Supplementary Materials: Intra-patient heterogeneity of circulating tumor cells and circulating tumor DNA in blood of melanoma patients

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Table S1. Overview CTC positive patients.

Patient_ID	Sex	Age	Melanoma_Type	Mutational_Status	TNM	Survival_Status	Detected_CTCs	Ulceration	S100 (µg/L)	LDH (U/L)	Number_of_ Follow_Ups
patient_1	m	50	SSM	unknown	T1bN0M0	alive	2	No	0.021	227	1
patient_2	m	46	nodular	BRAF	T3bN2cM0	alive	3	Yes	0.034	NS	1
patient_3	m	58	NS	unknown	T3aN0M0	alive	2	No	0.039	272	1
patient_4	m	57	unknown	BRAF	TxN0M1c	alive	4	NS	0.058	143	5
patient_5	m	65	desmoplastic	BRAF	NS	alive	1	NS	0.061	NS	2
patient_6	f	71	unknown	none	TxN0M1c	alive	8	NS	0.089	290	4
patient_7	m	39	unknown	unknown	TxNxM1c	dead	4	NS	0.09	804	1
patient_8	f	88	cutaneous	BRAF	T2aN1aM1b	alive	1	No	0.11	211	1
patient_9	m	74	cutaneous	BRAF	T4N2bM1a	alive	3	NS	0.122	269	4
patient_10	f	61	nodular	BRAF	T3aN2cM0	alive	1	No	0.151	NS	1
patient_11	m	88	cutaneous	unknown	T2aN2cM0	dead	2	No	0.254	NS	1
patient_12	m	69	unknown	NRAS	TxNxM1a	alive	3	NS	0.27	217	1
patient_13	f	69	cutaneous	BRAF	T3bN2cM1c	alive	1	Yes	0.394	NS	1
patient_14	m	46	nodular	BRAF	T4aN3M1c	dead	2	No	0.769	213	1
patient_15	f	NS	cutaneous	BRAF	T4aN2cM0	alive	1	No	0.9	216	1
patient_16	m	66	cutaneous	none	T4bN0M1c	dead	1	Yes	1.52	219	1
patient_17	m	74	unknown	BRAF	TxNxM1c	dead	3	NS	9.463	680	1
patient_18	f	52	cutaneous	BRAF	T3bN1aM1c	dead	62	Yes	19.71	493	1
patient_19	f	34	SSM	NRAS	T1bN1aMx	alive	3	Yes	NS	160	1
patient_20	m	44	uveal	unknown	TxN0M1c	alive	5	NS	NS	166	2
patient_21	m	76	SSM	unknown	T1aN0Mx	alive	1	No	NS	NS	1
patient_22	m	76	unknown	BRAF	TxNxM1a	alive	3	NS	NS	NS	2
patient_23	m	62	cutaneous	BRAF	T1bN2M1c	dead	1	Yes	NS	NS	1
patient_24	m	58	nodular	BRAF	T4bN3M1a	alive	1	NS	NS	NS	4
patient_25	f	76	amelanotic	unknown	T4bN0M0	alive	4	NS	NS	NS	4
patient_26	f	85	amelanotic	NRAS	T4bN3M0	dead	3	NS	NS	NS	4

patient_27	f	81	nodular	NRAS	T4bN0M0	dead	6	NS	NS	NS	3

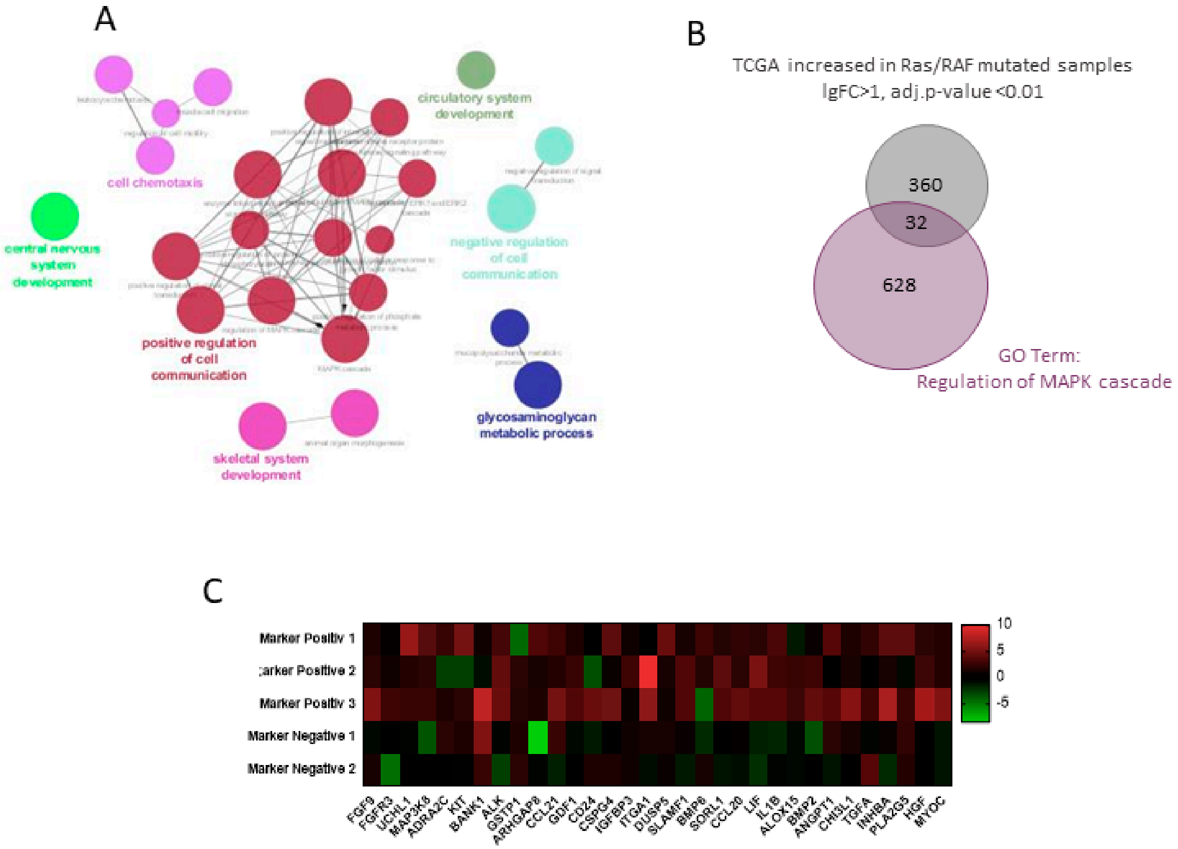

Figure S1. Pathway analysis in the TCGA cohort. mRNA analysis of single cells (**A**) GO-Terms enriched in Ras/RAF mutated samples from the TCGA cohort. Analysis was performed using Cytoscape. (**B**) Venn-diagram of genes significantly increased in Ras/RAF mutated samples compared to non-mutated samples (TCGA) and genes listed in the GO-term “Regulation of MAPK cascade”. (**C**) mRNA expression analysis of marker negative and marker positive single cells.