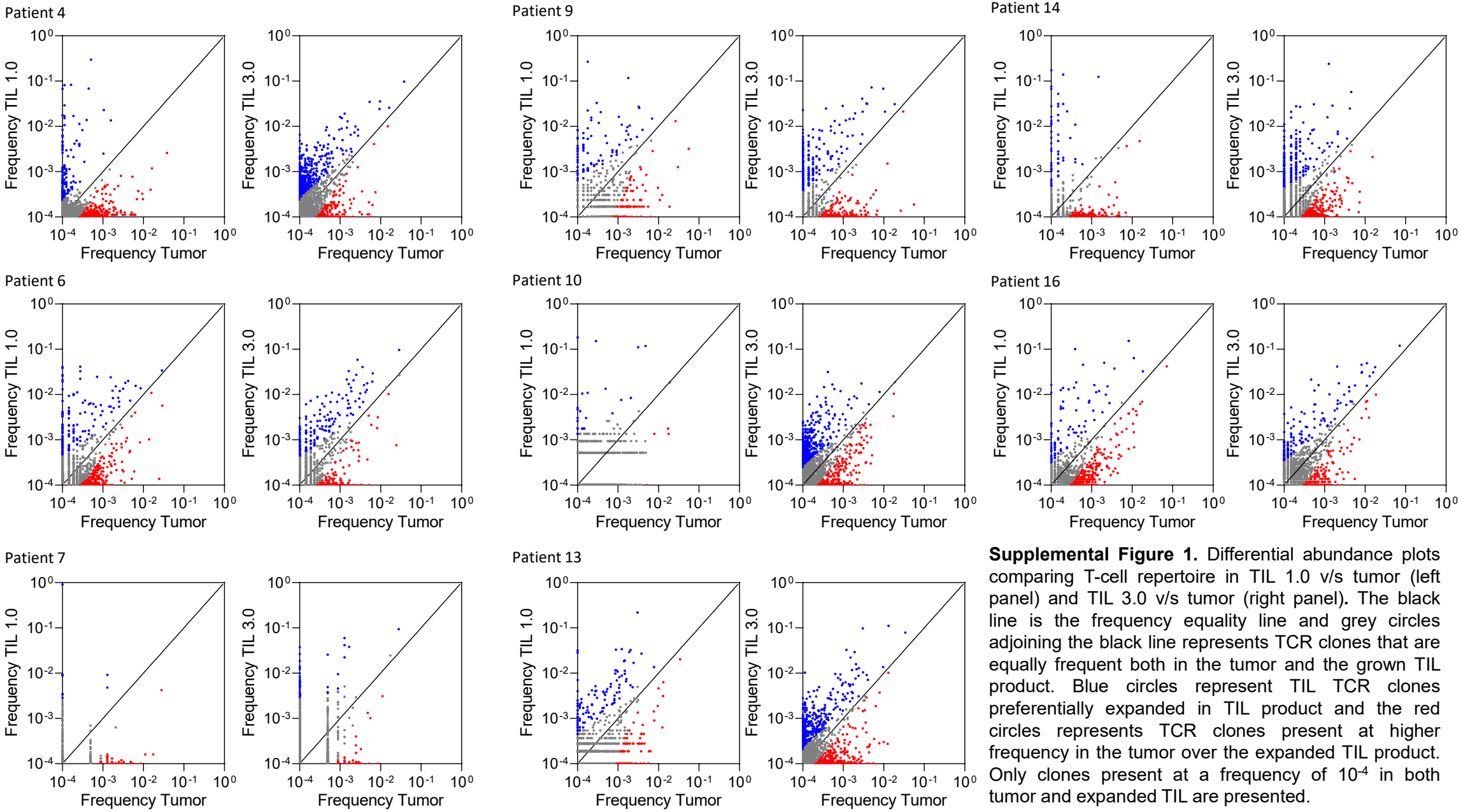
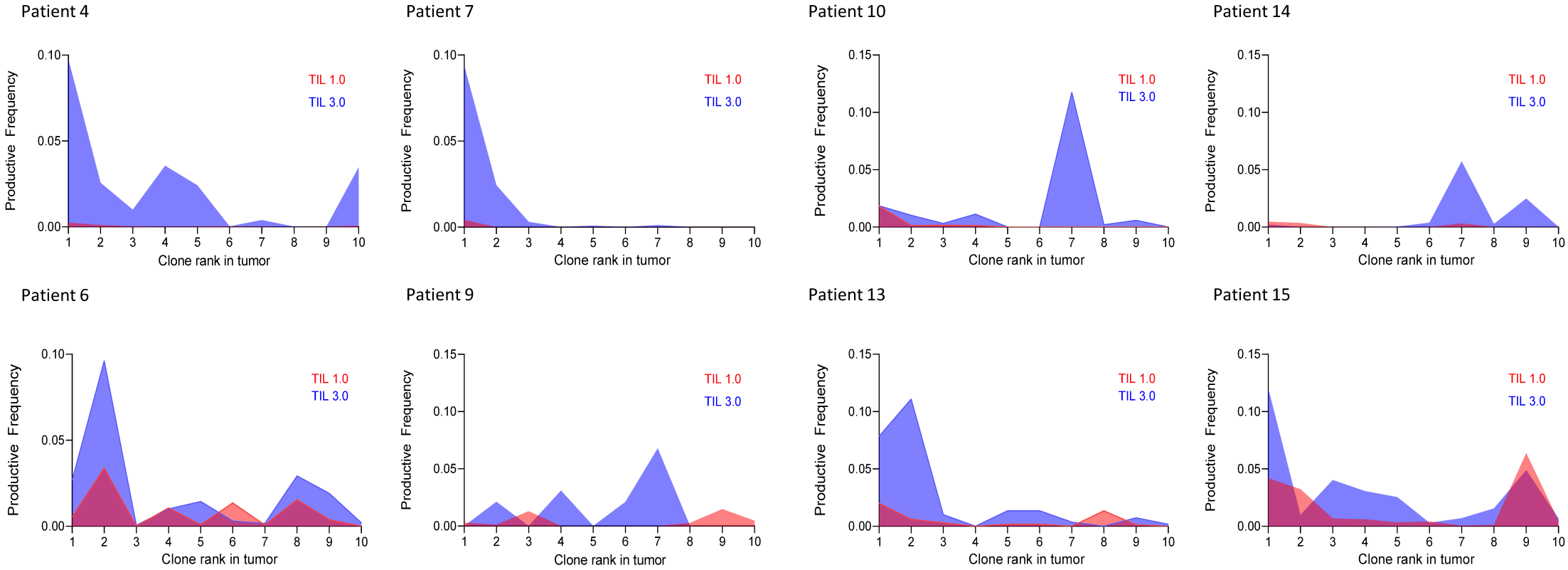
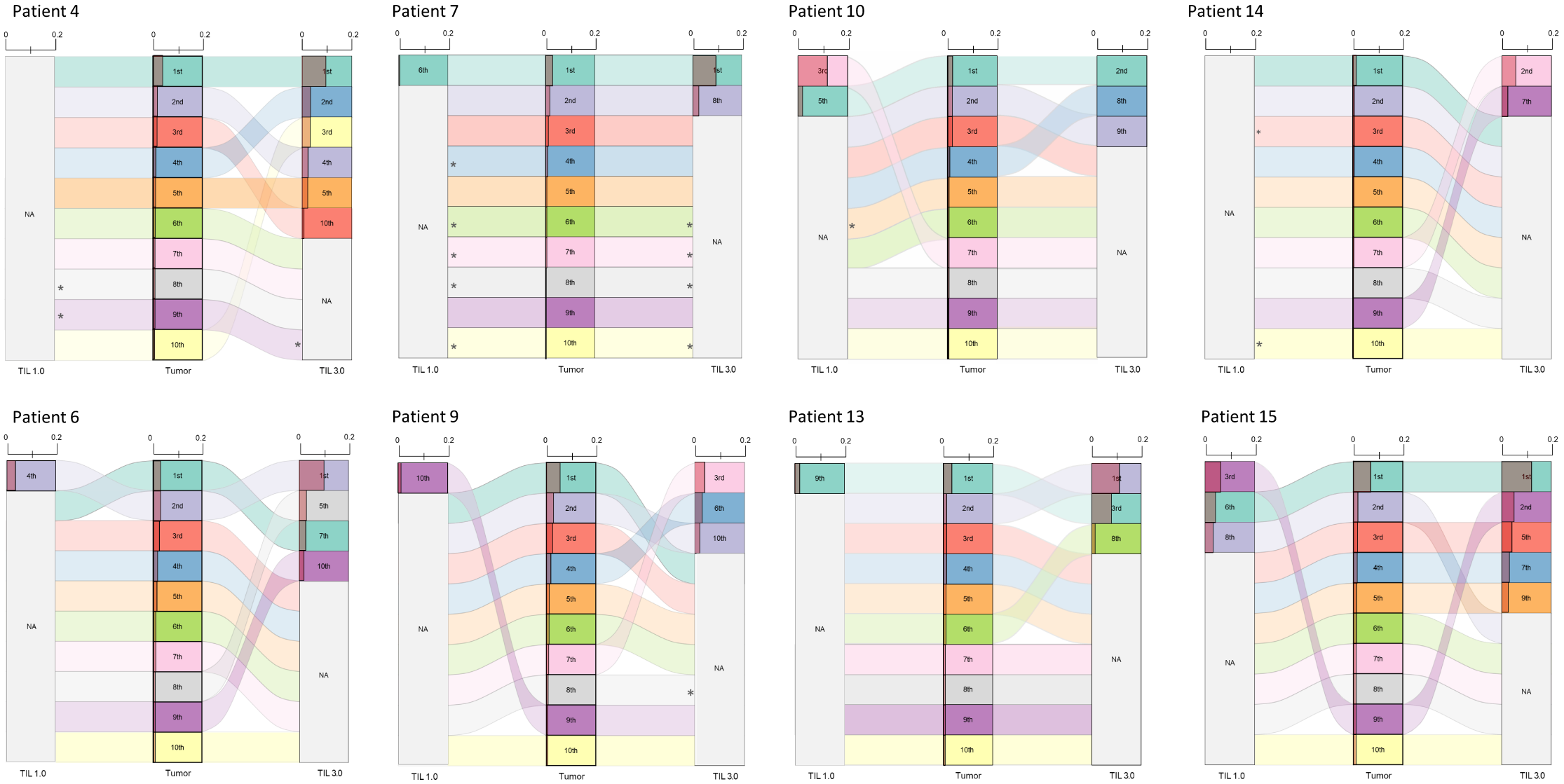


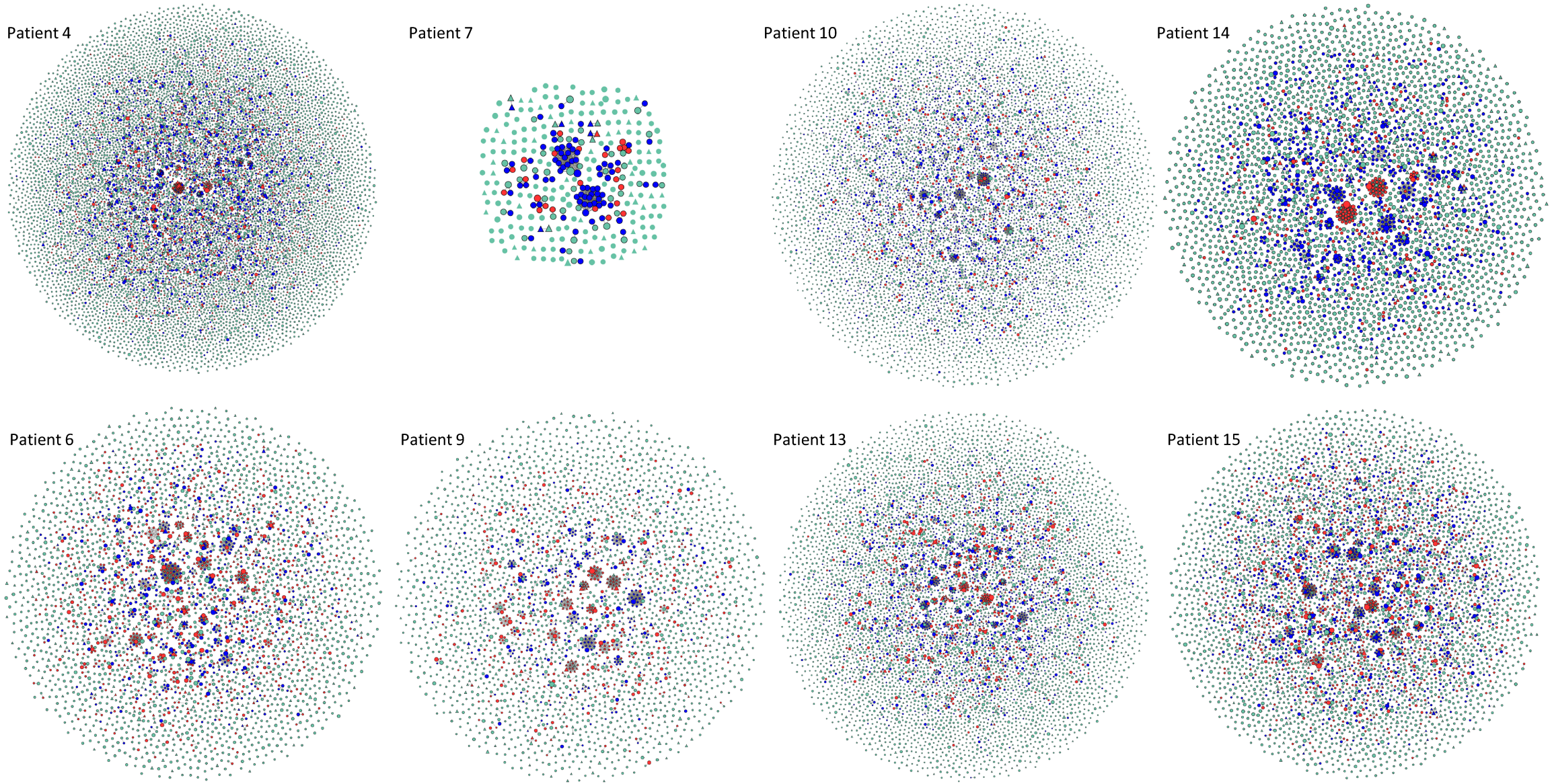
Supplemental Figure 1. Differential abundance plots comparing T-cell repertoire in TIL 1.0 v/s tumor (left panel) and TIL 3.0 v/s tumor (right panel). The black line is the frequency equality line and grey circles adjoining the black line represents TCR clones that are equally frequent both in the tumor and the grown TIL product. Blue circles represent TIL TCR clones preferentially expanded in TIL product and the red circles represents TCR clones present at higher frequency in the tumor over the expanded TIL product. Only clones present at a frequency of 10^{-4} in both tumor and expanded TIL are presented.



Supplemental Figure 2 : Comparison of the productive frequency of top 10 resected tumor T-cell clones found in grown TIL 1.0 and TIL 3.0 product.

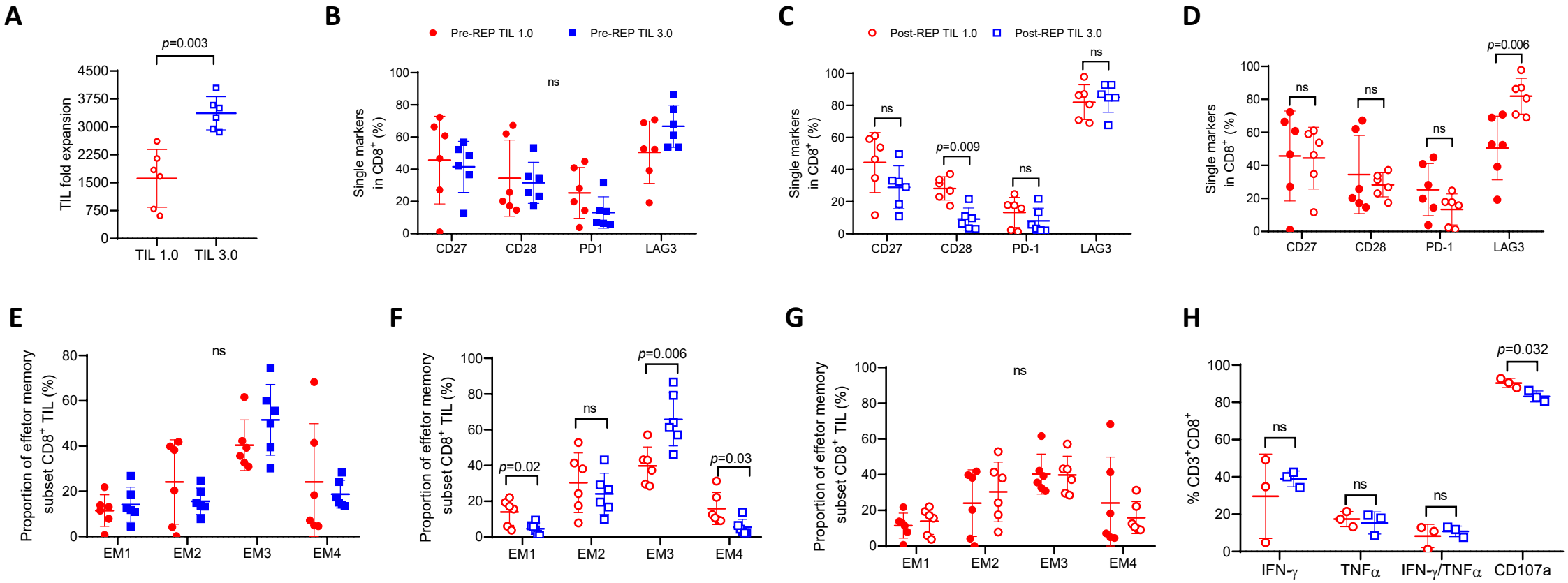


Supplemental Figure 3. Alluvial plot depicting the top 10 ranked TIL clones found in the tumor to their corresponding rank in TIL 1.0 and TIL 3.0 culture method. N/A means not present in top 10 and ∗ means they are not present in expanded TIL product. Shaded region in each clone represents the productive frequency (range from 0.0 – 0.2).



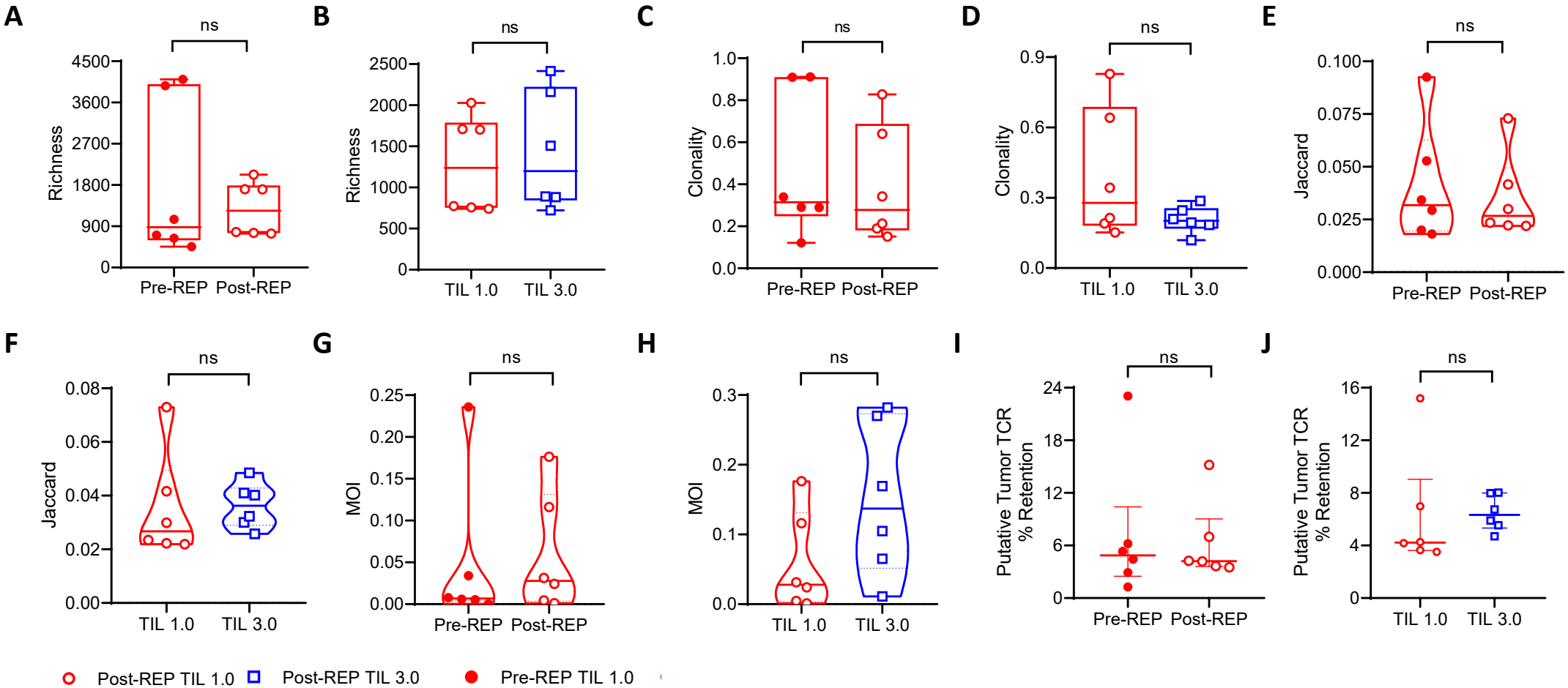
Supplemental Figure 4 : Graphs of putative tumor-specific TCR [clones (circles) and clusters (triangles)] found in the baseline NSCLC tissue (green), TIL expanded with TIL 1.0 (red) and TIL 3.0 (blue) for each patients.

Supplementary Figure 5



Supplemental Figure 5 : (A) Comparison of fold expansion obtained from the final expansion step to generate an infusion product (REP) using TIL 1.0 (red) and TIL 3.0 (blue) (paired, n=6) at day 14. (B) Assessment of the surface expression of the differentiation/activation CD27, CD28, PD-1 and LAG3 on pre-REP CD8+ TIL (in %) (paired, n=6), (C) Post-REP CD8+ TIL (paired, n=6) generated from TIL 1.0 and TIL 3.0 culture and (D) pre and post-REP TIL 1.0 CD8+ TIL (paired, n=6). (E) Comparison of proportion of effector memory subset [established from CD27 and CD28 expression signifying effector potential and differentiation states] of pre-REP $CD8^+$TIL (paired, n=6) (F) Post-REP CD8+ TIL (paired, n=6) generated from TIL 1. and 3.0 culture and (G) pre and post-REP TIL 1.0 CD8+ TIL (paired, n=6) . (H) Analysis of TIL functionality measured by intracellular IFN-γ, TNFα, IFN-γ/TNFα and CD107a of cryopreserved (right panel) post-REP $CD8^+$TIL (in %) upon PMA/Ionomycin activation (TIL 1.0 vs TIL 3.0, paired, n=3). Statistical analysis was performed by paired T test on (A), (B), (C), (D), (E), (F), (G) and (H).

Supplementary Figure 6



Supplemental Figure 6 : (A) Comparison of richness in pre and post-REP final product, (paired n=6) and between (B) post-REP TIL 1.0 and TIL 3.0 product, (paired=6). Comparison of clonality in (C) in TIL 1.0 pre and post-REP product and (D) post-REP TIL 1.0 and 3.0 product, (paired n=6). Comparison of Jaccard index in (E) in TIL 1.0 pre and post-REP product and (F) post-REP TIL 1.0 and 3.0 product, (paired n=6). Comparison of MOI index in (G) in TIL 1.0 pre and post-REP product and (H) post-REP TIL 1.0 and 3.0 product, (paired n=6). Comparison of retained putative tumor-specific TCR in (I) in TIL 1.0 pre and post-REP product and (J) post-REP TIL 1.0 and 3.0 product, (paired n=6). Statistical analysis was performed by paired T test on (A), (B), (C), (D), (E), (F), (G), (H) and (I).