address basic and other health-related self-care needs. The target population included people ages 18 and older. English speaking, living in 1 of 16 ZIP codes on Chicago’s south and west sides (160 mi²) who received care at ≥1 of 28 CommunityRx partner sites and had a diagnosis of asthma or COPD. Between December 2015 and December 2016, information about pulmonary research participation opportunities was included on the HealtheRx of eligible patients contemporaneously with usual registry recruitment methods. Usual methods, used since 2010 by the PR group, included public advertisements requiring the patient to call the research office for more information. Eligible patients identified during routine clinical care with a Pulmonary/Critical Care clinician or when enrolling in a pulmonary clinical trial. We hypothesized that, compared with usual recruitment practices, the HealtheRx recruitment strategy would increase the rate and decrease the per subject cost of patient recruitment to a prospective registry. Total annual recruitment costs for each method were calculated based on the number of consented PR patients per method. RESULTS/ANTICIPATED RESULTS: Between December 22, 2015 and December 15, 2016 13,437 HealtheRx (8762 for asthma, 3842 for COPD, and 833 for both asthma and COPD) were generated with the recruitment advertisement. In total, 41 participants responded to the ad and participated in the phone survey. In which 15 (36.5%) participants self-reported a diagnosis of asthma only (65% of all HealtheRxs with advertisement were for asthma only), 9 (22%) reported a diagnosis of COPD only (28.5% of all HealtheRxs with advertisement were for COPD only), and 17 (41.5%) reported diagnoses of both asthma and COPD (6.2% of all HealtheRxs with advertisement were for asthma and COPD). Most participants were female (n=28), non-Hispanic black (n=37), and not employed (n=39). The median age was 57. The majority (n=31) had never participated in health or medical research and was not aware of current opportunities to participate in research (n=25). All 41 participants expressed interest in joining PRR and were mailed a blank PRR consent form =39). The median age was 57. The majority (n=31) had never participated in health or medical research and was not aware of current opportunities to participate in research (n=25). All 41 participants expressed interest in joining PRR and were mailed a blank PRR consent form and a prepaid return envelope with their incentive check for the telephone survey. To date, 5 participants returned a signed consent form via mail and were enrolled in PRR. During the same period, 4 patients enrolled in PRR via usual recruitment methods. The cost per subject to enroll in PRR was $364.40 using the HealtheRx recruitment and $4590 using usual practice. DISCUSSION/SIGNIFICANCE OF IMPACT: NIH has called for innovation in research recruitment methodologies to increase enrollment especially of people who are under-represented in clinical trials research. This study demonstrates the feasibility and efficiency of using an EMR-integrated recruitment consent method to enroll people of under-represented minority groups to a research registry. 2302 Downregulation of mir-1207-3p is correlated to upregulation of FNDC1, FN1, AR, and c-MYC in aggressive prostate cancer in men of African ancestry Dibash K. Das, Akintunde T. Orumuyi, Gabriel Olabiyi Ogun, S. Adekola Adebayo, A. Ayo Salako, Adeodat Ilboudo, E. O. Olapade-Olaopa and Olorunseun O. Ogunwobi Department of Biological Sciences, Hunter College, New York, NY, USA OBJECTIVES/SPECIFIC AIMS: Prostate cancer is the second most common cancer in the world for men. For reasons still unclear, aggressive PCa disproportionately affects males of African ancestry (MoAA). Incidence and mortality rates are highest in MoAA as they have consistently shown a 2.3-3.0-fold higher risk of mortality compared with Caucasian men. This aggressiveness of PCa may be due to specific biological factors. Studies have established that microRNAs (miRNAs), essential in post-transcriptional gene regulation, are dysregulated in PCa. mir-1207-3p is encoded at the FNDC1 domain containing 1 (FNDC1) locus. The chromosomal regions are associated with a number of genes in cancer. To date, 5 miRNA (including mir-1207-3p) in PCa have never been investigated. Moreover, studies have shown that compound of miRNA androgen receptor (AR) acting on the 3′ UTR of FNDC1 increase the concentration of all miRNA in prostatic tissue. We have been linked to PCa aggression, and has been shown to be downstream of androgen receptor. (AR) in some PCa. However, the mechanisms regulating c-MYC have never been studied in MoAA. We have recently demonstrated that mir-1207-3p has prognostic value in PCa, and directly binds to the 3′ UTR of Fibronectin type III domain containing 1 (FNDC1) to regulate a novel FNDC1/fibronectin (FN1)/AR pathway upregulated in metastatic PCa. However, the relevance of this novel and clinically significant mir-1207-3p molecular pathway in PCa in MoAA is unknown. Therefore, we hypothesized that microRNA 1207-3p, encoded at the 8q24 PCa susceptibility locus, is a biomarker with clinical applications in MoAA. Our specific aim was to assess the clinical relevance of mir-1207-3p, FNDC1, FN1, AR, and MYC expression in aggressive PCa in a cohort of West African black males. METHODS/STUDY POPULATION: Consequently, we aimed to determine the expression profile of miRNA-1207-3p, FNDC1, FN1, AR, and MYC in histologically confirmed normal prostate (n=24), benign prostatic hyperplasia (n=44) and malignant prostate tissue (n=40) from prostatectomy or transrectal ultrasound-guided biopsies in patients recruited at the University College Hospital, Ibadan, Nigeria, a sub-Saharan Black African population. In total, 17 patients had tumors with Gleason score ≥8. Tissues were collected in compliance with Institutional Ethics Board approved protocols. RNA extraction, cDNA synthesis, and quantitative PCR were performed to analyze miRNA expression of miRNA-1207-3p, FNDC1, FN1, AR, and MYC. Statistical analysis were performed using SPSS software. All data were analyzed by the 1-way ANOVA test. Tukey post-hoc test was performed to determine the differences in mean expression between normal and tumor prostate tissues. p<0.02 was considered significant. RESULTS/ANTICIPATED RESULTS: We discovered that miR-1207-3p was significantly upregulated in prostate tumor tissues (0.09±0.02, 95% CI (0.04, 0.136), p=0.000) compared with normal prostate tissue in MoAA (0.92±0.15, 95% CI (0.60, 1.244), p=0.000). This is the first description of mir-1207-3p differential expression in human clinical PCa in MoAA. In contrast, FNDC1 was significantly overexpressed in prostate tumor tissues (21.93±8.21, 95% CI (4.97, 38.89), p=0.003) in comparison with normal prostate tissues in MoAA (1.57±0.45, 95% CI (0.625, 2.51), p=0.003). The same positive correlation with advanced disease held true for FN1 [tumor: 13.66±3.53, 95% CI (6.38, 20.93), p=0.000; normal: 1.07±0.235, 95% CI (0.58, 1.56), p=0.000], AR [tumor: 20.49±6.74, 95% CI (6.50, 34.48), p=0.000; normal: 9.94±0.20, 95% CI (0.52, 1.36), p=0.000], and c-MYC [tumor: 33.92±8.43, 95% CI (16.53, 51.33), p=0.000; normal: 1.94±0.36, 95% CI (1.18, 2.70)]. The significantly increased expression of FNDC1, FN1, AR, and c-MYC in prostate tumor tissues in comparison with normal prostate tissues indicate that their overexpression is associated with increased risk of cancer progression in MoAA. DISCUSSION/SIGNIFICANCE OF IMPACT: These results show that the underexpression of miR-1207-3p and the overexpression of FNDC1, FN1, AR and MYC is associated with aggressive PCa in MoAA, mir-1207-3p, and it molecular target of FNDC1, may be useful biomarkers for the prediction of PCAs in MoAA. 2307 Resting state network profiles of Alzheimer disease and frontotemporal dementia: A preliminary examination Joey Annette Contreras, Shannon L. Risacher, Mario Dzemidzic, John D. West, Brenna C. McDonald, Martin R. Farlow, Brandy R. Matthews, Liana G. Apostolova, Jared Brosch, Bernard Ghetti and Joaquin GoNi Indiana University School of Medicine, Indianapolis, IN, USA OBJECTIVES/SPECIFIC AIMS: Recent evidence from resting-state fMRI studies have shown that brain network connectivity is altered in patients with neuropsychiatric disorders such as Alzheimer disease (AD), schizophrenia, and autism spectrum disorder, but relatively little is known about how these brain changes correlate with the complete connectivity patterns of these well-reported RSNs. Here, we used advanced connectomic approaches to examine the connectivity of RSNs in Alzheimer disease (AD), Frontotemporal dementia (FTD), and age-matched control participants. METHODS/STUDY POPULATION: In total, 44 participants [27 controls (66.4±7 years), 13 AD (68.5.63±13.9 years), 4 FTD (59.57±12.2 years)] from an ongoing study at Indiana University School of Medicine were used. Resting-state fMRI data was processed using an in-house pipeline modeled after Power et al. (2014). Images were parcelled into 278 regions of interest (ROI) based on Shen et al. (2013). Connectivity between each ROI pair was described by Pearson correlation coefficient. Brain regions were grouped into 7 canonical RSNs as described by Yeo et al. (2015). Pearson correlation values were then averaged across pairs of ROIs in each network and averaged across individuals in each group. These values were used to determine relative expression of FC in each RSN (intranetwork) and create RSN profiles for each group. RESULTS/ANTICIPATED RESULTS: Our findings support previous literature which shows that limbic networks are disrupted in FTD participants compared with AD and age-matched controls. In addition, interactions between different RSNs was also examined and show a significant differentiation between controls and AD subjects was found between DP and DMN RSNs. Similarly, previous literature has reported a disruption between executive (frontoparietal) network and default mode network in AD compared with controls. DISCUSSION/SIGNIFICANCE OF IMPACT: Our approach allows us to create profiles that could help compare intranetwork FC in different neurodegenerative diseases. Future work with expanded samples will help us to draw more substantial conclusions regarding differences, if any, in the connectivity patterns between RSNs in various neurodegenerative diseases.