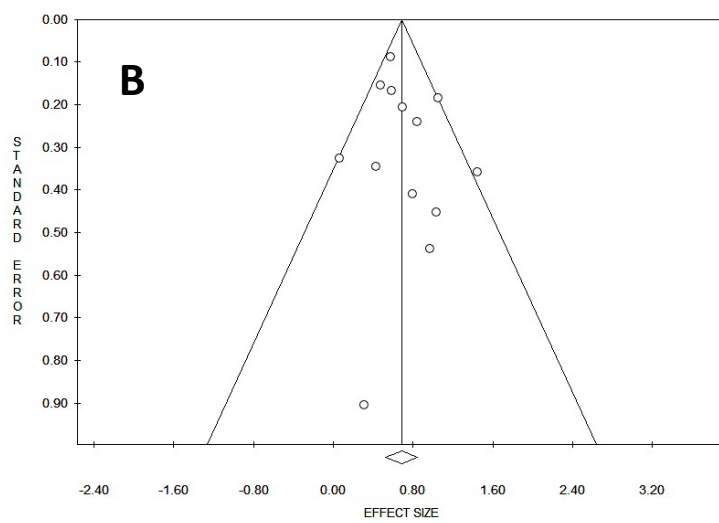
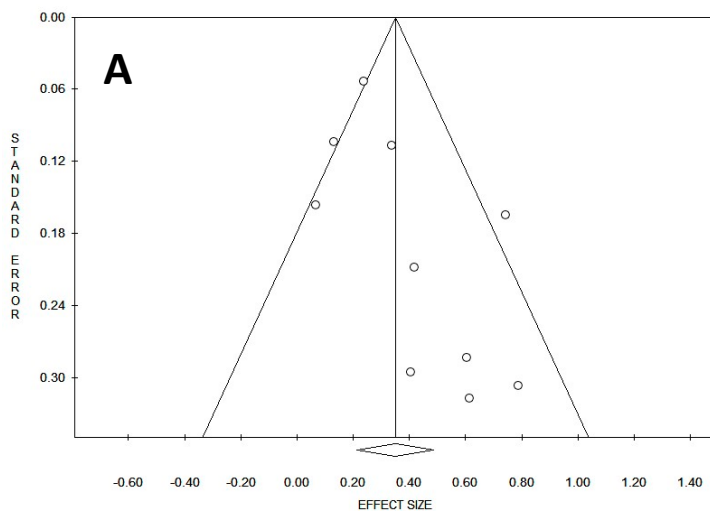




Supplementary Table S1. list of articles excluded from the meta-analysis and reasons for exclusion.

List of articles excluded	Reasons for exclusion (numbers)
Teng et al., 2023 [3]	Genetically predicted LTL by Mendelian randomization (7)
Cortez Cardoso Penha et al., 2023 [6]	
Gao et al., 2020 [9]	
Cao et al., 2019 [10]	
Kachuri et al., 2019 [11]	
Haycock et al., 2017 [14]	
Zhang et al., 2015 [16]	
Shiraishi et al., 2024 [1]	Genetically predicted LTL by SNPs variants (5)
Bhat et al., 2023 [4]	
Chang et al., 2021 [7]	
Rode et al., 2016 [15]	
Machiela et al., 2015 [18]	
Xue et al., 2020 [8]	Retrospective case-control (6)
Sun et al., 2015 [19]	
Sanchez-Espiridion et al., 2014 [20]	
Jang et al., 2008 [24]	
Wu et al., 2003 [25]	
Hosgood et al., 2009 [23]	
Belić et al., 2023 [5]	Not reporting the risk of lung cancer (outcome of interest) (4)
Autsavapromporn et al., 2018 [12]	
Willeit et al., 2010 [22]	
Weischer et al., 2013 [25]	
Doherty et al., 2018 [13]	Lung cancer mortality (1)
Fernández-Marcelo et al., 2015 [17]	DNA not extracted form blood (1)
Córdoba-Lanús et al., 2024 [2]	Considering subjects with COPD (1)

1. Shiraishi, K.; Takahashi, A.; Momozawa, Y.; Daigo, Y.; Kaneko, S.; Kawaguchi, T.; Kunitoh, H.; Matsumoto, S.; Horinouchi, H.; Goto, A.; et al. Identification of telomere maintenance gene variations related to lung adenocarcinoma risk by genome-wide association and whole genome sequencing analyses. *Cancer Commun (Lond)* **2024**, *44*, 287-293.
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