Lung Pre-cancer

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Lung cancer is the most common form of cancer as 12.3 % of all cancers (Minna, Roth, & Gazdar, 2002).
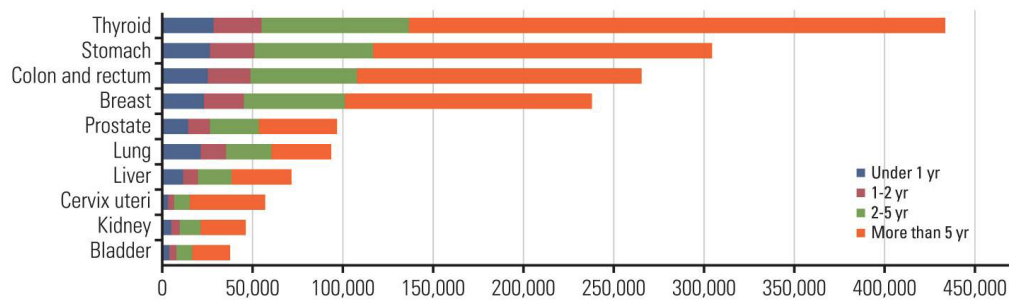
Figure 1: Common cancer survival rates (Hong et al., 2021)

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Carcinoma *in situ* (CIS)

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Adenocarcinoma *in situ* (AIS)

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Atypical adenomatous hyperplasia (AAH)

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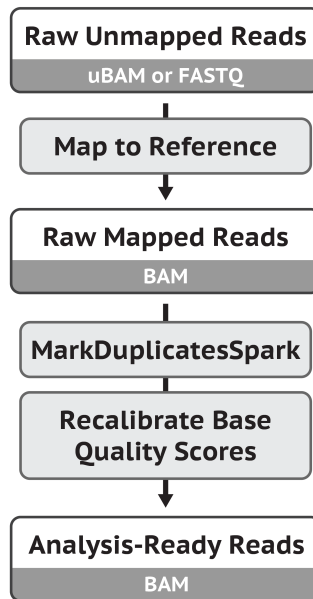Minimally invasive adenocarcinoma (MIA)

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DePristo, M. A., Banks, E., Poplin, R., Garimella, K. V., Maguire, J. R., Hartl, C., ... others (2011). A framework for variation discovery and genotyping using next-generation dna sequencing data. *Nature genetics*, *43*(5), 491.

Hong, S., Won, Y.-J., Lee, J. J., Jung, K.-W., Kong, H.-J., Im, J.-S., ... others (2021). Cancer statistics in korea: Incidence, mortality, survival, and prevalence in 2018. *Cancer Research and Treatment: Official Journal of Korean Cancer Association*, *53*(2), 301.

Minna, J. D., Roth, J. A., & Gazdar, A. F. (2002). Focus on lung cancer. *Cancer cell*, *1*(1), 49–52.

Van der Auwera, G. A., Carneiro, M. O., Hartl, C., Poplin, R., Del Angel, G., Levy-Moonshine, A., ... others (2013). From fastq data to high-confidence variant calls: the genome analysis toolkit best practices pipeline. *Current protocols in bioinformatics*, *43*(1), 11–10.
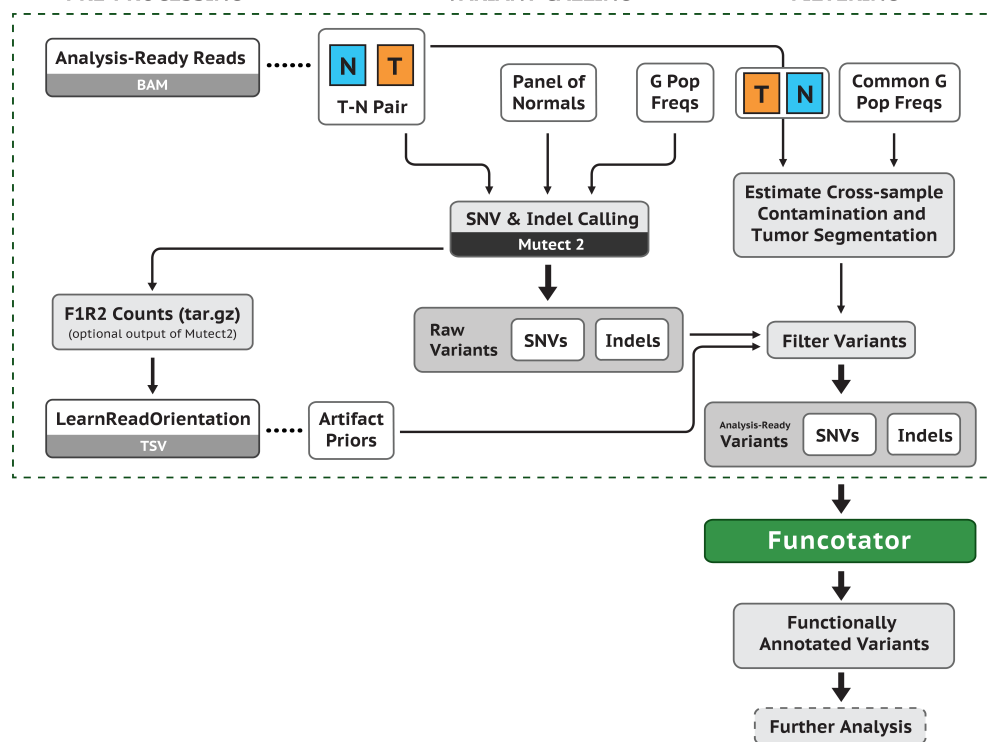
Figure 3: Somatic short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)
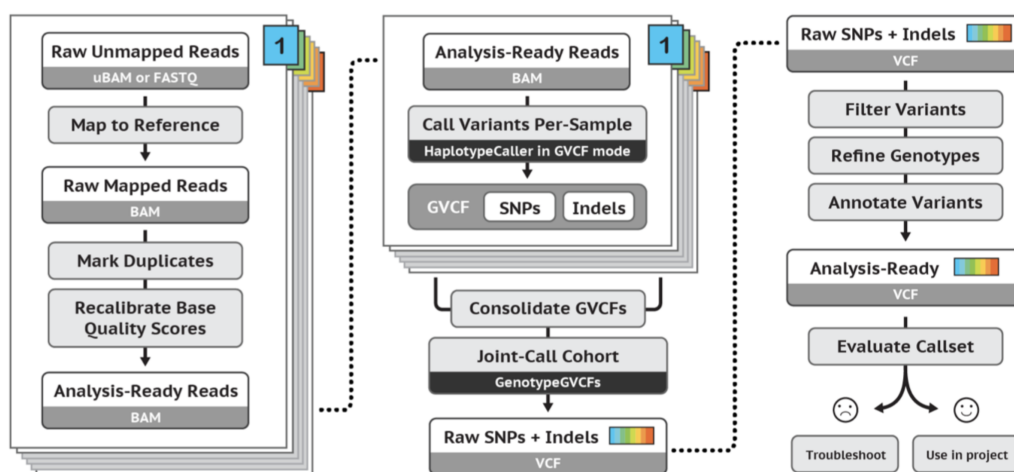

Figure 4: Germline short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)
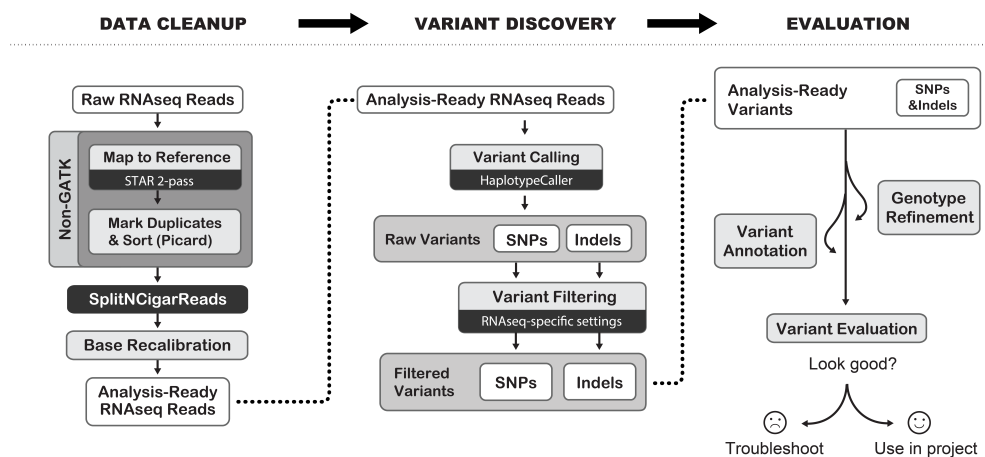
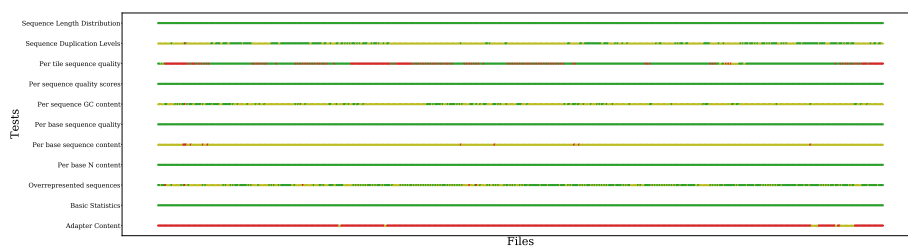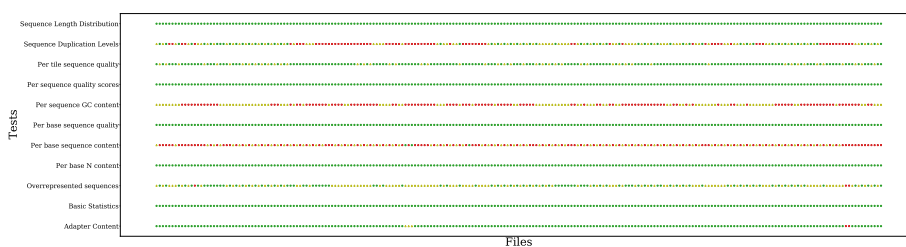Figure 5: RNA-seq short variant discovery workflow (Van der Auwera et al., 2013; DePristo et al., 2011)

Figure 6: FastQC results with WES data

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