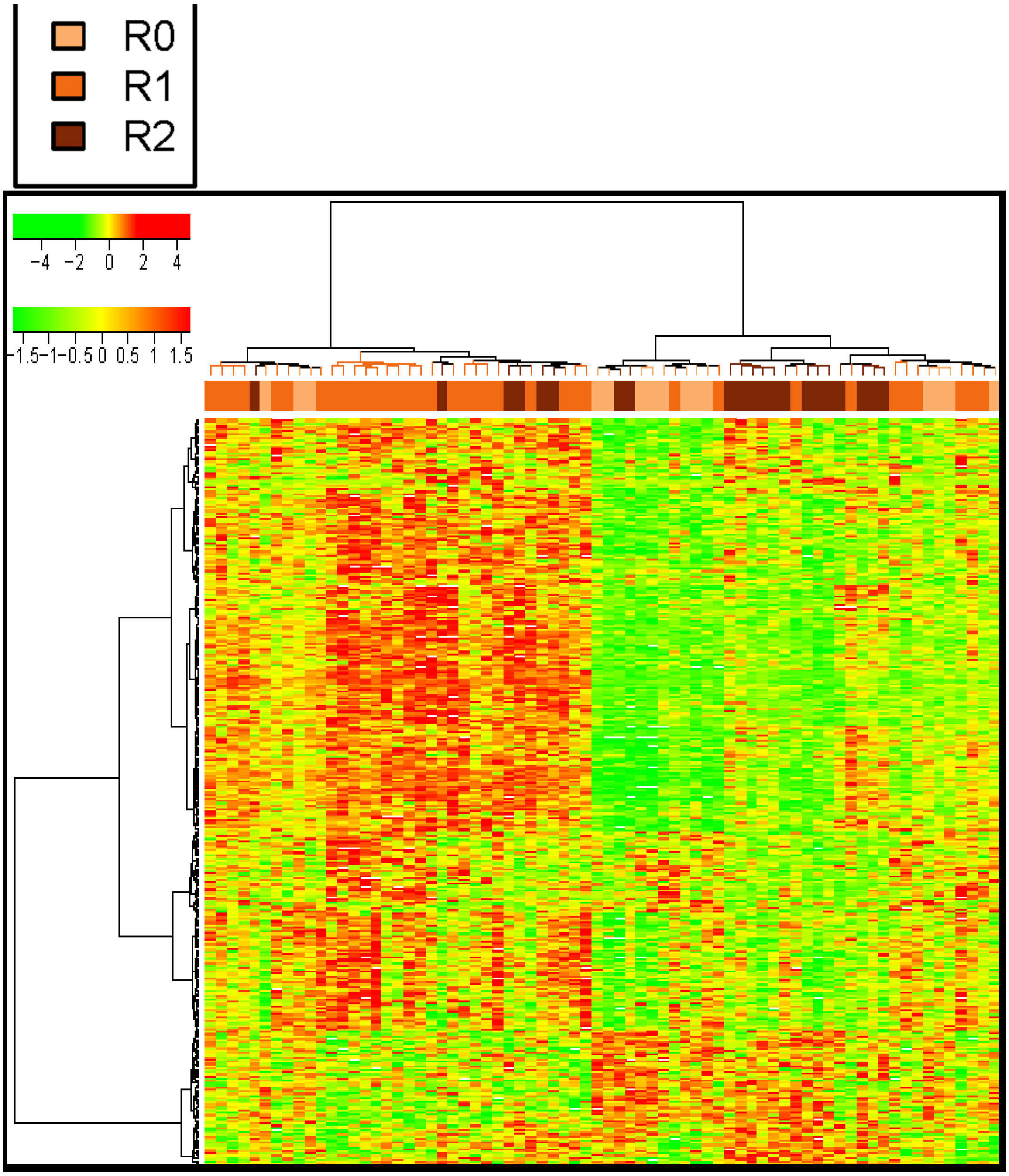
Residual tumor size

1. Hierarchical clustering: Dendrogram showes the relations between tumor samples from patients with different residual tumor size (R0<1cm, 5cm>R1>1cm, R2>5cm). Heat map shows relative intensity of genes expression. Samples are clustered into two main branches with distinct gene expression pattern, however this division seems unrelated with the size of residual tumor: samples R0, R1 and R2 are mixed together in both branches of the dendrogram.



2. Gene Ontology analysis was performed using annotated genes selected in Welch (p<0.001) for the difference between R0 *versus* R1/R2 tumors (R0<1cm, 5cm>R1>1cm, R2>5cm).

Gene Ontology class	**p-value**
GO:35107: appendage morphogenesis	0.000183
GO:35108: limb morphogenesis	0.000183
GO:30326: embryonic limb morphogenesis	0.000112
GO:35113: embryonic appendage morphogenesis	0.000112
GO:48598: embryonic morphogenesis	0.000434
GO:43009: embryonic development (sensu Vertebrata)	0.000896
GO:1701: embryonic development (sensu Mammalia)	0.000896
GO:48637: skeletal muscle development	0.000666
GO:48741: skeletal muscle fiber development	0.000666
GO:48747: muscle fiber development	0.000666

GO:48736: appendage development	0.000183

3. Signaling pathways (according to Biocarta repository) with significantly changed gene expression between R0 *versus* R1/R2 tumors (R0<1cm, 5cm>R1>1cm, R2>5cm).
Least square (LS) and Kolomogorov-Smirnoff (KS) tests were used for analysis of annotated genes selected in Welch (p<0.001) for the difference between R0 *versus* R1/R2 tumors.

	Signaling pathways (Biocarta)	**Signaling pathway name**	**p-value LS**	**p-value KS**
1	h_hSWI-SNFpathway	Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes	1e-05	0.0003721
2	h_iresPathway	Internal Ribosome entry pathway	1e-05	0.0124445
3	h_p35alzheimersPathway	Deregulation of CDK5 in Alzheimers Disease	1e-05	0.0224286
4	h_rarrxrPathway	Nuclear receptors coordinate the activities of chromatin remodeling complexes and coactivators to facilitate initiation of transcription in carcinoma cells	1e-05	0.0061562
5	h_il2rbPathway	IL-2 Receptor Beta Chain in T cell Activation	0.0001047	0.0023371
6	h_vdrPathway	Control of Gene Expression by Vitamin D Receptor	0.0003917	8e-04
7	h_carm-erPathway	CARM1 and Regulation of the Estrogen Receptor	0.0009617	0.0744877
8	h_aktPathway	AKT Signaling Pathway	0.0011545	0.0018995
9	h_HivnefPathway	HIV-I Nef: negative effector of Fas and TNF	0.0012251	0.0041861
10	h_aifPathway	Opposing roles of AIF in Apoptosis and Cell Survival	0.0018552	0.0430208
11	h_longevityPathway	The IGF-1 Receptor and Longevity	0.0028867	0.0004183
12	h_RELAPathway	Acetylation and Deacetylation of RelA in The Nucleus	0.0172831	0.0022354
13	h_cdc25Pathway	cdc25 and chk1 Regulatory Pathway in response to DNA damage	0.0888813	0.0027169
14	h_rbPathway	RB Tumor Suppressor/Checkpoint Signaling in response to DNA damage	0.0980191	0.0036151
15	h_igf1mtorpathway	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway	0.1458465	0.0042863

4. Signaling pathways (according to Biocarta repository) with significantly changed gene expression between R0 *versus* R1/R2 tumors (R0<1cm, 5cm>R1>1cm, R2>5cm). Hotelling test was used for analysis of annotated genes selected in Welch test (p<0.001) for the difference between R0 *versus* R1/R2 tumors.

	Signaling pathways (Biocarta)	**Signaling pathway name**	**p-value**
1	h_iresPathway	Internal Ribosome entry pathway	0.0001336
2	h_nfkbPathway	NF-kB Signaling Pathway	0.0004274
3	h_il4Pathway	IL 4 signaling pathway	0.0007516
4	h_tercPathway	Overview of telomerase RNA component gene hTerc Transcriptional Regulation	0.0007812
5	h_HivnefPathway	HIV-I Nef: negative effector of Fas and TNF	0.0009426
6	h_RELAPathway	Acetylation and Deacetylation of RelA in The Nucleus	0.0011095
7	h_rhoPathway	Rho cell motility signaling pathway	0.0013813
8	h_calcineurinPathway	Effects of calcineurin in Keratinocyte Differentiation	0.0014919
9	h_rarrxrPathway	Nuclear receptors coordinate the activities of chromatin remodeling complexes and coactivators to facilitate initiation of transcription in carcinoma cells	0.0016827
10	h_caspasePathway	Caspase Cascade in Apoptosis	0.0017188
11	h_smPathway	Spliceosomal Assembly	0.001745
12	h_bcellsurvivalPathway	B Cell Survival Pathway	0.0023689
13	h_rasPathway	Ras Signaling Pathway	0.0025734
14	h_aktPathway	AKT Signaling Pathway	0.0036686
15	h_ranMSpathway	Role of Ran in mitotic spindle regulation	0.0037095
16	h_aifPathway	Opposing roles of AIF in Apoptosis and Cell Survival	0.0040409
17	h_hSWI-SNFpathway	Chromatin Remodeling by hSWI/SNF ATP-dependent Complexes	0.0041561
18	h_trkaPathway	Trka Receptor Signaling Pathway	0.004251
19	h_rnaPathway	Double Stranded RNA Induced Gene Expression	0.004562
20	h_deathPathway	Induction of apoptosis through DR3 and DR4/5 Death Receptors	0.0046078
21	h_chemicalPathway	Apoptotic Signaling in Response to DNA Damage	0.0046144
22	h_vdrPathway	Control of Gene Expression by Vitamin D Receptor	0.0047563
23	h_p35alzheimersPathway	Deregulation of CDK5 in Alzheimers Disease	0.0048028
24	h_glycolysisPathway	Glycolysis Pathway	0.0048048