

Supplemental Material to:

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**Integrated analysis of DNA methylation and mRNA
expression profiling reveals candidate genes associated
with cisplatin resistance in non-small cell lung cancer**

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Supplementary Information

Figure S1. Integrated circos view of hypermethylated and downregulated genes in A549/DDP identified by microarrays. The outer ring (red) represents expression log fold change A549 vs. A549/DDP; the inner ring (blue) represents methylation Δ_{β} A549 vs. A549/DDP

Figure S2. Resistance index of A549/DDP was determined by MTT.

Table S1. Hypermethylated and downregulated genes in A549/DDP identified by microarrays.

Table S2. GO analysis: Biological Process

Table S3. GO analysis: Cellular Component

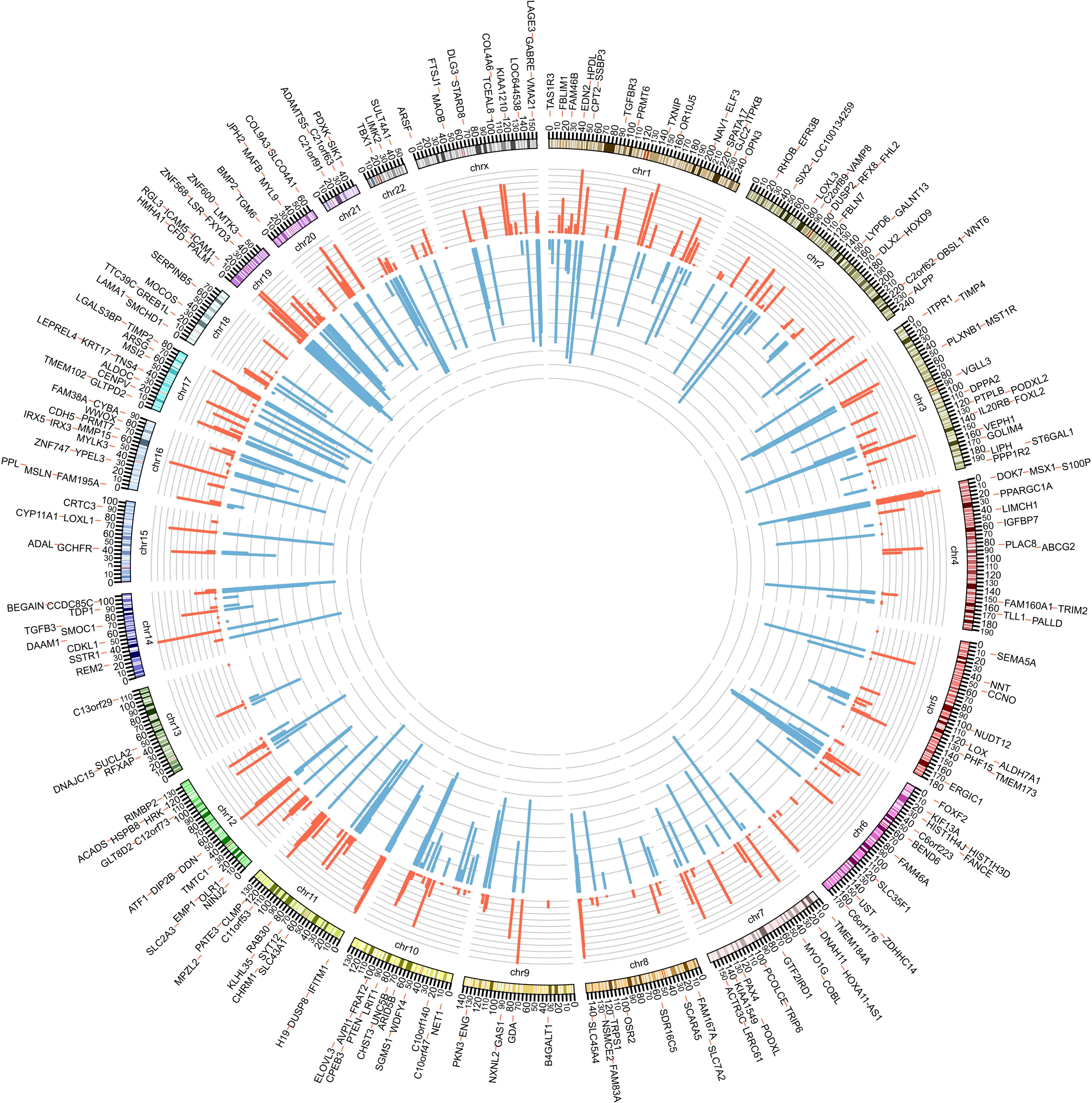
Table S4. GO analysis: Molecular Function

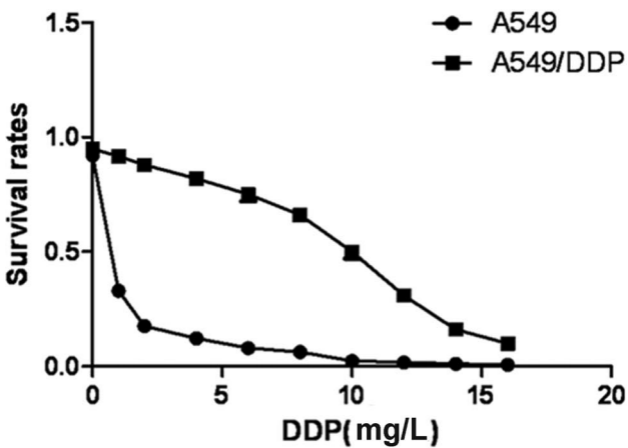
Table S5. KEGG Pathway analysis

Table S6. Gene expression validated by a self-assembling quantitative PCR array.

Table S7. Data of lung adenocarcinoma and squamous cell carcinoma publicly available from TCGA Project.

Table S8. List of primers.





Supplementary Table S8. List of primers used in realtime-PCR, quantitative methylation-specific PCR(M) and bisulphite sequencing (B)

Gene Name	Primer Sequence(5'-3')	Tm (°C)	Product (bp)
GAPDH	F: CAATGACCCCTTCATTGACC R: TGAAGATGGTGTGGGATT	55	135
GAS1	F:CCTCATTCAAGCTCAACCACA R:GAAGACTTTGCCGCAGTAGG	59	247
TIMP	F:GCCAGGACTATTCCCTTTCC R:TGCCAGTCAGCCTGTTTATG	59	162
ICAM1	F:GGCTGGAGCTGTTTGAAGA R:TCACACTGACTGAGGCCTTG	60	249
WISP2	F:AGGTATGGCAGAGGTGCAAG R:AGGGGAAGTCGGAGAGAAAG	60	155
BMP2(M)	F:GTAGGTCGATTATGGTGGTCG R:TCGTCAAAAACTAAAATAAAAAACG	57	154
CLMP (M)	F:GTCGATTAGGGTTTTTTTTATCGA R:TACACATTTTAACCAAAACCACGTA	54	249
GAS1(M)	F:TAGTTTTTCGGGTGATTAAGAGTTC R:ATACATAATAAAAAACACCGCGAC	59	135
ICAM1(M)	F:CGCGATTTTTTTGGTTTTTC R:TATTTACTTAACCACCGCCTATACG	54	169
LOXL1(M)	F:TAGTTGATTTAGTGGGAGAATAACG R:CCGAAAACACTCTCGAAACG	60	102
HSPB8(M)	F:GGTTAGGCGAGGTGGTTTAC R:CCAAACTAAAACGCAATTACG	55	257
S100P(M)	F:TATAGAGTGTTTTAAGAAAGGGATGA R:TACTAACACCCAACGTACTAACACG	57	108
WISP2(M)	F:ATTGGTTTAGGTTTTTATATATATACGC R:CAAACACACACAAACACACG	57	115
GDA(M)	F:GGTAACGTAGAGAGAATTTTGGC R:CTACTATCGAACCAATTATAACGTT	74	103
TIMP4(M)	F:GATTTTCGGATTTATTAAGTGTCGA R: AACCTAAAACGAAAAACACAACG	54	250
WISP2 (B)	F: GTTTTTGGTGTGGTATTGGTTTA R: CTCTCATATCCCCTACAAAACCA	60	345
TIMP4 (B)	F: AGAGTGGTAGATGTGTTGTTGAG R: TTAACCCTTAAAACCACCTCATA	59	252
ICAM1 (B)	F: TTTTTTTTTGGGAGTTGTAAAGA R: CTCCCTCCACTAAAAAATACCCC	60	256
GAS1 (B)	F: ATTGGTTGTAGGYGTAGTTGTA R: AACTATTCATTTCCAAAAAACCA	59	414

GDA (B)	F: TGAGGAGGTAGGGAGTTAGTTT R: CCAAATTCCTTACACCTATCCT	59	374
LOXL1 (B)	F: GAGTTGGGGTAAGTAAGGAGTT R: TATTCTCCCACTAAATCAACTACC	59	256
CLMP (B)	F: AAGTGGGTGYGAAGGTAGTTAG R: ACCAAAAAATTCTACTCCCTCT	59	327
HSP8 (B1)	F: TAGTTTGGGTAGTTTGGGAAGT R: CTACCCAAAATCACACAACAA	59	254
HSP8 (B2)	F: GTGGTTTTGTTTTTTGAGTTTT R: TCACACACACTTTCAAAACT	59	351
BMP2 (B)	F: TAAGTTAGGAGGGTATTTTGGA R: ACTAACTACCCTCTCCAACC	56	438
S100P (B1)	F: GGTTTTAGGGAATTTGATTTAATAGGT R: TCTATATCCTTCAAAAACCCAATT	59	328
S100P (B2)	F: GGGAGTTTTTTGTTTGGTTTTATAG R: CACAATAACATCCTCATTCTAAC	61	283
S100P (B3)	F: GAATGAGGATGTTATTGTGGTTTAGT R: CACCTCCTCCTAAAACTAACAAA	59	297
S100P (B4)	F: GGTGGGTTTGAATTTAGTATTATGA R: CAAAAACCTAATAACTCCTTCTCC	60	156
