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All other comments are mine. A: It would be easier to use Unix command, like this: $ head. | tr ' ''' | cut -d " " -f 1 | tr -d "$" .tst rarrar.dts for example. You can see all the patterns in.tst file, and you can use: $ grep -n '^[^;]*;'.tst to find the line that match with the pattern. Here we use the command without echo argument, it means that the text would be output, so we can view it: $ head. | tr ' ''' | cut -d " " -f 1 | tr -d "$" | less .tst rarrar.dts We can use: $ grep -n '^[^;]*;'.tst to find the number of lines that matches the pattern. However, you can use awk instead, like this: $ head. | awk -F'[;|]]' '/^[^;]*;/{ sub(/^[^;]*;/,""); print $1}' We can view the output with: $ awk -F'[;|]]' '/^[^;]*;/{ sub(/^[^;]*;/,""); print $1}'.tst or with other awk's options. The clinical and molecular genetics of microphthalmia with linear skin defects (MLS). MLS is a genetic disorder characterized by microphthalmia and linear skin defects. In this report, we examine the clinical and genetic heterogeneity of this disorder. Clinical and molecular genetic studies were performed in eight families. A quantitative trait locus (QTL) of the microphthalmia phenotype has been identified in multiplex families on chromosome 4q35. Another QTL for linear skin defects has been identified on chromosome 7p13. Additional evidence of a "double QTL" for microphthalmia and linear skin defects on chromosomes 5 and 7 has been obtained. The results of the genetic analysis, cellular expression patterns of the candidate gene NIPAL1 in MLS and a clinical study of patients with NIPAL1 mutations are discussed.