Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:29:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525017.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_SRR10525017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:29:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,656,385
Mapped reads	1,508,365 / 91.06%
Unmapped reads	148,020 / 8.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,054 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	46,079 / 2.78%
Duplication rate	2.14%
Clipped reads	1,510,958 / 91.22%

2.2. ACGT Content

Number/percentage of A's	20,864,144 / 24.17%
Number/percentage of C's	15,991,831 / 18.52%
Number/percentage of T's	27,847,024 / 32.26%
Number/percentage of G's	21,622,881 / 25.05%
Number/percentage of N's	778 / 0%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.258

2.4. Mapping Quality

Mean Mapping Quality	43.69

2.5. Mismatches and indels

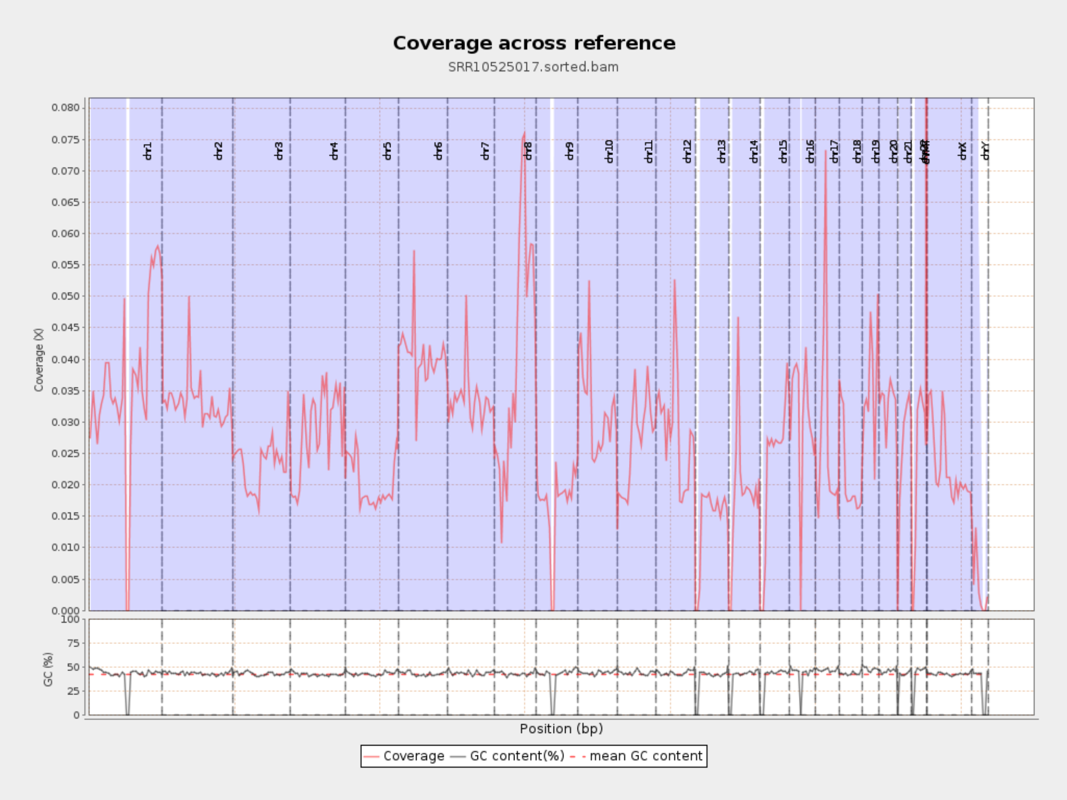
General error rate	0.5%
Mismatches	424,647
Insertions	5,051
Mapped reads with at least one insertion	0.33%
Deletions	16,601
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.8%

2.6. Chromosome stats

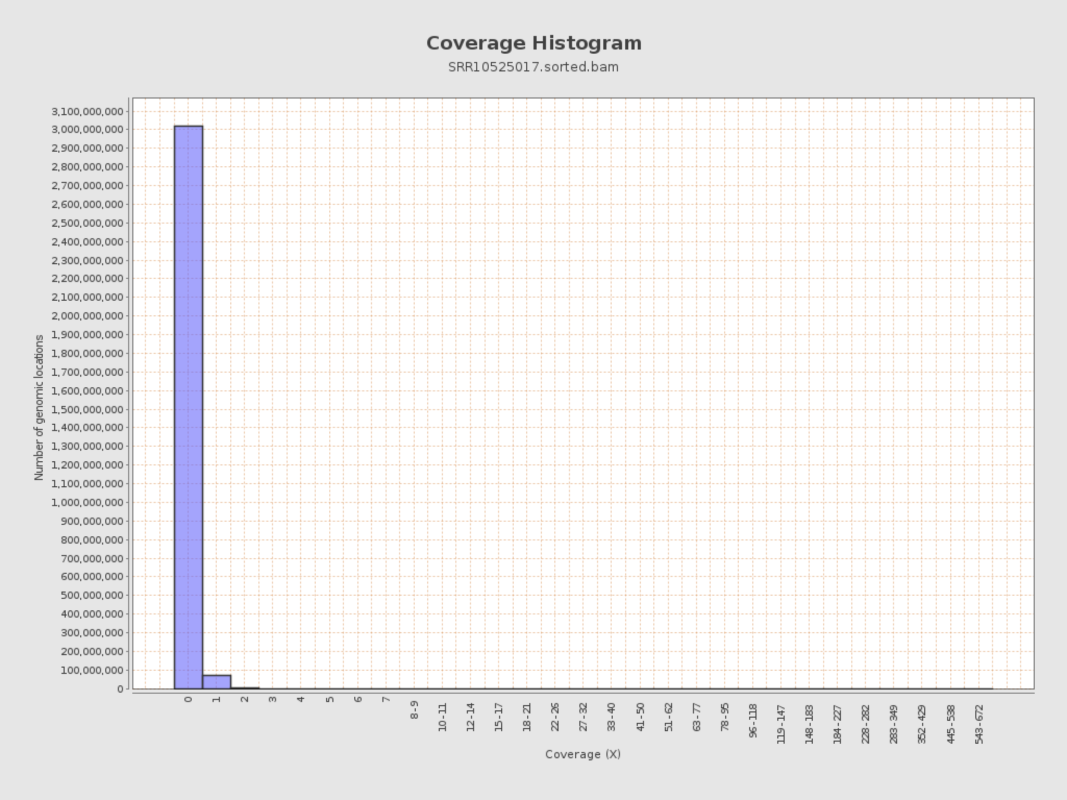
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9017808	0.0362	0.4821
chr2	243199373	8080611	0.0332	0.307
chr3	198022430	4627134	0.0234	0.1655
chr4	191154276	5463634	0.0286	0.1972
chr5	180915260	3660164	0.0202	0.1557
chr6	171115067	6943198	0.0406	0.2927
chr7	159138663	5355947	0.0337	0.3349

chr8	146364022	5945380	0.0406	0.2609
chr9	141213431	2364038	0.0167	0.1917
chr10	135534747	4368253	0.0322	0.2537
chr11	135006516	3570827	0.0264	0.2236
chr12	133851895	3800519	0.0284	0.1841
chr13	115169878	1647622	0.0143	0.1288
chr14	107349540	1983498	0.0185	0.1533
chr15	102531392	2378310	0.0232	0.1771
chr16	90354753	2763724	0.0306	0.1973
chr17	81195210	2238207	0.0276	0.2339
chr18	78077248	1680343	0.0215	0.3028
chr19	59128983	2136319	0.0361	0.3095
chr20	63025520	2079172	0.033	0.197
chr21	48129895	1228343	0.0255	0.1806
chr22	51304566	1153667	0.0225	0.1593
chrMT	16571	10864	0.6556	0.9224
chrX	155270560	3620389	0.0233	0.1921
chrY	59373566	236390	0.004	0.1014

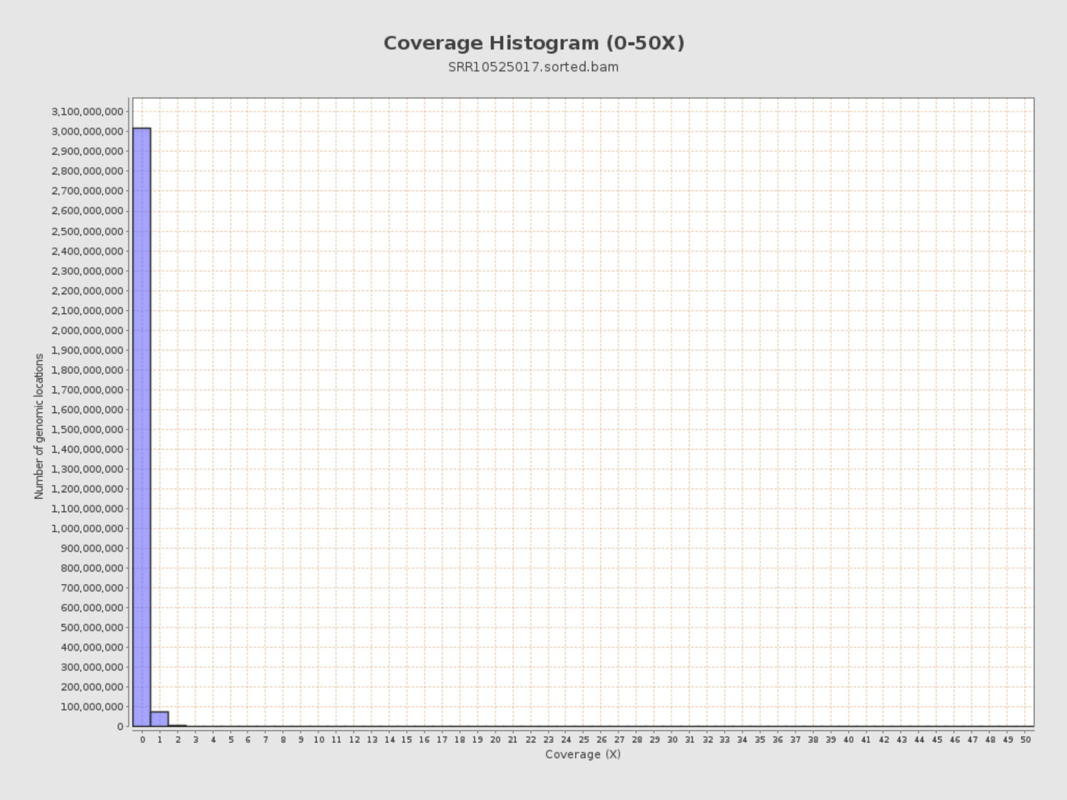
3. Results : Coverage across reference



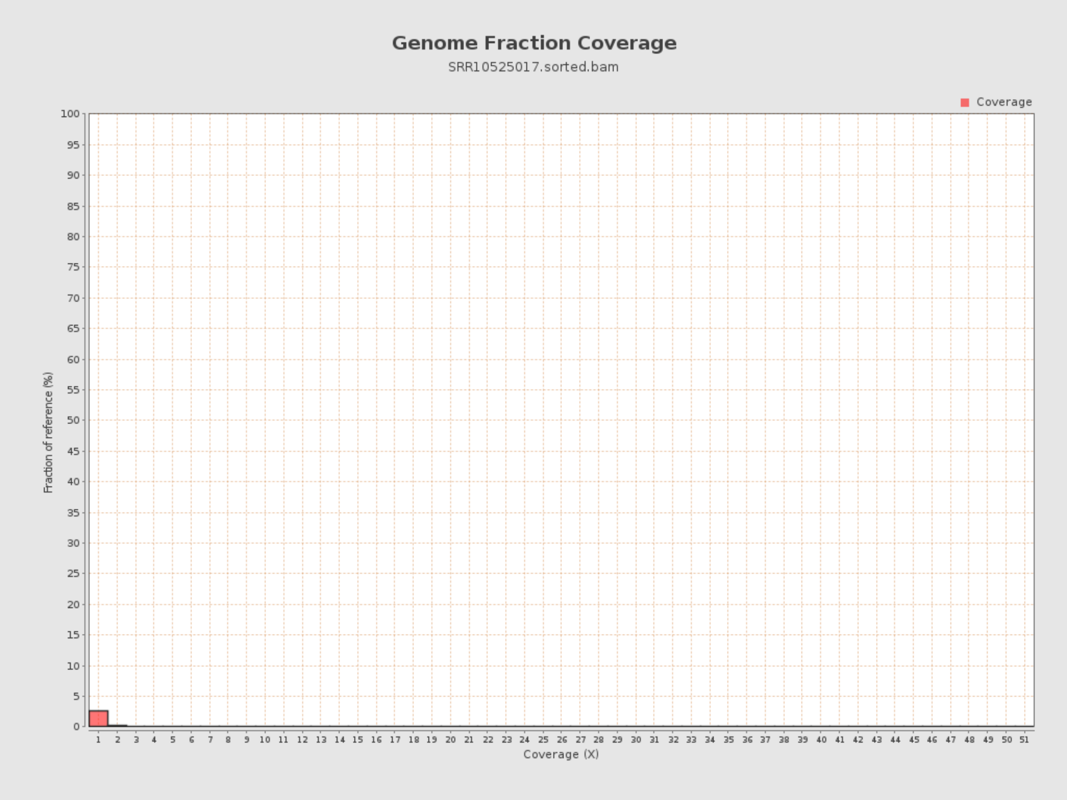
4. Results : Coverage Histogram



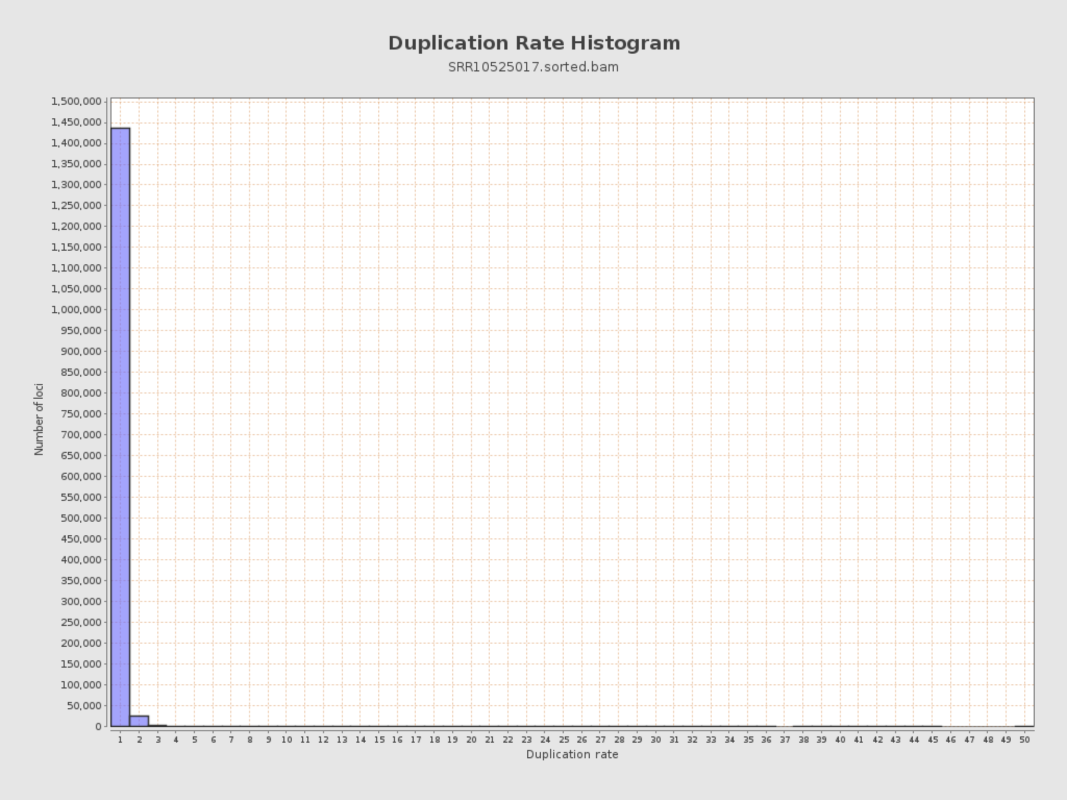
5. Results : Coverage Histogram (0-50X)



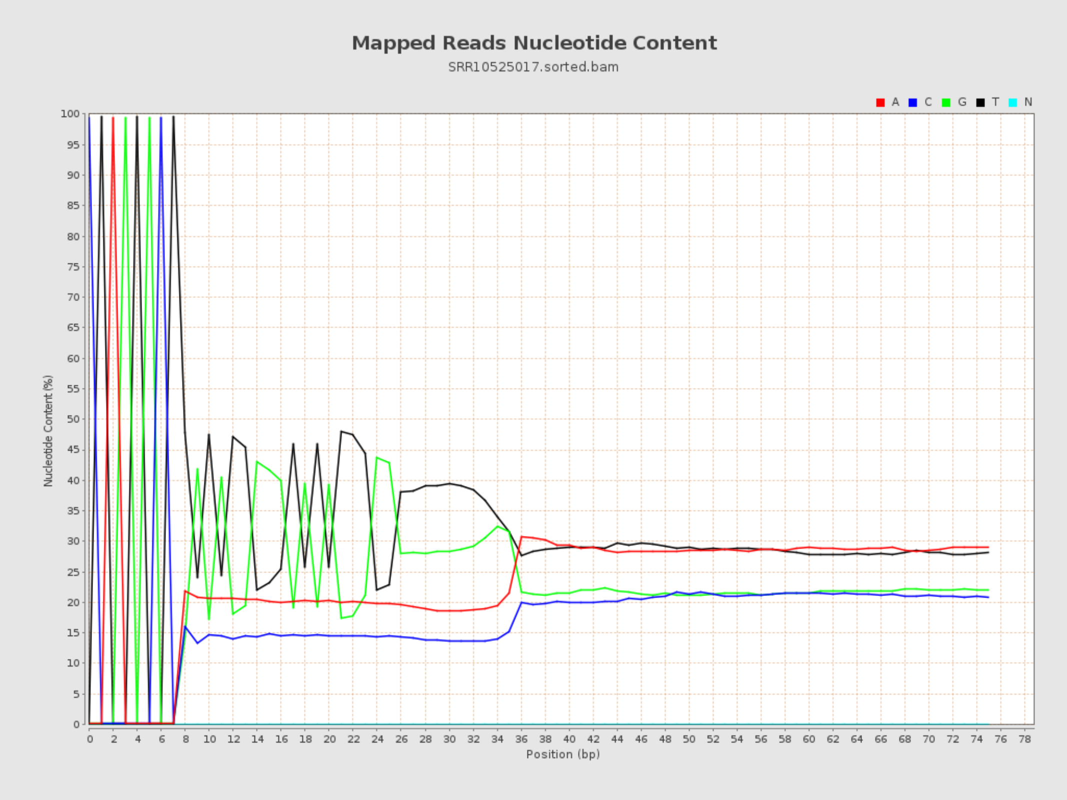
6. Results : Genome Fraction Coverage



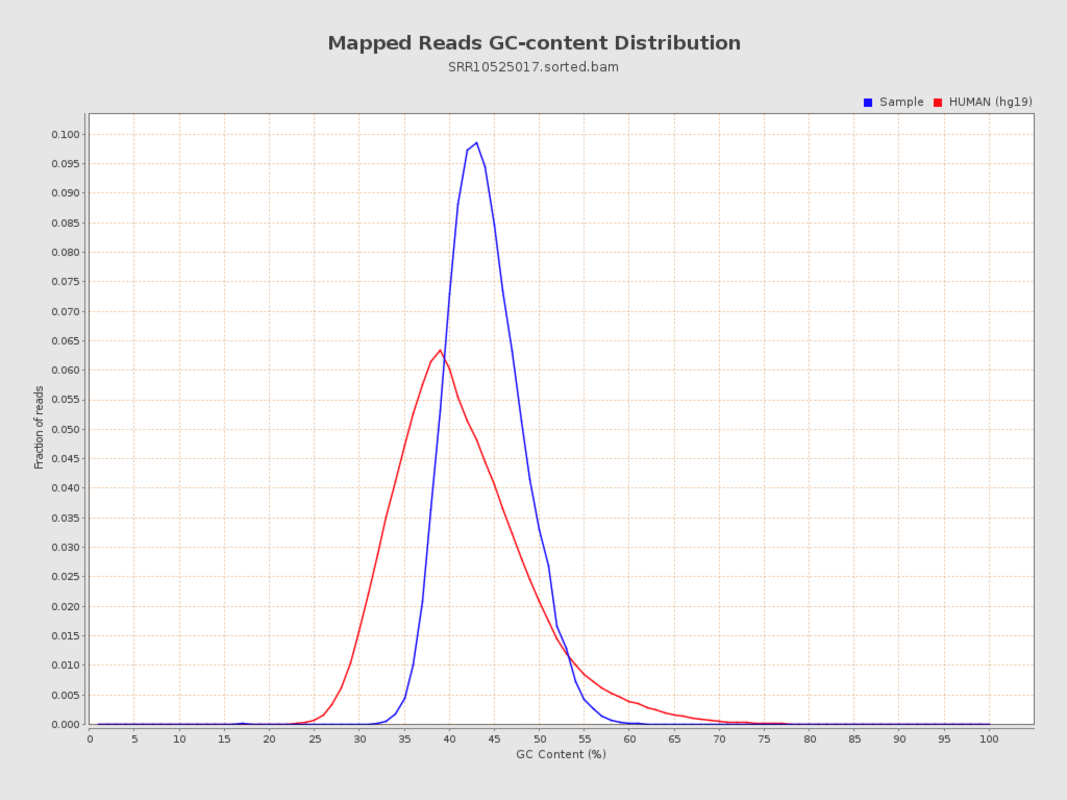
7. Results : Duplication Rate Histogram



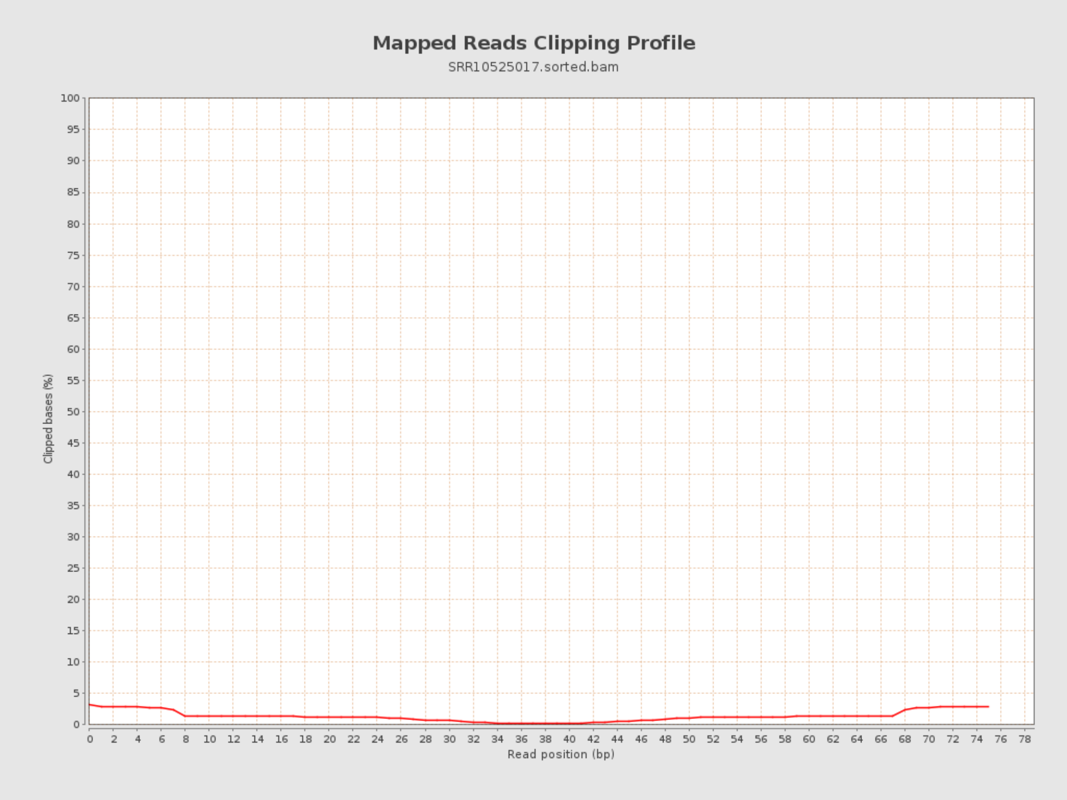
8. Results : Mapped Reads Nucleotide Content



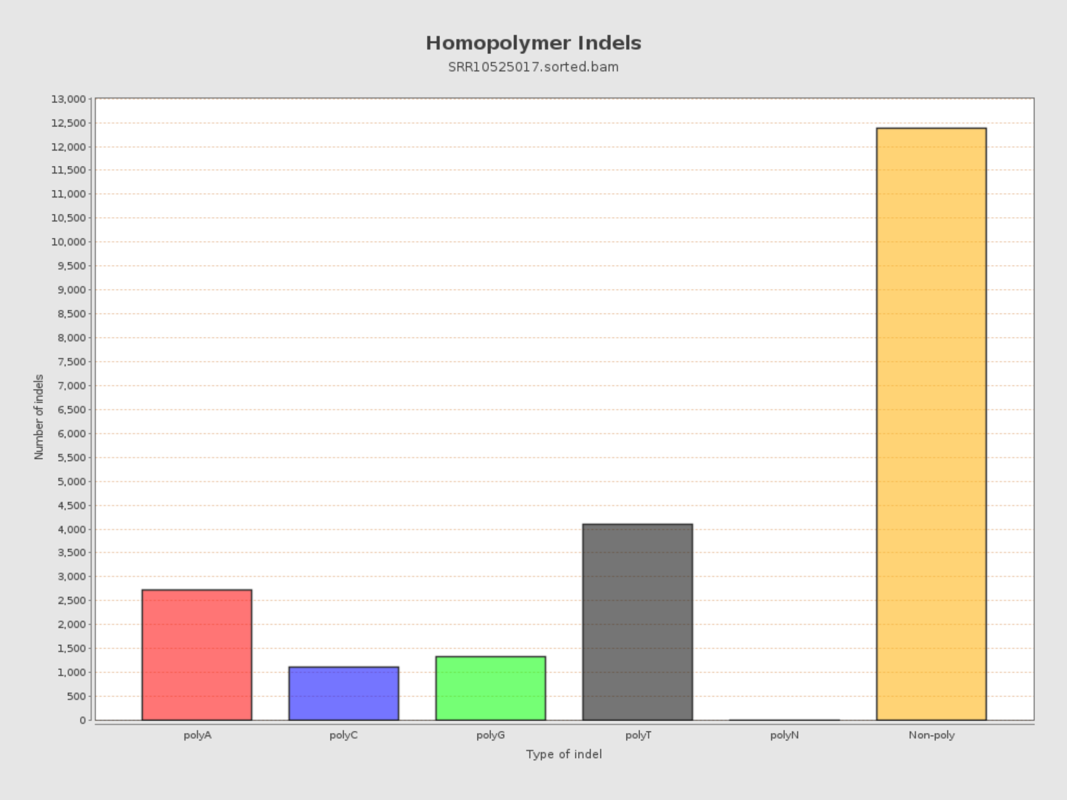
9. Results : Mapped Reads GC-content Distribution



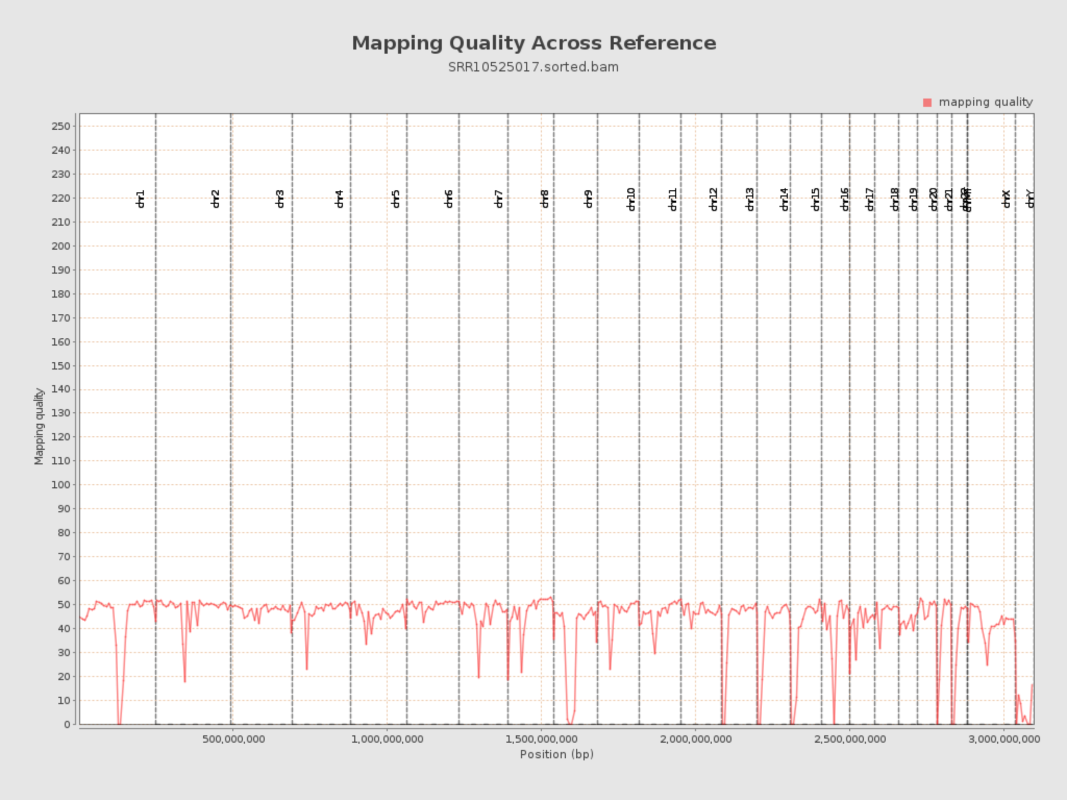
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram