Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 09:28:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090198.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_SRR090198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 09:28:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,537,121
Mapped reads	23,113,491 / 90.51%
Unmapped reads	2,423,630 / 9.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	157,619 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	3,967,071 / 15.53%
Duplication rate	11.41%
Clipped reads	11,907,743 / 46.63%

2.2. ACGT Content

Number/percentage of A's	405,119,783 / 26.9%
Number/percentage of C's	280,792,511 / 18.65%
Number/percentage of T's	469,109,773 / 31.15%
Number/percentage of G's	349,935,830 / 23.24%
Number/percentage of N's	927,177 / 0.06%
GC Percentage	41.88%

2.3. Coverage

Mean	0.4866

Standard Deviation	3.476

2.4. Mapping Quality

Mean Mapping Quality	46.28

2.5. Mismatches and indels

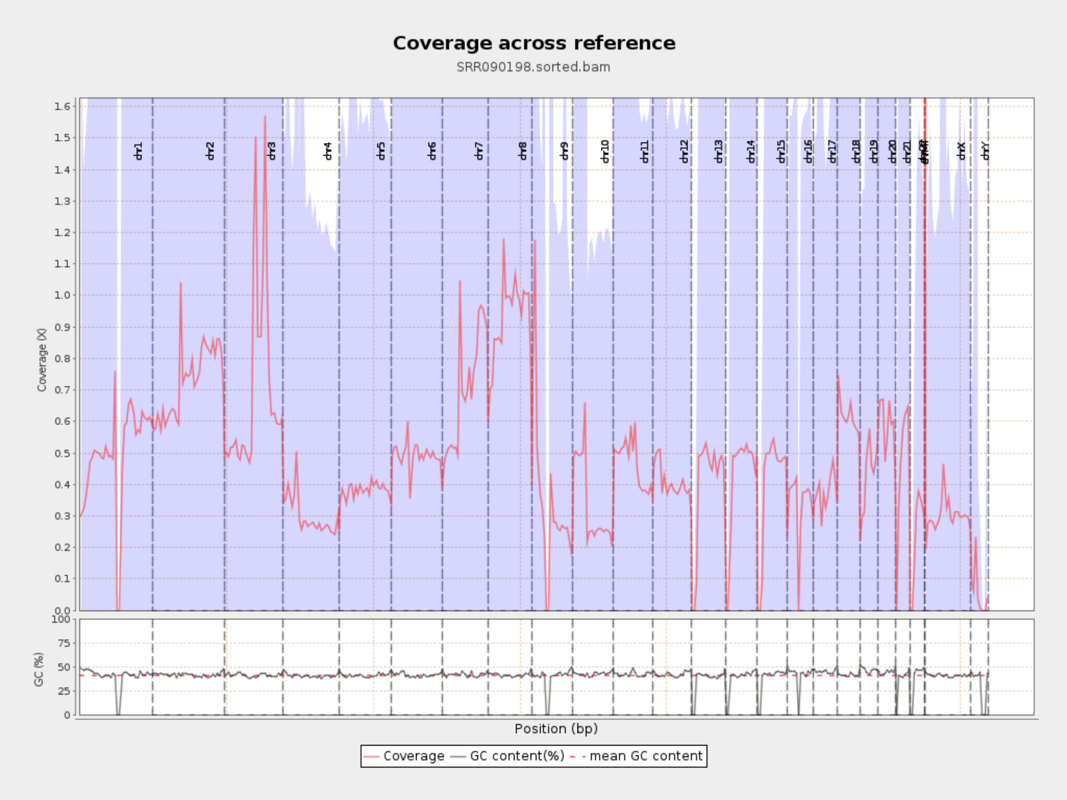
General error rate	0.81%
Mismatches	11,980,608
Insertions	99,238
Mapped reads with at least one insertion	0.43%
Deletions	299,392
Mapped reads with at least one deletion	1.28%
Homopolymer indels	46.4%

2.6. Chromosome stats

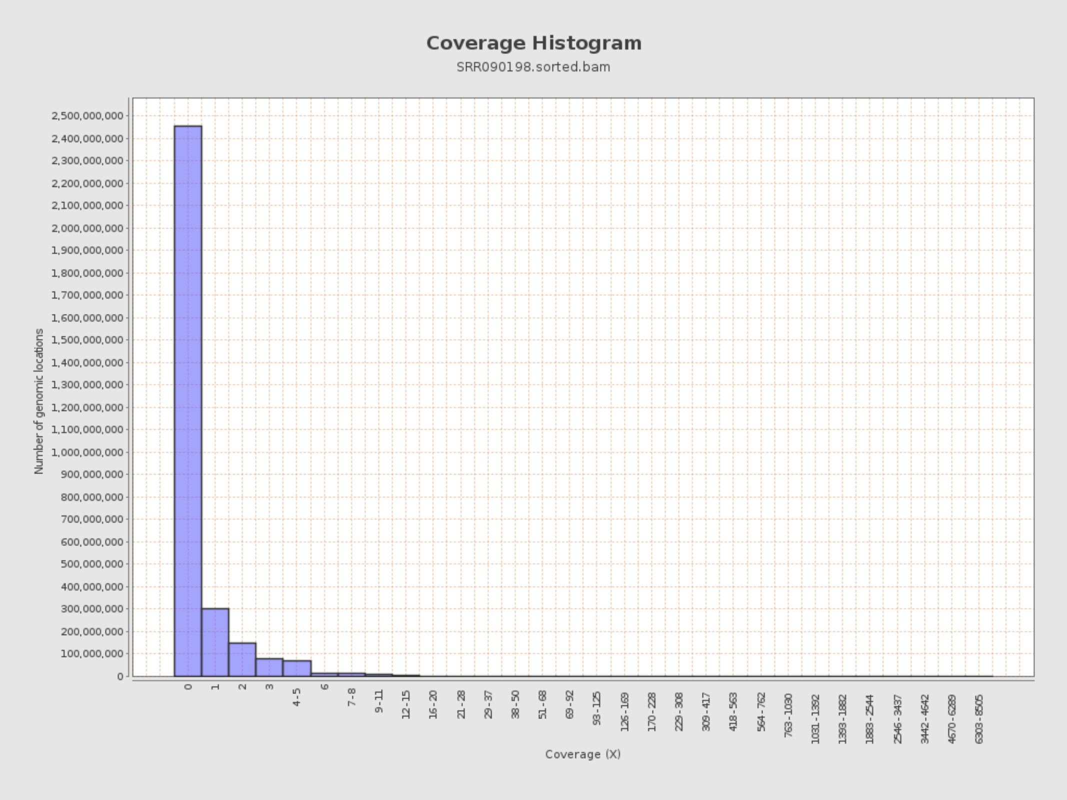
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	124197882	0.4983	6.512
chr2	243199373	178115015	0.7324	4.1864
chr3	198022430	141424366	0.7142	1.7177
chr4	191154276	57342362	0.3	1.3134
chr5	180915260	69017437	0.3815	1.2192
chr6	171115067	84583431	0.4943	1.9124
chr7	159138663	112635336	0.7078	7.0599

chr8	146364022	137098584	0.9367	5.6437
chr9	141213431	47807034	0.3385	2.8231
chr10	135534747	46040210	0.3397	3.0557
chr11	135006516	63218265	0.4683	2.3621
chr12	133851895	54921805	0.4103	1.3027
chr13	115169878	46113131	0.4004	1.1812
chr14	107349540	44801658	0.4173	1.3914
chr15	102531392	40393205	0.394	1.2086
chr16	90354753	30029270	0.3323	1.3045
chr17	81195210	30382195	0.3742	1.5821
chr18	78077248	48430606	0.6203	4.6305
chr19	59128983	25183955	0.4259	3.8307
chr20	63025520	37393582	0.5933	1.6168
chr21	48129895	22839672	0.4745	1.5508
chr22	51304566	12102512	0.2359	0.8883
chrMT	16571	2035304	122.8232	60.4929
chrX	155270560	46837243	0.3016	1.4759
chrY	59373566	3461792	0.0583	2.279

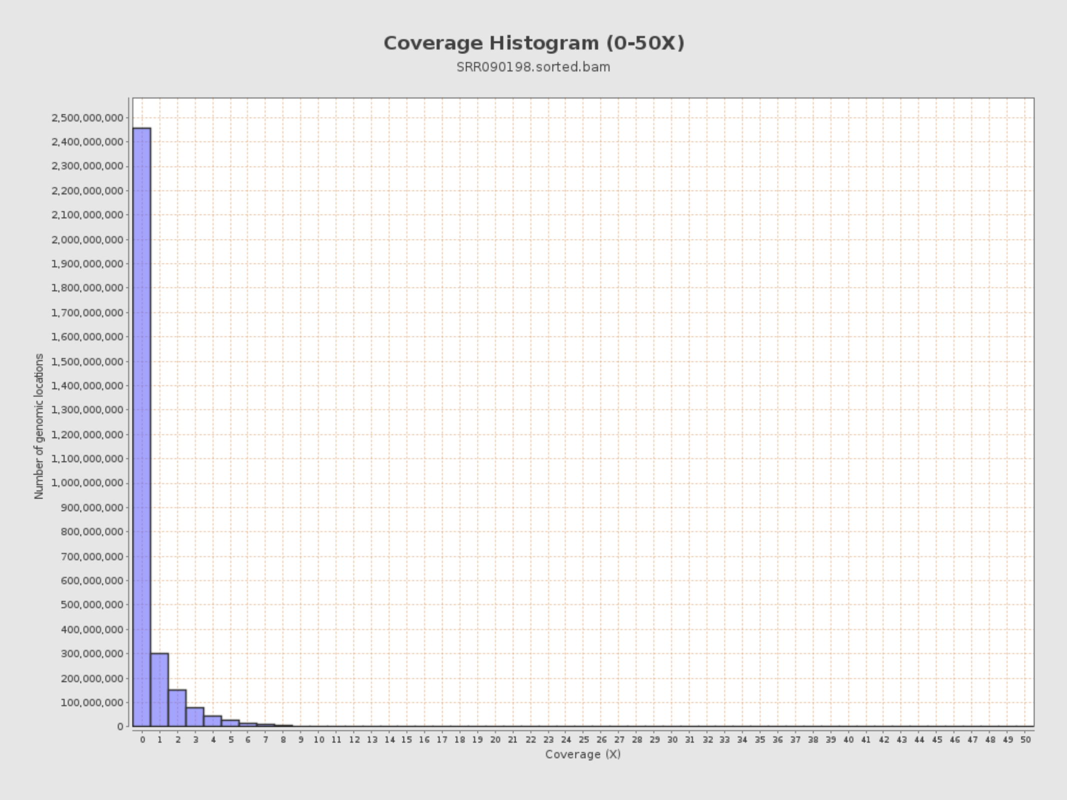
3. Results : Coverage across reference



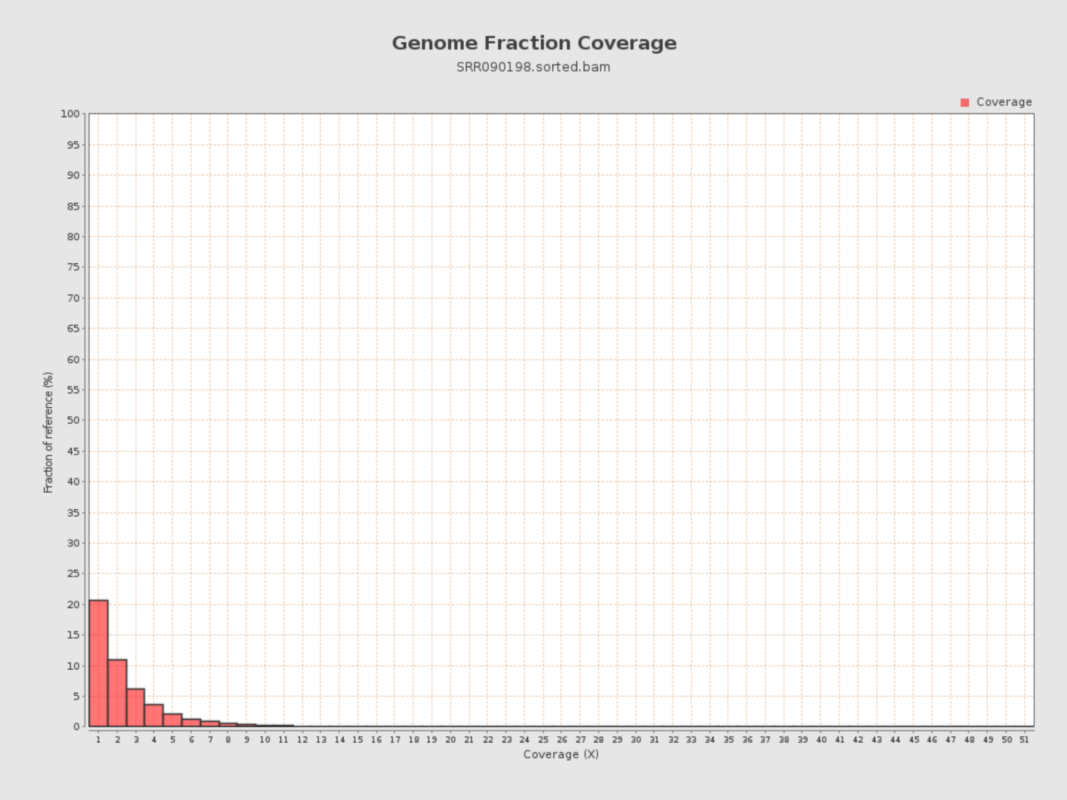
4. Results : Coverage Histogram



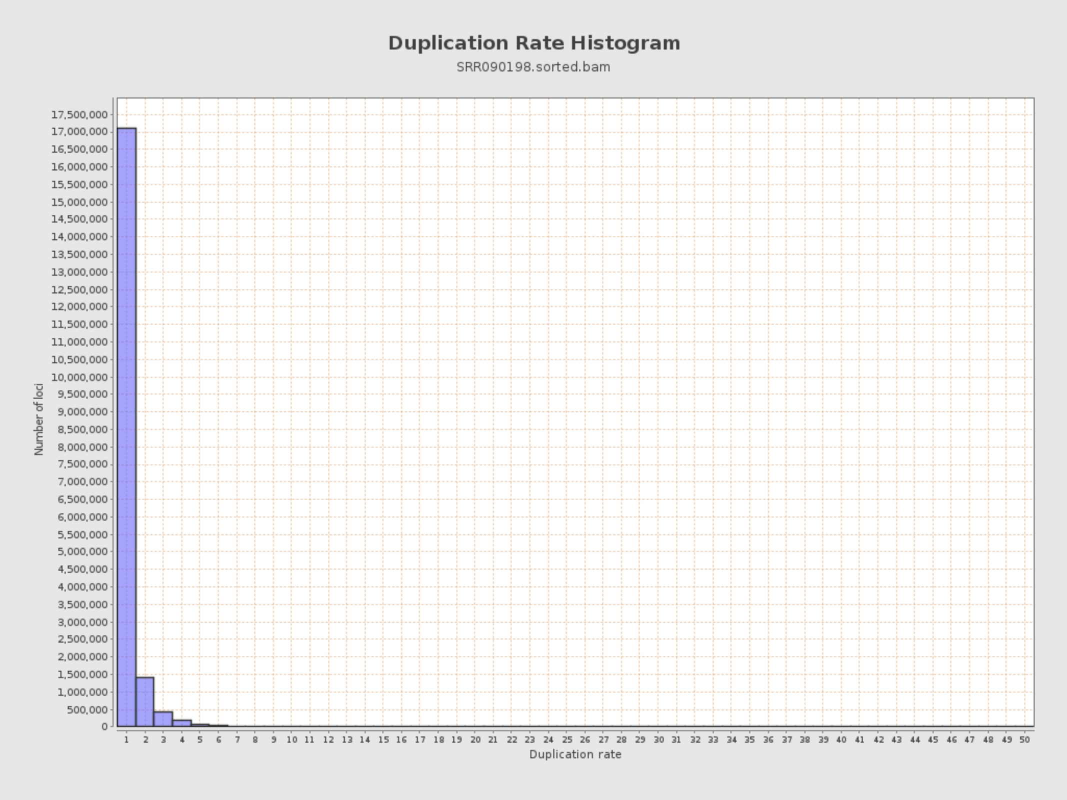
5. Results : Coverage Histogram (0-50X)



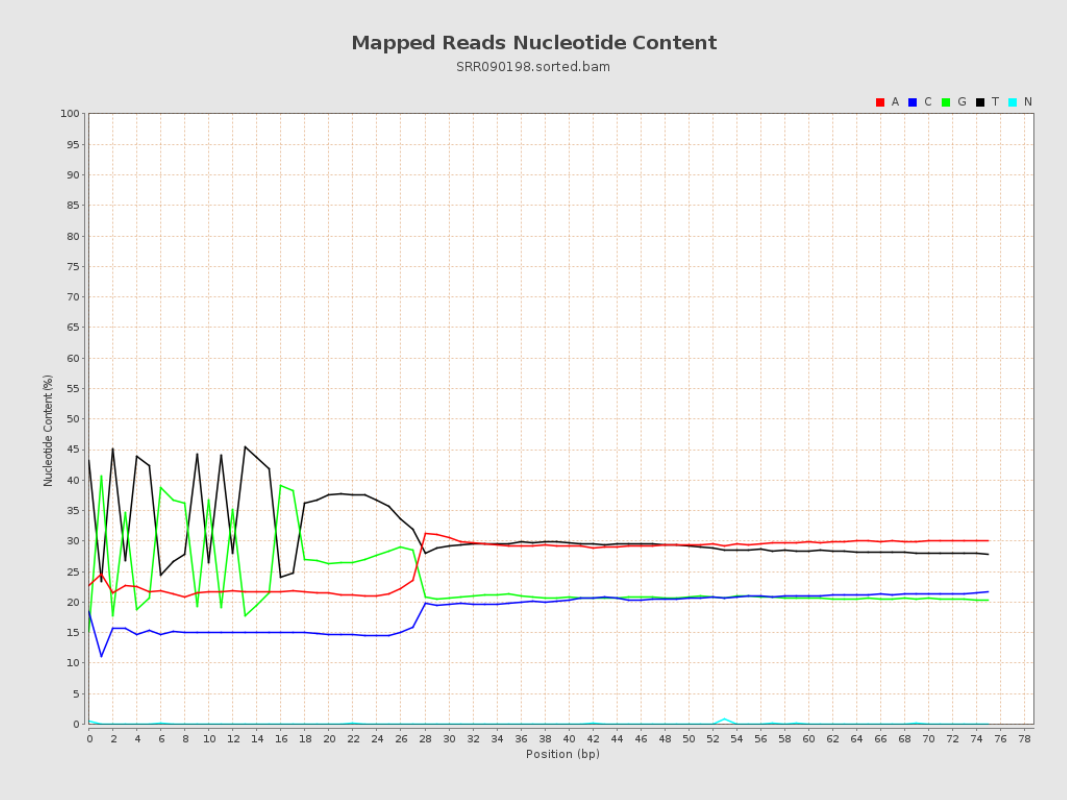
6. Results : Genome Fraction Coverage



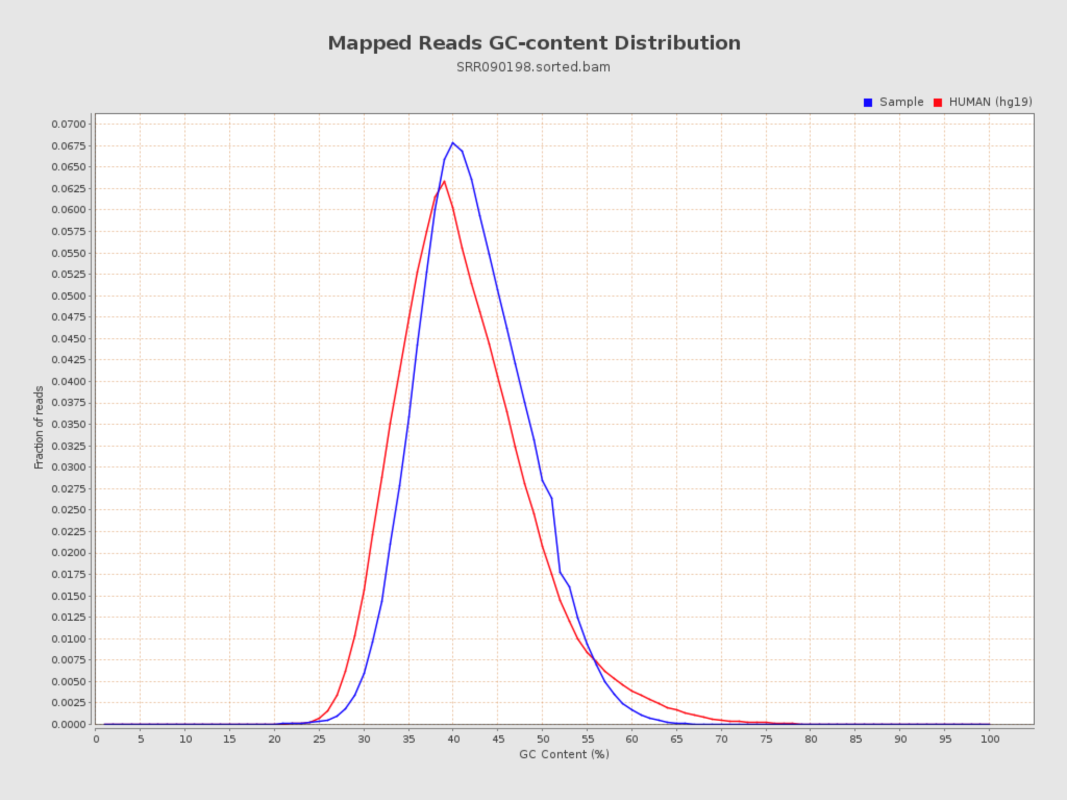
7. Results : Duplication Rate Histogram



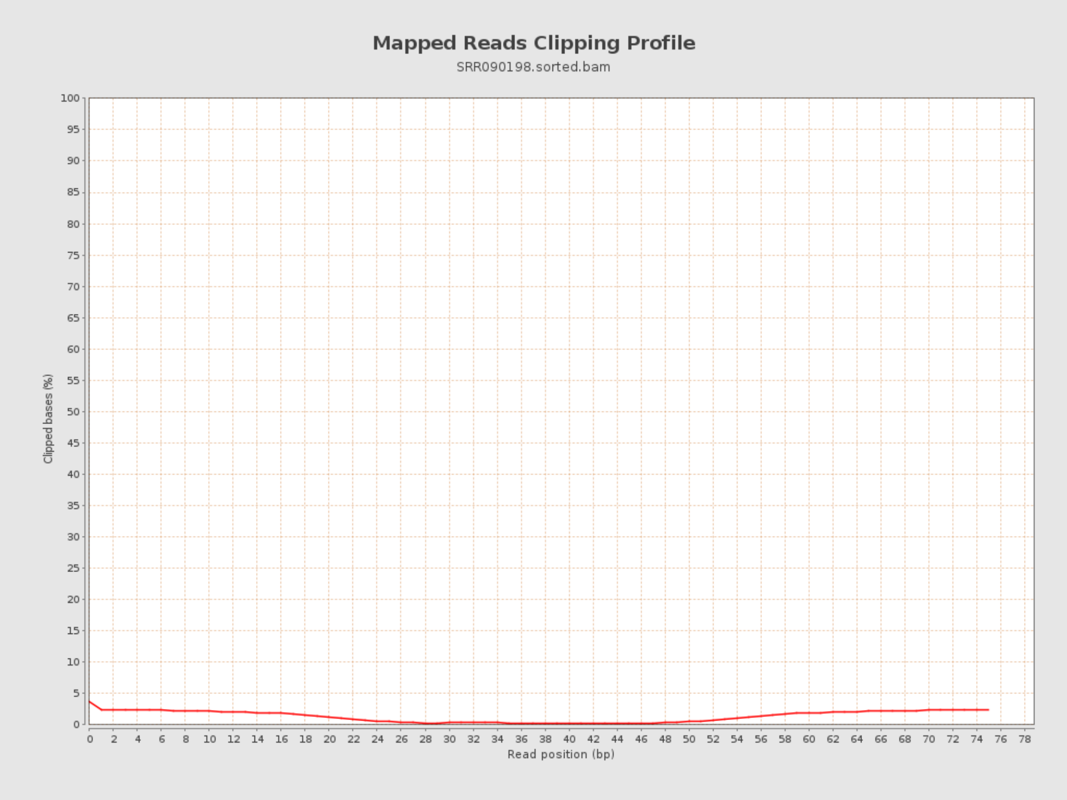
8. Results : Mapped Reads Nucleotide Content



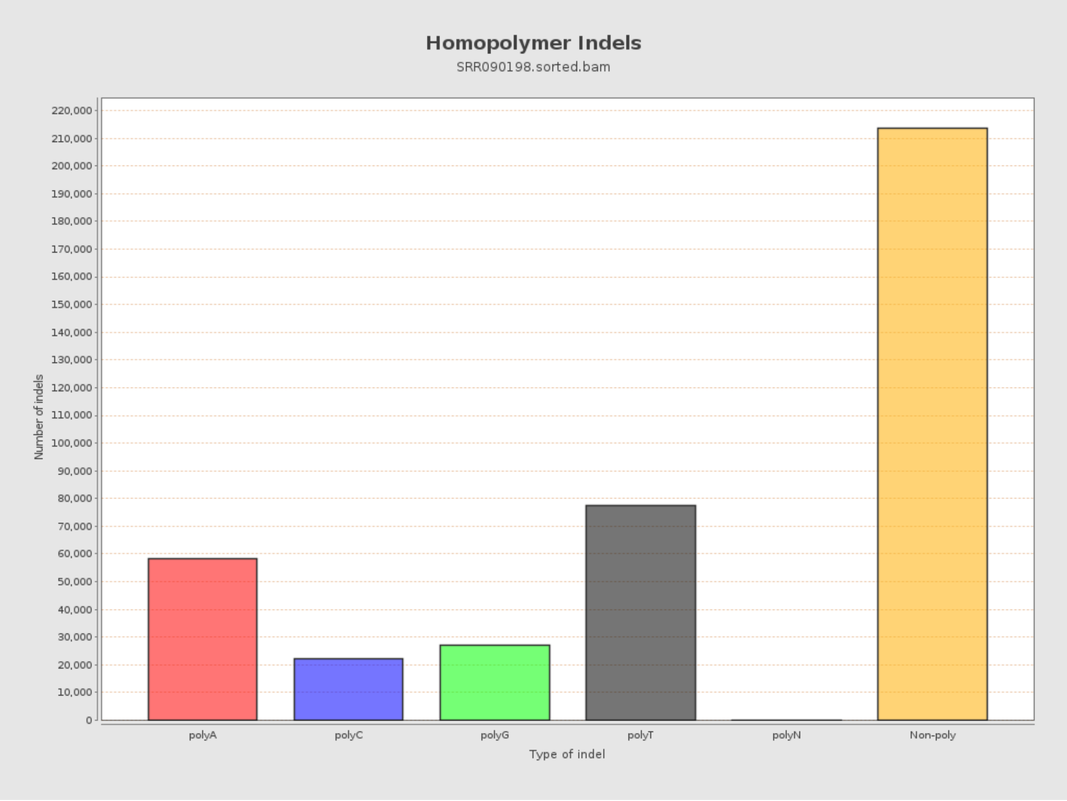
9. Results : Mapped Reads GC-content Distribution



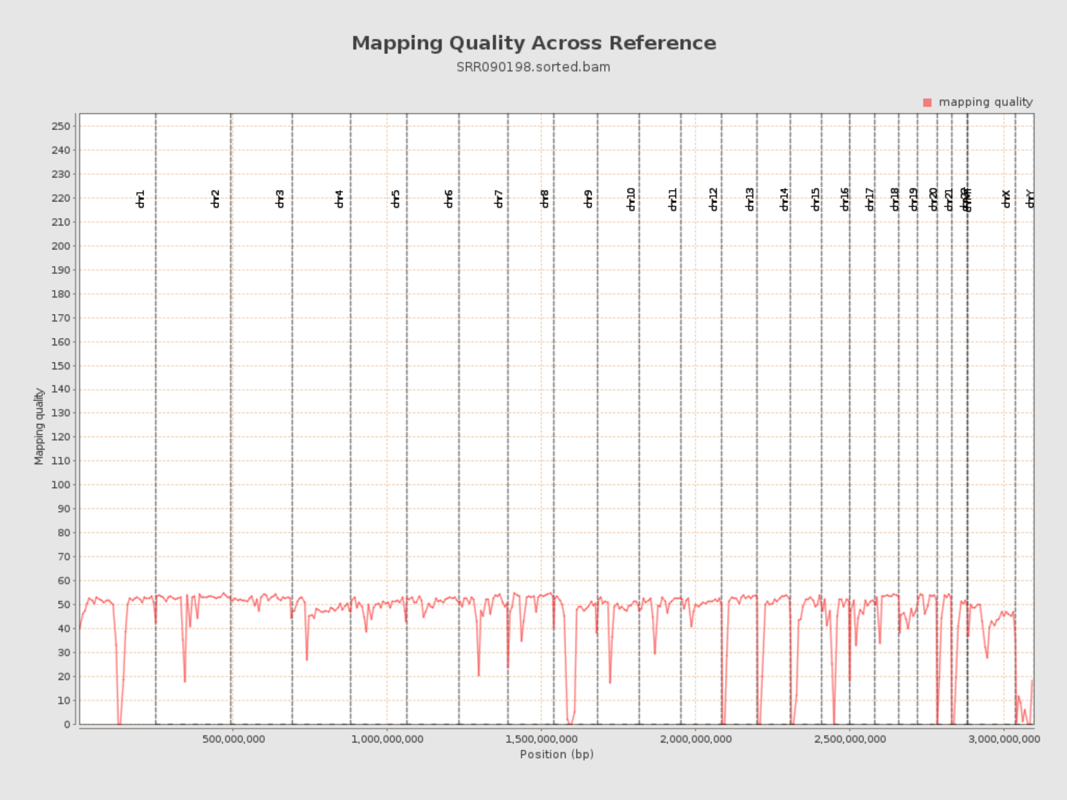
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram