

Supplementary Table S1. List of melanoma cells

Classification stage	Official name	Mutations
Melanocytes	Melanocyte 13	
	Normal Human Melanocyte (NHM)	
Malignant Non Invasive	WM35	BRAF V600E, IGF-R1 deficient
Malignant Locally Invasive	WM115	BRAF V600E, CDKN2A and PTEN deficient
	WM793	BRAF V600E
Metastases	A375	BRAF V600E, CDKN2A deficient
	1205Lu	BRAF V600E, PTEN deficient
	C8161	P53 mutation
	A375-M2	BRAF V600E, CDKN2A deficient

Supplementary Table S2. Top 10 of significantly upregulated and downregulated genes upon PPAR γ specific activation in A375 cells, as quantified by RNA-sequencing

Ensembl Gene ID	Gene symbol	Gene name	FDR^a	Fold change
ENSG00000170323	FABP4	fatty acid binding protein 4, adipocyte	0.000E+00	151.80
ENSG00000169442	CD52	CD52 molecule	5.556E-03	44.48
ENSG00000164972	C9orf24	chromosome 9 open reading frame 24	1.030E-02	39.45
ENSG00000091831	ESR1	estrogen receptor 1	2.719E-02	32.73
ENSG00000167772	ANGPTL4	angiopoietin-like 4	3.984E-61	29.51
ENSG00000135218	CD36	CD36 molecule (thrombospondin receptor)	2.077E-22	24.03
ENSG00000134240	HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	6.810E-17	19.43
ENSG00000073737	DHRS9	dehydrogenase/reductase (SDR family) member 9	7.112E-04	16.48
ENSG00000135447	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	5.366E-08	11.31
ENSG00000109321	AREG	amphiregulin	8.468E-49	11.02
ENSG00000158321	AUTS2	autism susceptibility candidate 2	1.716E-03	-52.26
ENSG00000164106	SCRG1	stimulator of chondrogenesis 1	1.691E-02	-35.53
	LOC338588	uncharacterized LOC338588	2.133E-02	-32.90
ENSG00000108370	RGS9	regulator of G-protein signaling 9	2.286E-02	-32.46
ENSG00000171345	KRT19	keratin 19	2.956E-02	-32.46
ENSG00000116031	CD207	CD207 molecule, langerin	3.169E-02	-29.60
ENSG00000237836	PHKA2-AS1	PHKA2 antisense RNA 1	3.171E-02	-29.60
ENSG00000196277	GRM7	glutamate receptor, metabotropic 7	3.943E-02	-28.93
ENSG00000213088	DARC	Duffy blood group, chemokine receptor	2.651E-03	-13.84
ENSG00000172733	PURG	purine-rich element binding protein G	2.133E-02	-10.44

^aFDR – False Discovery Rate

Supplementary Table S3. Top 20 of deregulated pathways in RGZ vs Ctrl A375-Media, after an in-depth MS analysis, analyzed with Reactome

Pathway identifier	Pathway name	Entities found	Entities total	Entities ratio	Entities P-value	Entities FDR ^a
R-HSA-168256	Immune System	71	2537	0.187	3.13E-05	4.39E-04
R-HSA-1280215	Cytokine Signaling in Immune system	39	961	0.071	1.15E-06	2.65E-05
R-HSA-109582	Hemostasis	27	801	0.059	1.09E-03	8.55E-03
R-HSA-449147	Signaling by Interleukins	37	642	0.047	3.19E-10	1.34E-08
R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	26	585	0.043	1.86E-05	2.97E-04
R-HSA-6798695	Neutrophil degranulation	23	480	0.035	1.83E-05	2.97E-04
R-HSA-1474244	Extracellular matrix organization	49	329	0.024	1.11E-16	1.30E-14
R-HSA-76002	Platelet activation, signaling and aggregation	21	305	0.023	1.69E-07	4.57E-06
R-HSA-6785807	Interleukin-4 and 13 signaling	20	212	0.016	2.10E-09	6.93E-08
R-HSA-3781865	Diseases of glycosylation	12	190	0.014	1.76E-04	1.93E-03
R-HSA-166658	Complement cascade	8	156	0.012	7.16E-03	4.30E-02
R-HSA-1474228	Degradation of the extracellular matrix	26	148	0.011	1.11E-16	1.30E-14
R-HSA-76005	Response to elevated platelet cytosolic Ca ²⁺	19	144	0.011	2.24E-11	1.16E-09
R-HSA-114608	Platelet degranulation	18	137	0.010	8.18E-11	3.84E-09
R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	25	127	0.009	1.11E-16	1.30E-14
R-HSA-8957275	Post-translational protein phosphorylation	22	109	0.008	1.11E-16	1.30E-14
R-HSA-1474290	Collagen formation	18	104	0.008	9.58E-13	5.56E-11
R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	7	98	0.007	2.00E-03	1.40E-02
R-HSA-6806667	Metabolism of fat-soluble vitamins	8	90	0.007	2.35E-04	2.35E-03

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