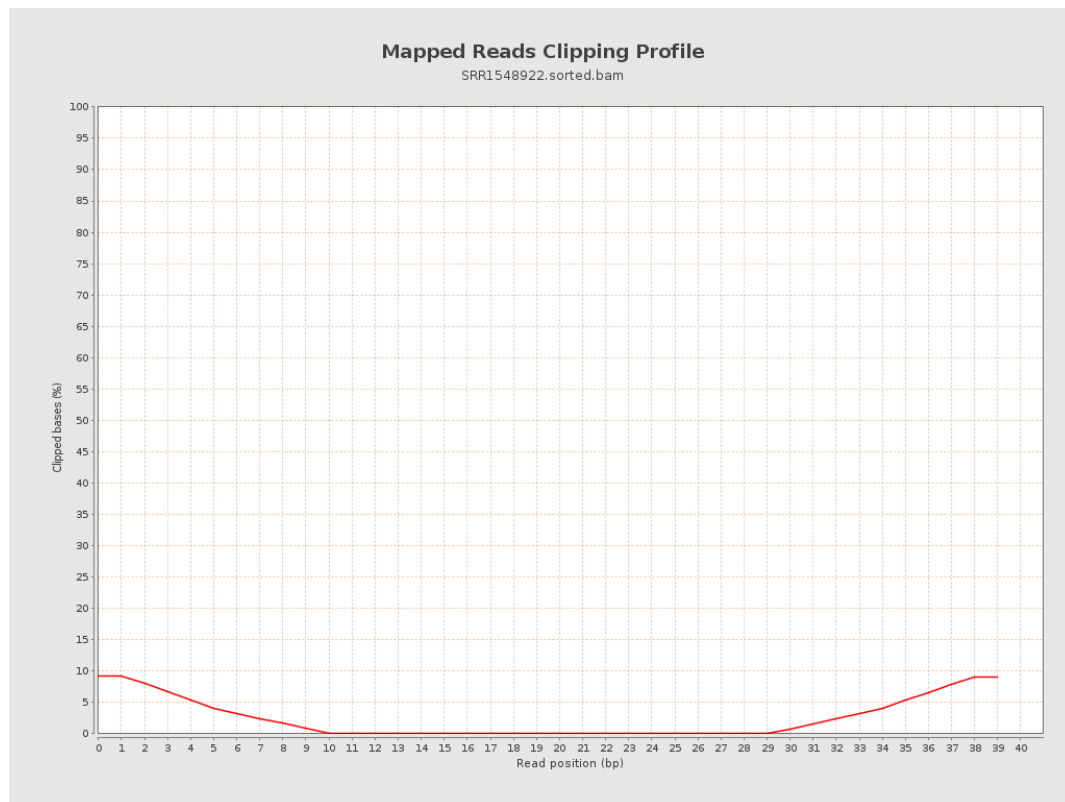
8. Results : Mapped Reads Nucleotide Content



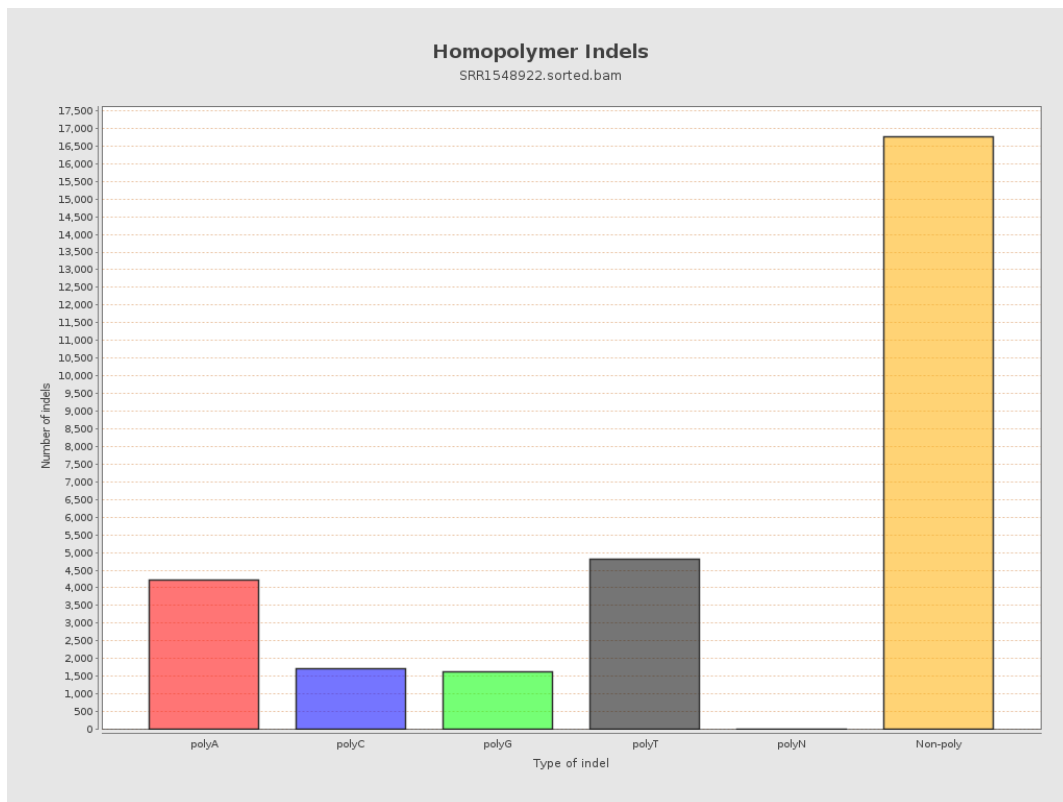
9. Results : Mapped Reads GC-content Distribution



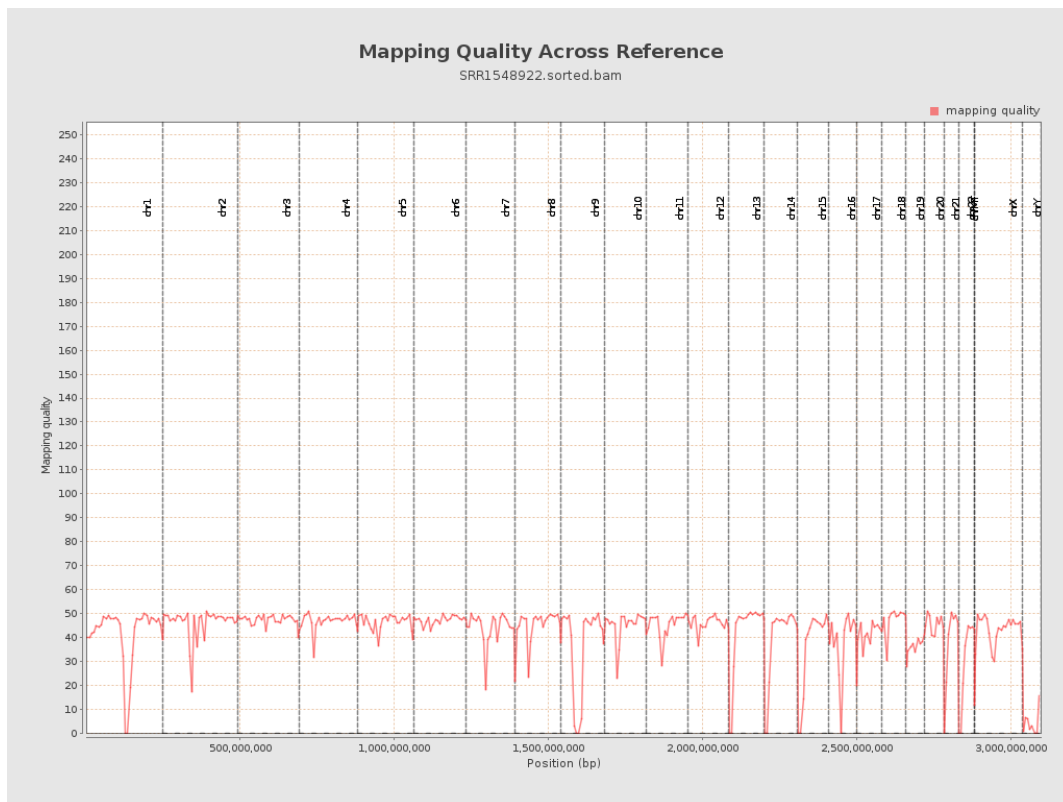
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

