Background: Identifying and monitoring HIV transmission networks provides a more informative picture of a local HIV epidemic than standard measures of incidence and prevalence. By inferring
potential transmission links between risk groups, demographic subpopulations, and geography, one may better understand the drivers of spread locally, and the links between epidemics outside the region. This study focused on the HIV-epidemic in two German cities with particularly high rates of new HIV diagnoses: Cologne and Munich.

**Material/methods:** Phylogenetic and network analyses were performed to infer putative relationships between HIV1 partial pol sequences from 2,181 unique individuals receiving care at the University Hospital of Cologne (n=1,507), LMU University Hospital Munich (n=641), or the Interdisciplinary HIV Centre, Technical University Munich (TUM; n=33), sampled between 1999 – 2016. After quality filtering, putative transmission linkages were inferred when two sequences were ≤1.5% genetically different. A computationally efficient network based approach was then used to analyze relationships between this sample and all publicly available HIV sequences from the Los Alamos National Laboratory HIV Sequence database.

**Results:** The sampled population was predominantly male (80%). The predominant risk factor for HIV infection was men reporting sex with men (MSM, 55%), while only 3.7% reported injection drug use as their main risk factor. A total of 358/2,181 (16.4%) of sequences linked with at least one other sequence, forming 121 transmission clusters, ranging in size from 2 (n=82 dyads) to 15 sequences (Figure). Sequences from Cologne were significantly more likely to be linked than sequences from Munich (19.1% vs 10.4% of sequences linked, p<0.001). We found that 10 transmission clusters (8.3%) included sequences from centers in Cologne and Munich, and 21 clusters (17.4%) included both heterosexual males and MSM. Clustering individuals were significantly more likely to be younger (median age 36 vs 40, p<0.001), men (90.8% vs 78.3%, p<0.001), of German (80.4% vs 66.5%, p<0.001) origin, reporting MSM contact as main risk factor (69% vs 52%, p<0.001), and infected with subtype B (86.6% vs 71%, p<0.001), when compared to non-clustering individuals. By combining the 2,181 sequences from Cologne and Munich with 152,577 publicly available HIV polymerase sequences, we found a total of 110 clusters that included both, our sequences [total n=130; 93/1,507 (6.2%) from Cologne and 37/674 (5.5%) from Munich] and publicly available sequences (total n=307; 131 from other German centers, 48 from other European countries, 110 from Asia and 18 from America).

**Conclusions:** In this analysis of the HIV1 epidemics in Cologne and Munich we found multiple links between these epidemics and those across Germany and around the world and also between risk groups. These results highlight the pitfalls of focusing prevention efforts and monitoring on specific risk groups or specific locales, and not taking into consideration the overall HIV epidemic.