

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:34:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548925.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_SRR1548925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548925.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:34:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,615,372
Mapped reads	4,880,527 / 86.91%
Unmapped reads	734,845 / 13.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	125,966 / 2.24%
Duplication rate	1.74%
Clipped reads	371,029 / 6.61%

2.2. ACGT Content

Number/percentage of A's	57,225,975 / 29.62%
Number/percentage of C's	39,319,303 / 20.35%
Number/percentage of T's	57,390,482 / 29.71%
Number/percentage of G's	39,230,705 / 20.31%
Number/percentage of N's	1,711 / 0%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0624
Standard Deviation	0.7676

2.4. Mapping Quality

Mean Mapping Quality	42.17
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2.5. Mismatches and indels

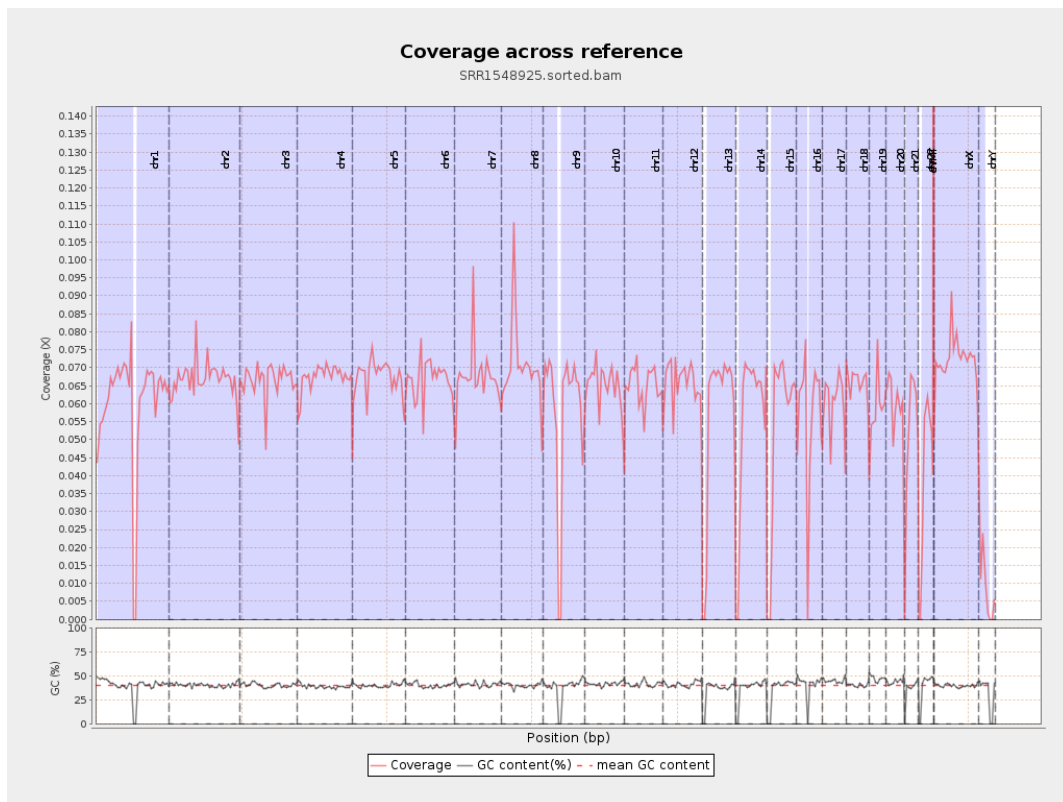
General error rate	0.28%
Mismatches	538,678
Insertions	6,359
Mapped reads with at least one insertion	0.13%
Deletions	16,646
Mapped reads with at least one deletion	0.34%
Homopolymer indels	41.56%

2.6. Chromosome stats

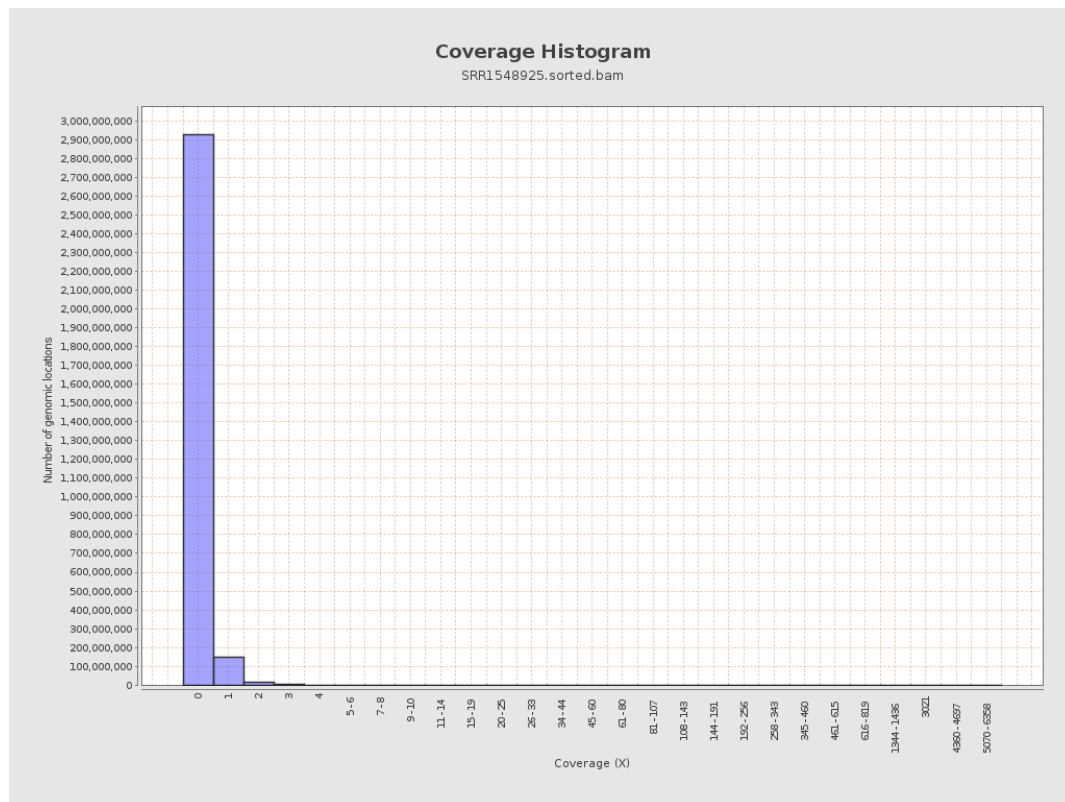
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15015470	0.0602	0.6495
chr2	243199373	16259967	0.0669	0.3769
chr3	198022430	13191899	0.0666	0.2885
chr4	191154276	12894748	0.0675	0.294
chr5	180915260	12213489	0.0675	0.2941
chr6	171115067	11417735	0.0667	0.3151
chr7	159138663	10789060	0.0678	0.5327
chr8	146364022	10296374	0.0703	3.0774

chr9	141213431	8156960	0.0578	0.3567
chr10	135534747	8855100	0.0653	0.3453
chr11	135006516	8757813	0.0649	0.4065
chr12	133851895	8814707	0.0659	0.2952
chr13	115169878	6456747	0.0561	0.2624
chr14	107349540	5915735	0.0551	0.2867
chr15	102531392	5532854	0.054	0.2589
chr16	90354753	5114407	0.0566	0.2821
chr17	81195210	4841529	0.0596	0.2907
chr18	78077248	5163933	0.0661	0.611
chr19	59128983	3501107	0.0592	0.5934
chr20	63025520	3750039	0.0595	0.2787
chr21	48129895	2469922	0.0513	0.2769
chr22	51304566	2003190	0.039	0.2444
chrMT	16571	5181	0.3127	0.6307
chrX	155270560	11224060	0.0723	0.3467
chrY	59373566	548359	0.0092	0.1337

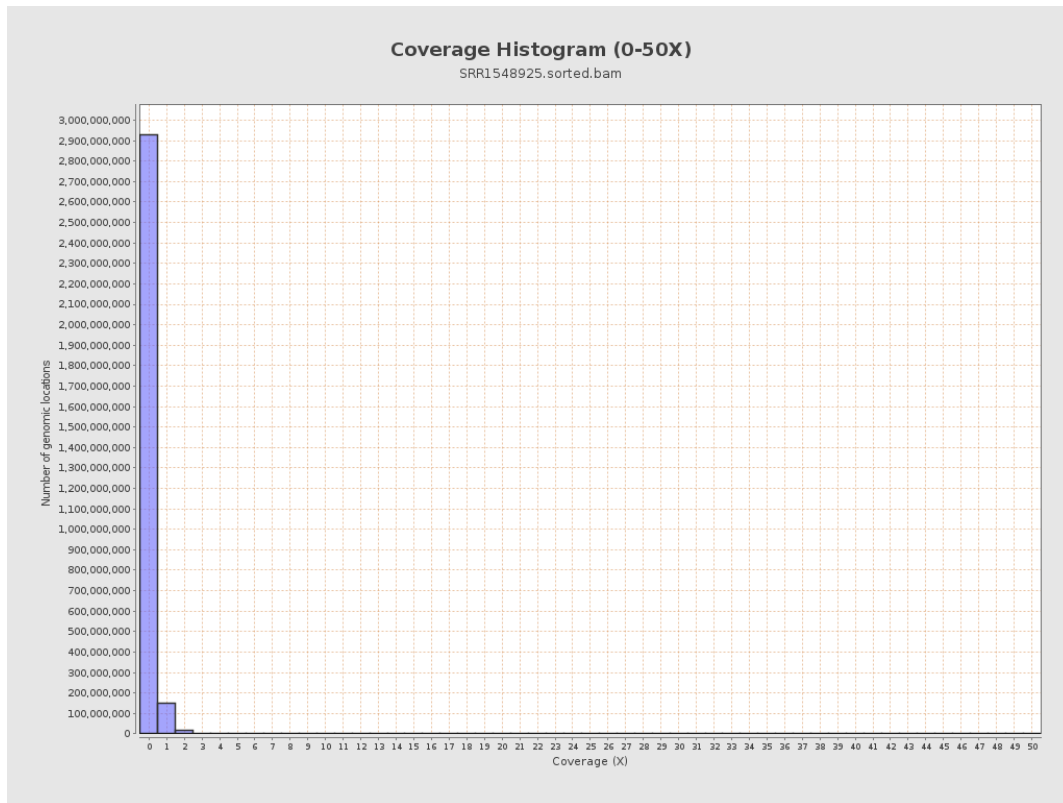
3. Results : Coverage across reference



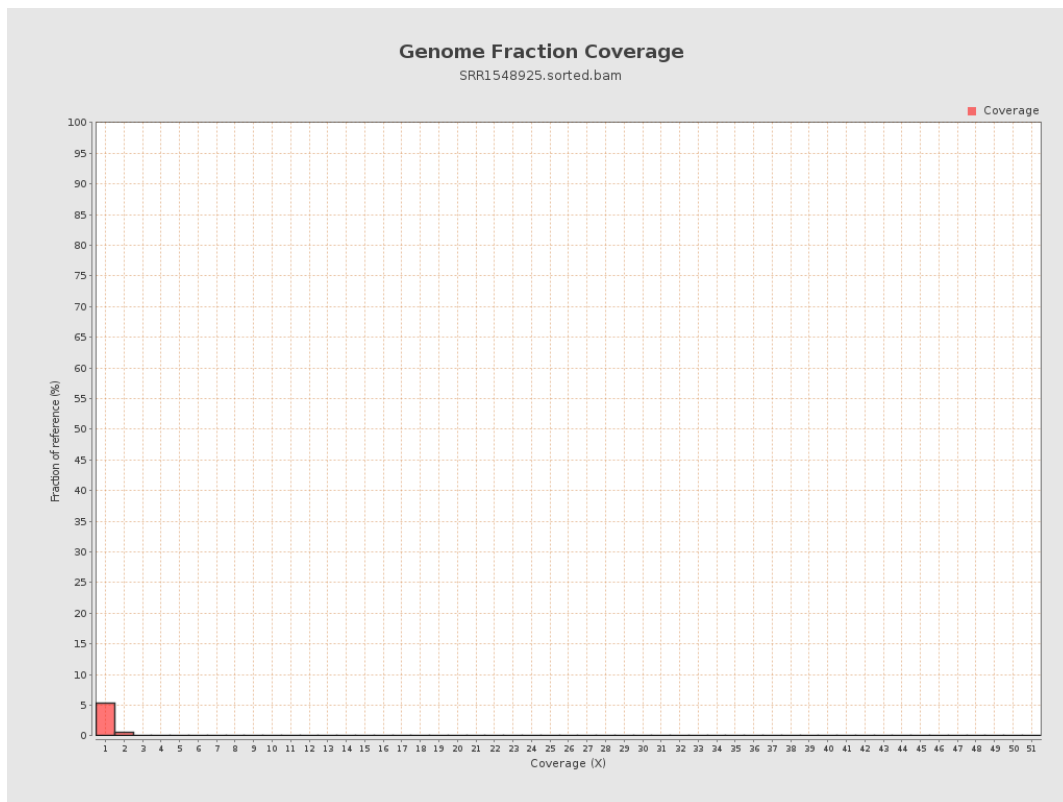
4. Results : Coverage Histogram



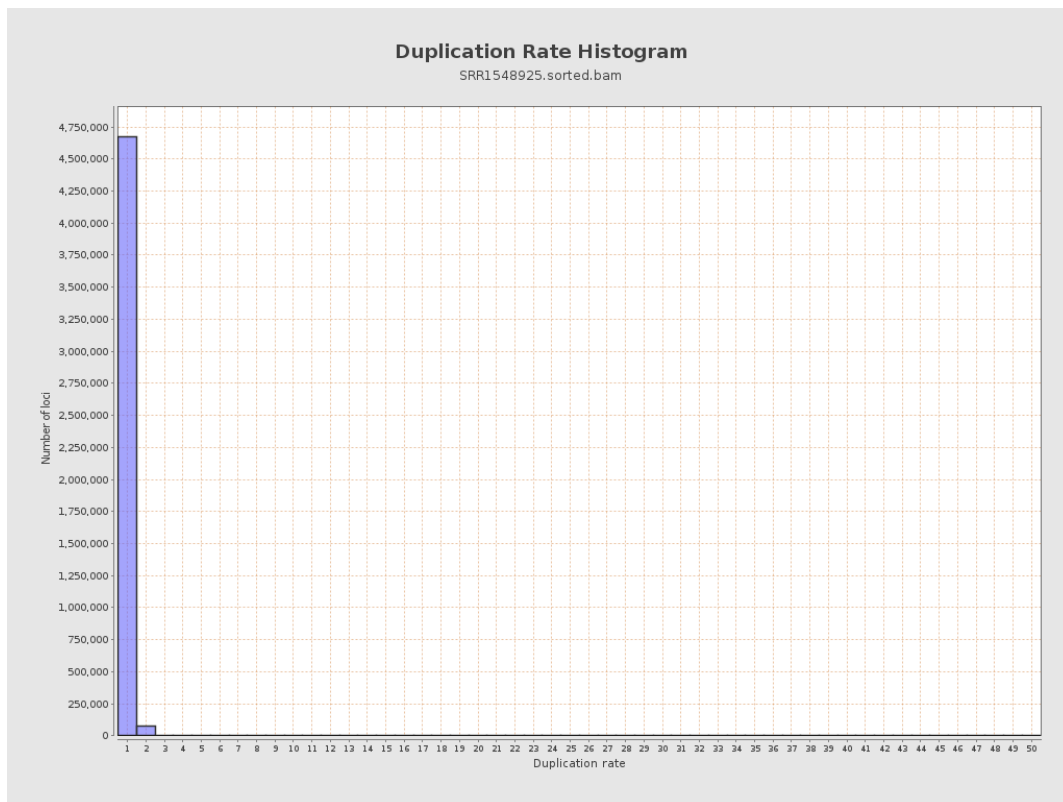
5. Results : Coverage Histogram (0-50X)



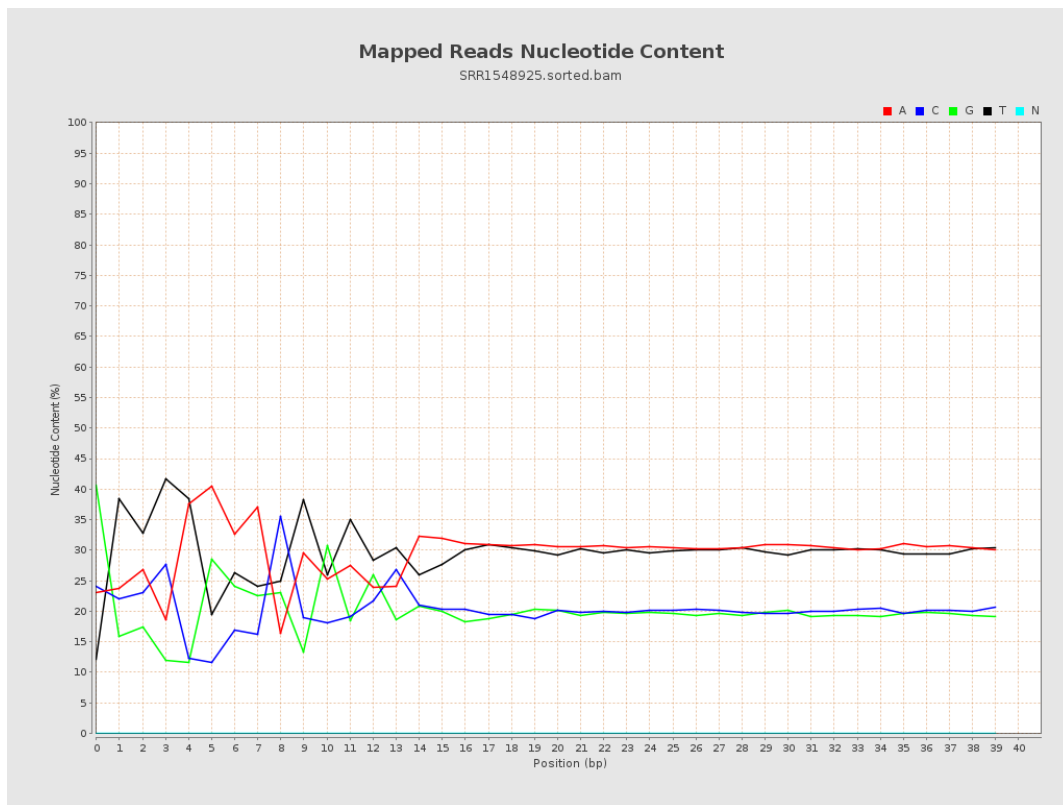
6. Results : Genome Fraction Coverage



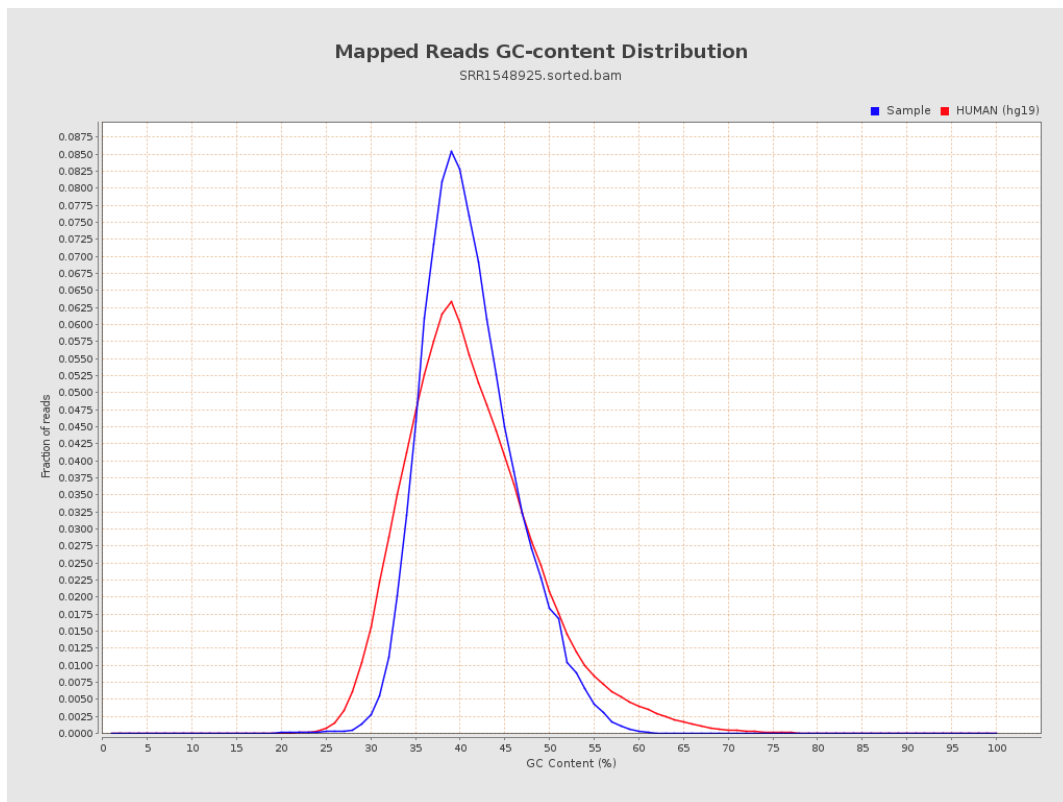
7. Results : Duplication Rate Histogram



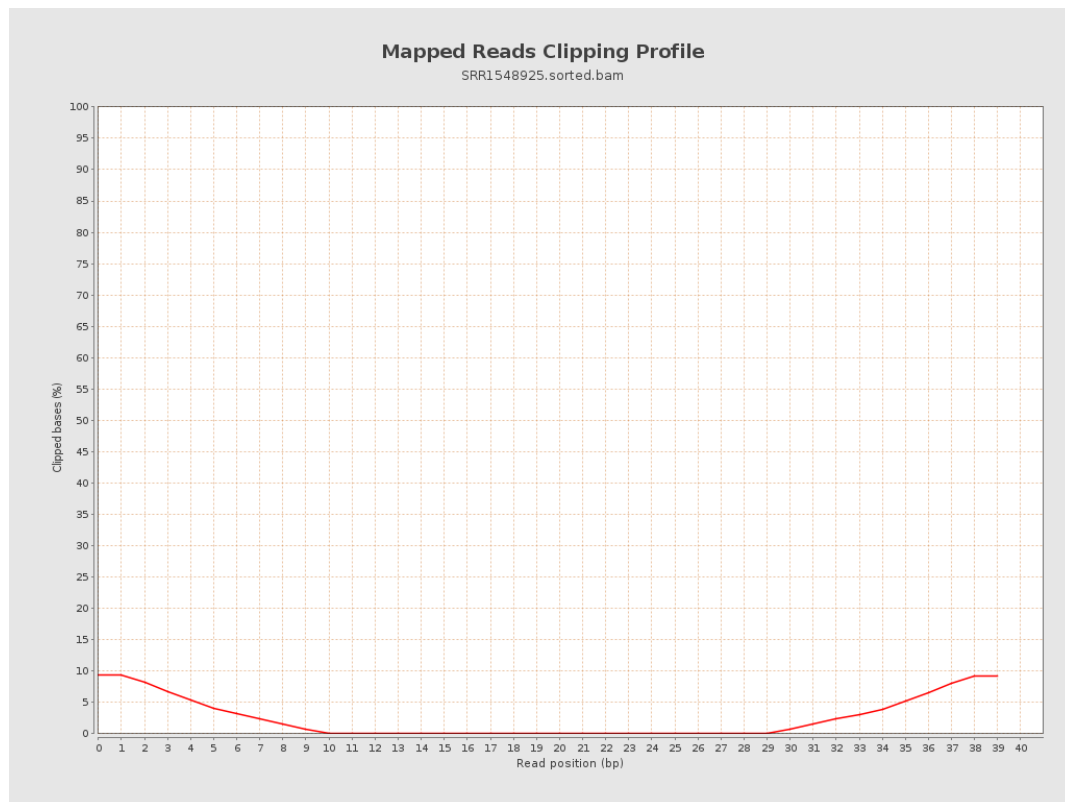
8. Results : Mapped Reads Nucleotide Content



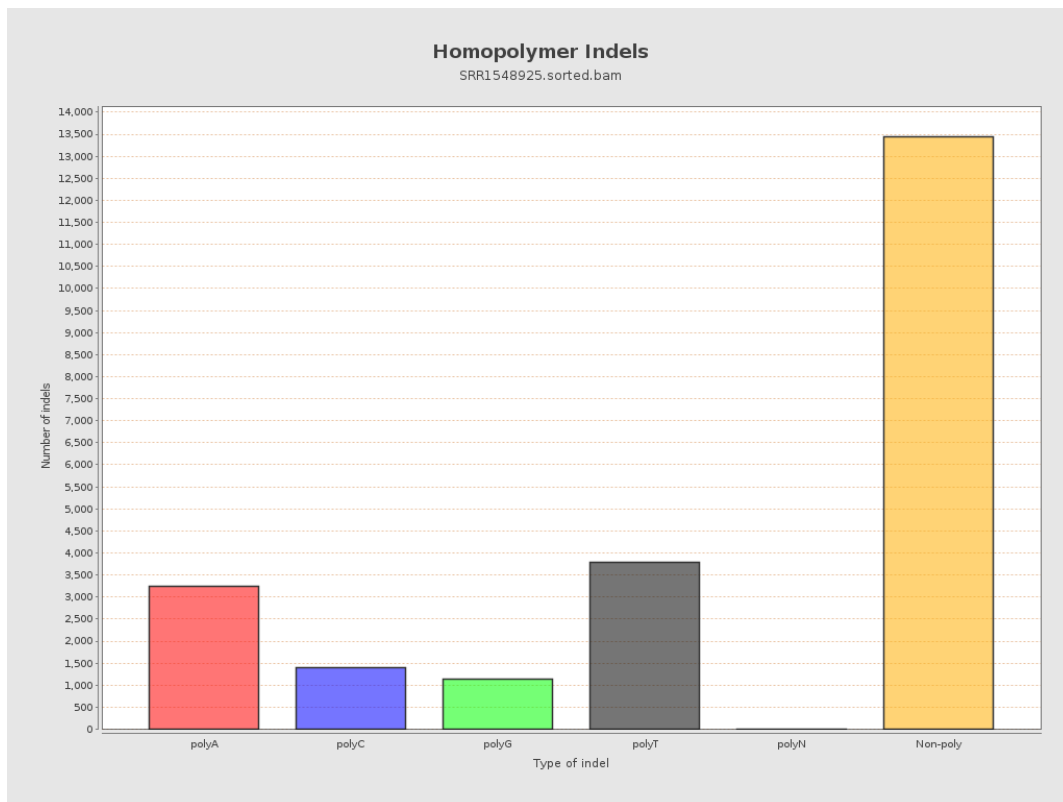
9. Results : Mapped Reads GC-content Distribution



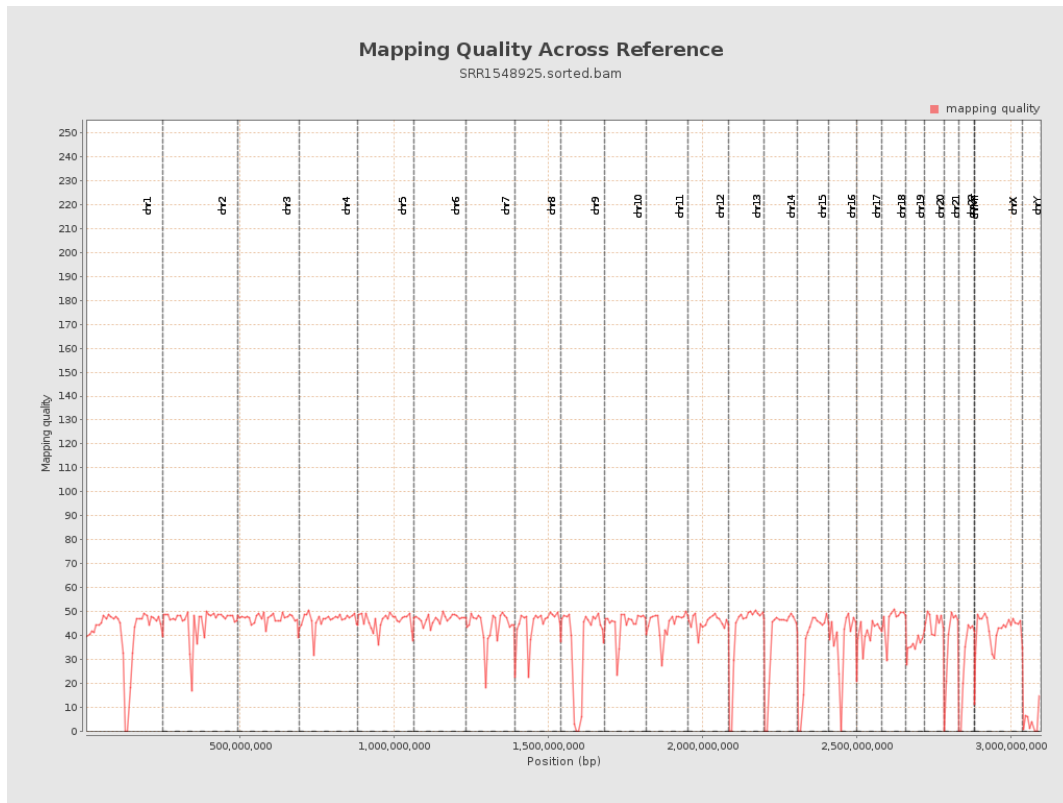
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

