Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:22:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818749.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_SRR1818749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:22:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,301,271
Mapped reads	2,250,647 / 97.8%
Unmapped reads	50,624 / 2.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,739 / 0.77%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	1,227,302 / 53.33%
Duplication rate	46.35%
Clipped reads	2,256,631 / 98.06%

2.2. ACGT Content

Number/percentage of A's	43,022,076 / 28.14%
Number/percentage of C's	32,353,327 / 21.16%
Number/percentage of T's	44,464,197 / 29.08%
Number/percentage of G's	33,059,975 / 21.62%
Number/percentage of N's	9,262 / 0.01%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0494

Standard Deviation	0.592

2.4. Mapping Quality

Mean Mapping Quality	47.73

2.5. Mismatches and indels

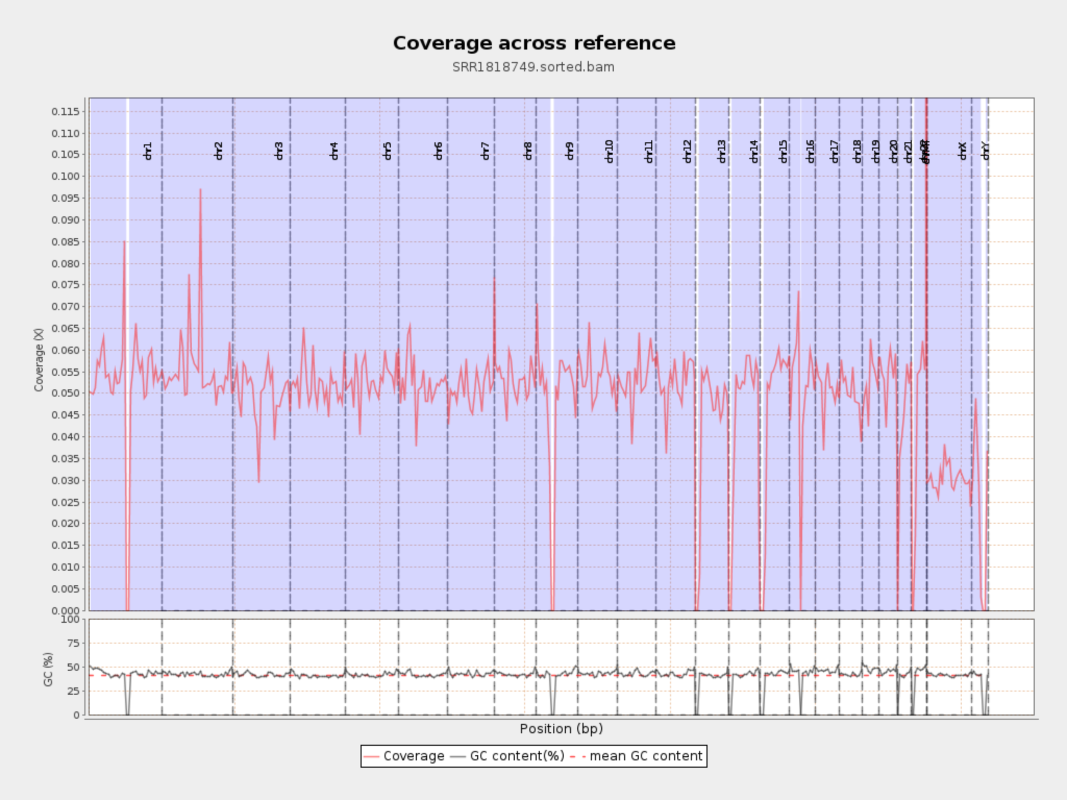
General error rate	0.51%
Mismatches	745,348
Insertions	17,917
Mapped reads with at least one insertion	0.79%
Deletions	39,337
Mapped reads with at least one deletion	1.73%
Homopolymer indels	40.87%

2.6. Chromosome stats

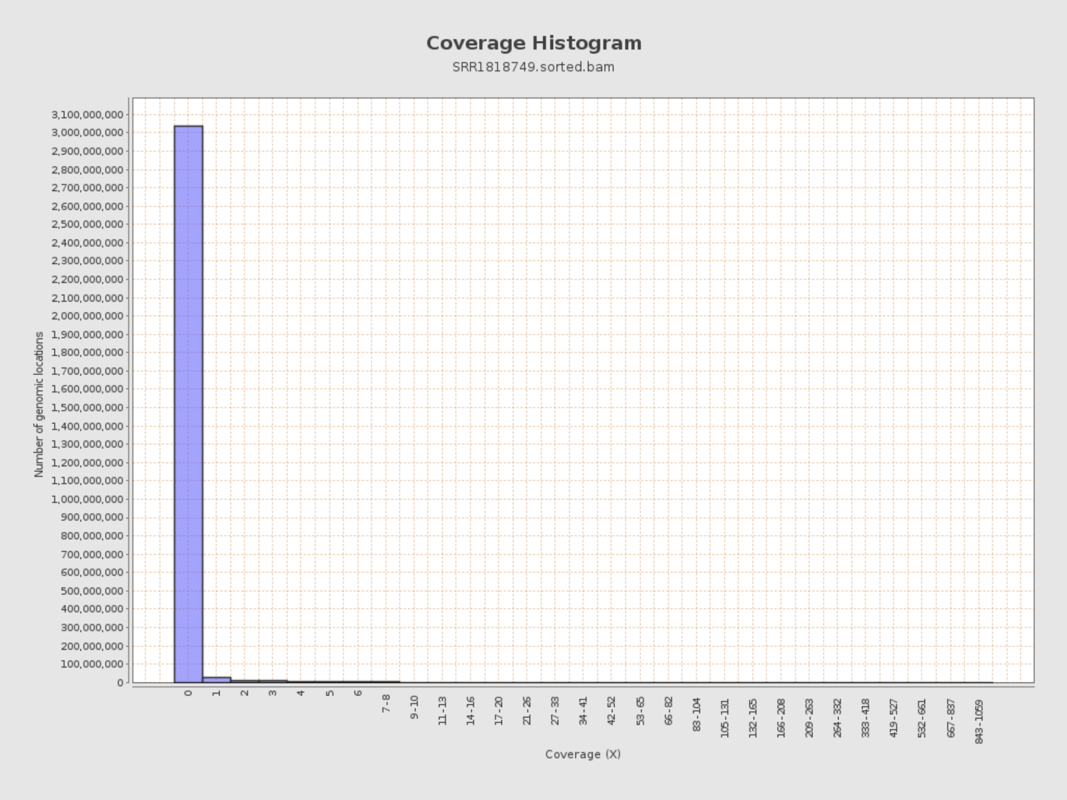
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13047435	0.0523	0.8637
chr2	243199373	13610382	0.056	0.8362
chr3	198022430	9892121	0.05	0.4592
chr4	191154276	9951217	0.0521	0.5176
chr5	180915260	9606830	0.0531	0.4818
chr6	171115067	8980453	0.0525	0.5077
chr7	159138663	8132113	0.0511	0.5282

chr8	146364022	7793633	0.0532	0.5291
chr9	141213431	6599006	0.0467	0.514
chr10	135534747	7304240	0.0539	0.6109
chr11	135006516	7236016	0.0536	0.5255
chr12	133851895	7075620	0.0529	0.4945
chr13	115169878	4824393	0.0419	0.4227
chr14	107349540	4821452	0.0449	0.4762
chr15	102531392	4583224	0.0447	0.4389
chr16	90354753	4593162	0.0508	0.6382
chr17	81195210	4154654	0.0512	0.496
chr18	78077248	3945018	0.0505	0.6638
chr19	59128983	3111837	0.0526	0.7581
chr20	63025520	3424119	0.0543	0.5145
chr21	48129895	2054068	0.0427	0.4465
chr22	51304566	2011139	0.0392	0.4503
chrMT	16571	138828	8.3778	9.0557
chrX	155270560	4727545	0.0304	0.4049
chrY	59373566	1353730	0.0228	0.9351

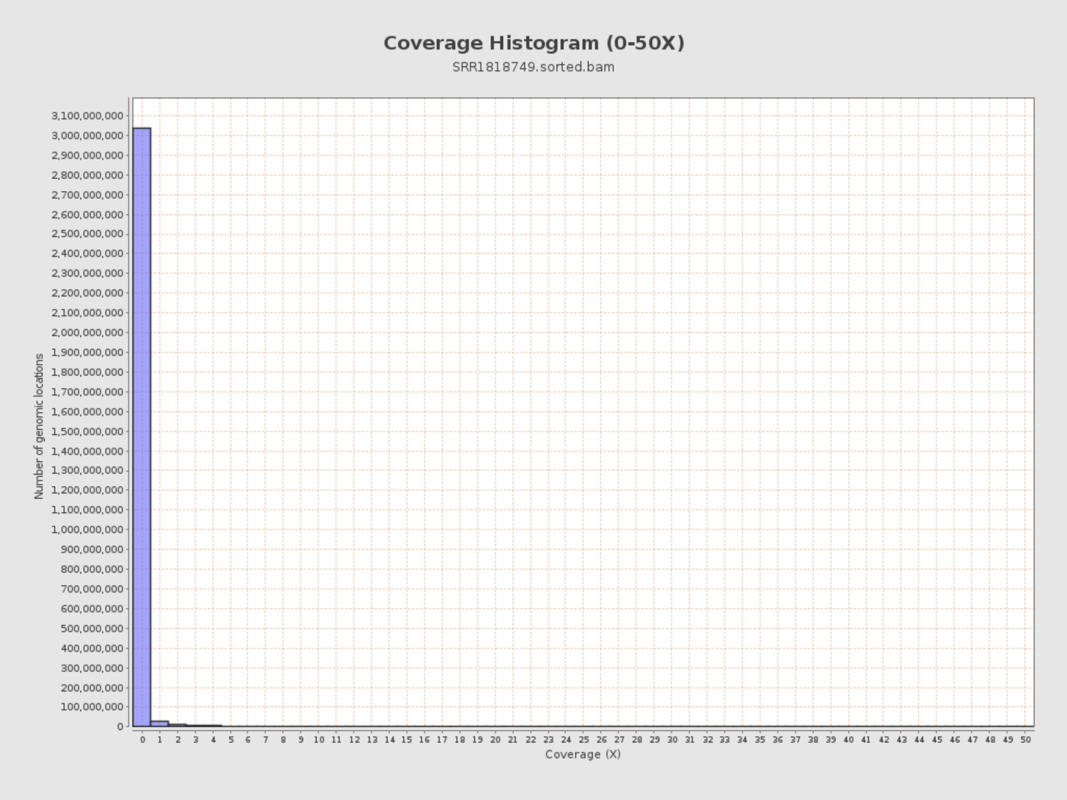
3. Results : Coverage across reference



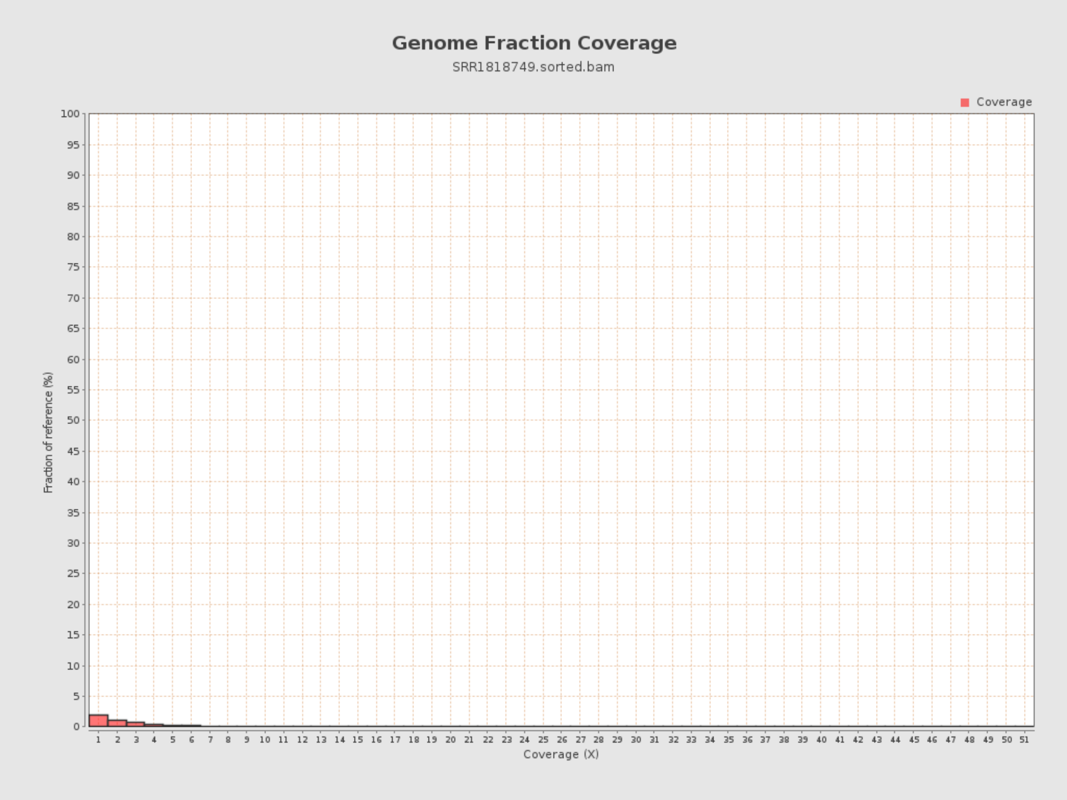
4. Results : Coverage Histogram



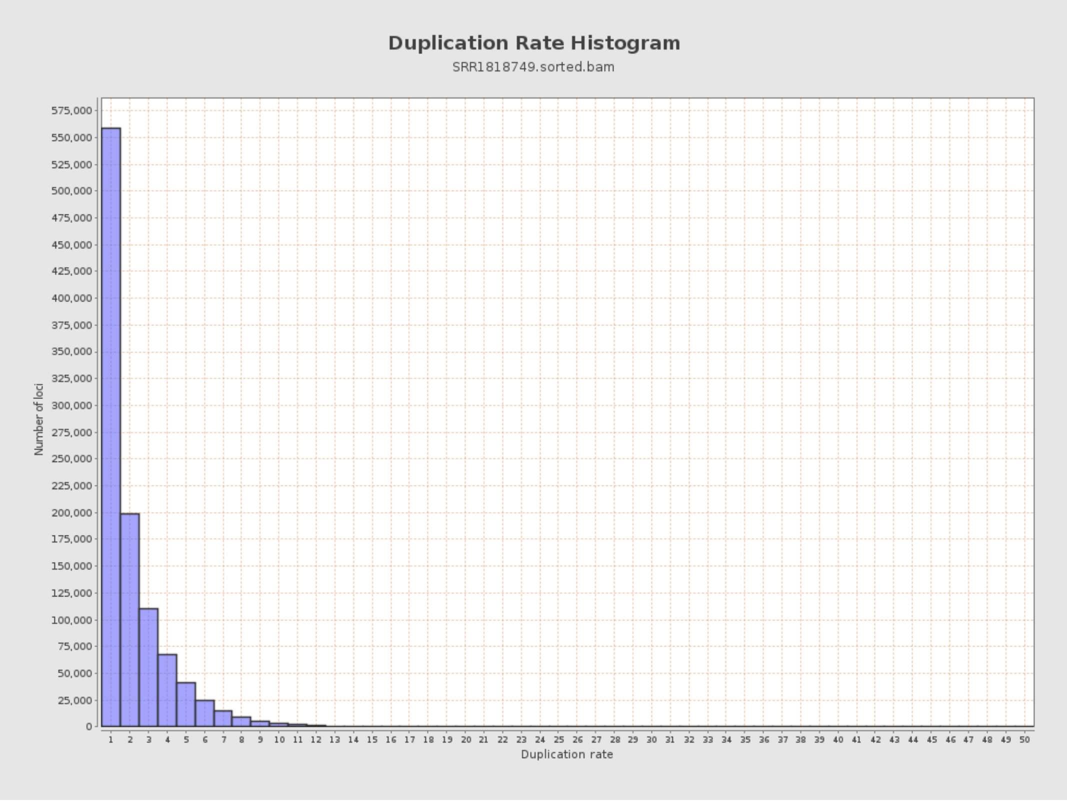
5. Results : Coverage Histogram (0-50X)



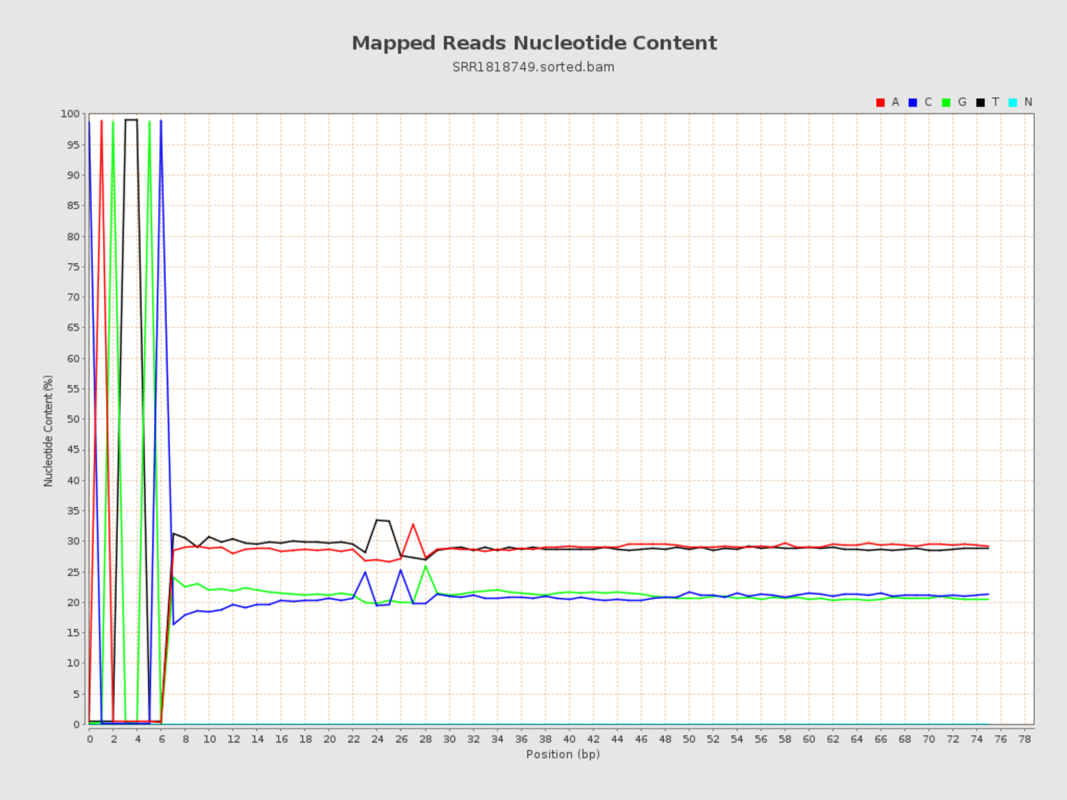
6. Results : Genome Fraction Coverage



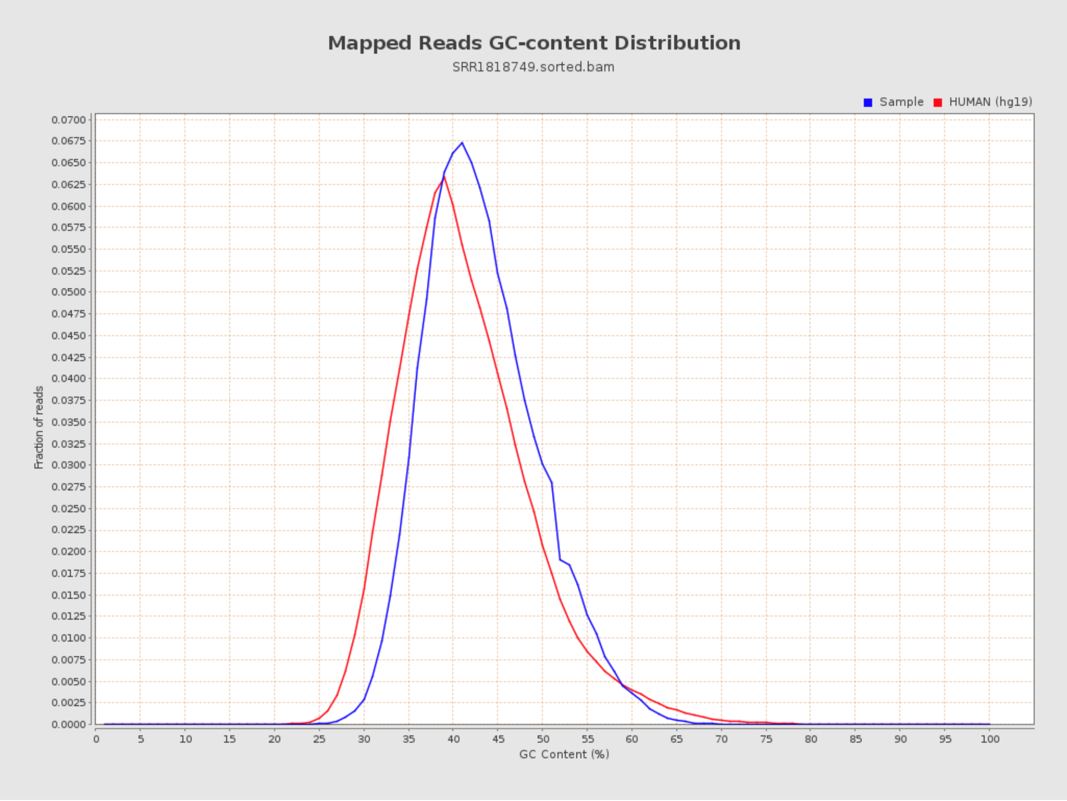
7. Results : Duplication Rate Histogram



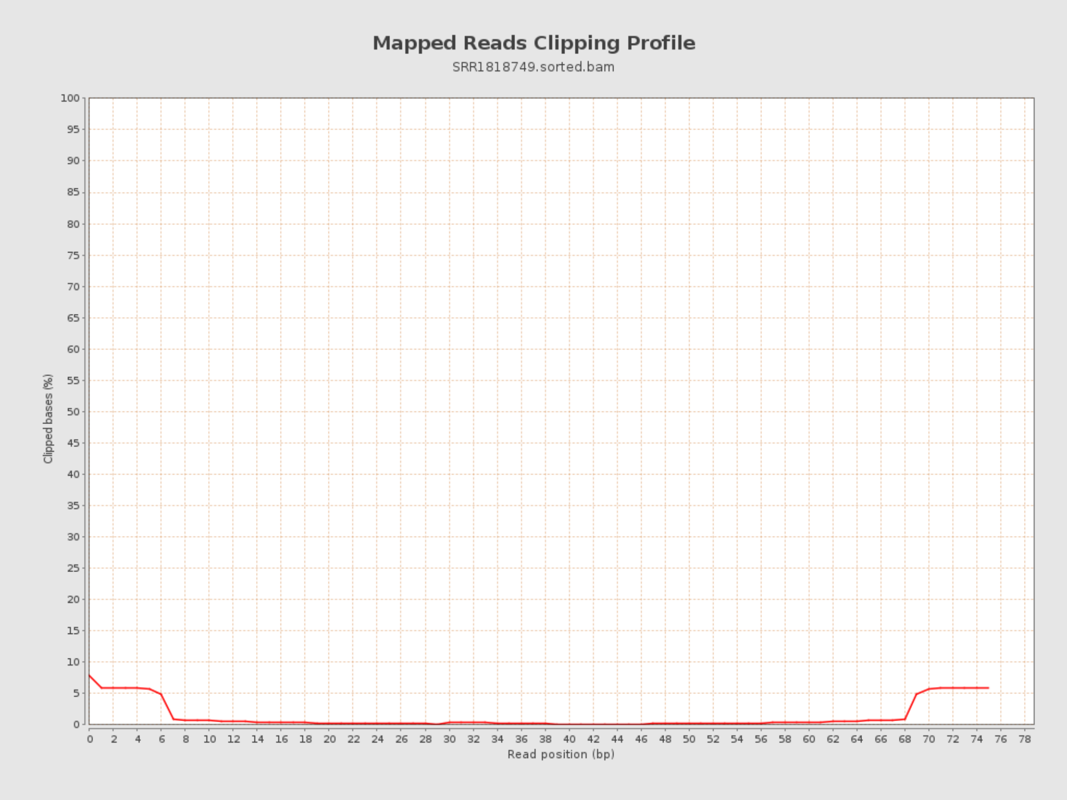
8. Results : Mapped Reads Nucleotide Content



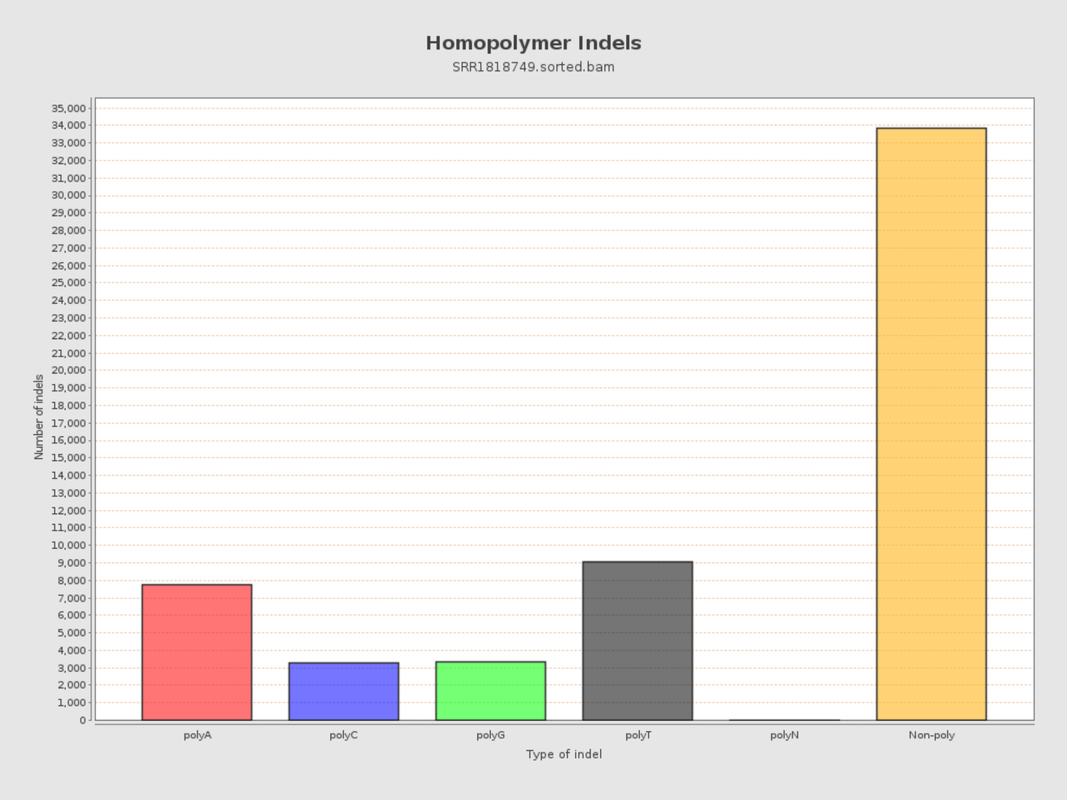
9. Results : Mapped Reads GC-content Distribution



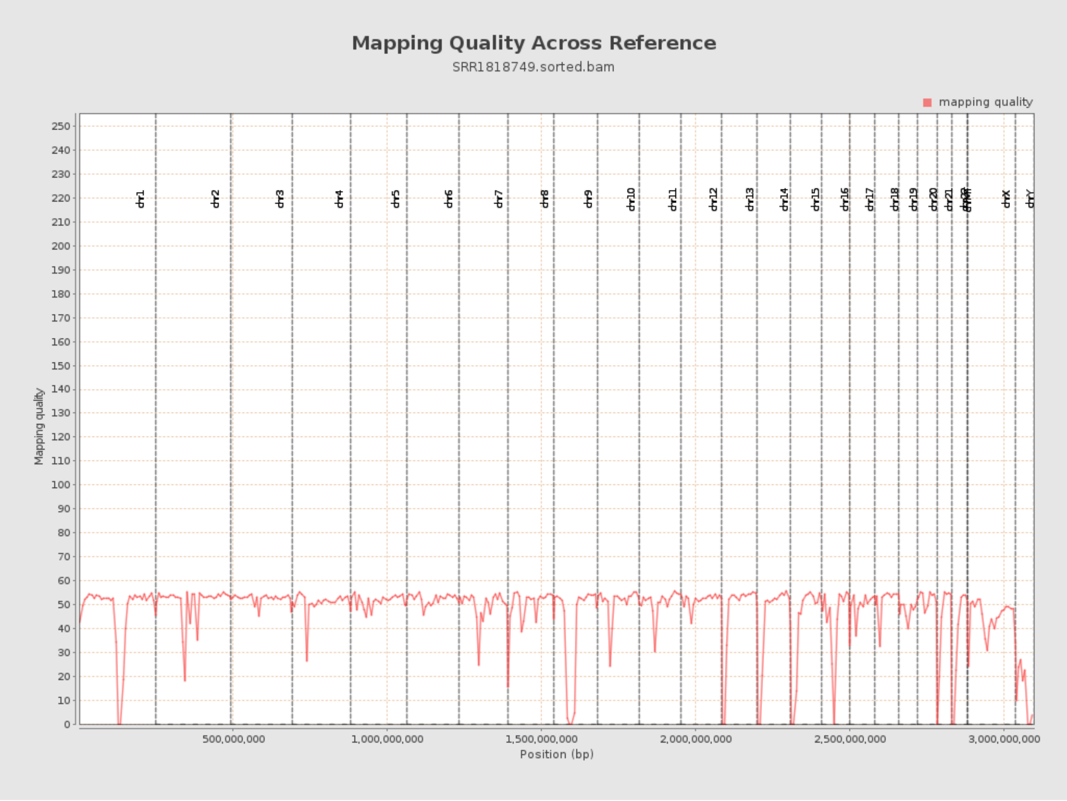
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram