Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 13:39:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089577.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_SRR089577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089577.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 13:39:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,423,807
Mapped reads	8,985,115 / 86.2%
Unmapped reads	1,438,692 / 13.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	309 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	941,430 / 9.03%
Duplication rate	8.18%
Clipped reads	972,481 / 9.33%

2.2. ACGT Content

Number/percentage of A's	122,429,125 / 29%
Number/percentage of C's	89,513,499 / 21.21%
Number/percentage of T's	120,100,971 / 28.45%
Number/percentage of G's	90,072,554 / 21.34%
Number/percentage of N's	12,198 / 0%
GC Percentage	42.54%

2.3. Coverage

Mean	0.1364

Standard Deviation	0.8433

2.4. Mapping Quality

Mean Mapping Quality	44.74

2.5. Mismatches and indels

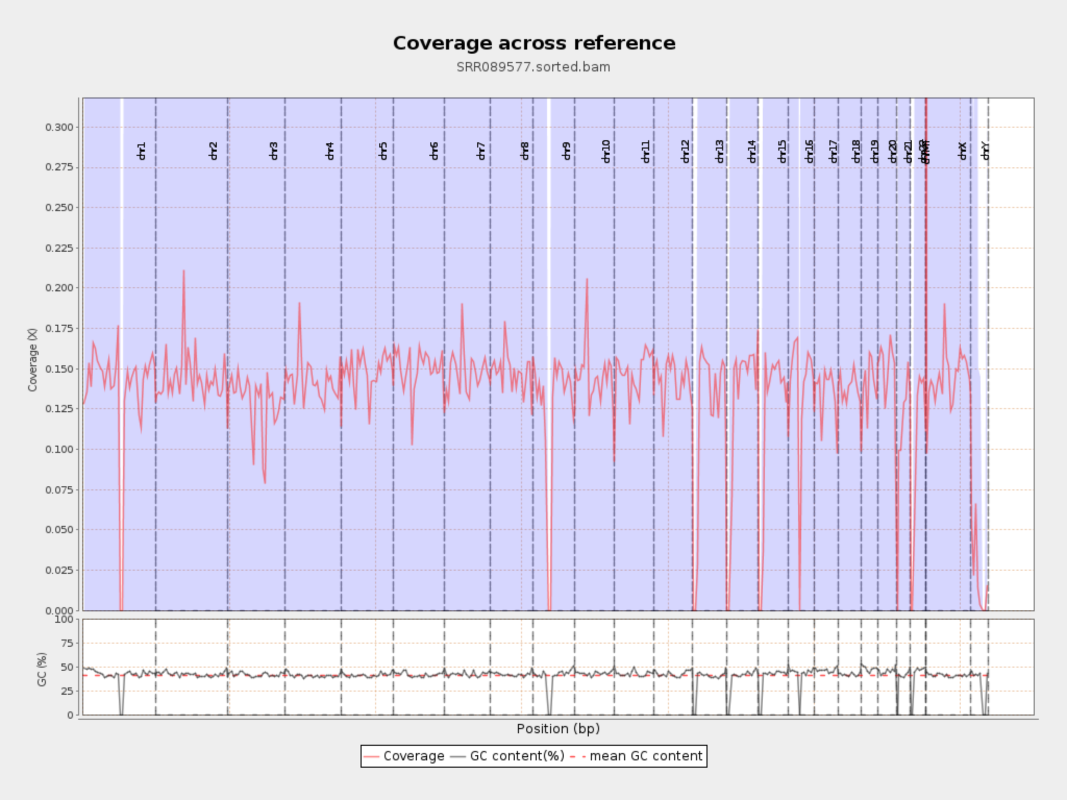
General error rate	0.43%
Mismatches	1,807,777
Insertions	16,235
Mapped reads with at least one insertion	0.18%
Deletions	55,850
Mapped reads with at least one deletion	0.62%
Homopolymer indels	44.53%

2.6. Chromosome stats

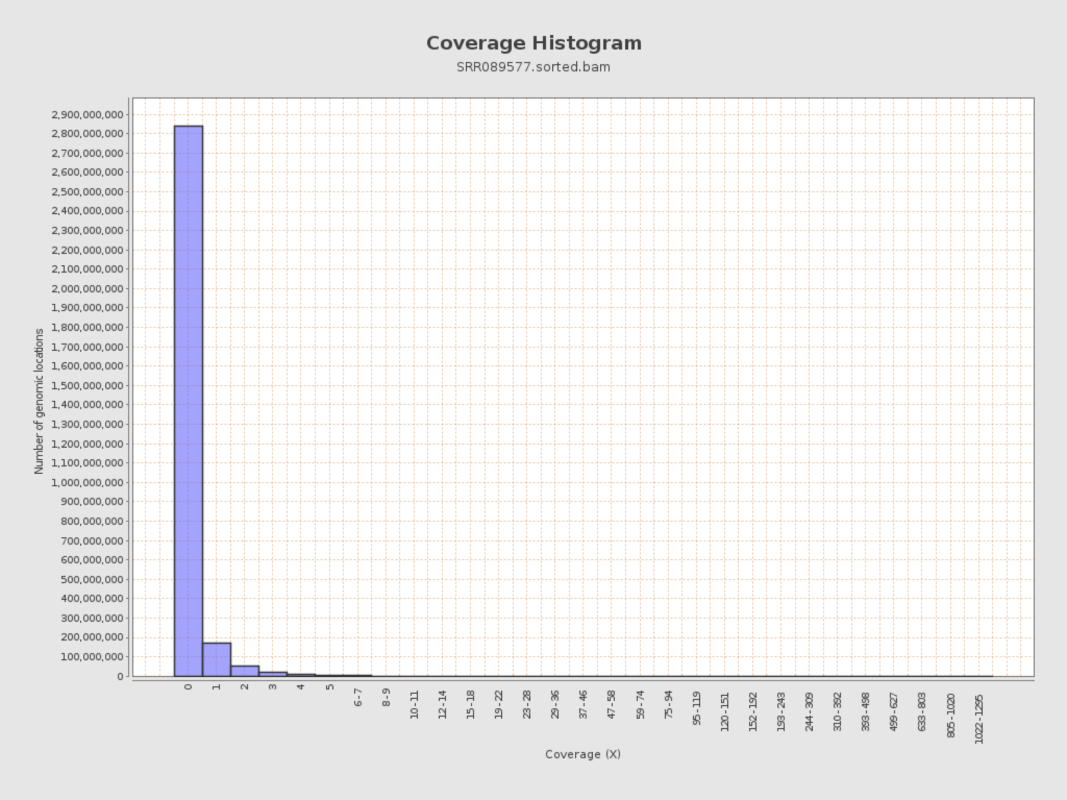
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34172546	0.1371	1.1383
chr2	243199373	35318181	0.1452	1.2295
chr3	198022430	25462171	0.1286	0.5543
chr4	191154276	27378674	0.1432	0.6442
chr5	180915260	26911603	0.1488	0.6068
chr6	171115067	25735991	0.1504	0.7285
chr7	159138663	23533729	0.1479	1.1311

chr8	146364022	21576855	0.1474	0.9072
chr9	141213431	17439394	0.1235	0.7936
chr10	135534747	19821813	0.1462	0.8731
chr11	135006516	19926237	0.1476	0.8377
chr12	133851895	19304664	0.1442	0.6327
chr13	115169878	13926947	0.1209	0.5439
chr14	107349540	13558894	0.1263	0.7146
chr15	102531392	12009983	0.1171	0.5327
chr16	90354753	12207527	0.1351	0.6427
chr17	81195210	11097832	0.1367	0.6617
chr18	78077248	10831262	0.1387	1.2614
chr19	59128983	8285060	0.1401	1.1159
chr20	63025520	9480019	0.1504	0.6639
chr21	48129895	5403291	0.1123	0.6423
chr22	51304566	4969857	0.0969	0.4876
chrMT	16571	126916	7.6589	7.4584
chrX	155270560	22516129	0.145	0.7488
chrY	59373566	1216101	0.0205	0.4112

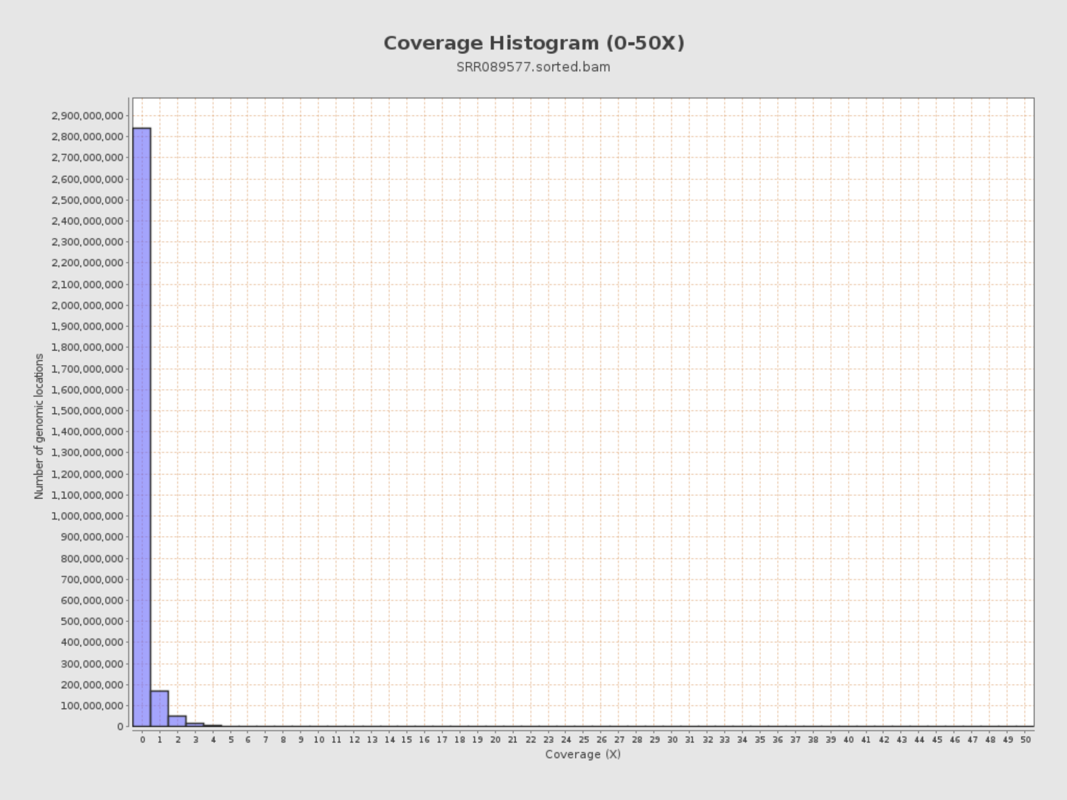
3. Results : Coverage across reference



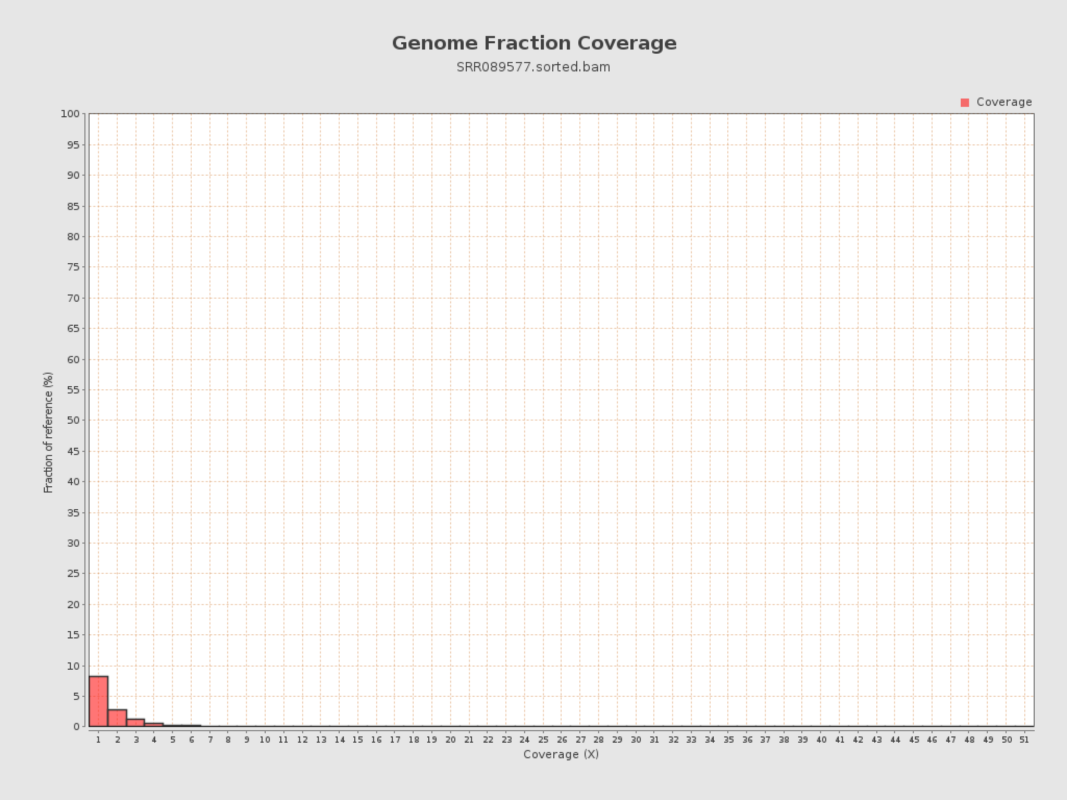
4. Results : Coverage Histogram



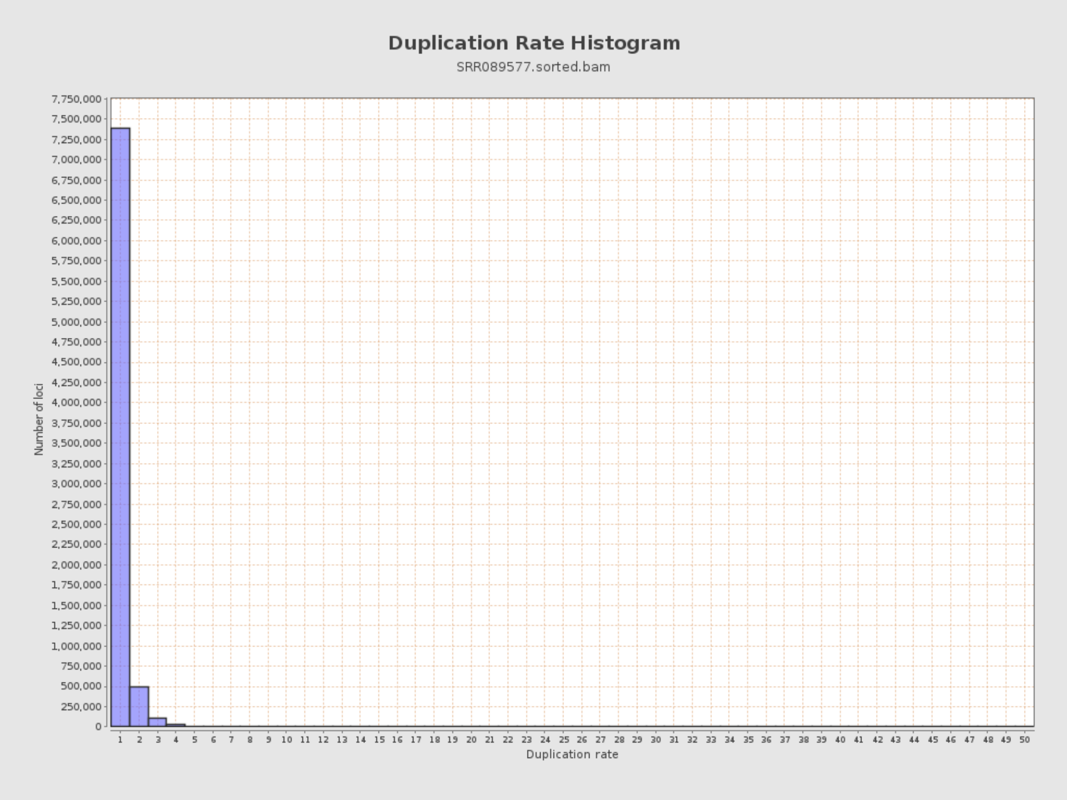
5. Results : Coverage Histogram (0-50X)



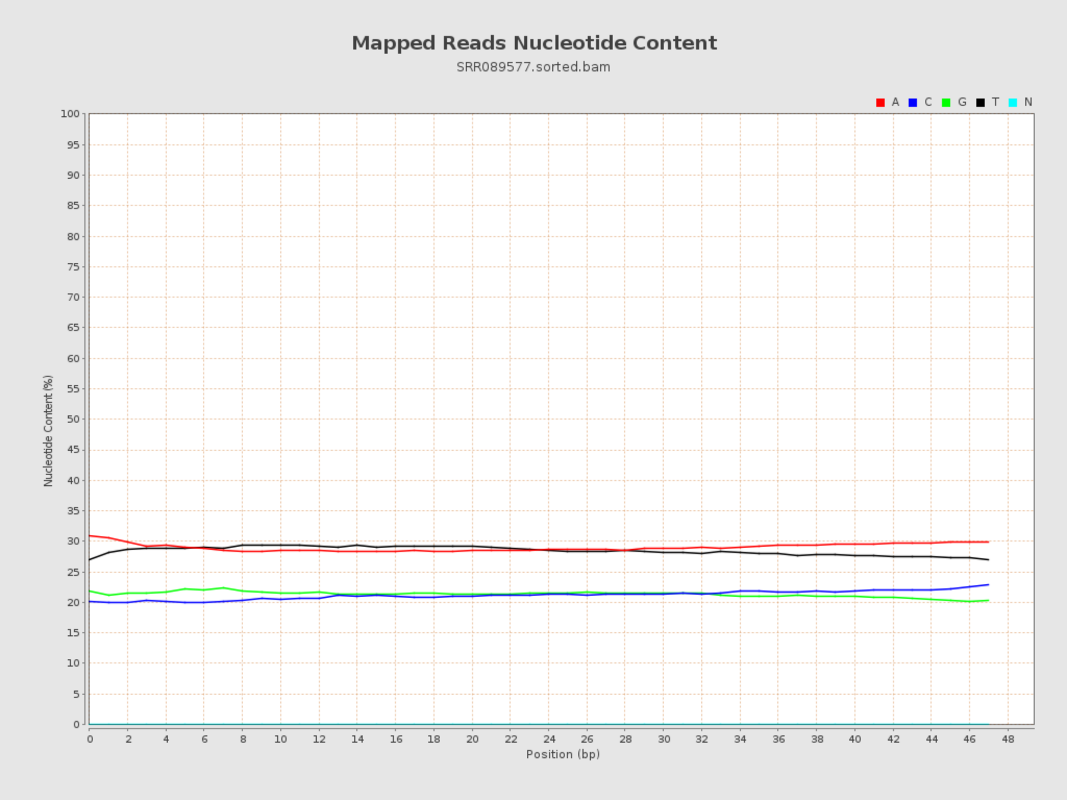
6. Results : Genome Fraction Coverage



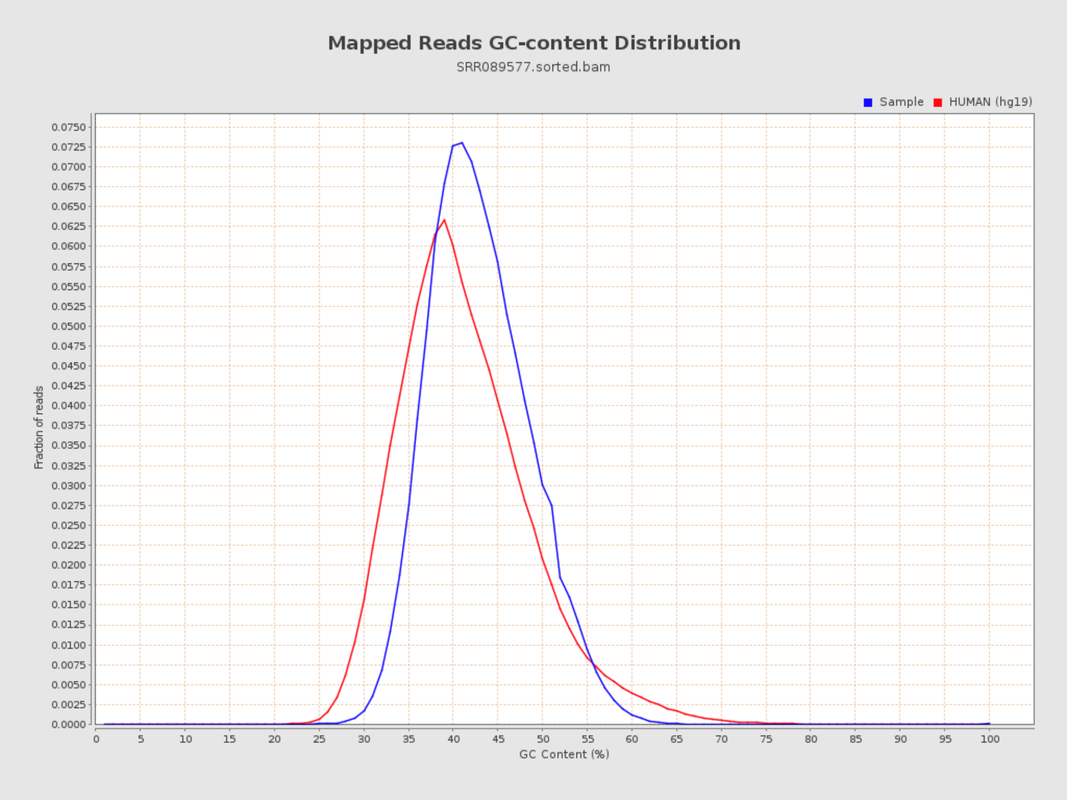
7. Results : Duplication Rate Histogram



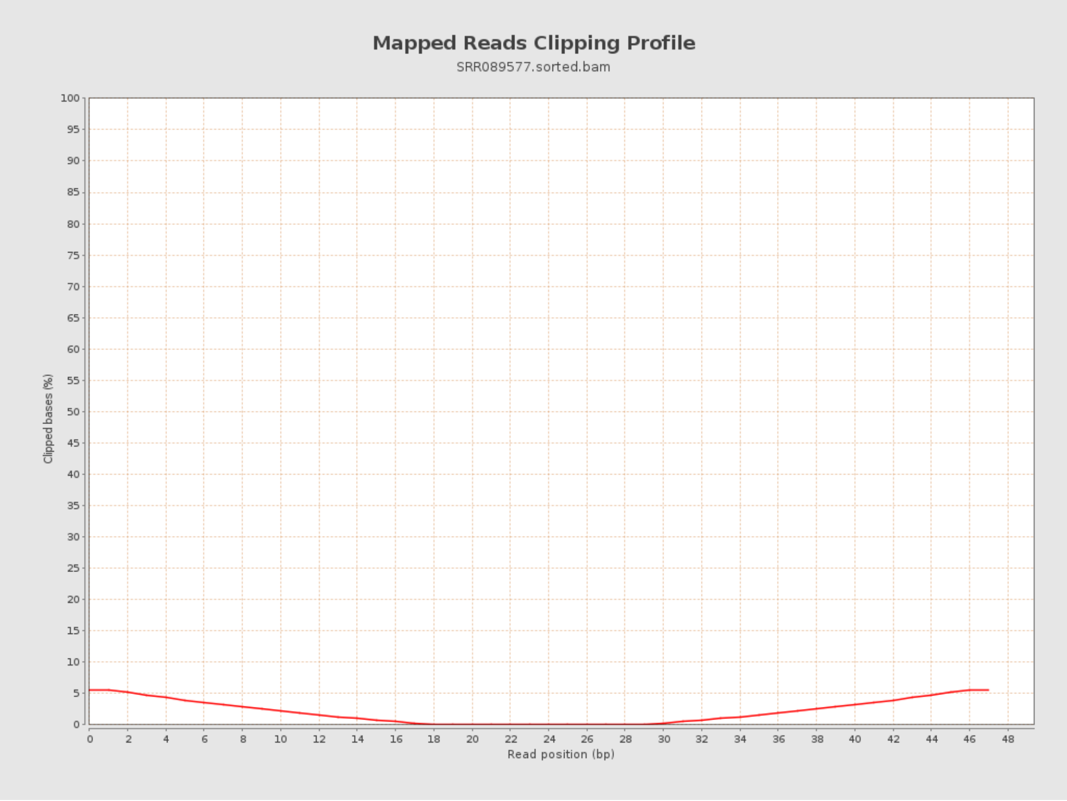
8. Results : Mapped Reads Nucleotide Content



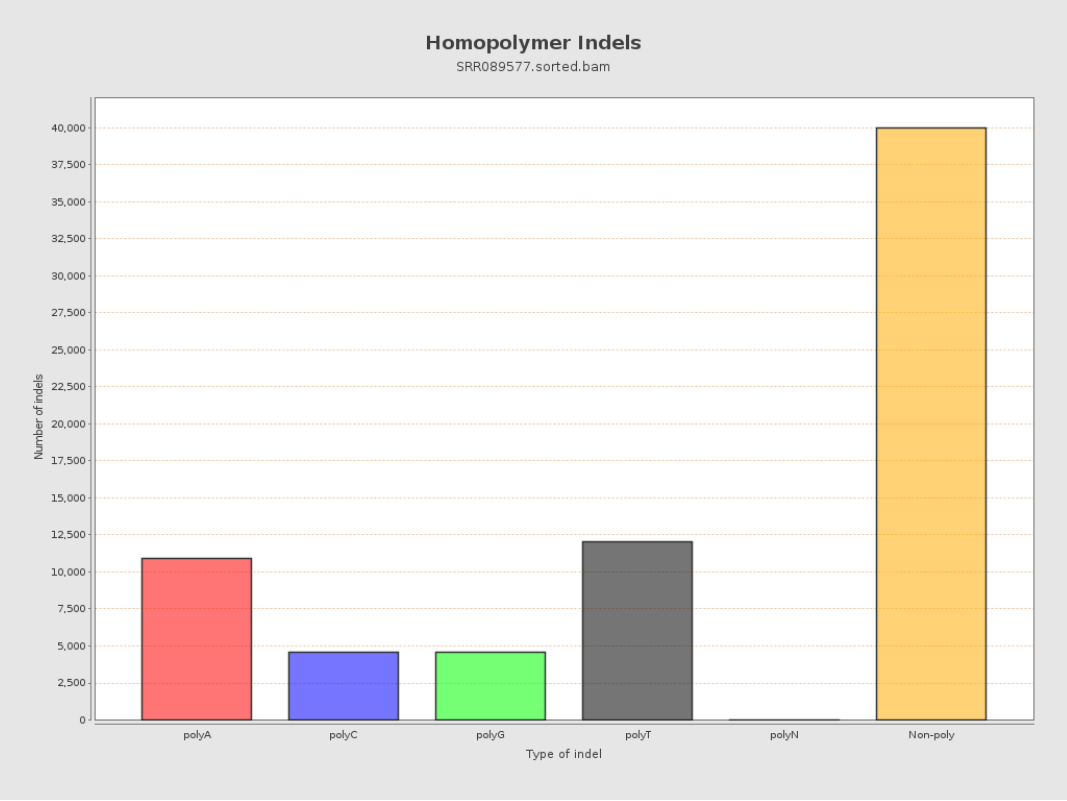
9. Results : Mapped Reads GC-content Distribution



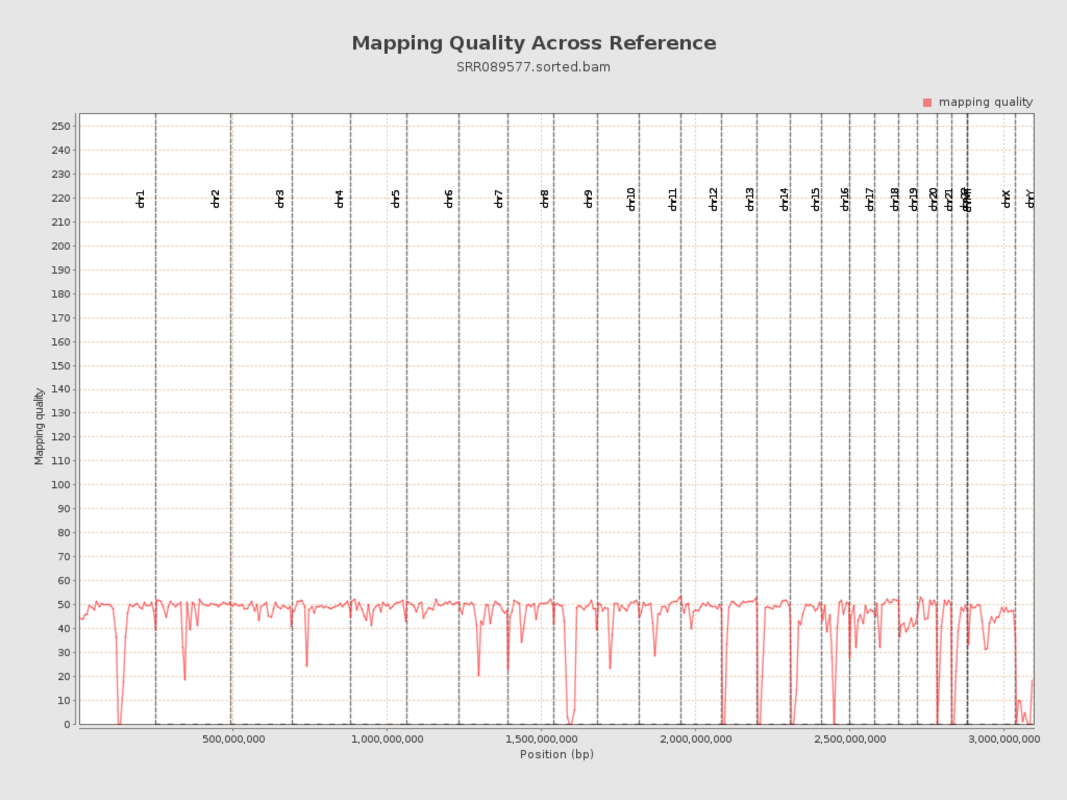
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram