

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:53:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548957.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_SRR1548957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548957.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:53:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,112,095
Mapped reads	6,780,913 / 83.59%
Unmapped reads	1,331,182 / 16.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	332,158 / 4.09%
Duplication rate	2.86%
Clipped reads	620,887 / 7.65%

2.2. ACGT Content

Number/percentage of A's	75,128,207 / 28.06%
Number/percentage of C's	58,089,747 / 21.7%
Number/percentage of T's	76,420,028 / 28.55%
Number/percentage of G's	58,059,104 / 21.69%
Number/percentage of N's	362 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.0865
Standard Deviation	0.8785

2.4. Mapping Quality

Mean Mapping Quality	35.62
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2.5. Mismatches and indels

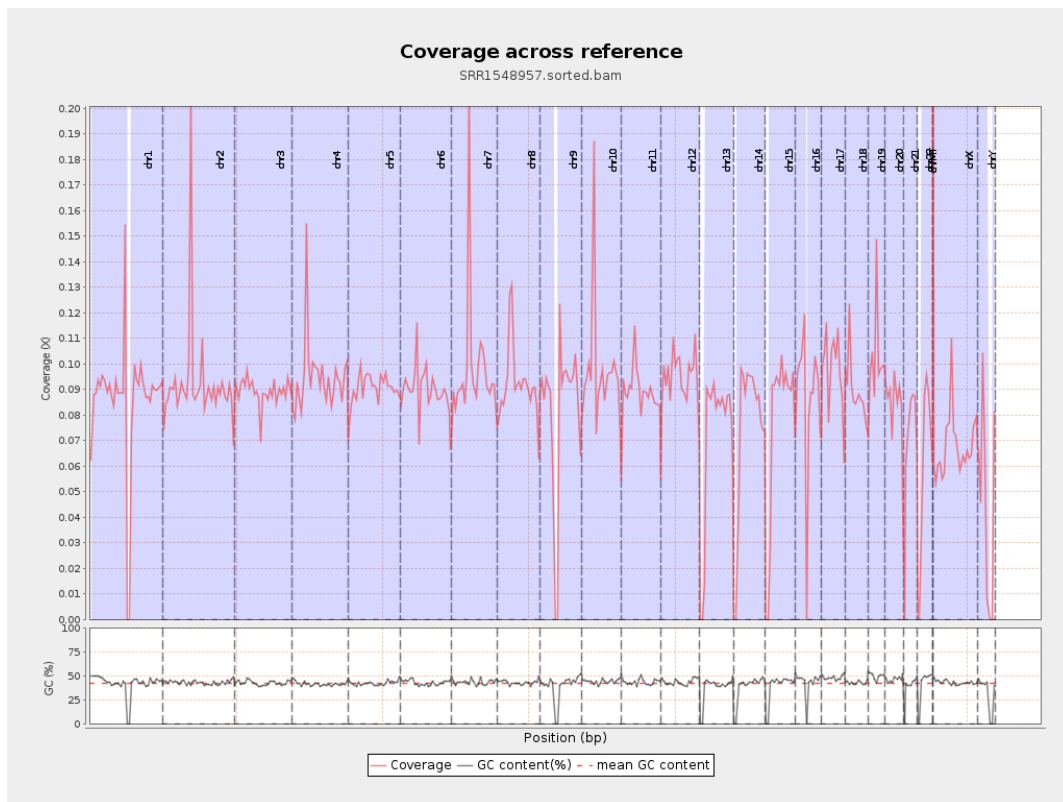
General error rate	0.34%
Mismatches	888,591
Insertions	9,610
Mapped reads with at least one insertion	0.14%
Deletions	19,290
Mapped reads with at least one deletion	0.28%
Homopolymer indels	37.88%

2.6. Chromosome stats

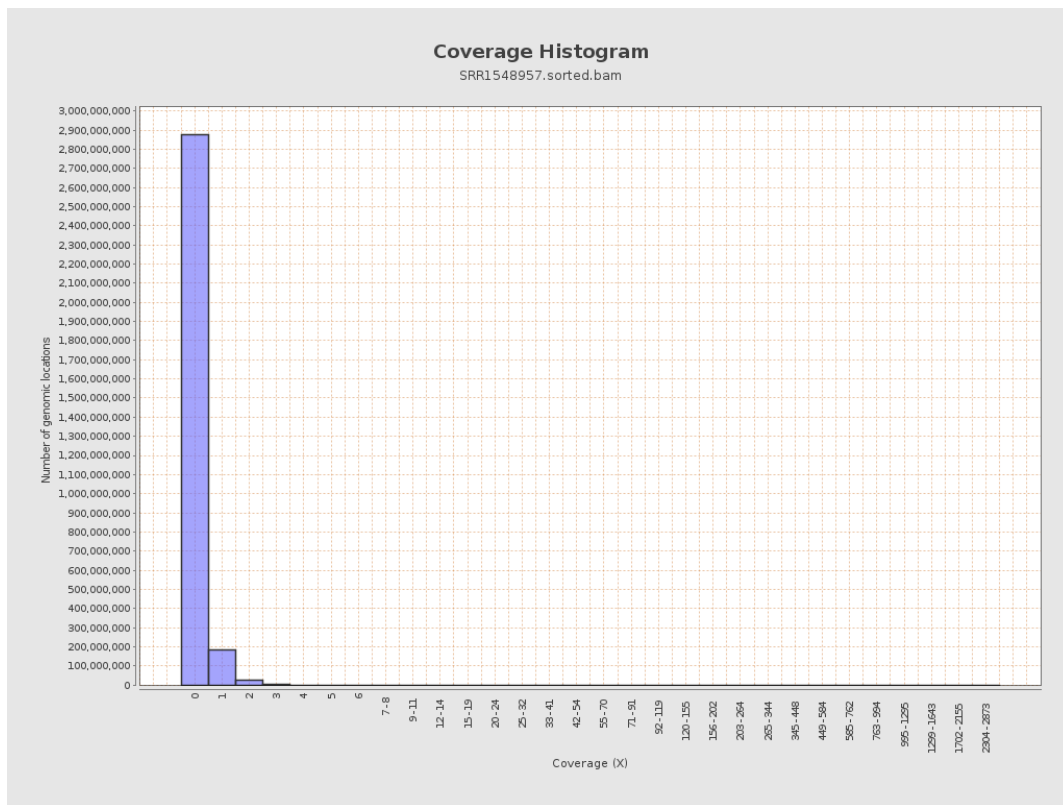
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21384553	0.0858	1.5407
chr2	243199373	22458980	0.0923	0.9499
chr3	198022430	17649906	0.0891	0.3558
chr4	191154276	18102599	0.0947	0.4511
chr5	180915260	16365180	0.0905	0.3851
chr6	171115067	15378071	0.0899	0.3931
chr7	159138663	15587585	0.0979	1.2697
chr8	146364022	13462276	0.092	1.5183

chr9	141213431	11510950	0.0815	0.9561
chr10	135534747	13177297	0.0972	0.7618
chr11	135006516	12039889	0.0892	0.6201
chr12	133851895	12814534	0.0957	0.4125
chr13	115169878	8194632	0.0712	0.3073
chr14	107349540	8071522	0.0752	0.5693
chr15	102531392	7722079	0.0753	0.3345
chr16	90354753	7681864	0.085	0.4867
chr17	81195210	8030696	0.0989	0.4351
chr18	78077248	7018070	0.0899	1.8009
chr19	59128983	6073756	0.1027	1.5815
chr20	63025520	5353968	0.0849	0.4084
chr21	48129895	3362816	0.0699	0.5224
chr22	51304566	3055206	0.0596	0.4302
chrMT	16571	8942	0.5396	0.8678
chrX	155270560	10523360	0.0678	0.52
chrY	59373566	2693222	0.0454	0.4826

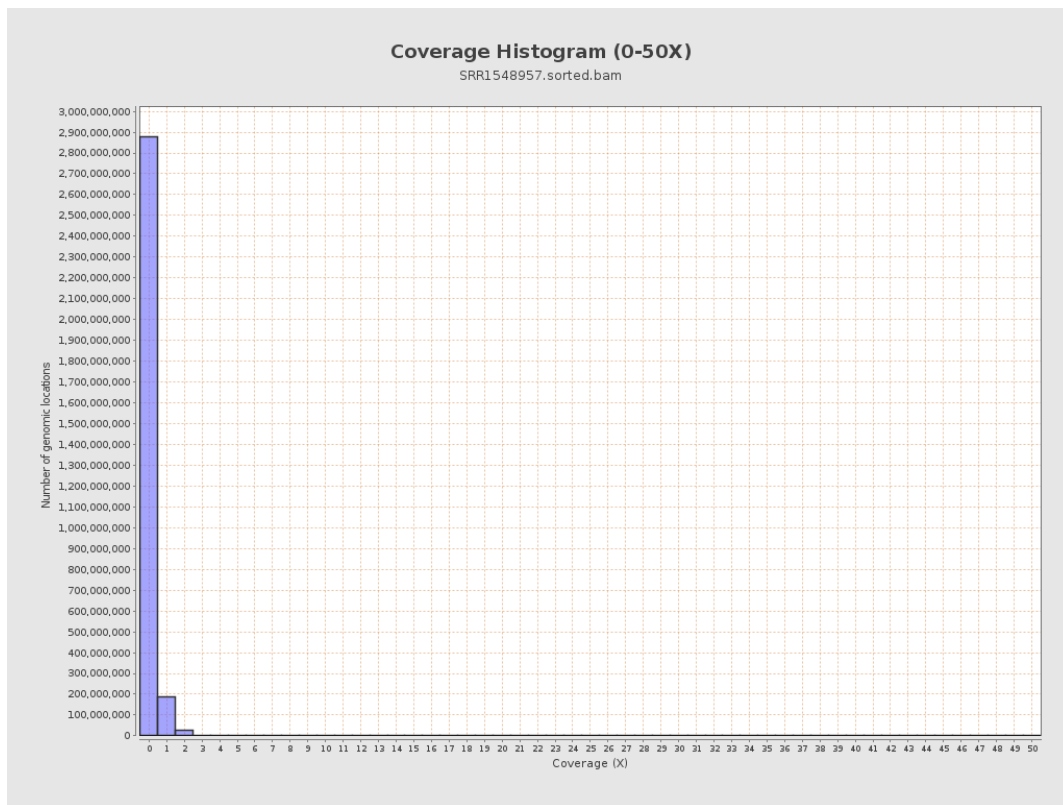
3. Results : Coverage across reference



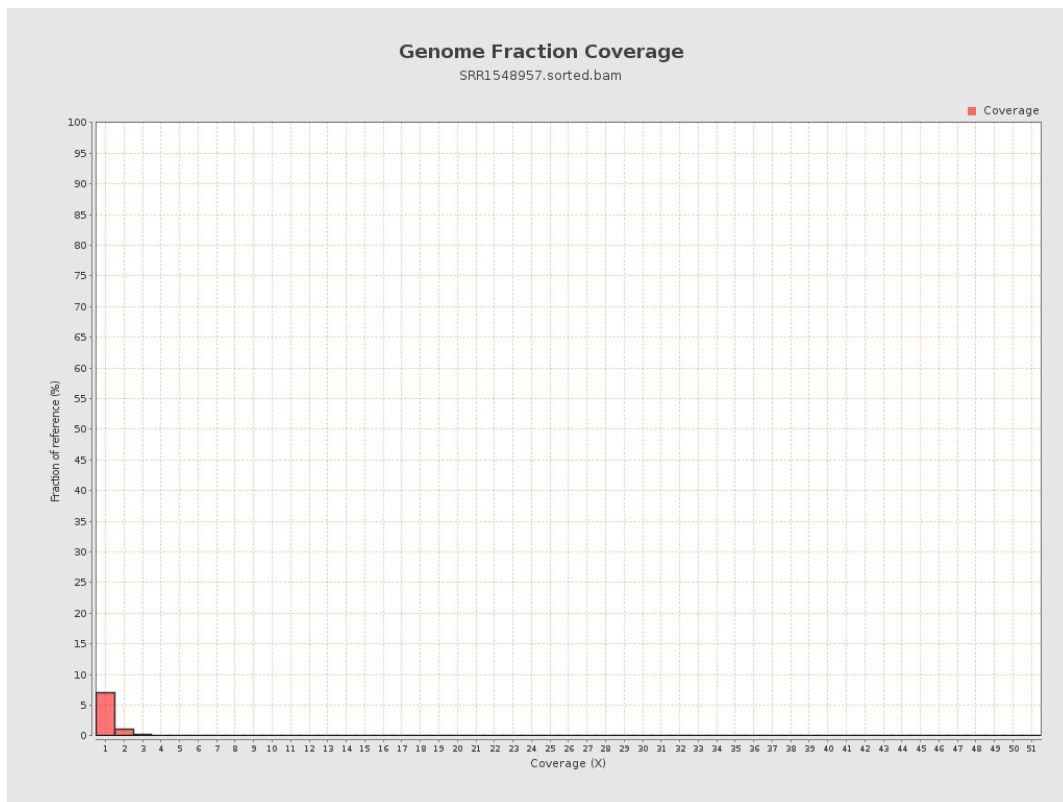
4. Results : Coverage Histogram



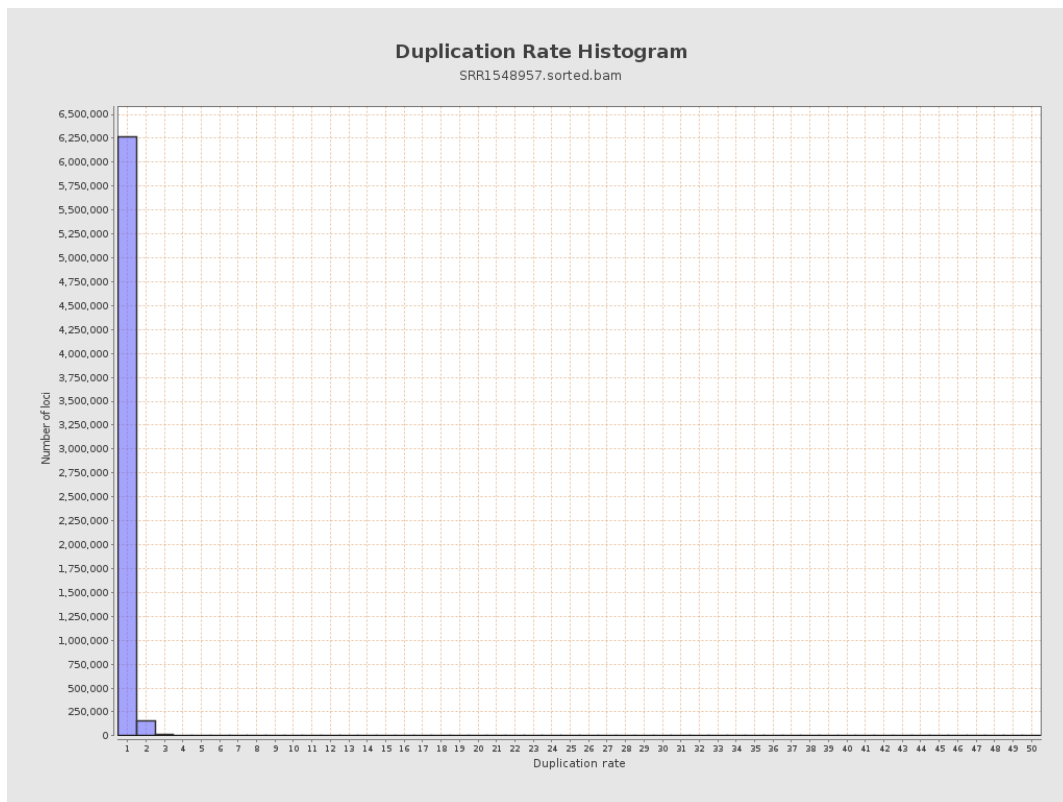
5. Results : Coverage Histogram (0-50X)



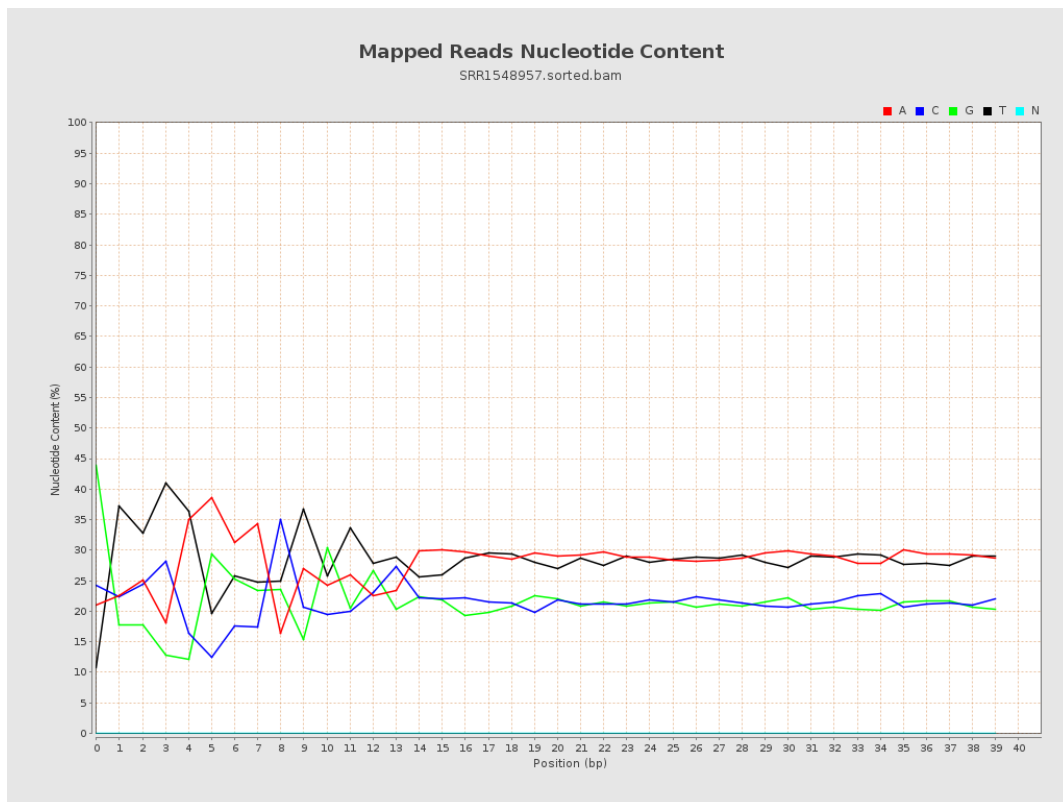
6. Results : Genome Fraction Coverage



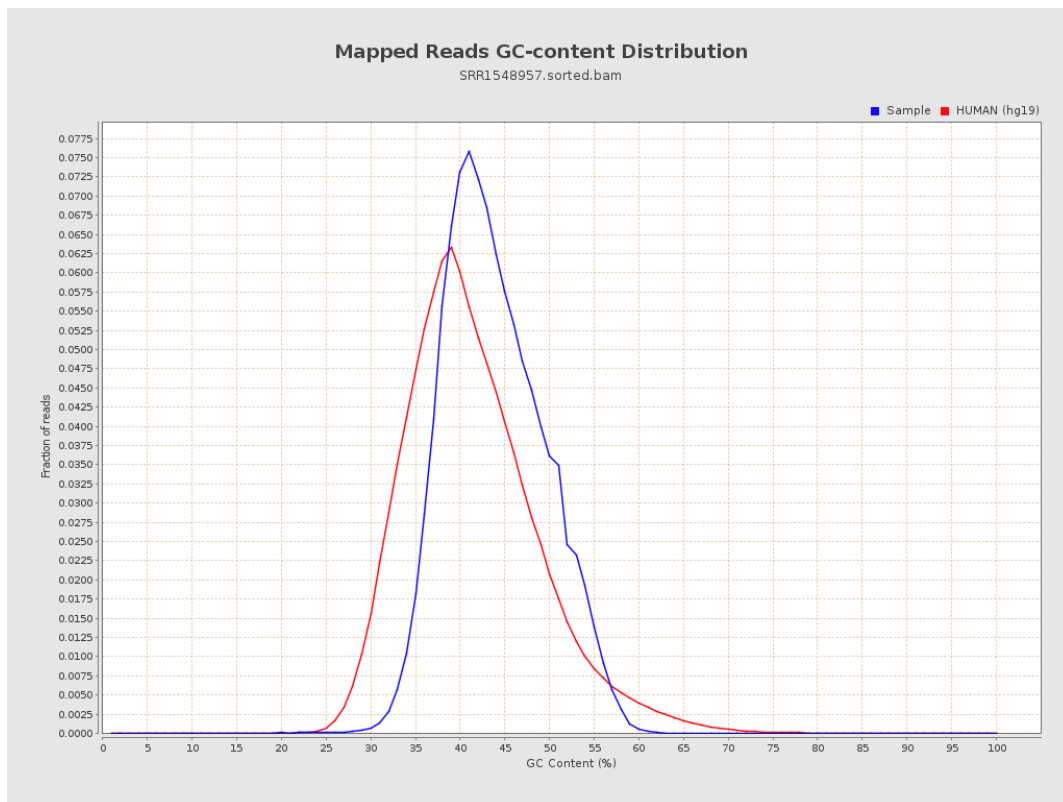
7. Results : Duplication Rate Histogram



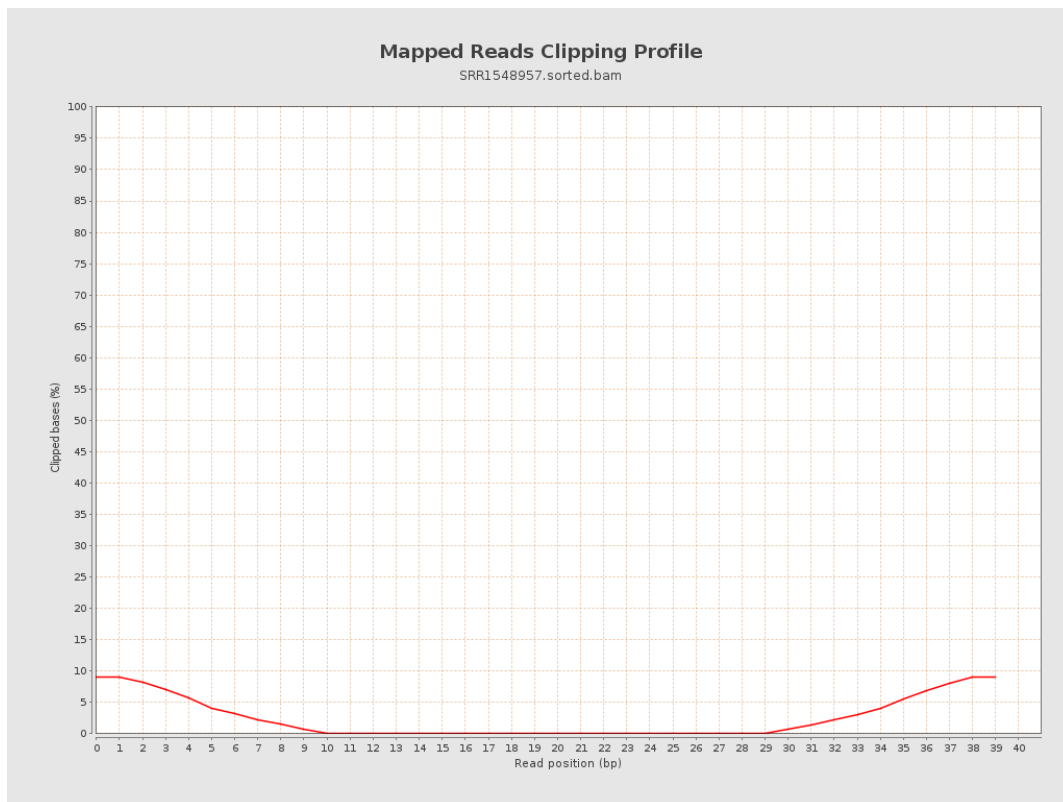
8. Results : Mapped Reads Nucleotide Content



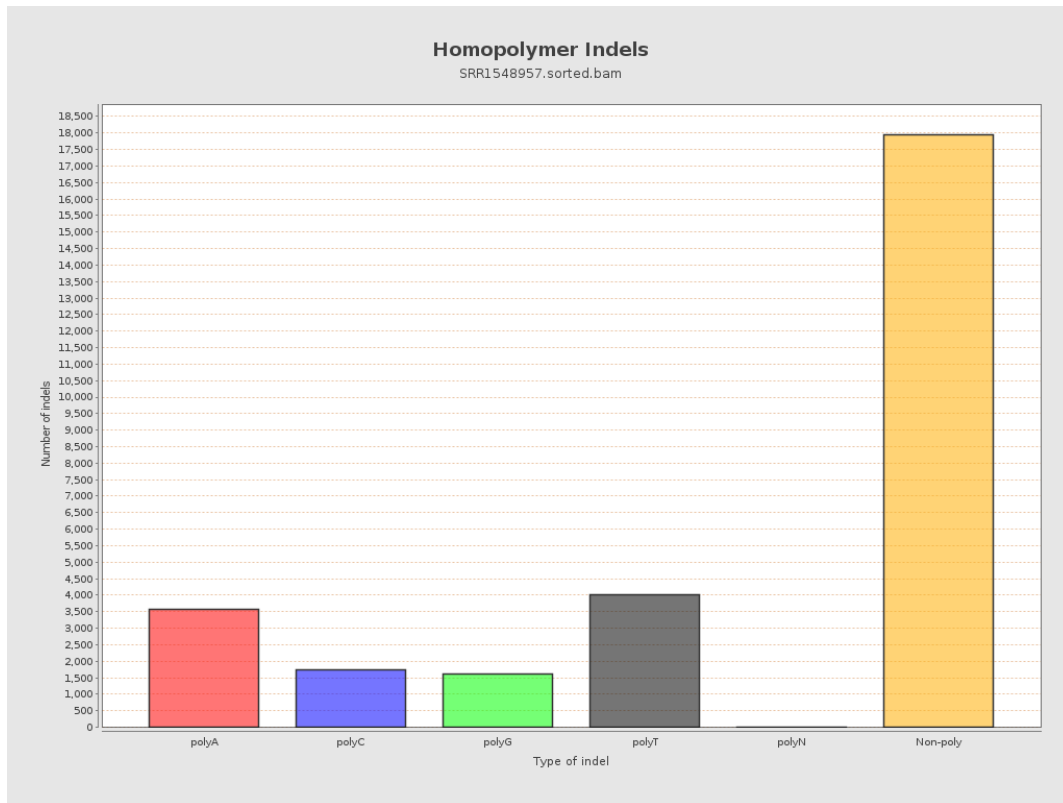
9. Results : Mapped Reads GC-content Distribution



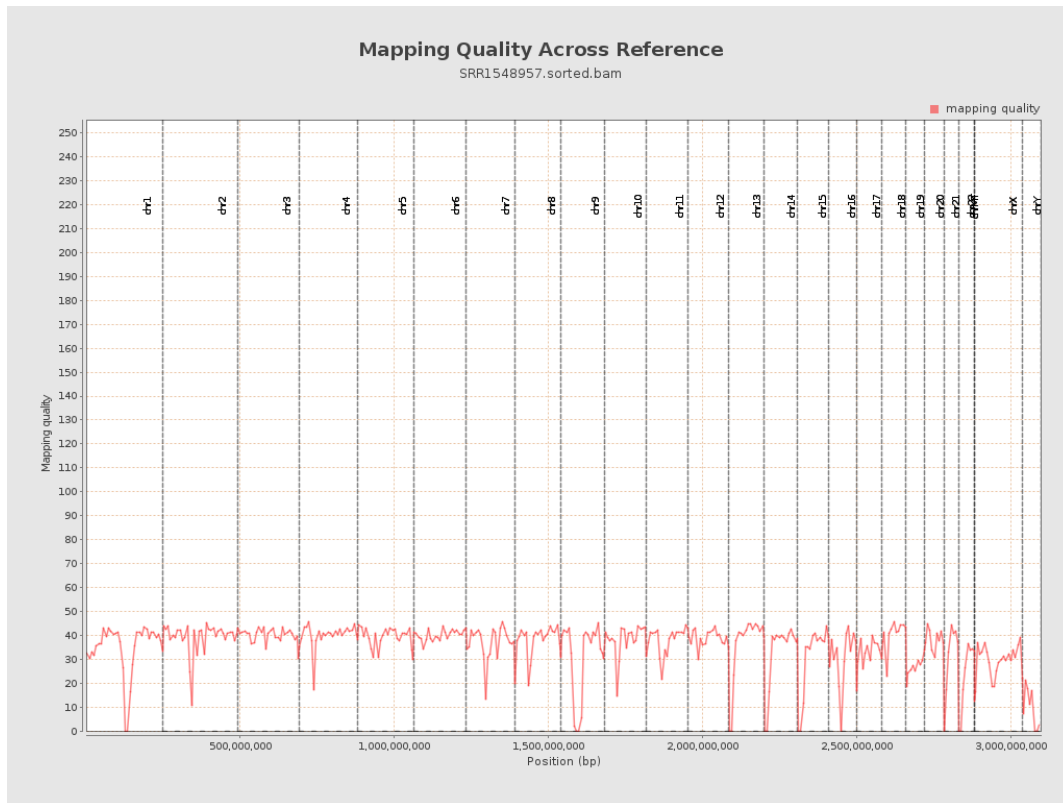
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

