Fig. S1, Kim DK, Lee CY, Han YJ et al.

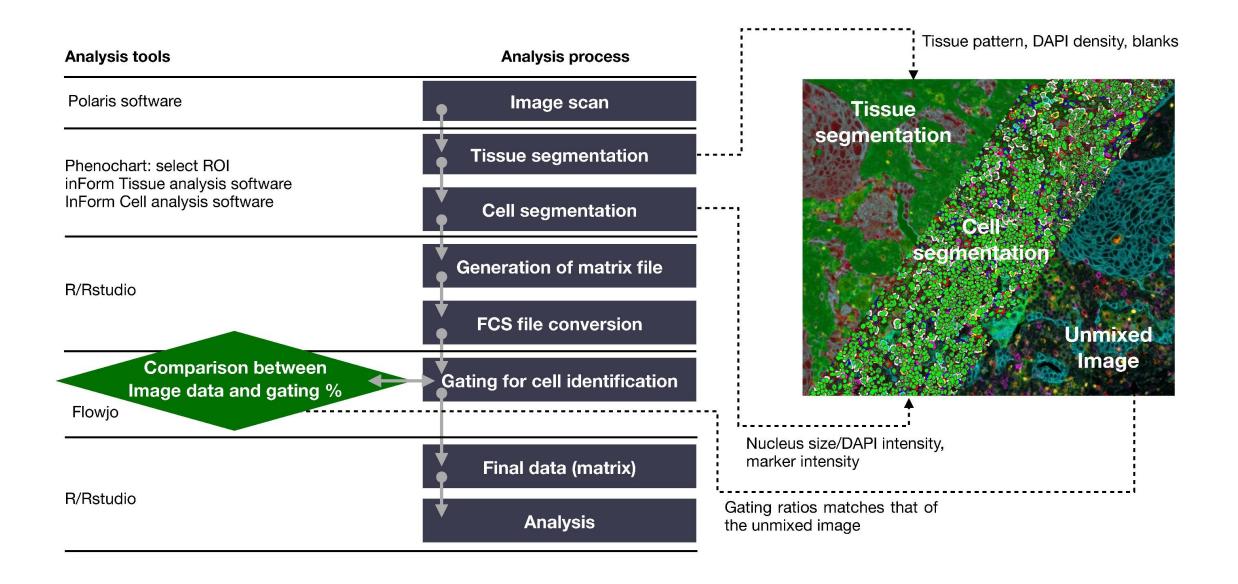


Figure S1. Schematic diagram of the softwares utilized throughout the investigation.

Fig. S2, Kim DK, Lee CY, Han YJ et al.

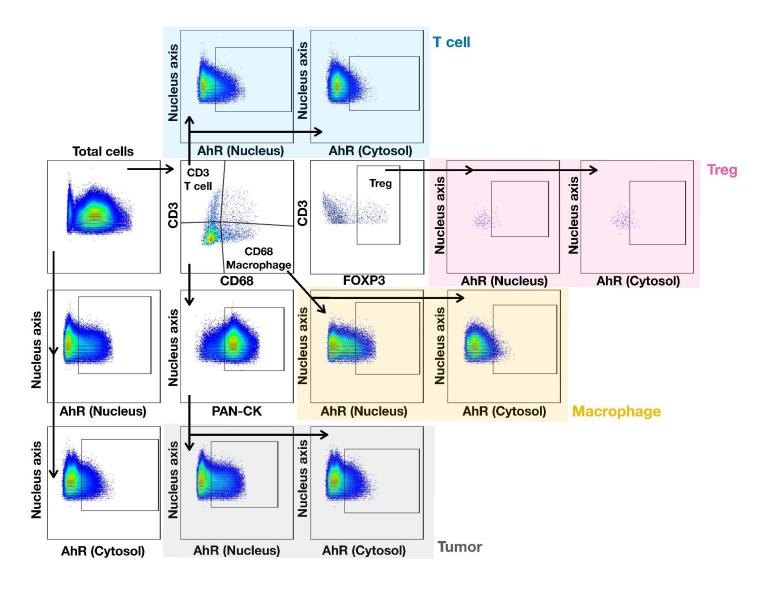


Figure S2. Gating strategy for cell phenotyping and AhR expression.

Fig. S3, Kim DK, Lee CY, Han YJ et al.

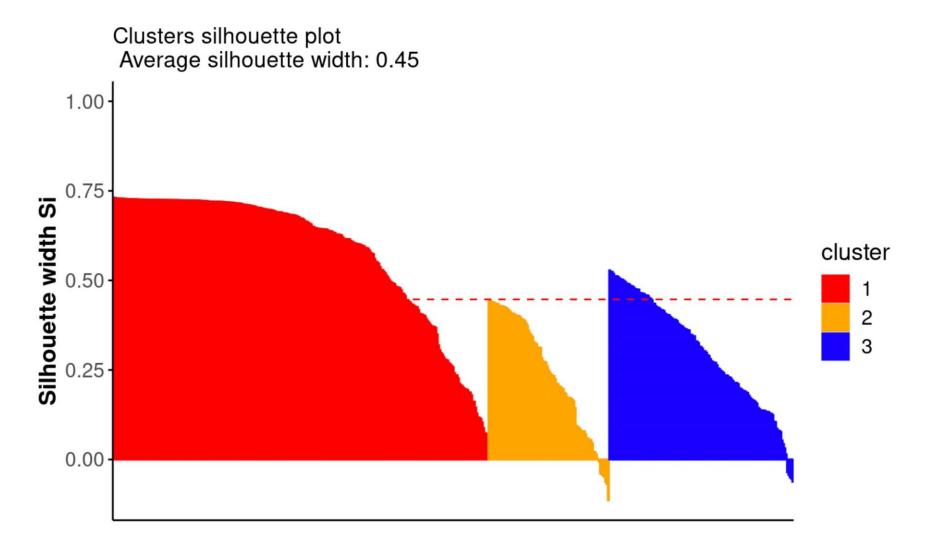


Figure S3. Silhouette plot illustrating a comprehensive comparison of five cancer types based on AhR expression using K-mean clustering.