

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:37:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549018.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_SRR1549018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549018.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:37:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,114,381
Mapped reads	6,154,989 / 86.51%
Unmapped reads	959,392 / 13.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	347,115 / 4.88%
Duplication rate	4.62%
Clipped reads	428,980 / 6.03%

2.2. ACGT Content

Number/percentage of A's	70,453,112 / 28.91%
Number/percentage of C's	51,047,538 / 20.95%
Number/percentage of T's	70,795,334 / 29.05%
Number/percentage of G's	51,403,820 / 21.09%
Number/percentage of N's	2,399 / 0%
GC Percentage	42.04%

2.3. Coverage

Mean	0.0787
Standard Deviation	0.769

2.4. Mapping Quality

Mean Mapping Quality	42.66
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2.5. Mismatches and indels

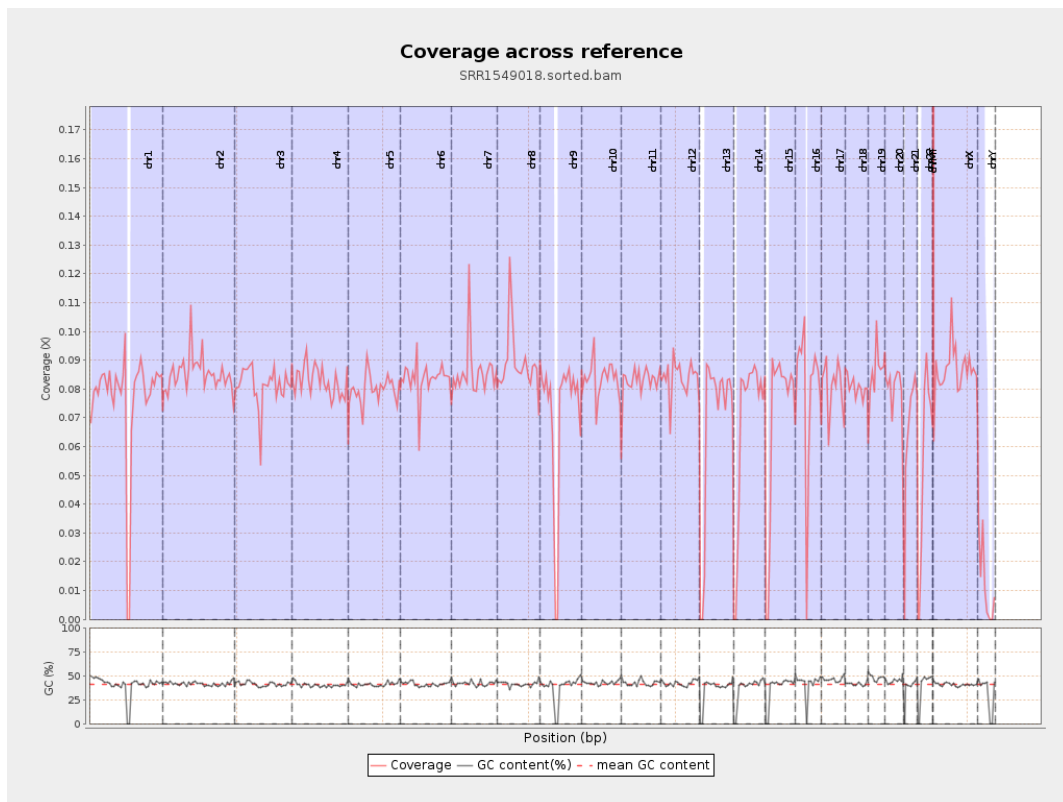
General error rate	0.26%
Mismatches	633,210
Insertions	6,871
Mapped reads with at least one insertion	0.11%
Deletions	18,409
Mapped reads with at least one deletion	0.3%
Homopolymer indels	43.95%

2.6. Chromosome stats

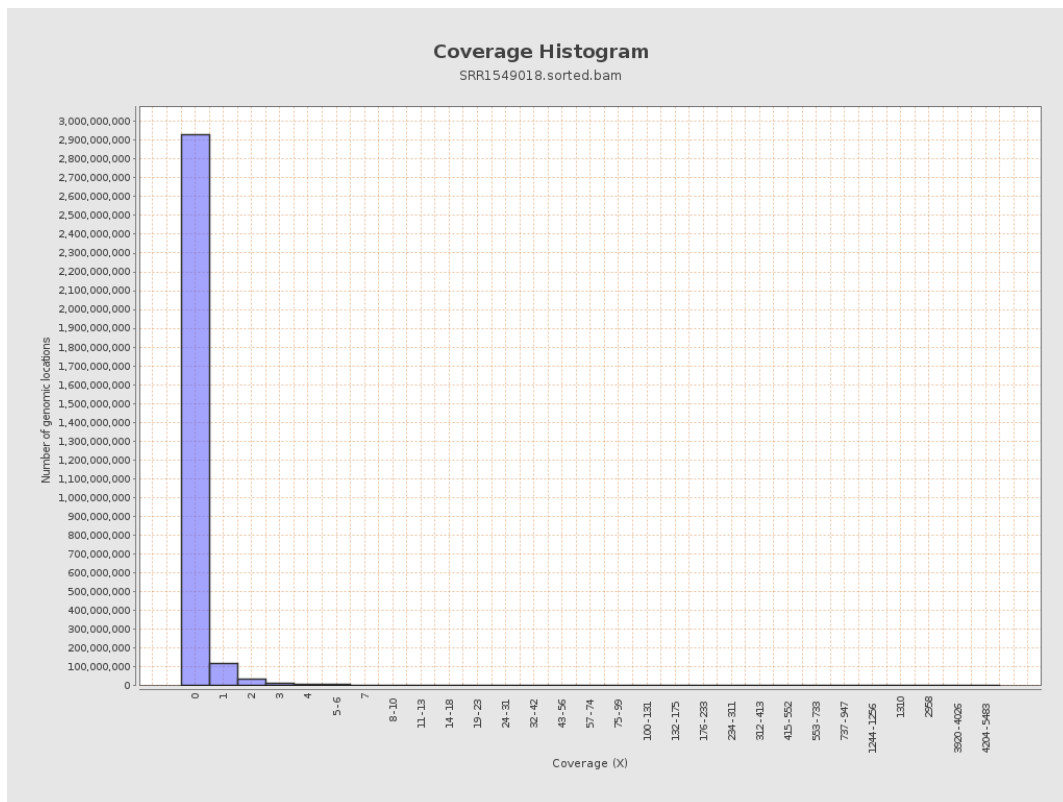
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19101002	0.0766	0.7849
chr2	243199373	20765020	0.0854	0.5248
chr3	198022430	16068522	0.0811	0.397
chr4	191154276	15816375	0.0827	0.4143
chr5	180915260	14451118	0.0799	0.3944
chr6	171115067	14315635	0.0837	0.4417
chr7	159138663	13665818	0.0859	0.669
chr8	146364022	13028908	0.089	2.6887

chr9	141213431	10024186	0.071	0.4698
chr10	135534747	11313547	0.0835	0.4721
chr11	135006516	11216899	0.0831	0.6566
chr12	133851895	11276858	0.0842	0.4115
chr13	115169878	7852180	0.0682	0.3626
chr14	107349540	7426290	0.0692	0.4147
chr15	102531392	7051775	0.0688	0.3612
chr16	90354753	7048989	0.078	0.4059
chr17	81195210	6604405	0.0813	0.4331
chr18	78077248	6316257	0.0809	0.7545
chr19	59128983	5108127	0.0864	0.7093
chr20	63025520	5045237	0.0801	0.4014
chr21	48129895	3158438	0.0656	0.3838
chr22	51304566	2851441	0.0556	0.3658
chrMT	16571	57559	3.4735	4.2802
chrX	155270560	13441501	0.0866	0.4703
chrY	59373566	720233	0.0121	0.1985

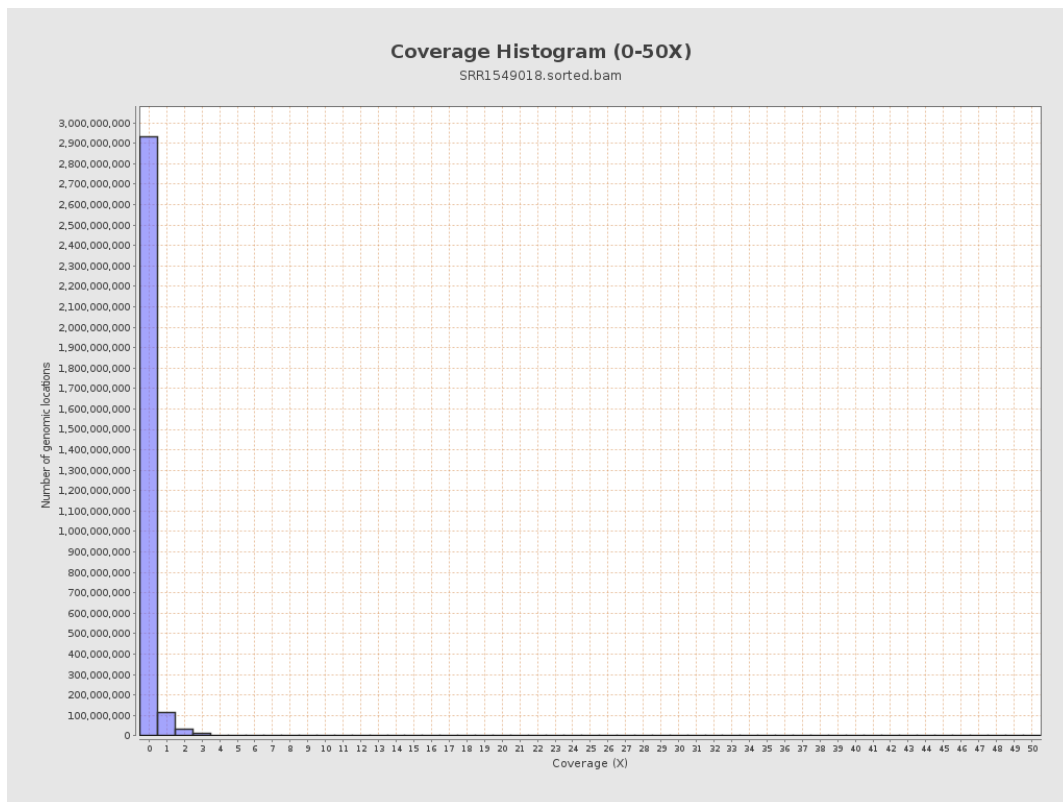
3. Results : Coverage across reference



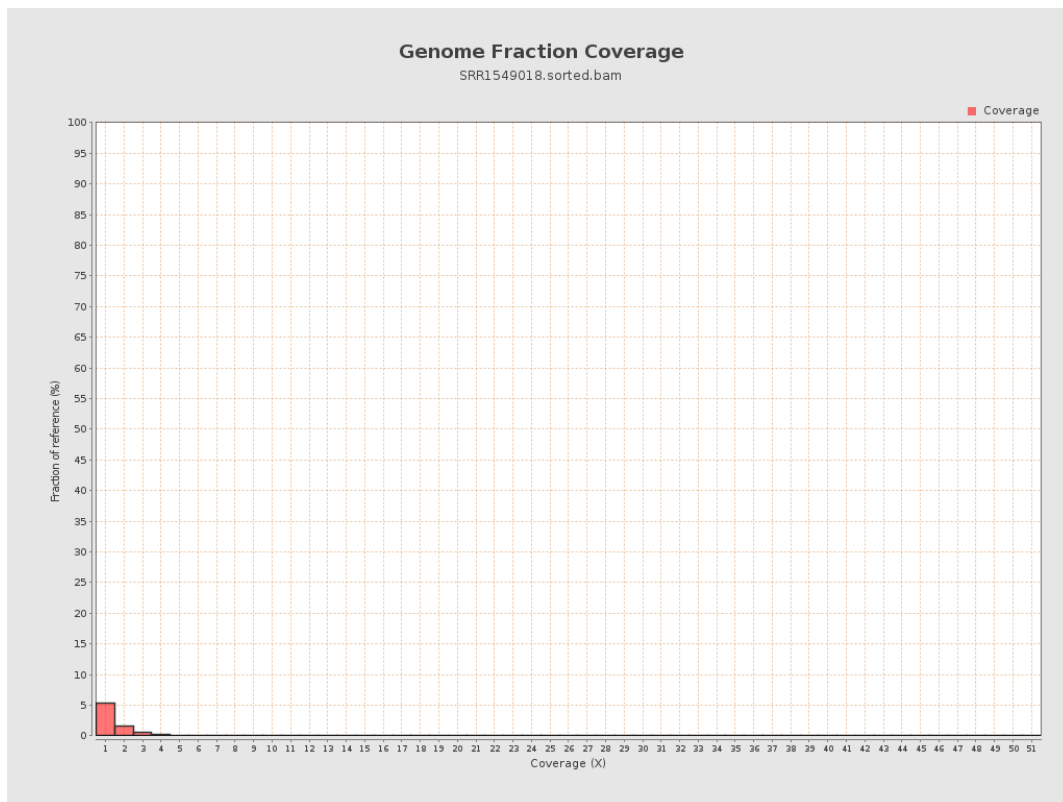
4. Results : Coverage Histogram



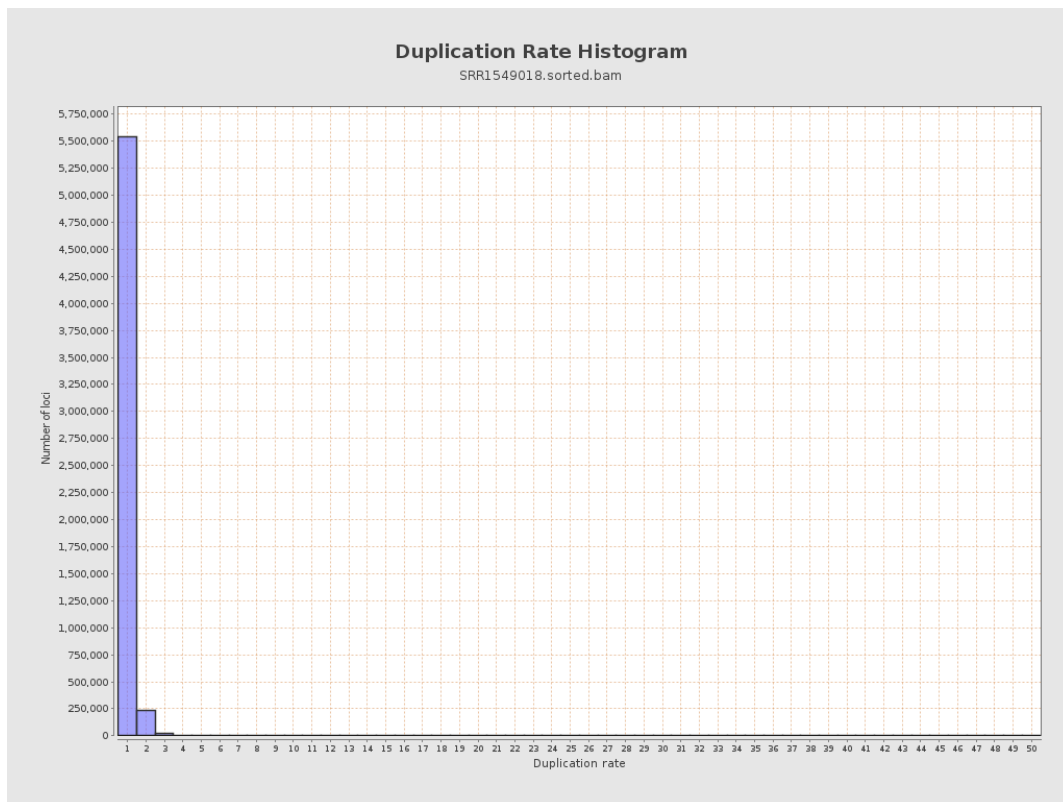
5. Results : Coverage Histogram (0-50X)



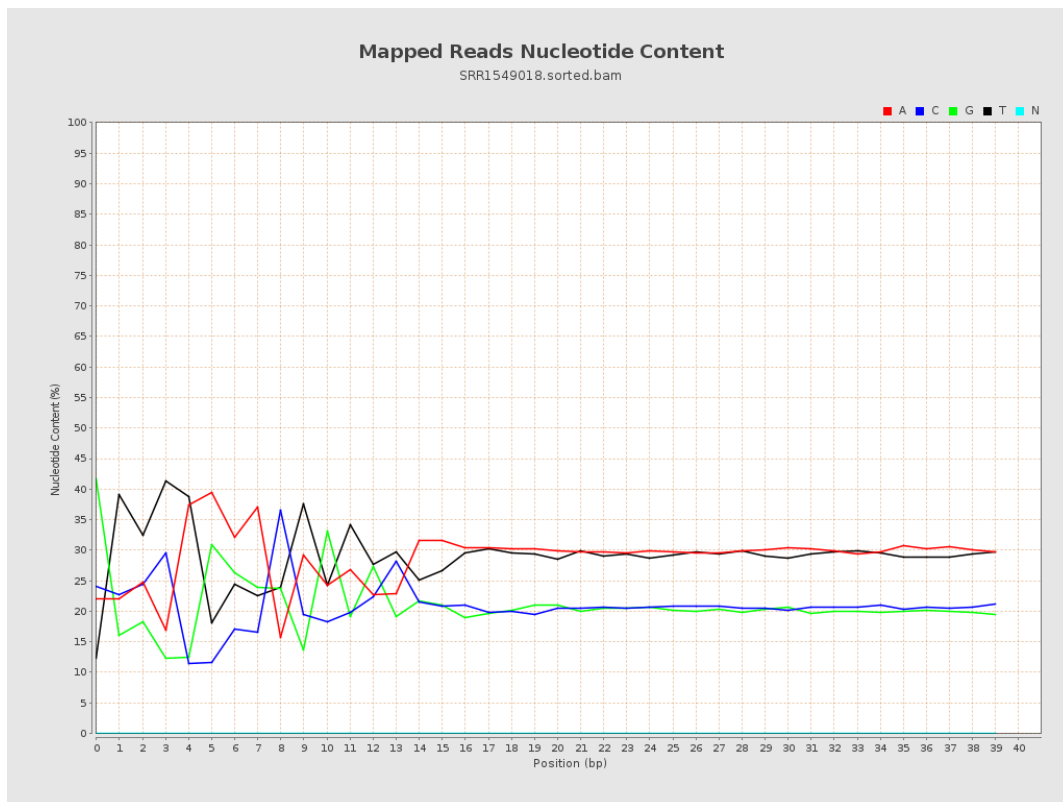
6. Results : Genome Fraction Coverage



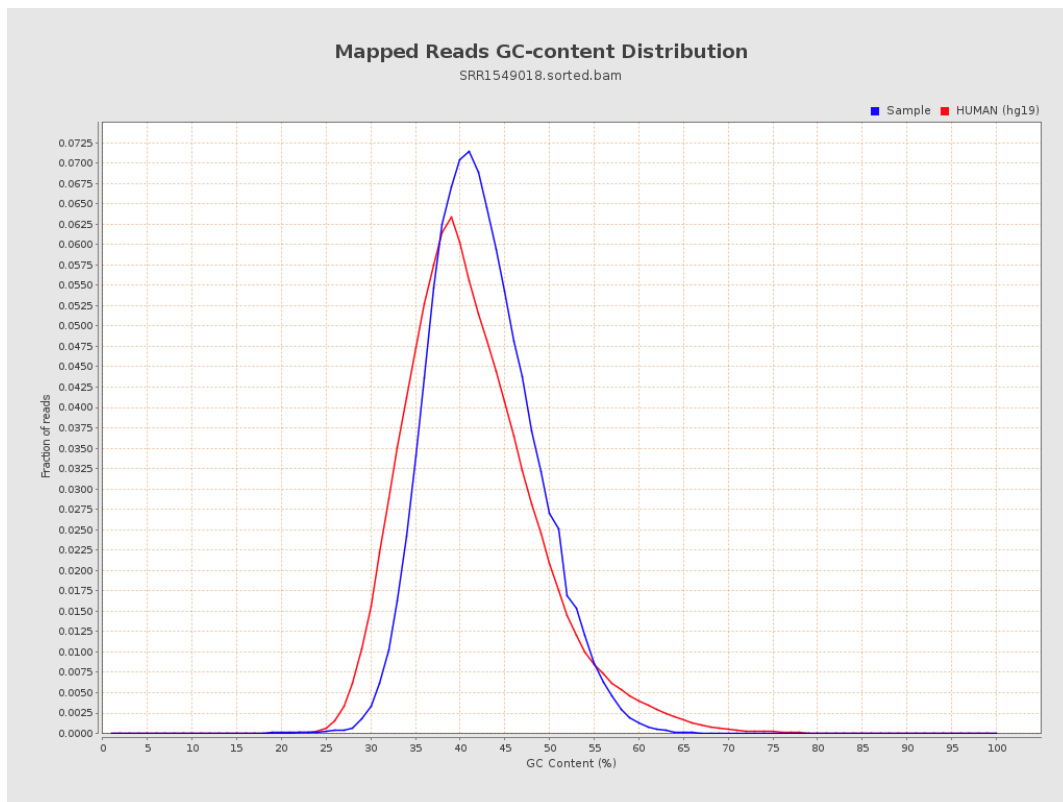
7. Results : Duplication Rate Histogram



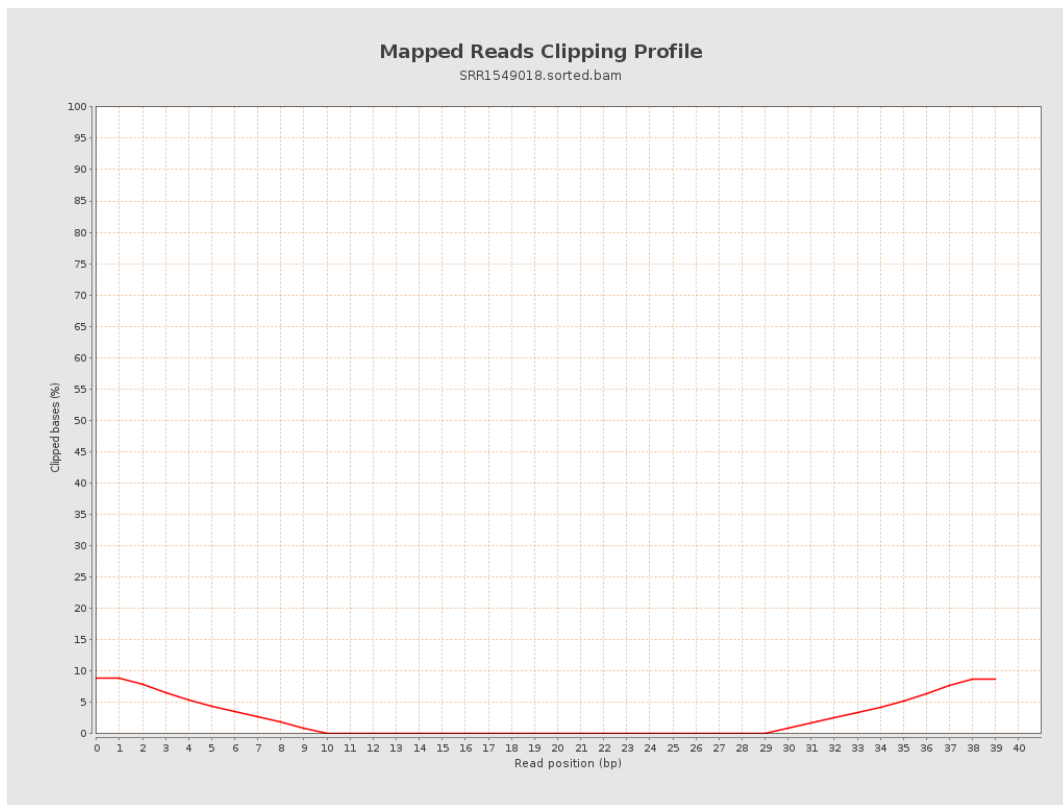
8. Results : Mapped Reads Nucleotide Content



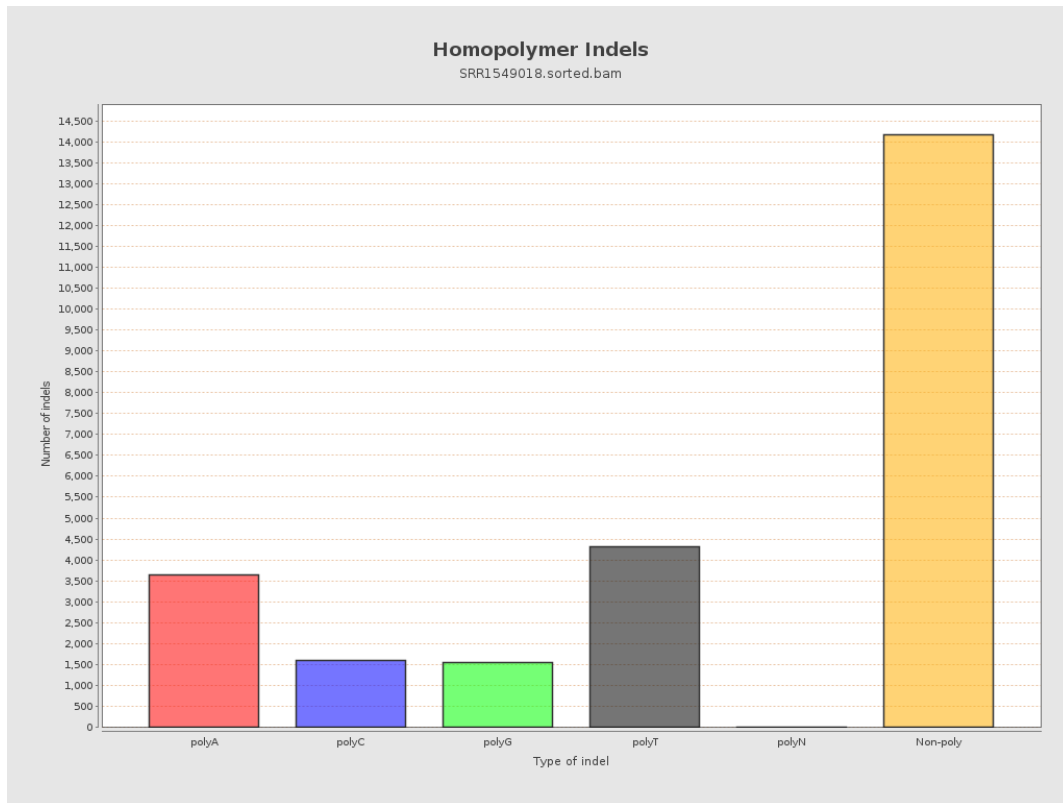
9. Results : Mapped Reads GC-content Distribution



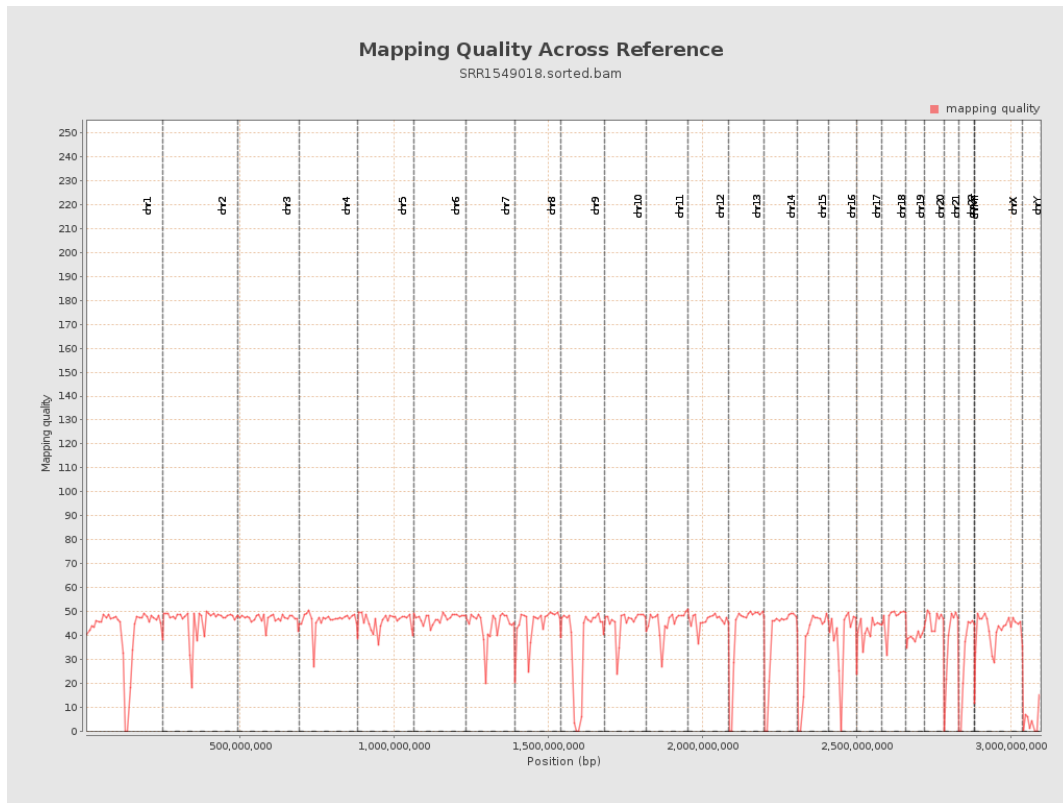
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

