

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:36:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818750.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_SRR1818750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:36:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,274,175
Mapped reads	1,239,957 / 97.31%
Unmapped reads	34,218 / 2.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,096 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	507,796 / 39.85%
Duplication rate	36.11%
Clipped reads	1,236,062 / 97.01%

2.2. ACGT Content

Number/percentage of A's	24,903,240 / 29.58%
Number/percentage of C's	17,903,707 / 21.27%
Number/percentage of T's	23,184,530 / 27.54%
Number/percentage of G's	18,189,319 / 21.61%
Number/percentage of N's	4,889 / 0.01%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.3667
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2.4. Mapping Quality

Mean Mapping Quality	47.52
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2.5. Mismatches and indels

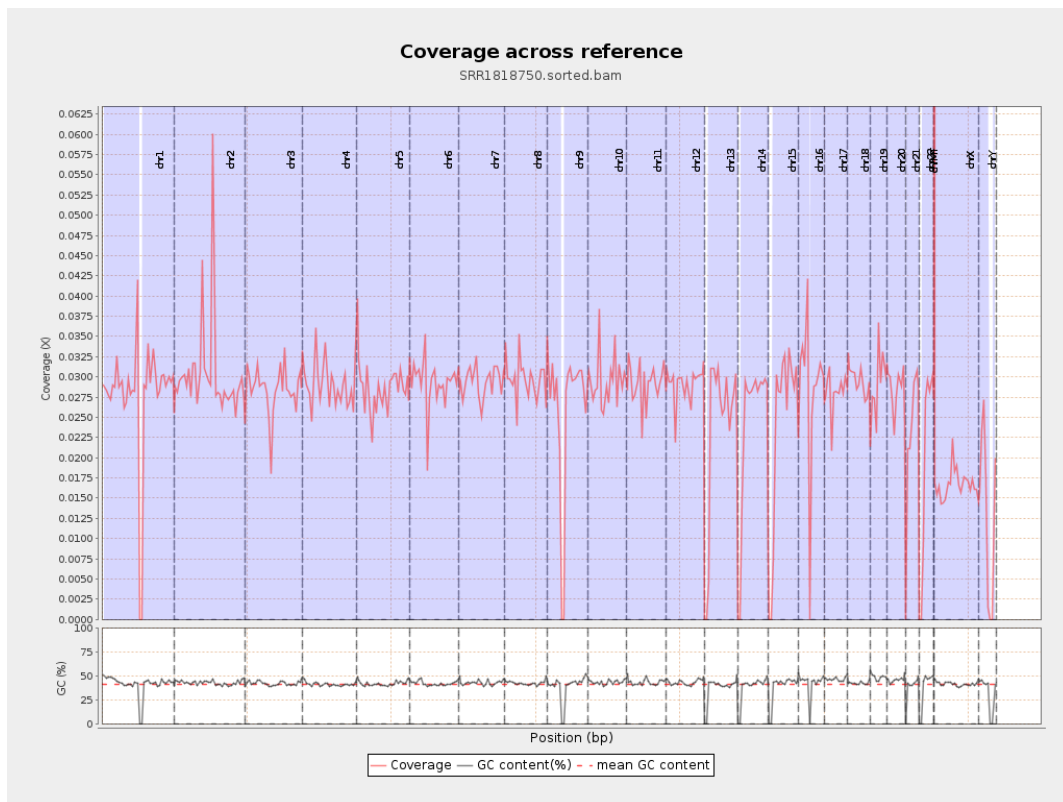
General error rate	0.55%
Mismatches	438,967
Insertions	10,581
Mapped reads with at least one insertion	0.84%
Deletions	21,858
Mapped reads with at least one deletion	1.74%
Homopolymer indels	40.17%

2.6. Chromosome stats

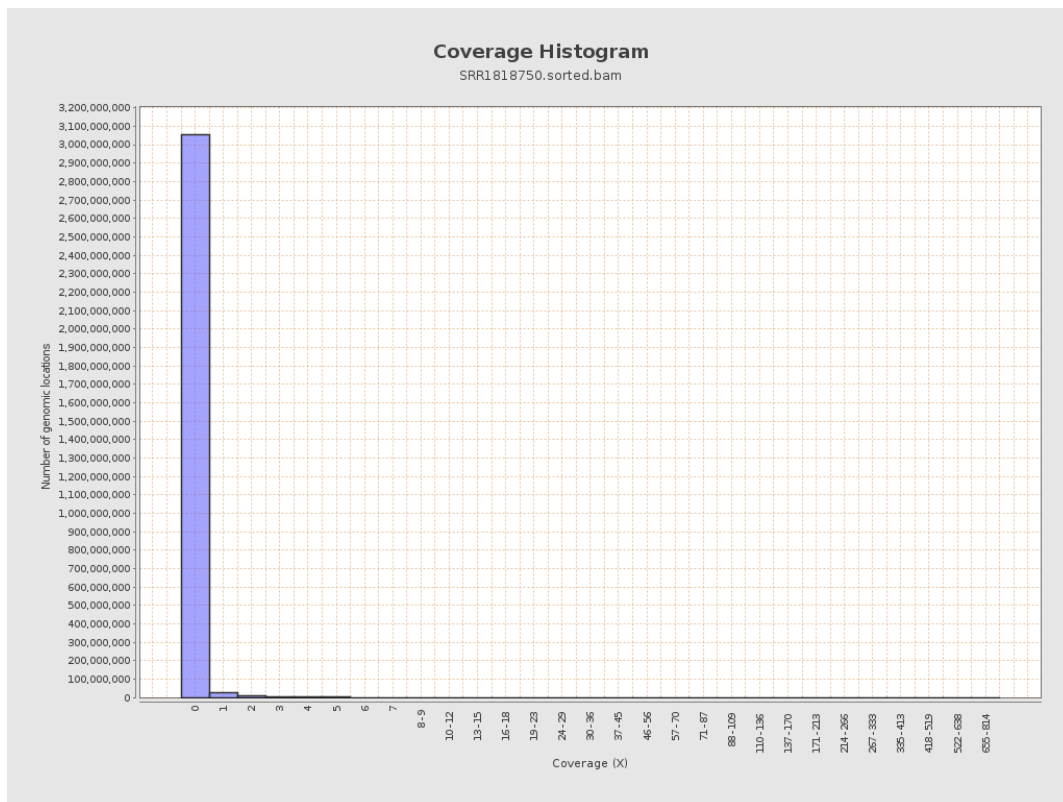
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6926594	0.0278	0.4663
chr2	243199373	7358739	0.0303	0.584
chr3	198022430	5633311	0.0284	0.2839
chr4	191154276	5569755	0.0291	0.3399
chr5	180915260	5143996	0.0284	0.293
chr6	171115067	5019572	0.0293	0.3104
chr7	159138663	4686325	0.0294	0.3304

chr8	146364022	4342761	0.0297	0.3181
chr9	141213431	3653721	0.0259	0.3051
chr10	135534747	4000432	0.0295	0.3819
chr11	135006516	3943687	0.0292	0.3224
chr12	133851895	3889117	0.0291	0.3069
chr13	115169878	2709549	0.0235	0.257
chr14	107349540	2583864	0.0241	0.2853
chr15	102531392	2467222	0.0241	0.2612
chr16	90354753	2552630	0.0283	0.4219
chr17	81195210	2284619	0.0281	0.2976
chr18	78077248	2304790	0.0295	0.4156
chr19	59128983	1731767	0.0293	0.439
chr20	63025520	1785771	0.0283	0.3001
chr21	48129895	1123901	0.0234	0.2674
chr22	51304566	1022020	0.0199	0.2621
chrMT	16571	114251	6.8946	6.7215
chrX	155270560	2600431	0.0167	0.2413
chrY	59373566	772732	0.013	0.6163

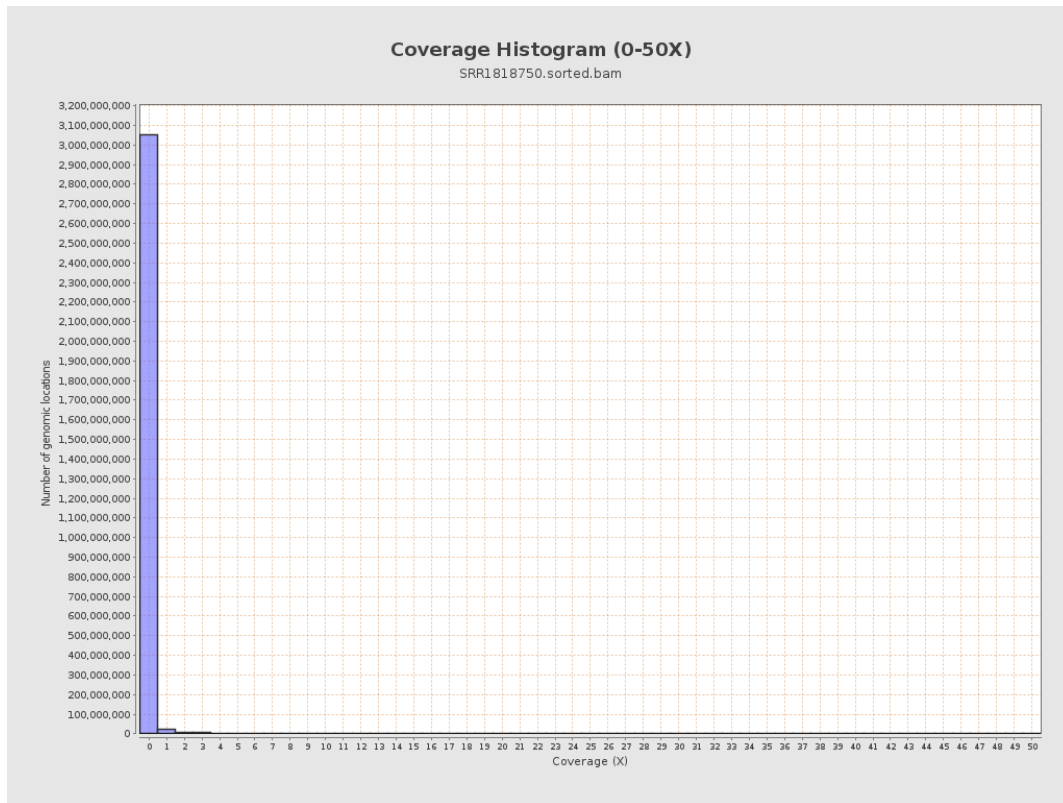
3. Results : Coverage across reference



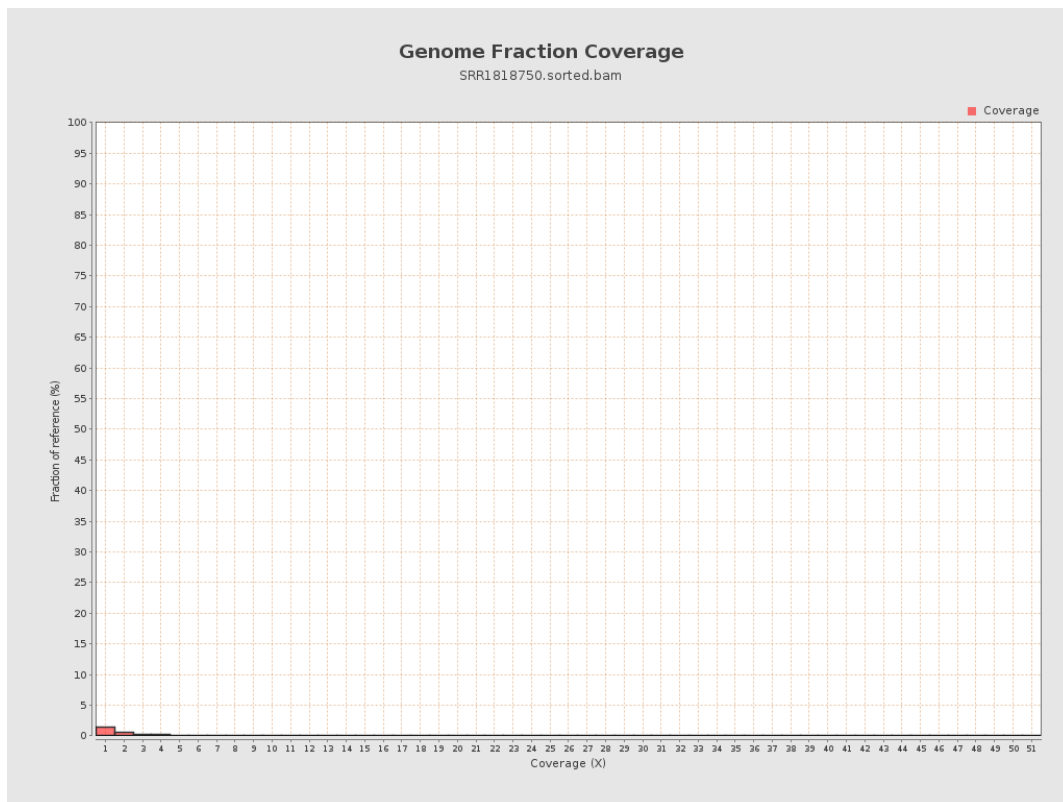
4. Results : Coverage Histogram



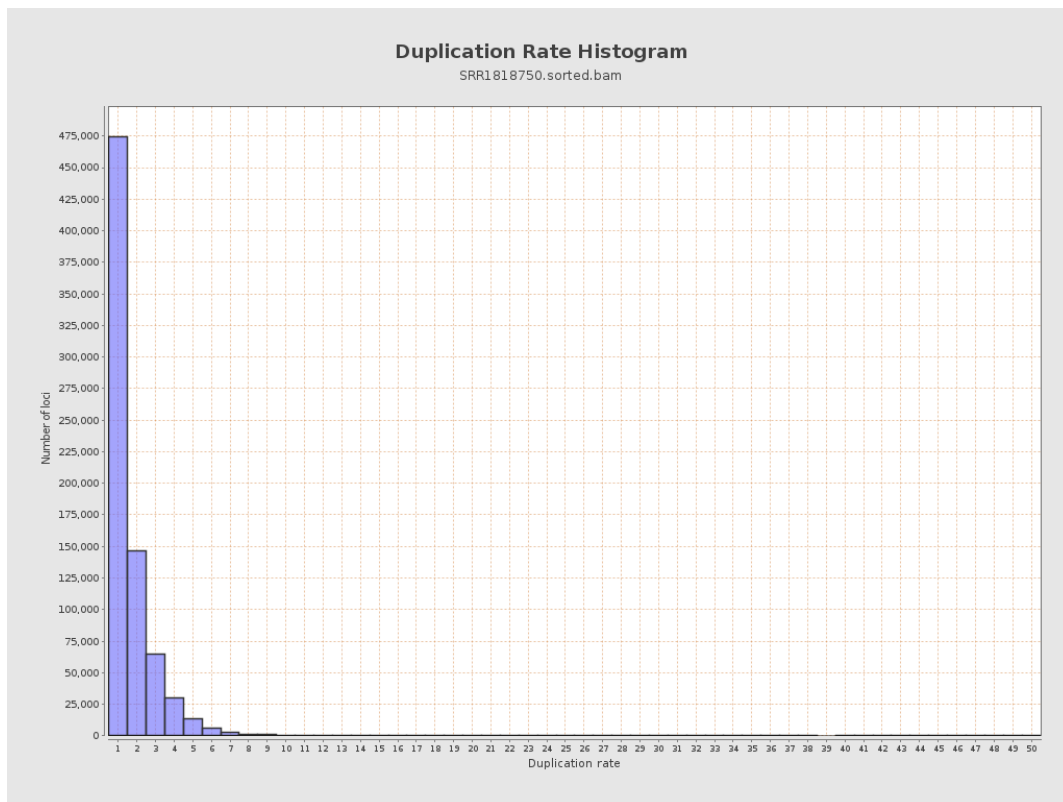
5. Results : Coverage Histogram (0-50X)



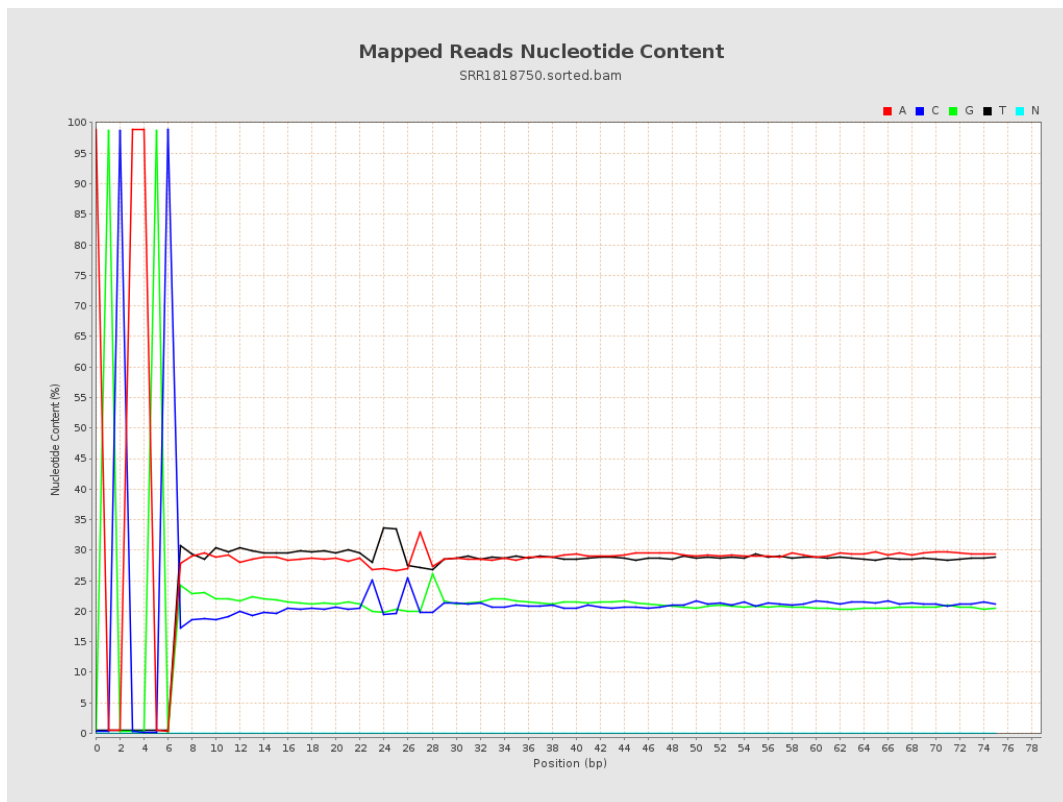
6. Results : Genome Fraction Coverage



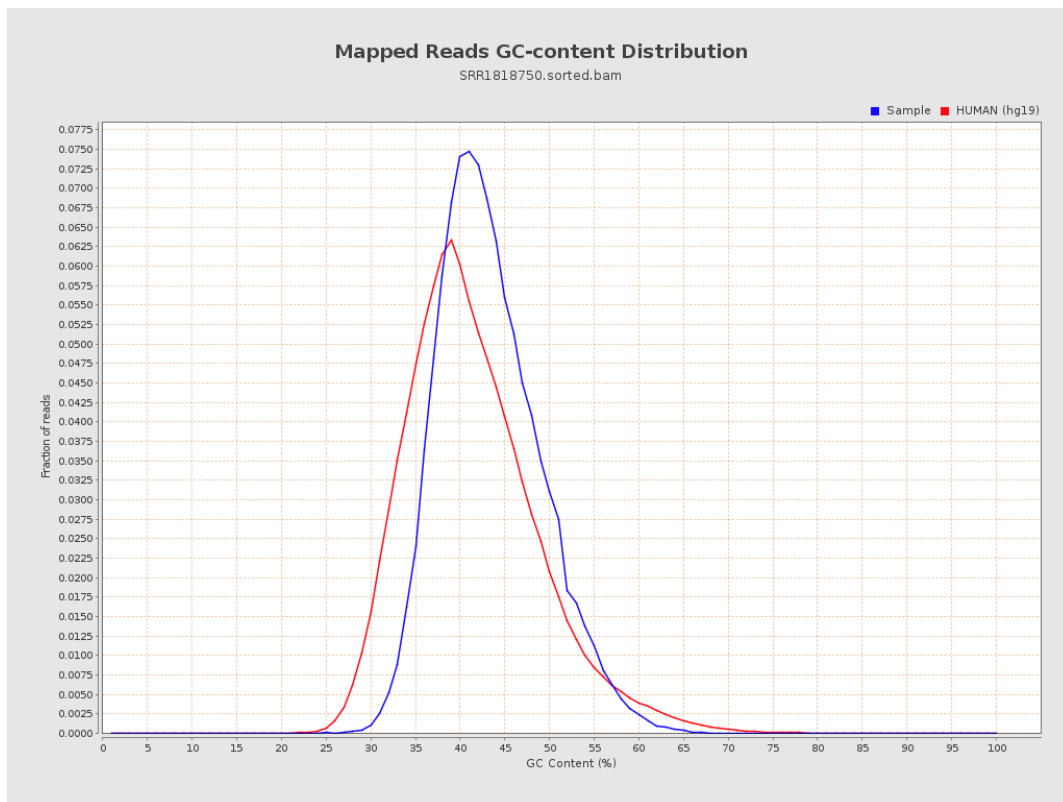
7. Results : Duplication Rate Histogram



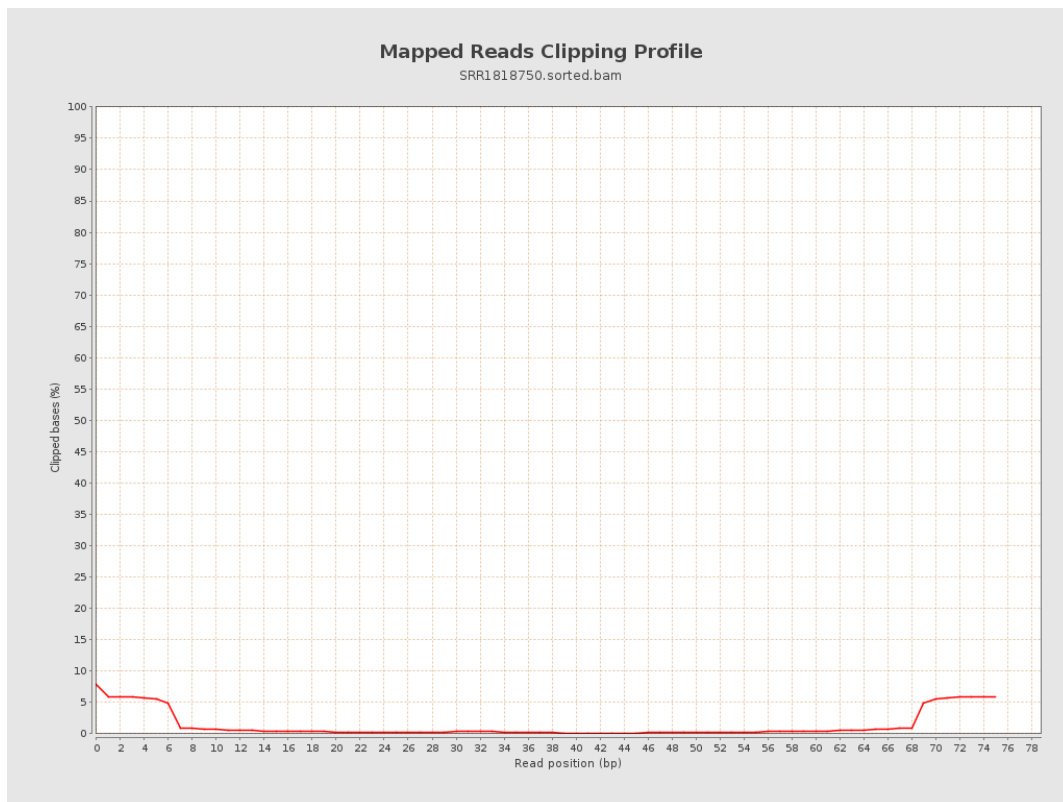
8. Results : Mapped Reads Nucleotide Content



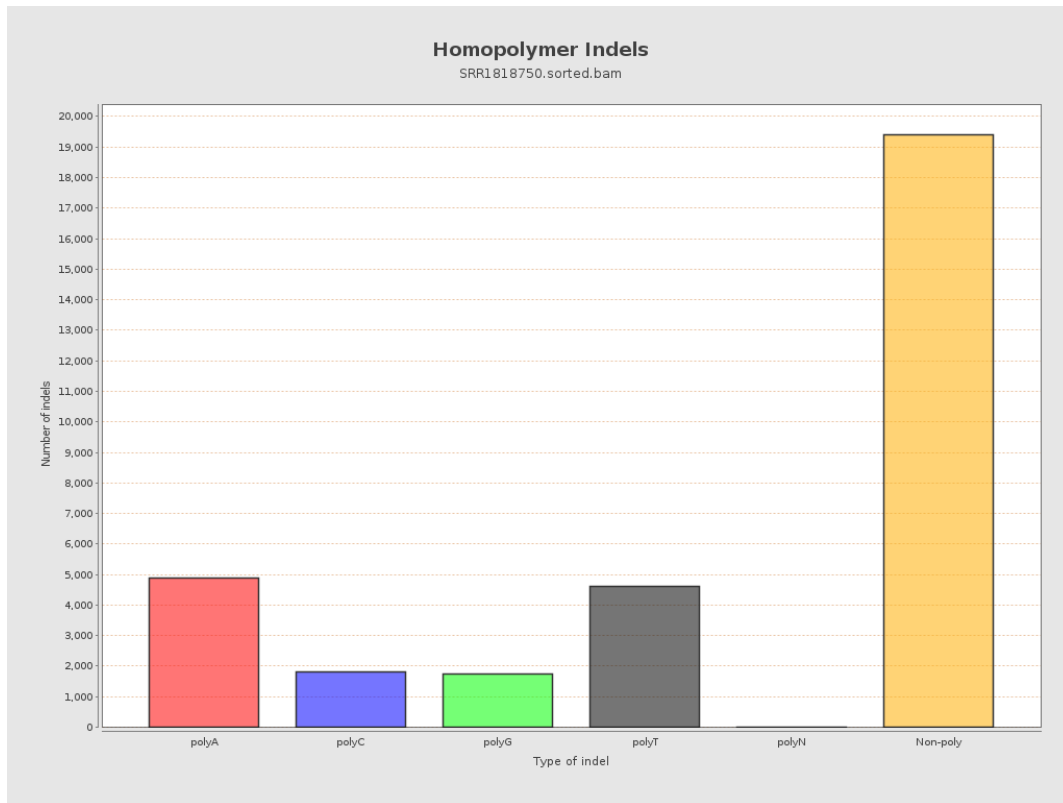
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

