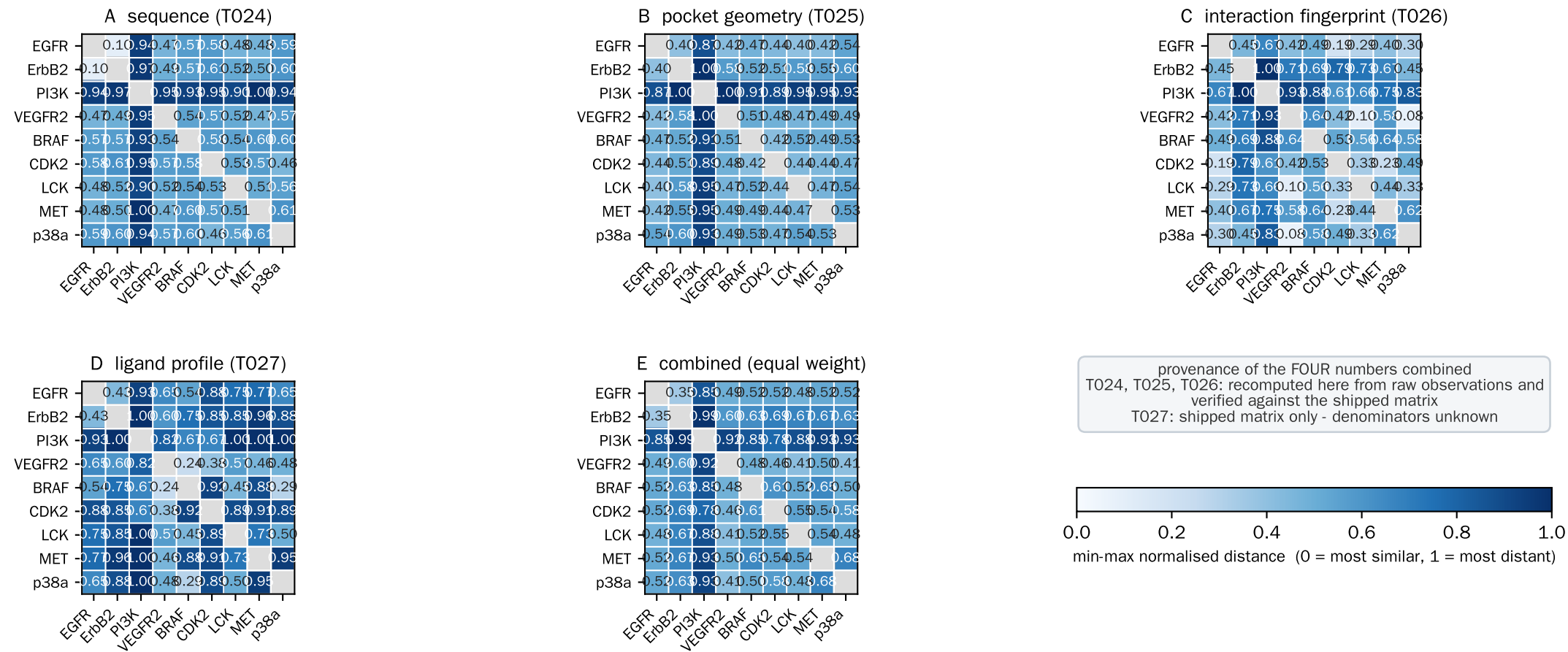


Four views of kinase similarity, all on one explicit kinase order



Each cell is a distance; each view is min-max normalised on its own scale (85-position pocket-sequence distance -> T024 sequence; KiSSim fingerprint distance -> T025 pocket geometry; Jaccard distance over 595 IFP bits -> T026 interaction fingerprint; 1 - shared-active fraction -> T027 ligand profile). Colours are therefore comparable across panels but absolute magnitudes are not. Grey diagonal = excluded self-comparison (defined 0). PI3K is the farthest kinase FROM EGFR in all four views; but it is not the farthest partner of every kinase (T026 interaction fingerprint: CDK2, LCK; T027 ligand profile: BRAF, CDK2). EGFR's own nearest neighbour is ErbB2 in the sequence view, ErbB2 in the pocket-geometry view, CDK2 in the interaction-fingerprint view and ErbB2 in the ligand-profile view - i.e. ErbB2 in three of the four. This is a statement about EGFR's nearest neighbour, not about the globally closest pair: the globally closest pair is EGFR-ErbB2 in T024 and T025, but VEGFR2-p38a in T026 and BRAF-VEGFR2 in T027. Panel E is the equal-weight mean of panels A-D, i.e. it inherits the asymmetric provenance noted above.