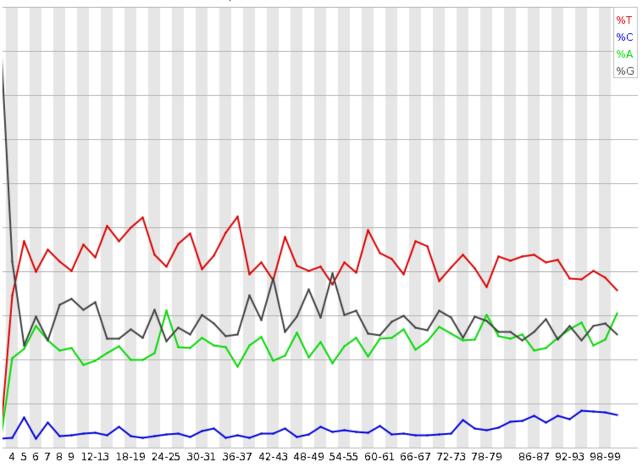
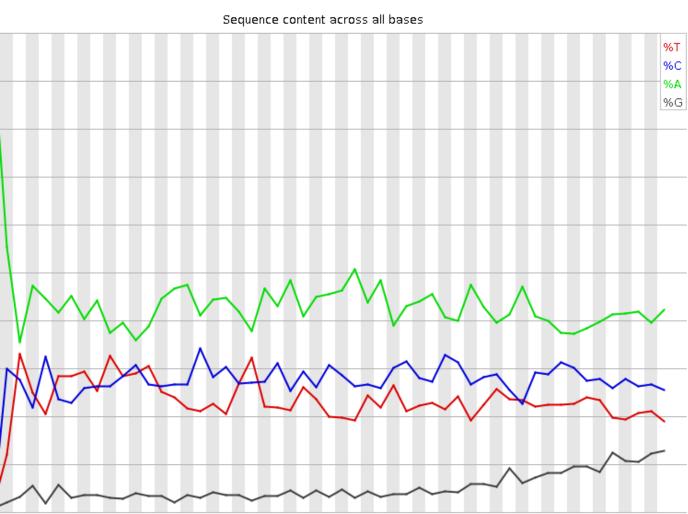
Sequence content across all bases



4 5 6 7 8 9 12-13 18-19 24-25 30-31 36-37 42-43 48-49 54-55 60-61 66-67 72-73 78-79 86-87 92-93 98-99 Read 1 Position in read (bp)



4 5 6 7 8 9 12-13 18-19 24-25 30-31 36-37 42-43 48-49 54-55 60-61 66-67 72-73 78-79 86-87 92-93 98-99 Position in read (bp)

Read2