

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:50:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708580.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_SRR1708580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708580.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:50:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,988,837
Mapped reads	4,903,381 / 98.29%
Unmapped reads	85,456 / 1.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	138 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	48,358 / 0.97%
Duplication rate	0.99%
Clipped reads	65,409 / 1.31%

2.2. ACGT Content

Number/percentage of A's	75,762,873 / 30.98%
Number/percentage of C's	46,330,503 / 18.95%
Number/percentage of T's	75,448,889 / 30.85%
Number/percentage of G's	46,996,798 / 19.22%
Number/percentage of N's	9,024 / 0%
GC Percentage	38.16%

2.3. Coverage

Mean	0.079

Standard Deviation	0.2942
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2.4. Mapping Quality

Mean Mapping Quality	46.73
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2.5. Mismatches and indels

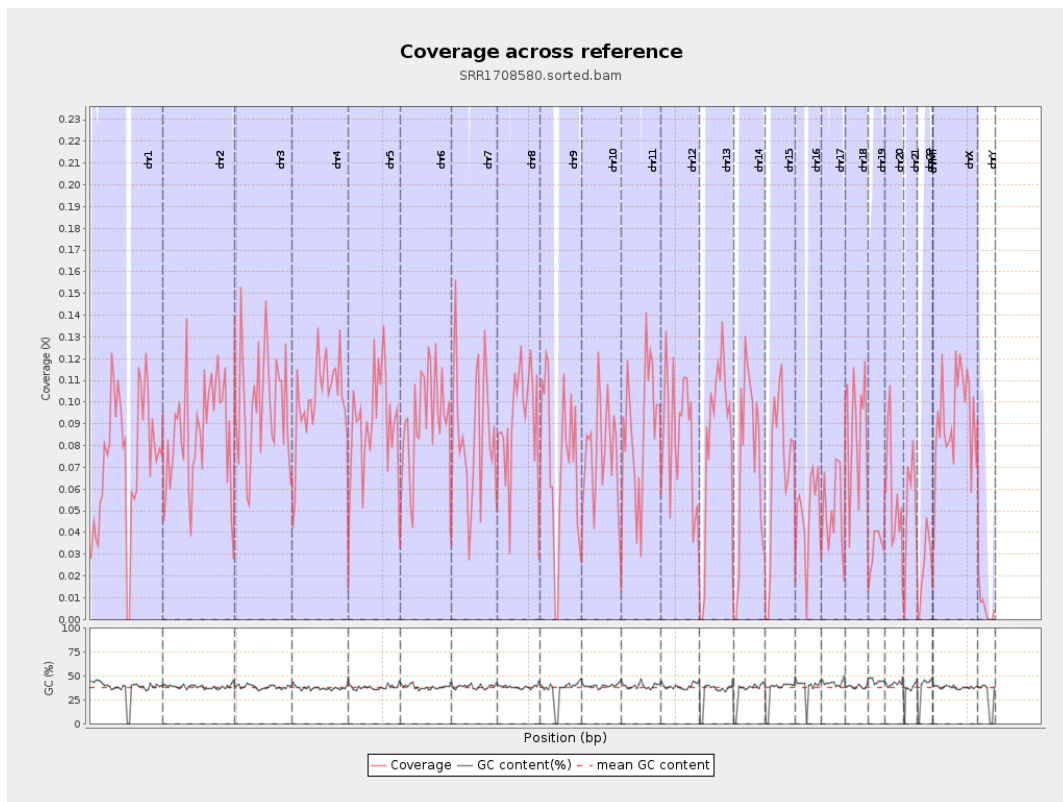
General error rate	0.15%
Mismatches	351,978
Insertions	15,182
Mapped reads with at least one insertion	0.31%
Deletions	12,328
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.91%

2.6. Chromosome stats

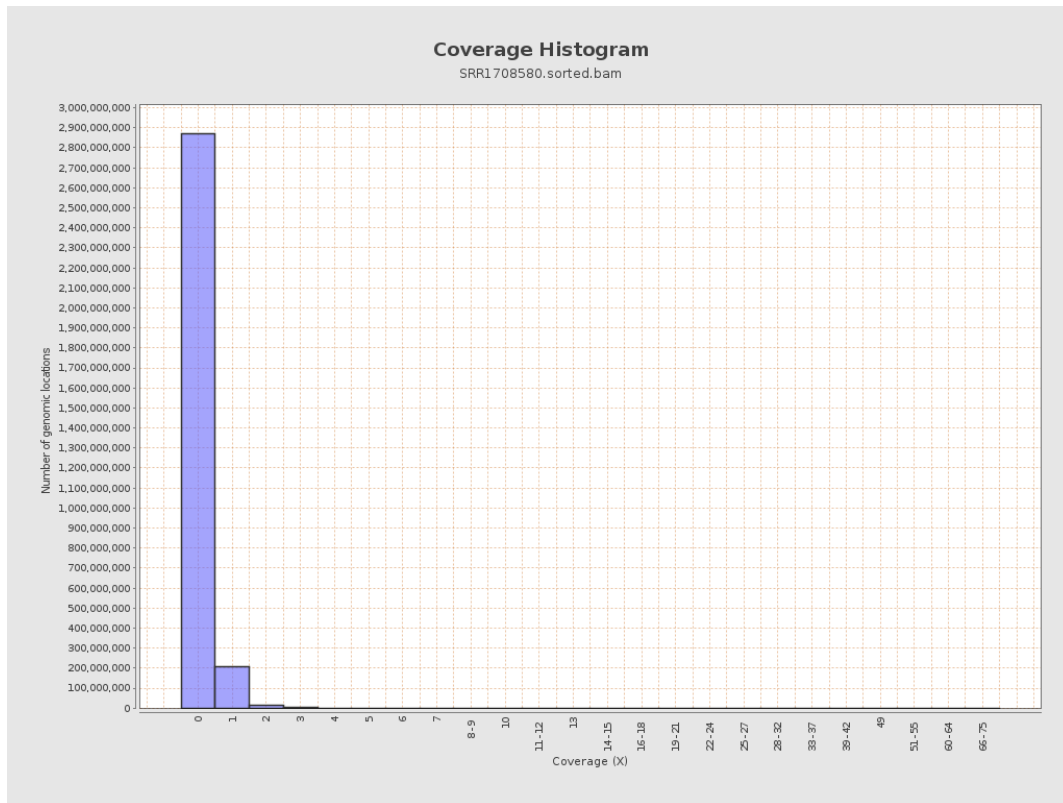
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18515753	0.0743	0.2868
chr2	243199373	20626603	0.0848	0.303
chr3	198022430	19655261	0.0993	0.3285
chr4	191154276	19470415	0.1019	0.3319
chr5	180915260	16088451	0.0889	0.3102
chr6	171115067	15786239	0.0923	0.3166
chr7	159138663	13410906	0.0843	0.3038

chr8	146364022	13363615	0.0913	0.3146
chr9	141213431	10336534	0.0732	0.2835
chr10	135534747	10470572	0.0773	0.2893
chr11	135006516	11847007	0.0878	0.3108
chr12	133851895	11168856	0.0834	0.3015
chr13	115169878	9498805	0.0825	0.3006
chr14	107349540	7797023	0.0726	0.2833
chr15	102531392	7092955	0.0692	0.2771
chr16	90354753	4316852	0.0478	0.2272
chr17	81195210	4137733	0.051	0.2357
chr18	78077248	6864314	0.0879	0.3086
chr19	59128983	2013897	0.0341	0.1912
chr20	63025520	3639054	0.0577	0.2511
chr21	48129895	2484947	0.0516	0.2388
chr22	51304566	1267505	0.0247	0.163
chrMT	16571	550	0.0332	0.1791
chrX	155270560	14389293	0.0927	0.3183
chrY	59373566	325998	0.0055	0.0777

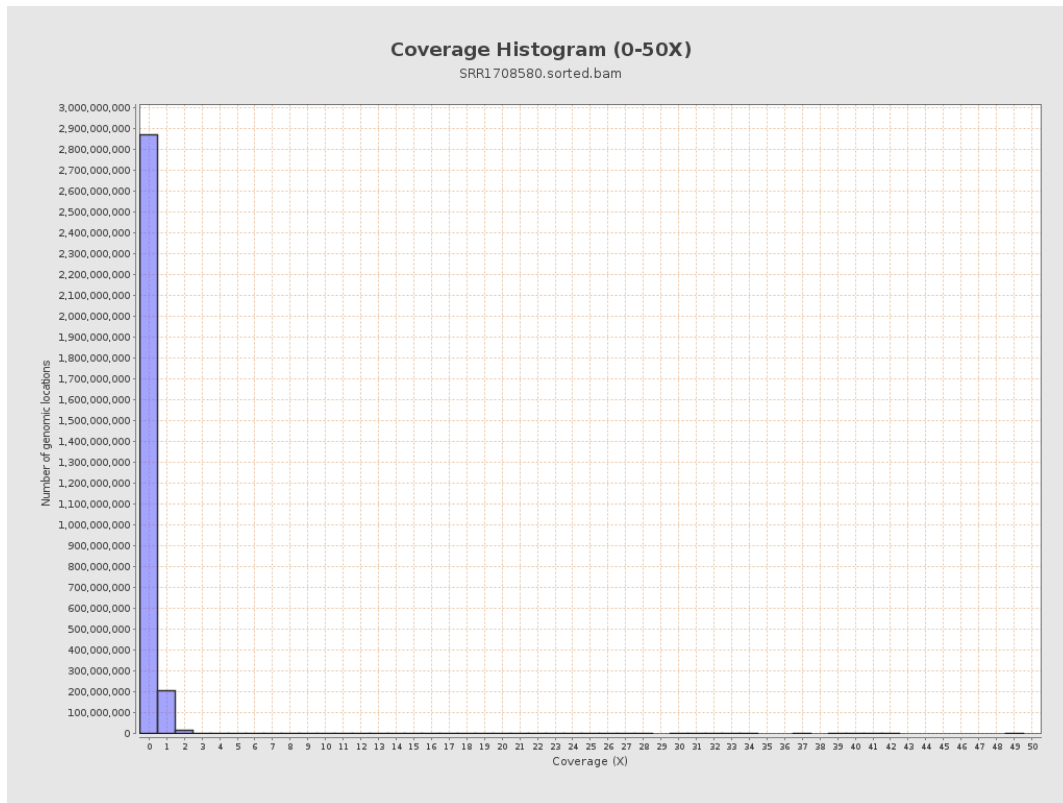
3. Results : Coverage across reference



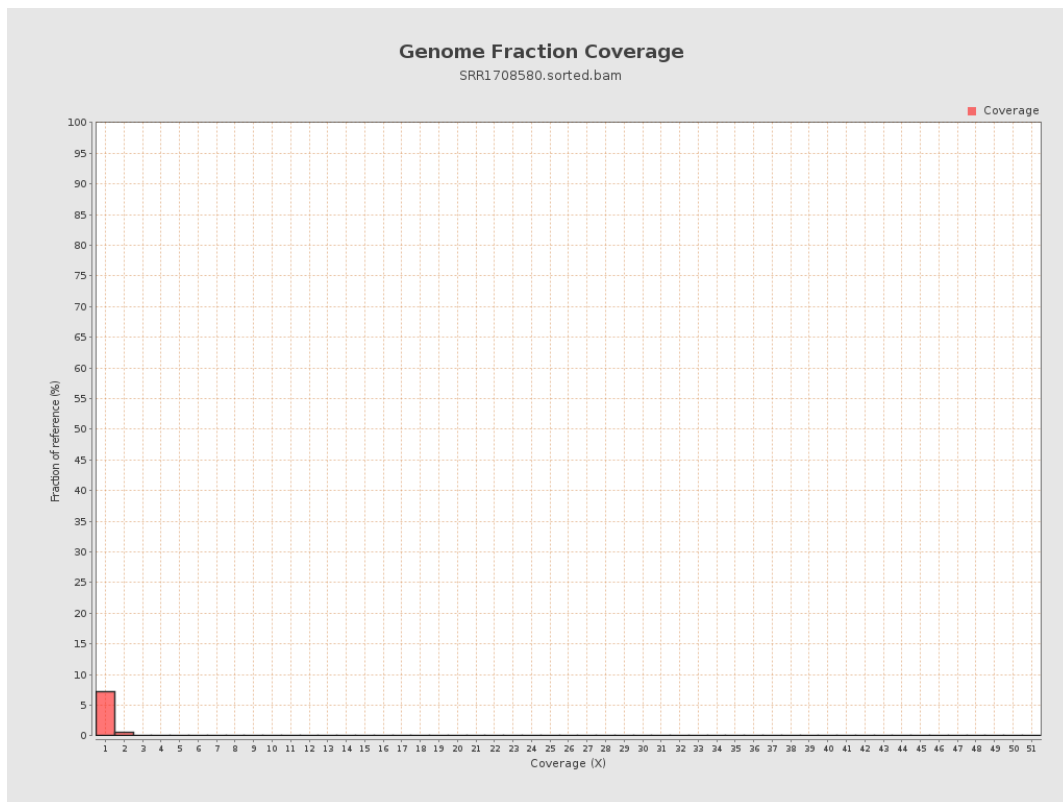
4. Results : Coverage Histogram



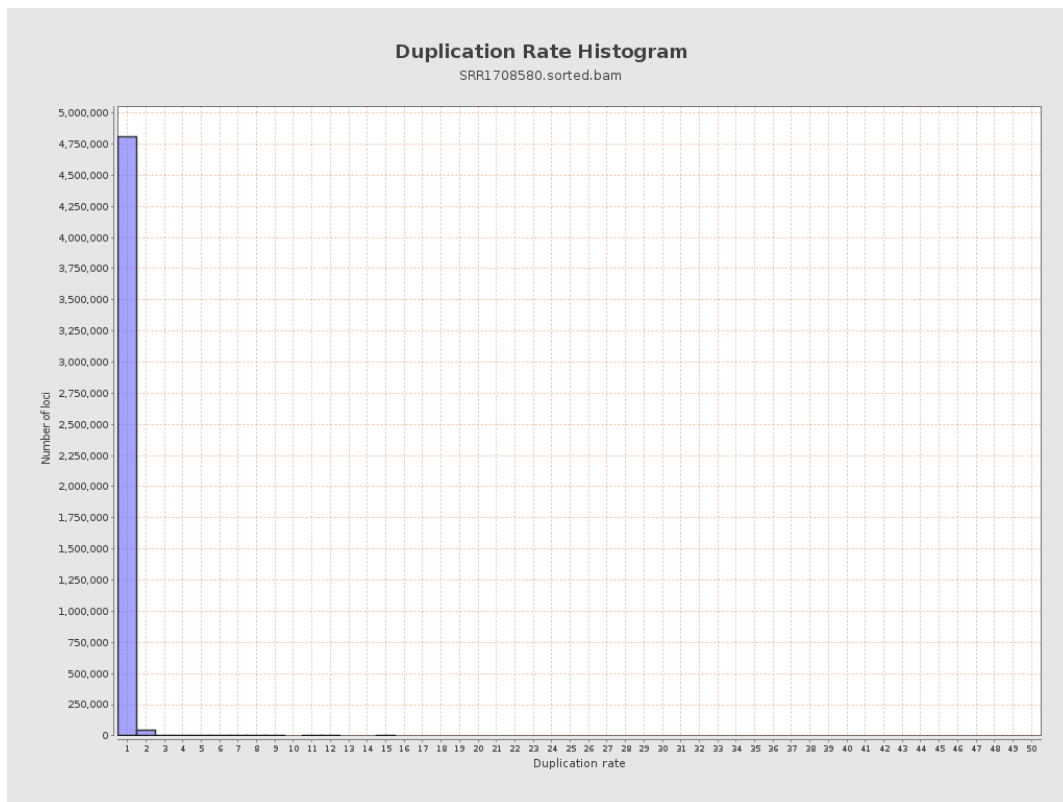
5. Results : Coverage Histogram (0-50X)



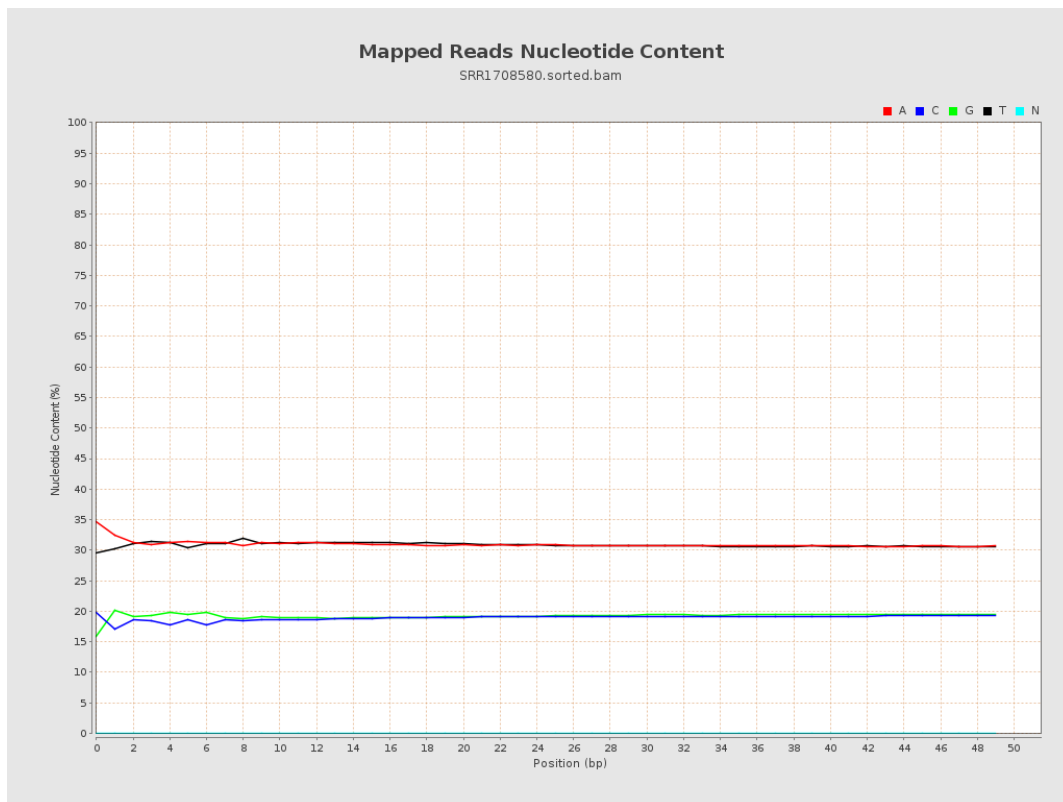
6. Results : Genome Fraction Coverage



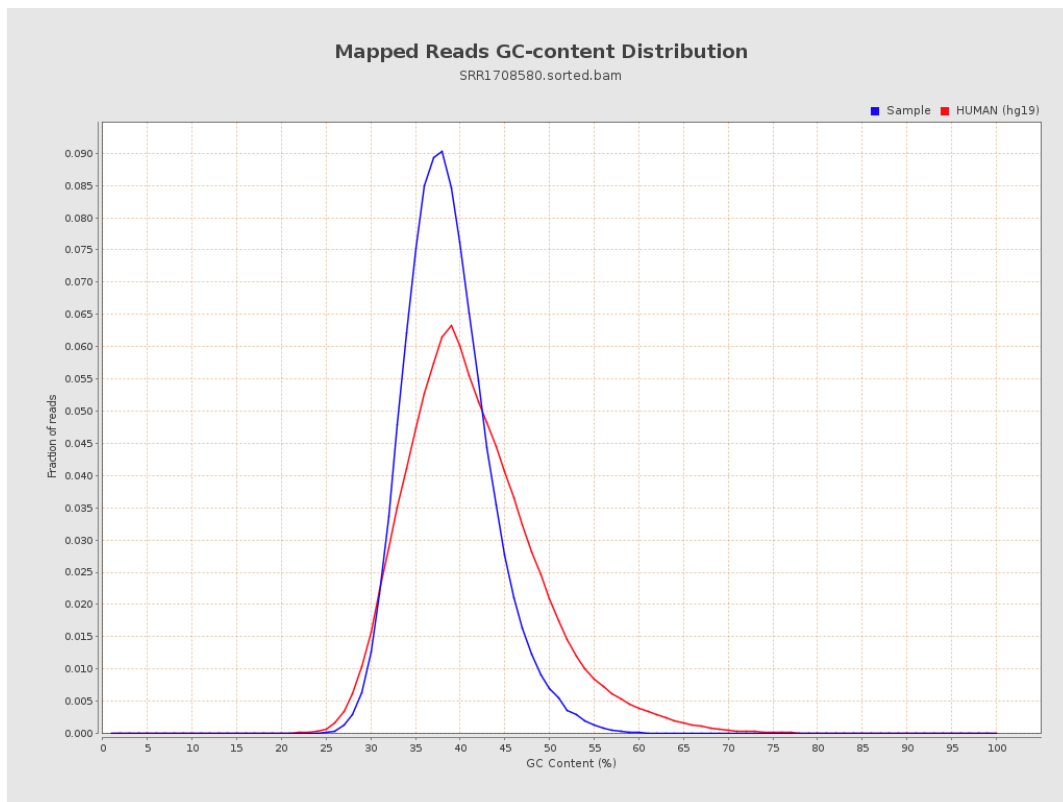
7. Results : Duplication Rate Histogram



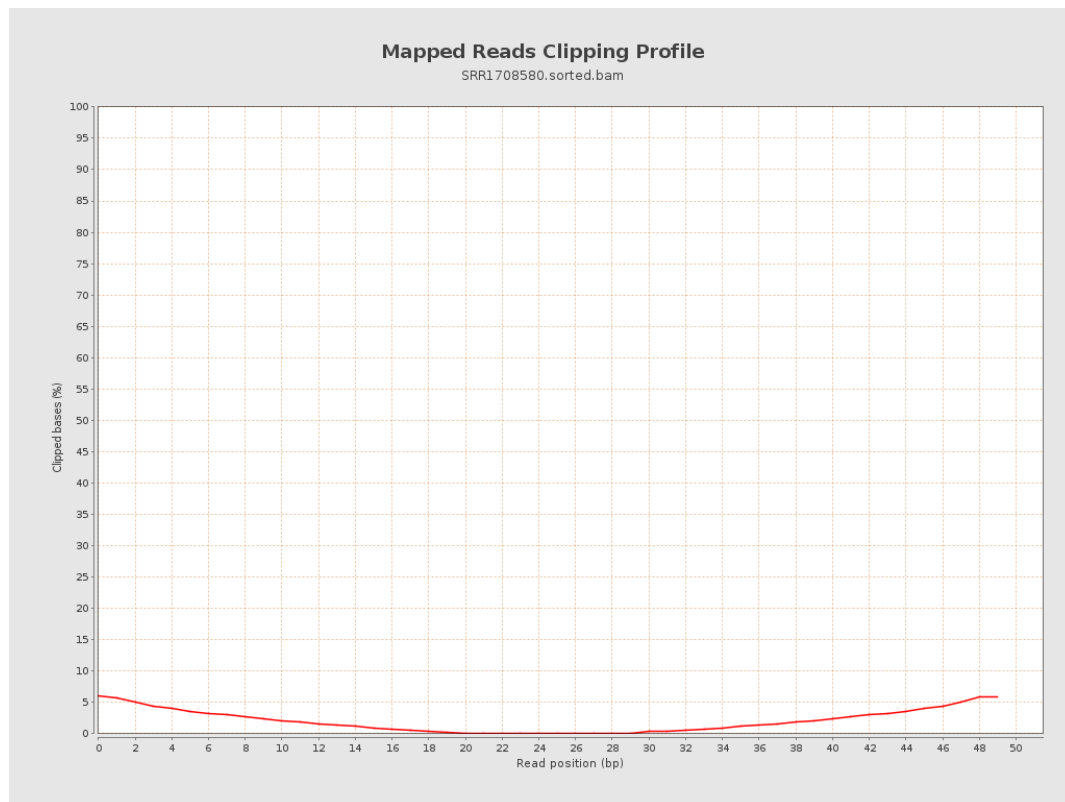
8. Results : Mapped Reads Nucleotide Content



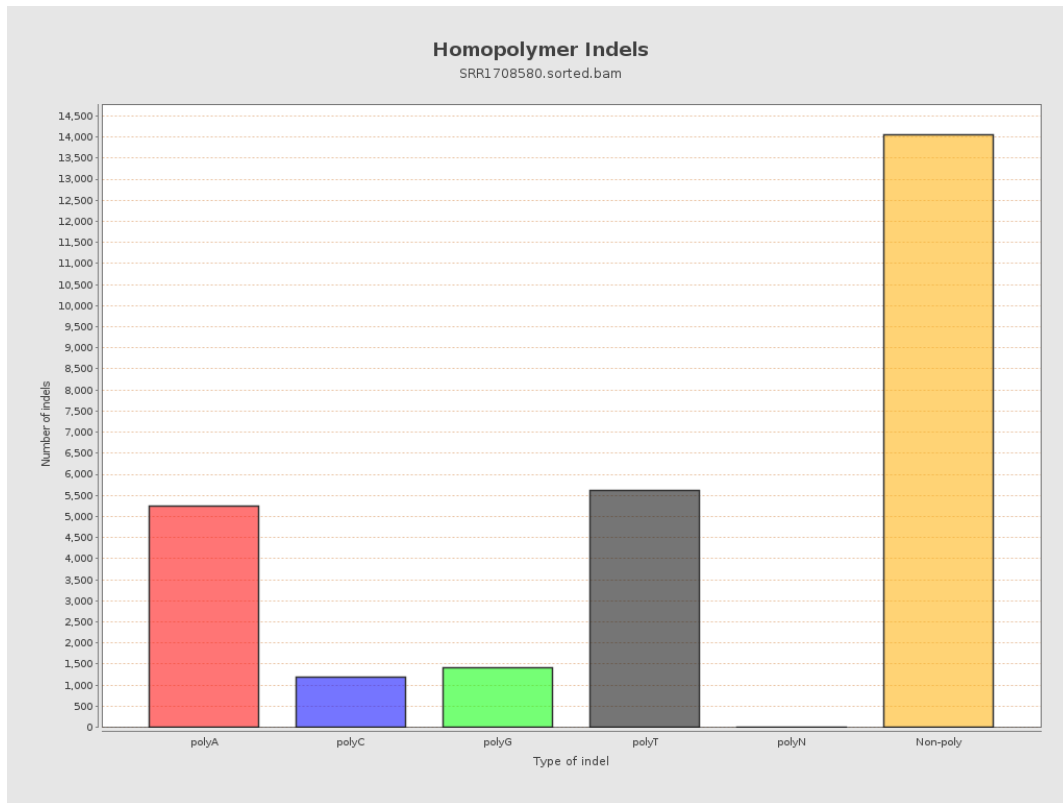
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

