Figure S1

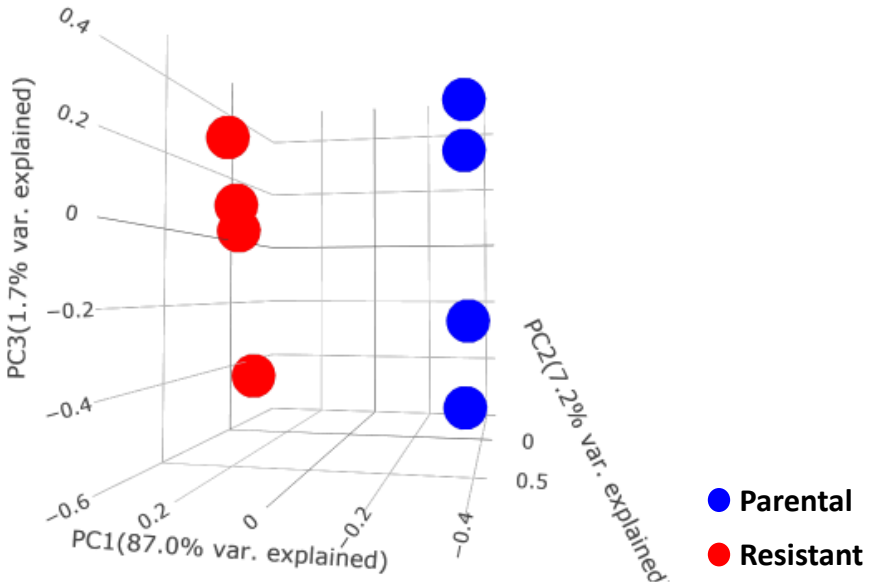

PC3(1.7% var. explained)
0.4
0.2
0
−0.2
−0.4
−0.6
PC1(87.0% var. explained)
0.2
0
−0.2
−0.4
PC2(7.2% var. explained)
0
0.5
Parental
Resistant

Figure S2

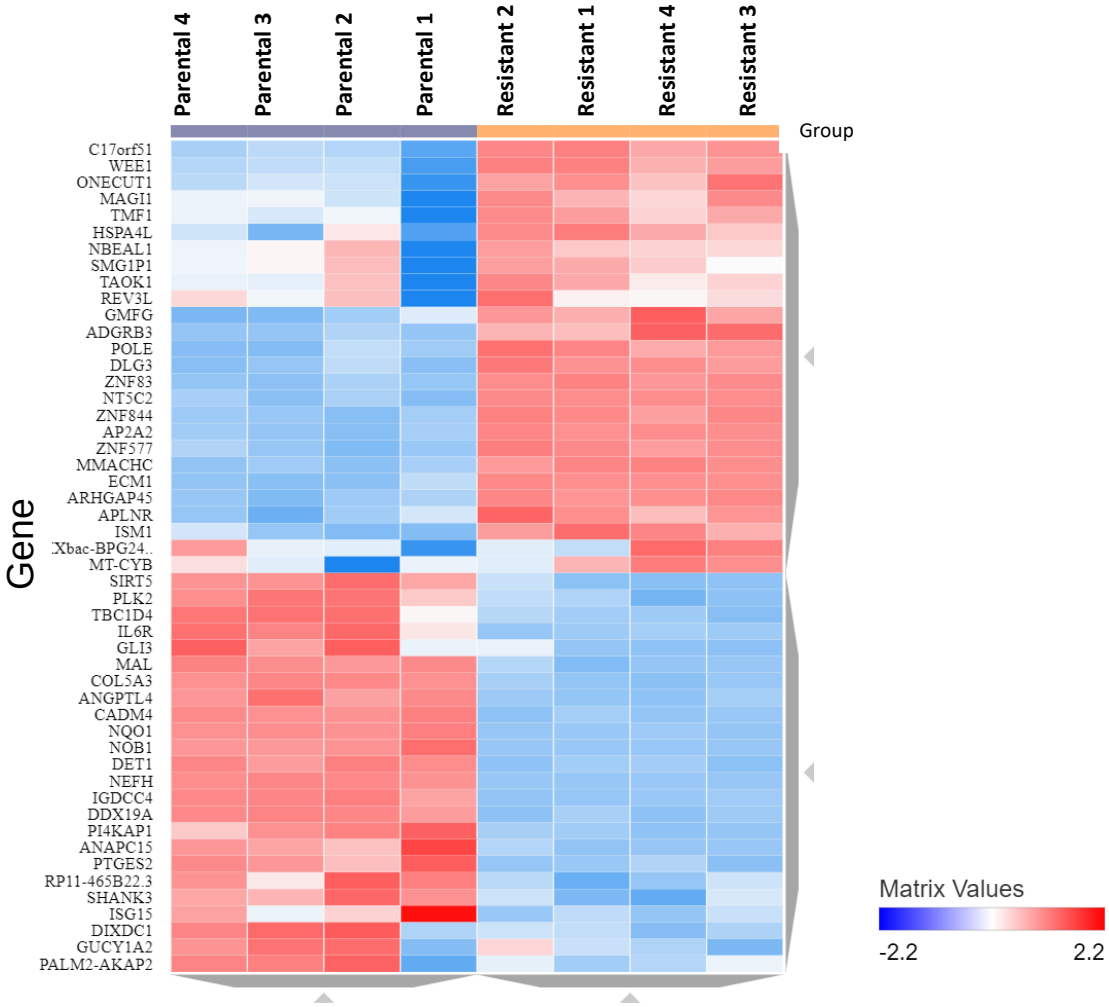

Parental 4
Parental 3
Parental 2
Parental 1
Resistant 2
Resistant 1
Resistant 4
Resistant 3
Group
Gene
C17orf51
WEE1
ONECUT1
MAGI1
TMF1
HSPA4L
NBEAL1
SMG1P1
TAOK1
REV3L
GMFG
ADGRB3
POLE
DLG3
ZNF83
NT5C2
ZNF844
AP2A2
ZNF577
MMACHC
ECM1
ARHGAP45
APLNR
ISM1
Xbac-BPG24...
MT-CYB
SIRT5
PLK2
TBC1D4
IL6R
GLI3
MAL
COL5A3
ANGPTL4
CADM4
NQO1
NOB1
DET1
NEFH
IGDCC4
DDX19A
PI4KAP1
ANAPC15
PTGES2
RP11-465B22.3
SHANK3
ISG15
DIXDC1
GUCY1A2
PALM2-AKAP2
Matrix Values
-2.2
2.2

Figure S3

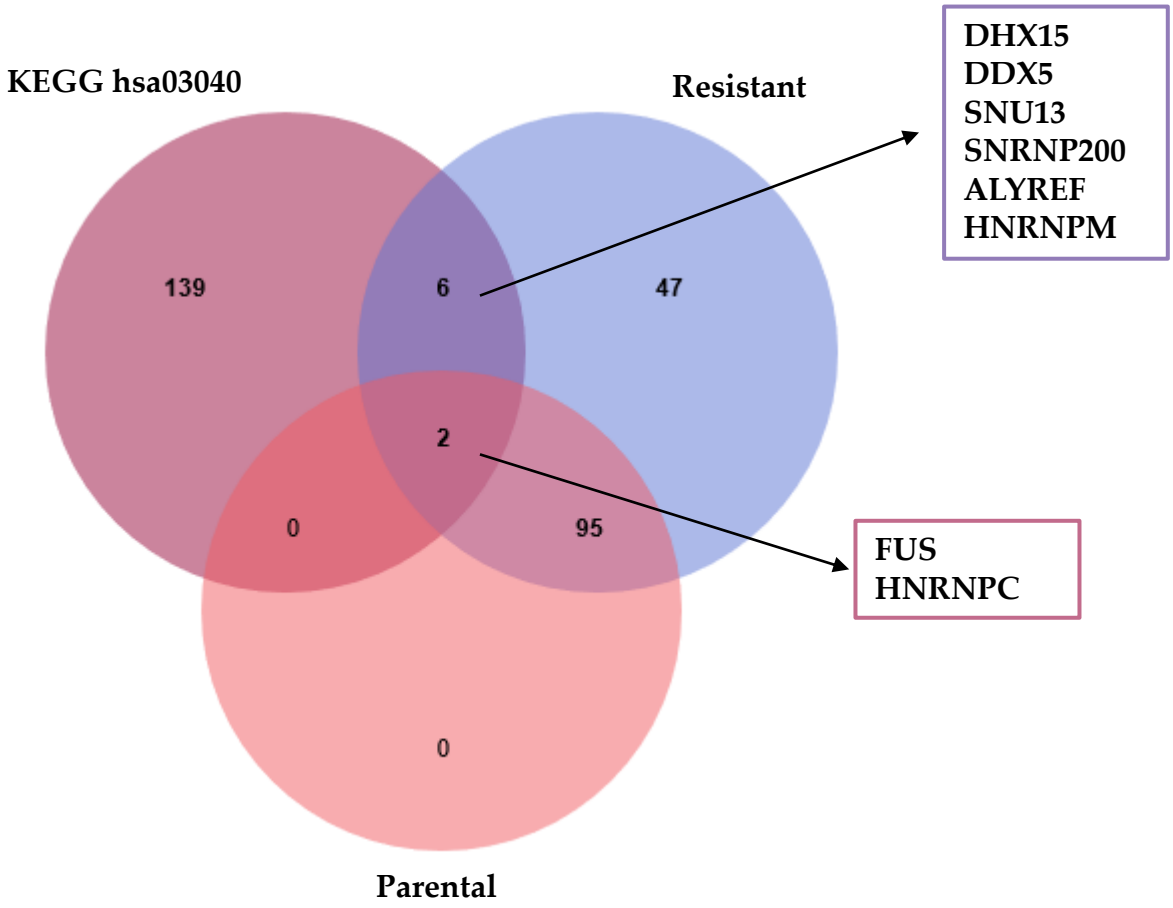

KEGG hsa03040
Resistant
Parental
139
6
47
2
0
95
0
DHX15
DDX5
SNU13
SNRNP200
ALYREF
HNRNPM
FUS
HNRNPC

Figure S4

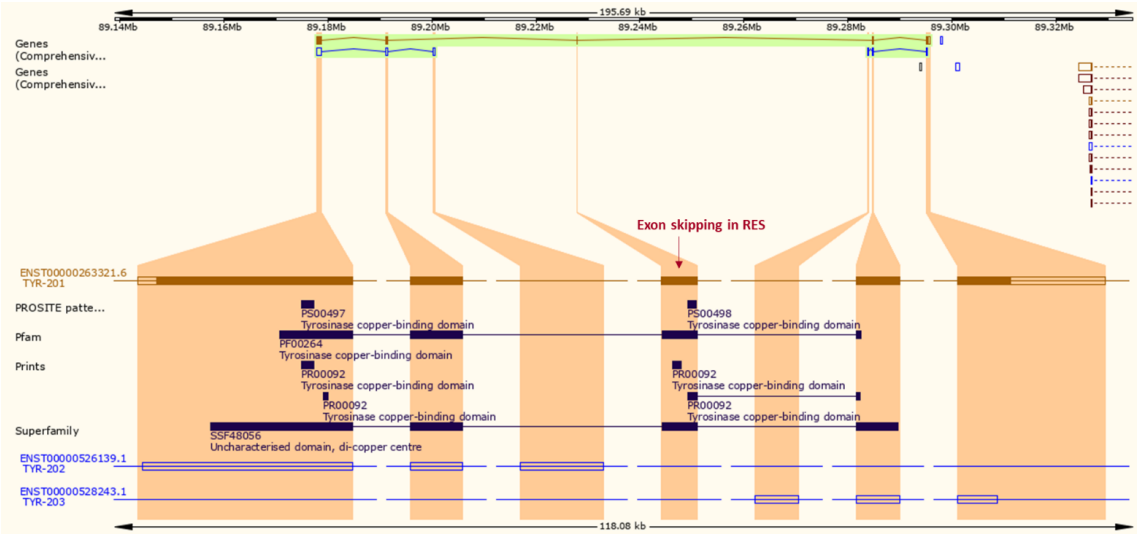
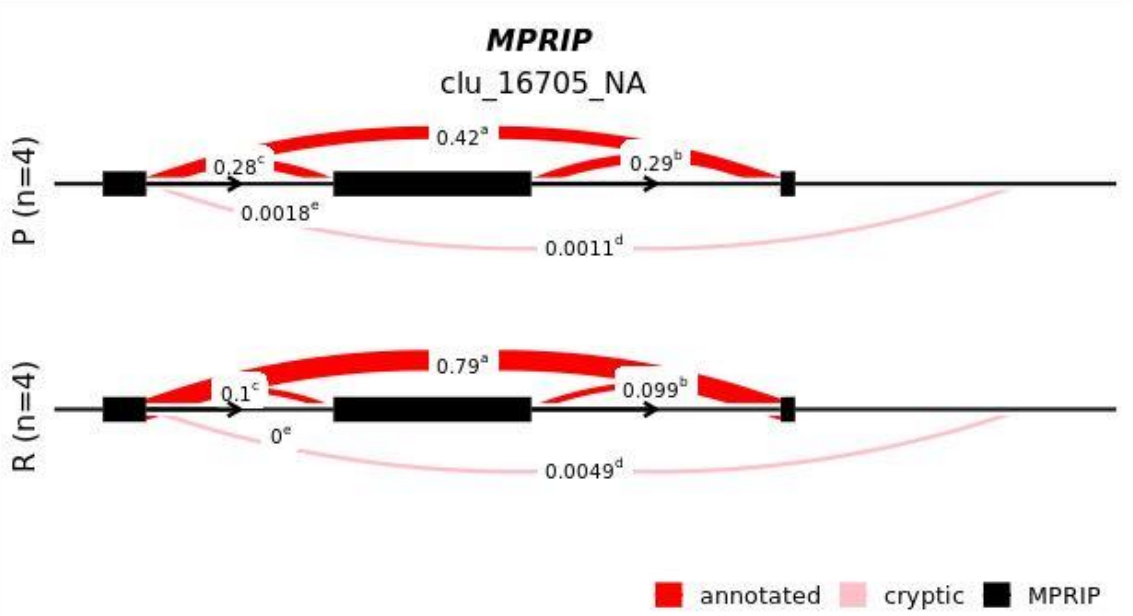

195.69 kb
89.14Mb
89.16Mb
89.18Mb
89.20Mb
89.22Mb
89.24Mb
89.26Mb
89.28Mb
89.30Mb
89.32Mb
Genes (Comprehensiv...
Genes (Comprehensiv...
Exon skipping in RES
ENST00000263321.6 TYR-201
PROSITE patte...
PS00497 Tyrosinase copper-binding domain
PS00498 Tyrosinase copper-binding domain
Pfam
PF00264 Tyrosinase copper-binding domain
Prints
PR00092 Tyrosinase copper-binding domain
PR00092 Tyrosinase copper-binding domain
PR00092 Tyrosinase copper-binding domain
PR00092 Tyrosinase copper-binding domain
Superfamily
SSF48056 Uncharacterised domain, di-copper centre
ENST00000526139.1 TYR-202
ENST00000528243.1 TYR-203
118.08 kb

Figure S5



	chr	start	end	verdict	ΔPSI
a	chr17	17180088	17184823	annotated	0.368
b	chr17	17180669	17184823	annotated	-0.184
c	chr17	17180088	17180607	annotated	-0.182
d	chr17	17180088	17188328	cryptic_threeprime	-0.002