

Supplementary Table 1. Genes differentially expressed modulated in the ccRCC compared to the HS with a fold change of 1.5 and a false discovery rate <0.05.

ProbeID	Entrez_Gene_ID	Symbol	FDR	FC	Definition
7380088	10180	RBM6	0.001031408	3.1675625	Homo sapiens RNA binding motif protein 6 (RBM6), mRNA.
7550341	25994	HIGD1A	0.016724395	3.0058818	Homo sapiens HIG1 domain family, member 1A (HIGD1A), mRNA.
1190717	9790	BMS1	0.013944148	2.4086955	Homo sapiens BMS1 homolog, ribosome assembly protein (yeast) (BMS1), mRNA.
5820195	1187	CLCNKA	0.021987725	2.349548	Homo sapiens chloride channel Ka (CLCNKA), transcript variant 2, mRNA.
1340360	55920	RCC2	0.028418759	2.3343458	Homo sapiens regulator of chromosome condensation 2 (RCC2), mRNA.
6590243	5306	PITPNA	0.019994108	2.2140698	Homo sapiens phosphatidylinositol transfer protein, alpha (PITPNA), mRNA.
610367	51696	HECA	0.037082594	2.1316395	Homo sapiens headcase homolog (Drosophila) (HECA), mRNA.
3890373	3689	ITGB2	0.029741324	2.0962887	Homo sapiens integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) (ITGB2), mRNA.
6280482	51388	NIP7	0.013367729	2.0863795	Homo sapiens nuclear import 7 homolog (S. cerevisiae) (NIP7), mRNA.
7150196	25963	TMEM87A	0.016734883	2.0647485	Homo sapiens transmembrane protein 87A (TMEM87A), mRNA.
5860369	23078	KIAA0564	0.016188184	1.9811081	Homo sapiens KIAA0564 (KIAA0564), transcript variant 1, mRNA.
2490730	57794	SF4	0.021231772	1.9511533	Homo sapiens splicing factor 4 (SF4), transcript variant b, mRNA.
5900682	6612	SUMO3	0.04308641	1.9218324	Homo sapiens SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae) (SUMO3), mRNA.
7050040	24149	ZNF318	0.04425512	1.92129	Homo sapiens zinc finger protein 318 (ZNF318), mRNA.
5220575	23047	PDSS5B	0.04098327	1.8796659	Homo sapiens PDSS5, regulator of cohesion maintenance, homolog B (S. cerevisiae) (PDSS5B), mRNA.
1500603	9933	KIAA0020	0.049261667	1.8674544	Homo sapiens KIAA0020 (KIAA0020), mRNA.
6560121	5289	PIK3C3	0.036196914	1.8480974	Homo sapiens phosphoinositide-3-kinase, class 3 (PIK3C3), mRNA.
1770685	4628	MYH10	0.03959929	1.8386456	Homo sapiens myosin, heavy chain 10, non-muscle (MYH10), mRNA.
1070047	23580	CDC42EP4	0.041125104	1.8240968	Homo sapiens CDC42 effector protein (Rho GTPase binding) 4 (CDC42EP4), mRNA.
7510392	57609	DIP2B	0.021691086	1.7807423	Homo sapiens DIP2 disco-interacting protein 2 homolog B (Drosophila) (DIP2B), mRNA.
4480180	7913	DEK	0.041712407	1.7670399	Homo sapiens DEK oncogene (DNA binding) (DEK), mRNA.
540221	4839	NOP2	0.033386216	1.6918228	Homo sapiens NOP2 nucleolar protein homolog (yeast) (NOP2), transcript variant 2, mRNA.
4280129	55250	ELP2	0.04456414	1.6766157	Homo sapiens elongation protein 2 homolog (S. cerevisiae) (ELP2), mRNA.
2510086	6667	SP1	0.024721734	1.5877315	Homo sapiens Sp1 transcription factor (SP1), transcript variant 1, mRNA.
6280240	83442	SH3BGL3	0.04871469	1.5650666	Homo sapiens SH3 domain binding glutamic acid-rich protein like 3 (SH3BGL3), mRNA.
5310605	219771	CCNY	0.035155393	1.5302719	Homo sapiens cyclin Y (CCNY), transcript variant 1, mRNA.
5900286	146198	ZFP90	0.04165755	1.5287553	Homo sapiens zinc finger protein 90 homolog (mouse) (ZFP90), mRNA.
60154	80755	AARSD1	0.02061157	-1.5412412	Homo sapiens alanyl-tRNA synthetase domain containing 1 (AARSD1), mRNA.
4860435	115209	OMA1	0.037150443	-1.5504347	Homo sapiens OMA1 homolog, zinc metallopeptidase (S. cerevisiae) (OMA1), mRNA.
5810129	6202	RPS8	0.049909446	-1.5602611	Homo sapiens ribosomal protein S8 (RPS8), mRNA.
5900746	54552	GNL3L	0.042122982	-1.6117707	Homo sapiens guanine nucleotide binding protein-like 3 (nucleolar)-like (GNL3L), mRNA.
7380138	90843	TCEAL8	0.044789072	-1.6353827	Homo sapiens transcription elongation factor A (SII)-like 8 (TCEAL8), transcript variant 1, mRNA.
5420487	51101	FAM164A	0.035849243	-1.6376764	Homo sapiens family with sequence similarity 164, member A (FAM164A), mRNA.
70300	10434	LYPLA1	0.045393478	-1.6384692	Homo sapiens lysophospholipase 1 (LYPLA1), mRNA.
2370538	51315	KRCC1	0.020030048	-1.6614183	Homo sapiens lysine-rich coiled-coil 1 (KRCC1), mRNA.
5820528	79042	TSEN34	0.0387222	-1.6850729	Homo sapiens tRNA splicing endonuclease 34 homolog (S. cerevisiae) (TSEN34), transcript variant 2, mRNA.
6290162	90668	LRRC16B	0.034195233	-1.7063369	Homo sapiens leucine rich repeat containing 16B (LRRC16B), mRNA.
2900050	2938	GSTA1	8.74E-04	-1.7277881	Homo sapiens glutathione S-transferase alpha 1 (GSTA1), mRNA.
4860142	51096	UTP18	0.049263574	-1.7333686	Homo sapiens UTP18, small subunit (SSU) processome component, homolog (yeast) (UTP18), mRNA.
460364	3400	ID4	0.030697007	-1.7787143	Homo sapiens inhibitor of DNA binding 4, dominant negative helix-loop-helix protein (ID4), mRNA.
7570603	55763	EXOC1	0.018828318	-1.8141791	Homo sapiens exocyst complex component 1 (EXOC1), transcript variant 1, mRNA.
7100632	125144	C17orf45	0.04659949	-1.8293931	Homo sapiens chromosome 17 open reading frame 45 (C17orf45), mRNA.
3610100	55692	LUC7L	0.019899437	-1.8566513	Homo sapiens LUC7-like (S. cerevisiae) (LUC7L), transcript variant 1, mRNA.
5340138	28973	MRPS18B	0.044734314	-1.8690472	Homo sapiens mitochondrial ribosomal protein S18B (MRPS18B), nuclear gene encoding mitochondrial protein, mRNA.
1430280	1050	CEBPA	0.013820265	-1.8994136	Homo sapiens CCAAT/enhancer binding protein (C/EBP), alpha (CEBPA), mRNA.
7160364	79176	FBXL15	0.035917003	-1.9105792	Homo sapiens F-box and leucine-rich repeat protein 15 (FBXL15), mRNA.
4850390	388796	LOC388796	0.023676366	-1.9124124	Homo sapiens hypothetical LOC388796 (LOC388796), non-coding RNA.
2350504	1890	ECGF1	0.020619152	-1.9274386	Homo sapiens endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA.
3440431	91120	ZNF682	0.018797306	-1.9390877	Homo sapiens zinc finger protein 682 (ZNF682), transcript variant 1, mRNA.
4150279	57827	C6orf47	0.043766014	-1.9477739	Homo sapiens chromosome 6 open reading frame 47 (C6orf47), mRNA.
4860184	5092	PCBD1	0.016106592	-2.0009947	Homo sapiens pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (PCBD1), mRNA.
3780021	286144	C8orf83	0.025248088	-2.007571	Homo sapiens chromosome 8 open reading frame 83 (C8orf83), non-coding RNA.
6560672	10236	HNRPR	0.006800589	-2.008213	Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA.
60148	552900	BOLA2	0.011920189	-2.0235174	Homo sapiens bolA homolog 2 (E. coli) (BOLA2), mRNA.
4490750	5874	RAB27B	0.04646747	-2.088229	Homo sapiens RAB27B, member RAS oncogene family (RAB27B), mRNA.
5340768	51335	NGRN	0.00405857	-2.1977782	Homo sapiens neugrin, neurite outgrowth associated (NGRN), transcript variant 1, mRNA.
7380634	55257	C20orf20	0.027539598	-2.2503464	Homo sapiens chromosome 20 open reading frame 20 (C20orf20), mRNA.
3060300	7316	UBC	0.044489328	-2.265785	Homo sapiens ubiquitin C (UBC), mRNA.
3870634	9774	BCLAF1	0.015827278	-2.3366969	Homo sapiens BCL2-associated transcription factor 1 (BCLAF1), transcript variant 1, mRNA.
7210717	221472	FGD2	0.01792776	-2.3666627	Homo sapiens FYVE, RhoGEF and PH domain containing 2 (FGD2), mRNA.
2970333	100131187	LOC100131187	0.018658912	-2.409087	Homo sapiens KAT protein (LOC100131187), mRNA.
670372	8537	BCAS1	0.001262682	-2.4287364	Homo sapiens breast carcinoma amplified sequence 1 (BCAS1), mRNA.
2640519	55672	NBPF1	0.046813827	-2.446864	Homo sapiens neuroblastoma breakpoint family, member 1 (NBPF1), mRNA. XM_934962 XM_934964 XM_934966 XM_934967 XM_934969 XM_934972 XM_934973 XM_934974 XM_934975 XM_934976 XM_934978
4390220	387522	TMEM189-UBE2V1	0.014259641	-2.4599235	Homo sapiens TMEM189-UBE2V1 readthrough transcript (TMEM189-UBE2V1), transcript variant 2, mRNA.
4250095	1340	COX6B1	0.021012627	-2.7241673	Homo sapiens cytochrome c oxidase subunit Vlb polypeptide 1 (ubiquitous) (COX6B1), nuclear gene encoding mitochondrial protein, mRNA.
5390202	54732	TMED9	2.58E-04	-2.833447	Homo sapiens transmembrane emp24 protein transport domain containing 9 (TMED9), mRNA.
6200367	10841	FTCD	0.002876448	-2.85685	Homo sapiens formiminotransferase cyclodeaminase (FTCD), transcript variant A, mRNA.
7050372	78989	COLEC11	0.020582838	-2.9213927	Homo sapiens collectin sub-family member 11 (COLEC11), transcript variant 1, mRNA.
5820133	79647	AKIRIN1	0.00907978	-2.9773476	Homo sapiens akirin 1 (AKIRIN1), mRNA.
5690132	84331	FAM195A	0.002724086	-3.2672496	Homo sapiens family with sequence similarity 195, member A (FAM195A), mRNA.

Supplementary Table 2. Biological pathways that were significantly differentially modulated in ccRCC patients compared to HS.

Category	p-value	Molecules
Cellular Development	0.003230	ID4, MED6, MYH10, AKIRIN1, SP1, CEBPA, SUMO3, PIK3C3, DEK
Cardiovascular Disease	0.003350	PDS5B, MYH10, ITGB2
Developmental Disorder	0.003350	DIP2B, TYMP, PDS5B, FTCD, MYH10, TSEN34, COLEC11, PCBD1
Organismal Injury and Abnormalities	0.003350	CLCNKA, TYMP, PDS5B, PITPNA, TIAL1, MYH10, ITGB2, TSEN34, PCBD1
Cancer	0.003600	ID4, TIAL1, MYH10, SP1, CEBPA, DEK
Carbohydrate Metabolism	0.003600	PITPNA, ITGB2, SP1, CEBPA, PIK3C3
Cell Cycle	0.003600	PITPNA, TIAL1, MYH10, SP1, CEBPA, PIK3C3, DEK
Cell Death and Survival	0.003600	TYMP, ITGB2, MYH10, GSTA1, CEBPA, PIK3C3
Cell Morphology	0.003600	YAE1D1, OMA1, TYMP, RAB27B, PDS5B, PITPNA, ITGB2, MYH10, CEBPA, PIK3C3, DEK
Cell-To-Cell Signaling and Interaction	0.003600	ITGB2, MYH10, DEK
Cellular Assembly and Organization	0.003600	MYO1C, OMA1, TYMP, RAB27B, PDS5B, PITPNA, FTCD, MYH10, CEBPA, PIK3C3, DEK
Cellular Compromise	0.003600	ITGB2, MYH10, GSTA1, PIK3C3
Cellular Function and Maintenance	0.003600	MYO1C, RAB27B, PITPNA, MYH10, ITGB2, CEBPA, PIK3C3, DEK
Cellular Growth and Proliferation	0.003600	ID4, MYH10, ITGB2, SP1, CEBPA
Cellular Movement	0.003600	MYH10, ITGB2, SP1, PIK3C3, DEK
Connective Tissue Disorders	0.003600	MYH10, ITGB2, COLEC11
DNA Replication, Recombination, and Repair	0.003600	TYMP, CEBPA, DEK
Gastrointestinal Disease	0.003600	PITPNA, ITGB2, CEBPA
Hereditary Disorder	0.003600	DIP2B, CLCNKA, TYMP, FTCD, PITPNA, MYH10, ITGB2, TSEN34, COLEC11, PCBD1
Inflammatory Response	0.003600	ITGB2, MYH10, CEBPA, DEK
Lipid Metabolism	0.003600	RAB27B, PITPNA, ITGB2, GSTA1, CEBPA, PIK3C3
Metabolic Disease	0.003600	CLCNKA, TYMP, FTCD, PITPNA, PCBD1
Molecular Transport	0.003600	OMA1, TYMP, RAB27B, PITPNA, MYH10, GSTA1, SP1, CEBPA, PIK3C3, PCBD1
Neurological Disease	0.003600	DIP2B, CLCNKA, TYMP, PITPNA, ITGB2, TSEN34, PIK3C3
Nucleic Acid Metabolism	0.003600	TYMP
Nutritional Disease	0.003600	PCBD1
Skeletal and Muscular Disorders	0.003600	TYMP, COLEC11
Small Molecule Biochemistry	0.003600	OMA1, TYMP, RAB27B, PITPNA, FTCD, ITGB2, GSTA1, SP1, CEBPA, PIK3C3, PCBD1
Tumor Morphology	0.003600	ITGB2, SP1, CEBPA
Hematological Disease	0.004540	ID4, RAB27B, PITPNA, MYH10, ITGB2, CEBPA, DEK

Supplementary Figure 1. Principal component analysis (PCA) showing the absence of a batch effect bias. PCA cannot separated samples by batch (shape represented different batch, red and blu colors represented ccRCC and HS, respectively).

