mergePairs says: denoised F1 is paired with R1, here is how abundance is found

F_Reads **F_drp$uniques** **F_dd$denoised**

F_drp$map F_dd$map

1 1 1

40195 12669 359

abundance = intersection of FW and RV IDs, to find actually paired reads, NB: demands FW and RV IDs in same order!

R_Reads **R_drp$uniques** **R_dd$denoised**

R_drp$map R_dd$map

1 1 1

42345 12745 275