Our samples have three treatment groups, 1) treatment naïve (TN), 2) residual disease (RD), and 3) progressive disease (PD)

We conducted three assays using the multiplex RNAscope kit to probe for nine gene probes using Opal dyes associated with each gene.

RNAscope assay #1:

RNAscope staining 1. SFTPD: C2 Opal dye 620

RNAscope staining 2. NFIX: C1 Opal dye 570

RNAscope staining 3. DLC1 C3 Opal dye 690

RNAscope assay #2:

RNAscope staining 4. NKX2-1: C2 Opal dye 620

RNAscope staining 5. SELENBP1: C3 Opal dye 690

RNAscope staining 6. IGFBP3: C1 Opal dye 570

RNAscope assay #3:

RNAscope staining 7. GJB3: C2 Opal dye 620

RNAscope staining 8. GJB2: C3 Opal dye 690

RNAscope staining 9. SERPINE1: C1 Opal dye 570

(HIGH PRIORITY) Question 1: Do we find there to be enriched expression of genes in any given treatment group? (TN, RD, PD)

(LOW PRIORITY) Question 2: Do we do we find co-expression of certain gene combinations enriched in any given group?

Example: NKX2-1 and SELENBP1, SFTPD and NFIX/NKX2-1