**Supplementary Tables**

**Supplementary Table1.** Primer summary for candidate variations

| Primer | Sequence 5' to 3' | Length (bp) |
|---|---|---|
| rs 113527563-F | GGTGTAGCTTATTTTCCGCG | 275 |
| rs 113527563-R | GATGATGACCAGCTTCGAGAG | |
| rs 11570255-F | GCGCCTGATCTAGGTTCATG | 253 |
| rs 11570255-R | CGTGCGGGTAGTCGTTGC | |
| rs 12536873-F | GGCTGAGTGGGAAGGTGTG | 182 |
| rs 12536873-R | CTTGGCATGAGCAGTTGTTG | |
| rs 13051496-F | CACAACTTTGACACCACCAAG | 296 |
| rs 13051496-R | AGCAGCAGCCTCTTCTTGG | |
| rs 28927681-F | AGGGTCAAACCAGGCCAG | 237 |
| rs 28927681-R | GCCACAGGATTCACCACG | |
| rs 3741231-F | AGCAGGTACCAGTGCTCCAG | 316 |
| rs 3741231-R | CCCGTGTTTGACGAGACCT | |
| rs 4251691-F | CTTTGGCTGTGTGCTTGGC | 353 |
| rs 4251691-R | TGCACACGGCCATAGAGG | |
| rs 6267-F | GAGTTCATCCTGCAGCCCAT | 234 |
| rs 6267-R | GCTTTGATGCCTGGTCCTG | |
| rs 8063446-F | CTCACTTTGCAGGAGCCTG | 214 |
| rs 8063446-F | GTAATCTCCGCGCCTCG | |

**Supplementary Table 2. Summarize of different genetic model**

| SNVs | Allele model | Dominant model | Recessive model | Homozygous model | Heterozygous model |
|---|---|---|---|---|---|
| ANKRD11 rs113527563 （G>C） | (GG*2+GC) vs. (CC*2+GC) | (CC+GC) vs. GG | CC vs. (GC+GG) | CC vs. GG | GC vs. GG |
| COL6A1 rs13051496（C>T） | (CC*2+CT) vs. (TT*2+CT) | (TT+CT) vs. CC | TT vs. (CT+CC) | TT vs. CC | CT vs. CC |
| COMT rs6267（G>T） | (GG*2+GT) vs. (TT*2+GT) | (TT+GT) vs. GG | TT vs. (GT+GG) | TT vs. GG | GT vs. GG |
| EDN3 rs11570255（G>A） | (GG*2+GA) vs. (AA*2+GA) | (AA+GA) vs. GG | AA vs. (GA+GG) | AA vs. GG | GA vs. GG |
| FAM129A rs28927681（A>G） | (AA*2+AG) vs. (GG*2+AG) | (GG+AG) vs. AA | GG vs. (AG+AA) | GG vs. AA | AG vs. AA |
| RECQL4 rs4251691（G>A） | (GG*2+GA) vs. (AA*2+GA) | (AA+GA) vs. GG | AA vs. (GA+GG) | AA vs. GG | GA vs. GG |
| SLC7A6OS rs8063446（A>C） | (AA*2+AC) vs. (CC*2+AC) | (CC+AC) vs. AA | CC vs. (AC+AA) | CC vs. AA | AC vs. AA |
| SSPO rs12536873（G>T） | (GG*2+GT) vs. (TT*2+GT) | (TT+GT) vs. GG | TT vs. (GT+GG) | TT vs. GG | GT vs. GG |
| SYT8 rs3741231（C>G） | (CC*2+CG) vs. (GG*2+CG) | (GG+CG) vs. CC | GG vs. (CG+CC) | GG vs. CC | CG vs. CC |

**Supplementary Table3.** Quality control of pooled whole-exome sequencing

| Sample | HC-pool | IBS-pool | DD-pool |
|---|---|---|---|
| Total effective reads | 42682142 | 102321372 | 125776375 |
| Reads uniquely mapped to genome% | 94.97 | 95.21 | 93.92 |
| Average read length (bp) | 150 | 150 | 147 |
| GC Content% | 53.00 | 54.32 | 52.00 |
| Mismatch rate in target region% | 0.33 | 0.33 | 0.30 |
| Mismatch rate in all effective sequence% | 0.30 | 0.29 | 0.29 |
| Base covered on target | 60429893 | 60448083 | 60446770 |
| Coverage of target region% | 99.96 | 99.99 | 99.98 |
| Base covered near target | 92590612 | 95557787 | 92465081 |
| Coverage of flanking region% | 95.18 | 98.23 | 95.05 |
| Fraction of target covered with at least 4x% | 99.68 | 99.93 | 99.94 |
| Fraction of target covered with at least 10x% | 98.17 | 99.71 | 99.79 |
| Fraction of target covered with at least 20x% | 99.49 | 98.78 | 99.28 |
| Fraction of target covered with at least 100x% | 91.01 | 85.54 | 81.28 |

Note: IBS: irritable bowel syndrome; DD: depressive disorder; HC: healthy control; G: guanine; C: cytosine

**Supplementary Table4.** Quality control of pooled whole-exome sequencing

| Group | Gene | avsnp150 | AltF | ClinVar |
|---|---|---|---|---|
| HI; HD | *COL6A1* | rs13051496 | 0.0615 | Collagen VI-related myopathy |
| HI; HD | *FAM129A* | rs28927681 | 0.0823 | Not Reported |
| HI; HD | *SSPO* | rs12536873 | 0.2361 | Not Reported |
| HI; HD | *SYT8* | rs3741231 | 0.3026 | Not Reported |
| HI | *ANKRD11* | rs113527563 | 0.245 | Not Reported |
| HI | *RECQL4* | rs4251691 | 0.4762 | Not Reported |
| HI | *SLC7A6OS* | rs8063446 | 0.0575 | Not Reported |
| HD | *COMT* | rs6267 | 0.0347 | Schizophrenia |
| HD | *EDN3* | rs11570255 | 0.0179 | Hirschsprung disease 4 |

Note: avsnp150: SNPs reference database; HI: IBS-pool compared with HC-pool; HD: DD-pool compared with HC-pool; AltF: frequency of altered variation in 1000 Genomes Asian population; ClinVar: Clinical Genome Resource.

**Supplementary Table 5.** Frequency of candidate variants validation

| SNVs | Detective rate (%) | Genotype | HC | IBS | DD | HC $P_{HWE}$ |
|---|---|---|---|---|---|---|
| ANKRD11 rs113527563 (G>C) | 99. 76 | GG | 79 | 62 | 86 | 0.21 |
| | | GC | 49 | 51 | 57 | |
| | | CC | 13 | 9 | 7 | |
| COL6A1 rs13051496 (C>T) | 98. 79 | CC | 105 | 106 | 129 | 0.57 |
| | | CT | 29 | 15 | 19 | |
| | | TT | 4 | 1 | 2 | |
| COMT rs6267 (G>T) | 99. 76 | GG | 121 | 100 | 131 | 0.01 |
| | | GT | 1 | 0 | 0 | |
| | | TT | 1 | 1 | 0 | |
| EDN3 rs11570255 (G>A) | 99. 76 | GG | 133 | 117 | 147 | 0.82 |
| | | GA | 7 | 5 | 3 | |
| | | AA | 0 | 0 | 0 | |
| FAM129A rs28927681 (A>G) | 100.00 | AA | 99 | 117 | 99 | 0.25 |
| | | AG | 23 | 24 | 23 | |
| | | GG | 0 | 0 | 0 | |
| RECQL4 rs4251691 (G>A) | 99. 76 | GG | 56 | 49 | 53 | 0.83 |
| | | GA | 77 | 79 | 54 | |
| | | AA | 17 | 13 | 15 | |
| SLC7A6OS rs8063446 (A>C) | 99. 76 | AA | 108 | 102 | 134 | 0.32 |
| | | AC | 30 | 20 | 16 | |
| | | CC | 1 | 0 | 0 | |
| SSPO rs12536873 (G>T) | 99. 52 | GG | 71 | 68 | 71 | 0.96 |
| | | GT | 44 | 66 | 44 | |
| | | TT | 7 | 7 | 7 | |
| SYT8 rs3741231 (C>G) | 95. 16 | CC | 90 | 80 | 119 | 0.01 |
| | | CG | 0 | 0 | 0 | |
| | | GG | 17 | 12 | 15 | |

Note: $P_{HWE}$: significance of H-W equilibrium analysis in healthy control

**Supplementary Table 6. Minor allele frequency of candidate SNPs**

| | HC | IBS | DD | Eastern Asian |
|---|---|---|---|---|
| ANKRD11rs113527563（G>C） | 0.266 | 0.283 | 0.237 | 0.245 |
| COL6A1rs13051496（C>T） | 0.077 | 0.070 | 0.134 | 0.062 |
| COMTrs6267（G>T） | 0.012 | 0.010 | 0.000 | 0.035 |
| EDN3rs11570255（G>A） | 0.021 | 0.025 | 0.010 | 0.018 |
| FAM129Ars28927681（A>G） | 0.094 | 0.085 | 0.097 | 0.082 |
| RECQL4rs4251691（G>A） | 0.344 | 0.372 | 0.370 | 0.476 |
| SLC7A6OSrs8063446（A>C） | 0.082 | 0.115 | 0.053 | 0.058 |
| SSPOrs12536873（G>T） | 0.238 | 0.284 | 0.211 | 0.236 |
| SYT8rs3741231（C>G） | 0.130 | 0.159 | 0.112 | 0.303 |

Note: 1000 Genomes of Eastern Asian, Released July 9, 2019