

ARCAP_M	gene	locus	sample_1	sample_2	status	value_1	value_2	log2(fold_change)	test_stat	p_value	q_value	significant	PC-3	value_1	value_2	log2(fold_change)	p_value	q_value
	CAMK2N1	chr1:2080888	shneg	shCHD1	OK	6,1168	17,9863	1.55605	7,78751	5,00E-05	0,0004193	yes		2,33023	3,38226	0.537515	0,0003	0,00430043
	CENPK	chr5:6481355	shneg	shCHD1	OK	12,2553	17,537	0.517003	2,49888	5,00E-05	0,0004193	yes		6,78965	9,7096	0.516074	5,00E-05	0,00089885
	DLC1	chr8:1294085	shneg	shCHD1	OK	6,91712	10,5343	0.606854	3,18032	5,00E-05	0,0004193	yes		0,545804	0,926068	0.762734	5,00E-05	0,00089885
	FOS	chr14:757454	shneg	shCHD1	OK	23,1548	33,1391	0.517226	2,52422	0,0001	0,00078473	yes		1,33334	2,34842	0.816649	5,00E-05	0,00089885
	HOXB6	chr17:466678	shneg	shCHD1	OK	21,682	40,3377	0.895631	3,46301	5,00E-05	0,0004193	yes		2,54889	4,07785	0.677943	5,00E-05	0,00089885
	IGFBP2	chr2:2174981	shneg	shCHD1	OK	16,2426	25,5209	0.651894	3,19515	5,00E-05	0,0004193	yes		8,57374	18,9506	1.14425	5,00E-05	0,00089885
	IL34	chr16:706133	shneg	shCHD1	OK	3,10729	4,60057	0.566156	2,0828	0,0003	0,0020738	yes		9,55609	13,9277	0.543466	5,00E-05	0,00089885
	RRM2	chr2:1026265	shneg	shCHD1	OK	43,8166	72,2153	0.720827	4,12368	5,00E-05	0,0004193	yes		32,0104	47,1503	0.558727	5,00E-05	0,00089885
	RUNX3	chr1:2522606	shneg	shCHD1	OK	0,73754	1,90169	1.36649	4,49992	5,00E-05	0,0004193	yes		0,888451	1,57665	0.827495	5,00E-05	0,00089885
	TGFA	chr2:7067441	shneg	shCHD1	OK	10,8952	36,2993	1.73625	9,38679	5,00E-05	0,0004193	yes		2,04268	2,92052	0.51576	5,00E-05	0,00089885
	TLR8-AS1	chrX:1292093	shneg	shCHD1	OK	8,537	12,1892	0.513805	2,42957	5,00E-05	0,0004193	yes		39,1201	58,1679	0.572314	5,00E-05	0,00089885
	ZNF618	chr9:1166385	shneg	shCHD1	OK	4,92597	6,99357	0.505621	2,67955	0,00015	0,00112331	yes		1,5847	2,46513	0.637454	5,00E-05	0,00089885