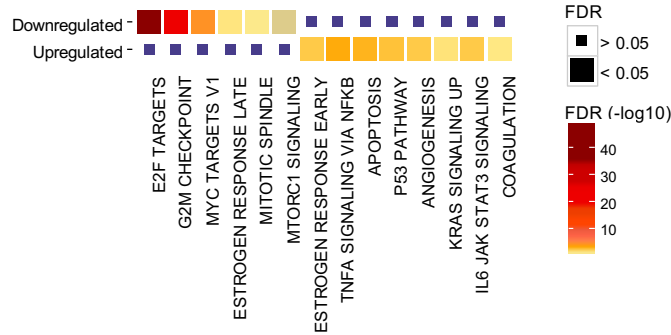
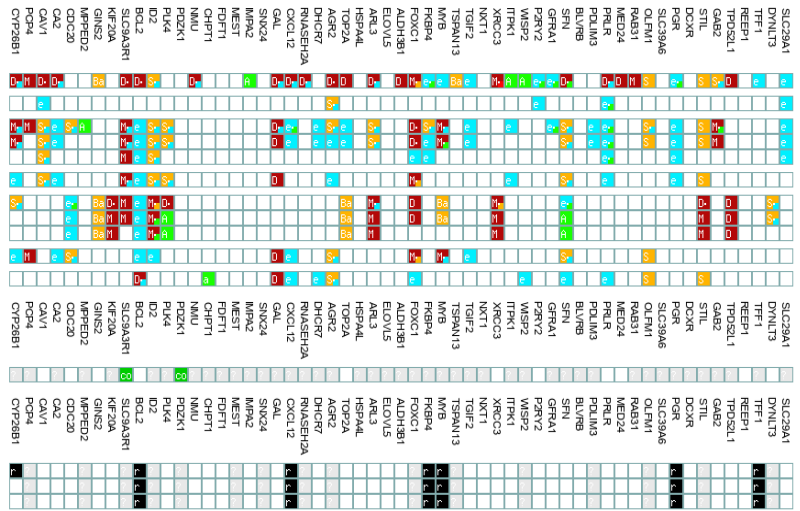


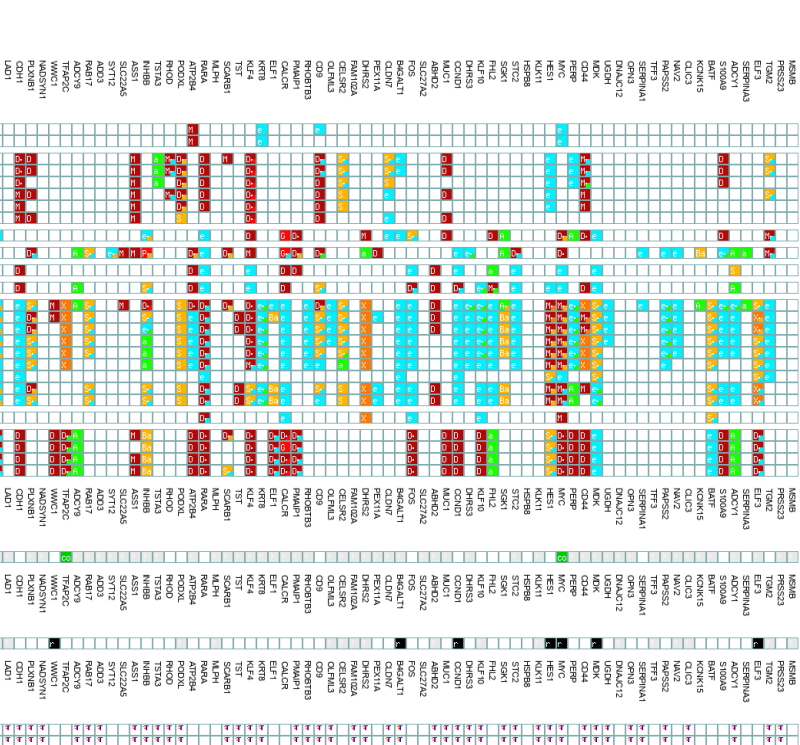
a **Hallmark pathways**
MCF7 LTED^{PaIboR} versus MCF7 LTED



source	term name	term ID	n. of term genes	n. of query genes	n. of common genes	corrected p-value
BP	cellular response to stimulus	GO:0051716	7303	57	38	2.01e-02
BP	body fluid secretion	GO:0007589	91	57	5	1.61e-02
BP	system development	GO:0048731	4669	57	30	7.29e-03
BP	animal organ development	GO:0048513	3415	57	25	8.61e-03
BP	gland development	GO:0048732	437	57	9	1.10e-02
BP	epithelium development	GO:0060429	1262	57	15	5.62e-03
BP	cell cycle	GO:0007049	1829	57	17	2.86e-02
BP	mitotic cell cycle	GO:0000278	985	57	16	3.30e-05
BP	mitotic cell cycle process	GO:1903047	821	57	12	6.67e-03
BP	positive regulation of developmental process	GO:0051094	1274	57	14	3.22e-02
BP	growth	GO:0040007	968	57	12	4.58e-02
source	term name	term ID	n. of term genes	n. of query genes	n. of common genes	corrected p-value
cor	Protein databases (CORUM protein complexes)					
cor	PDZK1-NHERF1-EZR complex	CORUM:6793	3	13	2	1.50e-02
source	term name	term ID	n. of term genes	n. of query genes	n. of common genes	corrected p-value
rea	Biological pathways (Reactome)					
rea	Signaling by Nuclear Receptors	R-HSA-9006931	198	41	7	3.24e-03
rea	ESR-mediated signaling	R-HSA-8939211	155	41	6	8.99e-03
rea	Estrogen-dependent gene expression	R-HSA-9018519	149	41	6	7.19e-03



source	term name	term ID	n. of term genes	n. of query genes	n. of common genes	corrected p-value
BP	response to water	GO:00009415	16	71	4	9.76e-04
BP	response to hydrostatic pressure	GO:0051959	7	71	3	5.46e-03
BP	biological adhesion	GO:0022610	1330	71	19	6.55e-04
BP	cell adhesion	GO:0007155	1323	71	18	3.03e-03
BP	cell-cell adhesion	GO:0098699	763	71	13	1.18e-02
BP	regulation of cell adhesion	GO:0093255	628	71	14	1.81e-04
BP	system development	GO:0048731	4669	71	36	3.79e-03
BP	negative regulation of cell adhesion	GO:0007162	242	71	8	9.59e-03
BP	regulation of cell death	GO:0010941	1645	71	19	1.62e-02
BP	regulation of biological quality	GO:0065908	3633	71	29	4.42e-02
BP	response to organic cyclic compound	GO:0014070	941	71	14	2.26e-02
BP	response to endogenous stimulus	GO:0009719	1570	71	19	8.13e-03
BP	multicellular organismal process	GO:0032501	7343	71	47	4.26e-03
BP	developmental process	GO:0032502	6118	71	43	1.54e-03
BP	anatomical structure development	GO:0048856	5699	71	40	6.82e-03
BP	multicellular organism development	GO:0002275	5232	71	38	6.78e-03
BP	animal organ development	GO:0048731	3415	71	31	3.79e-03
BP	gland development	GO:0048732	437	71	10	1.40e-02
BP	cellular developmental process	GO:0048869	4229	71	32	3.05e-02
BP	cell differentiation	GO:0092154	4057	71	31	4.59e-02
BP	myeloid leukocyte differentiation	GO:0000573	193	71	7	2.28e-02
BP	positive regulation of metabolic process	GO:0098693	3294	71	28	1.58e-02
BP	positive regulation of macromolecule metabolic process	GO:0010604	3417	71	26	4.06e-02
BP	positive regulation of nitrogen compound metabolic process	GO:0051173	2889	71	27	5.18e-03
BP	positive regulation of cellular metabolic process	GO:0033255	3001	71	28	3.07e-03
source	term name	term ID	n. of term genes	n. of query genes	n. of common genes	corrected p-value
cor	Protein databases (CORUM protein complexes)					
cor	TFAP2C-Hyg-KDPB complex	CORUM:6203	3	19	2	4.95e-02
source	term name	term ID	n. of term genes	n. of query genes	n. of common genes	corrected p-value
rea	Biological pathways (Reactome)					
rea	Signaling by NOTCH	R-HSA-197118	126	54	7	1.06e-03
source	term name	term ID	n. of term genes	n. of query genes	n. of common genes	corrected p-value
tf	Regulatory motifs in DNA (TRANSFAC TFBS)					
tf	Factor: SPI1; motif: GGGGAGGGGG	TF:MI01303	7863	71	46	3.75e-02
tf	Factor: SPI1; motif: GGGGAGGGGG; match class: 0	TF:MI01303_0	7863	71	46	3.75e-02



- [?] Gene Ontology ■ Biological process ■ Cellular component ■ Molecular function
- Inferred from experiment [IDA, IPI, IMP, IGI, IEP]
- Direct assay [IDA] / Mutant phenotype [IMP]
- Genetic interaction [IGI] / Physical interaction [IPI]
- Traceable author [TAS] / Non-traceable author [NAS] / Inferred by curator [IC]
- Expression pattern [IEP] / Sequence or structural similarity [ISS] / Genomic context [IGC]
- Biological aspect of ancestor [IBA] / Rapid divergence [IRD]
- Reviewed computational analysis [RCA] / Electronic annotation [IEA]
- No biological data [ND] / Not annotated or not in background [NA]
- Biological pathways ■ KEGG ■ Reactome
- [?] Regulatory motifs in DNA ■ TRANSFAC TFBS
- [?] Protein databases ■ Human Protein Atlas ■ CORUM protein complexes
- [?] Human Phenotype Ontology (sequence homologs in other species)