|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Pt ID | Cardiac anomaly | Additional anomalies | Microarray results (ISCN) | Nature/syndrome | Size | Pathogenicity | Contribution to phenotype | Gest. at testing (wks) | Outcome |
| CHD015 | VSD, HRHS, Pulmonary atresia | ACC, VM | 46,XX,der(8)t(?1;8)(q?31;p23.3) | Unbalanced translocation | NA | Pathogenic | Full | 20+6 | TOP |
| CHD029 | VSD | DWM | arr 22q11.21(18,894,820-21,457,610)x1 dn | Di George | ~2.6Mb | Pathogenic | Full | 19+3 | TOP |
| CHD042 | Pulmonary atresia |  | 46,XX.ish del(22)(q11.2q11.2)(TBX1-)  | Di George | NA | Pathogenic | Full | 33+6 | LB |
| CHD050 | Pulmonary atresia, VSD |  | arr [GRCh37] 22q11.21(18894820\_21457610)x1 dn | Di George | ~3Mb | Pathogenic | Full | 21 | TOP |
| CHD053 | TOF |  | 5q35 deletion | Deletion | UK | Pathogenic | Full | 23+4 | LB |
| CHD054 | COA | ACC, Left sided hydrothorax | Trisomy 8 Mosaicism | Trisomy 8 Mosaicism | NA | Pathogenic | Full | 24+5 | TOP |
| CHD055 | DORV, TOF | Small stomach | 46,XX,der(2)t(2;15)(q37;q26.1) | Unbalanced translocation | UK | Pathogenic | Full | 32+6 | UK |
| CHD080  | TGA | Omphalocele | 8p23.3-p21.3 microduplication9q24.3-p22.3 microdeletion | Unbalanced translocation | ~18.99 Mb~16.06Mb | Pathogenic | Full | 20+4 | TOP |
| CHD087 | HLHS |  | arr[GRCh37] 22q11.21(18894865\_21440485)x3 dn | Micro-duplication | ~2.8Mb | Pathogenic | Partial | 22+6 | LB |
| CHD089 | DORV, pulmonary valve atresia |  | arr[GRCh37] Xp21.1(76850115\_76,938,852)x2 mat | Micro-duplication | ~89Kb | Pathogenic | Full | 24+1 | NND |
| CHD091 | VSD, IAA, subaortic stenosis |  | arr[GRCh37] 22q11.21(18706023\_21561492)x1 dn | Di George | ~2.8Mb | Pathogenic | Full | 22+1 | LB |
| CHD096 | TOF | SUA | arr[GRCh37] 22q11.21(18847965\_21505388)x1 dn | Di George | ~2.7Mb | Pathogenic | Full | 20+4 | LB |
| CHD109 | VSD, DORV | Intra-abdominal cyst | 46,XX,der(15)t(15;20)(p11;p11.21 ) matarr [GRCh37] 20p13p11.21(60770\_24031345)x3 | Unbalanced translocation | ~24Mb | Pathogenic | Full | 27+6 | LB |
| CHD113 | TOF, DORV |  | arr[GRCh37] 22q11.21(18919972\_21540318)x1 dn | Di George | ~2.7Mb | Pathogenic | Full | 22+2 | SB |
| CHD127 | Pericardial effusion, ventricular hypertrophy | SUA, short long bones | 45,X[29]/46,X,r(X)(p1?1;p2?10[11].arr[GRCh37] Xp22.33p11.4(76118\_41735358)x1, Xp11.4q22.1(41746183\_100662690)x1~2, Xq22.1q28(100662909\_155246643)x1 | Turner mosaic | ~41.7 Mb Xp~54.6Mb Xq | Pathogenic | Full | 34+3 | LB |
| CHD143 | TOF, IAA |  | arr[GRCh37] 22q11.21(18661699\_21661435)x1 dn | Di George | ~3Mb | Pathogenic | Full | 22+2 | TOP |

Table S2 – Abnormal results detectable by chromosome microarray [Abbreviations ACC = Absent corpus callosum; COA = Coarctation of the aorta; DORV = Double outlet right ventricle; DWM = Dandy Walker Malformation; HLHS = Hypoplastic left heart syndrome; HRHS = Hypoplastic Right Heart Syndrome; IAA = Interrupted aortic arch; LB = Livebirth; NA = Non-applicable; NND = Neonatal death; SB=Stillbirth; SUA = Single umbilical artery; TGA = Transposition of the great arteries; TOF = tetralogy of Fallot; TOP = Termination of pregnancy; UK = Unknown; VM = Ventriculomegaly; VSD = Ventricular septal defect]