1308 ARTIFICIAL INTELLIGENCE (AI)-POWERED IMMUNE PHENOTYPING BASED ON PROGRAMMED DEATH LIGAND 1 (PD-L1) IMMUNOHISTOCHEMISTRY (IHC) IN TRIPLE NEGATIVE BREAST CANCER (TNBC)

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Background The tumor microenvironment has recently become important in cancer and immune phenotype (IP) has been proposed as a way to assess it. A variety of methods to assess IP in tumor tissue were proposed, mostly from histology slides of IHC including CD3 and CD8 or hematoxylin and eosin (H&E). However, methodology based on spatial tumor-infiltrating lymphocyte (TIL) analysis in PD-L1 IHC has been rarely investigated. Here, we performed AI-based IP classification in TNBC using PD-L1 22C3 IHC whole slide images (WSIs) as well as PD-L1 combined positive score (CPS) and its positivity.

Methods We employed Lunit SCOPE IO, an AI-powered H&E analyzer for spatial TIL analysis, identifying and quantifying TIL within cancer or stromal areas in H&E slides. For PD-L1 IHC analysis, Lunit SCOPE PD-L1 CPS, an AI-powered PD-L1 CPS analyzer was used. This model detects and quantifies PD-L1 status in tumor and immune cells and was developed with $3.35x10^5$ tumor cells and $3.45x10^5$ immune cells from PD-L1 IHC-stained WSI of breast cancer. To validate, 180 pairs of PD-L1 IHC and H&E WSIs from a cohort of TNBC were analyzed. The IPs were classified as inflamed (high TIL density in the cancer area, IIP) or non-inflamed (non-IIP) in H&E and PD-L1 IHC WSIs, using a standardized $0.5x0.5mm^2$ grid for both and a lymphocyte cutoff of 130/mm^2 for AI-based PD-L1 IHC analysis.

Results IPs were classified as inflamed in 69 cases (38.3%) in PD-L1 and 40 cases (22.2%) in H&E. The agreement in IPs between two models was 73.9% (table 1). The median PD-L1 CPS was 10 (interquartile range 2 - 25). AI-based PD-L1 IHC analysis revealed significant differences in median CPS levels between IIP and non-IIP, with values of 32.5 (15.6 - 77.2) and 2.9 (0.6 - 8.6), respectively ($p<0.001$). Moreover, median values of PD-L1 positivity in IIP were significantly higher than in the non-IIP across cell types: tumor cells (14.9% vs. 1.4%, $p<0.001$), lymphocytes (36.2% vs. 14.1%, $p<0.001$), and macrophages (14.9% vs. 9.7%, $p=0.001$).

Conclusions The IP determined by the AI-powered PD-L1 IHC analyzer showed a high concordance rate with the IP determined by the AI-powered H&E analyzer. Moreover, high PD-L1 expression of each respective cell type of tumor, lymphocyte, and macrophage was observed in the IIP. Consistent with previous knowledge of the IP, our PD-L1 results support use of immune-oncology approaches in this phenotype.

Abstract 1308 Table 1 Analysis of IPs by two AI-powered analyzers

		IPs by AI-powered H&E analyzers		
		Inflamed	non-Inflamed	Total
IPs by AI-powered PD-L1 CPS analyzers	Inflamed	31	38	69
	non-Inflamed	9	102	111
	Total	40	140	180

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