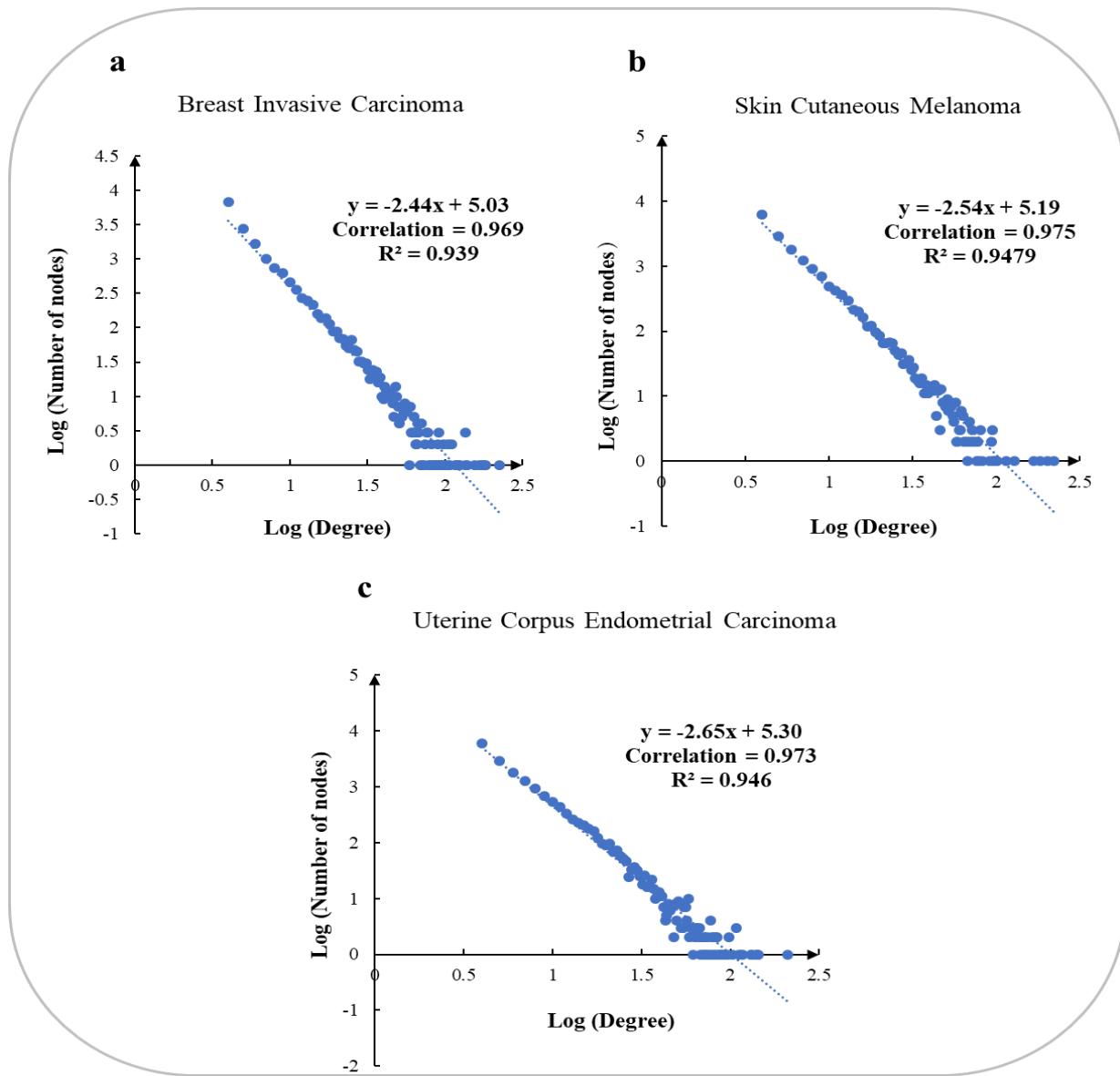


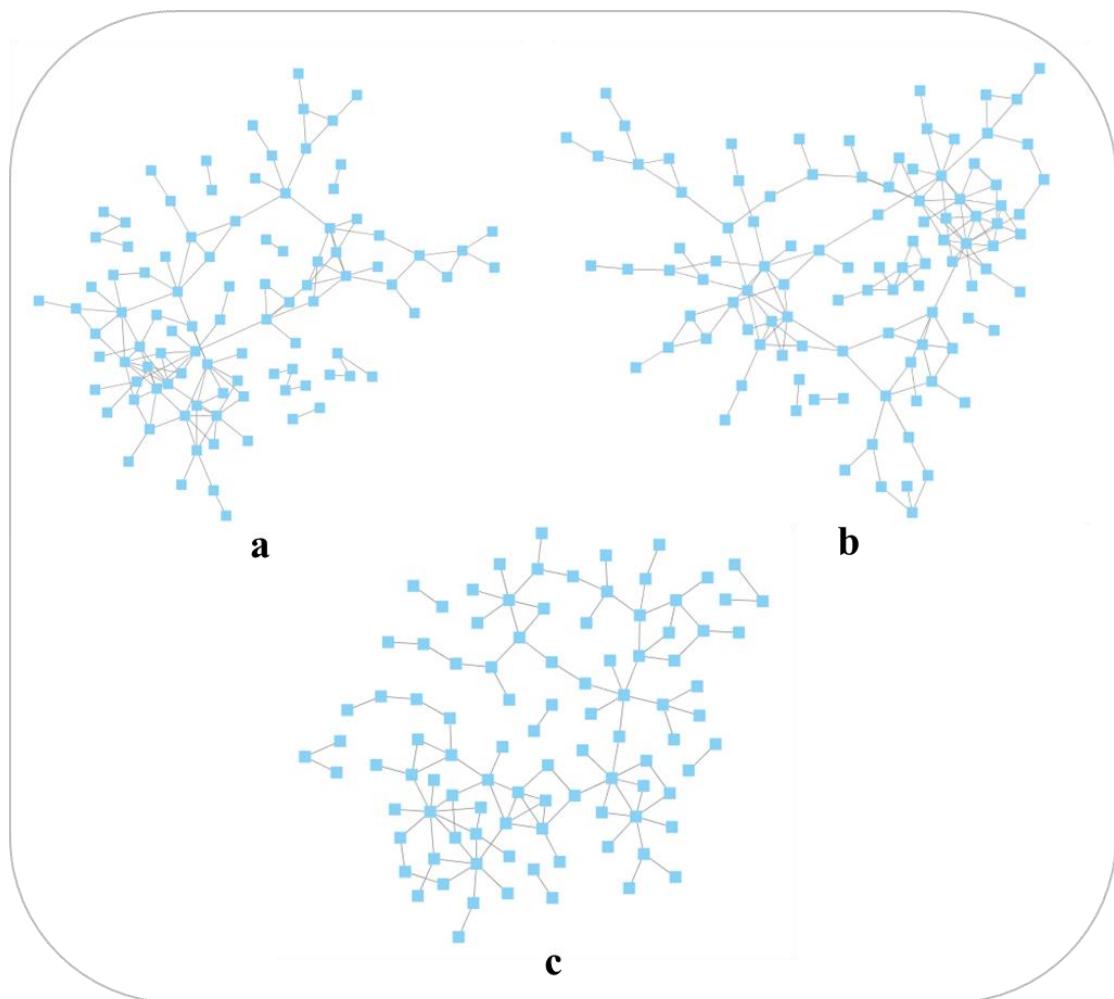
The file includes ten figures (Figure S1 – Figure S10) and four tables (Table S1- S4).

## Figures

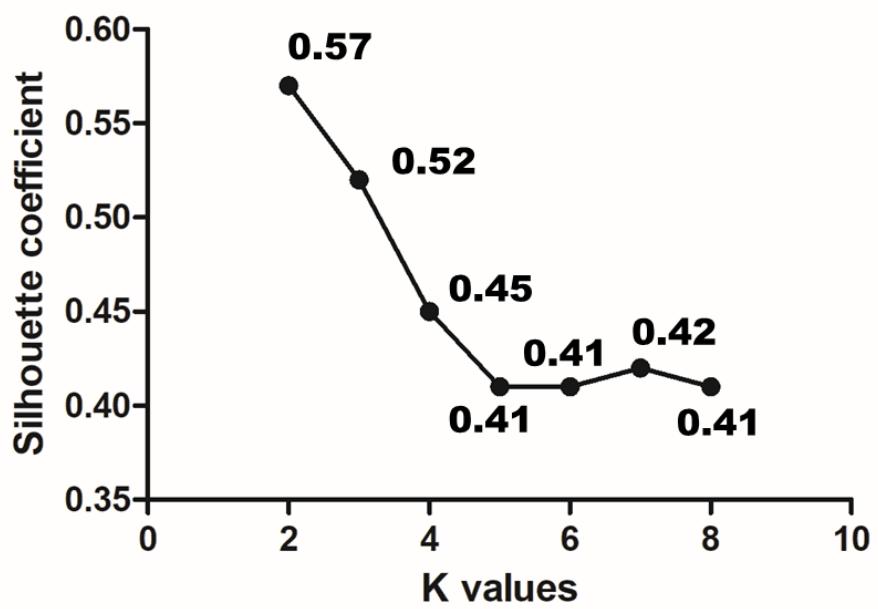


**Figure S1. Power-law distribution fitting of nodal degrees in three cancer co-methylation**

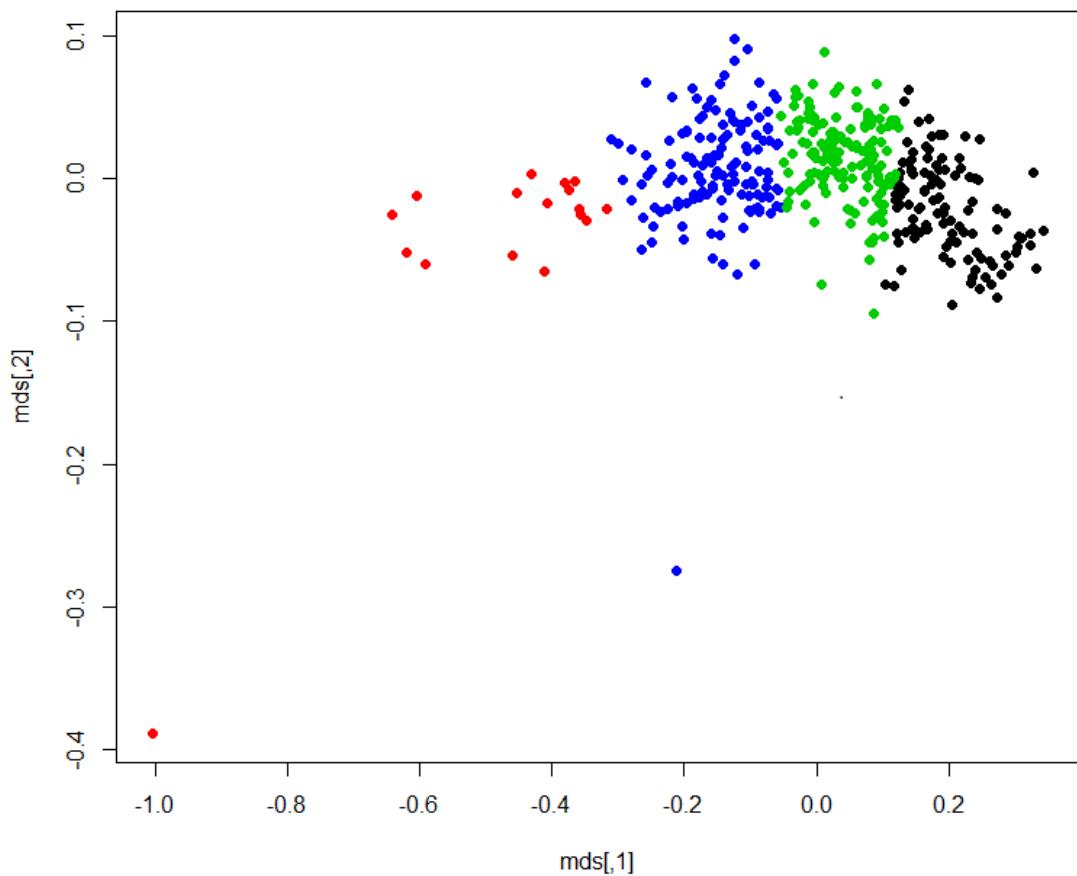
networks. a. The fitting results of node degrees in breast invasive carcinoma co-methylation network; b. The fitting results of nodal degrees in skin cutaneous melanoma co-methylation network; c. The fitting results of nodal degrees in uterine corpus endometrial carcinoma co-methylation network



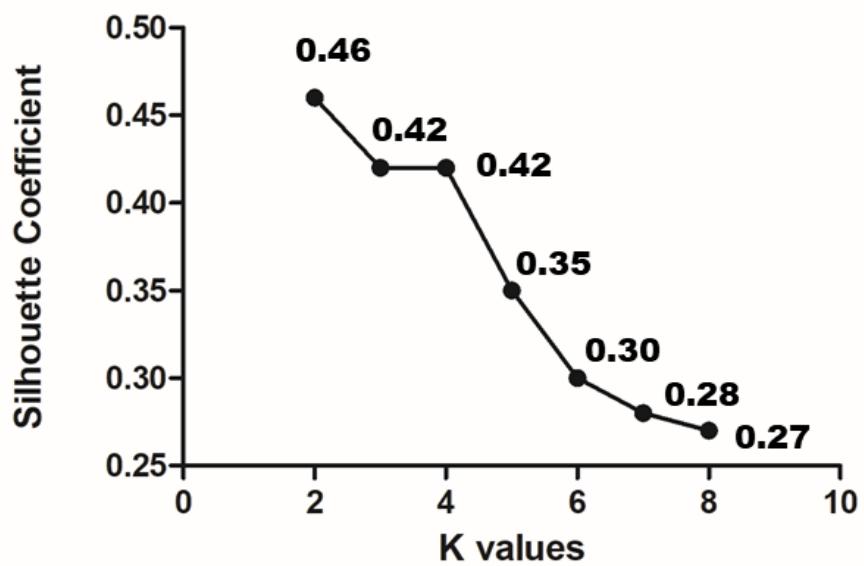
**Figure S2. The module networks of three cancers. a. The module network of breast invasive carcinoma; b. The module network of skin cutaneous melanoma; c. The module network of uterine corpus endometrial carcinoma**



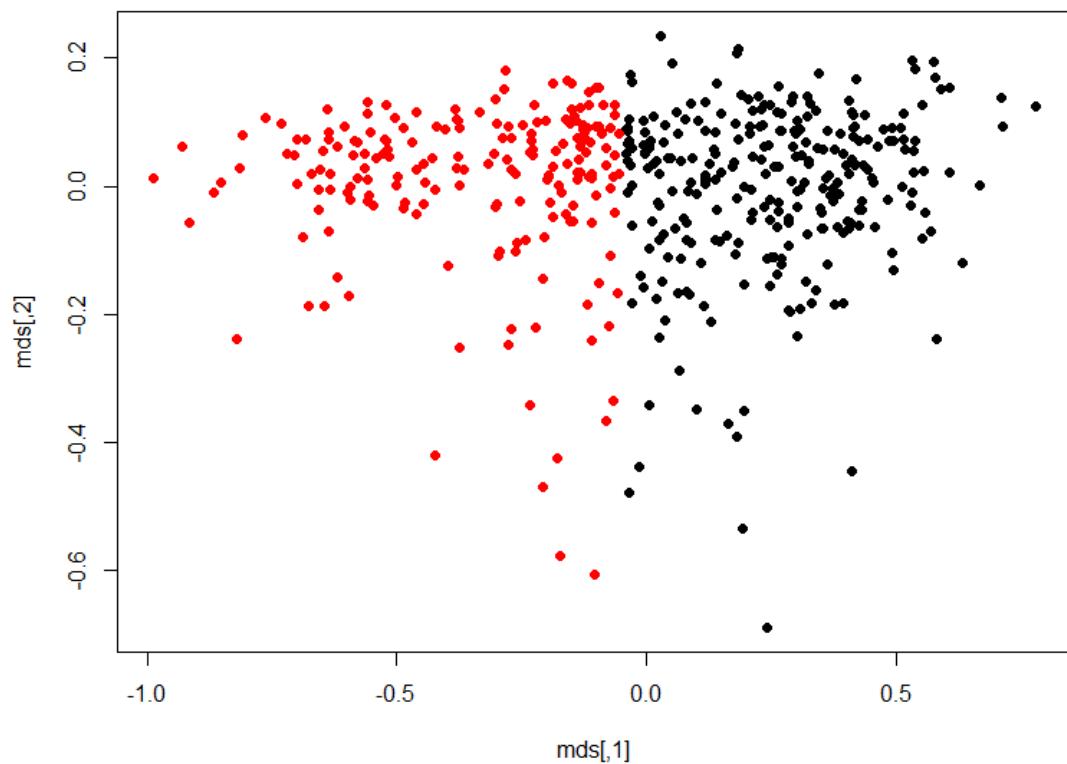
**Figure S3.** Silhouette coefficients of breast invasive carcinoma samples at different K values



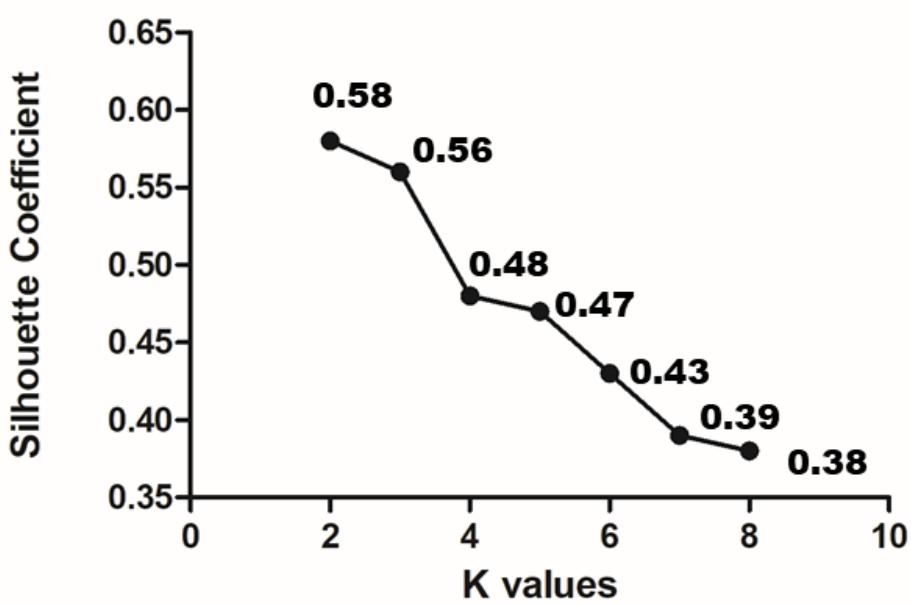
**Figure S4. Clustering results of breast invasive carcinoma samples by K-means algorithm  
(K = 4, after MSD conversion)**



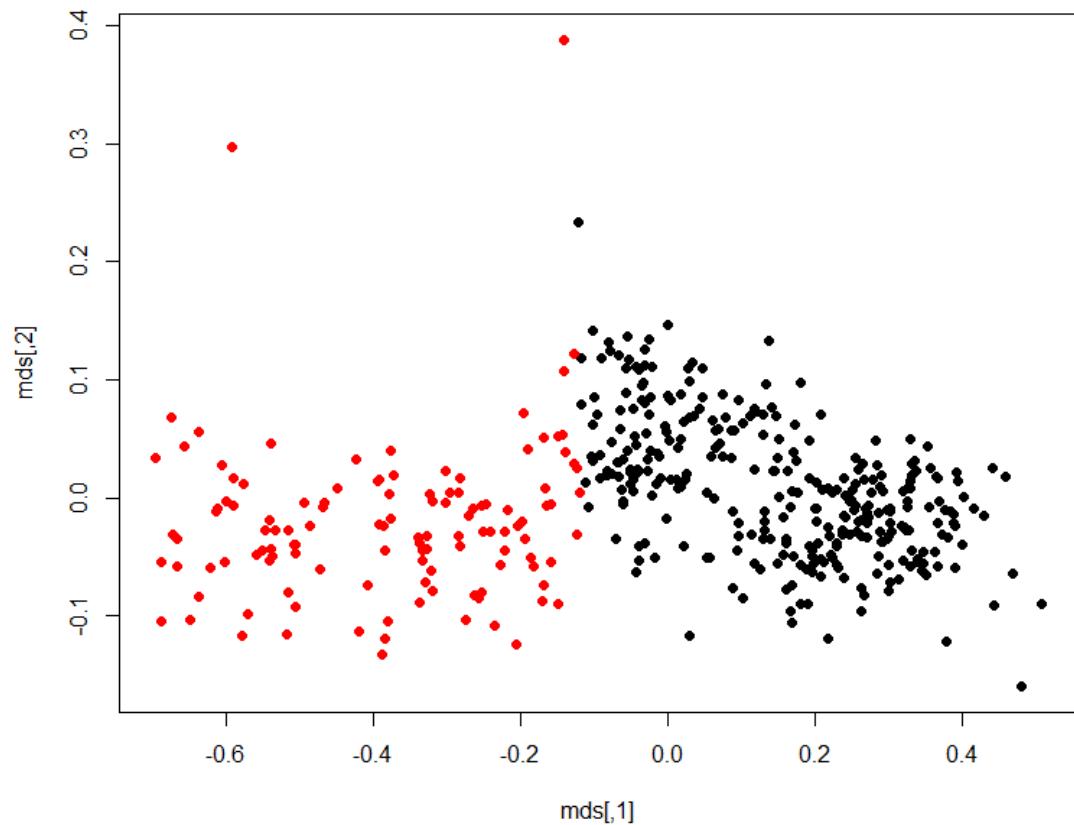
**Figure S5.** Silhouette coefficients of skin cutaneous melanoma samples at different K values



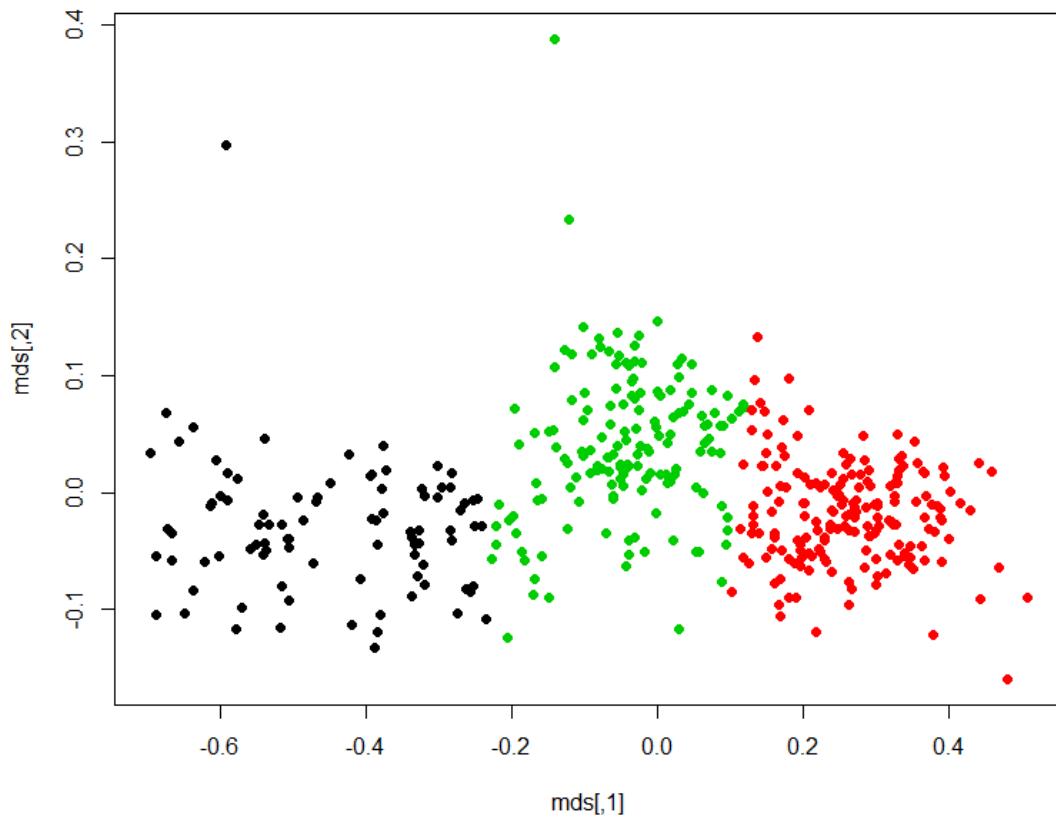
**Figure S6. Clustering results of skin cutaneous melanoma samples by K-means algorithm  
(K = 2, after MSD conversion)**



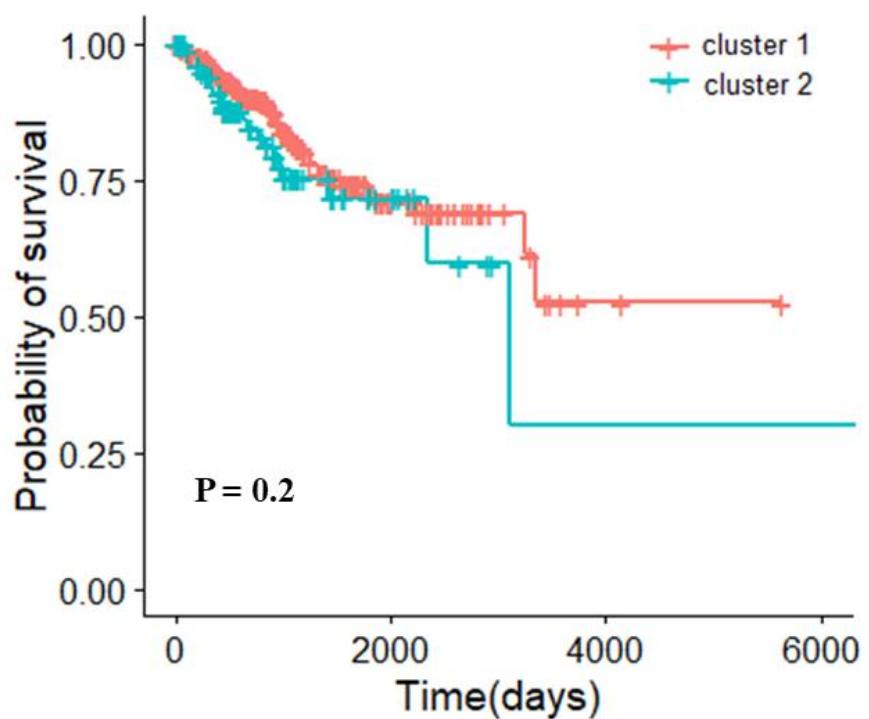
**Figure S7.** Silhouette coefficients of uterine corpus endometrial carcinoma samples at different K values



**Figure S8. Clustering results of uterine corpus endometrial carcinoma samples by K-means algorithm (K = 2, after MSD conversion)**



**Figure S9. Clustering results of uterine corpus endometrial carcinoma samples by K-means algorithm (K = 3, after MSD conversion)**



**Figure S10.** Survival analysis of different types of uterine corpus endometrial carcinoma samples after clustering ( $K = 2$ )

## Tables

**Table S1. The detailed results of preprocessing**

| Cancer type                          | Number of samples | Number of genes after expression data preprocessing | Number of genes after methylation data preprocessing |
|--------------------------------------|-------------------|---|--|
| Breast invasive carcinoma            | 780               | 18,955  | 16,850   |
| Skin cutaneous melanoma              | 468               | 18,955  | 17,031   |
| Uterine corpus endometrial carcinoma | 428               | 18,955  | 17,081   |

**Table S2. The list of genes included in the core modules of the breast invasive carcinoma**

| Module Number | Number of genes included in the module | Genes contained in the module  |
|---------------|--|--|
| 68            | 6                                      | AGBL5; CCT7; TBL3; RAB11B; PFKM; SNX5;   |
| 118           | 40                                     | CRTAP; FAM113A; TYW1; FBXO31; ACCN2; B9D1; RCHY1; SSBP3; AFG3L2; RPP38; AP1B1; C21orf66; RFC2; C18orf21; TRIM25; PAICS; C16orf62; STAG1; ORC3L; C7orf46; CIAO1; NCAPG2; CEP63; CTXN1; CUL4A; DHX57; GATSL2; ZNF594; GTF3C2; SGEF; IFT20; KDM1B; KIAA0494; MGC57346; NDUFC1; NAAA; SOS1; STRA13; UQCRCFS1; WDR91; |

**Table S3. The list of genes included in the core modules of the skin cutaneous melanoma**

| Module Number | Number of genes included in the module | Genes contained in the module   |
|---------------|--|---|
| 73            | 15                                     | ABCF1; LOC440926; UBE2N; GLI4; MADD; EEF2K; ANKRD50; APPL1; API5; TSG101; C1orf122; CTSD; ZNF580; PHF12; TBK1;  |
| 98            | 11                                     | SEPHS2; RBM16; BCL2L2; PDZRN3; MMP14; C21orf59; RHOJ; PROX1; SAMD5; LARGE; MPST;  |
| 122           | 15                                     | CCDC9; NR1H3; SPOPL; TRIM3; C17orf63; CCDC12; MIR572; PLCD4; PRELP; MIA; OTUB1; CARS; NAT14; TET3; VMO1;  |
| 123           | 57                                     | LAMC3; ABCC3; KCNJ5; SLC25A13; HCG11; ADAMTSL4; SDC1; ADIPOR1; CISH; PLK1S1; SLC25A35; YTHDF1; MAPK6; UGDH; UEVLD; TRAF4; C16orf5; FTO; OTUD1; RYBP; XKR9; FMNL2; C8orf45; PCGF6; C8orf73; C9orf3; MIR24-1; MIR23B; PHF2; CD9; IGFBP4; TMEM14A; HAP1; CREG1; CYB561; MAGI1; EFNA1; EPOR; EXT1; ETFA; PPP3CA; MEX3A; POLD2; MED24; PVRL3; TACR1; ITGA5; KIF18B; LSM11; MAGI2; PLOD1; PCBD2; PIGX; RGS9; RNF26; TSTD2; VAMP2; |

**Table S4. The list of genes included in the core modules of the uterine corpus endometrial carcinoma**

| Module Number | Number of genes included in the module | Genes contained in the module   |
|---------------|--|---|
| 37            | 8                                      | JMJD6; SETD3; POP1; RWDD2A; NDUFS3; CDH24; GCSH; HELLS;   |
| 68            | 78                                     | UBA5; AKAP5; DMXL2; FBXW7; AURKA; PSMB9; LIN37; FAM13B; ARF1; ALS2CR8; CCDC148; HELQ; PPP2R5E; CISD1; MIR636; ZNF808; ANO1; ARSJ; TBL3; ARFGAP1; STYX; ARHGDIA; ATP5I; RPS5; C17orf90; MNT; ILF3; NEK11; C17orf48; BAG2; UBE2F; PGD; C20orf43; SF3B2; C2orf76; ZNF148; MIR760; ZNF211; CAMSAP1L1; CARS2; DOCK4; WRB; ZNF862; LOC338758; CHTF18; EZH2; L2HGDH; PRKAG1; CIB2; UBE2L6; NIP7; DDX41; DDX46; SRPR; FAM134A; FGFR1OP2; WAPAL; FRAT2; HNRNPC; GGNBP2; GMDS; GTF2I; HAUS6; JAG1; PCM1; KIAA1377; LAMP3; LOC401431; ZNF598; Magmas; POLH; RFPL2; SAP30BP; SEMA3A; TDRD7; ZNF181; WDR90; ZCCHC17; |