**Supplementary Table 1** Genes those are located in 2.11 Mb deleted region on chromosome 13q34

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| **Gene** | **Description** |
| SPACA7 | sperm acrosome associated 7 |
| TUBGCP3 | tubulin, gamma complex associated protein 3. Necessary for microtubule nucleation at the centrosome. |
| ATP11A | ATPase, class VI, type 11A, an integral membrane ATPase. Likely drives the transport of ions such as calcium across membranes. |
| MCF2L | MCF.2 cell line derived transforming sequence-like. Guanine nucleotide exchange factor that potentially links pathways that signal through RAC1, RHOA and CDC42. Catalyzes guanine nucleotide exchange on RHOA and CDC42 and interacts specifically with the GTP-bound form of RAC1, suggesting that it functions as an effecter of RAC1. May also participate in axonal transport in the brain.  |
| F7 | coagulation factor VII (serum prothrombin conversion accelerator) of the blood coagulation cascade |
| F10 | coagulation factor X of the blood coagulation cascade |
| PROZ | protein Z, vitamin K-dependent plasma glycoprotein that regulates blood coagulation. Assist hemostasis by binding thrombin and promoting its association with phospholipid vesicles. Inhibits activity of the coagulation protease factor Xa in the presence of SERPINA10, calcium and phospholipids |
| PCID2 | PCI domain containing 2, expressed in immature and early-stage B lymphocytes and regulates expression of the mitotic checkpoint protein MAD2 |
| CUL4A | cullin 4A, a ubiquitin ligase component of a multimeric complex involved in the degradation of DNA damage-response proteins |
| LMAP1 | lysosomal-associated membrane protein 1, provides selectins with carbohydrate ligands |
| GRTP1 | growth hormone regulated TBC protein 1. May act as a GTPase-activating protein for Rab family protein(s) |
| ADPRHL1 | ADP-ribosylhydrolase like 1, involved in ADP-ribosylation, a posttranslational modification used to regulate protein function |
| DCUN1D2  | DCN1, defective in cullin neddylation 1, domain containing 2. May contribute to neddylation of cullin components of SCF-type E3 ubiquitin ligase complexes. Neddylation of cullins play an essential role in the regulation of SCF-type complexes activity. |
| TMCO3  | transmembrane and coiled-coil domains 3 |
| TFDP1 | transcription factor Dp-1, a member of a family of transcription factors that heterodimerize with E2F proteins to enhance their DNA-binding activity and promote transcription from E2F target genes, involved in cell cycle progression from G1 to S phase |
| ATP4B  | ATPase, H+/K+ exchanging, beta polypeptide |
| GRK1  | G protein-coupled receptor kinase 1, phosphorylates rhodopsin and initiates its deactivation |
| TMEM255B | transmembrane protein 255B  |
| GAS6 | growth arrest-specific 6, a gamma-carboxyglutamic acid (Gla)-containing protein. Ligand for tyrosine-protein kinase receptors AXL, TYRO3 and MER whose signaling is implicated in cell growth and survival, cell adhesion and cell migration. GAS6/AXL signaling plays a role in various processes such as endothelial cell survival during acidification by preventing apoptosis, optimal cytokine signaling during human natural killer cell development, hepatic regeneration, gonadotropin-releasing hormone neuron survival and migration, platelet activation, or regulation of thrombotic responses. |
| RASA3  | RAS p21 protein activator 3, a member of the GAP1 family of GTPase-activating proteins that acts as a suppressor of RAS function, control of cellular proliferation and differentiation |
| CDC16 | cell division cycle 16 homolog. Component of the anaphase promoting complex/cyclosome (APC/C), a cell cycle-regulated E3 ubiquitin ligase that controls progression through mitosis and the G1 phase of the cell cycle. The APC/C complex acts by mediating ubiquitination and subsequent degradation of target proteins |
| UPF3A | UPF3 regulator of nonsense transcripts homolog A, part of a post-splicing multiprotein complex involved in both mRNA nuclear export and mRNA surveillance. Involved in nonsense-mediated decay (NMD) of mRNAs containing premature stop codons by associating with the nuclear exon junction complex (EJC) and serving as link between the EJC core and NMD machinery. |
| CHAMP1 | chromosome alignment maintaining phosphoprotein 1. Required for proper alignment of chromosomes at metaphase and their accurate segregation during mitosis. Involved in the maintenance of spindle microtubules attachment to the kinetochore during sister chromatid biorientation. May recruit CENPE and CENPF to the kinetochore. |

Sources: UCSC Genome Browser and Ensembl Genome browser [www.genecards.org]