Targeting Melanoma-Initiating Cells by Caffeine: In Silico and In Vitro Approaches

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Table S1

Expression of CMT, according to the GDS1375 dataset from GEO database. Genes showing expression level with fold change lower than 1.6 or higher than 0.4 in melanoma vs nevi

Symbol	Mean expression in melanoma	Mean expression in nevi	t-test (p value)	Fold change (melanoma/nevi)
ATM	456.5	448.7	0.857	1.02
IL10	105.6	118.3	0.459	0.89
IGF1R	942.2	1346.6	0.012	0.69
EIF2A	1898.8	1378.2	5.03×10^{-6}	1.38
CASP3	342.5	388.3	0.019	0.88
BCL2	1041.6	884.3	0.113	1.18
MMP2	3179.8	3539.2	0.692	0.89
MMP9	2922.7	1018.5	0.329	2.87
PXN	1409.3	1112.8	0.0005	1.27
ADORA3	324.1	274.1	0.0614	1.18
ACHE	167.1	119.2	0.0501	1.41
TNFA	147.3	198.4	0.044	0.74
TGM2	389.8	267.5	0.0984	1.46
RBBP8 (*SAE2*)	1084.5	980.4	0.2311	1.11

ATM, ATM serine/threonine kinase; *IL10*, interleukin 10; *IGF1R*, insulin like growth factor 1 receptor; *EIF2A*, Eukaryotic Translation Initiation Factor 2A; *CASP3*, caspase 3; *BCL2*, BCL2 apoptosis regulator; *MMP*, matrix metalloproteinases; *PXN*, paxillin; *ADORA3*, adenosine receptor 3; *ACHE*, acetylcholinesterase; *TNFA*, tumor necrosis factor alpha; *TGM2*, transglutaminase 2; *RBBP8*, RB binding protein 8, endonuclease.
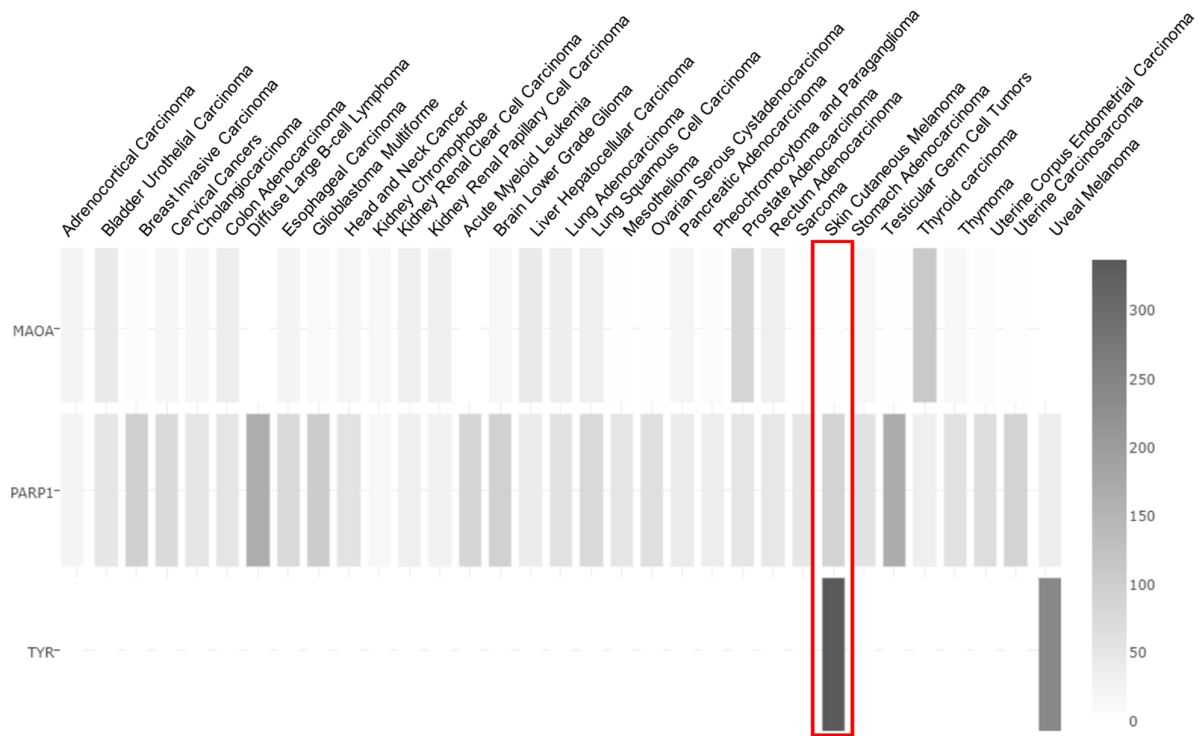
Figure S1. Gene expression comparison of *PARP1* (poly(ADP-ribose) polymerase 1), *MAOA* (monoamine oxidase A), *TYR* (tyrosinase) in different tumor tissues according to GEPIA2 database. Red box indicates the skin coutaneous melanoma.