Background Psychiatric illnesses such as bipolar disorder, schizophrenia and schizoaffective disorder are severe, disabling disorders associated with decreased quality of life (QOL) and functioning (Bobes, Garcia-Portilla, Bascaran, Saiz, & Bousoño, 2007; Latalova, Prasko, Diveky, Kamaradova, & Velartova, 2010; Merikangas et al., 2012). Stigmatization, co-morbidities, adverse effects of medications, care models with deficits in personal and social recovery needs and chronic symptoms due to treatment resistance are factors that can lead to severe reductions in quality of life and functioning (Kahn et al., 2015; Sum, Ho, & Sim, 2015). In this study we aim to characterize patients with good and poor outcomes according to QOL and functioning scores. Using cluster analysis, we sought to identify longitudinal trajectories and investigate whether levels of QOL and functioning are associated with polygenic risk scores. Determining clusters of patients at higher risk of poorer outcomes is critical to provide early and effective interventions.

Methods Longitudinal data was used from the Clinical Research Group 241 and PsyCourse studies in Germany. Participants were phenotyped using a comprehensive battery which included data on socio-demographics, history of illness, symptomatology, QOL and functioning. Data was collected at four equidistant time points over an 18-month period. The Infinium Psycharray from Illumina was used to genotype patients. Relevant questionnaire items (i.e. QOL, functioning scores, and socio-demographic data) were pre-selected and factor analysis for mixed data was applied to identify trends in the data. This allowed for the computation of abstract data dimensions which were used for calculation of longitudinal trajectories. These trajectories can be seen as a representation of the overall status of patients and both the overall level as well as the longitudinal change of this status were used as inputs for a k-mean clustering for longitudinal data (Genolini et al., 2013). This, in turn, resulted in the identification of three distinct subpopulations of patients. In a linear regression model we used clusters as predictive variables for polygenic risk scores at 11 thresholds.

Results The dimension which explained the most variance was used for cluster analysis. This dimension was mainly driven by scores for self-satisfaction, life
enjoyment, ability to cope with daily tasks, energy, and quality of life. In a sample of 198 patients, three clusters were observed; cluster A (39.4%) consisted of participants with the highest average scores for functioning and QOL, cluster B (33.8%) including participants with the lowest average scores for functioning and QOL, and cluster C (26.8%) consisting of participants who had great improvement in functioning and QOL scores over the course of the longitudinal study. Male patients were substantially overrepresented in cluster A and the inverse effect was observed in cluster B. No significant differences were seen for age of onset, age at interview, or duration of illness within the clusters. Polygenic risk scores at certain thresholds can be predicted by the clusters. In cluster B there was a trend for higher polygenic risk scores.

**Discussion** Phenotypic data provide insight to target sufferers of severe mental illness with worse outcomes. Levels of functioning and QOL seem to be associated with polygenic risk scores. Further investigations are needed.

**Disclosure:** Nothing to Disclose.