

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:51:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818792.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_SRR1818792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:51:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,258,031
Mapped reads	1,148,114 / 91.26%
Unmapped reads	109,917 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,109 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	392,188 / 31.17%
Duplication rate	30.02%
Clipped reads	1,151,753 / 91.55%

2.2. ACGT Content

Number/percentage of A's	22,535,503 / 28.89%
Number/percentage of C's	15,863,617 / 20.34%
Number/percentage of T's	22,116,407 / 28.35%
Number/percentage of G's	17,486,052 / 22.42%
Number/percentage of N's	4,617 / 0.01%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0252

Standard Deviation	0.3471
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2.4. Mapping Quality

Mean Mapping Quality	47.62
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2.5. Mismatches and indels

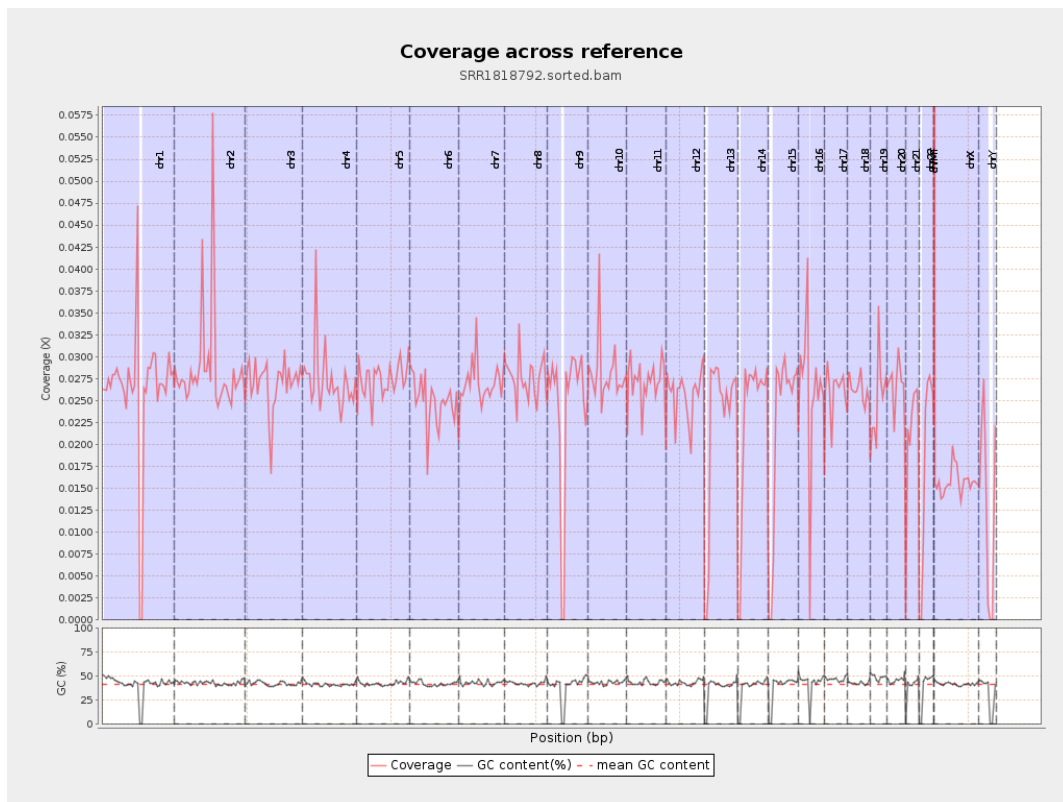
General error rate	0.52%
Mismatches	388,847
Insertions	7,731
Mapped reads with at least one insertion	0.66%
Deletions	19,715
Mapped reads with at least one deletion	1.7%
Homopolymer indels	43%

2.6. Chromosome stats

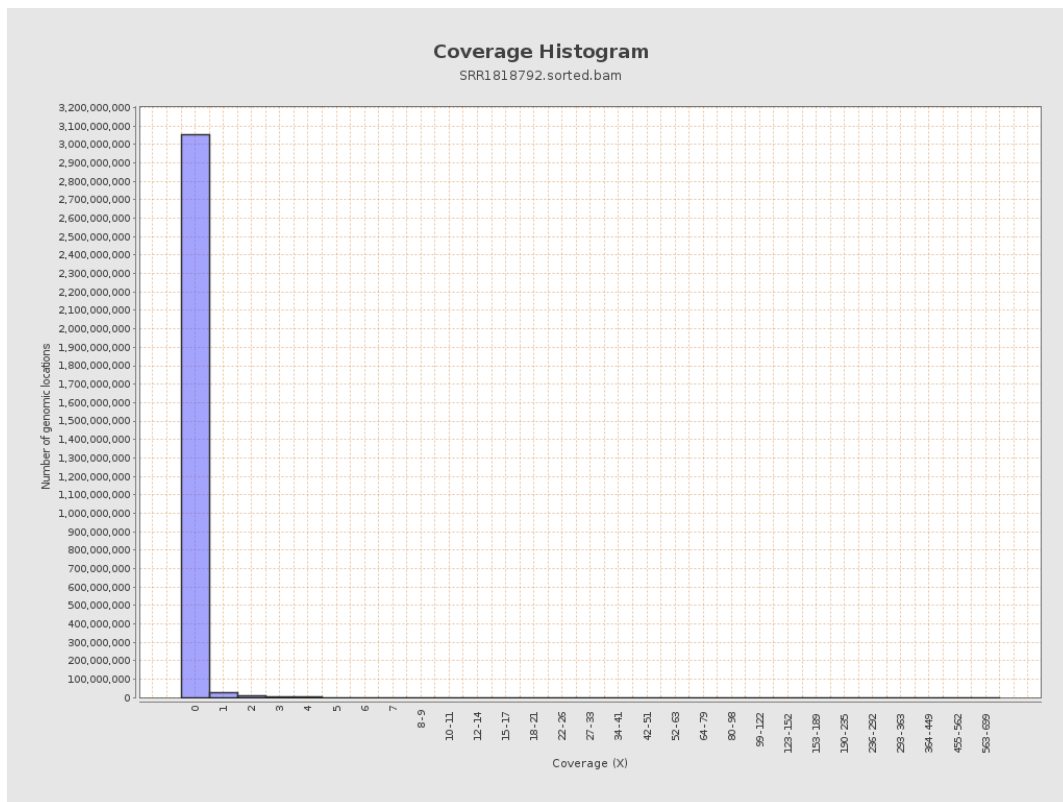
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6537738	0.0262	0.5217
chr2	243199373	6930660	0.0285	0.5504
chr3	198022430	5333704	0.0269	0.2611
chr4	191154276	5206873	0.0272	0.2988
chr5	180915260	4975603	0.0275	0.265
chr6	171115067	4251763	0.0248	0.2705
chr7	159138663	4303412	0.027	0.3061

chr8	146364022	4023868	0.0275	0.2987
chr9	141213431	3417482	0.0242	0.288
chr10	135534747	3814007	0.0281	0.3875
chr11	135006516	3677356	0.0272	0.2834
chr12	133851895	3431890	0.0256	0.2656
chr13	115169878	2555183	0.0222	0.2353
chr14	107349540	2449876	0.0228	0.2603
chr15	102531392	2278910	0.0222	0.2365
chr16	90354753	2319640	0.0257	0.4113
chr17	81195210	2121079	0.0261	0.2678
chr18	78077248	2054681	0.0263	0.3604
chr19	59128983	1496568	0.0253	0.4162
chr20	63025520	1683142	0.0267	0.2771
chr21	48129895	1021985	0.0212	0.2471
chr22	51304566	926651	0.0181	0.2278
chrMT	16571	6040	0.3645	0.9171
chrX	155270560	2445306	0.0157	0.2189
chrY	59373566	775443	0.0131	0.5268

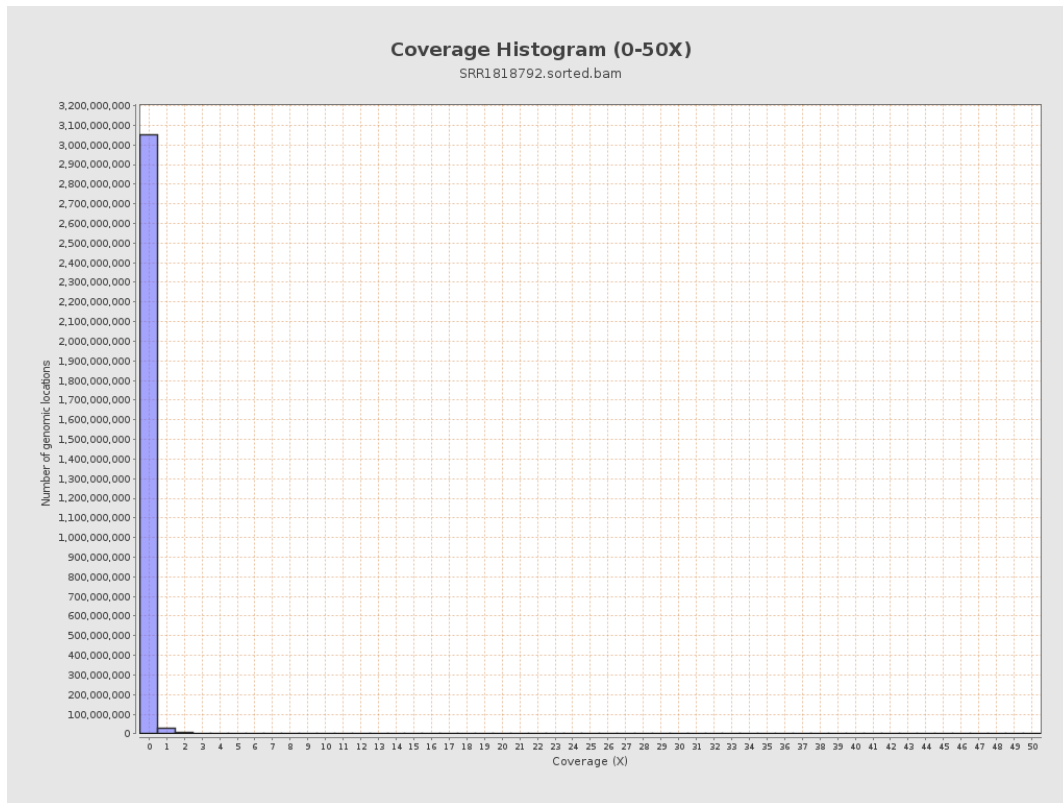
3. Results : Coverage across reference



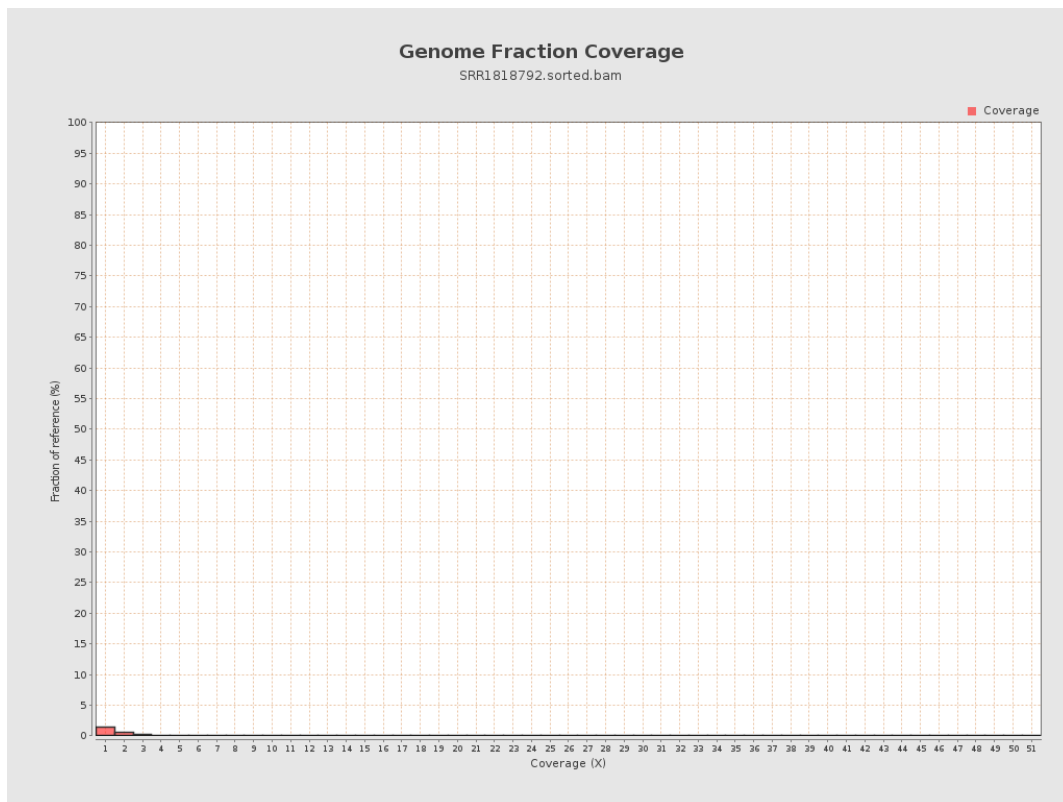
4. Results : Coverage Histogram



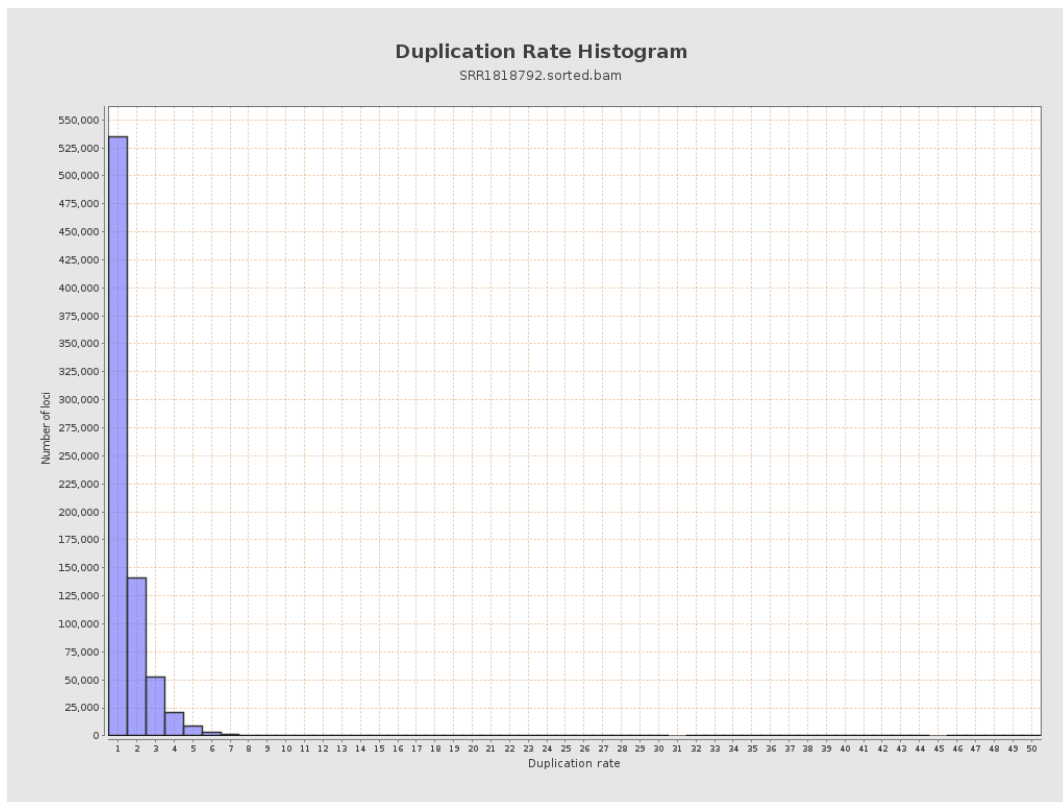
5. Results : Coverage Histogram (0-50X)



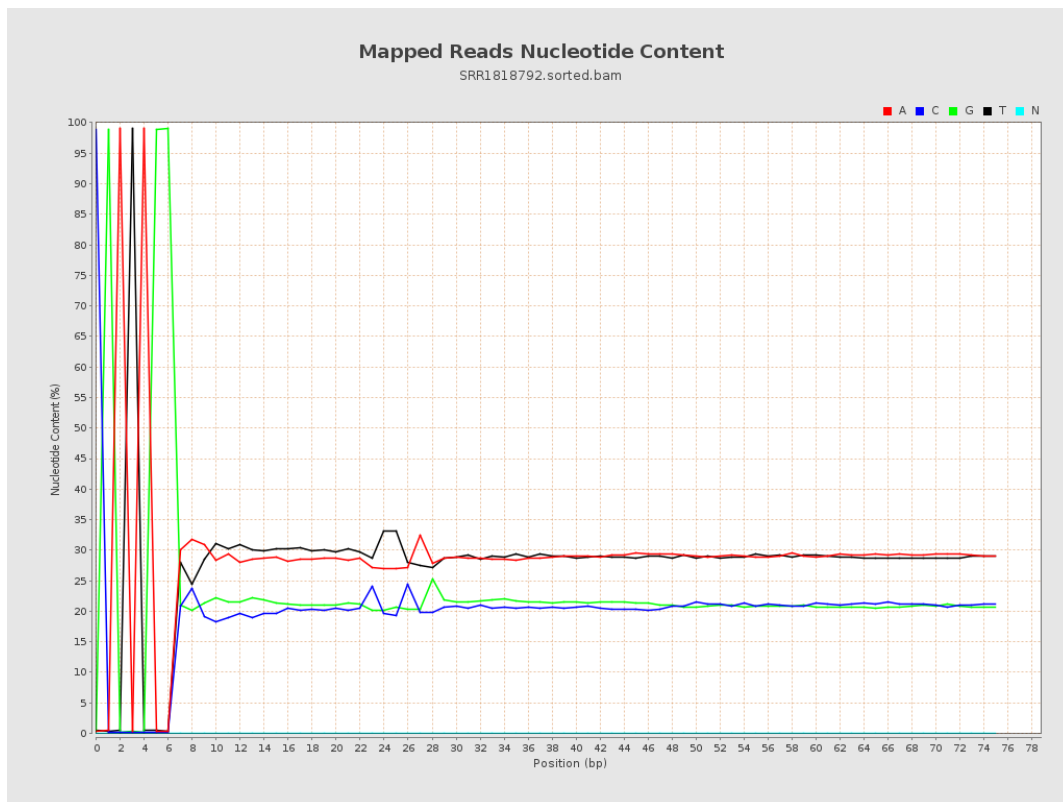
6. Results : Genome Fraction Coverage



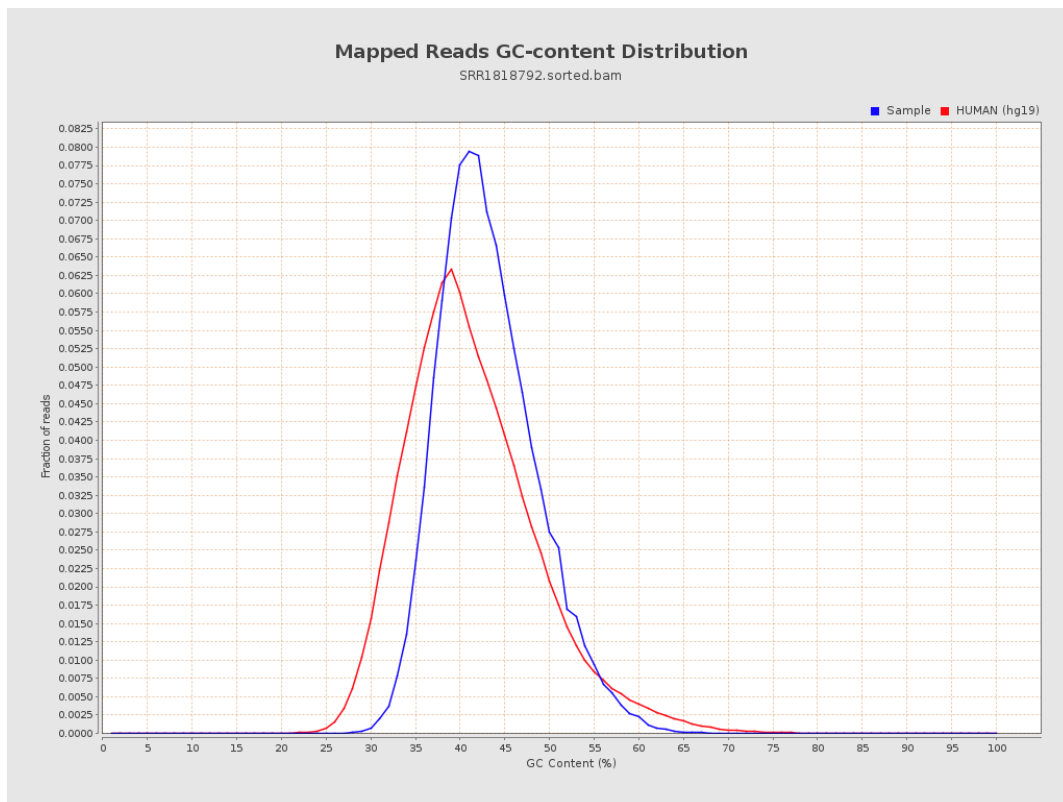
7. Results : Duplication Rate Histogram



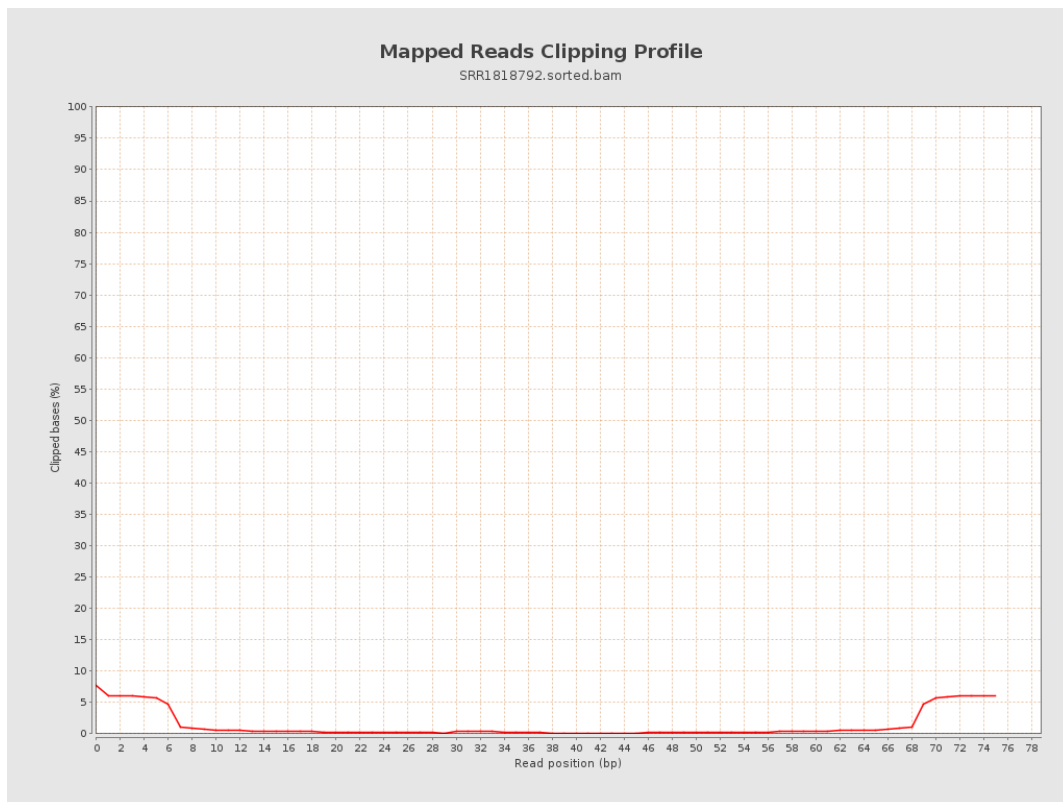
8. Results : Mapped Reads Nucleotide Content



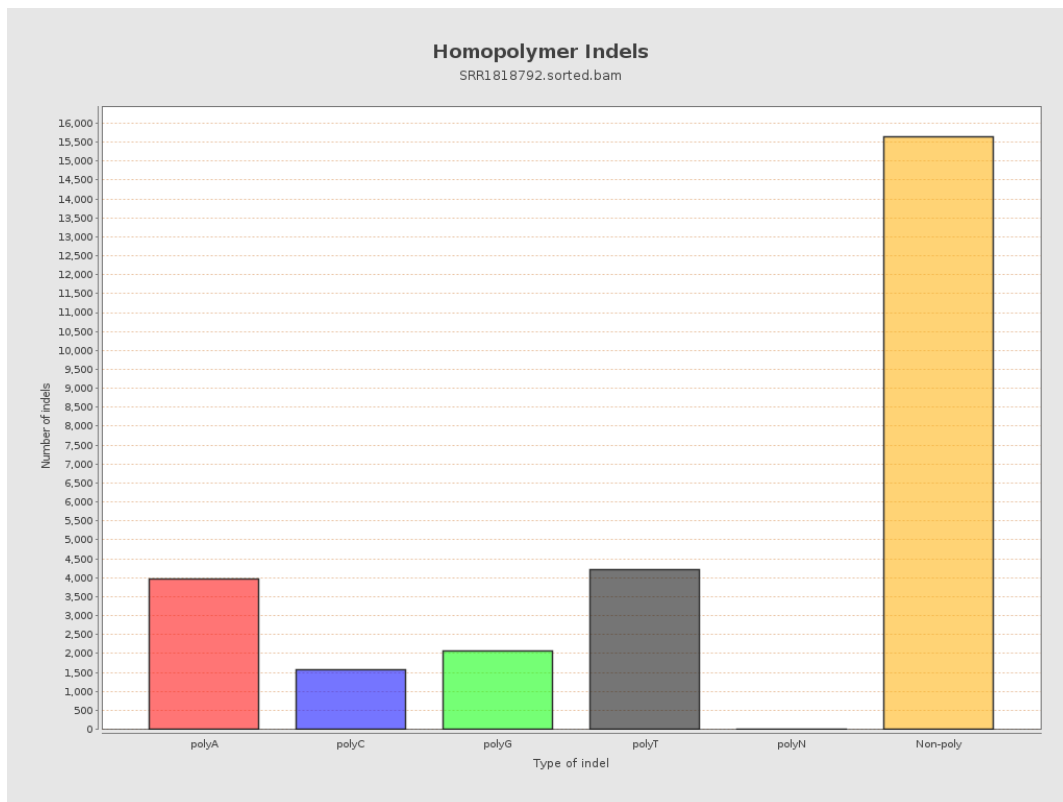
9. Results : Mapped Reads GC-content Distribution



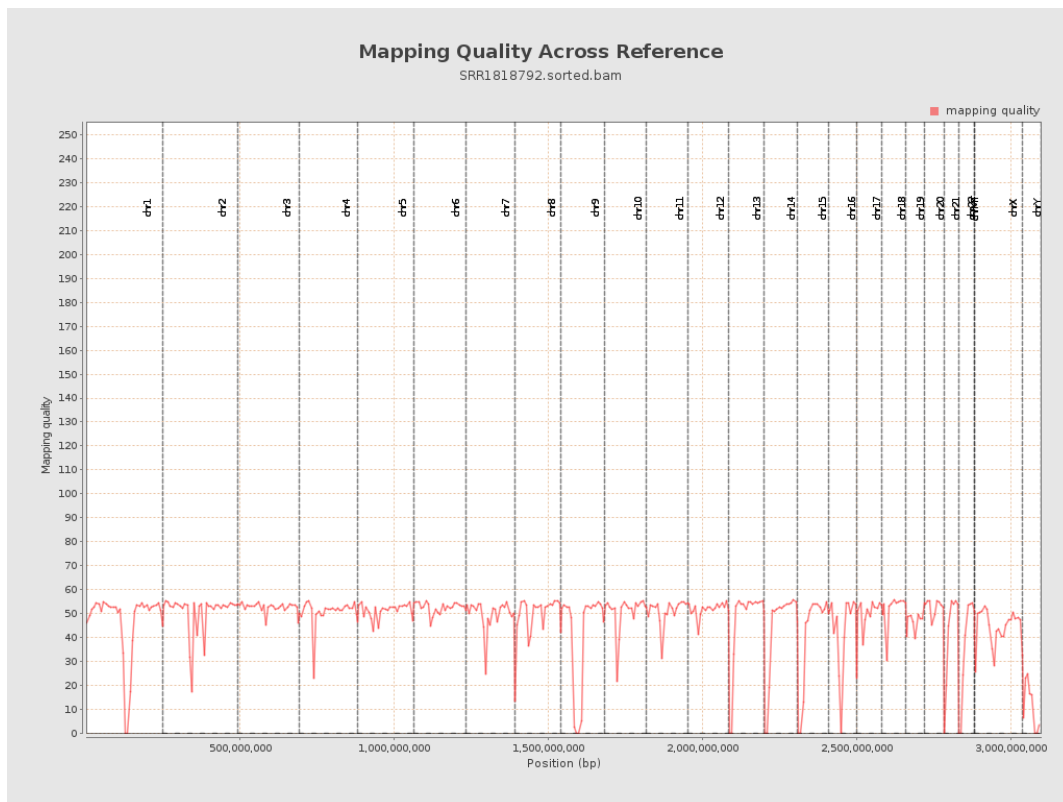
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

