Fig. S1. Functional annotation for DSGs and DRGs selected by different DSS parameters. (A) and (B) are the results of DSGs. (C) and (D) are the results of DRGs.

Fig. S2. The visualization of DSGs (A) and DRGs (B) in a genome-wide karyotype plot. The chromosomes are numbered from 1 to 22 and marked by gene locations. Skyblue, lightcoral and green represent low methylation, high and normal genes, respectively. The colors and numbers in bars represent the proportion of genes in chromosomes.

Fig. S3. The miRNA-TF co-regulatory networks for DSGs (A) and DRGs (B). The different nodes and edges are the same as defined in Fig. 2, and the node will be a yellow triangle when a transcription factor is also a gene.

Fig. S4. The structural features of two networks. (A) Degree distributions of dosage-sensitive regulatory network. Most of the nodes are lowly connected and only a few are relatively highly connected. The examination of the degree distribution of the dosage-sensitive regulatory network revealed a power-law with a slope of -0.877 and R2=0.4988. (B) Degree distributions of dosageresistant regulatory network. The examination of the degree distribution of the dosage-resistant regulatory network revealed a power-law with a slope of -0.902 and R2=0.5253.

Fig. S5. miRNA and TF in two regulatory networks. The number of miRNAs (A) and TFs (B) that were shared between two networks.

Fig. S6. Hub genes in the two networks. (A) The dosage sensitive network. (B) The dosage resistant network.

Fig. S7. The interaction status of the hub genes in the dosage sensitive network (A) and the resistant network (B). The different nodes and edges are the same as defined in Fig. 2.

Fig. S8. Regulatory relationships of MYC in the two networks. (A) The dosage sensitive network. (B) The dosage resistant network.

Fig. S9. The significance of survival analysis of hub motif between the training set and the test set. Red represents $p < -0.5$ in both train and test sample sets. (A) shows the result survival analysis in the sensitive hub subnetwork and (B) shows the result survival analysis in the resistant hub subnetwork.

Fig. S10. Survival-related hub motifs. (A) The hubs in the dosage sensitive network. (B) The hubs in the dosage resistant network.

Fig. S11. The significant performance of hub motif miR-98-5p-HOXA5-TP53 in survival analysis based on all OV patients. (A) Kaplan–Meier estimates of overall survival of OV train patients according to the motif signature. (B) Survival of patients in the test data set.

Fig. S12. Compared DSS of different datasets. (A)The same genes' DSS result of CCLE data with the change of DSS in TCGA dataset. (B)The changed trend between different sample sizes. Each point represents an independent gene. Orange, mediumaquamarine and lightblue points indicate the DSGs, DRGs and other genes in TCGA dataset, respectively.

Table S3 Summary of differential expressed miRNA and TF mediated dosage sensitive network

Motif types	Motifs	Genes	MiRNAs	TFs
Co-regulatory FFL	1	1	1	1
TF-mediated FFL	21	13	3	3
MiRNA-mediated FFL	626	132	96	20
Composite FFL	50	27	4	2
All network nodes	698	138	97	21

Table S4 Summary of differential expressed miRNA and TF mediated dosage resistant network

Motif types	Motifs	Genes	MiRNAs	TFs
Co-regulatory FFL	3	3	2	2
TF-mediated FFL	23	12	3	2
MiRNA-mediated FFL	788	138	106	28
Composite FFL	46	21	4	2
All network nodes	860	141	108	30