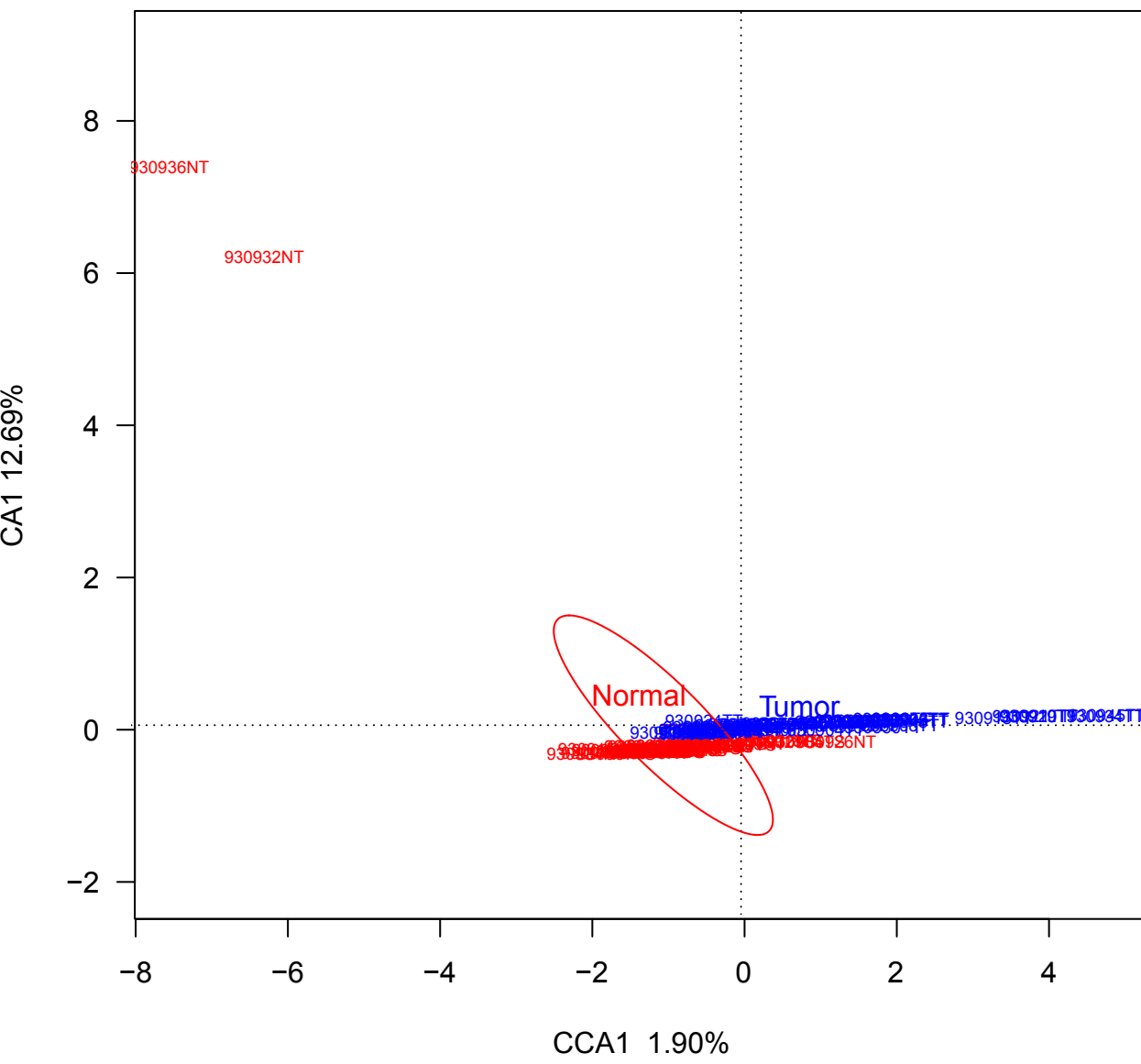


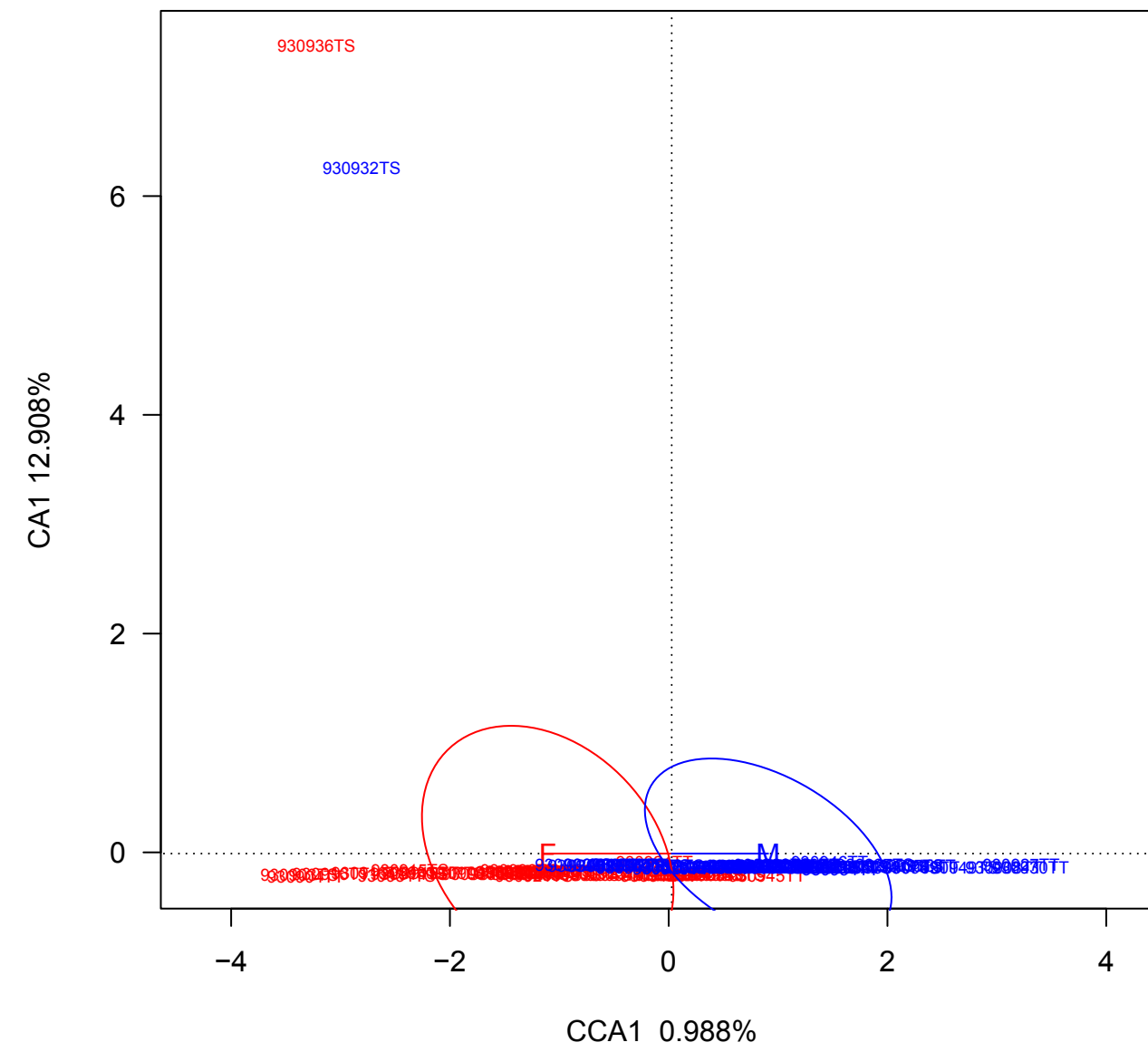
all tissue

ADONIS p-value 0.018



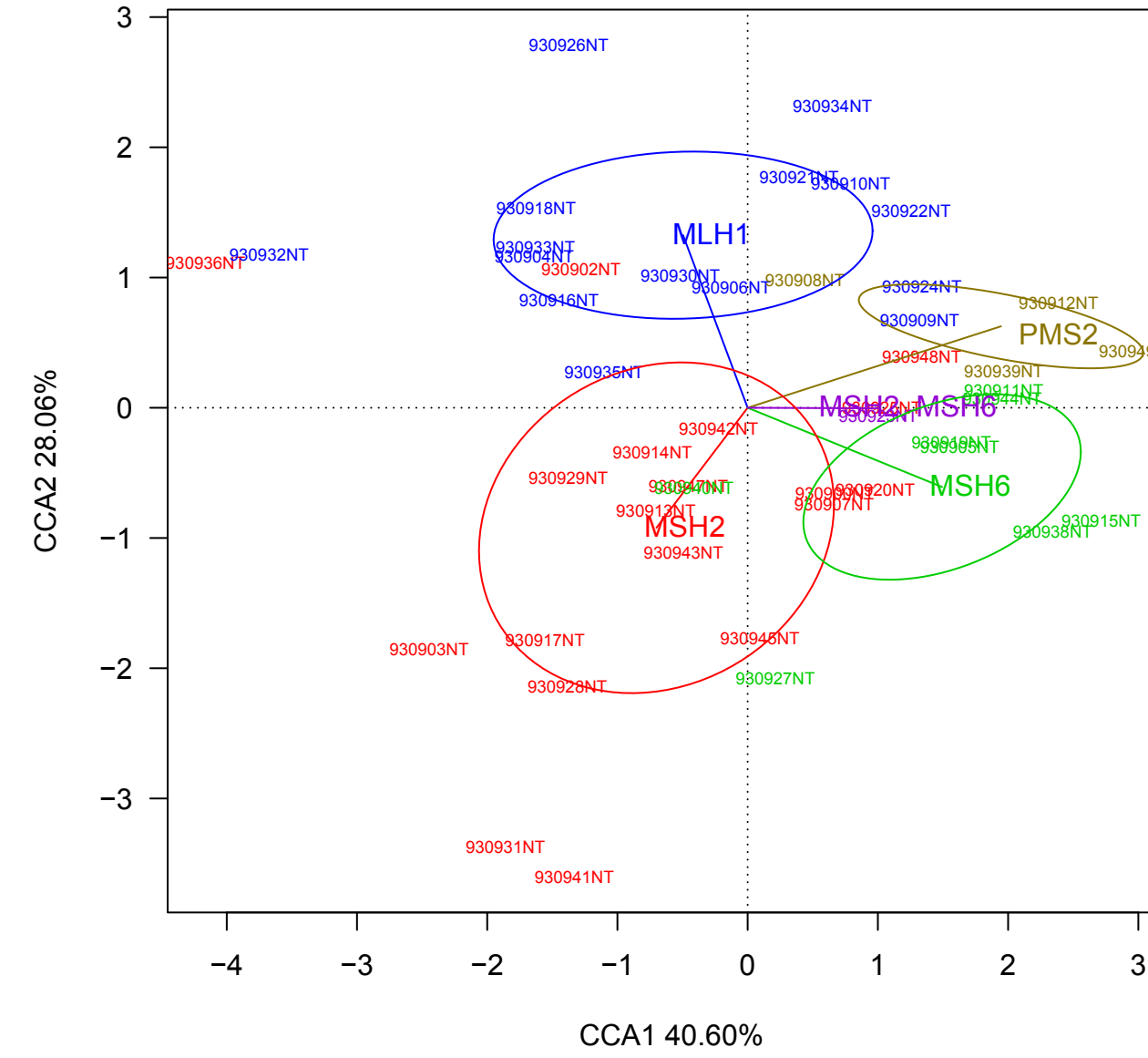
all gender

ADONIS p-value 0.66



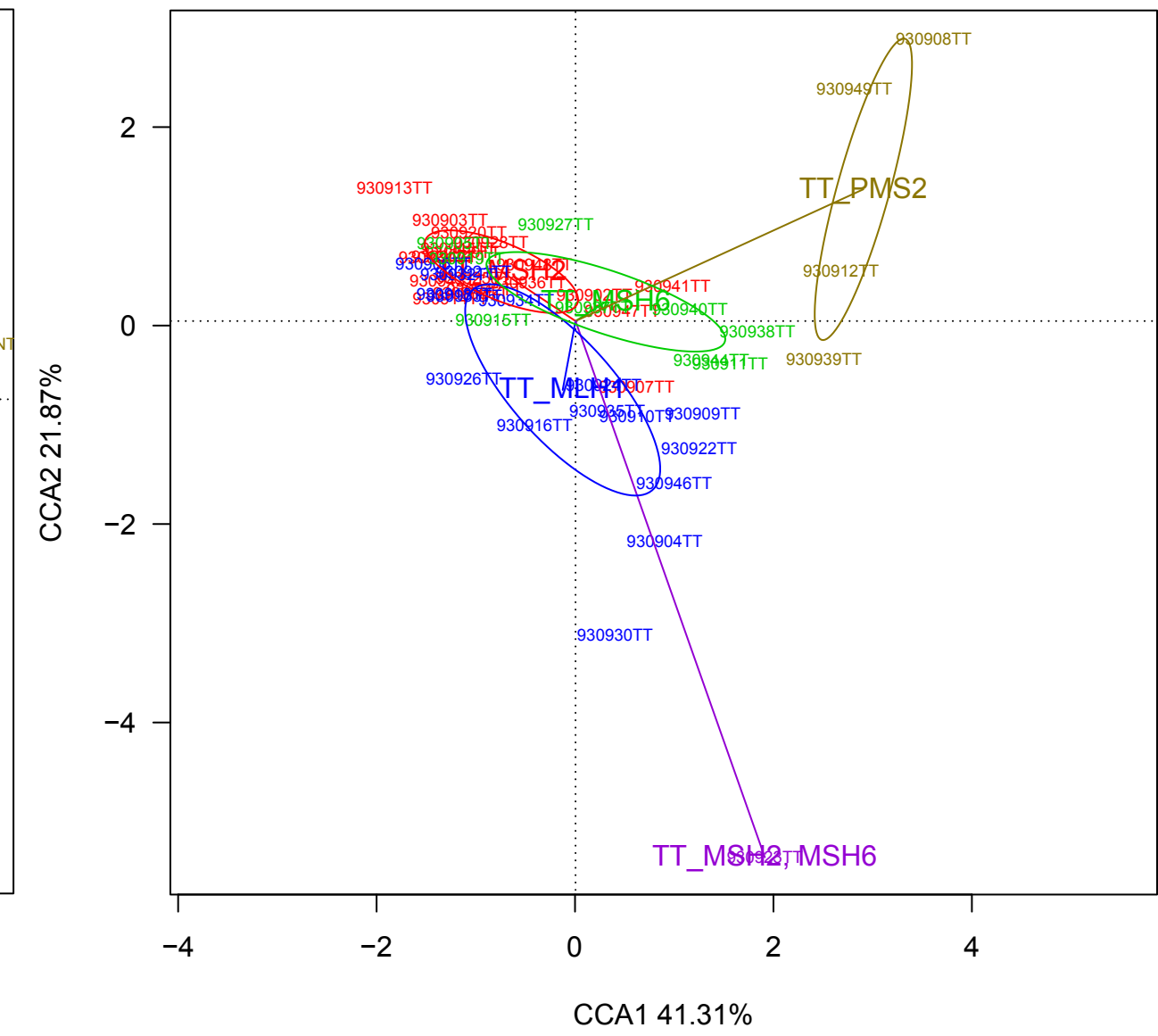
all gene NT

ADONIS p-value 0.36



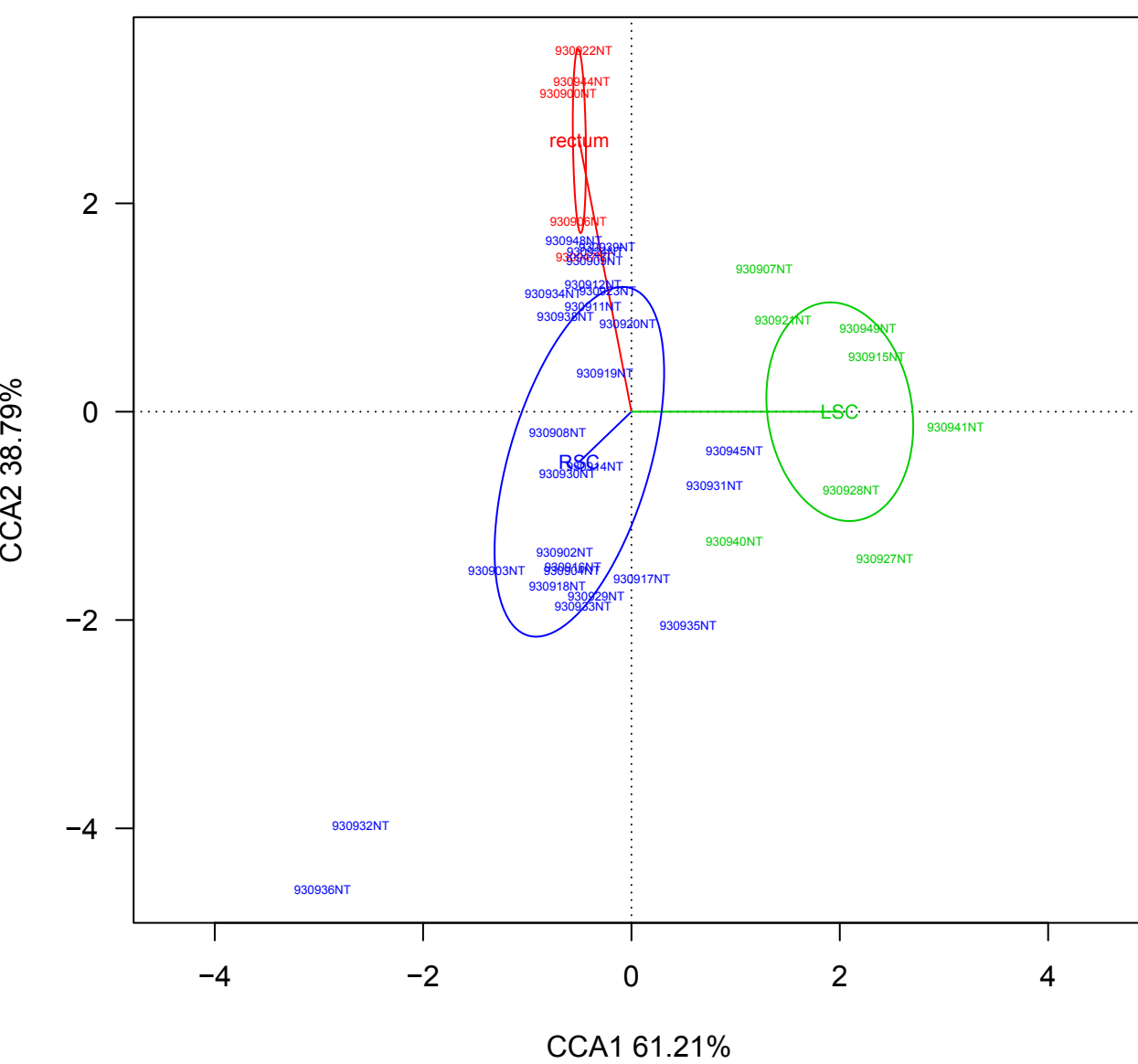
all gene TT

ADONIS p-value 0.15



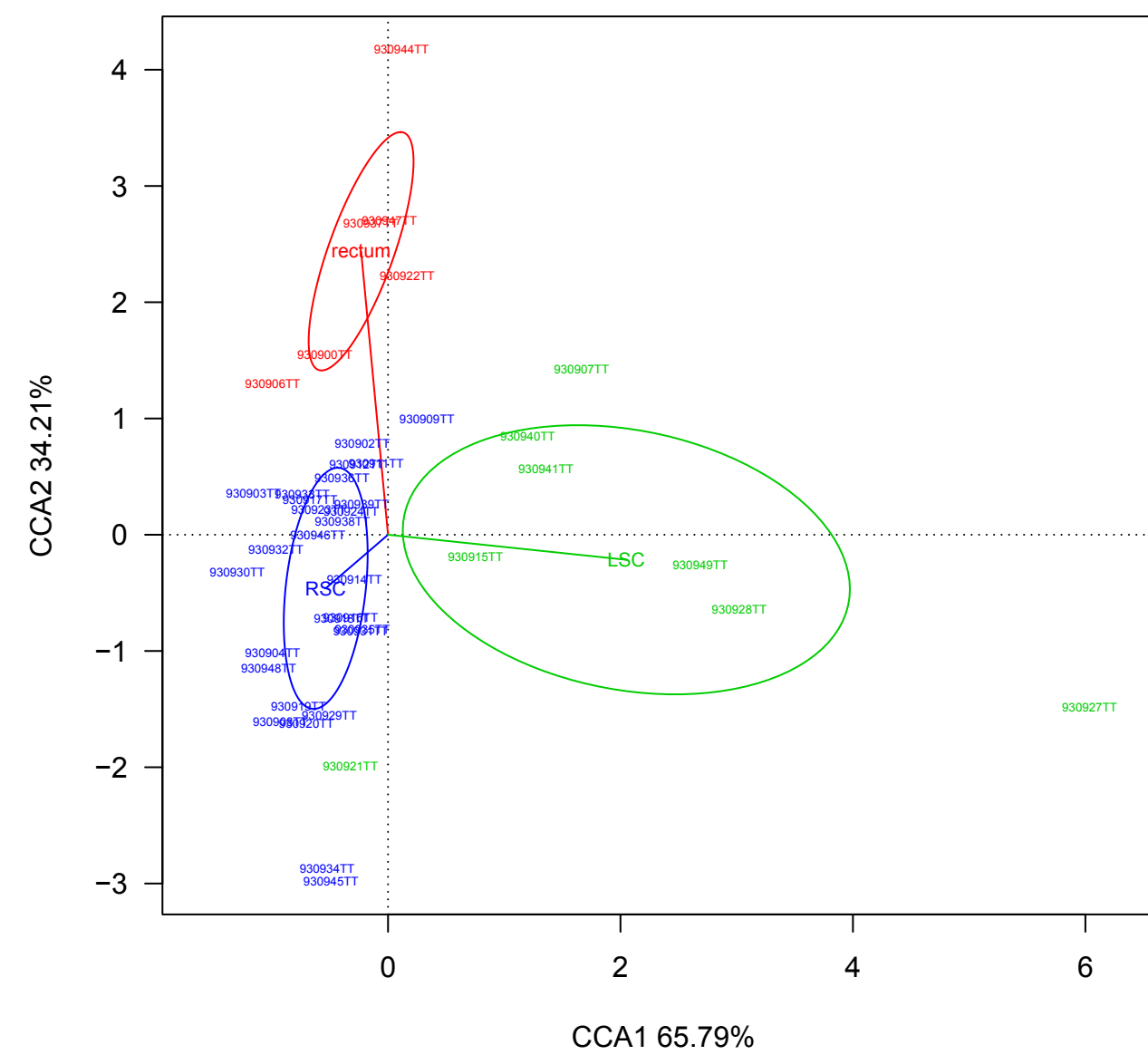
all location NT

ADONIS p-value 0.27



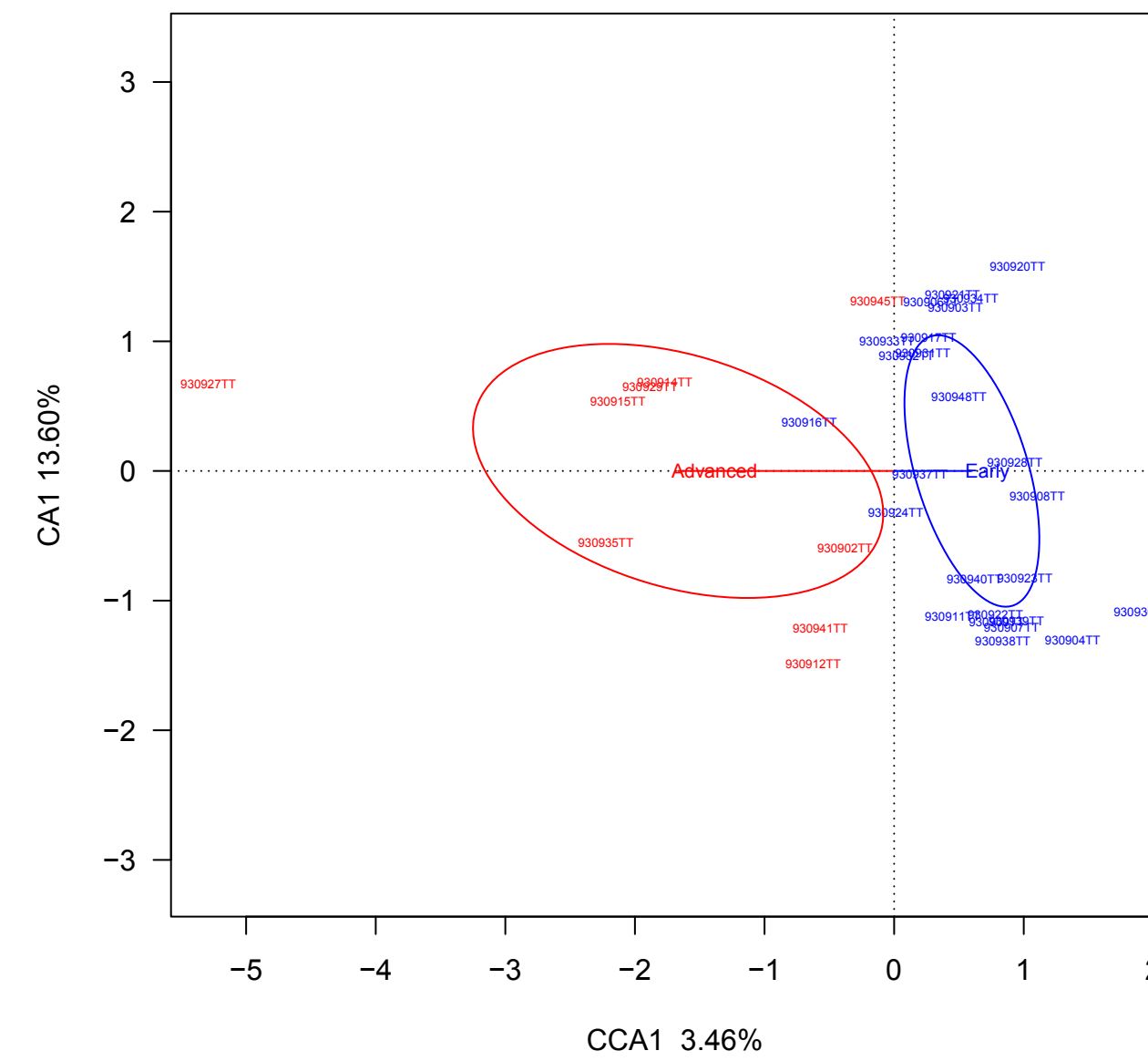
all location TT

ADONIS p-value 0.9



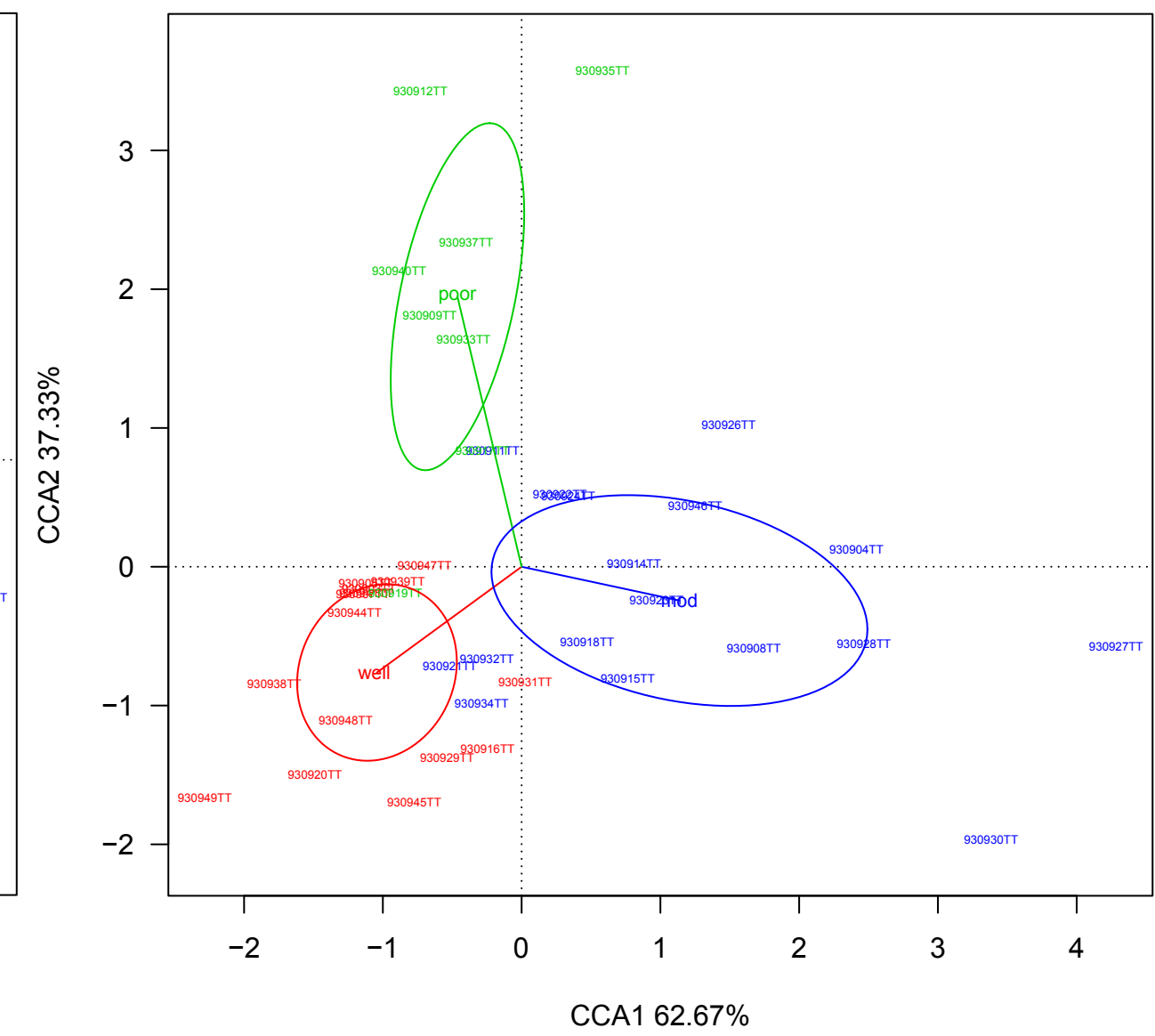
all stage

ADONIS p-value 0.37

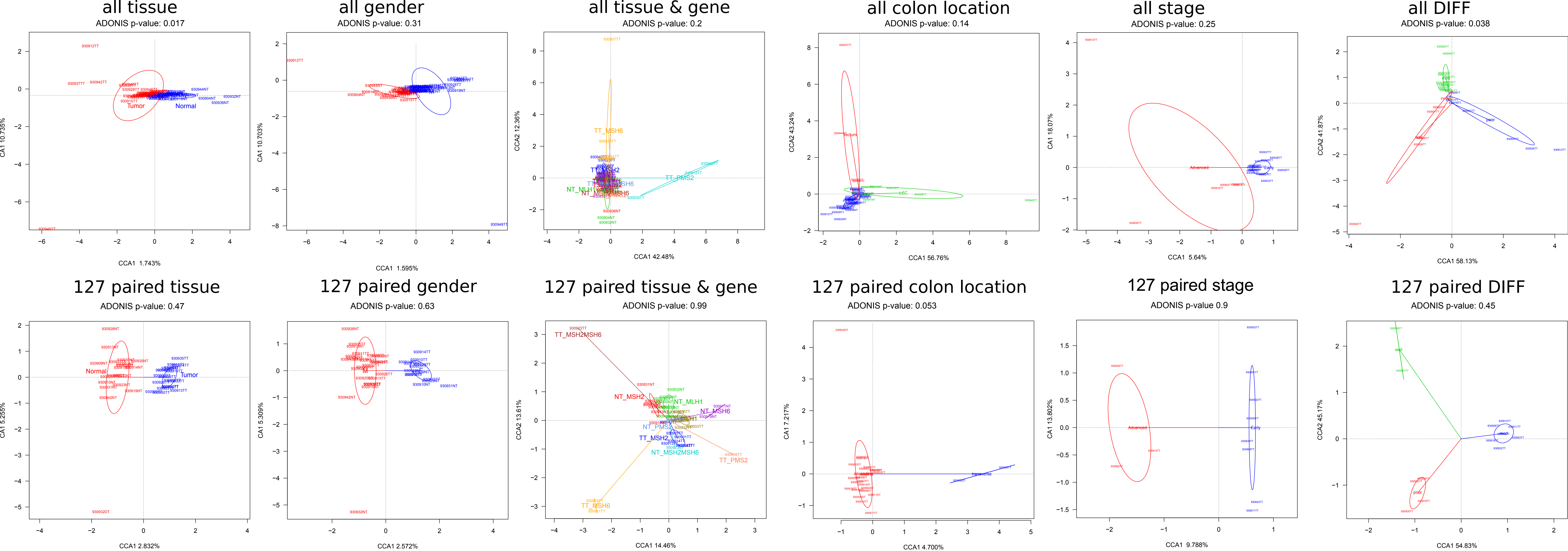


all DIFF

ADONIS p-value 0.96



Supplementary Figure S1. Canonical correspondence analysis of all, paired, and unpaired samples, with no further filtering and normalization step, based on the taxonomy, for the tissue type (normal mucosa tissue vs. tumor tissue), gender of the subjects (females vs.males), mutated gene and tumor location, with distinction between normal and tumor tissue, and by grade of differentiation (poorly, moderately and well differentiated) and stage (early vs. advanced) for tumor tissue samples.



Supplementary Figure S2. Canonical correspondence analysis of all, paired and unpaired samples, as well as of paired-only samples with more than 127 reads, based on function, for tissue type (normal mucosa tissue vs. tumor tissue), gender of the subjects (females vs. males), gene mutated for normal and tumor tissue, stage (early vs. advanced) and by grade of differentiation (poorly, moderately, and well differentiated) for tumor tissue samples . Statistical significance is indicated by the ADONIS tests p-values.