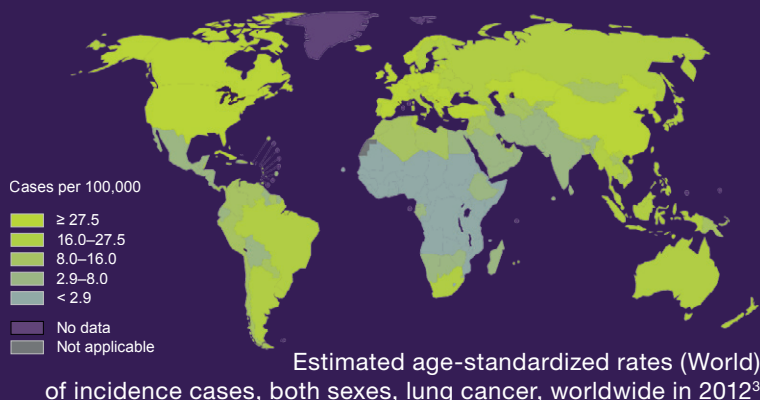


GLOBALLY, LUNG CANCER IS THE MOST COMMONLY DIAGNOSED TYPE OF CANCER...^{1,2}



...BUT LUNG CANCER IS NOT ONE DISEASE⁴



Small cell lung carcinoma	15%
Non-small cell carcinoma	80-85%
Adenocarcinoma	40%
Squamous cell carcinoma	30%
Large cell carcinoma	10%
Other	3%

Research has shown that there are a variety of different biomarkers associated with non-small cell lung cancer. Some biomarkers arise as a result of point mutations, and some reflect a range of protein expression. Both types can be used to help determine treatment options, and include:^{5,6}

10-40%*

The EGFR gene may play a role in cancer cell growth^{5,7}

10-25%*

KRAS gene mutations can cause cells to grow and divide in an uncontrolled manner^{8,9}

4-7%

The ALK gene, when rearranged, can result in tumour growth^{6,10}

2-4%

MET activation, through mutation or gene amplification, can drive growth of tumour cells^{11,12}

19%-100%¹⁴

Expression of **programmed death-ligand 1 (PD-L1)**, a protein expressed on the surface of cancer cells that helps them evade the immune system, may also help characterise the diversity of advanced NSCLC. Aberrant expression of PD-L1 has been found ranging from 19% to 100% of NSCLC patients.¹³⁻¹⁵

Lung cancer is staged on a scale of I to IV, according to the severity of disease:¹⁶

Stage I

Cancer is <5cm, localised and has not spread to lymph nodes

Stage II

Cancer is 5-7cm, localised and has potentially spread to lymph nodes close to the affected lung, the bronchus or pleura

Stage III

Cancer is >7cm, localised and has potentially spread to a major structure within the chest

Stage IV

Cancer is in both lungs or has metastasised to another part of the body or has caused a fluid collection around the lung or heart that contains cancer cells

Recommended treatments can vary depending on the stage of the lung cancer; however due to late manifestation of symptoms, a large proportion of lung cancer patients are diagnosed at Stage IV.¹⁷

* EGFR and KRAS gene mutations vary between ethnic populations. EGFR mutations are more prevalent among Asian populations (30-40%) as opposed to Caucasian populations (10-12%).^{5,6} The reverse is true for KRAS mutations (5-15% for Asian populations, 25-50% for Caucasian populations).¹⁸

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