

balanced trans skipped: (1, 'balanced_translocation', ['2.1.wt(35+).34+.4+', '4.2.mt(35+).4+.q-ter'])

- X
- X
- X

balanced trans skipped: (2, 'balanced_translocation', ['2.2.mt(4+).35+.q-ter', '4.1.wt(4+).3+.35+'])

- X
- X
- X

inv(9)(p13.3p13.1)

- inversion on Chr9: 33582925(p13.3) - 38561385(p13.1)
- all genes near breakpoints: ['FAM138A', 'ALDH1B1', 'PTENP1', 'AQP7', 'FAM201A', 'MIR1302-10', 'SUGT1P1', 'ANKRD18B', 'IGFBPL1', 'ANXA2P2', 'FAM138F', 'PRSS3', 'FOXD4', 'MIR6851', 'NOL6', 'CBWD1', 'MIR1302-9', 'MIR1302-11', 'FAM95C', 'ANKRD18A', 'DDX11L5', 'PGM5P3-AS1', 'FAM138C', 'PTENP1-AS', 'AQP3', 'WASHC1', 'MIR1302-2', 'LINC01251']
- genes near breakpoints documented in DDG2P: None

dup(15)(q21.3)

- tandem duplication on Chr15: 53582371(q21.3) - 54147634(q21.3)
- all genes near breakpoints: ['LOC645202', 'MIR4509-2', 'LOC100132202', 'MIR1268A', 'MIR4509-1', 'MIR4509-3', 'WDR72', 'GOLGA8F', 'GOLGA8G', 'HERC2', 'UNC13C']
- genes near breakpoints documented in DDG2P:
HERC2(605837): HERC2-related neurodevelopmental disorder(615516)
- all genes with +1 CN: ['WDR72', 'UNC13C']
- genes with +1 CN documented in DDG2P: None