Additional files

Additional file 1: Figure S1. All 42 clusters

Additional file 2: Figure S2. Cluster 33

Additional file 3: Figure S3. The predict accuracy of our method (Modules) and the cMap online tool with 28 drugs whose signature length were 300 (Drug300) and 500 (Drug500), respectively. In this case, we defined the accuracy of each drug as the proportion that the drugs whose attributes were same with the query drug's to all the output list of that drug.

Additional file 4: Table S1. The 'expression profile' obtained from our study, the first column represented Entrez Gene ID.

Additional file 5: Table S2. We predicted new indications for 42 drugs with unknown ATC codes

Additional file 6: Table S3. The details of drugs' indications within clusetr 10.

Additional file 7: Table S4. The signatures (Probe IDs) with 500 length about 28 drugs.

Additional file 8: Table S5. The similarity drugs obtained from cMap online tool with 28 drugs whose signature length was 500.

Additional file 9: Table S6. Literature validation for predicted indications of 143 drugs with ATC and Literature validation for indications predicted based on the third level of ATC.

Additional file 10: Supplementary materials