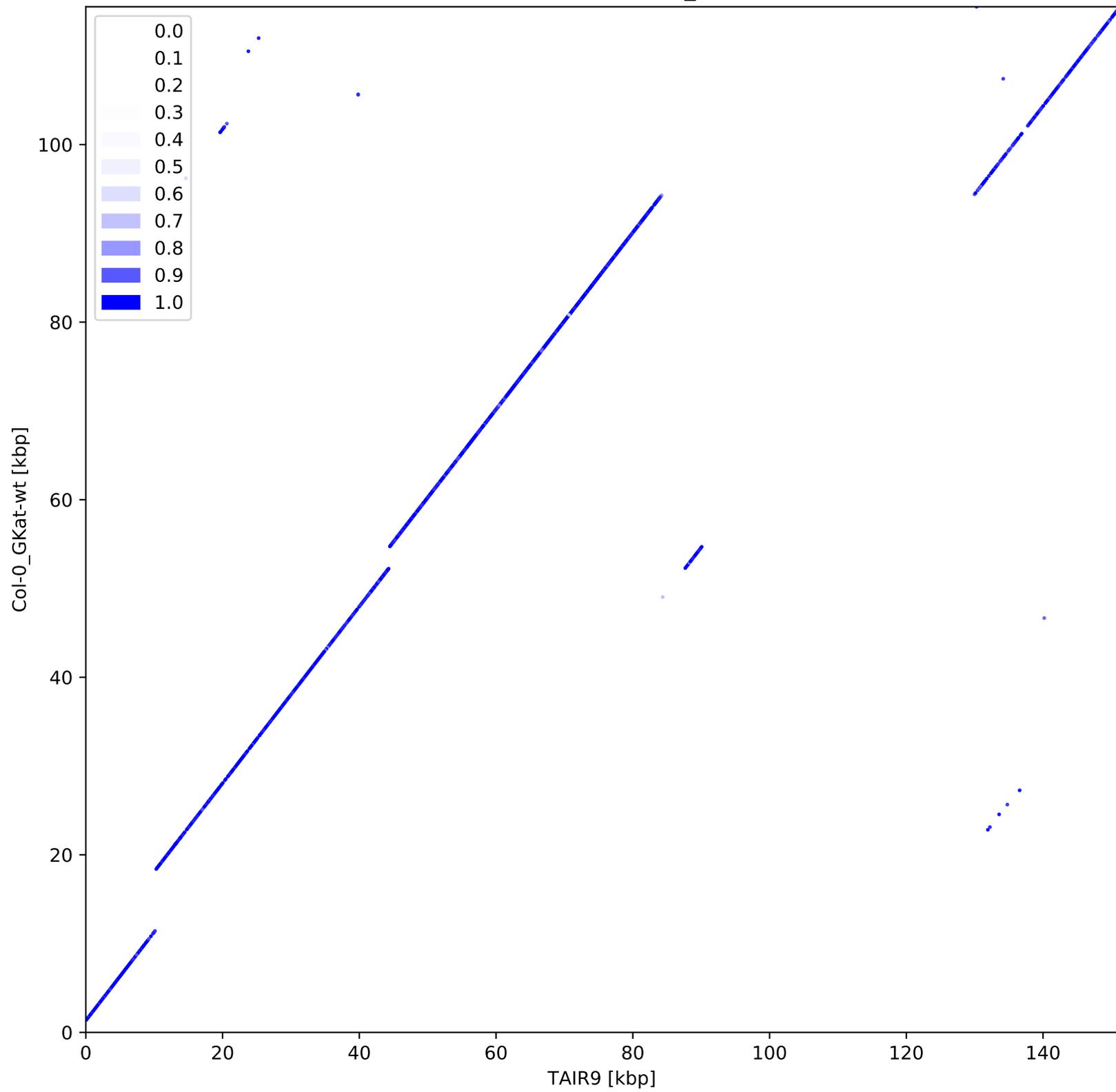


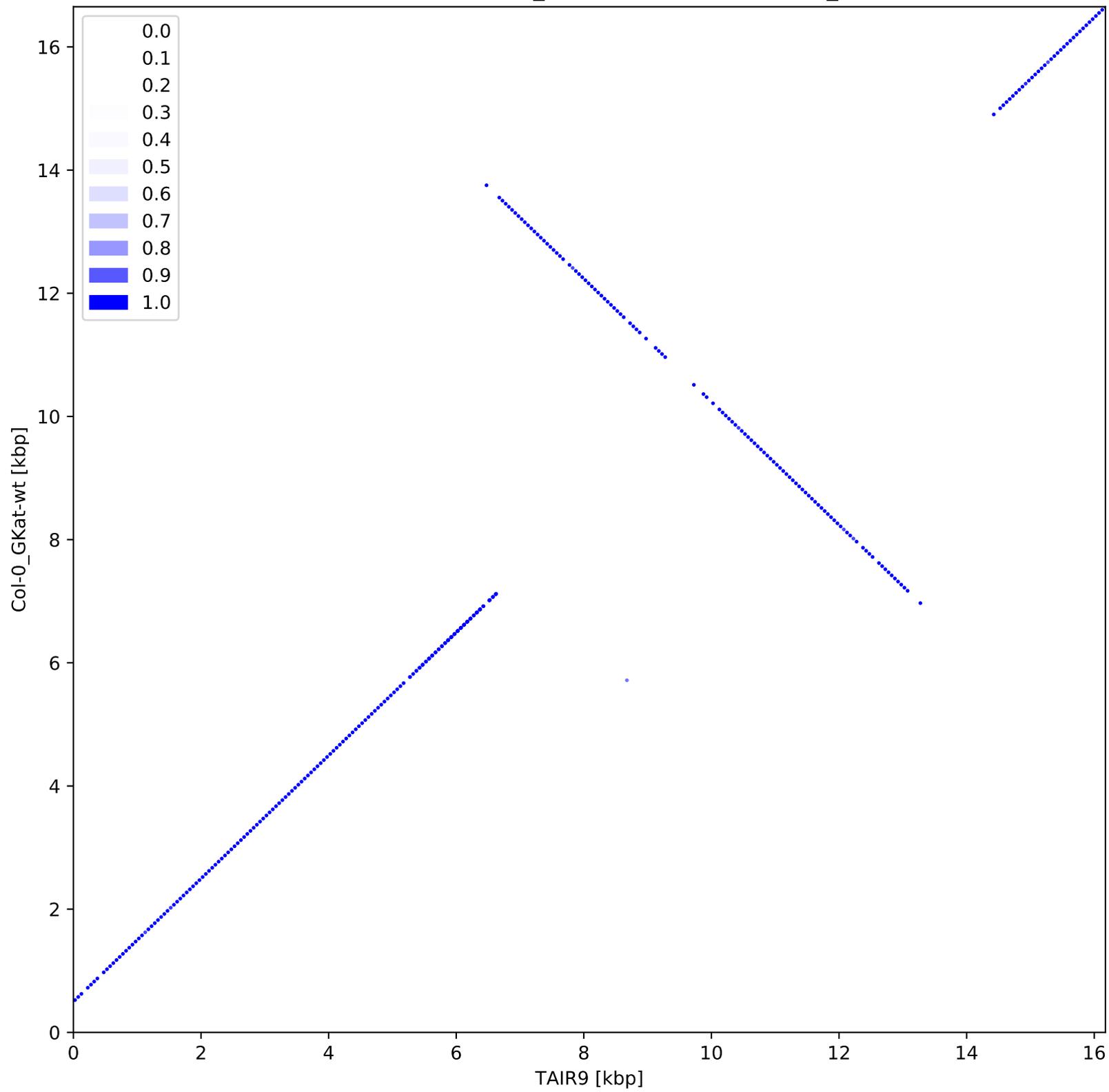
Additional file 11: Dot plots between TAIR9 and Col-0_GK-wt for potential errors in the reference sequence.

These figures were generated based on a previously described script (Pucker et al. (2019), PLoS-One 14:e0216233). The intensity of blue coloration indicates the sequence similarity of BLAST hits. Structural variants between both genome sequences are revealed by dots that are not located on the expected central diagonal line from lower left to upper right. Titles of individual figures indicate the displayed region of the TAIR9 reference sequence, the AGIs of effected genes, and the IDs of overlapping BACs.

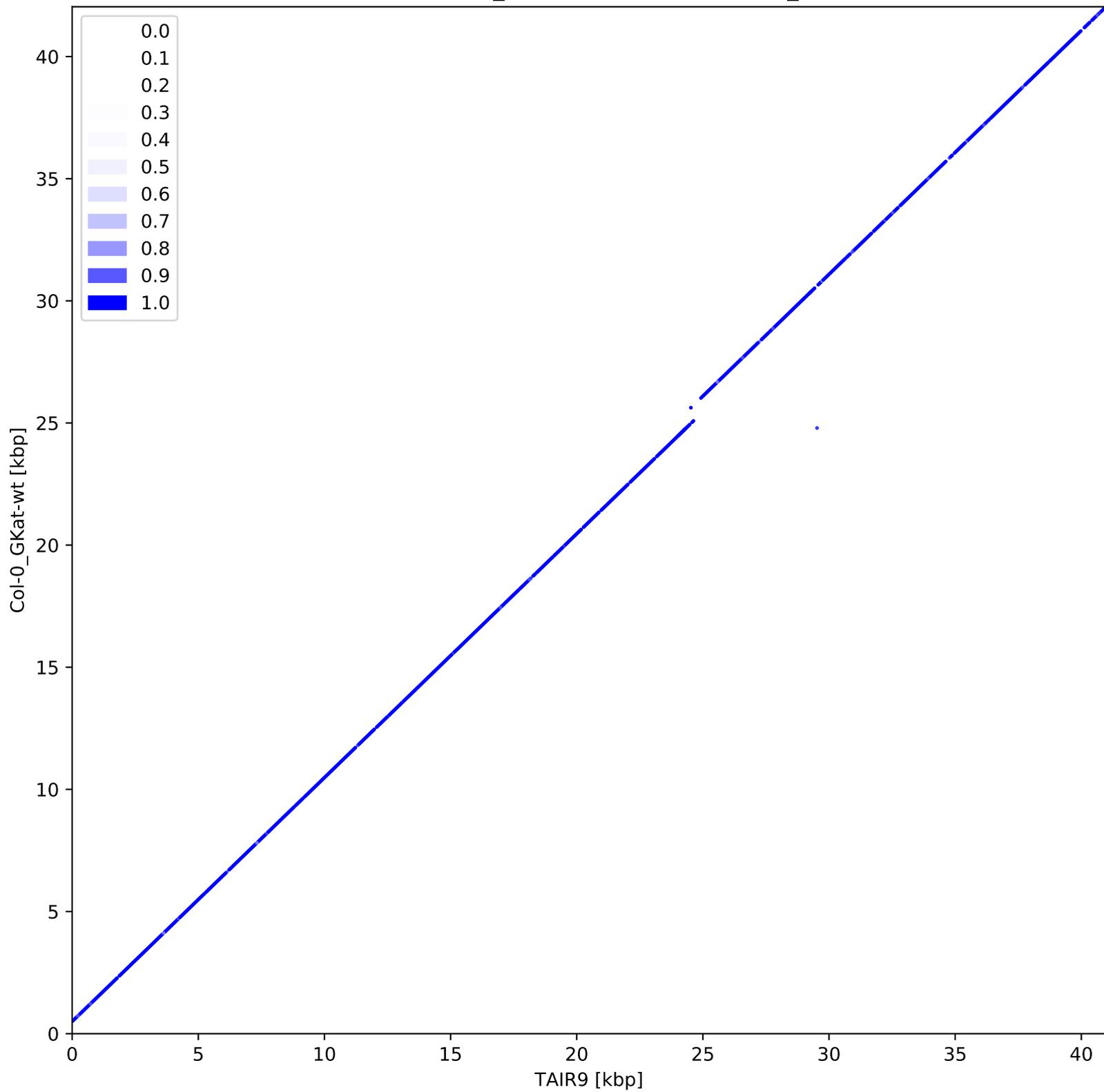
Chr1:14300000-14450000_F8L2;F2C1



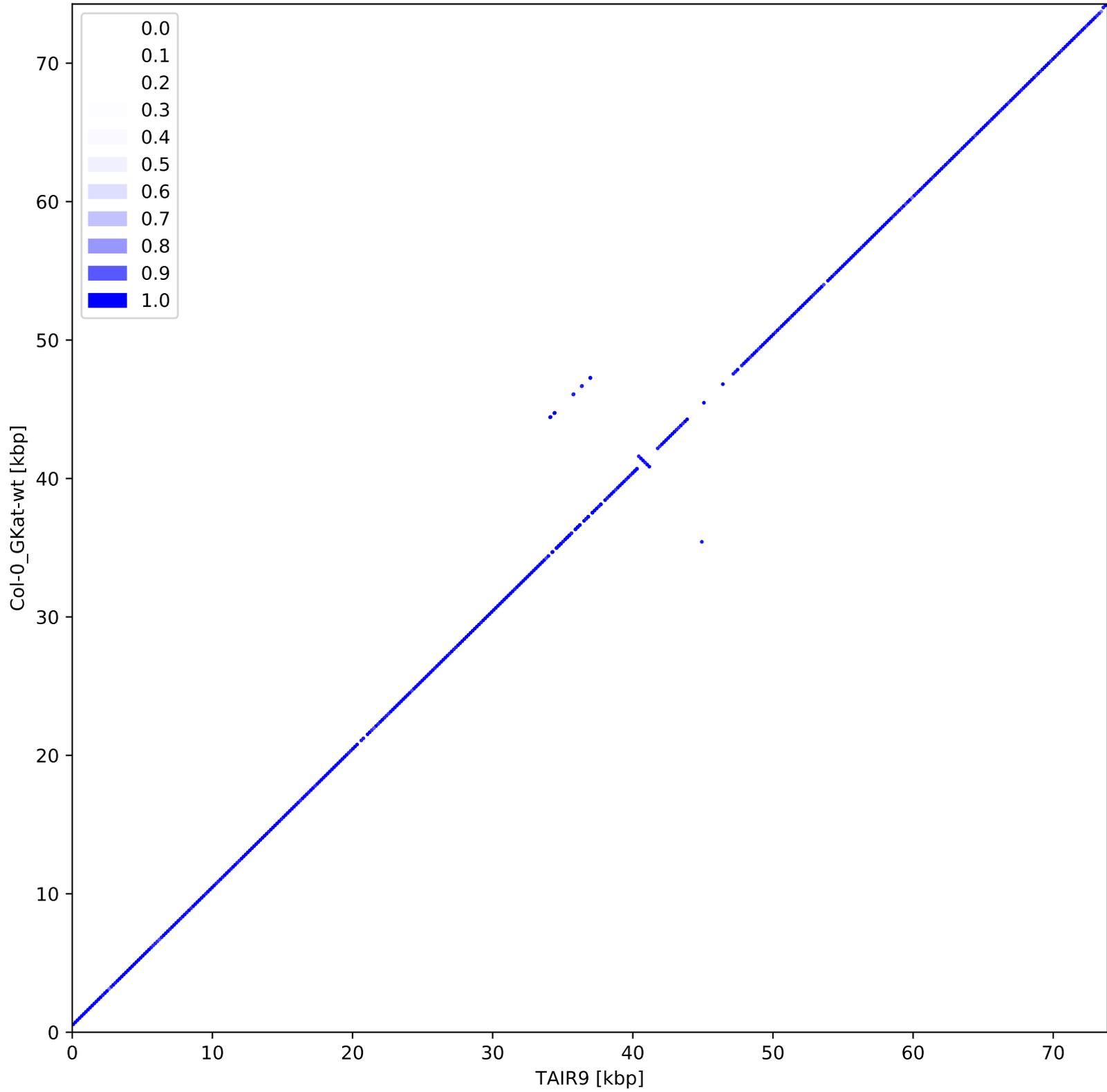
Chr1:2450800-2466000_AT1G07910...AT1G07950_T6D22



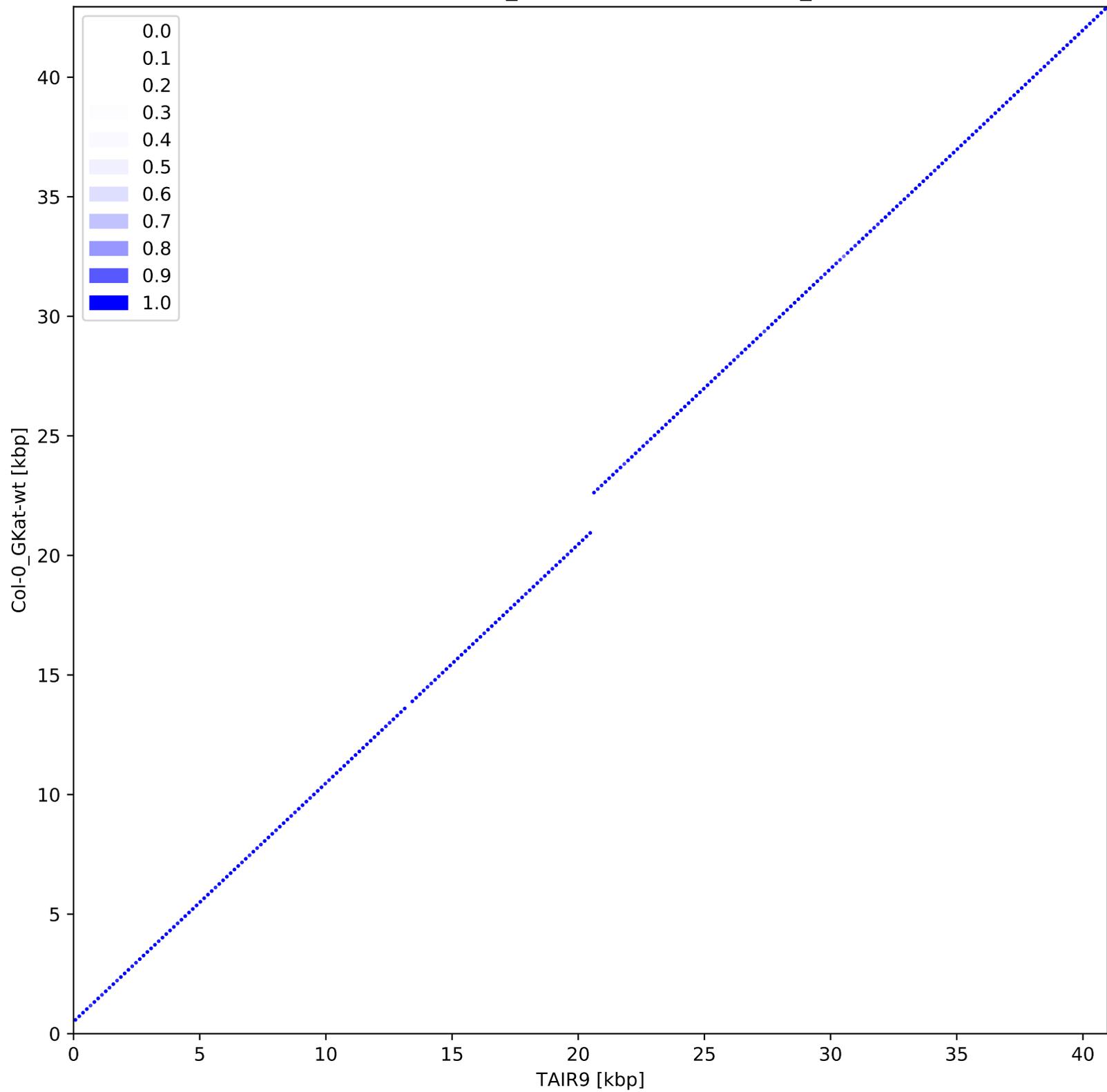
Chr1:7412700-7452700_AT1G21160...AT1G21280_T22I11;F16F4



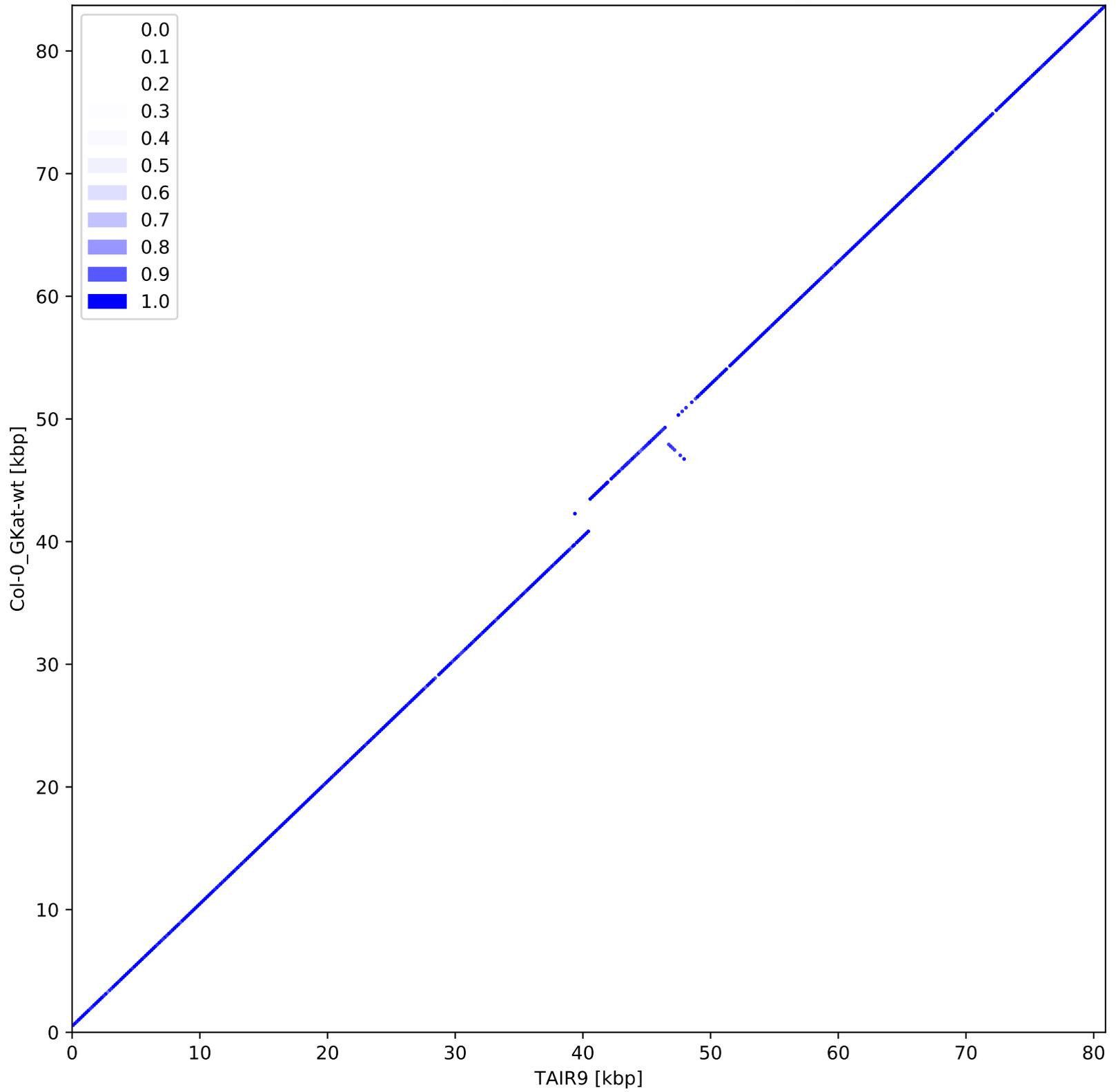
Chr2:851300-941300_AT2G02930...AT2G03130_T17M13;T18E12



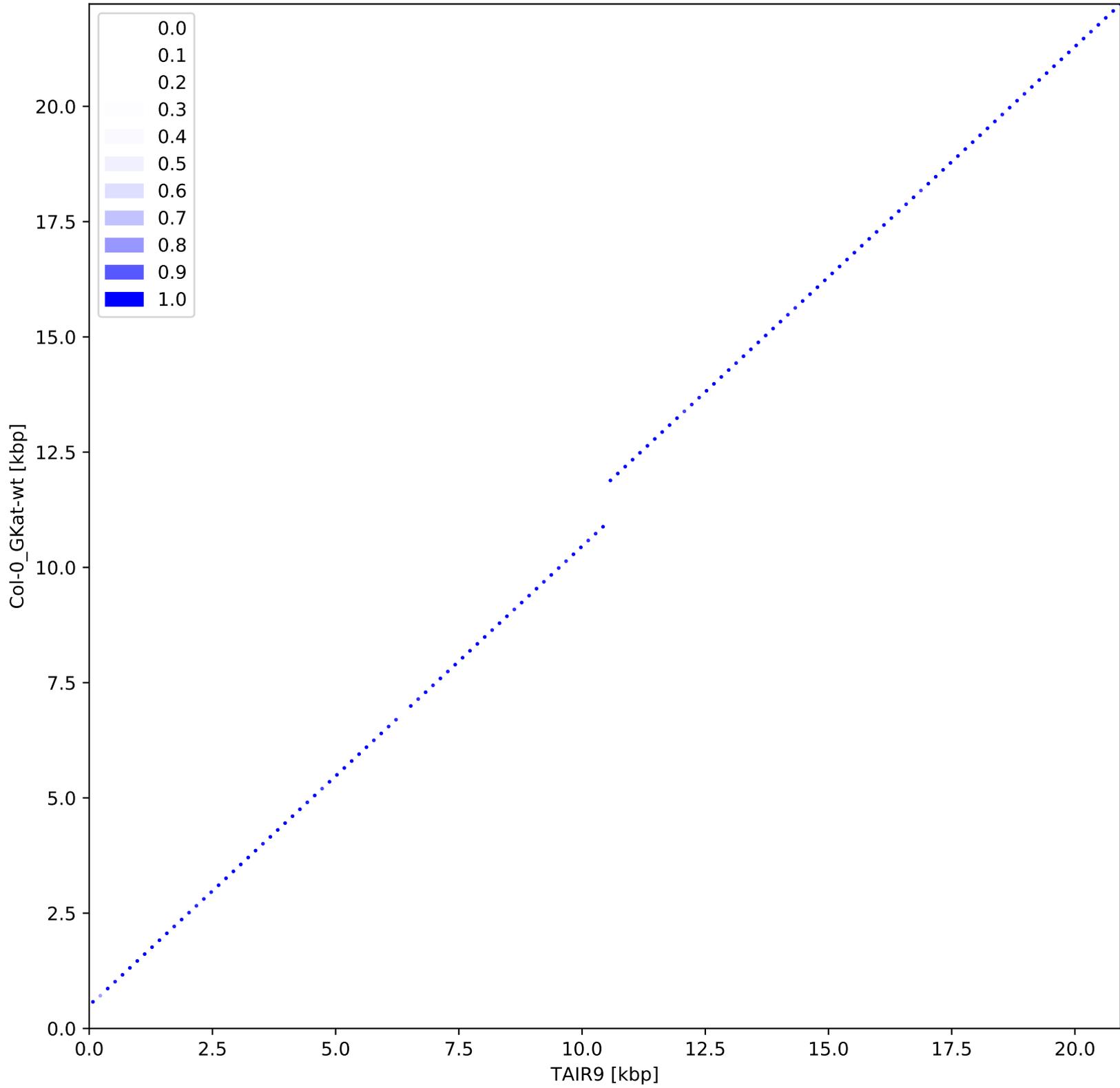
Chr2:13939000-13979000_AT2G32860...AT2G32950_F24L7;T21L14



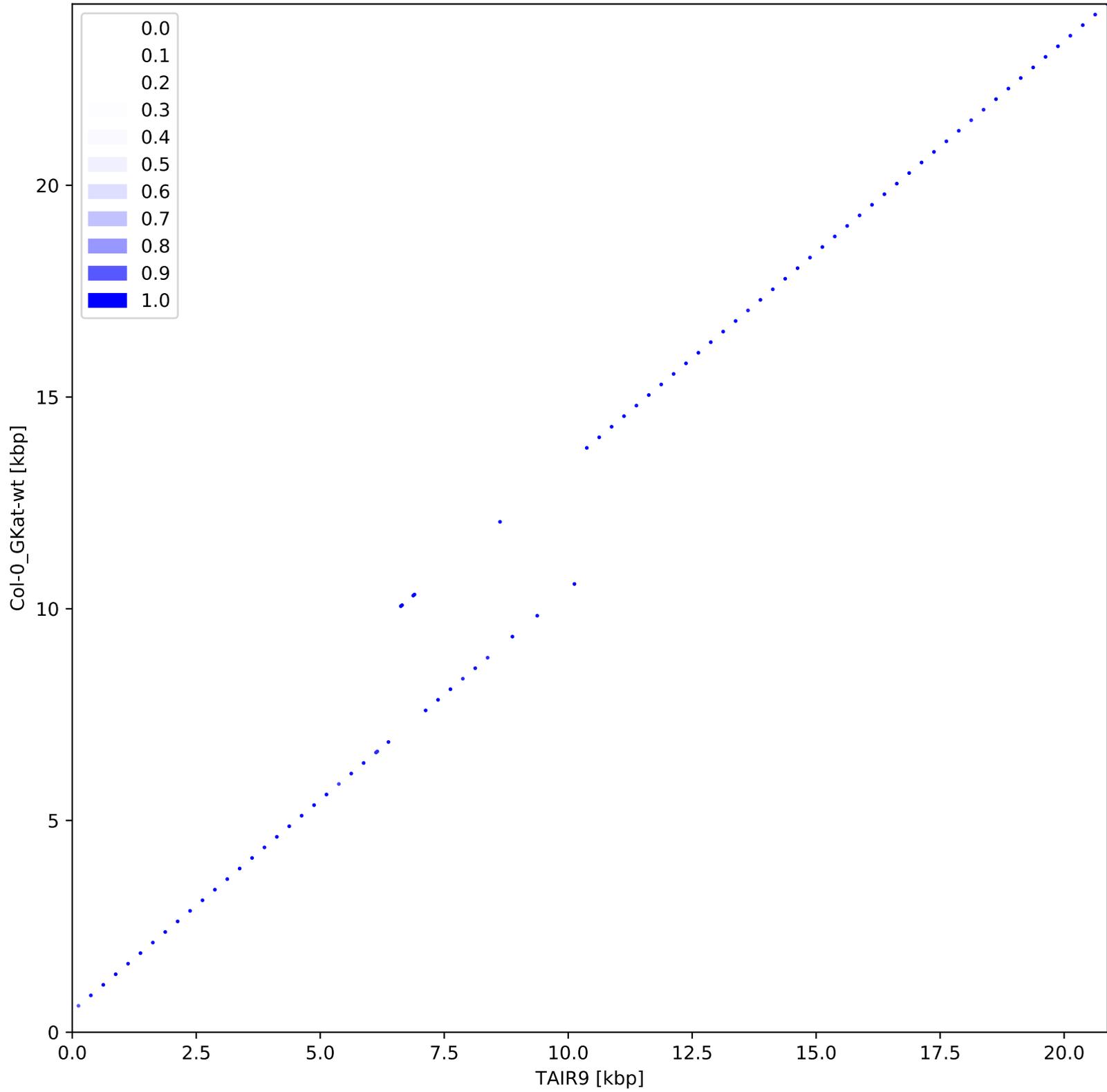
Chr3:1921700-2001700_AT3G06340...AT3G06483_F28L1;F5E6



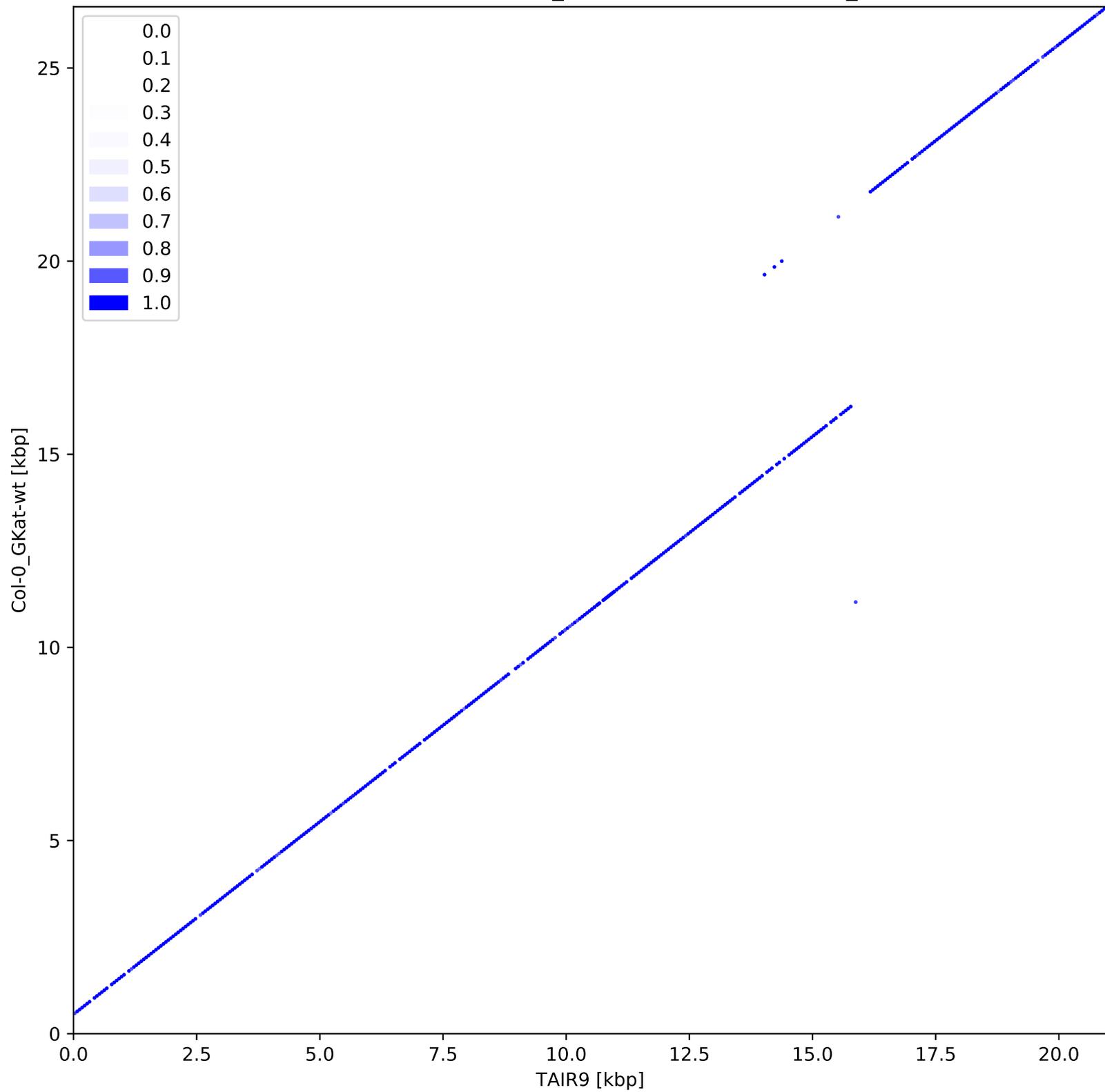
Chr3:8891300-8911300_AT3G24460...AT3G24490_MXP5;MOB24



Chr4:5576600-5596600_AT4G08730...AT4G08760_T32A17



Chr5:16385200-16405200_AT5G40890...AT5G40930_MHK7



Chr5:21221300-21421300_AT5G52270...AT5G52860_F17P19;MXC20

