### Supplementary Table 1. Genetic mutational profiles of MDS patients with or without AID

| Variable                          | AID (n = 16) | No AID (n = 57) | p value |
|-----------------------------------|--------------|----------------|---------|
| Presence of genetic mutation      | 11 (68.8)    | 46 (80.7)      | 0.32    |
| No. of mutated genes              |              |                | 0.32    |
| 0                                 | 5 (31.3)     | 11 (19.3)      |         |
| 1                                 | 3 (18.8)     | 13 (22.8)      |         |
| 2                                 | 3 (18.8)     | 10 (17.5)      |         |
| 3                                 | 1 (6.3)      | 12 (21.1)      |         |
| 4                                 | 4 (25.0)     | 4 (7.0)        |         |
| 5                                 | 0            | 2 (3.5)        |         |
| 6                                 | 0            | 4 (7.0)        |         |
| 7                                 | 0            | 1 (1.8)        |         |
| Classifier of mutated genes       |              |                |         |
| Chromatin modification             |              |                |         |
| *ASXL1*                           | 3 (18.8)     | 13 (22.9)      | 0.84    |
| *EZH2*                            | 1 (6.3)      | 4 (7.0)        | 1.0     |
| Splicing                          |              |                |         |
| *PRPF40B*                         | 0            | 1 (1.8)        | 1.0     |
| *SF3B1*                           | 2 (12.5)     | 4 (7.0)        | 0.61    |
| *SRSF2*                           | 2 (12.5)     | 3 (5.3)        | 0.3     |
| *U2AF1*                           | 0            | 9 (15.8)       | 0.19    |
| *U2AF2*                           | 0            | 1 (1.8)        | 1.0     |
| *ZRSR2*                           | 1 (6.3)      | 2 (3.5)        | 0.53    |
| DNA methylation                   |              |                |         |
| *DNMT3A*                          | 1 (6.3)      | 5 (8.8)        | 0.86    |
| *IDH2*                            | 0            | 3 (5.3)        | 1.0     |
| *TET2*                            | 5 (31.3)     | 3 (5.3)        | 0.001   |
| Transcription                     |              |                |         |
| *BCOR*                            | 0            | 4 (7.0)        | 0.57    |
| *BRD4*                            | 0            | 1 (1.8)        | 1.0     |
| *CEBPA*                           | 0            | 3 (5.3)        | 1.0     |
| *EGR2*                            | 0            | 1 (1.8)        | 1.0     |
| *ETV6*                            | 0            | 1 (1.8)        | 1.0     |
| *GATA1*                           | 0            | 1 (1.8)        | 1.0     |
| *GATA2*                           | 0            | 1 (1.8)        | 1.0     |
| *IKZF1*                           | 0            | 1 (1.8)        | 1.0     |
| *NPM1*                            | 0            | 2 (3.5)        | 1.0     |
| *RUNX1*                           | 1 (6.3)      | 4 (7.0)        | 1.0     |
| *TP53*                            | 2 (12.5)     | 12 (21.1)      | 0.31    |
| *WT1*                             | 1 (6.3)      | 2 (3.5)        | 0.53    |
| Receptor kinase                   |              |                |         |
| *BIRC3*                           | 0            | 1 (1.8)        | 1.0     |
| *CSF3R*                           | 0            | 3 (5.3)        | 1.0     |
| *JAK2*                            | 0            | 3 (5.3)        | 1.0     |
### Supplementary Table 1. Continued

| Variable         | AID (n = 16) | No AID (n = 57) | p value |
|------------------|--------------|-----------------|---------|
| **MPL**          | 0            | 2 (3.5)         | 1.0     |
| **NOTCH1**       | 0            | 4 (7.0)         | 0.57    |
| **RAS pathway**  |              |                 |         |
| **NF1**          | 0            | 2 (3.5)         | 1.0     |
| **NRAS**         | 0            | 2 (3.5)         | 1.0     |
| **PTPNII**       | 0            | 1 (1.8)         | 1.0     |
| **Signaling**    |              |                 |         |
| **PRKD3**        | 1 (6.3)      | 0               | 0.22    |
| **SH2B3**        | 0            | 1 (1.8)         | 1.0     |
| **Cell cycle/DNA repair** | | | |
| **RB1**          | 1 (6.3)      | 1 (1.8)         | 0.39    |
| **ATM**          | 0            | 3 (5.3)         | 1.0     |
| **BARD1**        | 0            | 1 (1.8)         | 1.0     |
| **Cohesin**      |              |                 |         |
| **SMC1A**        | 0            | 1 (1.8)         | 1.0     |
| **SMC3**         | 0            | 1 (1.8)         | 1.0     |
| **STAG2**        | 1 (6.3)      | 3 (5.3)         | 1.0     |
| **Others**       |              |                 |         |
| **DIS3**         | 0            | 1 (1.8)         | 1.0     |
| **FAT4**         | 0            | 3 (5.3)         | 1.0     |
| **LAMB4**        | 0            | 2 (3.5)         | 1.0     |
| **LRP1B**        | 0            | 2 (1.6)         | 1.0     |
| **PLEKHG5**      | 1 (6.3)      | 3 (5.3)         | 1.0     |
| **POLG**         | 1 (6.3)      | 1 (1.8)         | 0.39    |
| **RIPKI**        | 0            | 1 (1.8)         | 1.0     |
| **SCRIB**        | 0            | 1 (1.8)         | 1.0     |
| **SETBP1**       | 0            | 1 (1.8)         | 1.0     |
| **TGM7**         | 0            | 1 (1.8)         | 1.0     |

Values are presented as number (%). No mutation was found 39 of 88 genes; ATRX, SF1, SF3A1, IDH1, BRD2, PHF6, TCF22, CS-Fr, FBXW7, FLT3, KIT, BRAF, CBL, KRAS, ITPKB, MYD88, CCND1, CDKN2A, BRCC3, RAD21, CALR, CARD6, CHD2, DAP2, DDX3X, EEF1E1, FAM46C, HIST1H4E, KIAA0355, KLHL6, MED12, MAPK1, NFKBIE, POT1, PTEN, SAMND1, SMARCA2, XPO1, ZMYM3.

MDS, myelodysplastic syndrome; AID, autoimmune disease.