

Supplementary Table 3. Differential gene response of RCC4 VHL-deficient and -restored cells upon cystine deprivation

Probeset	Gene Symbol	Gene Title	Puro+C4	Puro+C3	Puro+C2	Puro-C4	Puro-C3	Puro-C1	VHL+C4	VHL+C3	VHL+C1	VHL-C4	VHL-C3	VHL-C2	Δlog2 Mean	p_value	Indicator
206029_at	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	0.014	-0.094	0.080	0.539	0.553	0.158	-0.582	-0.772	-0.366	0.068	-0.177	-0.178	0.417	0.137	1
207219_at	ZNF643	zinc finger protein 643	-0.059	0.093	-0.034	0.674	0.959	0.637	-0.622	-0.715	-0.817	-0.269	-0.102	-0.245	0.757	0.006	1
213804_at	INPP5B	inositol polyphosphate-5-phosphatase, 75kDa	0.027	0.028	-0.054	0.539	0.533	0.346	-0.451	-0.543	-0.558	-0.070	-0.299	-0.084	0.473	0.006	1
221865_at	C9orf91	chromosome 9 open reading frame 91	0.042	0.048	-0.090	0.717	0.738	0.680	-0.926	-1.037	-1.016	-0.072	-0.180	-0.192	0.711	0.002	1
204411_at	KIF21B	kinesin family member 21B	-0.092	-0.050	0.142	0.791	0.696	0.962	-1.082	-1.089	-1.005	-0.237	-0.242	-0.240	0.816	0.002	1
208892_s_at	DUSP6	dual specificity phosphatase 6	-0.135	0.006	0.129	0.477	0.642	0.555	-0.452	-0.908	-0.691	-0.302	0.062	0.190	0.558	0.014	1
205944_s_at	SARS	seryl-tRNA synthetase	-0.002	-0.023	0.025	0.587	0.671	0.625	-0.639	-0.638	-0.561	0.079	0.046	0.020	0.628	0.003	1
205944_s_at	CLTC1	clathrin, heavy chain-like 1	0.029	-0.076	0.047	0.665	0.887	0.874	-0.624	-0.714	-0.542	0.007	0.031	0.078	0.809	0.014	1
202672_s_at	ATF3	activating transcription factor 3	0.030	-0.007	-0.024	0.863	0.807	0.796	-1.335	-1.498	0.353	0.109	0.103	0.822	0.000	1	
204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	-0.152	0.147	0.005	0.579	0.744	0.763	-0.644	-0.922	-0.836	0.144	0.236	0.193	0.695	0.005	1
204285_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0.027	-0.086	0.060	0.728	0.612	0.675	-0.803	-1.118	-0.952	0.325	0.172	0.122	0.672	0.002	1
202014_at	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	-0.031	-0.121	0.152	0.695	0.674	0.729	-0.876	-0.751	0.292	0.159	0.161	0.683	0.014	1	
37028_at	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	-0.051	-0.067	0.118	0.619	0.655	0.530	-0.796	-0.884	-0.746	0.272	0.155	0.177	0.601	0.024	1
220892_s_at	PSAT1	phosphoserine aminotransferase 1	0.018	0.085	-0.104	0.699	0.621	0.107	-0.355	-0.281	-0.267	0.663	0.540	0.480	0.779	0.047	1
203204_s_at	JMD2A	jumonji domain containing 2A	0.178	-0.138	-0.041	0.641	0.623	0.752	-0.376	-0.239	-0.099	0.278	0.199	0.238	0.672	0.024	1
207629_s_at	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	-0.059	-0.082	0.142	0.364	0.624	0.522	-0.211	-0.358	-0.109	0.235	0.229	0.241	0.503	0.039	1
208813_at	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	0.032	-0.026	0.006	0.800	0.949	0.909	-0.274	-0.161	-0.150	0.359	0.457	0.336	0.886	0.005	1
213671_s_at	MARS	methionine-tRNA synthetase	-0.027	0.025	0.002	0.388	0.610	0.554	-0.171	-0.166	-0.227	0.165	0.318	0.164	0.517	0.010	1
203205_at	JMD2A	jumonji domain containing 2A	0.017	-0.090	0.073	0.569	0.315	0.580	-0.178	-0.240	-0.260	0.196	0.215	0.269	0.488	0.008	1
221778_at	KIAA1718	KIAA1718 protein	0.018	-0.135	0.117	1.037	0.815	0.806	-0.123	-0.498	-0.549	0.367	0.304	0.371	0.886	0.013	1
204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	0.040	-0.036	-0.004	0.717	0.666	0.773	-0.307	-0.501	-0.375	0.443	0.529	0.437	0.719	0.002	1
209435_s_at	ARHGEF2	rho/rac guanine nucleotide exchange factor (GEF) 2	-0.034	-0.031	0.065	0.604	0.602	0.530	-0.296	-0.387	-0.221	0.280	0.335	0.332	0.579	0.009	1
219959_at	PTHL /// MOCOS	parathyroid hormone-like hormone /// molybdenum cofactor sulfurase	0.043	-0.073	0.030	0.423	0.540	0.535	-0.150	-0.223	-0.170	0.219	0.214	0.170	0.499	0.018	1
221050_s_at	GTPBP2	GTP binding protein 2	0.063	-0.122	0.059	0.685	0.660	0.830	-0.281	-0.350	-0.148	0.407	0.340	0.367	0.725	0.005	1
201475_x_at	MARS	methionine-tRNA synthetase	-0.030	-0.046	0.076	0.545	0.527	0.619	-0.274	-0.287	-0.163	0.308	0.283	0.266	0.564	0.000	1
209205_s_at	LM04	LIM domain only 4	-0.028	-0.033	0.060	0.521	0.514	0.573	-0.177	-0.177	-0.260	0.330	0.247	0.268	0.536	0.001	1
217996_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-0.170	0.025	0.145	0.581	0.509	0.503	-0.050	-0.358	-0.274	0.056	0.216	0.242	0.531	0.044	1
202847_at	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.028	-0.067	0.039	1.256	1.282	1.383	-1.283	-1.326	-1.253	0.721	0.846	0.584	1.307	0.001	1
218145_at	TRIB3	tribbles homolog 3 (Drosophila)	0.055	-0.030	-0.025	0.844	0.858	0.750	-0.794	-0.130	-0.739	0.416	0.287	0.361	0.817	0.002	1
202402_s_at	CARS	cysteinyl-tRNA synthetase	0.022	-0.092	0.070	0.617	0.796	0.597	-0.426	-0.459	-0.467	0.355	0.340	0.328	0.670	0.026	1
212971_at	CARS	cysteinylytRNA synthetase	0.013	-0.055	0.042	0.576	0.652	0.477	-0.481	-0.486	-0.426	0.323	0.283	0.245	0.568	0.019	1
217997_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-0.014	-0.047	0.062	0.829	0.772	0.577	-0.374	-0.625	-0.481	0.400	0.255	0.307	0.786	0.003	1
203438_at	STC2	stanniocalcin 2	-0.006	-0.023	0.029	0.777	0.867	0.788	-0.787	-0.699	-0.758	0.672	0.655	0.587	0.814	0.002	1
201761_at	MTHFD2	methylene tetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	-0.024	-0.026	0.050	0.636	0.647	0.672	-0.543	-0.726	-0.637	0.603	0.698	0.650	0.652	0.001	1
212948_at	CAMTA2	calmodulin binding transcription activator 2	-0.029	-0.063	0.092	0.611	0.560	0.424	-0.325	-0.576	-0.412	0.465	0.567	0.397	0.532	0.034	1
215009_s_at	SEC31A	SEC31 homolog A (S. cerevisiae)	-0.104	0.215	-0.111	0.494	0.511	0.557	-0.088	-0.270	-0.271	-0.204	0.108	-0.003	0.520	0.045	1
203888_at	THBD	thrombomodulin	-0.035	-0.186	0.221	0.644	0.676	0.515	-0.399	-0.445	-0.299	-0.023	-0.036	-0.123	0.612	0.068	1
203887_s_at	THBD	thrombomodulin	-0.016	-0.087	0.103	0.766	0.629	0.567	-0.253	-0.598	-0.182	0.078	-0.072	-0.006	0.654	0.021	1
213763_at	HIPK2	Homeodomain interacting protein kinase 2	0.085	-0.020	-0.365	0.612	0.743	0.438	0.051	-0.034	-0.038	-0.106	-0.286	-0.199	0.597	0.084	1
202887_s_at	DDIT4	DNA-damage-inducible transcript 4	0.029	-0.015	-0.015	1.279	1.262	1.222	-2.873	-2.967	-2.974	-0.639	-0.706	-0.681	1.254	0.000	1
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	-0.108	-0.024	0.132	0.658	0.532	0.428	-1.186	-1.588	-1.507	-0.114	-0.594	-0.622	0.538	0.058	1
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.073	0.120	-0.192	0.614	0.514	0.561	-1.724	-2.155	-1.577	-0.990	-0.936	-0.673	0.563	0.032	1
218651_s_at	LARP6	La ribonucleoprotein domain family, member 6	-0.040	-0.075	0.015	0.542	0.509	0.584	-0.945	-1.306	-1.103	-0.497	-0.577	-0.547	0.545	0.005	1
202859_x_at	IL8	interleukin 8	-0.170	-0.090	0.260	0.684	0.429	0.548	-2.935	-3.727	-3.499	-0.748	-1.461	-1.466	0.554	0.078	1
211506_s_at	IL8	interleukin 8	-0.121	-0.080	0.202	0.862	0.445	0.770	-3.158	-3.437	-3.287	-0.866	-1.433	-1.755	0.692	0.042	1
212486_s_at	FYN	FYN oncogene related to SRC, FGR, YES	0.075	-0.009	-0.066	0.646	0.285	0.587	-0.734	-0.817	-0.931	-0.792	-0.787	-0.765	0.506	0.043	1
206969_at	KRT34	keratin 34	-0.031	-0.211	0.242	1.008	0.904	1.100	-1.808	-1.701	-1.692	-1.609	-1.685	-1.510	1.004	0.006	1
203665_at	HMOX1	heme oxygenase (decycling) 1	-0.053	-0.215	0.268	0.784	0.711	0.727	-1.509	-1.572	-1.497	-0.987	-1.094	-1.134	0.741	0.035	1
211015_s_at	FYN	FYN oncogene related to SRC, FGR, YES	0.042	-0.053	0.012	0.615	0.602	0.541	-2.505	-2.400	-2.382	-1.778	-1.944	-1.558	0.586	0.004	1
211669_s_at	PLAU	plasminogen activator, urokinase	0.026	-0.075	0.048	0.521	0.358	0.533	-2.358	-2.658	-2.178	-1.727	-2.021	-1.805	0.478	0.002	1
205479_s_at	PLAU	plasminogen activator, urokinase	-0.057	-0.061	0.118	0.524	0.519	0.456	-2.121	-2.469	-1.960	-1.579	-1.829	-1.705	0.500	0.025	1
221009_s_at	ANGPTL4	angiopoietin-like 4	-0.059	-0.186	0.245	0.618	0.591	0.560	-1.459	-1.797	-1.463	-1.434	-1.729	-1.741	0.590	0.052	1
221859_at	SYT13	synaptotagmin XIII	0.441	-0.073	-0.368	0.500	0.577	0.127	-1.846	-1.837	-1.586	-1.924	-1.784	-1.846	0.316	0.212	1
209305_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta	0.075	-0.045	0.030	0.525	0.288	0.688	-0.193	-0.129	-0.094	1.073	0.956	0.711	0.501	0.048	1
209383_at	DDT3	DNA-damage-inducible transcript 3	-0.089	-0.028	0.118	0.994	0.924	0.882	-0.417	-0.443	-0.393	1.196	1.081	1.077	0.934	0.010	1
203725_at	GADD45A	growth arrest and DNA-damage-inducible, alpha	-0.056	0.037	0.020	0.548	0.493	0.501	-0.046	-0.303	-0.336	0.762	0.793	0.755	0.514	0.008	1
206101_at	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	-0.105	0.083	0.022	0.690	0.656	0.435	0.253	0.098	-0.027	1.422	1.199	1.366	0.594	0.033	1
203439_s_at	STC2	stanniocalcin 2	0.029	0.008	0.037	1.013	0.969	0.845	-0.071	-0.048	-0.048	1.323	1.282	1.283	0.942	0.001	1
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219284_at	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	-0.109	0.087	0.022	0.758	0.687	0.727	0.187	0.353	0.073	0.649	0.730	0.736	0.724	0.011	1
200670_at	XBP1	X-box binding protein 1	-0.098	0.083	0.015	0.785	0.828	0.907	0.126	0.137	-0.033	0.532	0.759	0.807	0.840	0.003	1
202720_at	TES	testis derived transcript (3 LIM domains)	-0.056	0.027	0.029	0.488	0.527	0.547	0.337	0.160	-0.001	0.278	0.416	0.451	0.521	0.001	1
205194_at	PSPH	phosphoserine phosphatase	-0.074	0.360	-0.286	1.096	1.154	1.117	1.071	1.012	0.896	1.570	1.939	1.928	1.122	0.024	1
201000_at	AARS	alanyl-tRNA synthetase	0.047	-0.034	-0.013	0.435	0.542	0.517	0.484	0.588	0.636	1.146	1.069	1.077	0.498	0.013	1
221577_x_at	GDF15	growth differentiation factor 15	-0.064	-0.031	0.094	1.076	1.013	1.157	1.371	1.255	1.307	2.219	2.251	2.222	1.082	0.001	1
208763_s_at	TSC22D3	TSC22 domain family, member 3	0.020	0.022	-0.042	0.490	0.612	0.637	0.246	0.341	0.358	1.078	1.210	1.230	0.580	0.011	1
209230_S_at	NUPR1	nuclear protein 1	0.014	-0.029	0.015	0.905	0.943	1.020	0.152	0.279	0.322	1.493	1.568	1.465	0.956	0.001	1
210817_s_at	CALCOCO2	calcium binding and coiled-coil domain 2	0.058	-0.017	-0.042	0.530	0.564	0.604	0.253	0.292	0.257	0.732	0.784	0.599	0.566	0.008	1
206343_S_at	NRG1	neuregulin 1	0.000	-0.053	0.053	0.516	0.516	0.618	0.153	0.216	0.167	0.716	0.714	0.641	0.550	0.001	1
202638_s_at	ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	0.028	-0.196	0.168	0.623	0.491	0.517	0.383	0.249	0.355	1.058	0.805	0.869	0.543	0.033	1
201294_s_at	VWS81	WD repeat and SOCS box-containing 1	0.511	-0.440	-0.071	0.570	0.588	0.530	0.285	0.254	0.293	0.398	0.710	0.419	0.656	0.211	1
202481_at	DHRS3	dehydrogenase/reductase (SDR family) member 3	-0.078	0.003	0.074	0.502	0.036	0.619	1.279	1.222	1.220	1.534	1.713	1.453	0.385	0.161	1
204439_at	IFI4L	interferon-induced protein 44-like	-0.051	-0.089	0.140	0.624	0.420	0.567	1.774	1.539	1.575	1.616	1.942	1.885	0.537	0.018	1
214701_s_at	FN1	fibronectin 1	0.529	-0.537	0.008	0.020	-0.085	-0.095	1.008	0.999	1.036	1.276	1.142	1.086	-0.053	0.866	-1
210150_s_at	LAMAS	laminin, alpha 5	-0.106	-0.030	0.136	-0.005	-0.592	-0.588	2.647	2.621	2.269	2.482	2.503	2.538	-0.395	0.258	-1
218711_s_at	SDPR	serum deprivation response (phosphatidylserine binding protein)	0.090	0.179	-0.268	-0.481	-0.563	-0.644	3.061	3.274	3.204	2.381	2.994	2.923	-0.563	0.033	-1
202437_s_at	CYP181	cytochrome P450, family 1, subfamily B, polypeptide 1	-0.165	0.396	-0.230	-0.760	-0.570	-0.626	2.995	2.909	2.736	2.122	2.514	2.484	-0.652	0.060	-1
209446_s_at	C7orf44	chromosome 7 open reading frame 44	0.165	0.348	0.513	0.501	0.394	0.424	0.356	-0.572	-0.502	0.738	0.356	-0.337	0.440	0.236	-1
201996_s_at	SPEN	spen homolog, transcriptional regulator ( <i>Drosophila</i> )	-0.061	-0.114	0.175	-0.671	-0.817	-0.794	-0.138	-0.545	-0.308	-0.361	-0.627	-0.614	-0.760	0.019	-1
200664_s_at	DNAJB1	Dna (Hsp40) homolog, subfamily B, member 1	0.075	-0.060	-0.015	-0.525	-0.560	-0.343	-0.198	-0.341	-0.212	-0.876	-0.962	-0.987	-0.476	0.027	-1
202388_at	RGS2	regulator of G-protein signalling 2, 24kDa	0.051	-0.208	0.158	-0.371	-0.641	-0.502	-0.187	-0.592	-0.193	-1.474	-1.673	-1.613	-0.505	0.023	-1
200808_s_at	HSPA1A /// HSPA1B	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	0.096	-0.067	-0.029	-0.841	-0.732	-0.709	-0.543	-0.519	-0.414	-1.997	-2.140	-2.168	-0.761	0.013	-1
202581_at	HSPA1B	heat shock 70kDa protein 1B	-0.012	0.037	-0.025	-0.772	-0.865	-0.855	-0.470	-0.631	-0.615	-2.450	-2.443	-2.205	-0.831	0.002	-1
20799_at	HSPA1A	heat shock 70kDa protein 1A	-0.134	0.048	0.086	-0.609	-0.630	-0.522	-0.110	-0.177	-0.216	-1.571	-1.501	-1.552	-0.587	0.010	-1
214329_x_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10 /// tumor necrosis factor (ligand) superfamily, member 10	-0.150	0.260	-0.110	-0.656	-0.646	-0.645	0.104	-0.152	-0.622	-1.288	-0.983	-1.156	-0.649	0.037	-1
215073_s_at	NRF2	nuclear receptor subfamily 2, group F, member 2	-0.025	0.289	-0.264	-0.594	-0.394	-0.569	-0.389	-0.342	-0.635	-1.884	-1.065	-1.149	-0.519	0.043	-1
214724_at	DIXDC1	DIX domain containing 1	0.108	0.041	-0.149	-0.671	-0.564	-0.585	0.020	-0.168	-0.188	-0.577	-0.466	-0.535	-0.606	0.026	-1
212095_at	RHOB	ras homolog gene family, member B	0.010	0.055	-0.065	-0.681	-0.503	-0.543	-0.106	-0.102	-0.040	-1.018	-0.894	-0.864	-0.576	0.011	-1
218566_s_at	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	-0.102	0.186	-0.085	-0.625	-0.602	-0.515	0.161	0.055	-0.031	-0.783	-0.771	-0.753	-0.581	0.032	-1
219062_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	-0.006	-0.066	0.072	-0.525	-0.660	-0.497	0.229	0.041	0.110	-0.502	-0.554	-0.441	-0.561	0.002	-1
206928_at	ZNF124	zinc finger protein 124	-0.311	0.244	0.067	-0.557	-0.628	-0.423	0.129	0.105	0.007	-0.115	-0.119	-0.154	-0.536	0.099	-1
213268_at	CAMTA1	calmodulin binding transcription activator 1	-0.052	-0.075	0.127	-0.569	-0.665	-0.712	0.666	0.252	0.561	-0.307	-0.306	-0.070	-0.648	0.022	-1
205818_at	DBC1	deleted in bladder cancer 1	0.094	0.044	-0.138	-0.533	-0.400	-0.763	0.718	0.759	0.729	0.298	0.284	0.206	-0.565	0.011	-1
219250_s_at	FLRT3	fibronectin leucine rich transmembrane protein 3	-0.025	0.242	-0.217	-0.632	-0.435	-0.538	0.349	0.708	0.266	-0.315	0.191	-0.050	-0.535	0.039	-1
218807_at	VAV3	vav 3 oncogene	0.055	0.153	-0.208	-0.742	-0.507	-0.494	0.184	0.566	0.267	-0.158	0.168	0.126	-0.581	0.063	-1