

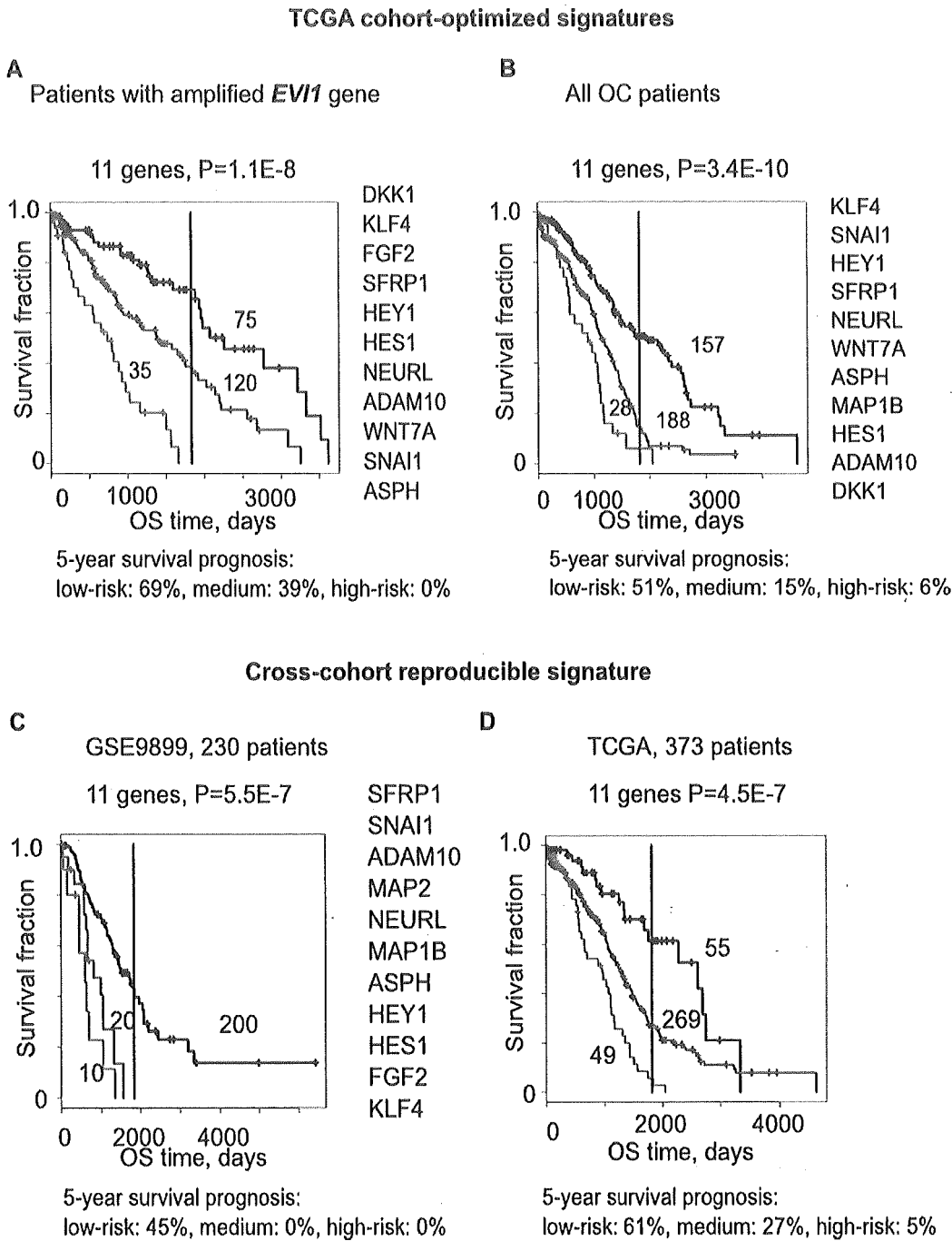
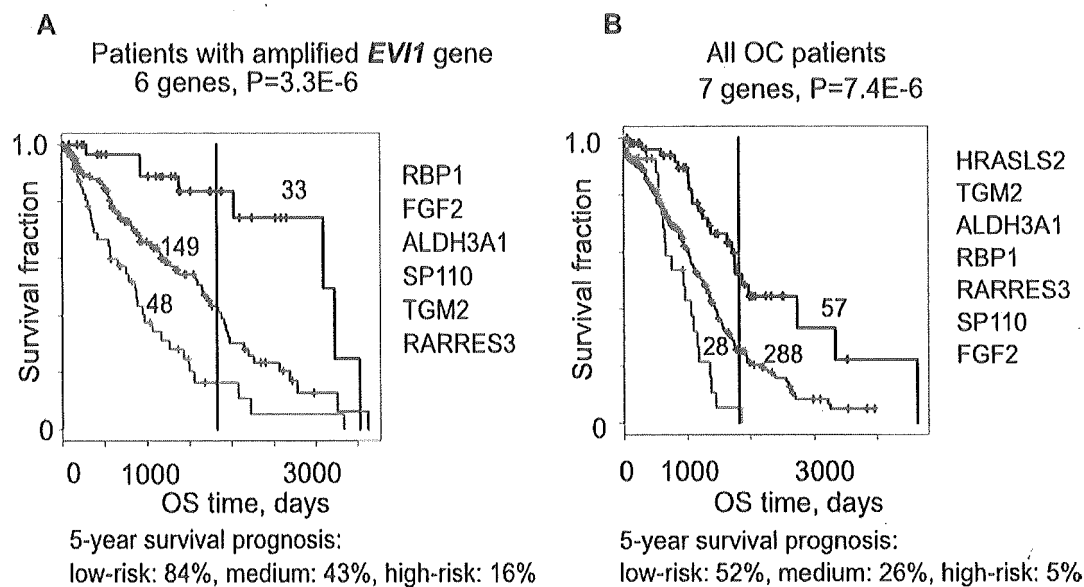


Figure 1

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TCGA cohort-optimized signatures



Cross-cohort reproducible signature

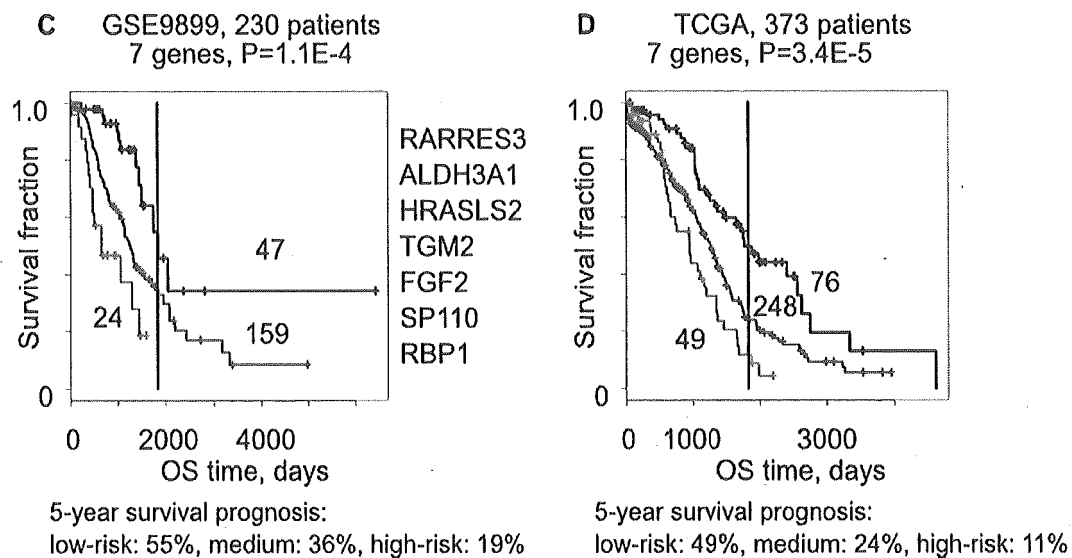


Figure 2

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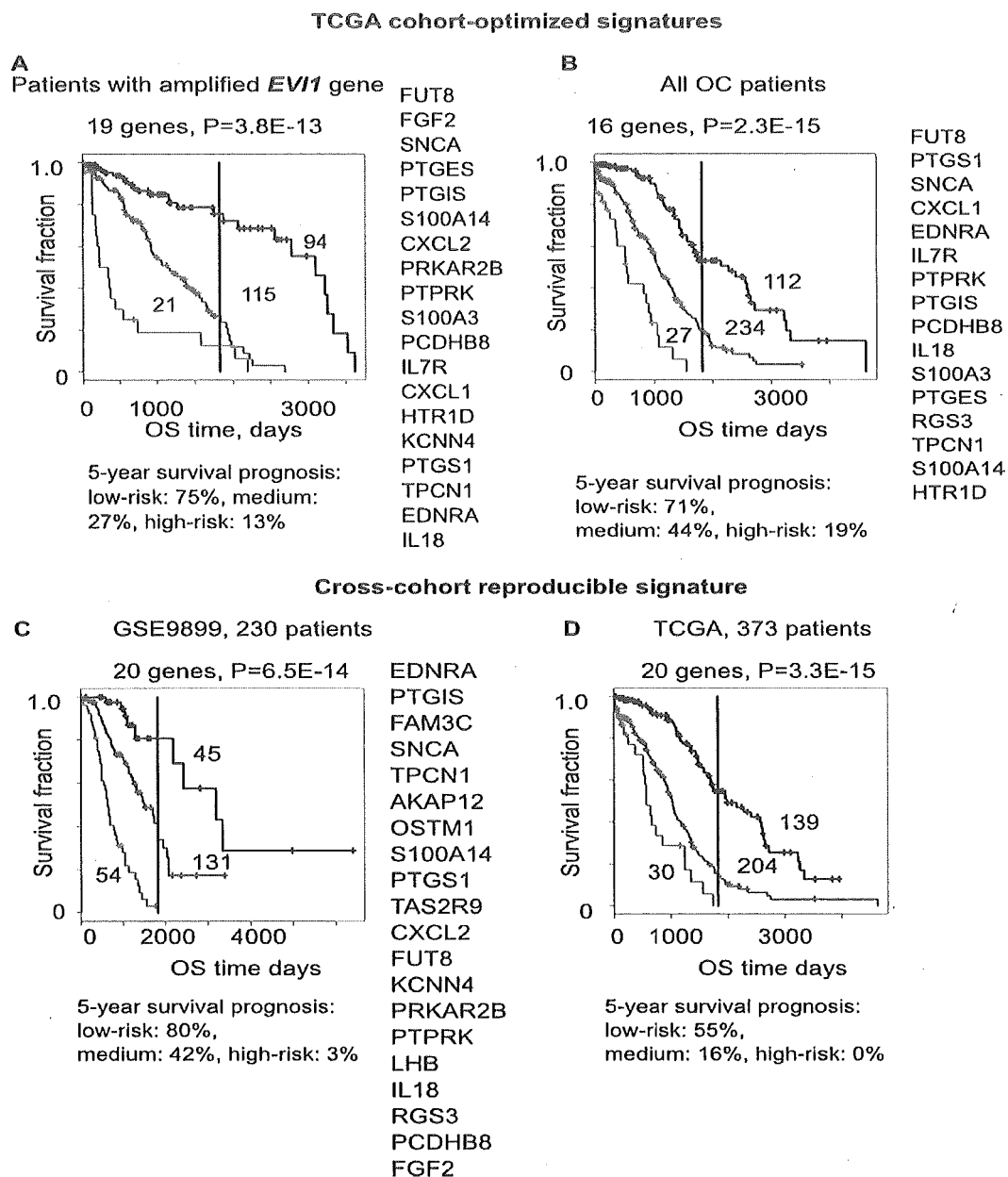
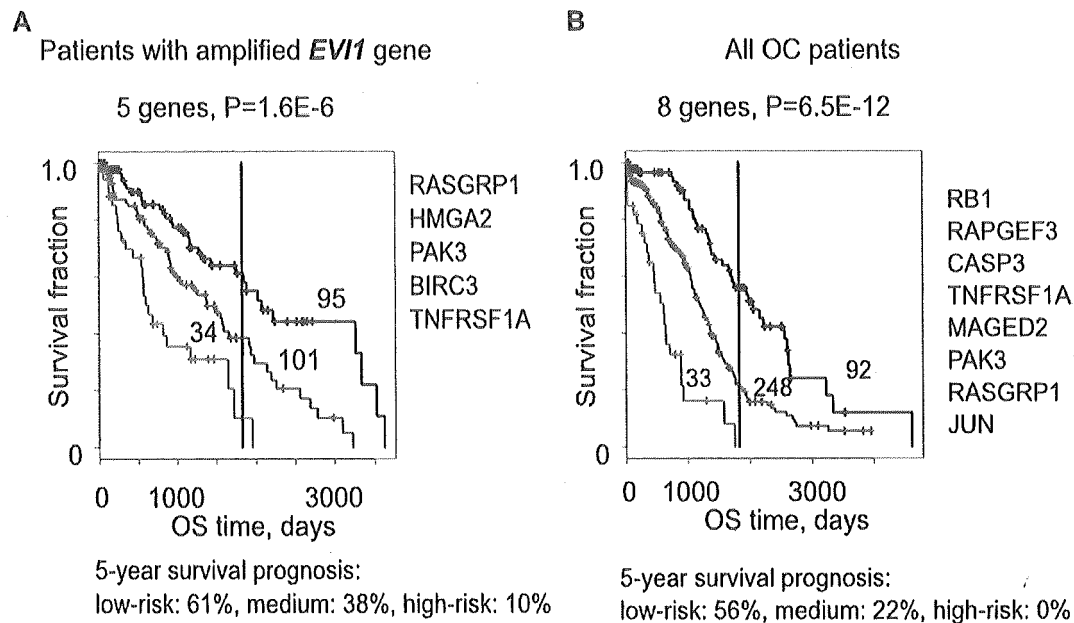


Figure 3

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TCGA cohort-optimized signatures



Cross-cohort reproducible signature

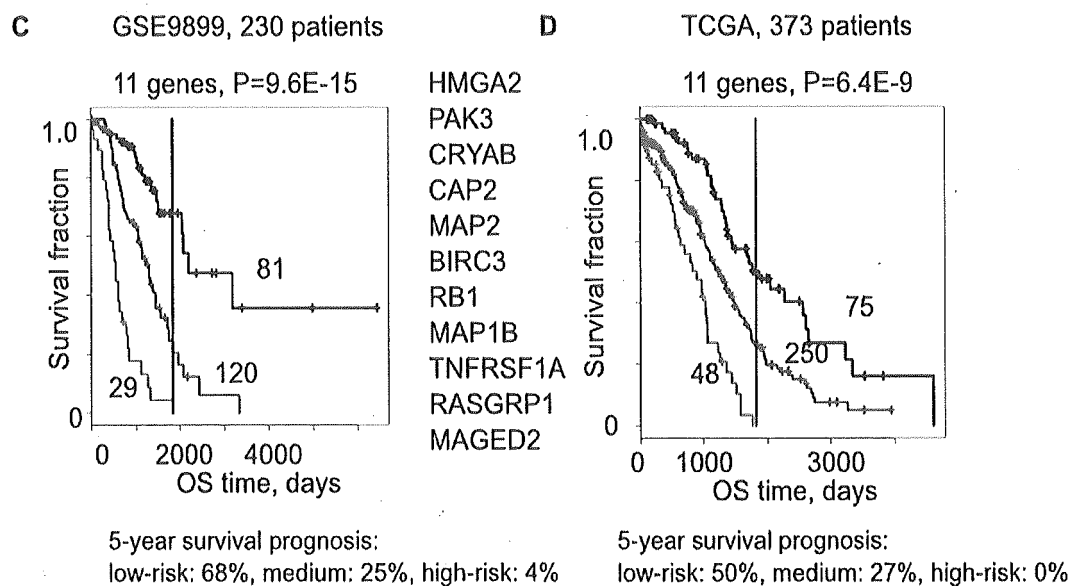
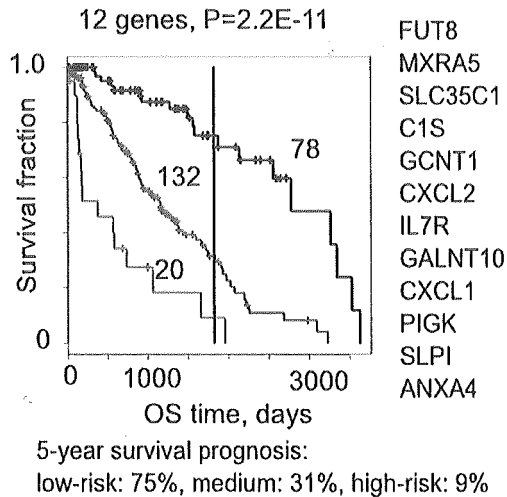


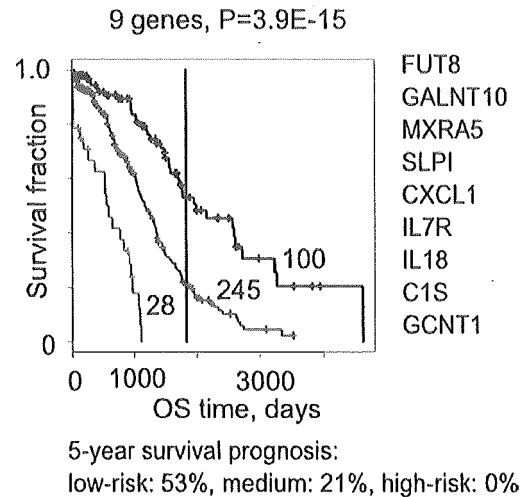
Figure 4

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TCGA cohort-optimized signatures

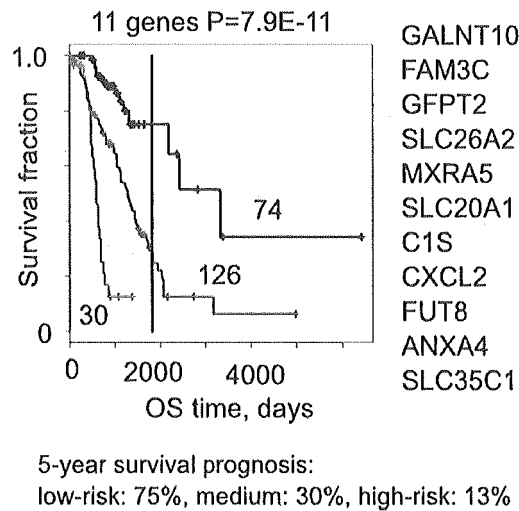
A Patients with amplified *EVI1* gene

B All OC patients



Cross-cohort reproducible signature

C GSE9899, 230 patients



D TCGA, 373 patients

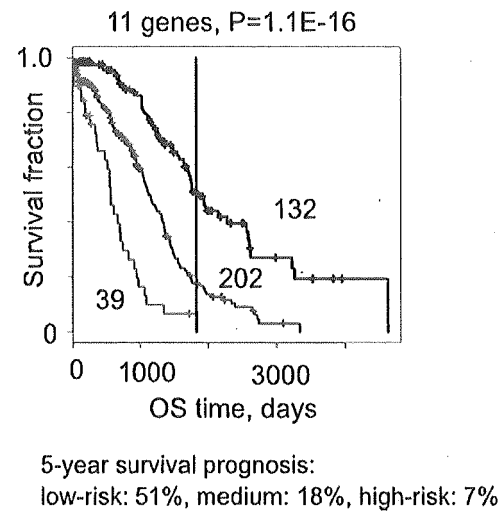
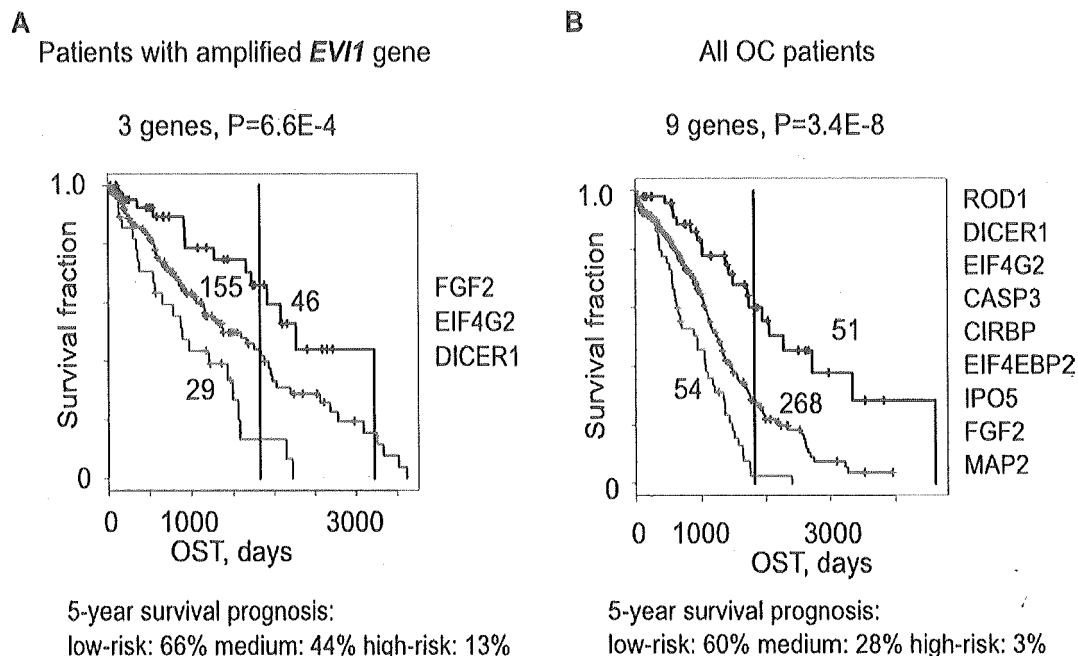


Figure 5

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TCGA cohort-optimized signatures



Cross-cohort reproducible signature

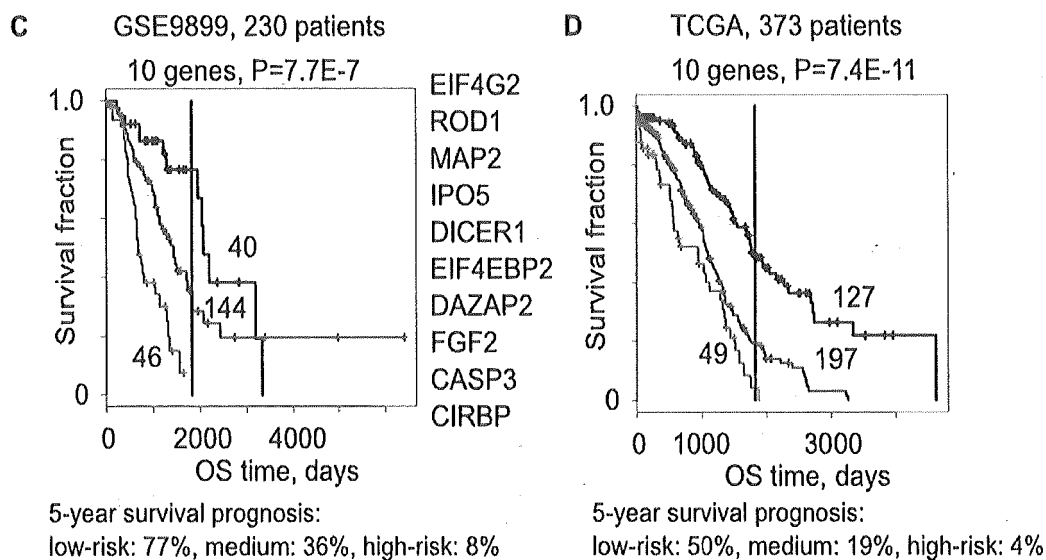


Figure 6

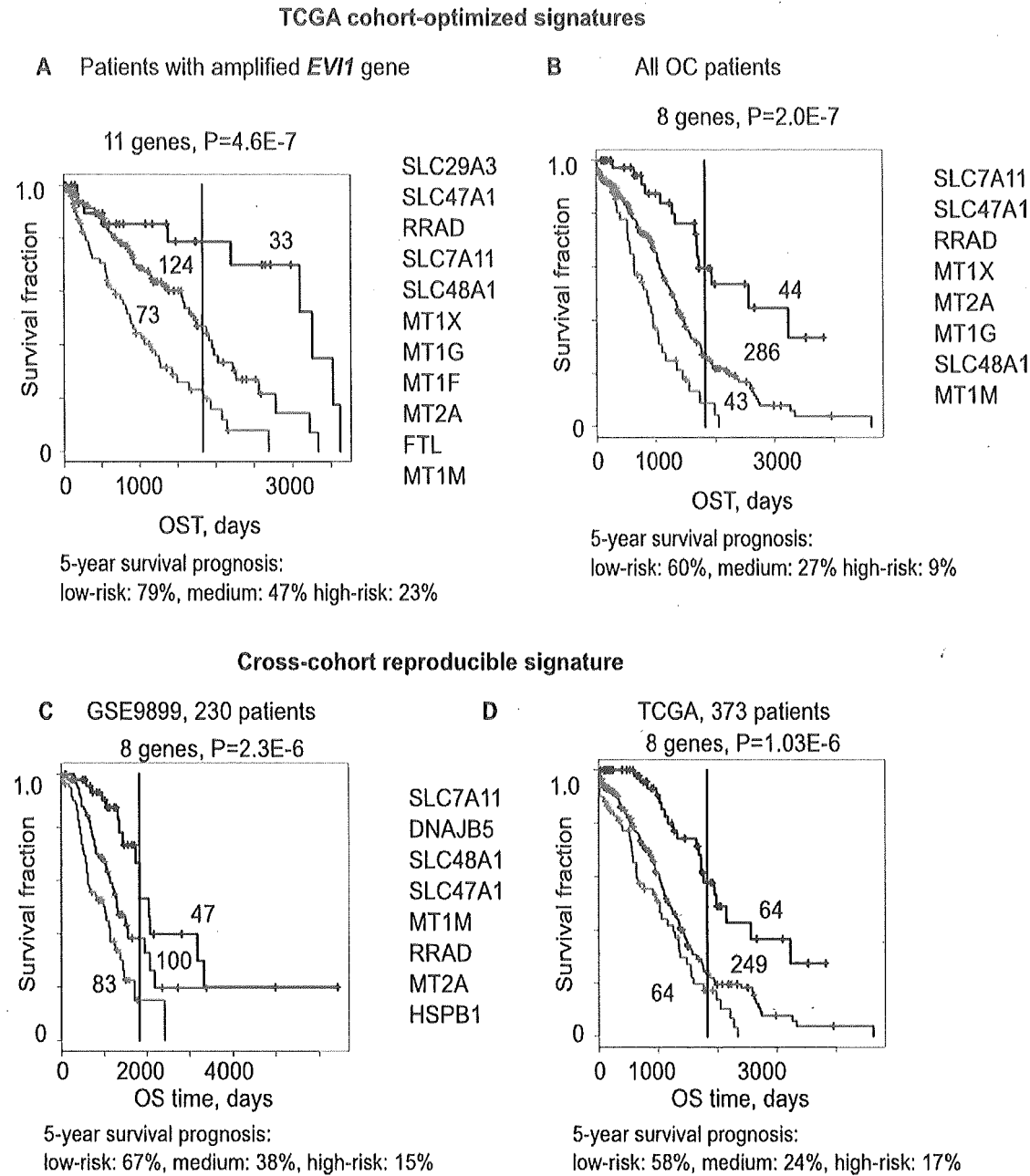


Figure 7

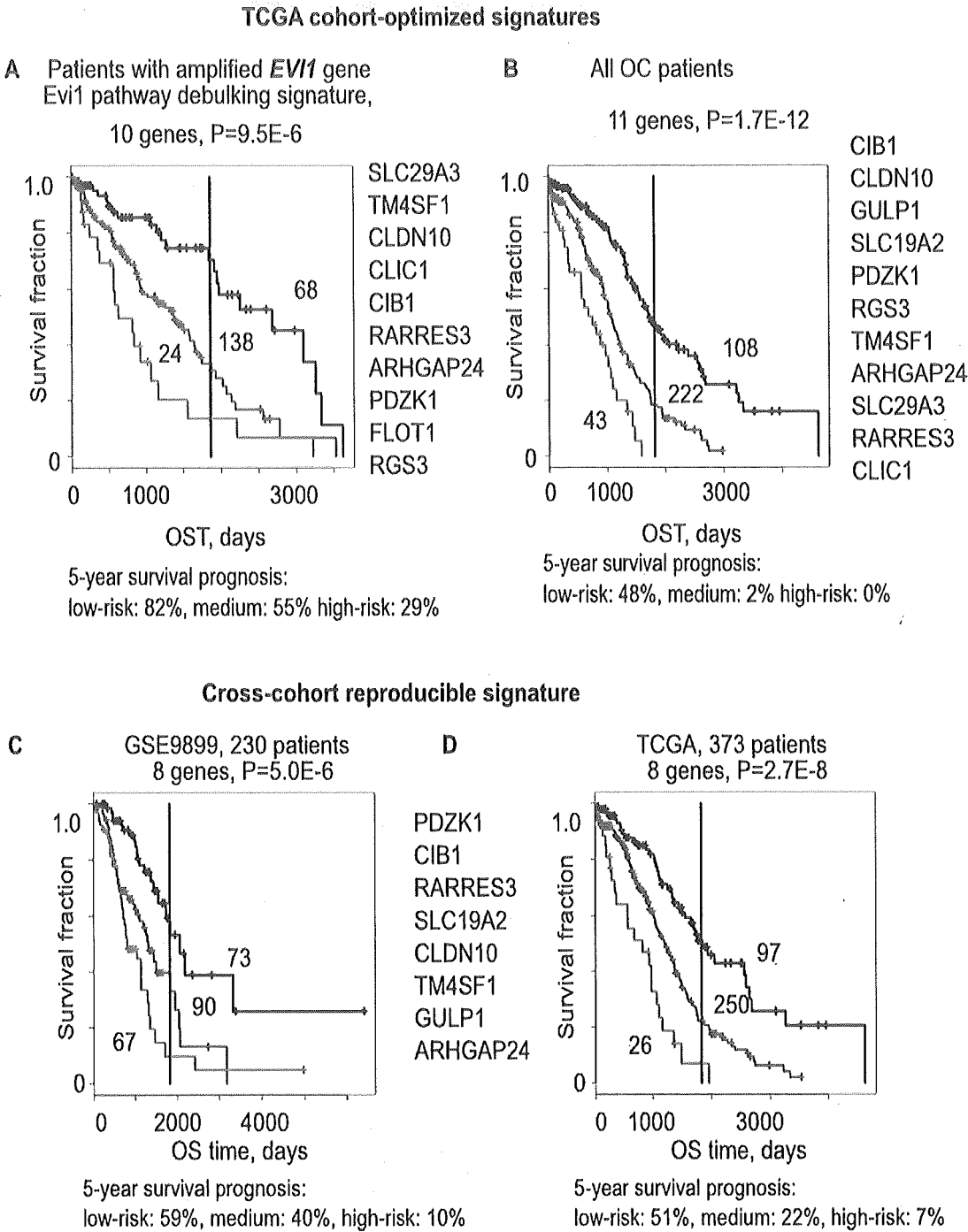
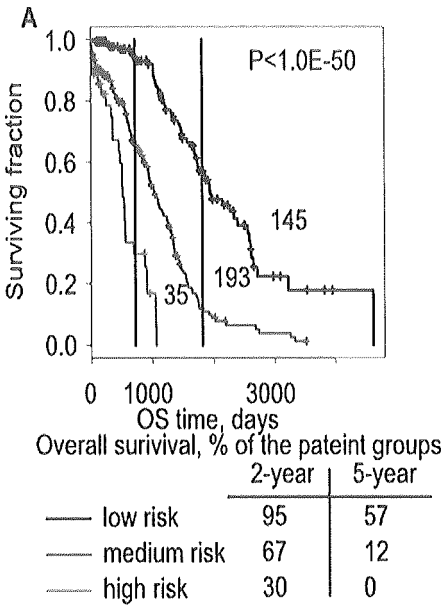
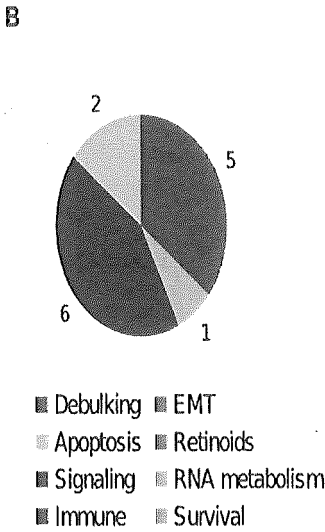
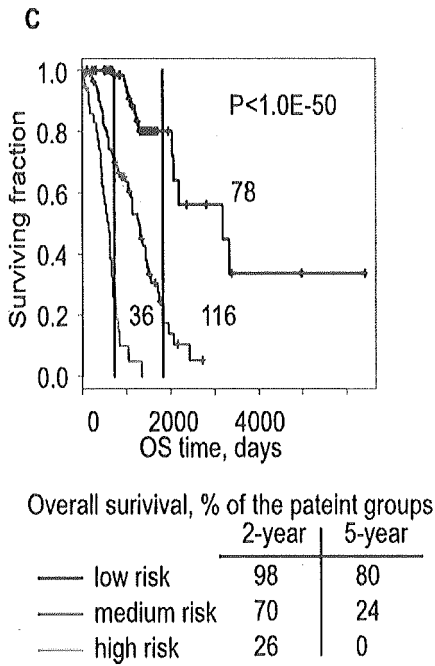


Figure 8



FUT8
ANXA4
RB1
CRYAB
ROD1
PIGK
TAS2R9
OSTM1
FAM3C
GALNT10
LHB
AKAP12



SFRP1
HMGA2
EDNRA
EIF4G2
PTGIS
GALNT10
FAM3C
SNCA
PAK3
SNAI1
SLC7A11
GFPT2
TPCN1
CRYAB
ROD1
SLC26A2

CAP2
DNAJB5
ADAM10
OSTM1
CIB1
MAP2
RARRES3
SLC19A2
CLDN10
S100A14
MXRA5
PTGS1
NEURL
IPO5
AKAP12
PDZK1

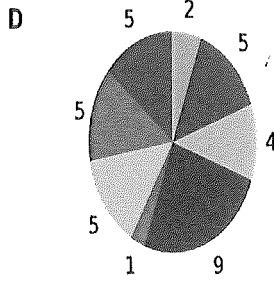
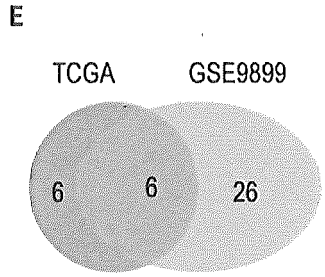


Figure 9

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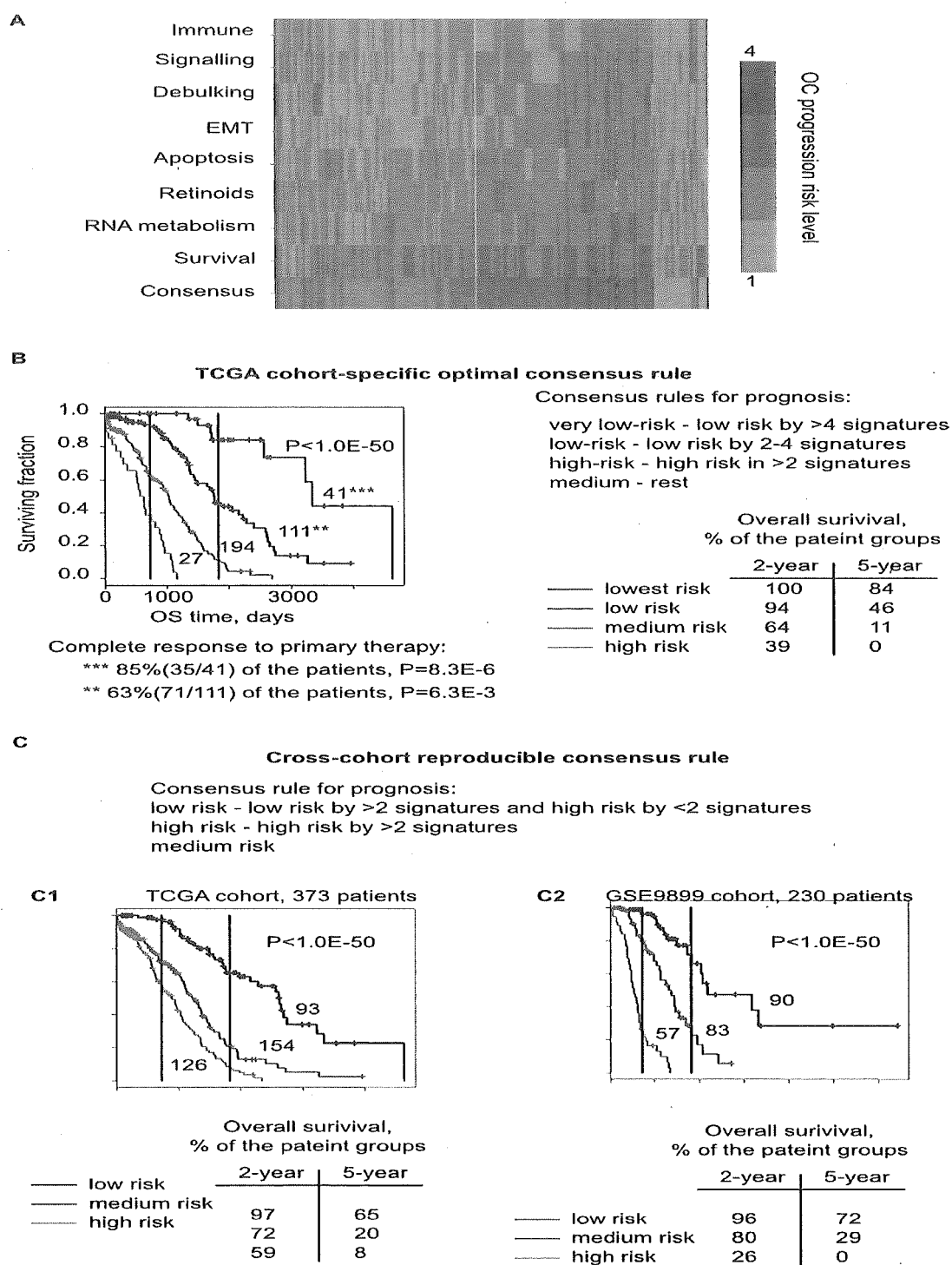


Figure 10

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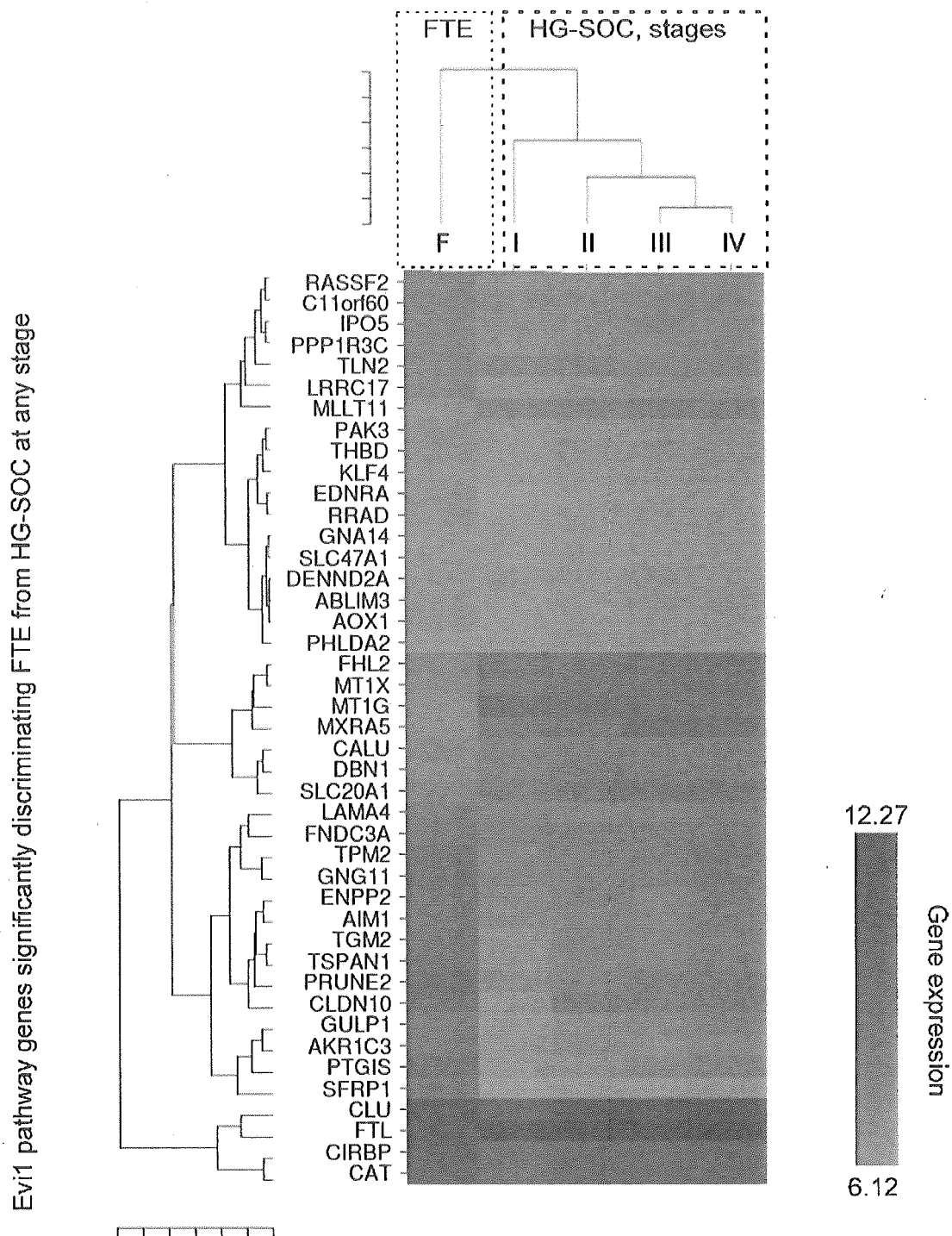


Figure 11

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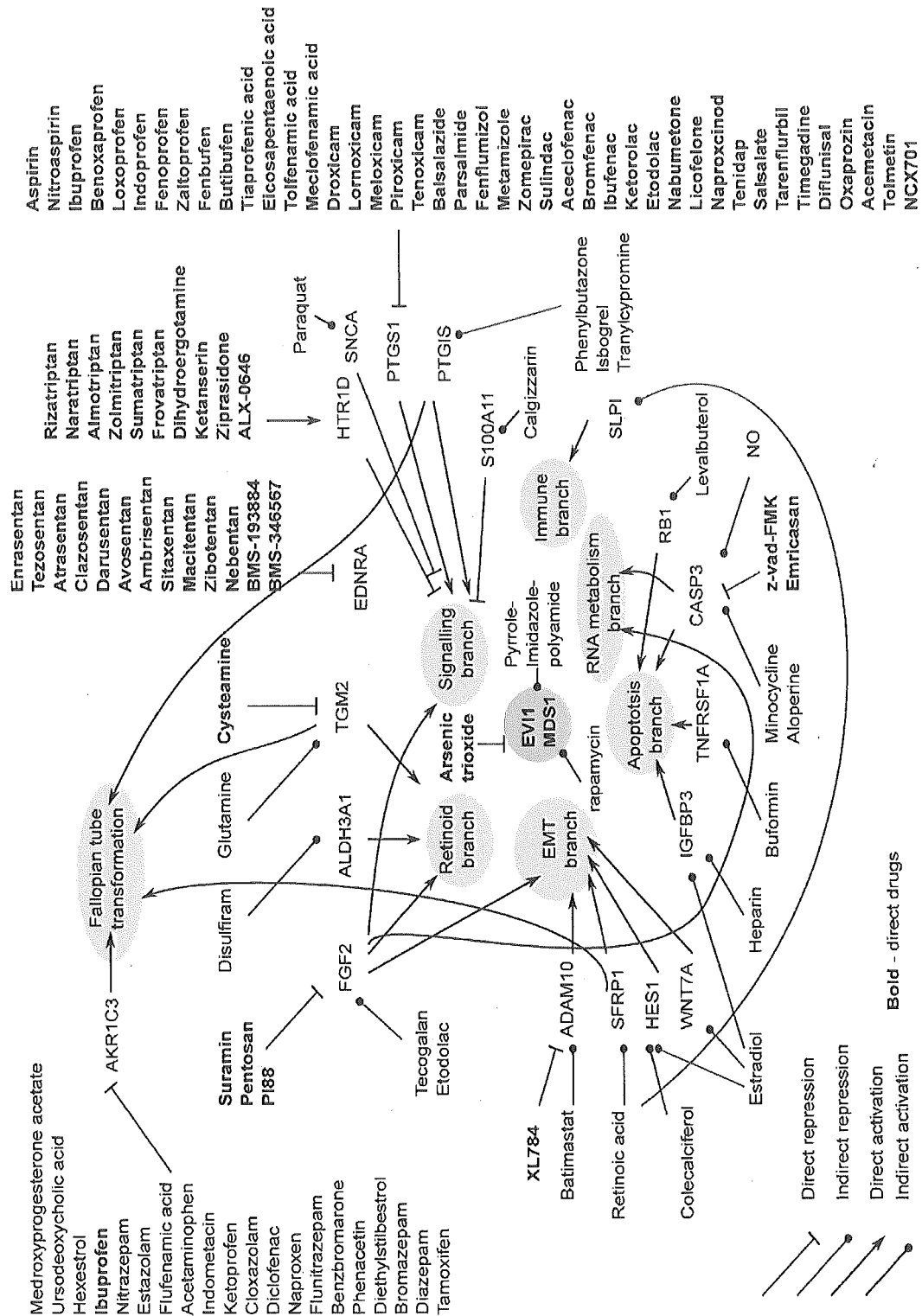


Figure 12

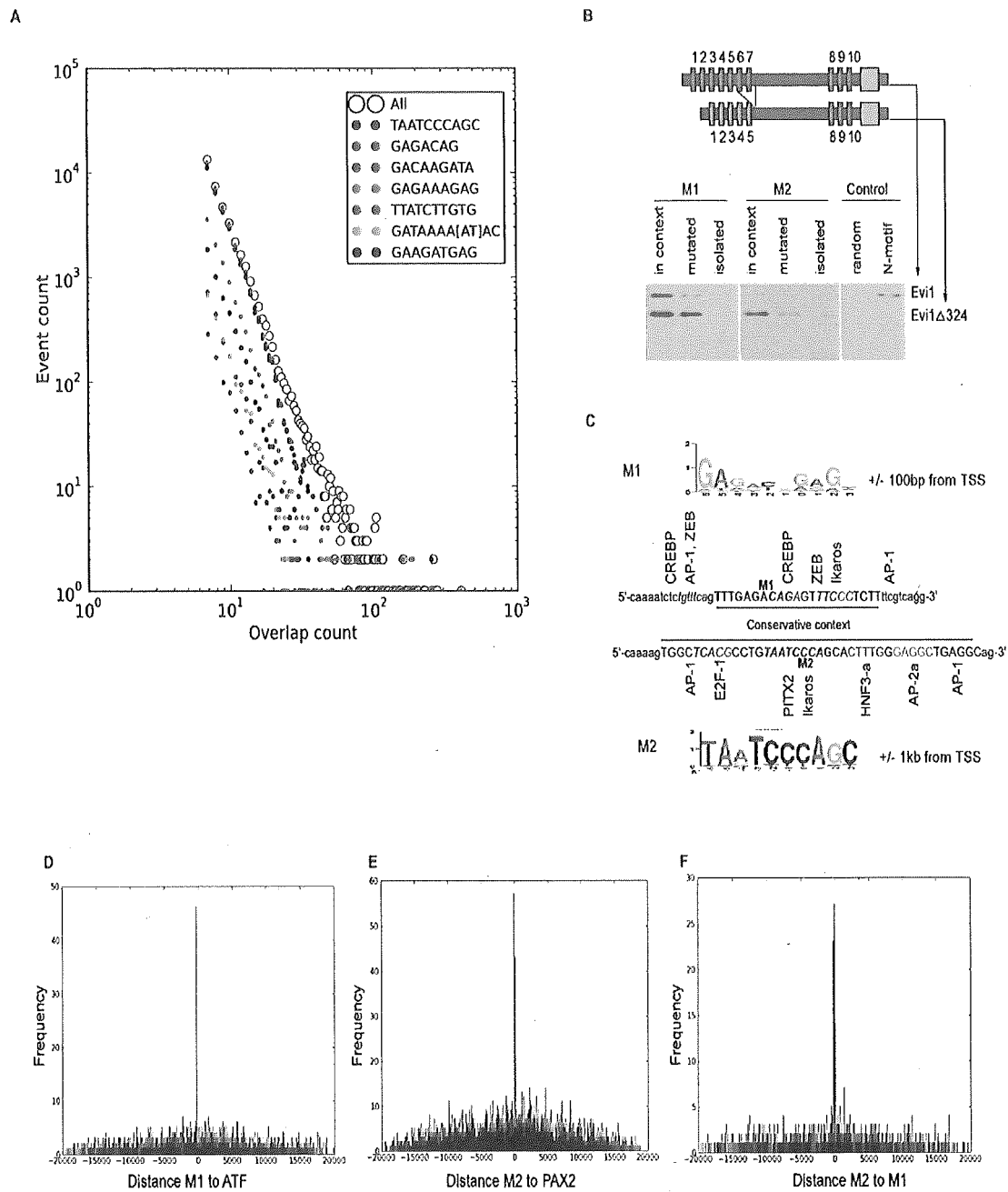
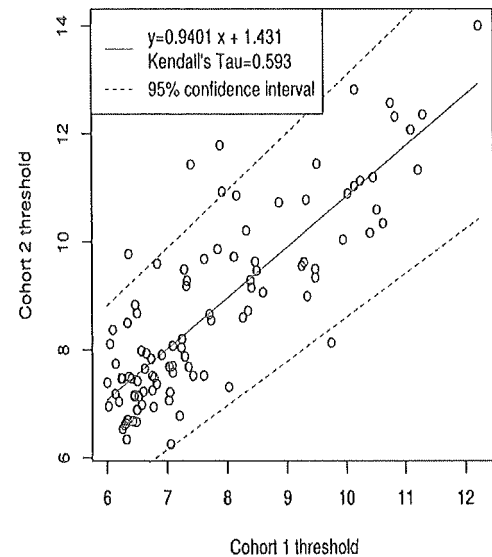


Figure 13

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```
fit=lm(threshold2~threshold1)
fit.c=coefficients(fit)
```

```
centroid=function(X,Y,fit.c,convfun=mean)
```

```
{
  a=fit.c[2]
  b=fit.c[1]
  nrX=nrow(X)
  if (!is.null(nrX)) {
    extrapX=matrix(0,nrX,ncol(X))
    extrapY=extrapX
    for (i in ncol(X)) {
      x=X[,i]
      y=Y[,i]
      extrapX[,i]=(a*y+x- a*b)/(a^2+1)
      extrapY[,i]=a*extrapX[,i]+b
    }

    return(cbind(apply(extrapX,1,convfun),apply(extrapY,1,convfun)))
  } else {
    extrapX=(a*Y+X- a*b)/(a^2+1)
    extrapY=a*extrapX+b
    return(apply(cbind(extrapX,extrapY),1,convfun))
  }
}
```

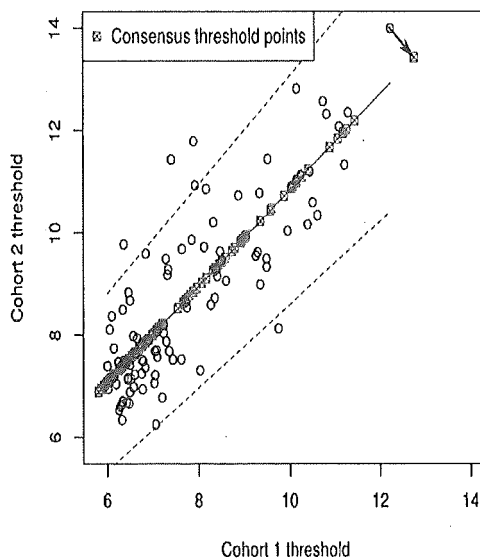


Figure 14

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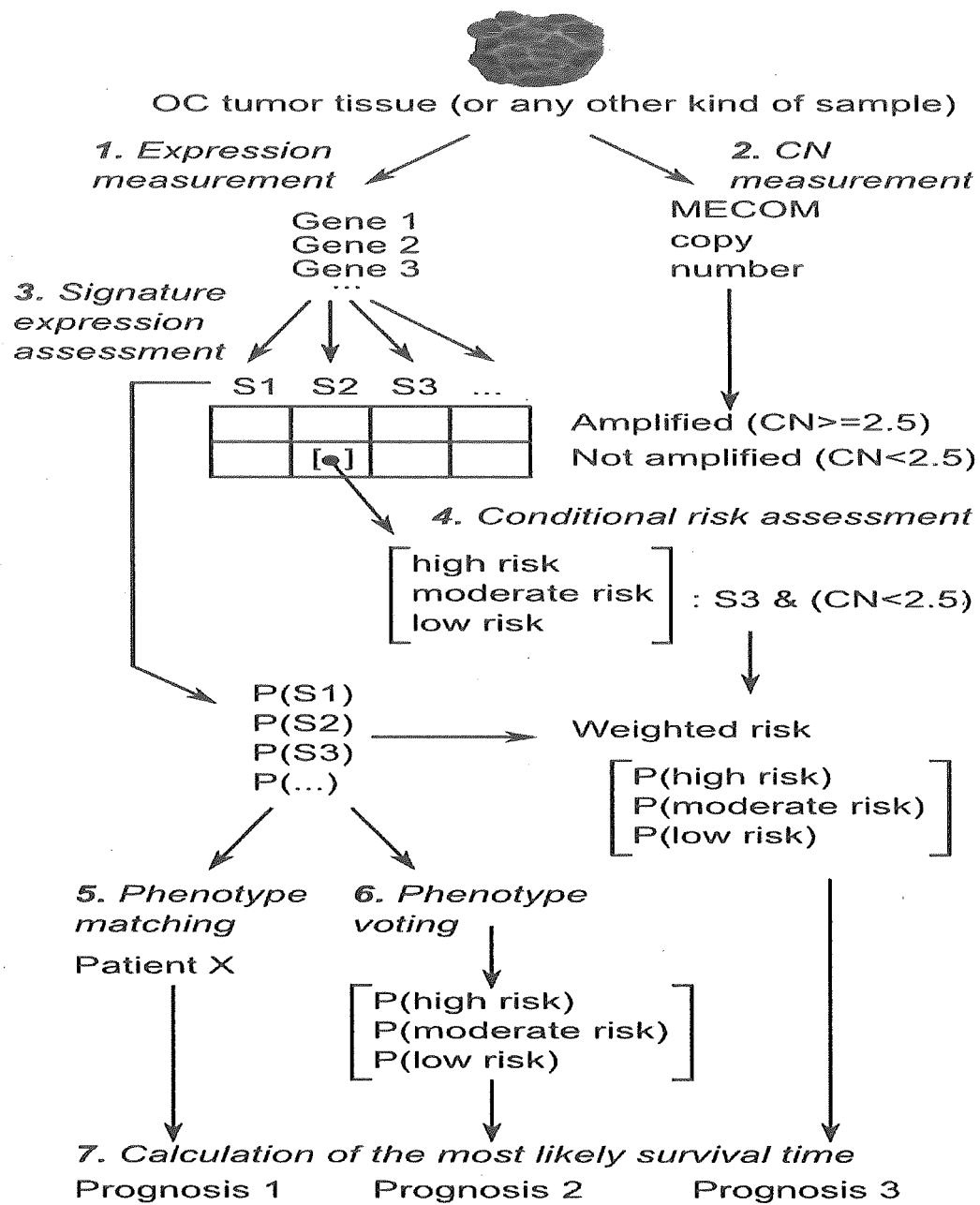


Figure 15

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Univariate Cox proportional hazard models of the patient survival, based on the criteria available at the operation time (TCGA cohort, 356 patients)

Factor	Group	beta	HR	CI_L	CI_U	z	Pr(> z)
immune	high risk	2.50	12.14	7.47	19.73	10.07	0.00E+00
immune	medium risk	1.31	3.71	2.63	5.23	7.46	8.57E-14
signalling	high risk	1.91	6.75	4.04	11.28	7.29	3.07E-13
apoptosis	high risk	1.85	6.35	3.83	10.52	7.18	7.00E-13
debulking	high risk	1.63	5.11	3.20	8.17	6.81	9.84E-12
-							
RiskGroup	low risk	1.37	0.25	0.17	0.39	-6.47	1.00E-10
rnametabolism	high risk	1.49	4.44	2.74	7.18	6.07	1.31E-09
Primary	PARTIAL RESPONSE	1.21	3.34	2.26	4.94	6.05	1.44E-09
chemotherapy	medium risk	0.95	2.60	1.89	3.57	5.86	4.68E-09
signalling	high risk	1.42	4.15	2.56	6.72	5.78	7.62E-09
emt	high risk	1.42	4.15	2.56	6.72	5.78	7.62E-09
-							
Neoplasm status	TUMOR FREE	3.02	0.05	0.02	0.14	-5.60	2.12E-08
rnametabolism	medium risk	0.95	2.58	1.84	3.61	5.49	3.92E-08
emt	medium risk	0.87	2.39	1.75	3.26	5.49	4.10E-08
debulking	medium risk	0.85	2.35	1.72	3.21	5.34	9.49E-08
surv	high risk	1.65	5.20	2.83	9.55	5.31	1.08E-07
Primary	PROGRESSIVE	1.27	3.56	2.21	5.74	5.23	1.72E-07
chemotherapy	DISEASE	1.27	3.56	2.21	5.74	5.23	1.72E-07
RiskGroup	high risk	1.41	4.08	2.30	7.22	4.83	1.39E-06
apoptosis	medium risk	0.87	2.40	1.64	3.51	4.50	6.89E-06
-							
Residual tumor	null	0.89	0.41	0.26	0.66	-3.72	1.98E-04
Age	>=67	0.72	2.05	1.40	3.00	3.69	2.24E-04
retinoic	medium risk	0.66	1.94	1.35	2.77	3.62	2.92E-04
surv	medium risk	0.92	2.51	1.50	4.22	3.49	4.84E-04
retinoic	high risk	1.02	2.78	1.49	5.18	3.21	1.31E-03
-							
Residual tumor	No Macroscopic disease	0.67	0.51	0.32	0.82	-2.76	5.83E-03
-							
Tumor stage	Stages I and II	1.16	0.31	0.13	0.76	-2.56	1.04E-02
Tumor grade	Grades 3 and 4	0.45	1.57	1.06	2.34	2.25	2.45E-02
Age	53-66	0.40	1.49	1.04	2.13	2.16	3.08E-02
Primary	STABLE DISEASE	0.72	2.05	1.06	3.97	2.14	3.27E-02
chemotherapy	STABLE DISEASE	0.72	2.05	1.06	3.97	2.14	3.27E-02
-							
Neoplasm status	WITH TUMOR	0.40	0.67	0.44	1.02	-1.87	6.09E-02
Residual tumor	11-20 mm	0.10	1.11	0.66	1.85	0.39	6.97E-01
Race	Other	0.10	1.10	0.65	1.87	0.36	7.19E-01
Residual tumor	>20 mm	0.04	1.05	0.73	1.50	0.24	8.11E-01

Figure 16

17/68

Univariate Cox proportional hazard models of the patient survival, based on the criteria available at the operation time (TCGA cohort, 356 patients)

Factor	Group	beta	HR	CI_L	CI_U	z	Pr(> z)
immune	high risk	2.50	12.14	7.47	19.73	10.07	0.00E+00
immune	medium risk	1.31	3.71	2.63	5.23	7.46	8.57E-14
signalling	high risk	1.91	6.75	4.04	11.28	7.29	3.07E-13
apoptosis	high risk	1.85	6.35	3.83	10.52	7.18	7.00E-13
debulking	high risk	1.63	5.11	3.20	8.17	6.81	9.84E-12
RiskGroup	low risk	-1.37	0.25	0.17	0.39	-6.47	1.00E-10
rnametabolism	high risk	1.49	4.44	2.74	7.18	6.07	1.31E-09
Primary chemotherapy	PARTIAL RESPONSE	1.21	3.34	2.26	4.94	6.05	1.44E-09
signalling	medium risk	0.95	2.60	1.89	3.57	5.86	4.68E-09
emt	high risk	1.42	4.15	2.56	6.72	5.78	7.62E-09
Neoplasm status	TUMOR FREE	-3.02	0.05	0.02	0.14	-5.60	2.12E-08
rnametabolism	medium risk	0.95	2.58	1.84	3.61	5.49	3.92E-08
emt	medium risk	0.87	2.39	1.75	3.26	5.49	4.10E-08
debulking	medium risk	0.85	2.35	1.72	3.21	5.34	9.49E-08
surv	high risk	1.65	5.20	2.83	9.55	5.31	1.08E-07
Primary chemotherapy	PROGRESSIVE DISEASE	1.27	3.56	2.21	5.74	5.23	1.72E-07
RiskGroup	high risk	1.41	4.08	2.30	7.22	4.83	1.39E-06
apoptosis	medium risk	0.87	2.40	1.64	3.51	4.50	6.89E-06
Residual tumor	null	-0.89	0.41	0.26	0.66	-3.72	1.98E-04
Age	>=67	0.72	2.05	1.40	3.00	3.69	2.24E-04
retinoic	medium risk	0.66	1.94	1.35	2.77	3.62	2.92E-04
surv	medium risk	0.92	2.51	1.50	4.22	3.49	4.84E-04
retinoic	high risk	1.02	2.78	1.49	5.18	3.21	1.31E-03
Residual tumor	No Macroscopic disease	-0.67	0.51	0.32	0.82	-2.76	5.83E-03
Tumor stage	Stages I and II	-1.16	0.31	0.13	0.76	-2.56	1.04E-02
Tumor grade	Grades 3 and 4	0.45	1.57	1.06	2.34	2.25	2.45E-02
Age	53-66	0.40	1.49	1.04	2.13	2.16	3.08E-02
Primary chemotherapy	STABLE DISEASE	0.72	2.05	1.06	3.97	2.14	3.27E-02
Neoplasm status	WITH TUMOR	-0.40	0.67	0.44	1.02	-1.87	6.09E-02
Residual tumor	11-20 mm	0.10	1.11	0.66	1.85	0.39	6.97E-01
Race	Other	0.10	1.10	0.65	1.87	0.36	7.19E-01
Residual tumor	>20 mm	0.04	1.05	0.73	1.50	0.24	8.11E-01

Figure 17

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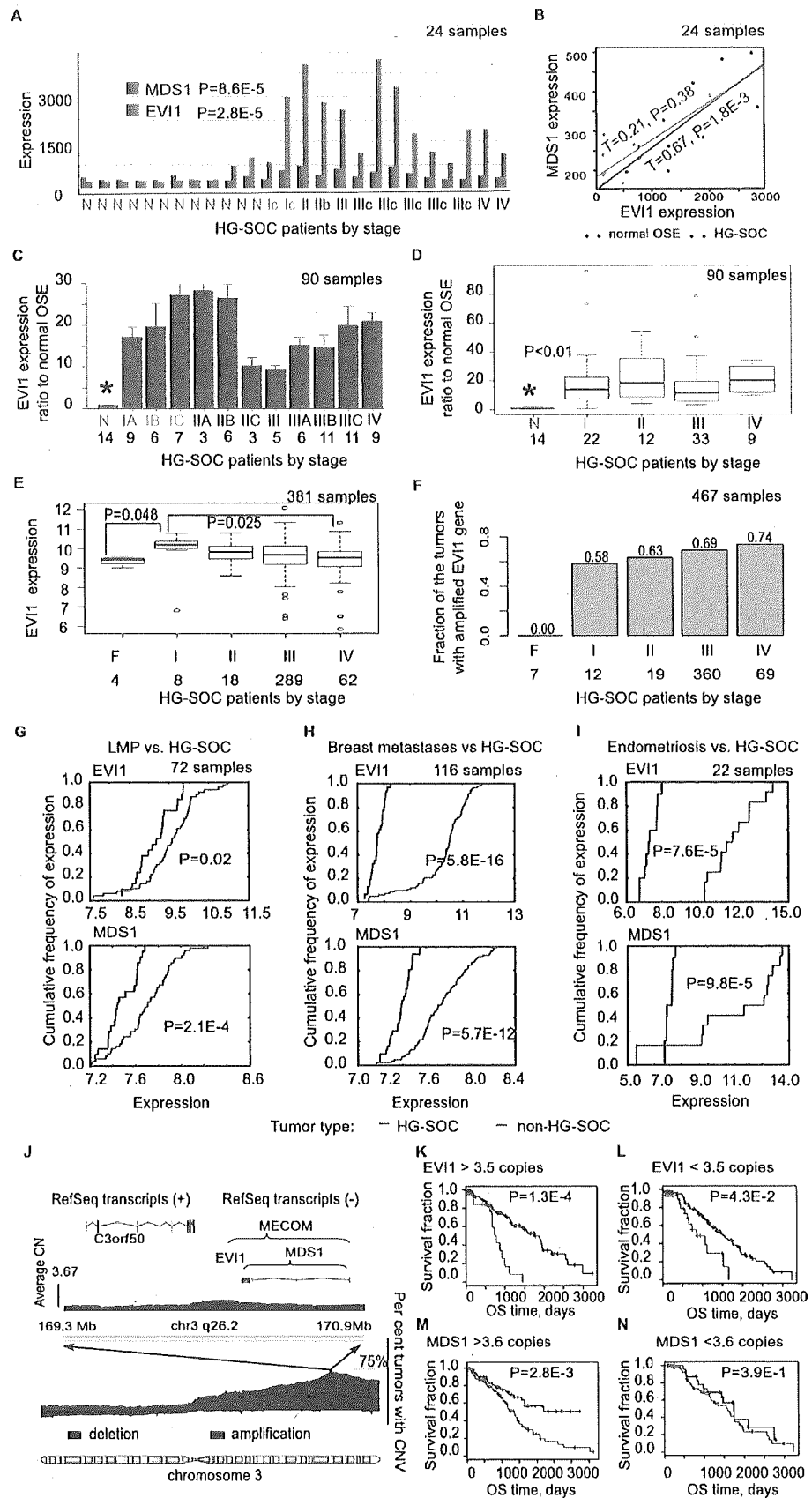


Figure 18

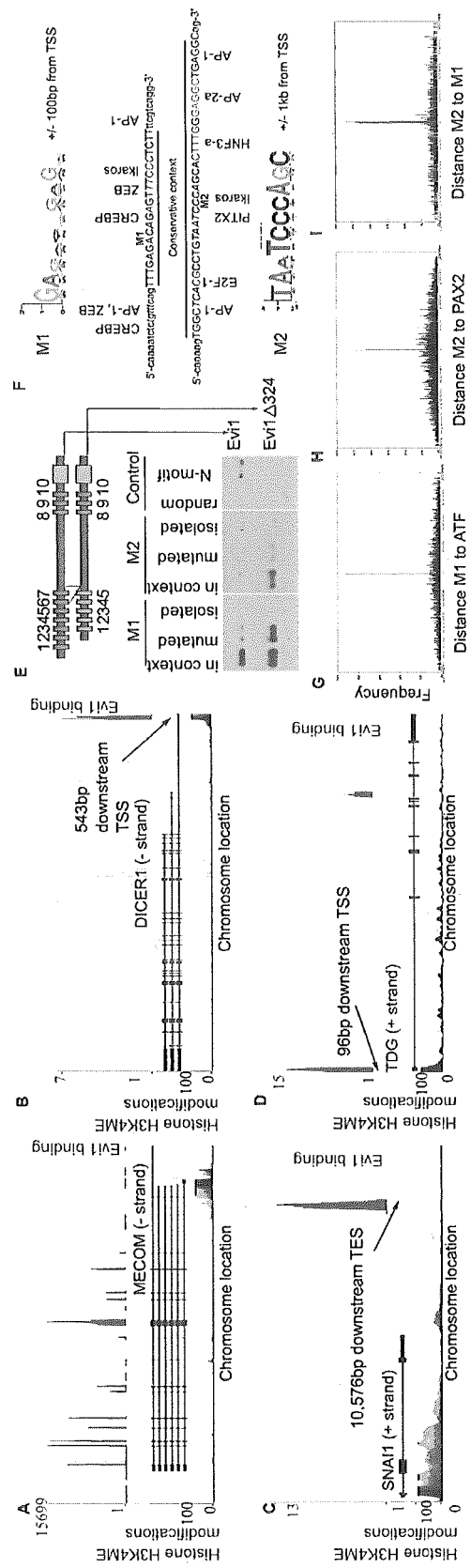


Figure 19

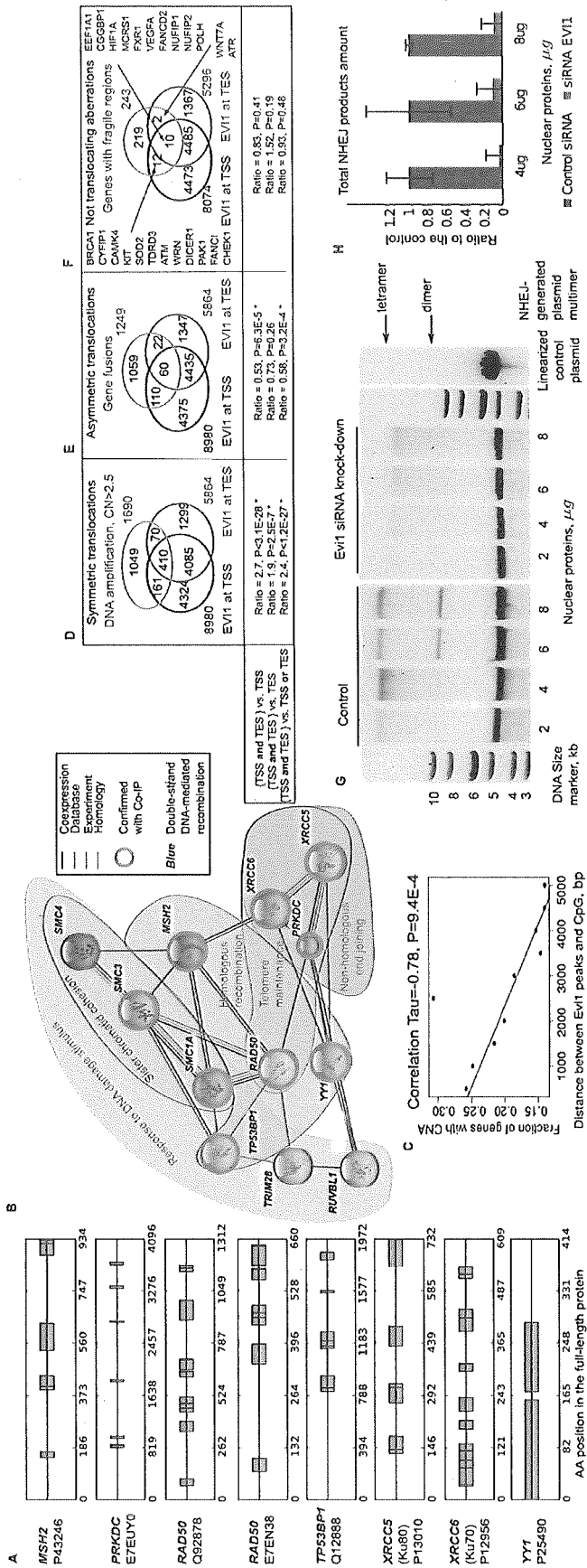


Figure 20

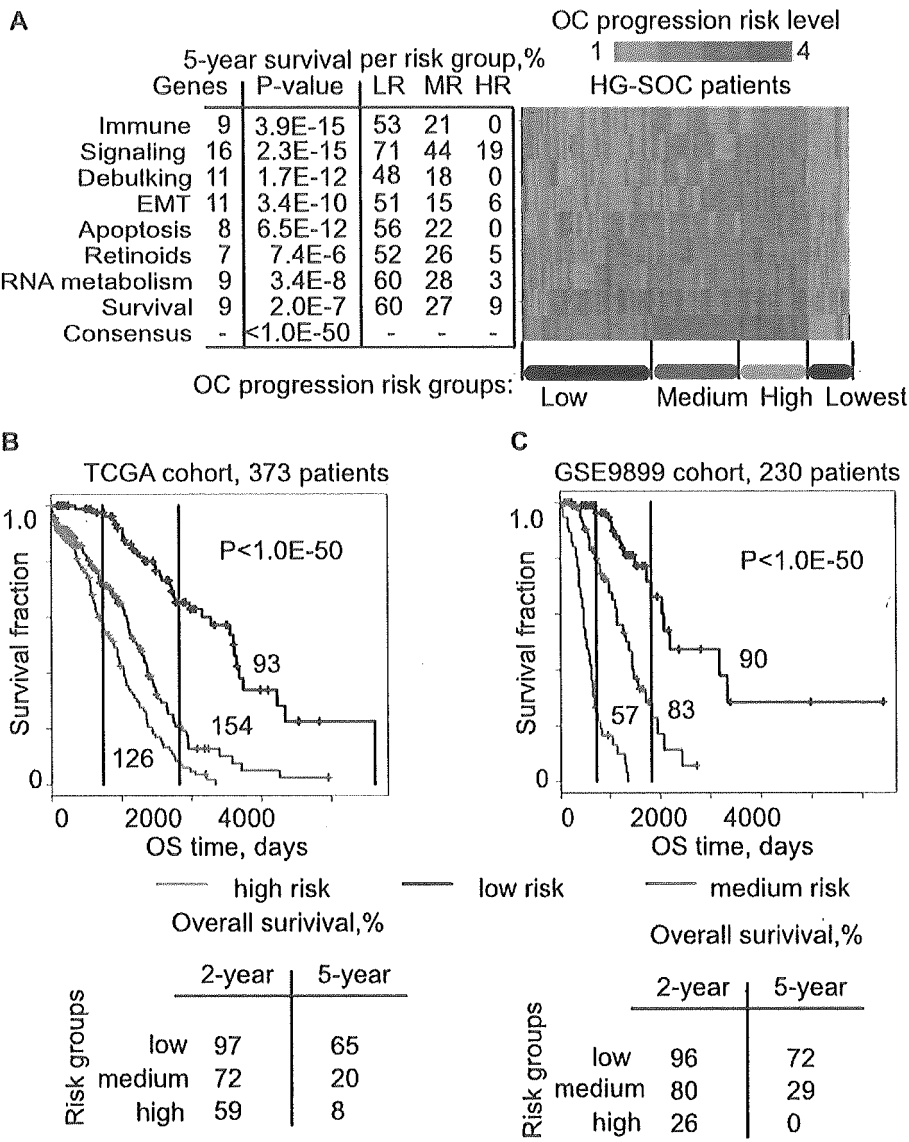


Figure 21

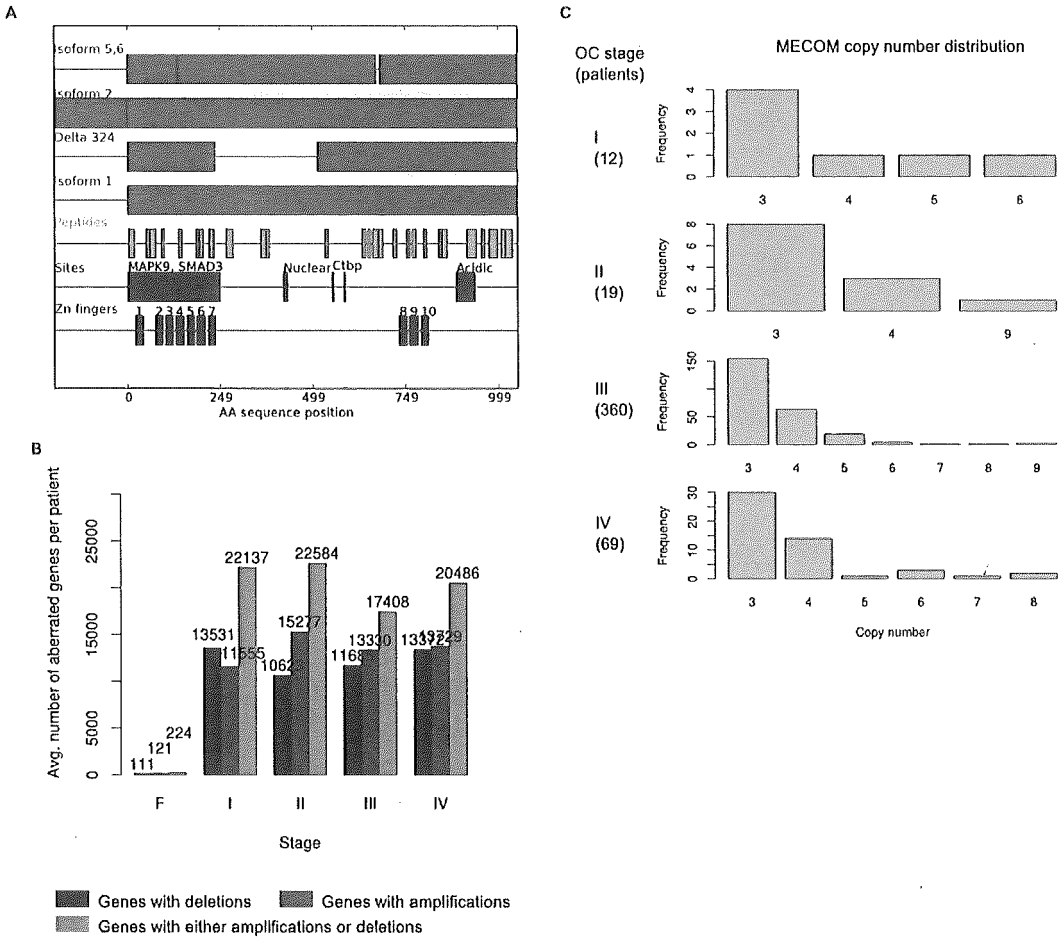


Figure 22: Figure S1

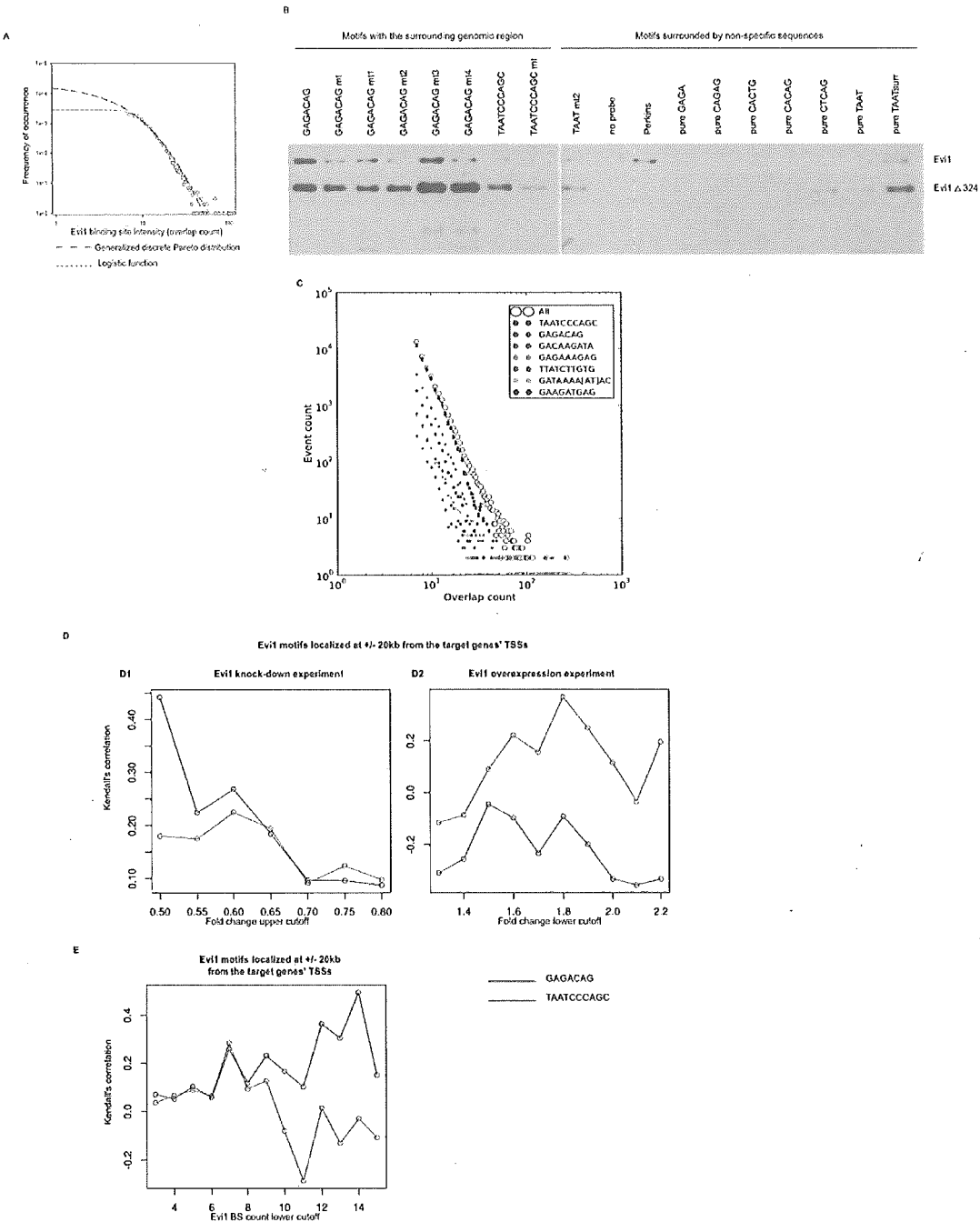


Figure 23: Figure S2

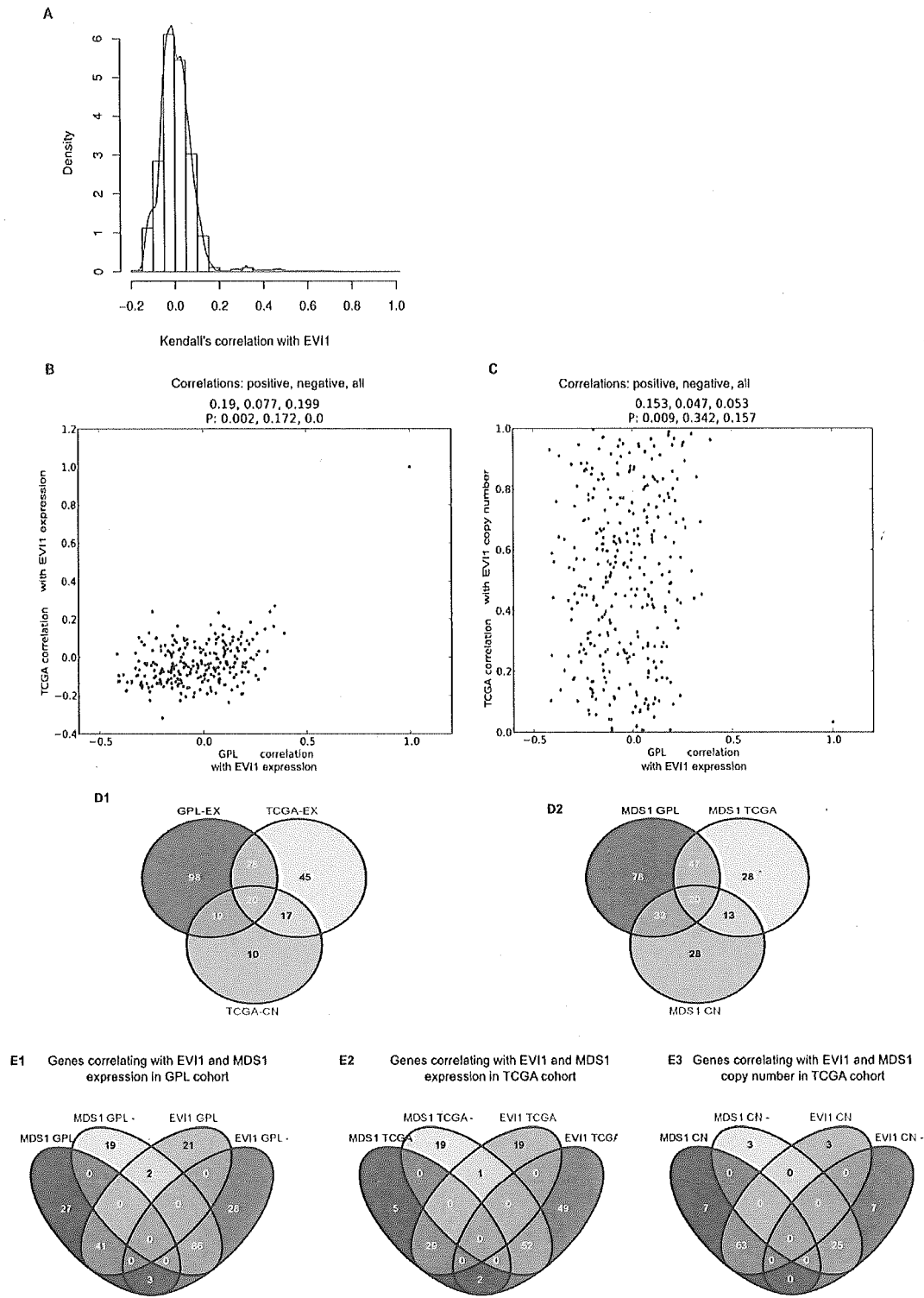


Figure 24: Figure S3

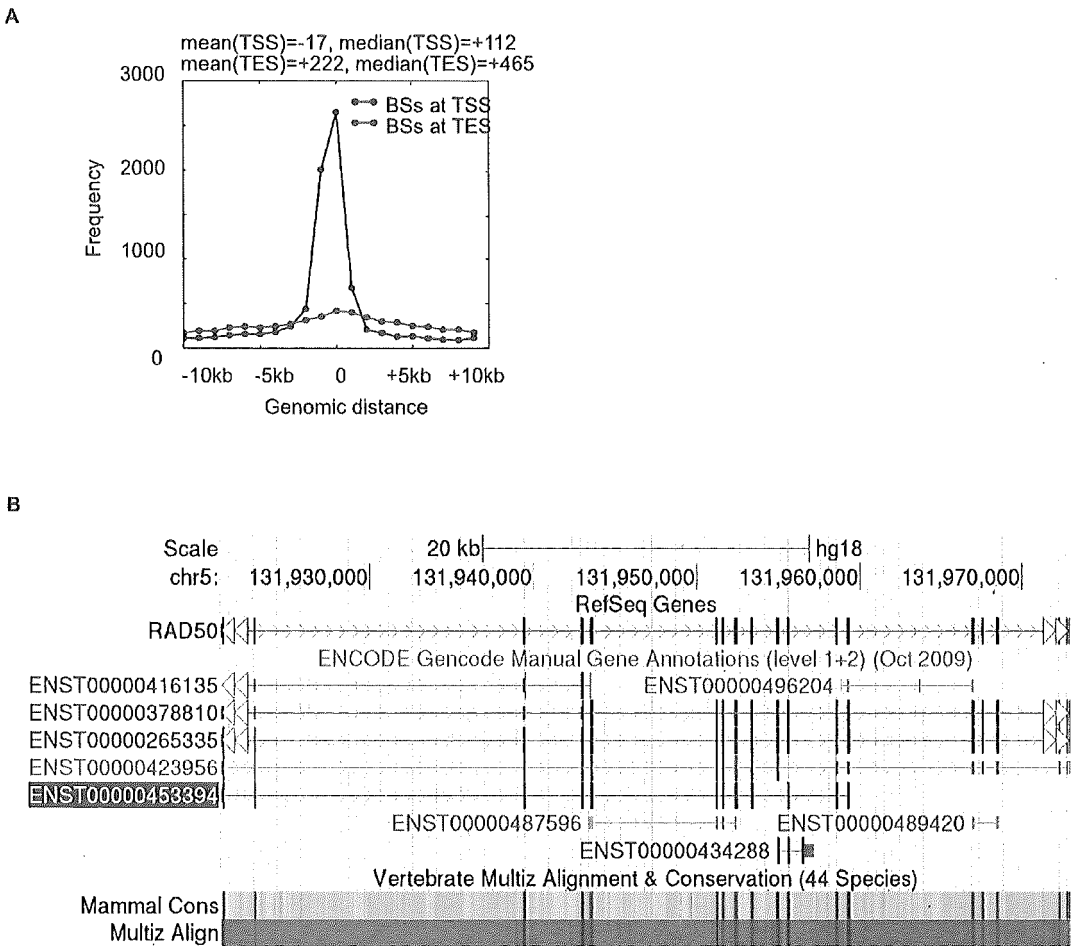


Figure 25: Figure S4

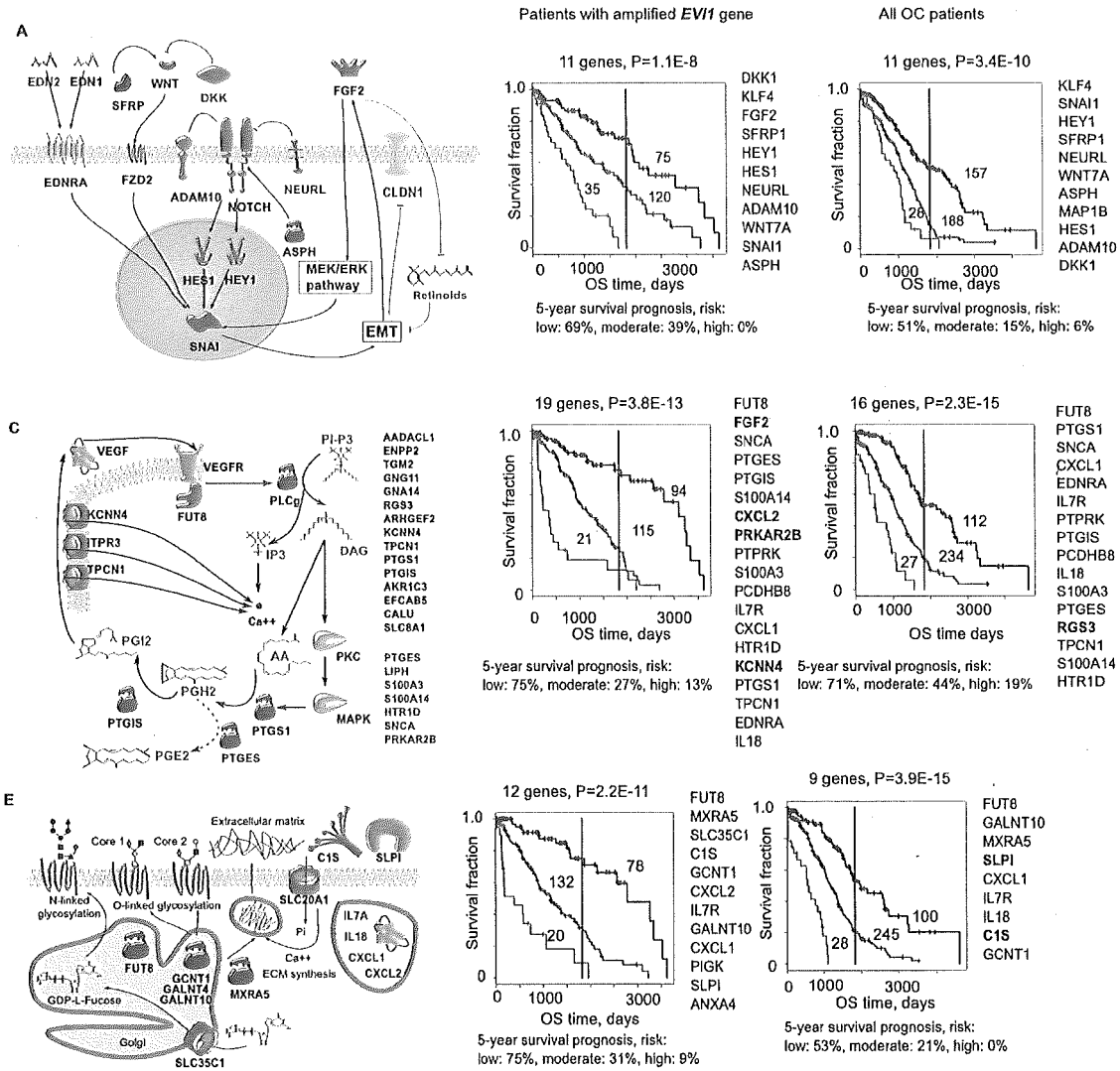


Figure 26: Figure S5

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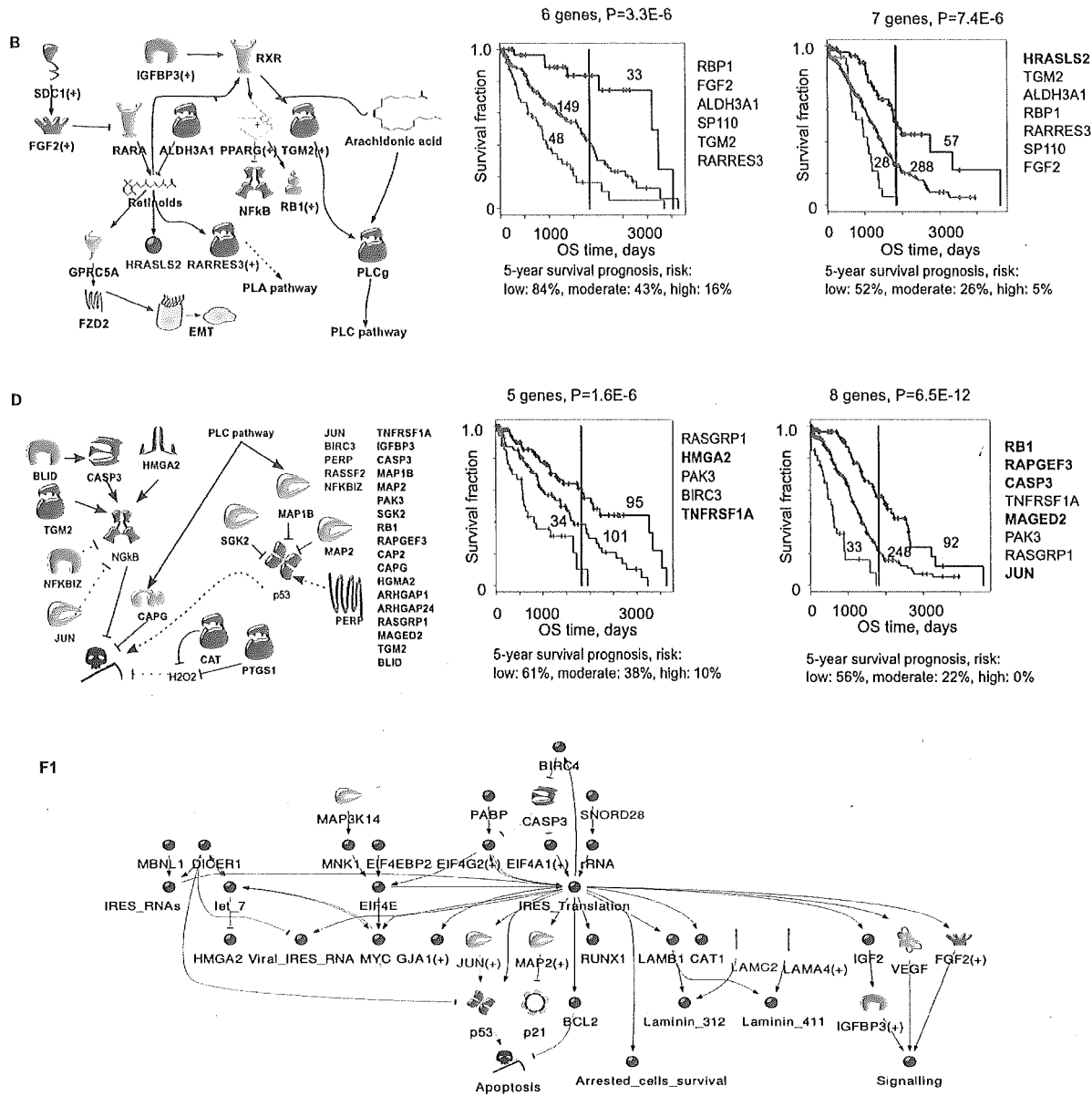


Figure 26: Figure S5

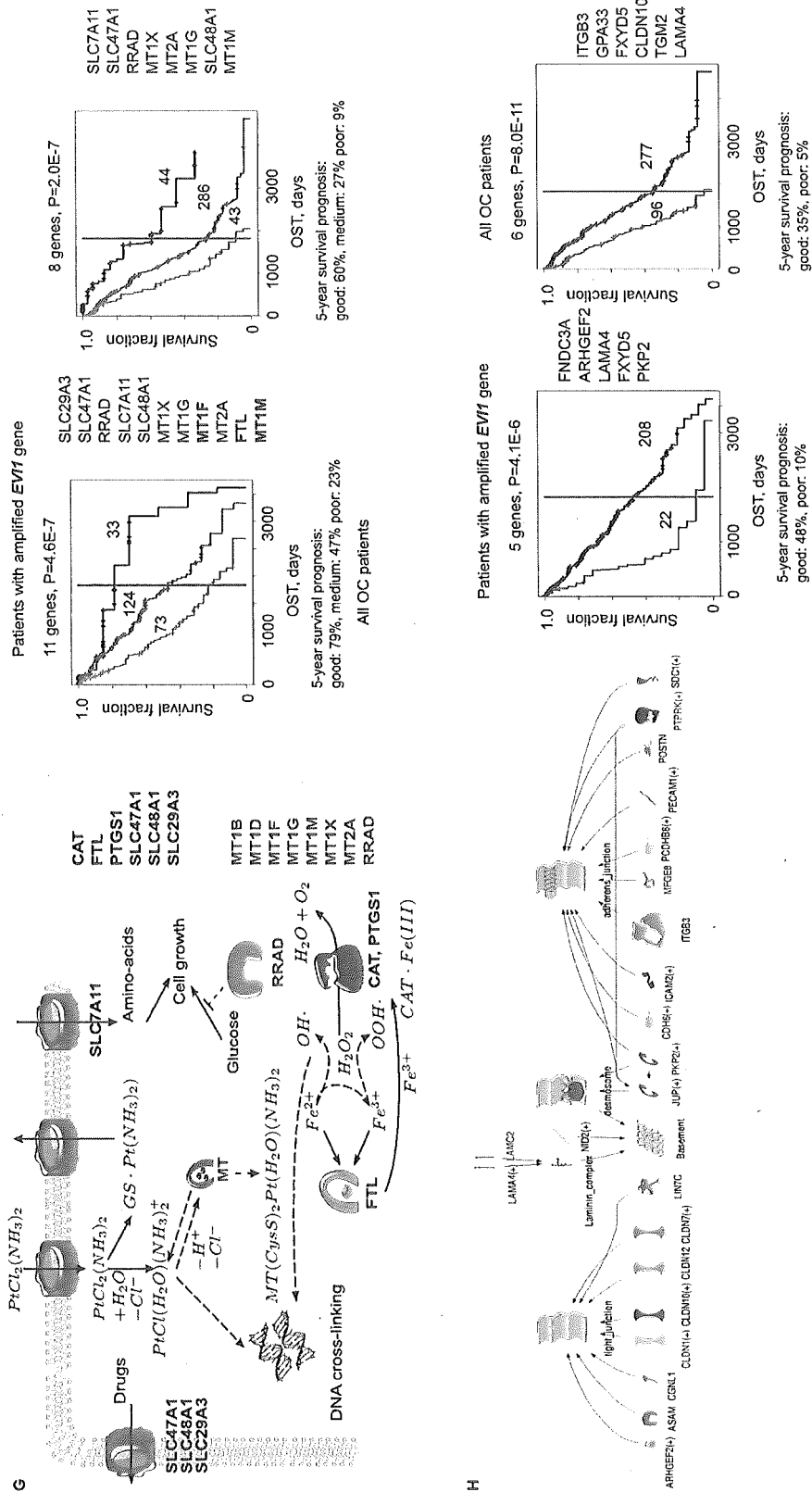
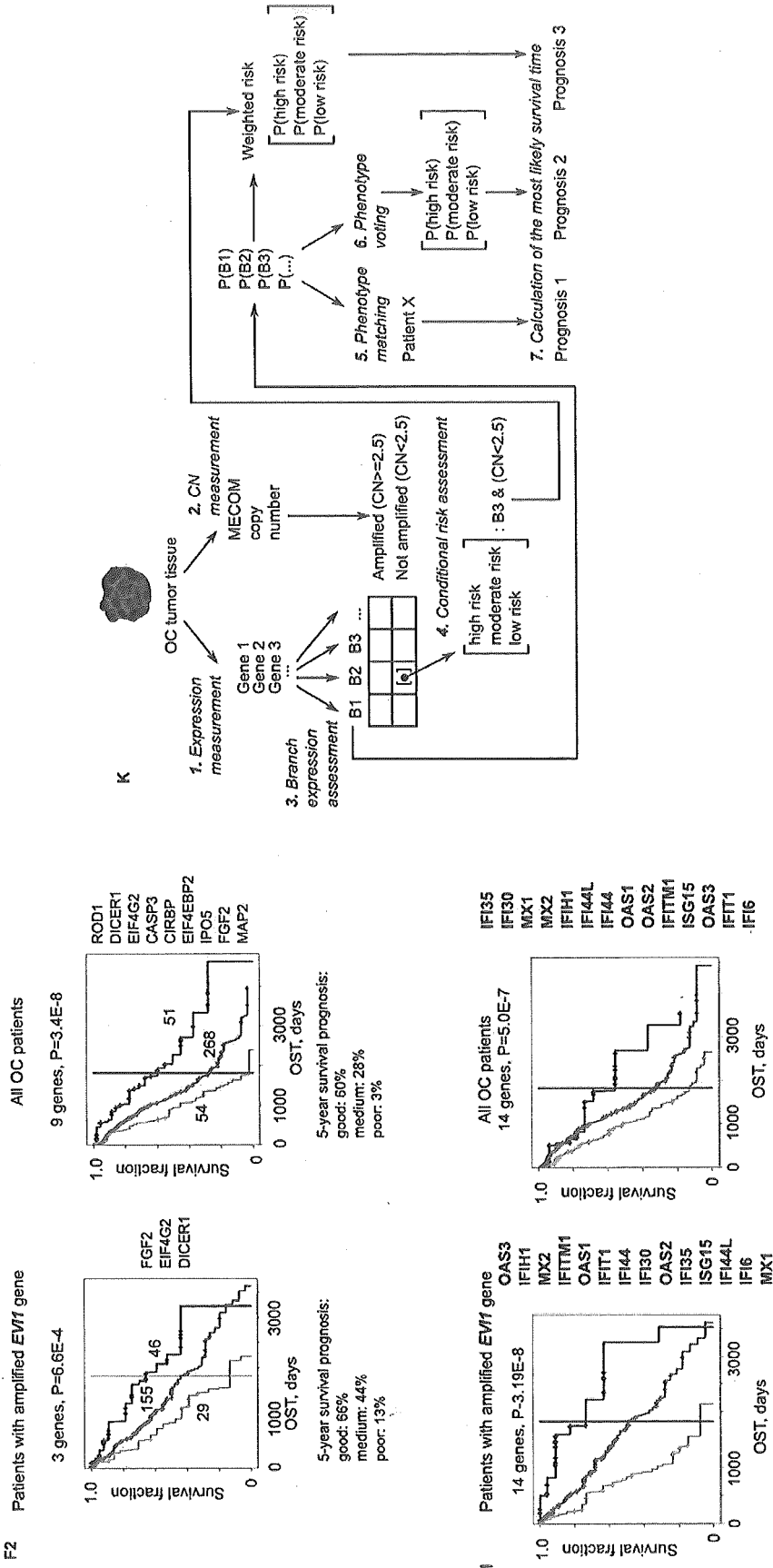


Figure 26: Figure S5



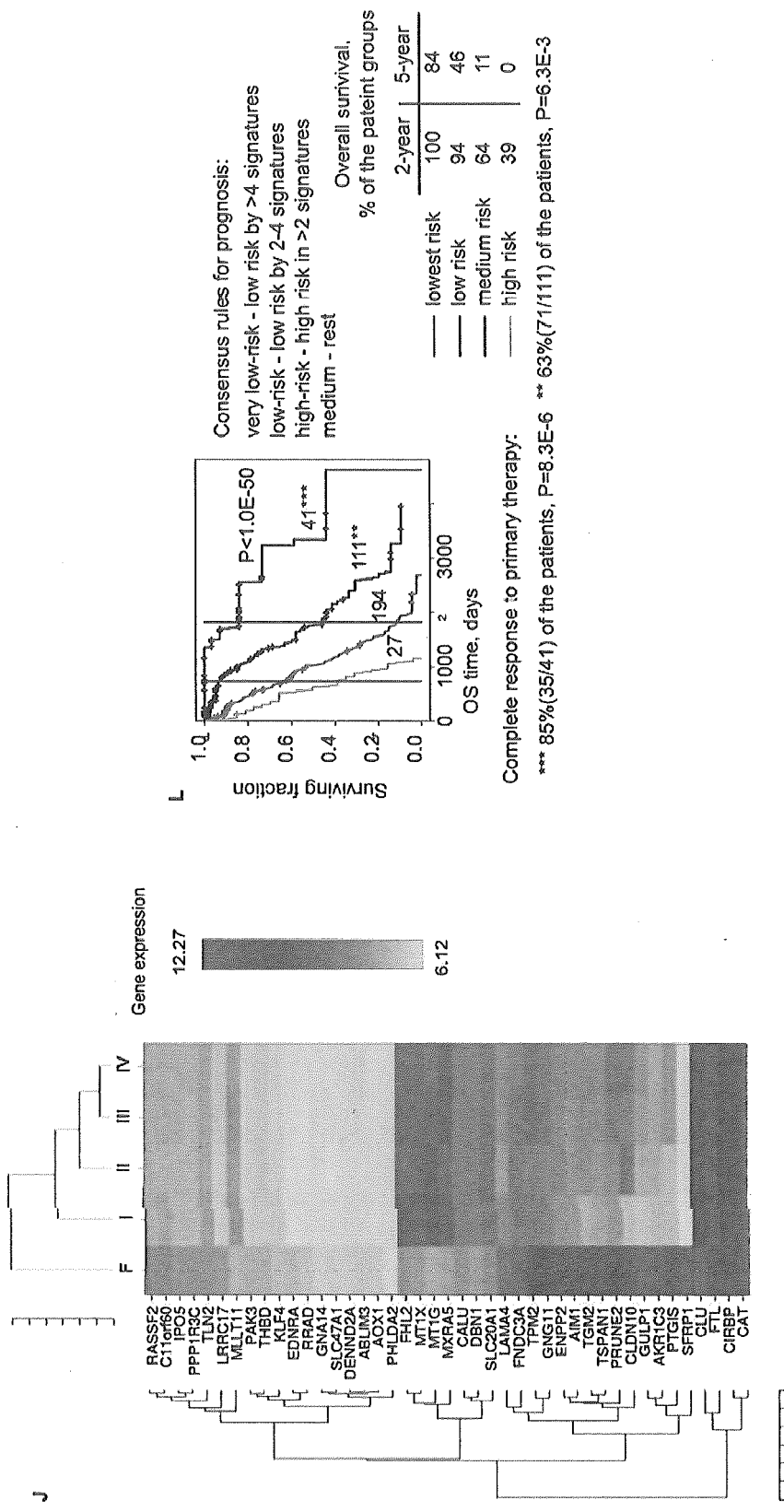


Figure 26: Figure S5

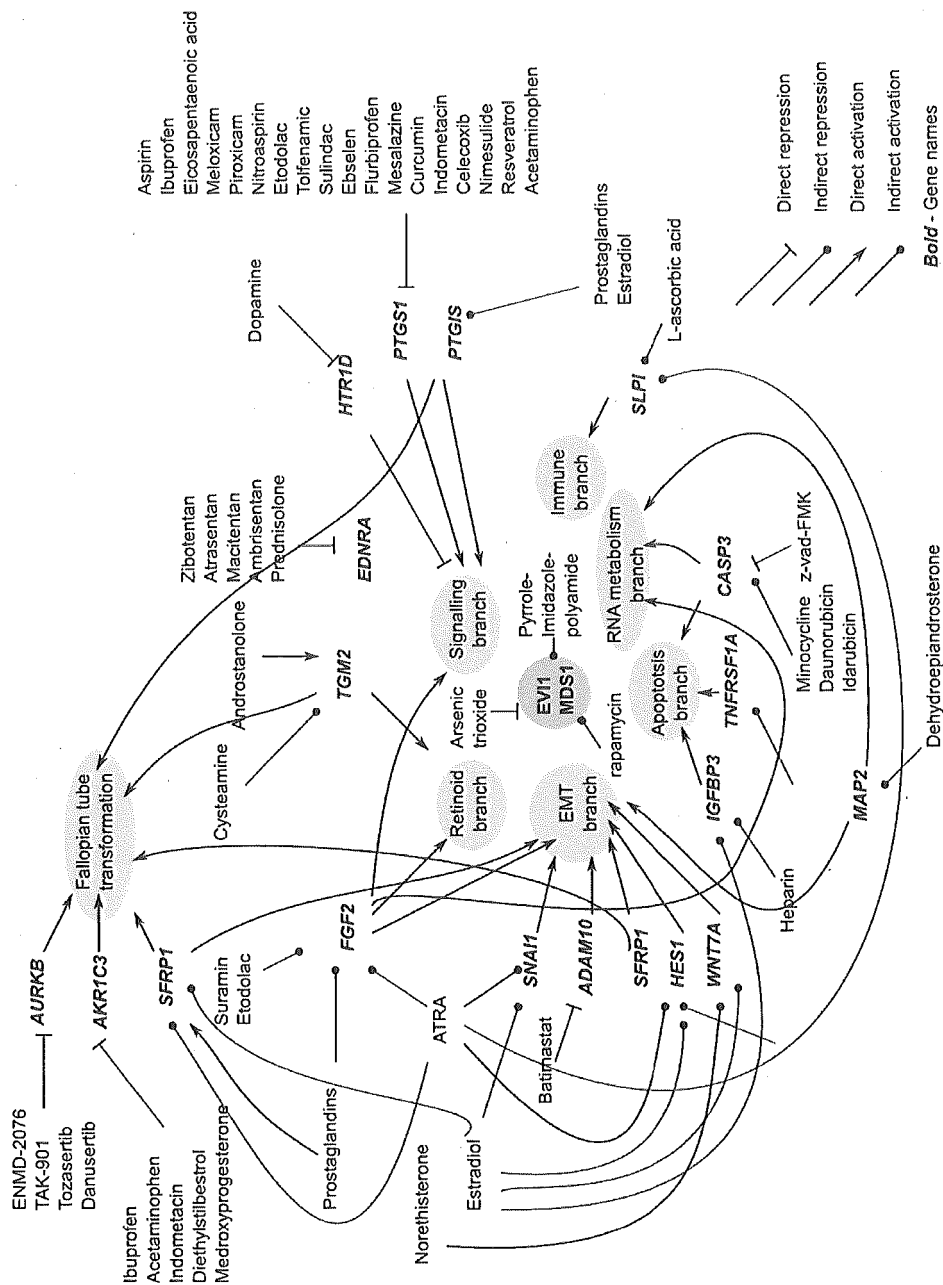


Figure 27: Figure S6

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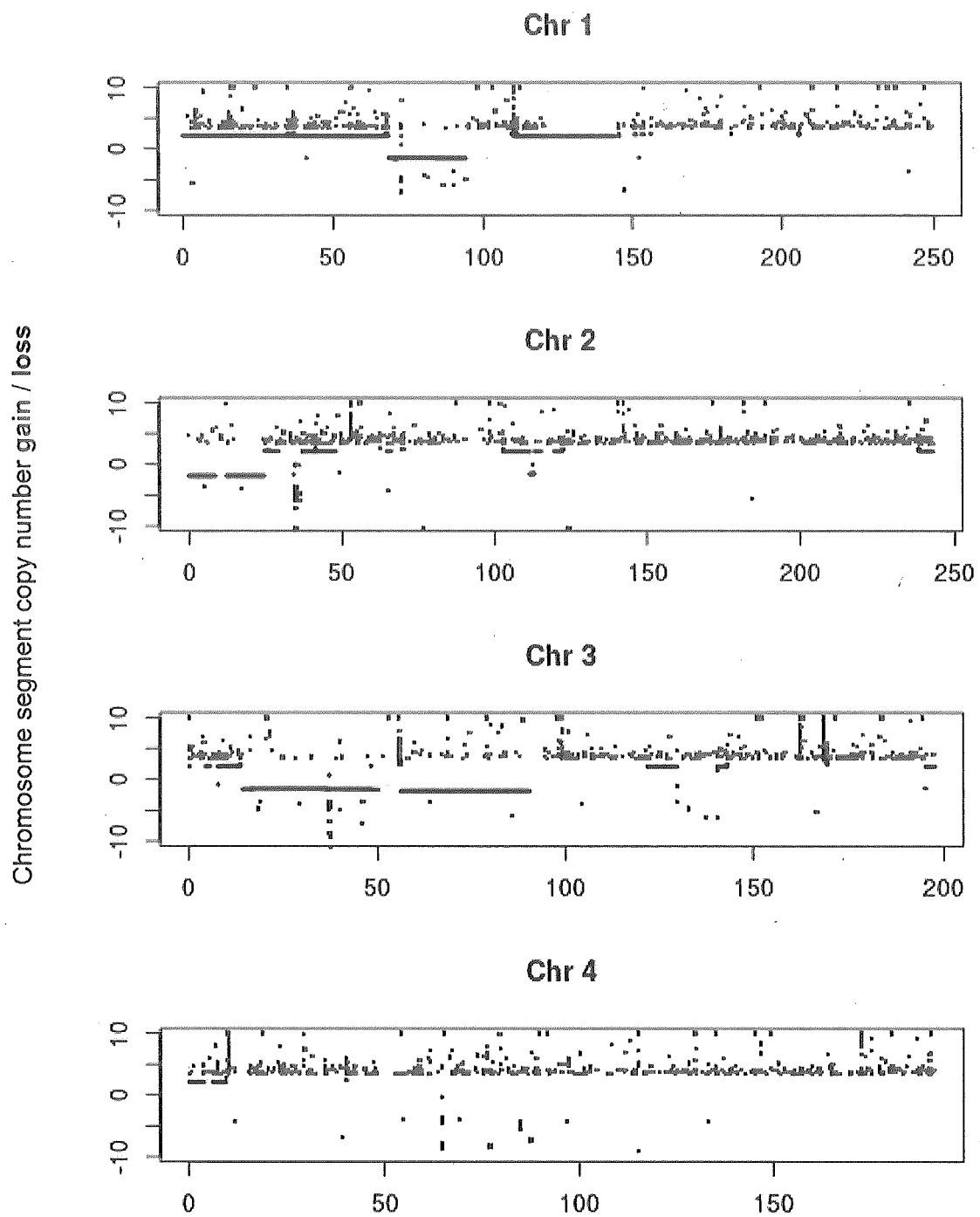
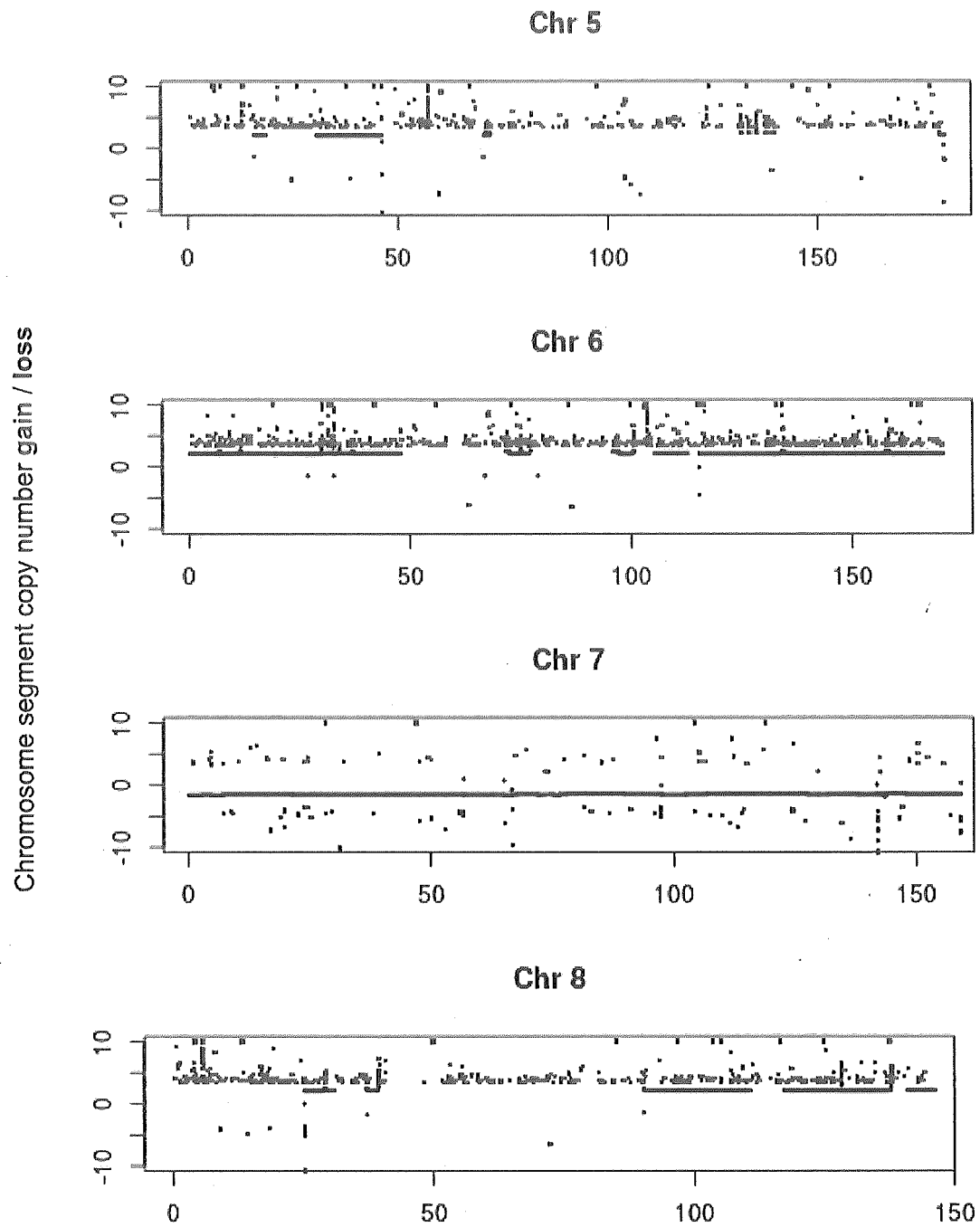


Figure 28: Figure S7

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Figure 28: Figure S7

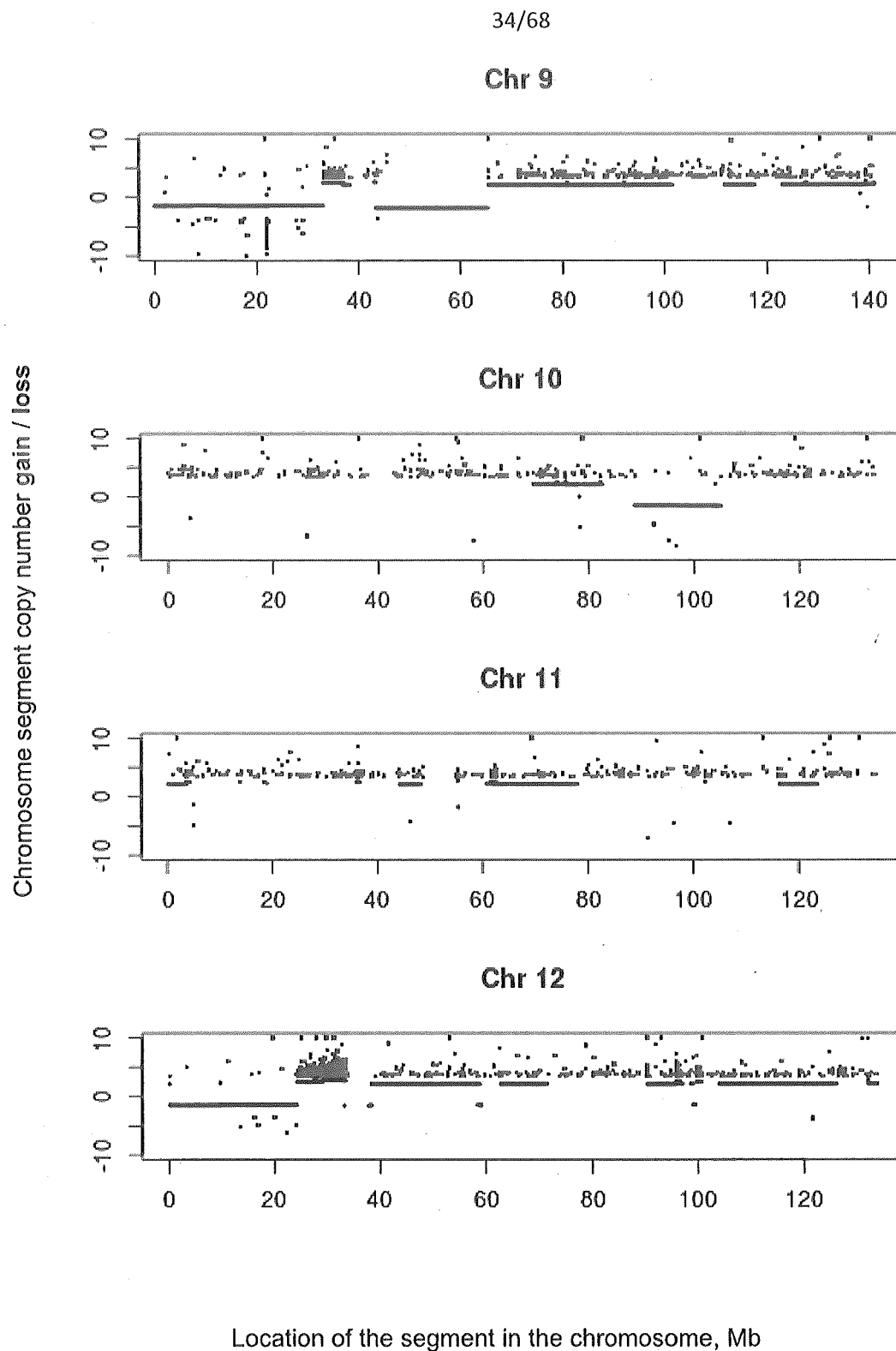


Figure 28: Figure S7

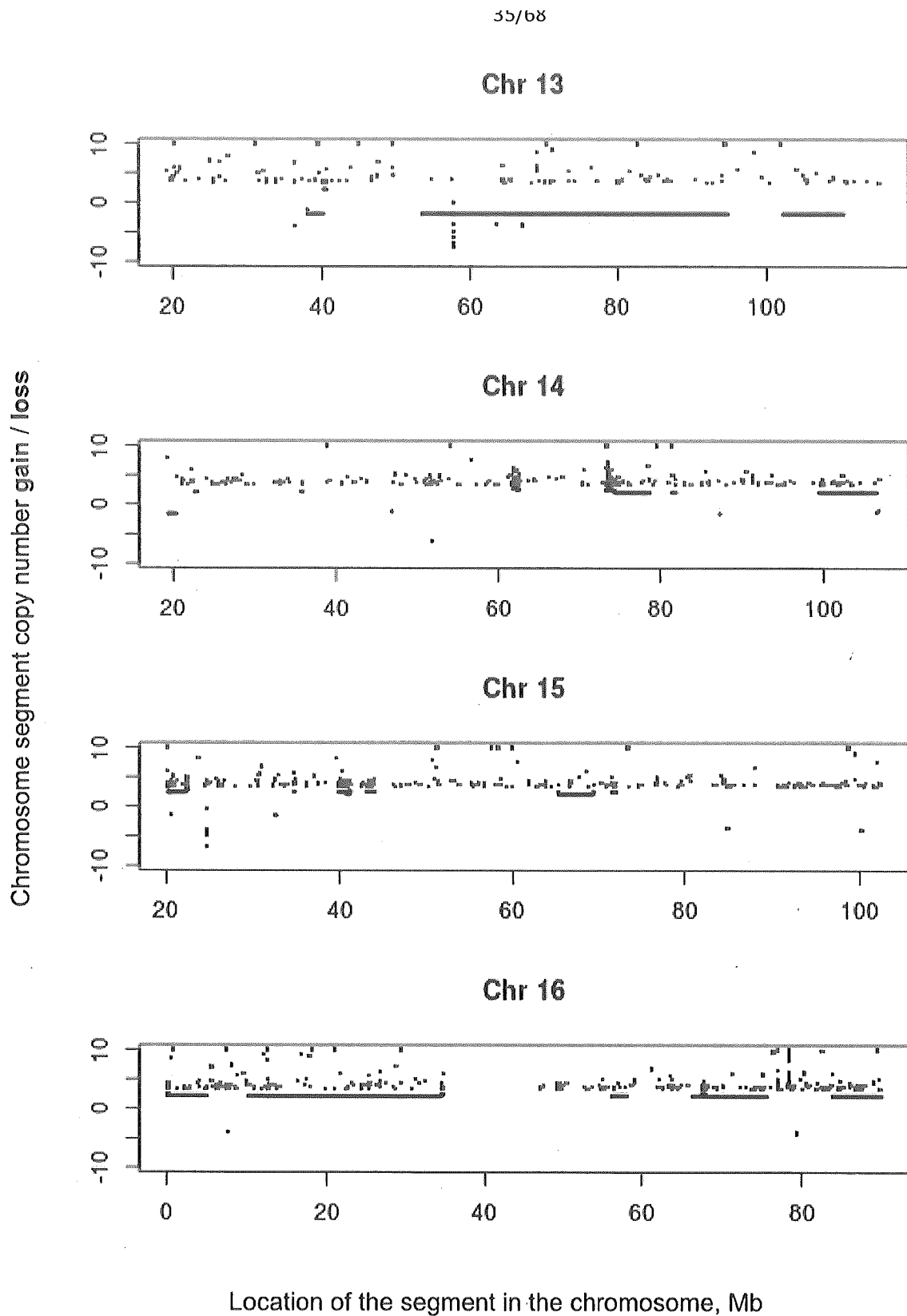


Figure 28: Figure S7

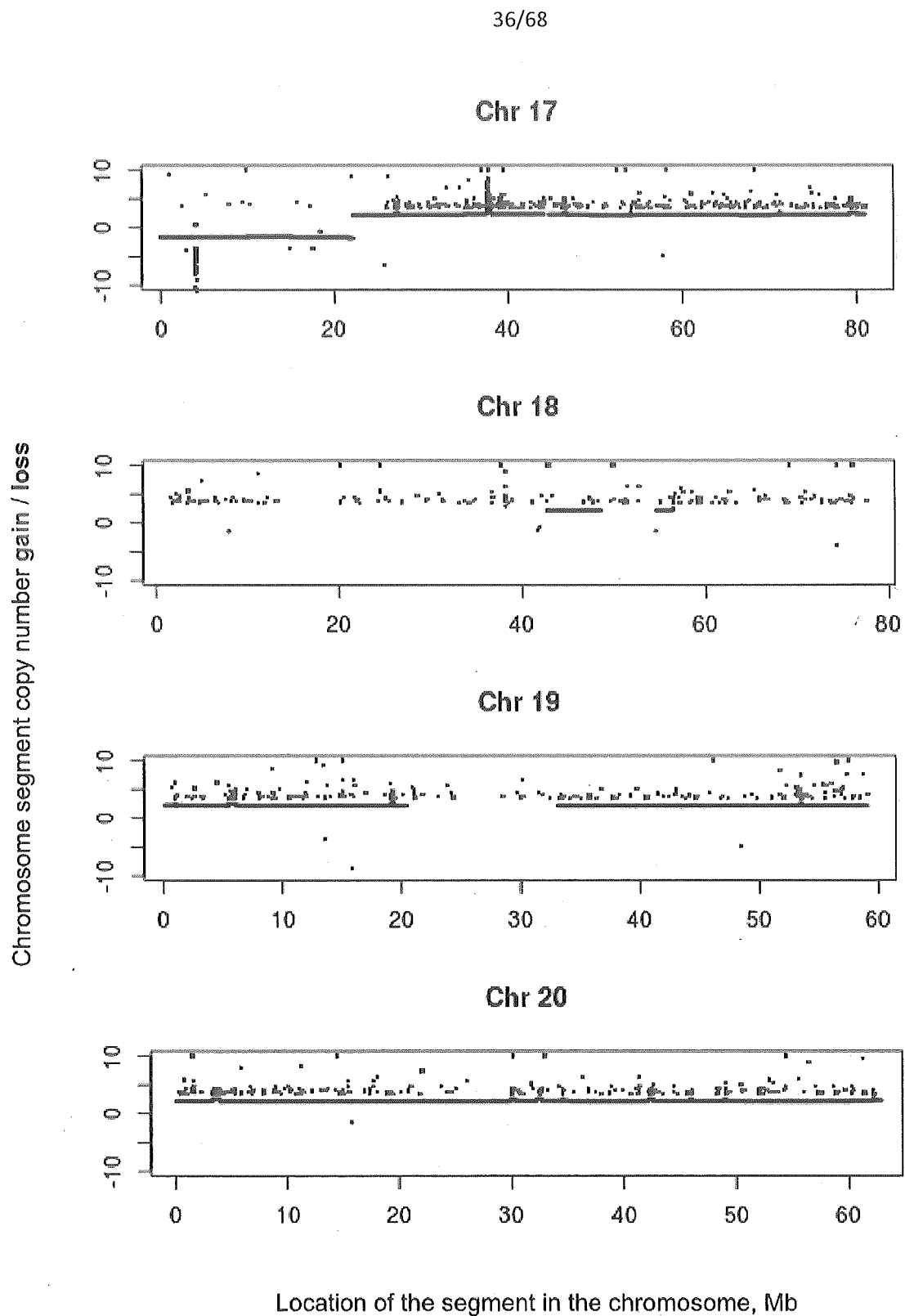


Figure 28: Figure S7

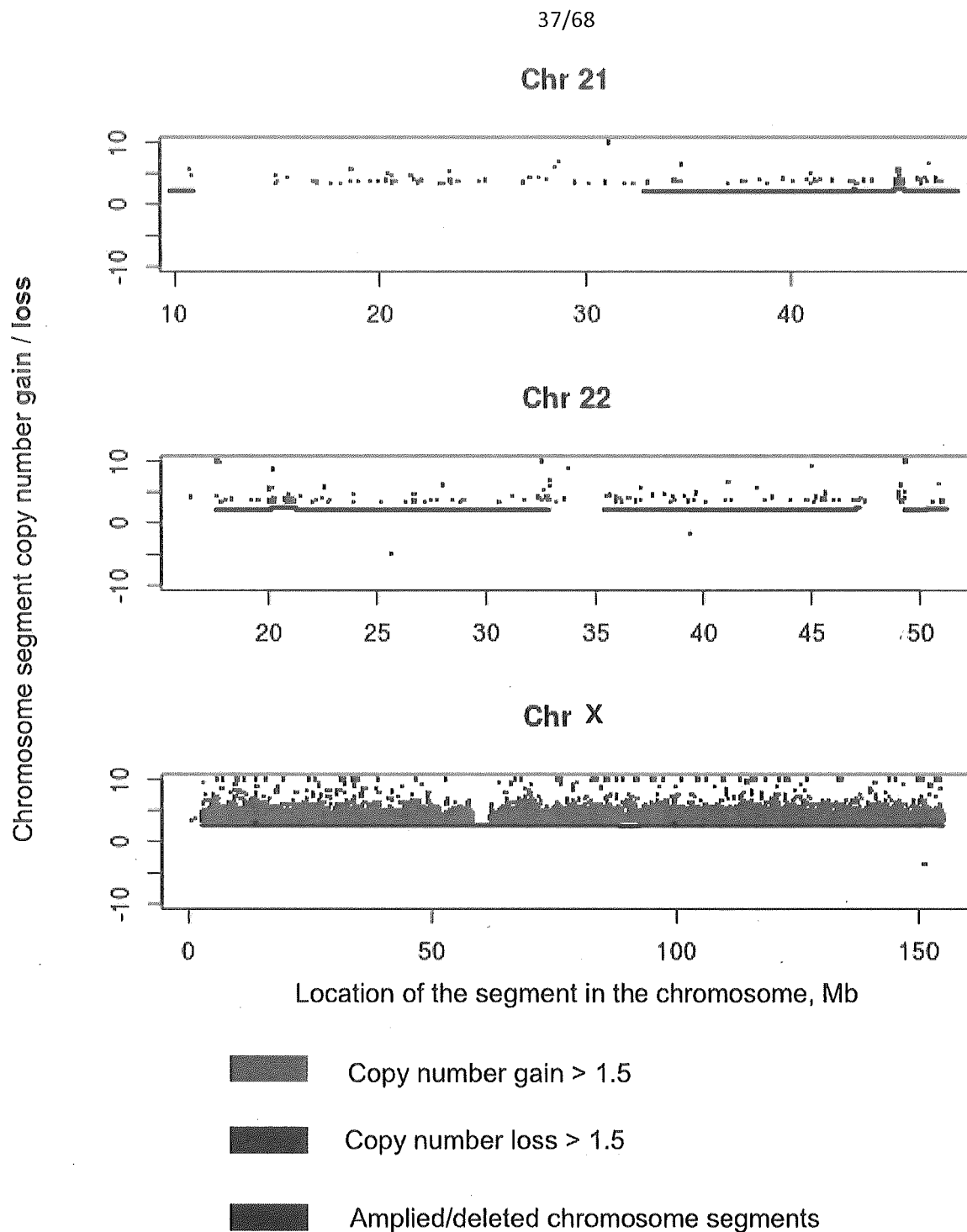


Figure 28: Figure S7

Association of EVI1 and MDS1 genes expression and copy number with HGS-OC stages

<i>EVI1</i> expression				
Tumor stage	I	II	III	IV
F	0.048	0.081	0.277	0.563
I	0.000	0.129	0.060	0.025
II	0.000	0.000	0.454	0.103
III	0.000	0.000	0.000	0.144
IV	0.000	0.000	0.000	0.000

MDS1 expression

Tumor stage	I	II	III	IV
F	0.073	0.195	0.141	0.116
I	0.000	0.429	0.227	0.234
II	0.000	0.000	0.754	0.840
III	0.000	0.000	0.000	0.906
IV	0.000	0.000	0.000	0.000

EVI1 copy number

Tumor stage	II	III	IV
II	0.400	0.240	0.395
III	0.000	0.877	0.963
IV	0.000	0.000	0.860

MDS1 copy number

Tumor stage	II	III	IV
II	0.400	0.183	0.186
III	0.000	0.799	0.762
IV	0.000	0.000	0.935

Figure 29: Table S1

Figure 30: Table S2(A): ChIP-seq peak clusters used for qPCR validation of Evi1 binding sites

Peak id	cluster overlap count	foldChange	qPCR enrichment	qPCR stdev	foldchange group
6.2556836	0	1.00	0.85	0.11	neg control
10.8226227	0	1.00	1.05	0.22	neg control
13.9769965	0	1.00	1.24	0.39	neg control
15.6827701	0	1.00	0.96	0.23	neg control
17.447453	0	1.00	1.14	0.20	neg control
20.482766	0	1.00	1.91	0.02	neg control
3.17031559	402	1.25	3.38	0.00	1 to 2
12.314877	8	1.91	0.89	0.10	1 to 2
15.6403176	10	1.94	2.03	0.02	1 to 2
18.6599927	14	1.99	1.28	0.78	1 to 2
2.8663888	7	2.12	1.23	1.20	2 to 3
Y.11932263	53	2.29	1.91	0.38	2 to 3
2.20842074	8	2.38	2.72	0.86	2 to 3
4.88360245	11	2.54	4.11	0.65	2 to 3
6.43986366	9	2.65	1.46	0.76	2 to 3
9.12993884	12	2.75	2.36	0.15	2 to 3
6.1115335	10	2.91	2.91	0.91	2 to 3
4.656848	8	3.18	2.51	0.14	3 to 4
8.24916764	8	3.18	5.25	0.92	3 to 4
14.1021159	8	3.18	1.95	1.45	3 to 4
14.1046288	8	3.18	4.85	0.29	3 to 4
18.2237946	8	3.18	4.30	1.25	3 to 4
12.4804774	11	3.18	4.10	1.05	3 to 4
11.3402303	12	3.44	6.71	3.44	3 to 4
2.55943279	9	3.53	3.29	0.01	3 to 4
4.13502111	9	3.53	2.03	0.53	3 to 4
4.40977842	9	3.53	1.18	0.02	3 to 4
10.7214531	9	3.53	2.57	1.76	3 to 4
12.508437	9	3.53	3.45	2.27	3 to 4
13.1056063	9	3.53	5.64	1.24	3 to 4
16.455002	9	3.53	2.47	0.19	3 to 4
17.1605845	9	3.53	6.53	1.93	3 to 4
20.2061772	9	3.53	1.90	0.11	3 to 4
20.3205066	9	3.53	1.40	0.03	3 to 4
22.3484966	9	3.53	3.74	1.79	3 to 4
1.41730971	13	3.71	2.97	1.71	3 to 4
4.14766269	10	3.88	4.17	1.91	3 to 4
10.4641828	10	3.88	2.90	1.68	3 to 4
14.6849331	10	3.88	3.59	2.53	3 to 4
17.7237463	10	3.88	2.11	0.68	3 to 4

X.13597365	10	3.88	6.42	0.19	3 to 4
2.21824451	7	4.23	0.94	0.13	4 to 5
4.83191225	7	4.23	0.40	0.26	4 to 5
6.12184483	7	4.23	2.93	0.27	4 to 5
7.23111674	7	4.23	7.62	0.43	4 to 5
8.12561902	7	4.23	1.25	0.50	4 to 5
8.67999362	7	4.23	7.42	2.90	4 to 5
9.73934033	7	4.23	1.88	0.01	4 to 5
10.7327825	7	4.23	3.02	0.48	4 to 5
12.110354	7	4.23	1.81	0.20	4 to 5
12.2859495	7	4.23	2.38	0.47	4 to 5
18.29492	7	4.23	1.69	0.61	4 to 5
18.5472564	7	4.23	4.29	0.13	4 to 5
20.8782314	7	4.23	4.17	1.38	4 to 5
21.2149429	7	4.23	4.93	0.69	4 to 5
22.2303016	7	4.23	0.96	0.11	4 to 5
8.67629951	11	4.23	2.49	0.59	4 to 5
3.87358784	12	4.59	6.21	0.79	4 to 5
6.21856341	8	4.76	2.24	0.45	4 to 5
2.45105279	8	4.76	11.11	5.02	4 to 5
5.1333589	8	4.76	1.30	0.82	4 to 5
6.26510125	8	4.76	3.60	0.09	4 to 5
6.31912594	8	4.76	2.73	0.31	4 to 5
9.10603563	8	4.76	1.21	0.56	4 to 5
16.2506876	8	4.76	2.17	1.04	4 to 5
17.2452993	8	4.76	4.22	0.14	4 to 5
17.7768523	8	4.76	1.51	0.40	4 to 5
18.2820642	8	4.76	2.90	0.14	4 to 5
19.4741355	8	4.76	4.50	1.30	4 to 5
19.5204427	8	4.76	5.91	0.49	4 to 5
22.402665	8	4.76	1.22	0.13	4 to 5
X.19687563	8	4.76	4.80	2.38	4 to 5
X.48461857	8	4.76	1.84	0.09	4 to 5
14.6109889	13	4.94	3.82	1.63	4 to 5
21.4517178	18	5.03	9.27	2.23	5 to 6
4.90336197	9	5.29	4.17	0.22	5 to 6
1.1546925	9	5.29	5.14	0.76	5 to 6
1.38168499	9	5.29	2.52	0.08	5 to 6
6.43256729	9	5.29	3.33	1.37	5 to 6
8.41712088	9	5.29	4.52	3.83	5 to 6
12.8127585	9	5.29	1.78	0.41	5 to 6
15.323979	9	5.29	5.83	0.52	5 to 6
15.3903214	9	5.29	2.19	1.33	5 to 6
16.4556573	9	5.29	2.15	0.30	5 to 6
18.2970325	9	5.29	5.91	0.32	5 to 6
19.1827256	9	5.29	2.14	0.28	5 to 6
21.3508941	9	5.29	2.80	0.76	5 to 6
X.129301266	9	5.29	6.50	4.55	5 to 6
9.12713117	10	5.29	2.67	1.48	5 to 6
8.81949316	10	5.82	2.80	0.59	5 to 6
12.451536	10	5.82	2.41	0.28	5 to 6
17.4168683	10	5.82	4.25	0.05	5 to 6

18.4404446	10	5.82	4.88	3.59	5 to 6
19.4523324	10	5.82	3.74	3.47	5 to 6
20.3205552	10	5.82	2.93	0.69	5 to 6
22.3937182	10	5.82	3.64	0.25	5 to 6
1.20524497	11	6.35	2.58	0.54	6 to 10
3.18449902	13	7.41	2.72	0.68	6 to 10
2.11589904	7	8.47	2.78	0.25	6 to 10
2.23917055	7	8.47	1.45	0.23	6 to 10
4.22125681	7	8.47	7.22	3.89	6 to 10
4.73404319	7	8.47	4.92	1.01	6 to 10
6.11475226	7	8.47	1.95	0.07	6 to 10
11.1169969	7	8.47	1.24	0.14	6 to 10
11.6455106	7	8.47	7.92	0.72	6 to 10
13.4470015	7	8.47	1.81	0.04	6 to 10
14.7481686	7	8.47	2.94	0.21	6 to 10
15.688743	7	8.47	6.81	1.12	6 to 10
16.8420384	7	8.47	2.38	0.06	6 to 10
17.4315359	7	8.47	1.90	0.05	6 to 10
19.3944324	7	8.47	5.74	1.36	6 to 10
6.29028658	7	8.47	6.34	2.47	6 to 10
X.23717817	7	8.47	1.49	0.03	6 to 10
X.3429852	7	8.47	0.82	0.03	6 to 10
1.20263407	8	9.53	5.16	1.92	6 to 10
2.2197153	8	9.53	4.09	0.51	6 to 10
10.359756	8	9.53	3.54	0.71	6 to 10
12.3220334	8	9.53	2.30	0.43	6 to 10
12.9305144	8	9.53	3.99	0.63	6 to 10
15.3930982	8	9.53	4.95	0.14	6 to 10
19.1956298	8	9.53	2.32	1.67	6 to 10
20.6519815	8	9.53	3.53	0.44	6 to 10
21.4482426	8	9.53	1.52	0.18	6 to 10
22.1677331	8	9.53	9.69	0.13	6 to 10
3.18967472	9	10.59	2.03	0.66	10 +
9.2043983	9	10.59	1.09	0.33	10 +
17.5905273	9	10.59	5.12	1.73	10 +
18.4470869	9	10.59	4.41	0.18	10 +
22.3537023	9	10.59	3.64	0.48	10 +
X.7011993	9	10.59	8.58	2.95	10 +
9.35507897	60	10.76	13.81	2.45	10 +
1.21072542	30	10.94	13.13	2.59	10 +
1.15962589	10	11.60	3.54	0.36	10 +
1.14415124	10	11.65	10.76	0.37	10 +
1.38844367	10	11.65	4.78	0.22	10 +
2.13897651	10	11.65	6.47	0.46	10 +
2.95362583	10	11.65	2.98	0.54	10 +
4.12453772	10	11.65	3.07	0.06	10 +
11.1019754	10	11.65	3.67	0.47	10 +
16.7125545	10	11.65	5.68	2.06	10 +
6.21839484	11	12.70	5.87	2.01	10 +
11.1128503	11	12.70	4.90	1.55	10 +
15.2925267	80	14.29	13.85	0.67	10 +
1.43178969	30	16.41	11.77	3.29	10 +

5.40790862	18	20.12	4.19	1.01	10 +
11.7079888	100	26.73	5.95	1.39	10 +
5.52130901	25	27.53	5.81	0.97	10 +
3.14050372	30	32.82	8.01	0.12	10 +
13.1133261	99	35.29	16.20	0.45	10 +
4.88753979	101	36.00	14.46	1.05	10 +
10.1349833	72	38.64	18.28	0.62	10 +
20.613585	159	56.47	17.55	0.11	10 +
21.4464837	107	57.17	10.18	2.13	10 +
2.24078549	103	110.11	11.29	1.31	10 +

Figure 30: Table S2(B) (exemplary only)

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Figure 31: Table S3(A) (exemplary only)

Characteristics of the genes, whose expression is directly regulated by Evi1, revealed in EVI1 siRNA knockdown experiment.																
ProbeID	RefSeq ID	Symbol	Description	PAM (dlt)	EDGE P-value	Median control	Median siRNA	Fold change	Number of TES peaks	Evil-gene binding confidence	Average copy number of the BSs	Copy number-adjusted confidence	Number of Motifs 1 within +/-20k from TSS	Number of Motifs 2 within +/-20k from TSS	Number of Motifs 1 within +/-1 kb from TSS	Number of Motifs 2 within +/-1 kb from TSS
8091972	NM_005241	EVI1	MDS1 and EVI1 complex locus protein EVI1 isoform b	1.7	0	11.58	10.02	0.34	13	36	1.00	6.74	1	13	1	
8047922	NM_001039532	MAP2	microtubule-associated protein 2 isoform 5	0.26	0	8.00	6.80	0.43	4	2	1.00	2.00	1	10	7	
7903467	NM_001132228	NTNG1	netrin-G1 isoform 2 precursor	3.98	6.54E-005	8.40	7.34	0.48	3	0	1.00	2.00	1	7	2	
7971077	NM_001358934	POSTN	periostin isoform 2 precursor	2.38	0	6.63	5.59	0.48	1	0	1.00	1.66	1	6	7	
8066493	NM_003064	SLPI	antileukoprotease precursor	-0.28	0	11.42	10.37	0.48	4	4	1.00	2.00	1	15	7	
8171172	NM_015419	MDR45	matrix-remodeling-associated protein 5 precursor	-0.42	0	8.87	7.91	0.51	6	5	1.00	3.57	1	18	11	
8096166	NM_001025616	ARHGAP24	rho GTPase-activating protein 24 isoform 1	0.2	0	7.55	6.60	0.52	3	3	1.00	2.00	1	16	11	
8092177	NM_020792	AADACL1	neutral cholesterol ester hydrolase 1 isoform b	-0.02	5.13E-008	10.42	9.47	0.52	4	7	1.00	2.00	1	25	11	
8122222	NM_018845	PDE7B	cAMP specific 3',5'-cyclic phosphodiesterase 7B	0.02	0	8.13	7.21	0.53	2	1	1.00	2.00	1	14	7	
7902541	NM_006820	IFI44L	interferon-induced protein 44-like	2.56	0	6.25	5.33	0.53	1	1	0.97	1.06	1	7	3	
8007931	NM_000212	ITGB3	integrin beta-3 precursor	3.1	0	9.67	8.78	0.54	8	6	1.00	2.00	1	24	21	
8156706	NM_003275	TMOD1	tropomodulin-1	-0.72	0	10.26	9.38	0.54	2	1	1.00	2.00	1	26	11	
7983367	NM_032866	CGNL1	cingulin-like protein 1	2.46	0	9.11	8.24	0.55	5	6	1.00	2.00	1	25	21	
7962822	NM_001098531	RAPGEF3	rap guanine nucleotide exchange factor 3 isoform a	3.44	0	8.19	7.33	0.55	7	9	1.00	2.00	1	13	3	
7901177	NM_005727	TSPAN1	transpanin-1	2.36	0	11.31	10.45	0.55	11	9	1.00	2.00	1	30	21	
7926084	NM_031923	TAF3	transcription initiation factor TFIID subunit 3	2.98	0	8.25	7.40	0.55	3	1	1.00	2.00	1	21	21	
8017132	NM_182820	FAM33A	spindle and kinesin-associated protein 2 isoform 1	0.58	0	10.61	9.80	0.57	4	4	1.00	2.00	1	33	37	
7985222	NM_005447	RASSF9	ras association domain-containing protein 9	2.09	0	6.83	6.02	0.57	1	1	1.00	2.00	1	14	11	
8138238	NM_004956	EVI1	ETS translocation variant 1 isoform a	0.12	0	6.41	5.61	0.57	1	0	0.55	1.11	1	12	11	
8135211	NM_001031692	LRRG17	leucine-rich repeat-containing protein 17 isoform 1 precursor	0.12	0	8.17	7.37	0.57	1	0	0.77	1.07	1	21	21	
8004511	NM_001040059	EIF4A1 CD68	macrophage-specific protein 4 precursor	3.64	3.55E-003	8.95	8.18	0.58	2	2	0.96	1.17	1	21	17	
7986351	NM_183376	ARRDC4	arrestin domain-containing protein 4	2.58	0	8.55	7.79	0.59	3	3	1.00	2.00	1	16	11	
8083217	NM_004267	CHST2	carbohydrate sulfotransferase 2	0.56	0	10.33	9.57	0.59	4	2	1.00	2.00	1	24	11	
8135937	NM_001097634	GNT1	beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase	-0.62	0	9.89	9.13	0.59	1	2	1.00	2.00	1	22	21	
8066922	NM_000961	PTGIS	prostaglandin synthase precursor	-1.04	0	10.58	9.83	0.59	17	4	1.00	2.00	1	27	21	
8091411	NM_014220	TM4SF1	transmembrane 4 L6 family member 1	0.8	0	11.17	10.42	0.59	7	8	1.00	2.00	1	14	11	
7976872	NM_001376	DYNL1H1	cytoplasmic dynein 1 heavy chain 1	2.36	0	11.06	10.32	0.60	5	3	1.00	2.00	1	26	21	
7938448	NM_017944	USP47	ubiquitin carboxyl-terminal hydrolase 47 isoform b	2.7	0	10.08	9.34	0.60	4	7	1.00	2.00	1	7	14	
8039292	NM_031883	CSB	chromatin gonadotropin, beta polypeptide 8 precursor	1.68	0	8.29	7.61	0.62	1	4	1.00	2.00	1	30	11	
7905322	NM_006818	Clorf66 MLLT11	protein AF1q	2.44	0	9.91	9.24	0.63	13	12	1.00	2.72	1	38	41	
8030161	NM_000984	CSB	luteal protein subunit beta precursor	0.2	0	8.24	7.59	0.64	8	8	1.00	2.00	1	30	32	
7939591	NM_018389	SLC35C1	GDP- <i>D</i> -glucose transporter 1 isoform a	2.7	0	7.69	7.04	0.64	4	5	1.00	2.00	1	25	21	
7969061	NM_014923	JUNC3A	fibronectin type-III domain-containing protein 3A isoform 2	2.64	0	10.08	9.43	0.64	1	2	1.00	1.68	1	10	4	
8015343	NM_002276	JUP RRT19	keratin, type I cytoskeletal 19	-0.16	0	10.84	10.19	0.64	4	4	1.00	2.45	1	20	14	
8109192	NM_000112	SLC28A2	solute carrier family 28 member 2	0.2	0	10.76	10.12	0.64	1	10	1.00	2.00	1	33	24	

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Figure 31: Table S3(B)

Transcription factor-specific DNA motifs co-localized with Evi1-specific DNA motifs M1 and M2

Transcription factor name	Transfac matrix ID	M1: GAGACAG	M2: TAATCCAGC	Different species	Evidence of interaction in SILAC	M1-specific in Evi1 targets	M2-specific in Evi1 targets
Ahr2	M00778		1				
Aml1	M00751		1				
Ap-1	M00173		1		1		1
Ap-1	M00174		1				
Ap-1	M00188		1				
Ap-2rep	M00468	1				1	1
ATF	M00017	1					
ATF	M00338	1					
ATF-1	M00691	1			1		1
Atf4	M00514	1	1				
Atf6	M00483	1					1
Bach2	M00490	1					
Ben (Gtf2lrd1)	M01229	1		Mus		1	
c-Ets-1	M01078		1				
c-Ets-1	M00340	1					
Cacd	M01113	1		Mus			
Chx10	M00437		1				

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Creb	M00178			1		1		
Creb	M00113		1					
Creb	M00916		1	1		1		
Creb	M00917		1					
Crx	M00623			1				1
Ctf1	M01196			1				
E2A	M00693			1				
E2F4	M00803			1				
E4F1	M00694		1				1	
Elf	M00695			1				
FoxJ1b	M00809		1					
FoxJ2	M00422			1				1
FoxL1	M00293			1				1
Gr	M00192			1				
Gr	M00955		1					
Helios (Ikzf2)	M01003			1				1
Hnf3	M00791			1				1
HoxA4	M00640			1				1
Ikaros	M00141			1				1
Ikaros	M00087		1					
Lhx3	M00510		1					
MafA	M01139			1				1
Meis	M00419			1				1
MizF	M01182			1			1	
Myogenin	M00712			1				
Myogenin	M00804		1					
Coup-Tf1 (Nr2F1)	M00965		1					
p300	M00033			1				1
Pax2	M00098			1				1
Pax4	M00380			1				
Pbx	M01013			1				
Pitx2	M00482			1				1
Pou3f2	M00145			1				
Rbtf2 (LMO2)	M00277		1				1	1

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Rfx	M00975	1					1	
Sf1	M01132	1						
Smad2	M00792		1					1
Srebp1	M00221		1					
Srebp2	M01177		1					1
Strat13 (BHLHE40)	M00985	1		Mus				
Tbx5	M01044		1					
Tf2A	M00707	1						1
Tf2D	M00216		1					1
Vdr	M00961		1					
Zeb	M00413		1					
Zeb	M00073		1					
Zeb	M00414	1						
Total		26	40	0	4	6	21	

Figure 31: Table S3(C) (exemplary only)

Mutations in TP53 genes in the TCGA HG-SOC patient genomes												
Hugo_Symbol	Entrez_GeneID	Chrom	Start_Position	End_Position	Variant_Classification	Variant_Type	Reference_Allele	Tumor_Seq_Allele1	Tumor_Seq_Allele2	Sample_Barcode	Validation_Status	Mutation_Status
TP53	7157	36.1	7514707	7514707	Nonsense_Mutation	SNP	C	A	A	TCGA-13-0727-10B-01W-0371-08	Valid	Somatic
TP53	7157	36.1	7514708	7514708	Missense_Mutation	SNP	C	A	A	TCGA-13-0727-10B-01W-0371-08	Valid	Somatic
TP53	7157	36	7514709	7514710	Frame_Shift_Ins	INS		0	0	AGCCCTT	Valid	Somatic
TP53	7157	36	7514720	7514720	Frame_Shift_Del	DEL	C	C		TCGA-24-1434-10A-01W-0545-08	Valid	Somatic
TP53	7157	36	7514728	7514728	Nonsense_Mutation	SNP	G	G	A	TCGA-61-2097-11A-01W-0723-08	Valid	Somatic
TP53	7157	36.1	7515756	7515756	Splice_Site_SNP	SNP	A	A	G	TCGA-13-0725-10B-01W-0371-08	Valid	Somatic
TP53	7157	36	7515757	7515757	Splice_Site	SNP	C	C	T	TCGA-23-2072-10A-01W-0722-08	Valid	Somatic
TP53	7157	36	7515777	7515777	Splice_Site	SNP	C	C	T	TCGA-59-2355-10A-01W-0800-08	Valid	Somatic
TP53	7157	36	7517610	7517610	Nonsense_Mutation	SNP	T	T	A	TCGA-24-2271-10A-01W-0799-08	Valid	Somatic
TP53	7157	36	7517622	7517622	Nonsense_Mutation	SNP	G	G	A	TCGA-13-0899-10A-01D-0399-08	Valid	Somatic
TP53	7157	36	7517625	7517626	Frame_Shift_Ins	INS			0	TCGA-24-1603-10A-01W-0551-08	Valid	Somatic
TP53	7157	36	7517744	7517745	Frame_Shift_Del	DEL	CT		0	CT	Unknown	Unknown
TP53	7157	36	7517747	7517747	Nonsense_Mutation	SNP	G	G	A	TCGA-04-1331-10A-01W-0486-08	Valid	Somatic
TP53	7157	36.1	7517747	7517747	Nonsense_Mutation	SNP	G	A	G	TCGA-13-0758-10A-01W-0371-08	Valid	Somatic
TP53	7157	36	7517807	7517807	Missense_Mutation	SNP	C	C	T	TCGA-25-1326-10A-01W-0492-08	Valid	Somatic
TP53	7157	36	7517813	7517813	Frame_Shift_Del	DEL	T		0	TCGA-24-2267-11A-01W-0799-08	Valid	Somatic
TP53	7157	36.1	7517822	7517822	Missense_Mutation	SNP	C	G	G	TCGA-13-0764-10A-01W-0371-08	Valid	Somatic
TP53	7157	36	7517827	7517827	Missense_Mutation	SNP	C	C	T	TCGA-13-0904-10A-01D-0399-08	Valid	Somatic
TP53	7157	36	7517830	7517830	Missense_Mutation	SNP	G	G	C	TCGA-13-0913-10A-01D-0399-08	Valid	Somatic
TP53	7157	36	7517830	7517830	Missense_Mutation	SNP	G	G	T	TCGA-24-1552-10A-01W-0551-08	Valid	Somatic
TP53	7157	36.1	7517831	7517831	Missense_Mutation	SNP	G	A	G	TCGA-13-0757-10A-01W-0371-08	Unknown	Unknown
TP53	7157	36	7517842	7517842	Missense_Mutation	SNP	A	A	C	TCGA-24-2290-10A-01W-0799-08	Valid	Somatic
TP53	7157	36	7517845	7517845	Missense_Mutation	SNP	C	C	T	TCGA-10-0934-11A-01W-0420-08	Valid	Somatic
TP53	7157	36.1	7517845	7517845	Missense_Mutation	SNP	C	C	T	TCGA-13-0751-10A-01W-0371-08	Valid	Somatic
TP53	7157	36	7517845	7517845	Missense_Mutation	SNP	C	C	G	TCGA-13-0905-10A-01W-0492-08	Valid	Somatic
TP53	7157	36	7517845	7517845	Missense_Mutation	SNP	C	C	A	TCGA-13-1512-10A-01W-0546-08	Valid	Somatic

Figure 31: Table S3(D)

The comparison of Evi1 copy number distributions among patients with various mutations in TP53 genes in TCGA patient tumors.

Above the main diagonal the tumors with Evi1 copy number higher than 3 copies/genome are selected.

Below the main diagonal the tumors with Evi1 copy number lower than 3 copies/genome are selected. Wilcoxon test p-values are given.

Variant_Class	Frame_Shift_Del	Frame_Shift_Ins	In_Frame_Del	In_Frame_Ins	Missense_Mutation	Nonsense_Mutation	Nonstop_Mutation	RNA	Silent	Splice_Site	Splice_Site_Indel	Splice_Site_SNP	Translation_Start_Site
Frame_Shift_Del	1.000	0.510	1.000	1.000	0.857	0.090	1.000	1.000	1.000	0.643	1.000	1.000	1.000
Frame_Shift_Ins	0.286	1.000	1.000	1.000	0.669	0.225	1.000	1.000	1.000	0.880	1.000	1.000	1.000
In_Frame_Del	0.400	0.071	1.000	1.000	0.756	0.120	1.000	1.000	1.000	0.947	1.000	1.000	1.000
In_Frame_Ins	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Missense_Mutation	0.149	0.059	0.185	1.000	1.000	0.005	1.000	1.000	1.000	0.546	1.000	1.000	1.000
Nonsense_Mutation	0.396	0.496	0.212	1.000	0.386	1.000	1.000	1.000	1.000	0.039	1.000	1.000	1.000
Nonstop_Mutation	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
RNA	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Silent	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Splice_Site	0.374	0.099	0.469	1.000	0.728	0.549	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Splice_Site_Indel	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Splice_Site_SNP	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Translation_Start_Site	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

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Figure 32: Table S4(A)

ProbesetID	Refseq	Symbol	EV11 Tau (GSE20565 expression)	P, adj	Significant	EV11 Tau (TCGA expression)	P, adj	Significant (P<0.05)	EV11 Tau (TCGA copy number)	P, adj	Significant (P<0.05)	MDS1 Tau (TCGA expression)	P, adj	Significant (P<0.05)	MDS1 Tau (TCGA copy number)	P, adj	Significant (P<0.05)
7952036 NM_198275	MPZL3		4.82E-02	4.41E-01	0.00E+00	N.A.	N.A.	0.00E+00	4.41E-02	4.81E-01	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
8149927 NM_001831	CLU		4.01E-02	5.24E-01	0.00E+00	N.A.	N.A.	0.00E+00	6.31E-02	3.15E-01	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7938301 NM_182901	C11orf17		-3.35E-01	4.82E-06	1.00E+00	N.A.	N.A.	0.00E+00	-2.85E-01	1.84E-05	1.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
8005603 NM_018242	SLC47A1		3.24E-02	6.07E-01	0.00E+00	2.19E-02	5.18E-01	0.00E+00	-6.60E-02	2.93E-01	0.00E+00	-5.98E-02	7.80E-02	0.00E+00	N.A.	N.A.	0.00E+00
8124562 NM_030899	ZNF323		6.28E-02	3.17E-01	0.00E+00	1.88E-02	5.81E-01	0.00E+00	5.11E-02	4.14E-01	0.00E+00	-6.34E-02	6.21E-02	0.00E+00	N.A.	N.A.	0.00E+00
7900072 NM_018891	UAMC2		1.09E-02	8.64E-01	0.00E+00	1.81E-02	5.94E-01	0.00E+00	-1.14E-01	6.85E-02	0.00E+00	1.21E-01	3.78E-04	0.00E+00	N.A.	N.A.	0.00E+00
8038286 NM_033377	CGB5 CGB CGBT CG		1.52E-01	1.55E-02	1.00E+00	2.99E-02	3.79E-01	0.00E+00	1.96E-01	1.73E-03	1.00E+00	-1.37E-03	9.68E-01	0.00E+00	N.A.	N.A.	0.00E+00
8038290 NM_000737	CGB CGB8 LHB CGE		1.52E-01	1.55E-02	1.00E+00	-2.99E-02	3.79E-01	0.00E+00	1.96E-01	1.73E-03	1.00E+00	-1.37E-03	9.68E-01	0.00E+00	N.A.	N.A.	0.00E+00
8038282 NM_033183	CGB CGB8 LHB CGE		1.52E-01	1.55E-02	1.00E+00	2.99E-02	3.79E-01	0.00E+00	1.96E-01	1.73E-03	1.00E+00	-1.37E-03	9.68E-01	0.00E+00	N.A.	N.A.	0.00E+00
8062728 NM_170693	SGK2		-1.39E-01	2.58E-02	1.00E+00	-6.05E-02	7.48E-02	0.00E+00	-7.99E-02	2.03E-01	0.00E+00	-5.79E-02	8.83E-02	0.00E+00	N.A.	N.A.	0.00E+00
7908459 NM_001014975	CFH		-3.18E-01	2.81E-07	1.00E+00	-9.37E-02	5.78E-03	0.00E+00	-3.45E-01	1.80E-08	1.00E+00	-7.84E-02	2.09E-02	0.00E+00	N.A.	N.A.	0.00E+00
8004510 NM_001040039	EJF4A1 CD68		7.69E-02	2.20E-01	0.00E+00	-1.23E-01	1.48E-04	0.00E+00	1.28E-01	4.05E-02	1.00E+00	-2.96E-02	3.84E-01	0.00E+00	N.A.	N.A.	0.00E+00
7951686 NM_001562	IL18		-2.58E-01	3.60E-05	1.00E+00	-2.26E-01	3.07E-11	0.00E+00	-1.08E-01	8.34E-02	0.00E+00	-1.19E-01	4.37E-04	0.00E+00	N.A.	N.A.	0.00E+00
7897987 NM_023014	PRAMEF2		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7922412 NR_003943	SNORD77		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7948904 NR_002562	SNORD28		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7948908 NR_002564	SNHG1 SNORD26		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
795298 NM_001080825	TMEM120B		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7962165 NR_004854	AMNT		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7968232 NR_002574	SNORD102		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7971653 NR_002612	DLU2		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00
7985787 NM_176870	MTIM		N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00	N.A.	N.A.	0.00E+00

Figure 32: Table S4(B) (exemplary only)

Information on EVI1 copy number and expression improves prognostic value of 99% of EVI1 pathway genes.

Probeset	Symbol	P(Original)	P2d(Original)	P(Not amplified)	P(Amplified)	P2d(Amplified)	Improved (EVI1 expr)	Improved (EVI1 cn)	Improved
201118_at	PGD	0.053	0.014	1.000	0.013	0.041	TRUE	TRUE	TRUE
202026_at	SDHD	0.059	0.005	1.000	0.004	0.017	TRUE	TRUE	TRUE
209114_at	TSPAN1	0.011	0.008	1.000	0.070	0.094	TRUE	FALSE	TRUE
204439_at	IFI44L	0.061	0.000	1.000	0.010	0.058	TRUE	TRUE	TRUE
206713_at	NTNG1	0.120	0.055	1.000	0.137	0.173	TRUE	FALSE	TRUE
205380_at	PDZK1	0.042	0.015	1.000	0.011	0.019	TRUE	TRUE	TRUE
211071_s_at	MLLT11	0.195	0.009	1.000	0.079	0.147	TRUE	TRUE	TRUE
221210_s_at	NPL	0.018	0.005	1.000	0.261	0.295	TRUE	FALSE	TRUE
202267_at	LAMC2	0.135	0.023	1.000	0.030	0.073	TRUE	TRUE	TRUE
213800_at	CFH	0.069	0.004	1.000	0.093	0.164	TRUE	FALSE	TRUE
213524_s_at	G0S2	0.138	0.010	1.000	0.004	0.002	TRUE	TRUE	TRUE
205306_x_at	KMO	0.172	0.029	1.000	0.077	0.091	TRUE	TRUE	TRUE
203911_at	RAP1GAP	0.001	0.000	1.000	0.280	0.219	TRUE	FALSE	TRUE
207368_at	HTR1D	0.089	0.008	1.000	0.080	0.113	TRUE	TRUE	TRUE
201720_s_at	LPTM5	0.021	0.014	1.000	0.024	0.062	TRUE	FALSE	TRUE
219630_at	PDZK1IP1	0.040	0.015	1.000	0.020	0.081	TRUE	TRUE	TRUE
205924_at	RAB3B	0.076	0.003	1.000	0.202	0.317	TRUE	FALSE	TRUE
201464_x_at	JUN	0.024	0.000	1.000	0.182	0.103	TRUE	FALSE	TRUE
215506_s_at	DIRAS3	0.234	0.002	1.000	0.007	0.014	TRUE	TRUE	TRUE
209707_at	PIGK	0.000	0.000	1.000	0.079	0.079	FALSE	FALSE	FALSE
204363_at	F3	0.134	0.004	1.000	0.099	0.161	TRUE	TRUE	TRUE

Figure 32: Table S4(C)

Targets of Evi1 overlapping with HG-SOC debulking gene signature

Gene Symbol	Description	Survival analysis in the TCGA cohort			Correlations with Evi1 gene expression		
		Parametric p-value	Cox Hazard Ratio	Rank(p-value)	Corr(GSE12172 and GSE20565 datasets)	r	Corr(TCGA) P(TCGA)
FLOT1	Flotillin 1	3.94E-05	0.293	4	0.310	0.000	0.031 0.368
PDZK1	PDZ domain containing 1	0.000212	4.803	11	-0.154	0.014	- 0.110 0.001
CLIC1	chloride intracellular channel 1	0.000331	0.595	14	0.130	0.037	- 0.054 0.113
SLC29A3	solute carrier family 29 (nucleoside transporters), member 3	0.001105	5.25	32	0.128	0.041	- 0.081 0.017
RGS3	regulator of G-protein signaling 3	0.001448	0.363	43	0.065	0.297	- 0.005 0.889
SLC19A2	solute carrier family 19 (thiamine transporter), member 2	0.00225	1.717	61	-0.271	0.000	- 0.031 0.356
CIB1	calcium and integrin binding 1 (calmyrin)	0.003906	0.634	101	-0.070	0.266	- 0.050 0.142
ARHGAP24	Rho GTPase activating protein 24	0.004331	2.634	110	0.029	0.644	N.A. N.A.
CLDN10	Claudin 10	0.004925	0.675	125	-0.141	0.024	0.025 0.455
RARRES3	retinoic acid receptor responder (tazarotene induced) 3	0.005989	0.745	151	-0.025	0.695	- 0.107 0.002

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GULP1	GULP, engulfment adaptor PTB domain containing 1	0.006808	2.628	168	-0.384	0.000	-	0.008
NTNG1	netrin G1	0.008983	2.388	229	0.021	0.744	N.A.	N.A.
TM4SF1	transmembrane 4 L six family member 1	0.00907	0.711	231	-0.111	0.077	-	0.001

Figure 33: Table S5(A)

Association between the Evi1 pathway-based classification system of patients by survival risk groups with therapy in 373 TCGA patients.

Gene class	Clinical parameter	Parameter value	TCGA best kappa	TCGA fisher's P	FDR
signalling	CHEMOTHERAPY	YES	0.218	0.008389446	0.025692215
immune	CHEMOTHERAPY	YES	0.228	0.007024135	0.025692215
debulking	PRIMARYTHERAPYOUTCOMESUCCESS	COMPLETE RESPONSE	-0.247	1.55752E-05	0.000249204
debulking	PRIMARYTHERAPYOUTCOMESUCCESS	PROGRESSIVE DISEASE	-0.107	0.001615144	0.01776658
apoptosis	PRIMARYTHERAPYOUTCOMESUCCESS	COMPLETE RESPONSE	0.276	0.002124656	0.019121908
signalling	PRIMARYTHERAPYOUTCOMESUCCESS	COMPLETE RESPONSE	0.343	0.000000409	6.95E-006
signalling	PRIMARYTHERAPYOUTCOMESUCCESS	null	0.278	0.00168928	0.01776658
metabolism	PRIMARYTHERAPYOUTCOMESUCCESS	PROGRESSIVE DISEASE	0.176	0.005181379	0.025692215
immune	PRIMARYTHERAPYOUTCOMESUCCESS	COMPLETE RESPONSE	0.203	0.000127657	0.001531889
immune	PRIMARYTHERAPYOUTCOMESUCCESS	null	0.345	3.10E-005	0.000443234
surv	PRIMARYTHERAPYOUTCOMESUCCESS	COMPLETE RESPONSE	-0.177	0.0000295	0.001659547
consensus	TUMORRESIDUALDISEASE	null	-0.294	0.002822738	0.022581905
emt	PERSONNEOPLASMCANCERSTATUS	TUMOR FREE	-0.194	0.009232563	0.025692215
apoptosis	PERSONNEOPLASMCANCERSTATUS	TUMOR FREE	-0.22	0.004282036	0.025692215
signalling	PERSONNEOPLASMCANCERSTATUS	null	0.188	0.00313727	0.022581905
immune	PERSONNEOPLASMCANCERSTATUS	null	0.227	0.004568412	0.025692215
consensus	PRIMARYTHERAPYOUTCOMESUCCESS	COMPLETE RESPONSE	0.606	4.31948931986068E-08	7.77508077574922E-07
consensus	TUMORRESIDUALDISEASE	null	-0.294	0.002822738	0.022581905
consensus	PERSONNEOPLASMCANCERSTATUS	TUMOR FREE	-0.387	0.000193889	0.002326664

Signalling	Chemotherapy		
Risk	YES	REST	18
Moderate		182	7
Low		130	8
High		28	
Immune	Chemotherapy		
Risk	YES	REST	20
Moderate		166	

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Low	158	8
High	16	5
debulking		
Risk	PRIMARYTHERAPYOUTCOMESUCCESS	
Moderate	COMPLETE RESPONSE	REST
Low	78	105
High	103	50
	16	21
debulking		
Risk	PRIMARYTHERAPYOUTCOMESUCCESS	
Moderate	REST	PROGRESSIVE DISEASE
Low	160	23
High	149	4
	35	2
apoptosis		
Risk	PRIMARYTHERAPYOUTCOMESUCCESS	
Moderate	COMPLETE RESPONSE	REST
Low	125	123
High	61	31
	11	22
signalling		
Risk	PRIMARYTHERAPYOUTCOMESUCCESS	
Moderate	COMPLETE RESPONSE	REST
Low	98	102
High	92	45
	7	29
metabolism		
Risk	PRIMARYTHERAPYOUTCOMESUCCESS	
Moderate	REST	PROGRESSIVE DISEASE
Low	244	15
High	68	5
	32	9
immune		
Risk	PRIMARYTHERAPYOUTCOMESUCCESS	
	COMPLETE RESPONSE	REST

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signalling Risk Moderate Low High	PERSONNEOPLASMCANCERSTATUS		null	182 119 25	18 18 11
immune Risk Moderate Low High	PERSONNEOPLASMCANCERSTATUS		null	167 146 13	19 20 8
consensus Risk Moderate Low Very low High	PRIMARYTHERAPYOUTCOMESUCCESS COMPLETE RESPONSE		REST	87 70 33 7	104 40 7 25
consensus Risk Moderate Low Very low High	TUMORRESIDUALDISEASE		null	163 97 25 29	28 13 15 3
consensus Risk Moderate Low Very low High	PERSONNEOPLASMCANCERSTATUS		TUMOR FREE	156 78 24 31	35 32 16 1

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Figure 33: Table S5(B)

Univariate Cox proportional hazard models of the patient survival (TCGA cohort, 356 patients)							
Factor	Group	beta	HR	CI_L	CI_U	z	Pr(> z)
immune	high risk	2.50	12.14	7.47	19.73	10.07	0.00E+00
immune	medium risk	1.31	3.71	2.63	5.23	7.46	8.57E-14
signalling	high risk	1.91	6.75	4.04	11.28	7.29	3.07E-13
apoptosis	high risk	1.85	6.35	3.83	10.52	7.18	7.00E-13
debulking	high risk	1.63	5.11	3.20	8.17	6.81	9.84E-12
RiskGroup	low risk	-	0.25	0.17	0.39	-6.47	1.00E-10
metabolism	high risk	1.49	4.44	2.74	7.18	6.07	1.31E-09
Primary chemotherapy	PARTIAL RESPONSE	1.21	3.34	2.26	4.94	6.05	1.44E-09
signalling	medium risk	0.95	2.60	1.89	3.57	5.86	4.68E-09
emt	high risk	1.42	4.15	2.56	6.72	5.78	7.62E-09
Neoplasm status	TUMOR FREE	-	0.05	0.02	0.14	-5.60	2.12E-08
metabolism	medium risk	0.95	2.58	1.84	3.61	5.49	3.92E-08
emt	medium risk	0.87	2.39	1.75	3.26	5.49	4.10E-08
debulking	medium risk	0.85	2.35	1.72	3.21	5.34	9.49E-08
surv	high risk	1.65	5.20	2.83	9.55	5.31	1.08E-07
Primary chemotherapy	PROGRESSIVE DISEASE	1.27	3.56	2.21	5.74	5.23	1.72E-07
RiskGroup	high risk	1.41	4.08	2.30	7.22	4.83	1.39E-06
apoptosis	medium risk	0.87	2.40	1.64	3.51	4.50	6.89E-06
Residual tumor	null	-	0.41	0.26	0.66	-3.72	1.98E-04
Age	>=67	0.72	2.05	1.40	3.00	3.69	2.24E-04
retinoic	medium risk	0.66	1.94	1.35	2.77	3.62	2.92E-04
surv	medium risk	0.92	2.51	1.50	4.22	3.49	4.84E-04
retinoic	high risk	1.02	2.78	1.49	5.18	3.21	1.31E-03
Residual tumor	No Macroscopic disease	-	0.51	0.32	0.82	-2.76	5.83E-03
Tumor stage	Stages I and II	1.16	0.31	0.13	0.76	-2.56	1.04E-02
Tumor grade	Grades 3 and 4	0.45	1.57	1.06	2.34	2.25	2.45E-02
Age	53-66	0.40	1.49	1.04	2.13	2.16	3.08E-02

Primary chemotherapy	STABLE DISEASE	0.72	2.05	1.06	3.97	2.14	3.27E-02
Neoplasm status	WITH TUMOR	0.40	0.67	0.44	1.02	-1.87	6.09E-02
Residual tumor	11-20 mm	0.10	1.11	0.66	1.85	0.39	6.97E-01
Race	Other	0.10	1.10	0.65	1.87	0.36	7.19E-01
Residual tumor	>20 mm	0.04	1.05	0.73	1.50	0.24	8.11E-01

Figure 33: Table S5(C)

Multivariate Cox proportional hazard model of the patient survival, based on the diagnostic criteria available at the operation time (TCGA cohort, 356 patients)

Factor	Group	beta	HR	CI_L	CI_U	z	Pr(> z)
immune	high risk	1.45	4.27	2.39	7.62	4.91	9.06E-07
metabolism	high risk	1.31	3.70	2.07	6.62	4.40	1.06E-05
immune	medium risk	0.79	2.19	1.50	3.21	4.04	5.30E-05
Age	>=67	0.84	2.32	1.54	3.49	4.03	5.64E-05
debulking	high risk	1.09	2.97	1.71	5.14	3.87	1.08E-04
metabolism	medium risk	0.70	2.02	1.39	2.94	3.70	2.15E-04
debulking	medium risk	0.64	1.90	1.34	2.71	3.59	3.36E-04
apoptosis	high risk	1.00	2.72	1.52	4.87	3.36	7.80E-04
signalling	medium risk	0.49	1.64	1.16	2.32	2.80	5.05E-03
retinoic	medium risk	0.52	1.69	1.14	2.51	2.60	9.23E-03
Age	53-66	0.45	1.57	1.07	2.29	2.32	2.02E-02
signalling	high risk	0.70	2.02	1.12	3.65	2.32	2.03E-02
emt	medium risk	0.36	1.44	1.03	2.02	2.11	3.45E-02
apoptosis	medium risk	0.32	1.38	0.90	2.12	1.49	1.37E-01
surv	high risk	0.44	1.56	0.79	3.06	1.28	1.99E-01
emt	high risk	0.36	1.44	0.82	2.53	1.26	2.08E-01
retinoic	high risk	-0.47	0.62	0.28	1.39	-1.16	2.48E-01
Tumor stage	Stages I and II	-0.46	0.63	0.25	1.62	-0.95	3.42E-01
Tumor grade	Grades 3 and 4	0.11	1.11	0.72	1.72	0.49	6.27E-01
surv	medium risk	0.07	1.07	0.61	1.90	0.24	8.07E-01
Race	Other	0.05	1.05	0.60	1.86	0.19	8.53E-01

Figure 33: Table S5(D)

Multivariate Cox proportional hazard models of the survival of the patients with different response to the primary chemotherapy, based on the diagnostic area

Complete response (195 patients)

Factor	Group	beta	HR	CI_L	CI_U
<i>mammetabolism</i>					
Age	medium risk		1.284	3.612	2.037
<i>immune</i>	>=67		1.433	4.191	2.200
Age	medium risk		0.866	2.378	1.363
<i>emt</i>	53-66		0.894	2.445	1.337
<i>mammetabolism</i>	medium risk		0.821	2.272	1.294
emt	high risk		1.344	3.836	1.427
	high risk		1.035	2.815	1.169
	high risk		0.988	2.687	1.045
apoptosis	Other		-1.157	0.315	0.091
Race	medium risk		0.470	1.601	0.870
apoptosis	high risk		0.881	2.413	0.737
<i>immune</i>	Stages I and II		-1.032	0.356	0.075
Tumor stage	high risk		0.589	1.802	0.742
debulking	medium risk		-0.453	0.636	0.286
retinoic	high risk		0.614	1.848	0.573
retinoic	Grades 3 and 4		0.295	1.344	0.664
Tumor grade	high risk		-0.399	0.671	0.208
signalling	medium risk		-0.139	0.870	0.500
debulking	high risk		0.236	1.266	0.483
surv	medium risk		-0.046	0.955	0.449
surv	medium risk		0.029	1.029	0.631
signalling					

No complete response (partial response, stable disease, progressive disease; 161 patients)

Factor	Group	beta	HR	CI_L	CI_U
<i>debulking</i>	medium risk		1.753	5.771	2.872
<i>retinoic</i>	medium risk		1.505	4.504	2.442
<i>mammetabolism</i>	high risk		1.856	6.401	2.462
Race	Other		1.404	4.073	1.850
<i>signalling</i>	medium risk		1.186	3.274	1.676
<i>immune</i>	high risk		1.244	3.469	1.357

apoptosis	high risk	1.351	3.859	1.345
signalling	high risk	1.366	3.918	1.311
debulking	high risk	1.301	3.673	1.238
mammetabolism	medium risk	0.566	1.762	0.948
immune	medium risk	0.549	1.732	0.902
retinoic	high risk	-1.044	0.352	0.086
emt	high risk	0.657	1.929	0.774
apoptosis	medium risk	0.547	1.728	0.750
Tumor stage	Stages I and II	-0.961	0.383	0.050
Tumor grade	Grades 3 and 4	-0.205	0.814	0.415
Age	>=67	-0.210	0.810	0.388
surv	medium risk	-0.211	0.810	0.288
Age	53-66	0.115	1.122	0.628
emt	medium risk	0.044	1.045	0.587
surv	high risk	-0.021	0.980	0.284

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Figure 34: Table S6

Evi1 pathway genes correlating with patients risk groups

By expression	Gene	Tau	p	Significant	By gene to EVI1 expression ratio	Gene	Tau	p	Significant	EVI1 improved significance	EVI1 improved P-value
ADAM10		2.43E-02	5.42E-01	FALSE	ADAM10		1.42E-01	3.57E-04	TRUE	TRUE	TRUE
NEURL		-6.65E-02	9.55E-02	FALSE	NEURL		1.20E-01	2.54E-03	TRUE	TRUE	TRUE
SFRP1		6.79E-02	8.87E-02	FALSE	SFRP1		1.24E-01	1.88E-03	TRUE	TRUE	TRUE
DKK1		3.30E-02	4.08E-01	FALSE	DKK1		1.48E-01	2.05E-04	TRUE	TRUE	TRUE
WNT7A		5.48E-02	1.69E-01	FALSE	WNT7A		1.28E-01	1.27E-03	TRUE	TRUE	TRUE
SNAI1		3.31E-02	4.07E-01	FALSE	SNAI1		1.51E-01	1.56E-04	TRUE	TRUE	TRUE
HES1		2.29E-02	5.66E-01	FALSE	HES1		1.48E-01	1.99E-04	TRUE	TRUE	TRUE
HEY1		-1.88E-01	2.50E-06	TRUE	HEY1		-2.82E-03	9.44E-01	FALSE	FALSE	FALSE
FGF2		1.04E-01	9.07E-03	TRUE	FGF2		1.63E-01	4.26E-05	TRUE	FALSE	TRUE
MAP1B		-1.32E-01	9.57E-04	TRUE	MAP1B		-3.32E-02	4.05E-01	FALSE	FALSE	FALSE

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MAP2	1.85E-02	6.43E-01	FALSE	MAP2		1.39E-01	5.07E-04	TRUE	TRUE	TRUE
ASPH	3.80E-02	3.40E-01	FALSE	ASPH		1.54E-01	1.08E-04	TRUE	TRUE	TRUE
KLF4	-4.98E-02	2.12E-01	FALSE	KLF4		1.14E-01	4.18E-03	TRUE	TRUE	TRUE
CLDN10	-8.83E-02	2.69E-02	TRUE	CLDN10		-8.29E-03	8.35E-01	FALSE	FALSE	FALSE
EDNRA	7.04E-03	8.60E-01	FALSE	EDNRA		1.01E-01	1.11E-02	TRUE	TRUE	TRUE
TPCN1	1.23E-01	2.11E-03	TRUE	TPCN1		1.91E-01	1.63E-06	TRUE	FALSE	TRUE
PCDHB8	-7.50E-02	6.01E-02	FALSE	PCDHB8		1.24E-01	1.86E-03	TRUE	TRUE	TRUE
PTGES	-1.10E-02	7.82E-01	FALSE	PTGES		6.92E-02	8.26E-02	FALSE	FALSE	TRUE
PTGIS	2.50E-02	5.31E-01	FALSE	PTGIS		9.30E-02	1.96E-02	TRUE	TRUE	TRUE
PTGS1	-9.56E-03	8.10E-01	FALSE	PTGS1		1.14E-01	4.29E-03	TRUE	TRUE	TRUE
PTPRK	4.54E-02	2.54E-01	FALSE	PTPRK		1.43E-01	3.43E-04	TRUE	TRUE	TRUE
RGS3	-2.84E-02	4.76E-01	FALSE	RGS3		8.69E-02	2.93E-02	TRUE	TRUE	TRUE
IL7R	-6.31E-02	1.14E-01	FALSE	IL7R		3.02E-02	4.49E-01	FALSE	FALSE	FALSE
IL18	1.27E-01	1.40E-03	TRUE	IL18		1.63E-01	4.27E-05	TRUE	FALSE	TRUE
S100A3	3.40E-02	3.94E-01	FALSE	S100A3		1.35E-01	7.42E-04	TRUE	TRUE	TRUE
S100A14	7.16E-02	7.25E-02	FALSE	S100A14		1.09E-01	6.45E-03	TRUE	TRUE	TRUE
KCNN4	7.01E-02	7.87E-02	FALSE	KCNN4		1.52E-01	1.43E-04	TRUE	TRUE	TRUE
HTR1D	4.03E-02	3.12E-01	FALSE	HTR1D		1.49E-01	1.90E-04	TRUE	TRUE	TRUE
PRKAR2B	-1.89E-02	6.36E-01	FALSE	PRKAR2B		7.46E-02	6.13E-02	FALSE	FALSE	TRUE

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SNCA	1.56E-01	9.27E-05	TRUE	SNCA		1.94E-01	1.10E-06	TRUE	FALSE	TRUE
CXCL1	-6.77E-02	8.93E-02	FALSE	CXCL1		2.79E-02	4.84E-01	FALSE	FALSE	FALSE
CXCL2	-4.18E-02	2.94E-01	FALSE	CXCL2		5.61E-02	1.60E-01	FALSE	FALSE	TRUE
FUT8	-1.92E-01	1.49E-06	TRUE	FUT8		-6.19E-02	1.21E-01	FALSE	FALSE	FALSE
TNFRSF1A	6.77E-02	8.97E-02	FALSE	TNFRSF1A		1.44E-01	3.12E-04	TRUE	TRUE	TRUE
IGFBP3	-3.76E-02	3.46E-01	FALSE	IGFBP3		5.76E-02	1.49E-01	FALSE	FALSE	TRUE
CASP3	-9.43E-02	1.80E-02	TRUE	CASP3		7.55E-02	5.82E-02	FALSE	FALSE	FALSE
PAK3	-2.50E-02	5.31E-01	FALSE	PAK3		1.16E-01	3.59E-03	TRUE	TRUE	TRUE
SGK2	1.28E-01	1.29E-03	TRUE	SGK2		1.73E-01	1.36E-05	TRUE	FALSE	TRUE
JUN	1.07E-02	7.89E-01	FALSE	JUN		1.28E-01	1.33E-03	TRUE	TRUE	TRUE
RB1	1.49E-01	1.91E-04	TRUE	RB1		2.17E-01	5.09E-08	TRUE	FALSE	TRUE
RAPGEF3	1.63E-01	4.43E-05	TRUE	RAPGEF3		2.11E-01	1.26E-07	TRUE	FALSE	TRUE
CAP2	2.68E-02	5.02E-01	FALSE	CAP2		1.21E-01	2.31E-03	TRUE	TRUE	TRUE
BIRC3	1.18E-02	7.67E-01	FALSE	BIRC3		9.09E-02	2.27E-02	TRUE	TRUE	TRUE
HMG2	-7.59E-02	5.71E-02	FALSE	HMG2		-1.83E-02	6.46E-01	FALSE	FALSE	FALSE
ARHGAP1	3.11E-02	4.35E-01	FALSE	ARHGAP1		1.56E-01	9.53E-05	TRUE	TRUE	TRUE
ARHGAP24	-6.85E-02	8.60E-02	FALSE	ARHGAP24		1.29E-01	1.23E-03	TRUE	TRUE	TRUE
RASGRP1	4.02E-03	9.20E-01	FALSE	RASGRP1		1.07E-01	7.33E-03	TRUE	TRUE	TRUE
MAGED2	-1.16E-01	3.75E-03	TRUE	MAGED2		2.81E-02	4.81E-01	FALSE	FALSE	FALSE

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RBP1	-1.57E-01	7.92E-05	TRUE	RBP1		-2.33E-02	5.59E-01	FALSE	FALSE	FALSE
ALDH3A1	1.51E-01	1.50E-04	TRUE	ALDH3A1		1.79E-01	7.50E-06	TRUE	FALSE	TRUE
HRASLS2	1.05E-01	8.38E-03	TRUE	HRASLS2		1.64E-01	3.92E-05	TRUE	FALSE	TRUE
RARRES3	1.53E-02	7.02E-01	FALSE	RARRES3		8.02E-02	4.43E-02	TRUE	TRUE	TRUE
SP110	2.02E-02	6.12E-01	FALSE	SP110		1.22E-01	2.20E-03	TRUE	TRUE	TRUE
TGM2	2.24E-02	5.75E-01	FALSE	TGM2		9.31E-02	1.96E-02	TRUE	TRUE	TRUE
DICER1	-1.46E-01	2.57E-04	TRUE	DICER1		5.60E-02	1.60E-01	FALSE	FALSE	FALSE
IPO5	1.45E-02	7.15E-01	FALSE	IPO5		1.26E-01	1.53E-03	TRUE	TRUE	TRUE
CIRBP	-9.45E-02	1.77E-02	TRUE	CIRBP		7.10E-02	7.50E-02	FALSE	FALSE	FALSE
EIF4EBP2	-7.73E-03	8.46E-01	FALSE	EIF4EBP2		1.48E-01	2.03E-04	TRUE	TRUE	TRUE
EIF4G2	-1.45E-01	2.76E-04	TRUE	EIF4G2		1.09E-01	6.48E-03	TRUE	FALSE	FALSE
C1S	-3.63E-02	3.63E-01	FALSE	C1S		7.88E-02	4.81E-02	TRUE	TRUE	TRUE
SLPI	1.33E-01	8.83E-04	TRUE	SLPI		1.74E-01	1.32E-05	TRUE	FALSE	TRUE
MXRA5	-5.76E-02	1.49E-01	FALSE	MXRA5		4.46E-02	2.63E-01	FALSE	FALSE	FALSE
SLC20A1	-7.03E-02	7.77E-02	FALSE	SLC20A1		9.39E-02	1.85E-02	TRUE	TRUE	TRUE
SLC26A2	-2.46E-02	5.37E-01	FALSE	SLC26A2		6.72E-02	9.20E-02	FALSE	FALSE	TRUE
GCNT1	-5.80E-02	1.46E-01	FALSE	GCNT1		9.01E-02	2.38E-02	TRUE	TRUE	TRUE
SLC35C1	8.51E-02	3.29E-02	TRUE	SLC35C1		1.59E-01	6.57E-05	TRUE	FALSE	TRUE
MT1F	2.04E-02	6.08E-01	FALSE	MT1F		9.71E-02	1.49E-02	TRUE	TRUE	TRUE

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MT1G	4.44E-02	2.65E-01	FALSE	MT1G	1.05E-01	8.34E-03	TRUE	TRUE	TRUE
MT1M	7.61E-04	9.85E-01	FALSE	MT1M	7.21E-02	7.05E-02	FALSE	FALSE	TRUE
MT1X	6.65E-02	9.53E-02	FALSE	MT1X	1.39E-01	5.07E-04	TRUE	TRUE	TRUE
MT2A	5.53E-02	1.66E-01	FALSE	MT2A	1.51E-01	1.50E-04	TRUE	TRUE	TRUE
SLC47A1	1.18E-02	7.67E-01	FALSE	SLC47A1	1.56E-01	9.35E-05	TRUE	TRUE	TRUE
SLC48A1	9.79E-02	1.40E-02	TRUE	SLC48A1	1.62E-01	4.81E-05	TRUE	FALSE	TRUE
SLC29A3	8.85E-02	2.64E-02	TRUE	SLC29A3	1.65E-01	3.57E-05	TRUE	FALSE	TRUE
FTL	2.90E-02	4.67E-01	FALSE	FTL	1.42E-01	3.55E-04	TRUE	TRUE	TRUE
GALNT10	1.36E-01	6.30E-04	TRUE	GALNT10	1.72E-01	1.56E-05	TRUE	FALSE	TRUE
SLC7A11	-1.03E-01	9.70E-03	TRUE	SLC7A11	1.05E-01	8.59E-03	TRUE	FALSE	TRUE
RRAD	1.17E-01	3.32E-03	TRUE	RRAD	1.69E-01	2.19E-05	TRUE	FALSE	TRUE
Sum			0				0	0	0

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Figure 35: Table S7

Characteristic TCGA HG-SOC genes (from Domcke et al., 2013) with CNA alterations in SKOV3

NMID	Symbol	chromosome	cytoband	# samples	Copy Number change	average CN
NM_001904	CTNNB1	3	3p22.2 - 3p22.1	4	Deletion	1.10383
NM_001105077	MECOM	3	3q26.2	4	Amplification	6.74439
NM_004333	BRAF	7	7q34	4	Deletion	1.06632
NM_000314	PTEN	10	10q23.2 - 10q23.31	4	Deletion	1.1311
NM_004985	KRAS	12	12p12.1	4	Amplification	3.13603
NM_000321	RB1	13	13q14.2 - 13q21.1	2	Deletion	1.68343
NM_000546	TP53	17	17p13.2 - 17p13.1	4	Deletion	1.17478
NM_001005862	ERBB2	17	17q12	4	Amplification	7.65166
NM_007299	BRCA1	17	17q21.2 - 17q21.31	4	Amplification	2.44655
NM_007299	BRCA1	17	17q21.31	4	Amplification	2.4595

Figure 36: Table S8

Correspondence of Evi1 pathway-based patients classification by predicted risk groups to the TCGA transcriptional subtype system. 357 patients

Risk groups \ subtypes	TCGA transcriptional subtype system			
	Differentiated	Immunoreactive	Mesenchymal	Proliferative
1	8	11	7	21
2	37	32	21	31
3	44	34	46	42
4	7	8	7	1

Fisher's exact test P: 0.01467

Non-proliferative Proliferative

Risk group 1	26	21
Risk groups 2-4	262	74

Fisher's exact test P: 0.0043