|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Defect type** | **Gene** | **Chromosome** | **Location** | **Base change** | **Amino Acid change** | **Isoform**  | **Variant Type** | **Zygosity** | **Inheritance** | **Frequency (gnomAD)** | **CADD** | **CLINVAR** | **HGMD** | **Phenotypic Group** |
| **VEOIBD**  | **EOIBD**  | **PIBD**  |
|  |  |  |
| **UC**  | **CD** | **CD** | **UC** | **CD** |
| **M** | **M** | **M** | **M** | **M** | **M** | **M** | **M** | **M** | **M** | **M** | **F** | **M** | **M** | **M** | **M** | **M** | **M** | **M** | **F** |
| T + B cell defects | CD40LG | X | Exon 5 | G655A | G219R | NM\_000074 | NS | Hem Hom | XL | 0.0092 | 13.0 | B/LB | DFP |  |  |  | **●○** |  |  | **●○** |  | **●○** |  |  |  | **●○** |  |  | **●○** |  |  |  |  |
| WAS | X | Exon 4 | G391A | E131K | NM\_000377 | NS | Hem | XL | 0.0029 | 27.9 | B/LB | DM |  |  |  |  |  |  |  |  |  |  |  |  |  |  | **●○** |  | **●○** |  |  |  |
| WAS | X | Exon 11 | C1378T | P460S | NM\_000377 | NS | Hem | XL | 0.0023 | 15.4 | B/LB | DM? |  |  |  |  |  |  |  |  |  | **●○** | **●○** |  |  |  |  |  |  |  |  |  |
| DKC1 | X | UTR5 | 142C>G |  | NM\_001142463 |  | Hem | XL | 0.0021 | 6.5 | C | DM |  |  |  |  | **●○** |  |  | **●○** |  |  |  |  |  |  |  |  |  |  |  |  |
| Immunoregulation | TRIM22 | 11 | Exon 8 | G962A | R321K | NM\_006074 | NS | Hom | AR | 0.0255 | 25.0 |  | DM |  |  |  |  |  |  |  |  |  |  |  |  |  | **●●** |  |  |  |  |  |  |
| STAT1 | 2 | Exon 10 | G796A | V266I | NM\_139266 | NS | Het | AD | 0.0027 | 8.0 | LB | DM |  | **●** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | **●** | **●** |
| Autoinflammatory | XIAP | X | Exon 7 | A1408T | T470S | NM\_001204401 | NS | Hem | XL | 0.0003 | 11.2 |  | DM? |  |  | **●○** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Phagocytic defects | NCF2 | 1 | Exon 13 | C1167A | H389Q | NM\_001127651 | NS | Hom | AR | 0.0333 | 23.0 | B/LB | DFP |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | **●●** |  |  |
| NCF1 | 7 | Exon 4 | G269A | R90H | NM\_000265 | NS | Hom | AR | 0.0728 | 25.0 |  | DFP | **••** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Others | MASP2 | 1 | Exon 3 | A359G | D120G | NM\_139208 | NS | Hom | AR | 0.0252 | 27.2 | C | DFP |  |  |  |  |  |  |  |  |  |  |  | **••** |  |  |  |  |  |  |  |  |

Supplementary table 3- Variants identified that are ‘Disease-associated polymorphisms with supporting functional evidence’, ‘Disease causing mutation’, ‘Probable/possible pathological mutation’ (HGMD) or CADD >20, MAF <0.01, in the correct zygosity to cause disease.

NS- nonsynonymous, S- synonymous, Hom- homozygote, Het- heterozygote, XL- x-linked recessive, AR- autosomal recessive, AD- autosomal dominant, M- male, F- Female, UC- ulcerative colitis, CD- Crohn’s disease

CLINVAR- B- benign, LB- likely benign, C- conflicting evidence, U- uncertain significance

HGMD- DFP- Disease-associated polymorphism with supporting functional evidence, DM- Disease causing mutation, DM?- probable/possible pathological mutation

**●○** Hemizygous variant

● Heterozygous variant

●● Homozygous variant