

## Supplementary information

### Supplementary Materials and Methods

#### Gene mutations, chromosome imbalance, quantification of HBV

For all samples, tumor and non-tumor DNAs were dissected and stored at -80°C until DNA and RNA extraction using Qiaquick and Rneasy extraction kits, respectively (Qiagen). DNAs were quantified by fluorometry (Fluoroskan Thermo Lab-system), RNA were quantified using a spectrophotometer at 260nm (Nanodrop). The quality of DNA and RNA was controlled by gel electrophoresis followed by staining with ethidium bromide and Agilent 2100 bioanalyser. RNAs were qualified if the 28S/18S ratio was more than 1.5 for Affymetrix experiments and more than 1 for quantitative RT-PCR analyses. In the whole series of tumors, gene mutations were assessed for *TP53* (exon 2 to 11), *CTNNB1* coding for β-catenin (exon 2 to 4), *AXIN1* (exon 1 to 10), *PIK3CA* (exon 1 to 20), *EGFR* (exon 18 to 20), *KRAS*, *NRAS* and *HRAS* (exon 2 and 3) by direct sequencing using a 3100 Applied Biosystems sequencer. Allelic losses and chromosome imbalance were assessed by genotyping 400 markers from LMS2 microsatellites panel (Applied Biosystems) as previously described(23). Sequences of HBS and HBX DNA were determined in all tumors to ensure that primers used for quantification were chosen in regions outside viral polymorphisms or mutation. Quantification of viral DNA was related to a chromosome 22 PCR amplification (sequence of primers are available upon request). Efficacy of PCR amplification was measured at 95, 97 and 94% for HBS, HBX and chromosome 22, respectively. Tumor and non-tumor DNA samples were also carefully quantified using fluorimetry with Hoechst and concentrations were checked by agarose gel electrophoresis. A low number of viral DNA copies in tumors was defined by a ratio HBX/reference and HBS/reference inferior to 0.5 (mean: 0.01, range: 0.002-0.5, standard error: 0.14). A high number of viral DNA copies in tumors was defined by a ratio HBX/reference and HBS/reference superior to 1.5 (mean: 25, range: 1.6-212, standard error: 46). No value was found between 0.5 and 1.6.

#### Gene expression analysis

Raw feature data from Affymetrix HG-U133A GeneChip<sup>TM</sup> microarrays were normalized and log<sub>2</sub> intensity expression summary values for each probe set were calculated using robust multi-

array average (package affy V1.4.32). Probe sets corresponding to control genes or having a “\_x\_” annotation were masked yielding a total of 19,787 probe sets available for further analyses.

### **Unsupervised classification of samples**

We used the following steps:

**1. Unsupervised probe sets selection** based on the two following criteria : (i) a p-value of a variance test (see below) less than 0.01, and (ii) a “robust” coefficient of variation (rCV) less than 10 and superior to a given rCV percentile. Eight rCV percentile thresholds were used (60%; 70%; 80%; 90%; 95%; 97.5%; 99%; 99.5%), yielding 8 lists of probe sets.

- **Variance test:** For each probe set (P) we tested whether its variance across samples was different from the median of the variances of the 19,987 probe sets. The statistic used was  $((n-1)\times\text{Var}(P) / \text{Var}_{\text{med}})$ , where n refers to the number of samples. This statistic was compared to a percentile of the Chi-square distribution with  $(n-1)$  degrees of freedom (this criteria is used in the BRB ArrayTools filtering tool, described in the User’s Manual) and yielded a p-value for each probe set.
- **Robust coefficient of variation:** rCV for each probe set was calculated by dividing the standard deviation by the mean, eliminating the highest and lowest expression value across the samples for each probe set.

**2. Hierarchical clustering** of the 65 samples, using data restricted to each of 8 probe sets lists, for 3 different linkage methods (average, complete and Ward’s), using 1-Pearson correlation as a distance metric (package cluster V1.9.3) produced 24 dendograms.

### **3. Stability assessment:**

The intrinsic stability of each of the 24 dendograms was assessed by comparing each dendrogram to cluster results (dendograms) obtained after data “perturbation” or “resampling” (100 iterations for each). This comparison yielded a reproducibility score (see below). Here, perturbation refers to the addition of random Gaussian noise ( $\mu = 0$ ,  $\sigma = 1.5 \times$  median variance calculated from the data set) to the data matrix, and resampling refers to random substitution of 5% of the samples by virtual samples. Virtual samples were generated by random crossing of existing profiles. To verify that the obtained partition did not depend on the number of probe sets nor of the clustering method, we calculated similar

reproducibility scores based on partitions derived from a decreasing number of probe sets and different linkage methods.

- **Reproducibility score:** To compare two dendograms, both were cut into k clusters ( $k = 2..18$ ) yielding a “partition” for each dendrogram. We then calculated a reproducibility score by comparing the two partitions for each k. To compare two partitions, we calculated the proportion of pairs of samples that are in the same cluster retained in both partitions.

The overall stability of the classification was assessed by calculating a mean reproducibility score (for different values of k), using all pairs of dendograms obtained for a given clustering method with the 8 probe sets lists.

**4. Choice of a representative dendrogram:** To choose a representative dendrogram of the series of 24 dendograms, we identified “consensus” clusters of samples, and kept the dendrogram the most related to these “consensus” clusters. The “consensus” clusters were built using the sample-pairs that were retained in more than 50% of the 24 dendograms (using partitions in 8 clusters).

#### Determination of the specific HCC subgroup differentially expressed genes and subsequent GO analyses

The determination of specific HCC subgroup ( $G_x$ ) differentially expressed genes was based on statistical tests using the 19,787 Affymetrix probe set data (see Materials and Methods). Probe sets that were significant in a  $G_x$  versus  $G_{\text{non-}x}$  t test and significant in a  $G_x$  versus  $G_{\text{non-tumor}}$  t test and had a fold difference either  $< 0.5$  or  $> 2.0$  in  $G_x$  versus  $G_{\text{non-tumor}}$ , uniquely found with  $G_x$ , were considered to be  $G_x$  specific. Threshold hold for significance in either of the t tests were a p value  $< 0.001$  or 10% false discovery rate based on a multivariate test using 1,000 permutations (BRB ArrayTools v3.2 b5). In addition, the following subgroups were combined and tested as described above:  $G_1+G_2$ ;  $G_2+G_3$ ;  $G_5+G_6$ ;  $G_1+G_2+G_3$ . We identified 783 genes specifically deregulated in one or more HCC subgroups based on the criteria described above. We performed independent analyses of gene ontology categories for both over-expressed and under-expressed genes relative to non-tumors. We used hypergeometric tests (GOstats, V1.1.1) to measure the enrichment of GO terms in each of the subgroup specific gene lists. Independent tests were performed for molecular function (MF), biological process (BP) and cellular compartment (CC)

categories. We used the December 2004 mapping of probe set identifiers to Entrez Gene identifiers provided by Affymetrix (<http://www.affymetrix.com/support/technical/>) in combination with hgu133a meta-data library (January 12, 2005, <http://www.bioconductor.org/>) to map Entrez Gene identifiers to GO terms.

### **Construction and evaluation of an Affymetrix global HCC classification predictor**

Analyses were based on (i) random partition of the samples into a training set (Affymetrix : 36 HCC ; QRT-PCR : 28 HCC) and a validation set (Affymetrix : 21 HCC ; QRT-PCR : 81 HCC) (ii) gene supervised selection based on the training set, using sub-sampling (iii) gene filtering based on overall intensity levels (iv) random generation of genes combinations (v) rule learning using 5 prediction algorithms (R packages SVM (e1071, V1.4-1), PAM (pamr, V1.14.2), k-NN (class, V7.2-2), DQDA and DLDA (sma, V0.5.14)) (vi) rule selection based on the success rate of the prediction for the training and test sets. Except when mentioned, success rates are related to the validation set. Below is a detailed description of the steps used to construct and evaluate 6 HCC subgroups predictor derived from the Affymetrix data. The sample population was divided into a training set (S1, n = 36 HCC) and a validation set (S2, n = 21 HCC + 3 adenomas + 5 non-tumor pools).

**1. Gene selection:** using S1, we performed an F-test using a multivariate permutation test based on 1000 permutations of sample labels to correct for multiple testing (BRB ArrayTools v3.0.beta2). This test yielded 1,041 probe sets that contained less than 10 false discoveries.

We performed the same test on a sub-selection of 18 samples in S1 (3 randomly selected cases per group) and found 515 significant probe sets (here a p value < 0.001 was used as the threshold criteria due to the low number of samples per class which renders the permutation test un-reliable). The intersection of these two lists and filtering out probe sets that had a maximal intensity less than 100 units in all 6 HCC cluster groups yielded 258 probe sets. For the probe sets corresponding to the same HUGO gene symbol, we kept one probe set per symbol by eliminating probe sets having a lower F statistic reducing the list to 225 probe sets.

**2. Random sub-selections of genes:** **(i)** Starting from the 225 probe sets list, we generated, at random, 1000 sub-lists of k number of probe sets (k = 8..25) per list (total of 18,000 sub-lists). **(ii)** From the 225 probe sets list, we generated 1,000 sub-lists of k number of probe sets (k = 15, 30, total of 2,000 sub-lists), by choosing the same proportion of genes from individual gene-cluster bins. Gene-cluster bins were constructed based on complete linkage clustering

of the 225 probe sets (using 1-Pearson coefficient as the distance metric), and then cutting the dendrogram to yield 15 cluster nodes ( $n = 4$  to 49 probe sets by cluster bin); (iii) We also generated 1,000 sub-lists of  $k$  probe sets ( $k = 8, 16, 24$ , a total of 3,000 sub-lists) equally representing gene-cluster bins derived from an average linkage clustering, (1-Pearson coefficient) and cutting the dendrogram into 20 nodes, merging small cluster nodes (represented by less than 10 probe sets or a correlation higher than 0.3 with closest neighboring node) yielding a total of 8 major gene-cluster bins ( $n = 9 - 87$  probe sets by cluster bin).

**3. Rule learning:** The expression data from the set S1, restricted to the 23,000 sub-lists of probe sets, served to train 5 prediction algorithms (SVM (e1071, v1.4-1), PAM (pamr, v1.14.2), k-NN (class, v7.2-2), DQDA and DLDA (sma, v0.5.14)), yielding 115,000 predictors.

**4. Rule selection:** For each algorithm, in combination with each value of  $k$  ((i)  $k = 8..25$ ; (ii)  $k = 15,30$ ; (iii)  $k = 8, 16, 24$ ), we selected the best sub-list among 1,000, based on success rate of the corresponding predictor (trained with training set) to classify validation set samples (in case of equality the first sub-list encountered was kept); this selection gave 115 predictors. Among those, 7 predictors, related to 6 distinct sub-lists, gave a success rate to classify samples from the validation set higher than 93%. We selected the 24 genes sub-list related to 2 predictors (algorithms SVM and PAM) among those 6 sub-lists. We observed that this sub-list had a success rate of 97% using Nearest Shrunken Centroids (PAM) of predicting true class membership of the 36 samples in the training set (100% for SVM) and 93.1% of the 29 samples in the validation group (see supplemental Table 2 for list of genes and associated statistics).

**5. Rule validation:** RT-PCR data were obtained for 23 out of the 24 genes in the previously selected sub-list (no primers were available for CD24), along a series of 109 tumors, including 46 samples previously analysed with Affymetrix HG-U133A GeneChip<sup>TM</sup> microarrays (28 in the original training set (S1a), and 18 HCC in the original validation set (S2a)). Using  $\Delta Ct$  data (with 18S as control gene) for the set S1a, we trained 5 prediction algorithms (SVM, PAM, k-NN, DQDA and DLDA) : applied to set S2a, the predictor derived from SVM yielded 81% success rate (100% for S1a).

## **Construction and evaluation of a Quantitative RT-PCR global HCC classification predictor**

Given the partial success of the 24 genes predictor transferred from Affymetrix data to PCR data, we searched for a new predictor, starting the process from an initial list of 103 genes. These 103 genes corresponded to the supervised statistical tests comparing the different cluster groups, using all 65 samples in the Affymetrix data set. We then followed the same learning strategy as described for Affymetrix data: random sub-selections of genes; rule learning; rule selection; rule validation. We generated, at random, 500 sub-lists of k number of probe sets ( $k = 5..16$ ) per list (total of 6,000 sub-lists). Using  $\Delta Ct$  data (control gene 18S), we trained 5 prediction algorithms (SVM, PAM, kNN, DQDA, DLDA) on set S1a and obtained 30,000 predictors. For each algorithm, in combination with each value of k, we selected the best sub-list among 500, based on success rate of the corresponding predictor (trained with set S1a) to classify test set S2a (in case of equality the first sub-list encountered was kept); this selection gave 60 predictors. Among those, 3 predictors gave the highest success rate to classify test set S2a, one of which, yielded a success rate higher than 88% for 3 different algorithms (for S2a), and was therefore considered as the best. This predictor was obtained with DLDA algorithm, and predicted set S1a with 100% success rate and set S2a with 94% success rate. As a validation of the selected predictor, we assessed the relevance of predicted classes for the independent series of 63 HCC (set S3) via the p-value of a Fisher exact test measuring the level of association between predicted classes (1,2,3 vs 4,5,6) and FAL ( $<0.128, \geq 0.128$ ) ( $P = 8.5 \cdot 10^{-4}$ ), as well as between predicted classes (4 vs 5,6) and CTNNB1 mutation ( $P = 5 \cdot 10^{-5}$ ).

## **Quantitative RT-PCR data processing**

For quantitative RT-PCR analyses, 3 µg of total RNA was reverse transcribed using the High capacity Archive kit and random hexamers (Applied Biosystems). For each sample and tested gene, 1 µl of cDNA, corresponding to 2 ng of reverse transcribed RNA, were analyzed by TaqMan PCR analysis, in duplicate, using TaqMan® Low Density Array and the ABI PRISM® 7900HT System (Applied Biosystems). The quality of cDNAs was assessed using a R18S quantification by real time PCR (coefficient of variation 7% for the entire series). The variability of duplicates was evaluated at less than 5% in each measure therefore we used the mean of duplicate measures to estimate the level of gene expression. The relative amount of the tested

mRNA in samples, was determined using the  $2^{-\Delta\Delta CT}$  method where  $\Delta\Delta CT = (CT_{TESTED}-CT_{R18S})_{sample} - (CT_{TESTED}-CT_{R18S})_{calibrator}$ (26).

### **Survival analysis**

Survival time was calculated from the date of surgical resection. Patients who were lost to follow-up, alive at the time of the study or dead from another cause than liver cancer were treated as censored events. Among the 120 patients presenting HCC, patients treated by liver transplantation (16 cases) or by palliative resection (3 cases), patients who died during the two months following surgery (4 cases) were excluded from the survival analysis. Survival curves were calculated according to the Kaplan-Meier method (R package survival V2.17) and differences were assessed using the log rank test.

**Supplementary Table 1: Clinical and genetic characteristics of tumors**

	Affymetrix tumors % (n=57)	Validation set % (n=63)	All tumors % (n=120)
<b>Age (years) (mean +/- SD)</b>	62 +/- 14	58 +/- 12	60 +/- 13
<b>Gender (male)</b>	82	79	81
<b>AFP &lt;100</b>	67	61	64
<b>Cirrhosis or HCA</b>	63	71	68
<b>HBV infection</b>	30	30	30
<b>HCV infection</b>	19	30	25
<b>Alcohol</b>	32	35	33
<b>Hemochromatosis</b>	5	5	5
<b>Diameter (cm) (mean +/- SD )</b>	7.9 +/- 5.1	6.4 +/- 3.7	7.1 +/- 4.5
<b>Intact capsule</b>	23	18	20
<b>Satellite nodule</b>	40	44	42
<b>Edmondson grade :</b>			
<b>I</b>	7	7	7
<b>II</b>	51	47	49
<b>III</b>	35	44	39
<b>IV</b>	7	2	4
<b>Microscopic vascular emboli</b>	30	45	38
<b>Macroscopic portal invasion</b>	12	15	14
<b>TP53 mutations</b>	25	27	26
<b>CTNNB1 mutations</b>	32	25	28
<b>AXIN1 mutations</b>	11	11	11

**Supplementary Table 2: *TP53*, *CTNNB1*, *AXIN1*, *PIK3CA* and *KRAS* gene mutations**

CTNNB1 mutations			
<b>Id HCC</b>	<b>NC change</b>	<b>AA change</b>	<b>Group</b>
HCC211T*	IVS2 + 352_IVS3 + 61del	A5_A80del	G2
HCC217T*	134C>T	S45F	G3
HCC301T	104T>G	I35S	G3
HCC030T*	133T>C	S45P	G4
HCC040T*	134C>T	S45F	G4
HCC013T*	121A>G	T41A	G5
HCC037T*	134C>T	S45F	G5
HCC051T*	98C>T	S33L	G5
HCC097T*	133T>C	S45P	G5
HCC099T*	97T>C	S33P	G5
HCC113T*	133T>C	S45P	G5
HCC115T*	131T>C	S45P	G5
HCC121T*	131T>G	S45A	G5
HCC130T*	98C>T	S33F	G5
HCC164T*	107A>C	H36P	G5
HCC302T	134C>A	S45Y	G5
HCC303T	107A>C	H36P	G5
HCC317T	121A>G	T41A	G5
HCC333T	104T>G	I35S	G5
HCC429T	98C>G	S33Y	G5
HCC433T	95A>G	D32G	G5
HCC437T	121A>G	T41A	G5
HCC028T*	95A>G	D32G	G6
HCC059T*	121A>G	T41A	G6
HCC072T*	67A>C	S23R	G6
HCC131T*	133T>C	S45P	G6
HCC168T*	98C>G	S33C	G6
HCC197T*	134C>T	S45F	G6
HCC242T*	133T>C	S45P	G6
HCC305T	102_113del	I35_G38del	G6
HCC320T	110C>G	S37C	G6
HCC335T	97T>C	S33P	G6
HCC399T	98C>G	S33Y	G6
HCC432T	65_193del	V22_Y6del	G6

TP53 mutations				
	First Mutation		Second Mutation Loss of 17p	Group
<b>Id HCC</b>	<b>NC change</b>	<b>AA change</b>		
HCC016T*	747G>T	R249S	LOH	G2
HCC023T*	747G>T	R249S	LOH	G2
HCC080T*	522G>T	R175L	LOH	G2
HCC084T*	712T>C	C238R	-	G2
HCC098T*	IVS4 + 1G>C	Splicing exon 4	LOH	G2
HCC100T*	857A>T	E286V	LOH	G2
HCC245T*	731G>A	G244D	LOH	G2
HCC402T	746G>A	R249K	LOH	G2
HCC014T*	747G>T	R249S	LOH	G3
HCC022T*	747G>T	R249S	LOH	G3
HCC043T*	747G>T	R249S	LOH	G3
HCC126T*	851G>A	E285K	LOH	G3
HCC208T*	659A>C	Y220S	LOH	G3
HCC226T*	747G>T	R249S	LOH	G3
HCC229T*	637C>T	R213X	LOH	G3
HCC254T*	713G>T	C238F	LOH	G3
HCC304T	248_289 dup	A83_S96dup	LOH	G3
HCC008T	577C>G	H193D	LOH	G4
HCC009T*	574C>T	Q192X	LOH	G4
HCC015T*	764T>C	I255T	LOH	G4
HCC024T*	658T>A	Y220N	LOH	G4
HCC123T	182G>C	R181P	-	G4
HCC129T*	485T>G	I162S	LOH	G4
HCC154T*	679-680del	S227X	LOH	G4
HCC198T*	747G>T	R249S	LOH	G4
HCC314T	535C>T	H179Y	LOH	G4
HCC013T*	725G>T	C242F	LOH	G5
HCC037T*	267-268ins	S90fs	-	G5
HCC082T*	621insT	D208X	-	G5
HCC099T*	747G>T	R249S	LOH	G5
HCC137T*	1015G>T	E339X	LOH	G5

<b><i>AXIN1</i> mutations</b>				
	<b>First Mutation</b>		<b>Second Mutation</b>	<b>Group</b>
<b>Id HCC</b>	<b>NC change</b>	<b>AA change</b>		
HCC012T*	HD	HD	HD	G1
HCC018T*	568C>T	Q190X	LOH	G1
HCC079T*	1184G>C	R395P	LOH	G1
HCC237T*	1005_1011insGTCCCTC	T336fs	-	G1
HCC250T*	1871C>A	S624X	-	G1
HCC080T*	362G>T	C121F	-	G2
HCC339T	HD	HD	HD	G2
HCC438T	64C>T	R22X	1372insT ; C457fs	G2
HCC226T*	1744_1745del	S581fs	LOH	G3
HCC190T*	1839del	G613fs	-	G4
HCC204T*	865del	G289fs	LOH	G4
HCC306T	793G>T	G256X	960del ; D320fs	G4
HCC314T	1021del	D341fs	-	G4
HD=homozygous deletion				

<b><i>TCF1</i> mutations</b>				
	<b>First Mutation</b>		<b>Second Mutation</b>	<b>Group</b>
<b>Id HCC</b>	<b>NC change</b>	<b>AA change</b>		
CHC154T*	872_873insC	P291fs	749A>C ; Q250P	G4
CHC196T*	379A>T	N127Y	495G>T ; W165C	G4
ADE340	685C>T	R229X	LOH	G4
ADE358	617G>T	W206L	872_884del ; P291fs	G4
ADE373	82T>C	Q28X	LOH	G4

<b><i>PIK3CA</i> mutations</b>			
<b>Id HCC</b>	<b>NC change</b>	<b>AA change</b>	<b>Group</b>
HCC189T	398A>T	D133V	G2
HCC438T	3140A>T	H1047L	G2

<b><i>KRAS</i> mutation</b>			
<b>Id HCC</b>	<b>NC change</b>	<b>AA change</b>	<b>Group</b>
HCC037T	183A>T	Q61H	G5

**Supplementary Table 3: genes included in the Affymetrix data predictor of the classification**

HG-U133A Probe Set ID	Gene Symbol	Gene Title	F statistic	G1	G2	G3	G4	G5	G6
218146_at	AD-017	glycosyltransferase AD-017	8.5	471	433	463	542	933	868
208650_s_at	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	10.7	511	235	274	66	75	17
209619_at	CD74	CD74 antigen	5.7	1343	2008	2481	1896	1121	4973
206539_s_at	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	8.4	341	347	243	461	595	459
205963_s_at	DNAJA3	DnaJ (Hsp40) homolog, subfamily A, member 3	6.8	412	521	621	662	727	658
215253_s_at	DSCR1	Down syndrome critical region gene 1	5.5	139	134	136	205	170	265
205977_s_at	EPHA1	EphA1	16.2	432	972	189	530	230	120
202894_at	EPHB4	EphB4	9.3	538	264	204	261	288	220
204231_s_at	FAAH	fatty acid amide hydrolase	5.6	140	134	127	258	169	186
208228_s_at	FGFR2	fibroblast growth factor receptor 2	20.8	373	515	71	47	25	29
207874_s_at	FHR-3	complement factor H related 3	5.8	368	1000	174	2527	1567	980
218974_at	FLJ10159	hypothetical protein FLJ10159	11.9	896	289	168	116	89	40
205208_at	FTHFD	formyltetrahydrofolate dehydrogenase	13.1	221	226	766	993	2213	2123
217521_at	HAL	histidine ammonia-lyase	27.7	380	1065	139	298	83	66
202350_s_at	MATN2	matrilin 2	10.4	291	180	114	190	60	37
217932_at	MRPS7	mitochondrial ribosomal protein S7	6.5	321	389	725	403	438	448
208875_s_at	PAK2	p21 (CDKN1A)-activated kinase 2	7.6	297	199	337	143	150	119
215807_s_at	PLXNB1	plexin B1	6.9	482	343	194	207	304	217
208724_s_at	RAB1A	RAB1A, member RAS oncogene family	6.5	1960	2490	2388	1820	1601	1722
212117_at	RHOQ	ras homolog gene family, member Q	5.2	220	389	366	259	191	204
219733_s_at	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5	12.2	282	564	437	2309	2147	2152
203021_at	SLPI	secretory leukocyte protease inhibitor (antileukoproteinase)	18.0	1148	2766	313	1829	159	141
211989_at	SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	7.3	439	395	489	265	303	253
209478_at	STRA13	stimulated by retinoic acid 13	13.7	433	570	1170	583	959	1151

Listed are the 24 genes that were identified as the global HCC predictor for the Affymetrix samples using the Affymetrix data. Included are the corresponding probe set identifier (ID), the HUGO gene symbol and gene title, the F-statistic from an ANOVA between all 6 classes of samples and associated geometric mean of non-log intensity values per HCC sub-group (G1 – G6).

## Supplementary Table 4: HCC subgroup(s) specific genes with associated expression information based on Affymetrix data.

Each sheet (9 total sheets) in the Excel file corresponds to a subgroup ( $G_x$ ) or a combination of subgroups ( $G_{x,y}$ ). In each sheet we have provided the HUGO gene symbols, the associated Entrez Gene identifier, group specificity, and indication if the gene is up-regulated (“up”) or down-regulation (“down”) in respect to the non-tumor samples as well as the fold difference ( $G_x/n$ ) between the average expression of this gene in  $G_x$  and non-tumor samples. We have appended the probe set(s) identifiers that passed the statistical criteria described in Supplementary Information section. Values are color coded as follows: red,  $(G_x/n) > 2.0$ ; green,  $(G_x/n) < 0.5$ .

Gene Symbol	Entrez Gene	specificity	up_down	G1/n	Probe set
IGF2	3481	G1	up	15.53	210881_s_at;202409_at
PEG3	5178	G1	up	10.82	209242_at;209243_s_at
SOX9	6662	G1	up	6.36	202936_s_at;202935_s_at
SPINT2	10653	G1	up	4.3	210715_s_at
MGC11242	79170	G1	up	4.04	219127_at
SPINT1	6692	G1	up	4.01	202826_at
ZNF83	55769	G1	up	3.95	221645_s_at
ST14	6768	G1	up	3.85	216906_at;216905_s_at;202005_at
C5orf13	9315	G1	up	3.84	201310_s_at
MAP4K4	9448	G1	up	3.82	218181_s_at;206571_s_at
JARID1B	10765	G1	up	3.67	201548_s_at;211202_s_at
CTNND2	1501	G1	up	3.62	209617_s_at;209618_at
MGP	4256	G1	up	3.51	202291_s_at
PPAP2C	8612	G1	up	3.3	209529_at
IKBKAP	8518	G1	up	3.21	202491_s_at;202490_at
CLDN7	1366	G1	up	3.13	202790_at
PDGFA	5154	G1	up	3.06	205463_s_at
NUP133	55746	G1	up	2.98	202184_s_at
MAPK13	5603	G1	up	2.97	210059_s_at;210058_at
MATN2	4147	G1	up	2.91	202350_s_at
TPR	7175	G1	up	2.91	201731_s_at;201730_s_at;215220_s_at
LLGL2	3993	G1	up	2.86	203713_s_at
ARID3A	1820	G1	up	2.8	205865_at
CDK11	23097	G1	up	2.79	212897_at;212899_at
HOOK2	29911	G1	up	2.78	218780_at
ARHGEF3	50650	G1	up	2.77	218501_at
ZNF165	7718	G1	up	2.76	206683_at
MARCH-III	115123	G1	up	2.75	213256_at
LBR	3930	G1	up	2.68	220644_at;201795_at
ATP2B1	490	G1	up	2.65	209281_s_at;215716_s_at;212930_at
F11R	50848	G1	up	2.64	221664_s_at
GPR56	9289	G1	up	2.63	212070_at;206582_s_at
FLJ12895	65982	G1	up	2.61	217593_at;218312_s_at
KCTD3	51133	G1	up	2.59	217894_at
UBAP2	55833	G1	up	2.59	219192_at;221839_s_at
SOX13	9580	G1	up	2.58	38918_at;209736_at
DHRS7	51635	G1	up	2.57	210788_s_at

MMP11	4320	G1	up	2,56	203876_s_at;203878_s_at
N2N	388677	G1	up	2,56	214722_at
RKHD1	399664	G1	up	2,55	91816_f_at
S100A14	57402	G1	up	2,55	218677_at
CXADR	1525	G1	up	2,54	203917_at
SETDB1	9869	G1	up	2,54	203155_at
TAX1BP3	30851	G1	up	2,53	215464_s_at;209154_at
MGC22679	151230	G1	up	2,52	213610_s_at
NRXN3	9369	G1	up	2,52	205795_at;215020_at;215021_s_at
ADAR	103	G1	up	2,51	201786_s_at
ABCC10	89845	G1	up	2,5	213485_s_at
LAD1	3898	G1	up	2,5	216641_s_at;203287_at
TJP3	27134	G1	up	2,5	35148_at;213412_at
SSA2	6738	G1	up	2,48	213027_at;212839_s_at;212852_s_at
TTC3	7267	G1	up	2,48	208662_s_at;208663_s_at;208664_s_at;210645_s_at;208661_s_at
KIAA0792	9725	G1	up	2,46	215583_at;214833_at;202700_s_at
B4GALT3	8703	G1	up	2,43	210243_s_at
TLR5	7100	G1	up	2,43	210166_at
CACNA1D	776	G1	up	2,42	210108_at
FLJ36754	133993	G1	up	2,38	217608_at
ABHD3	171586	G1	up	2,37	213017_at
RPLP0	6175	G1	up	2,36	214167_s_at
SMARCC1	6599	G1	up	2,36	201073_s_at;201074_at;201075_s_at
PAIP1	10605	G1	up	2,35	208051_s_at
KIAA0794	26043	G1	up	2,34	212840_at;217100_s_at
DCPS	28960	G1	up	2,33	218774_at
SFI1	9814	G1	up	2,31	36545_s_at;214402_s_at
MYO5C	55930	G1	up	2,29	218966_at
LOC90333	90333	G1	up	2,28	214751_at
RPL17	6139	G1	up	2,28	200038_s_at
ST5	6764	G1	up	2,27	202440_s_at
XTP2	23215	G1	up	2,27	211944_at;211947_s_at;211946_s_at
C1orf22	80267	G1	up	2,25	220926_s_at
HRIHFB2122	11078	G1	up	2,25	210276_s_at
PLXNA2	5362	G1	up	2,25	213030_s_at;207290_at;222159_at
TNFSF4	7292	G1	up	2,25	207426_s_at
C1orf16	9887	G1	up	2,24	201794_s_at;217189_s_at
NCOA3	8202	G1	up	2,24	207700_s_at;211352_s_at;209061_at
C6orf64	55776	G1	up	2,23	218784_s_at
DNAJC9	23234	G1	up	2,22	213088_s_at
TTLL4	9654	G1	up	2,22	203702_s_at
RBM9	23543	G1	up	2,2	212104_s_at;216215_s_at
CRNLK1	51340	G1	up	2,19	219913_s_at
NTAN1	123803	G1	up	2,19	213062_at;213061_s_at
RBM8A	9939	G1	up	2,19	214113_s_at;217856_at;217857_s_at
IDUA	3425	G1	up	2,18	205057_s_at;205059_s_at
AHSA2	130872	G1	up	2,17	212980_at
EPHB4	2050	G1	up	2,17	216680_s_at;202894_at
HIC2	23119	G1	up	2,17	212964_at;212966_at;212965_at
LMNA	4000	G1	up	2,14	203411_s_at;212089_at
SEPHS1	22929	G1	up	2,14	208941_s_at;208939_at;208940_at
ZNF551	90233	G1	up	2,14	211721_s_at
PDCD4	27250	G1	up	2,14	212594_at;212593_s_at;202730_s_at
BRD3	8019	G1	up	2,12	203825_at
C7orf28A	51622	G1	up	2,12	201973_s_at;201974_s_at
SEC5L1	55770	G1	up	2,12	219349_s_at
HNRPA0	10949	G1	up	2,11	201054_at;201055_s_at
NAP1L1	4673	G1	up	2,09	213864_s_at;208754_s_at;204528_s_at;208753_s_at
SREBF2	6721	G1	up	2,09	201247_at;201248_s_at
ITM1	3703	G1	up	2,08	202223_at

POGZ	23126	G1	up	2,07	212153_at
RPA1	6117	G1	up	2,07	201528_at;201529_s_at
DDR1	780	G1	up	2,06	1007_s_at
INPP5A	3632	G1	up	2,06	203006_at
PIAS4	51588	G1	up	2,06	212881_at
ATP5G2	517	G1	up	2,05	208764_s_at
MPZL1	9019	G1	up	2,05	201875_s_at;210087_s_at;201874_at;210210_at
FNBP1	23048	G1	up	2,04	213940_s_at
PRPF4B	8899	G1	up	2,04	211090_s_at;202126_at
C11orf9	745	G1	up	2,03	204073_s_at
RABGAP1	23637	G1	up	2,03	204028_s_at;213313_at
RABIF	5877	G1	up	2,03	204477_at
LOC130074	130074	G1	up	2,02	212017_at
TIA1	7072	G1	up	2,02	201447_at;201446_s_at;201450_s_at;201449_at
RPS19	6223	G1	up	2,01	213414_s_at
AHNAK	195	G1	up	2	211986_at
KIAA0528	9847	G1	up	2	212943_at
SMARCA1	6594	G1	up	2	203875_at;215294_s_at;203874_s_at
ZNF143	7702	G1	up	2	221873_at
VKORC1	79001	G1	down	0,49	217949_s_at;214226_at
AK2	204	G1	down	0,49	212173_at;208967_s_at;205996_s_at;212174_at;212175_s_at
BLCAP	10904	G1	down	0,48	201032_at
CDC14B	8555	G1	down	0,48	211347_at;208022_s_at;211348_s_at;221556_at
ZNF593	51042	G1	down	0,48	204175_at
TRIM2	23321	G1	down	0,48	202342_s_at;215945_s_at;214248_s_at;202341_s_at
GCLC	2729	G1	down	0,47	202922_at;202923_s_at
ZNF330	27309	G1	down	0,47	209814_at
CTBS	1486	G1	down	0,47	218924_s_at;218923_at
DKFZP434K046	57017	G1	down	0,46	212228_s_at
HADH2	3028	G1	down	0,46	202282_at
HMOX2	3163	G1	down	0,46	218120_s_at;218121_at
SSB1	80176	G1	down	0,46	219677_at
ALDH1A1	216	G1	down	0,45	212224_at
PCAF	8850	G1	down	0,45	203845_at
LAP3	51056	G1	down	0,44	217933_s_at
MBNL2	10150	G1	down	0,44	203640_at;205018_s_at;205017_s_at
ACYP2	98	G1	down	0,42	206833_s_at
TLR3	7098	G1	down	0,42	206271_at
ABHD2	11057	G1	down	0,4	205566_at;63825_at;221815_at
CGI-100	50999	G1	down	0,4	202194_at;202195_s_at
CTSB	1508	G1	down	0,39	200839_s_at;213274_s_at;200838_at
CYP7B1	9420	G1	down	0,39	207386_at
SDHB	6390	G1	down	0,39	202675_at;214166_at
BTN3A2	11118	G1	down	0,38	209846_s_at;212613_at
BTN3A3	10384	G1	down	0,38	204821_at;38241_at;204820_s_at
SLC16A1	6566	G1	down	0,38	202234_s_at;202236_s_at;202235_at
GCHFR	2644	G1	down	0,35	204867_at
GCLM	2730	G1	down	0,35	203925_at
MPDZ	8777	G1	down	0,35	205079_s_at;213306_at
GLRX	2745	G1	down	0,34	206662_at;209276_s_at
BTEB1	687	G1	down	0,33	203541_s_at;203542_s_at;203543_s_at
GBE1	2632	G1	down	0,31	203282_at
C14orf159	80017	G1	down	0,28	218298_s_at
SLC39A8	64116	G1	down	0,27	219869_s_at;209266_s_at;209267_s_at
GADD45A	1647	G1	down	0,26	203725_at
CYP4F11	57834	G1	down	0,23	206153_at
AIM1	202	G1	down	0,19	212543_at
ABCB1	5243	G1	down	0,12	209993_at

Gene Symbol	Entrez Gene	specificity	up_down	G1/n	G2/n	Probe set
AFP	174	G1_2	up	34,6	3,88	204694_at
MYH4	4622	G1_2	up	12,42	2	208148_at
SMYD3	64754	G1_2	up	4,86	4,94	218788_s_at
TOR3A	64222	G1_2	up	3,51	2,43	218459_at
FAM34A	9926	G1_2	up	3,41	3,35	202651_at
FGFR4	2264	G1_2	up	3,19	2,03	204579_at;211237_s_at
KIAA0117	23029	G1_2	up	3,15	2,26	212591_at;214942_at;214943_s_at
TTC13	79573	G1_2	up	3,01	2,28	219481_at
PIGC	5279	G1_2	up	2,99	2,41	215242_at;216593_s_at;202846_s_at
C14orf101	54916	G1_2	up	2,91	2,01	219757_s_at
ZNF281	23528	G1_2	up	2,8	2,37	218401_s_at
RCOR3	55758	G1_2	up	2,79	2,16	218344_s_at
FBXW2	26190	G1_2	up	2,76	2,46	209630_s_at;218941_at
YAP	55249	G1_2	up	2,64	2,09	217836_s_at
PRCC	5546	G1_2	up	2,61	2,32	208938_at
ATRN	8455	G1_2	up	2,61	2,28	211852_s_at
WDR26	80232	G1_2	up	2,59	2,04	218107_at
SLC29A1	2030	G1_2	up	2,58	2,53	201801_s_at;201802_at
SYNJ2	8871	G1_2	up	2,56	2	216180_s_at;210612_s_at;212828_at
CEBPA	1050	G1_2	up	2,54	3,26	204039_at
FLJ11273	54664	G1_2	up	2,54	2,54	218930_s_at
RAP2A	5911	G1_2	up	2,54	2,45	221830_at
FLJ20618	55000	G1_2	up	2,54	2,12	222244_s_at
EFNA1	1942	G1_2	up	2,51	3,06	202023_at
GORASP2	26003	G1_2	up	2,42	2,03	207812_s_at;208843_s_at;208842_s_at
RPS6KC1	26750	G1_2	up	2,37	2,07	218909_at
TI-227H	29793	G1_2	up	2,26	2,04	212725_s_at;212337_at
CREB3L2	64764	G1_2	up	2,24	2,31	212345_s_at
NCK2	8440	G1_2	up	2,23	2	203315_at
ARF1	375	G1_2	up	2,22	2,03	200065_s_at;208750_s_at
H1F0	3005	G1_2	up	2,2	2,19	208886_at
UNC84A	23353	G1_2	up	2,18	2	206487_at;212074_at
ARK5	9891	G1_2	up	2,15	2,11	204589_at
SCAMP3	10067	G1_2	up	2,13	2,1	201771_at
C1orf37	92703	G1_2	up	2,1	2,12	212165_at
UXS1	80146	G1_2	up	2,06	2,19	219675_s_at
CHKA	1119	G1_2	up	2,06	2,16	204266_s_at;204233_s_at
C2orf33	56947	G1_2	up	2,03	2,19	219137_s_at
MKKS	8195	G1_2	up	2,02	2,14	218138_at
HSPA14	51182	G1_2	up	2,02	2,04	219212_at
KIAA1078	23271	G1_2	up	2,02	2,03	217196_s_at;212765_at
GSTA3	2940	G1_2	down	0,47	0,47	222102_at
GCKR	2646	G1_2	down	0,41	0,49	206867_at
HGD	3081	G1_2	down	0,41	0,33	214308_s_at;214307_at;205221_at
PIK3C2G	5288	G1_2	down	0,4	0,5	215129_at
HLF	3131	G1_2	down	0,4	0,2	204754_at;204753_s_at
QDPR	5860	G1_2	down	0,36	0,45	209123_at
FAM13A1	10144	G1_2	down	0,34	0,45	202972_s_at;217047_s_at
FAH	2184	G1_2	down	0,31	0,48	202862_at
IHLA3	11147	G1_2	down	0,29	0,5	220387_s_at
MTCBP-1	55256	G1_2	down	0,28	0,34	217761_at
ACSL5	51703	G1_2	down	0,27	0,29	218322_s_at
RPIB9	154661	G1_2	down	0,21	0,41	215321_at
TSK	25987	G1_2	down	0,21	0,23	218245_at
ABCG2	9429	G1_2	down	0,19	0,29	209735_at
FTHFD	10840	G1_2	down	0,18	0,19	205208_at;215798_at

Gene Symbol	Entrez Gene	specificity	up_down	G2/n	Probe set
NAV3	89795	G2	up	6,15	204823_at
ENPP2	5168	G2	up	3,71	209392_at;210839_s_at
AF1Q	10962	G2	up	3,64	211071_s_at
EPHA1	2041	G2	up	3,54	205977_s_at
MEIS2	4212	G2	up	2,92	207480_s_at
DEGS	8560	G2	up	2,81	207431_s_at;209250_at
RRAS2	22800	G2	up	2,78	208456_s_at;212590_at;212589_at
CD58	965	G2	up	2,76	211744_s_at;216942_s_at
INHBB	3625	G2	up	2,7	205258_at
MOSPD1	56180	G2	up	2,7	218853_s_at
AMIGO2	347902	G2	up	2,64	222108_at
MCTP1	79772	G2	up	2,51	220122_at
MOAP1	64112	G2	up	2,48	212508_at
ALDOC	230	G2	up	2,44	202022_at
KLHL7	55975	G2	up	2,41	220239_at;220238_s_at
SATB2	23314	G2	up	2,35	213435_at;215591_at
KIF14	9928	G2	up	2,33	206364_at
FHOD3	80206	G2	up	2,25	218980_at
FLJ10357	55701	G2	up	2,18	220326_s_at;58780_s_at
HIP1	3092	G2	up	2,15	205425_at
RPN2	6185	G2	up	2,11	208689_s_at
SDF2L1	23753	G2	up	2,09	218681_s_at
DKFZP434B168	25896	G2	up	2,08	218783_at;222250_s_at
SLC2A6	11182	G2	up	2,08	220091_at
ITGA5	3678	G2	up	2,06	201389_at
SAP130	79595	G2	up	2,03	220367_s_at
TMEM4	10330	G2	up	2	209797_at;209796_s_at;202857_at
LOC157567	157567	G2	down	0,47	212731_at

Gene Symbol	Entrez Gene	specificity	up_down	G2/n	G3/n	Probe set
IMP-3	10643	G2_3	up	5,94	6,05	203820_s_at;203819_s_at;216493_s_at
SFN	2810	G2_3	up	2,67	5,36	33322_i_at;209260_at;33323_r_at
PKM2	5315	G2_3	up	2,78	4,78	201251_at
TFPI	7035	G2_3	up	2,7	3,9	215447_at;214378_at;210665_at
DLG7	9787	G2_3	up	2,66	3,83	203764_at
UBE2S	27338	G2_3	up	3,37	3,78	202779_s_at
TUBG1	7283	G2_3	up	2,33	3,6	201714_at
SLC38A1	81539	G2_3	up	3,17	3,44	218237_s_at
TYMS	7298	G2_3	up	2,77	3,37	202589_at
BUB1B	701	G2_3	up	2,01	3,37	203755_at
ECT2	1894	G2_3	up	2,36	3,36	219787_s_at
NEK2	4751	G2_3	up	2,55	3,31	211080_s_at;204641_at
NPC1	4864	G2_3	up	2,49	3,31	202679_at
KIF4A	24137	G2_3	up	2	3,2	218355_at
RRAGD	58528	G2_3	up	3,31	3,18	221524_s_at;221523_s_at
MLF1IP	79682	G2_3	up	2,84	3,11	218883_s_at
TFRC	7037	G2_3	up	2,57	3,08	207332_s_at
MCM2	4171	G2_3	up	2,21	3,08	202107_s_at
XK	7504	G2_3	up	2,55	3,05	206698_at
USP1	7398	G2_3	up	2,22	3	202413_s_at;202412_s_at
C14orf109	26175	G2_3	up	3,22	2,95	213246_at
H2AFZ	3015	G2_3	up	2,32	2,91	213911_s_at;200853_at
CENPA	1058	G2_3	up	2,75	2,87	204962_s_at
SLC26A2	1836	G2_3	up	2,29	2,83	205097_at
SLC39A6	25800	G2_3	up	2,18	2,8	202088_at;202089_s_at
IARS	3376	G2_3	up	2,33	2,72	204744_s_at

SMC2L1	10592	G2_3	up	2,11	2,57	204240_s_at
SMARCA3	6596	G2_3	up	2,91	2,47	202983_s_at
ASK	10926	G2_3	up	2,14	2,46	204244_s_at
FEN1	2237	G2_3	up	2,41	2,43	204768_s_at;204767_s_at
MCM6	4175	G2_3	up	2,11	2,43	201930_s_at
PTK9	5756	G2_3	up	2,23	2,42	201745_at;214007_s_at
LOC56901	56901	G2_3	up	2,02	2,39	218484_s_at
ARFGEF2	10564	G2_3	up	2,62	2,37	218098_at;215931_s_at
JJAZ1	23512	G2_3	up	2,39	2,37	212287_at;213971_s_at
OIP5	11339	G2_3	up	2,21	2,37	213599_s_at
DDOST	1650	G2_3	up	2,09	2,37	208675_s_at
NARF	26502	G2_3	up	2,03	2,34	219862_s_at
MKI67	4288	G2_3	up	2,02	2,3	212022_s_at;212023_s_at;212021_s_at;212020_s_at
UPF3B	65109	G2_3	up	2,18	2,28	218757_s_at
COCH	1690	G2_3	up	4,09	2,25	205229_s_at
CCNE2	9134	G2_3	up	2	2,25	211814_s_at;205034_at
MCM3	4172	G2_3	up	2,07	2,22	201555_s_at
SLBP	7884	G2_3	up	2,04	2,21	206052_s_at
PTHR2	5746	G2_3	up	2,96	2,2	206772_s_at
ABCG1	9619	G2_3	up	2,43	2,17	204567_s_at;211113_s_at
RRM1	6240	G2_3	up	2,14	2,17	201476_s_at;201477_s_at
ARPC1A	10552	G2_3	up	2,02	2,17	200950_s_at
LOC55974	55974	G2_3	up	2,15	2,16	219125_s_at
KIAA0100	9703	G2_3	up	2,13	2,13	201729_s_at
DNAJC6	9829	G2_3	up	2	2,07	204720_s_at
MAPK1	5594	G2_3	up	2,13	2,06	212271_at;208351_s_at
C2orf4	51072	G2_3	up	2,24	2	219065_s_at
STARD5	80765	G2_3	down	0,5	0,44	213820_s_at
PTHR1	5745	G2_3	down	0,5	0,44	205911_s_at
ACO1	48	G2_3	down	0,5	0,42	207071_s_at
SORD	6652	G2_3	down	0,44	0,42	201563_at;201562_s_at
CG018	90634	G2_3	down	0,47	0,39	213375_s_at
PDE2A	5138	G2_3	down	0,45	0,38	204134_s_at
COBLL1	22837	G2_3	down	0,47	0,37	211032_at;203642_s_at;203641_s_at;215393_s_at
RAMP3	10268	G2_3	down	0,45	0,36	205326_s_at
CDO1	1036	G2_3	down	0,42	0,33	204154_s_at
SERPINF2	5345	G2_3	down	0,34	0,26	205075_s_at

Gene Symbol	Entrez Gene	specificity	up_down	G3/n	Probe set
G6PD	2539	G3	up	5,53	202275_at
HN1	51155	G3	up	3,74	217755_at
PFN2	5217	G3	up	3,52	204992_s_at
NDRG1	10397	G3	up	3,36	200632_s_at
PHB	5245	G3	up	3,3	200658_s_at;200659_s_at
MAD2L1	4085	G3	up	3,21	203362_s_at
NRAS	4893	G3	up	3,17	202647_s_at;202646_s_at
ENO1	2023	G3	up	3,1	201231_s_at;217294_s_at
NME1	4830	G3	up	3,06	201577_at
HCAP-G	64151	G3	up	2,97	218663_at;218662_s_at
TRIP13	9319	G3	up	2,9	204033_at
PAPOLA	10914	G3	up	2,89	209388_at;212720_at;212718_at;222035_s_at
POLR2K	5440	G3	up	2,87	202635_s_at
CGI-48	51096	G3	up	2,78	203721_s_at
PHLDA2	7262	G3	up	2,77	209803_s_at
TCEB1	6921	G3	up	2,74	202824_s_at
CCNA2	890	G3	up	2,73	203418_at;213226_at
GMFB	2764	G3	up	2,69	202544_at;202543_s_at
CGI-141	51026	G3	up	2,66	218193_s_at

TTK	7272	G3	up	2,66	204822_at
TBL1XR1	79718	G3	up	2,63	221428_s_at
HMMR	3161	G3	up	2,61	207165_at;209709_s_at
PGD	5226	G3	up	2,61	201118_at
P15RS	55197	G3	up	2,58	218209_s_at
PDCD2	5134	G3	up	2,58	213581_at;213585_s_at
USP14	9097	G3	up	2,58	201672_s_at
FAM11B	79134	G3	up	2,57	219253_at
UCK2	7371	G3	up	2,57	209825_s_at
CDC6	990	G3	up	2,56	203967_at;203968_s_at
ARPP-19	10776	G3	up	2,54	214553_s_at;221482_s_at
LRP12	29967	G3	up	2,54	219631_at;220253_s_at;220254_at
MMD	23531	G3	up	2,54	203414_at
BOP1	23246	G3	up	2,53	216397_s_at;212563_at
NME2	4831	G3	up	2,53	201268_at
RIT1	6016	G3	up	2,53	209882_at
HIST2H2BE	8349	G3	up	2,52	202708_s_at
SLC38A6	145389	G3	up	2,52	214830_at
C1orf39	54874	G3	up	2,51	215017_s_at
DR1	1810	G3	up	2,5	216652_s_at;209187_at;216653_at
KIAA0196	9897	G3	up	2,5	201985_at
KNTC2	10403	G3	up	2,5	204162_at
TPD52	7163	G3	up	2,48	201690_s_at;201688_s_at
SLC16A3	9123	G3	up	2,47	202855_s_at;202856_s_at
FLJ20485	54517	G3	up	2,46	218984_at
KNS2	3831	G3	up	2,45	212877_at;213656_s_at;212878_s_at
PSME3	10197	G3	up	2,44	200988_s_at;209853_s_at
RAD21	5885	G3	up	2,43	200607_s_at;200608_s_at
BUB1	699	G3	up	2,42	209642_at
RBM28	55131	G3	up	2,42	218593_at
SKB1	10419	G3	up	2,39	217786_at
KIF2	3796	G3	up	2,38	203087_s_at
GTF3C3	9330	G3	up	2,37	218343_s_at
EDD	51366	G3	up	2,37	208884_s_at;208883_at;208882_s_at
PGK1	5230	G3	up	2,36	217356_s_at;200737_at;200738_s_at
PRIM1	5557	G3	up	2,36	205053_at
TXN	7295	G3	up	2,36	208864_s_at
FLJ12443	79888	G3	up	2,35	201818_at
CLIC1	1192	G3	up	2,34	208659_at
FLJ10204	55093	G3	up	2,34	219060_at
ITGB1BP1	9270	G3	up	2,34	203336_s_at
RPL8	6132	G3	up	2,34	200936_at
KPNB1	3837	G3	up	2,33	213507_s_at;208975_s_at
ACTL6A	86	G3	up	2,33	202666_s_at
UGCG	7357	G3	up	2,33	221765_at;204881_s_at
WDR12	55759	G3	up	2,33	218512_at
NUP155	9631	G3	up	2,32	206550_s_at
CCT4	10575	G3	up	2,32	200877_at
CCT5	22948	G3	up	2,32	208696_at
SLC7A1	6541	G3	up	2,31	212295_s_at;212290_at
C1orf33	51154	G3	up	2,29	220688_s_at
CNAP1	9918	G3	up	2,29	201774_s_at
FLJ10407	55706	G3	up	2,29	218073_s_at
IPO7	10527	G3	up	2,29	200993_at;200992_at;200994_at;200995_at
GPR172A	79581	G3	up	2,28	222155_s_at
TGIF	7050	G3	up	2,28	203313_s_at
GLA	2717	G3	up	2,28	214430_at
DKFZP586L0724	25926	G3	up	2,27	221970_s_at
PC4	10923	G3	up	2,27	214512_s_at
SRI	6717	G3	up	2,27	208921_s_at

EZH2	2146	G3	up	2,26	203358_s_at
MELK	9833	G3	up	2,26	204825_at
TPD52L2	7165	G3	up	2,26	201379_s_at
USP3	9960	G3	up	2,26	221654_s_at
CCT2	10576	G3	up	2,24	201946_s_at;201947_s_at
COIL	8161	G3	up	2,24	203653_s_at;203654_s_at
KIF2C	11004	G3	up	2,24	211519_s_at;209408_at
CKLF	51192	G3	up	2,23	219161_s_at;221058_s_at
TRIM31	11074	G3	up	2,23	210159_s_at;215444_s_at;208170_s_at
EBNA1BP2	10969	G3	up	2,22	201323_at
MARCKS	4082	G3	up	2,22	201670_s_at;201669_s_at
ARPC4	10093	G3	up	2,21	217818_s_at;211672_s_at
DDX48	9775	G3	up	2,21	201303_at
TEBP	10728	G3	up	2,21	200627_at
NUP107	57122	G3	up	2,2	218768_at
ADSL	158	G3	up	2,2	202144_s_at
FXR1	8087	G3	up	2,2	201637_s_at;201635_s_at
NUP37	79023	G3	up	2,2	218622_at
PPARBP	5469	G3	up	2,2	203497_at
EIF3S3	8667	G3	up	2,19	201592_at
EVA1	10205	G3	up	2,18	203780_at;203779_s_at
PLOD2	5352	G3	up	2,18	202619_s_at;202620_s_at
RBBP4	5928	G3	up	2,18	210371_s_at
SNRPA1	6627	G3	up	2,18	206055_s_at;215722_s_at
DKC1	1736	G3	up	2,17	201479_at;216212_s_at;201478_s_at
PRO1855	55379	G3	up	2,17	222231_s_at
DUSP3	1845	G3	up	2,16	201538_s_at;201537_s_at
EIF3S9	8662	G3	up	2,16	211501_s_at
COPS5	10987	G3	up	2,15	201652_at
WDR45L	56270	G3	up	2,15	209076_s_at
ANP32E	81611	G3	up	2,14	221505_at;208103_s_at
C22orf18	79019	G3	up	2,14	218741_at
LANCL1	10314	G3	up	2,14	202020_s_at
SMC1L1	8243	G3	up	2,14	201589_at
UBE2V2	7336	G3	up	2,14	209096_at
HNRPR	10236	G3	up	2,13	208766_s_at;208765_s_at
NPEPPS	9520	G3	up	2,13	201454_s_at;201455_s_at
PAK1IP1	55003	G3	up	2,13	218886_at
AGA	175	G3	up	2,12	216064_s_at;204333_s_at
BRD7	29117	G3	up	2,12	221776_s_at
CANT1	124583	G3	up	2,12	46323_at;221732_at
EIF2S1	1965	G3	up	2,12	201144_s_at;201142_at
PPP1CC	5501	G3	up	2,12	200726_at
PSMD14	10213	G3	up	2,12	212296_at
TXNDC	81542	G3	up	2,12	208097_s_at;209476_at
JMJD1A	55818	G3	up	2,11	212689_s_at
SCYE1	9255	G3	up	2,11	202541_at;202542_s_at
HGS	9146	G3	up	2,1	210428_s_at
MGC2574	79080	G3	up	2,1	203119_at
MRPL42	28977	G3	up	2,1	217919_s_at
SEC61G	23480	G3	up	2,1	203484_at
SRM	6723	G3	up	2,1	201516_at
TSN	7247	G3	up	2,1	201504_s_at;201513_at;201515_s_at
ACACA	31	G3	up	2,09	212186_at
MAPRE1	22919	G3	up	2,09	200713_s_at;200712_s_at
PRKAR1A	5573	G3	up	2,09	200605_s_at;200604_s_at;200603_at
PSMC4	5704	G3	up	2,09	201252_at
PWP1	11137	G3	up	2,09	201606_s_at;201608_s_at
STMN1	3925	G3	up	2,09	200783_s_at
VMP1	81671	G3	up	2,09	220990_s_at

PSMD11	5717	G3	up	2,08	208777_s_at
TOPBP1	11073	G3	up	2,08	202633_at
KIF1B	23095	G3	up	2,08	209234_at
SMAD2	4087	G3	up	2,08	203077_s_at;203076_s_at;203075_at
CASC3	22794	G3	up	2,07	207842_s_at
CGI-121	51002	G3	up	2,07	219030_at
DDEF1	50807	G3	up	2,07	221039_s_at
DKFZp762E1312	55355	G3	up	2,07	218726_at
FLJ10036	55055	G3	up	2,07	218349_s_at
FLJ10458	54475	G3	up	2,07	203867_s_at;203866_at
FLJ20516	54962	G3	up	2,07	219258_at
C14orf10	55012	G3	up	2,06	218852_at
EML4	27436	G3	up	2,06	220386_s_at
KIAA0090	23065	G3	up	2,06	215991_s_at;212395_s_at;212396_s_at
PSMC6	5706	G3	up	2,06	201699_at
SNRPD2	6633	G3	up	2,06	200826_at
SNX7	51375	G3	up	2,06	205573_s_at
DHX15	1665	G3	up	2,05	201385_at;201386_s_at
GNB1	2782	G3	up	2,05	200744_s_at;200746_s_at;200745_s_at
HCNGP	29115	G3	up	2,05	217965_s_at
MASA	58478	G3	up	2,05	217956_s_at
PIGF	5281	G3	up	2,05	205078_at;205077_s_at
RFC3	5983	G3	up	2,05	204128_s_at;204127_at
TACC3	10460	G3	up	2,05	218308_at
XPO1	7514	G3	up	2,04	208775_at
CBX3	11335	G3	up	2,04	201091_s_at;200037_s_at
FLJ11193	55322	G3	up	2,04	203738_at
MPV17	4358	G3	up	2,04	203466_at
NARS	4677	G3	up	2,04	200027_at
NEUGRIN	51335	G3	up	2,04	217722_s_at
NSF	4905	G3	up	2,04	202395_at
CSNK1D	1453	G3	up	2,03	207945_s_at;208774_at
FLJ10587	55181	G3	up	2,03	218514_at
FLJ10719	55215	G3	up	2,03	213007_at;213008_at
NS	26354	G3	up	2,03	217850_at
PTP4A2	8073	G3	up	2,03	216988_s_at;208617_s_at;208616_s_at;208615_s_at
TAF2	6873	G3	up	2,03	209523_at
TDG	6996	G3	up	2,03	203743_s_at;203742_s_at
DNAJC10	54431	G3	up	2,02	221781_s_at;221782_at
PTBP2	58155	G3	up	2,02	218683_at
XAB1	11321	G3	up	2,01	209313_at
FTH1	2495	G3	up	2,01	200748_s_at
RANBP5	3843	G3	up	2	211954_s_at;211953_s_at;211952_at;211955_at
ATIC	471	G3	up	2	208758_at
C10orf3	55165	G3	up	2	218542_at
CYB5-M	80777	G3	up	2	201633_s_at;201634_s_at
FAM50A	9130	G3	up	2	203262_s_at
PLEKHF2	79666	G3	up	2	218640_s_at
RAD51AP1	10635	G3	up	2	204146_at
THRAP4	9862	G3	up	2	213043_s_at
C16orf30	79652	G3	down	0,49	219315_s_at
FXYD6	53826	G3	down	0,49	217897_at
GIMAP5	55340	G3	down	0,49	64064_at;218805_at
SMARCA2	6595	G3	down	0,49	206542_s_at
ALAD	210	G3	down	0,48	218487_at;218489_s_at
COX7A1	1346	G3	down	0,48	204570_at
PRG2	5553	G3	down	0,48	211743_s_at
ACADVL	37	G3	down	0,47	200710_at
FLJ20699	55020	G3	down	0,47	218272_at;216434_at
MAT2A	4144	G3	down	0,47	200768_s_at;200769_s_at;213705_at

CA5A	763	G3	down	0,46	207421_at
PIK3R1	5295	G3	down	0,46	212239_at;212240_s_at;212249_at
MASP1	5648	G3	down	0,45	210680_s_at;206449_s_at
SELENBP1	8991	G3	down	0,45	214433_s_at
TENC1	23371	G3	down	0,45	212494_at
TMPRSS6	164656	G3	down	0,45	214955_at
AGTRL1	187	G3	down	0,44	213592_at
FMO4	2329	G3	down	0,44	206263_at
TNXB	7148	G3	down	0,44	216339_s_at;208609_s_at
C10orf56	219654	G3	down	0,44	212423_at;212419_at
SLC25A20	788	G3	down	0,43	203658_at
TF	7018	G3	down	0,41	214064_at;214063_s_at
SARDH	1757	G3	down	0,41	210862_s_at;211322_s_at;210063_at
ECHS1	1892	G3	down	0,4	201135_at
LR8	28959	G3	down	0,4	220532_s_at
PCSK6	5046	G3	down	0,4	207414_s_at;211262_at
MGMT	4255	G3	down	0,39	204880_at
CRYL1	51084	G3	down	0,38	220753_s_at
TST	7263	G3	down	0,38	209605_at
GAMT	2593	G3	down	0,37	205354_at
CPN2	1370	G3	down	0,36	216223_at
CFHL1	3078	G3	down	0,35	215388_s_at
CYP27A1	1593	G3	down	0,35	203979_at
ALDH5A1	7915	G3	down	0,34	203609_s_at;203608_at
FLJ20605	54996	G3	down	0,34	221636_s_at;219527_at
ARGBP2	8470	G3	down	0,33	204288_s_at
F7	2155	G3	down	0,33	207300_s_at
COL18A1	80781	G3	down	0,32	209082_s_at;209081_s_at
GPLD1	2822	G3	down	0,32	206264_at;215554_at;206265_s_at;206266_at
SERPING1	710	G3	down	0,32	200986_at
SLC38A3	10991	G3	down	0,32	205972_at
RARRES2	5919	G3	down	0,31	209496_at
IFIT1	3434	G3	down	0,29	203153_at
ACAT1	38	G3	down	0,28	205412_at
ASGR2	433	G3	down	0,28	206130_s_at
CPB2	1361	G3	down	0,28	206651_s_at
PON1	5444	G3	down	0,27	206344_at;206345_s_at
DCL-1	9936	G3	down	0,26	203799_at
DHTKD1	55526	G3	down	0,26	209916_at
SERPINF1	5176	G3	down	0,2	202283_at
KNG1	3827	G3	down	0,18	206054_at
SLC2A2	6514	G3	down	0,18	206535_at

Gene Symbol	Entrez Gene	specificity	up_down	G1/n	G2/n	G3/n	G4/n	G5/n	G6/n	Probe set
CD24	934	G123	up	10,22	4,7	5,26	1,58	1,66	0,32	208650_s_at;266_s_at;209772_s_at
KPNA2	3838	G123	up	2,06	2,97	4,42	1,47	1,85	1,47	211762_s_at;201088_at
PEG10	23089	G123	up	26,27	7,58	4,11	1,62	1,66	1,3	212094_at;212092_at
FABP5	2171	G123	up	2,28	2,56	4,09	1,73	1,28	1,82	202345_s_at
PLCB1	23236	G123	up	2,77	5,49	3,91	1,67	1,18	1,69	211925_s_at;213222_at
KIAA0186	9837	G123	up	2,76	2,57	3,65	1,3	1,88	1,34	206102_at
PRKDC	5591	G123	up	2,2	2,25	3,61	1,55	1,61	1,98	215757_at;208694_at;210543_s_at
PNMA1	9240	G123	up	2,83	2,95	3,55	1,13	0,8	0,95	218224_at
RFC4	5984	G123	up	2,84	3,21	3,47	1,5	1,76	1,48	204023_at
CBX1	10951	G123	up	2,65	2,62	3,35	1,42	1,47	1,51	201518_at
ATAD2	29028	G123	up	3,38	2,5	3,32	1,63	1,5	1,75	218782_s_at
CPD	1362	G123	up	3,9	3,24	3,14	1,35	1,49	1,54	201941_at;201943_s_at;201940_at;201942_s_at
SMC4L1	10051	G123	up	2,4	3,36	3,07	1,45	1,6	1,46	201664_at;201663_s_at
RBM3	5935	G123	up	3,09	3	3	1,85	1,83	1,42	208319_s_at

CCT3	7203	G123	up	3,12	2,06	2,94	1,68	1,83	1,8	200910_at
KIF20A	10112	G123	up	2	2	2,8	1,3	1,8	1,57	218755_at
SNRPD1	6632	G123	up	2,02	2,02	2,79	1,17	1,35	1	202690_s_at;202691_at
ACLY	47	G123	up	2,02	2,07	2,75	1,6	1,31	1,65	201127_s_at;201128_s_at;210337_s_at
MRPL9	65005	G123	up	2,94	2,34	2,72	1,68	1,76	1,65	209609_s_at;211594_s_at
CCNB2	9133	G123	up	2,07	2,55	2,67	1,22	1,8	1,38	202705_at
SHC1	6464	G123	up	2,12	2,4	2,59	1,55	1,48	1,88	214853_s_at;201469_s_at
ENAH	55740	G123	up	2,76	2,19	2,58	1,54	1,09	0,96	217820_s_at
FLJ12442	64943	G123	up	3,95	3	2,55	1,2	1,6	1,83	218051_s_at
HSU79266	29901	G123	up	2,49	2,22	2,53	1,21	1,48	1,32	205449_at
BARD1	580	G123	up	2,17	2,4	2,5	1,45	1,63	1,22	205345_at
HAT1	8520	G123	up	2,12	2,11	2,38	1,37	1,53	1,3	203138_at
TUFT1	7286	G123	up	3,03	2,12	2,36	1,43	1,25	1,37	205807_s_at
CPSF6	11052	G123	up	2,42	2,35	2,35	1,36	1,25	1,28	202469_s_at;202470_s_at
KIAA0217	23185	G123	up	2,09	2,03	2,26	1,55	1,65	1,22	208952_s_at;208953_at;208954_s_at
M11S1	4076	G123	up	2,01	2	2,23	1,44	1,56	1,55	200723_s_at;200722_s_at
PRKCI	5584	G123	up	2,29	2,09	2,21	1,4	1,36	1,01	209678_s_at;213518_at;209677_at
UBAP2L	9898	G123	up	2,23	2	2,2	1,47	1,62	1,77	201378_s_at;201377_at
DUSP12	11266	G123	up	2,51	2,07	2,18	1,63	1,75	1,48	218576_s_at
SGCE	8910	G123	up	6,93	3,94	2,16	1,52	1,27	0,76	204688_at
SIP	27101	G123	up	2,3	2,03	2,16	1,44	1,64	1,5	210691_s_at;211761_s_at
VIL1	7429	G123	up	6	4,89	2,15	1,28	1,98	1,1	205506_at
C1orf9	51430	G123	up	2,5	2,02	2,14	1,49	1,55	1,55	203429_s_at
SNRPE	6635	G123	up	3,06	2,46	2,13	1,64	1,84	1,65	203316_s_at
SNRPB	6628	G123	up	2,09	2,06	2,13	1,22	1,47	1,11	213175_s_at;208821_at
FLJ12671	81875	G123	up	2,51	2,17	2,12	1,47	1,48	1,44	216502_at;212766_s_at;208114_s_at
CKAP4	10970	G123	up	2,88	3,25	2,07	1,15	1,18	1,65	200999_s_at;200998_s_at
TMPO	7112	G123	up	2,06	2,06	2,06	1,3	1,62	1,27	203432_at;209754_s_at
MAP4K3	8491	G123	up	2,2	2	2,03	1,33	1,13	1	218311_at
PON2	5445	G123	up	2,08	2,27	2,01	1,42	1,56	1,36	210830_s_at;201876_at
POGK	57645	G123	up	2,52	2,29	2	1,36	1,43	1,48	218229_s_at
PRODH2	58510	G123	down	0,32	0,44	0,49	0,53	0,91	0,59	216696_s_at
HADHSC	3033	G123	down	0,34	0,47	0,48	0,89	0,83	1,31	201036_s_at;211569_s_at;201035_s_at
SLAC2-B	23086	G123	down	0,38	0,45	0,47	0,83	0,78	2,05	214734_at
GOT2	2806	G123	down	0,43	0,36	0,47	0,74	0,68	0,55	200708_at
MLYCD	23417	G123	down	0,48	0,48	0,46	0,72	0,95	0,96	218869_at
ASPA	443	G123	down	0,39	0,46	0,46	0,81	0,73	0,58	206030_at
SLC28A1	9154	G123	down	0,4	0,45	0,46	0,91	0,64	0,62	207560_at
EPHX2	2053	G123	down	0,22	0,47	0,45	0,72	0,72	0,59	209368_at
ECM2	1842	G123	down	0,41	0,47	0,42	0,89	1,05	2,18	206101_at
MTHFD1	4522	G123	down	0,19	0,42	0,42	0,62	0,92	1,02	202309_at
NR1I2	8856	G123	down	0,37	0,36	0,42	0,98	0,69	0,68	207203_s_at;207202_s_at
HYAL1	3373	G123	down	0,21	0,5	0,41	0,77	0,82	0,85	210619_s_at
TNFRSF6	355	G123	down	0,4	0,39	0,41	0,6	0,67	1,22	204780_s_at;204781_s_at
SLC16A2	6567	G123	down	0,33	0,46	0,4	0,79	0,8	1,02	204462_s_at
ETNK2	55224	G123	down	0,35	0,45	0,39	0,82	0,9	0,87	219268_at
ACAA2	10449	G123	down	0,35	0,35	0,38	0,71	0,73	0,72	202002_at;202003_s_at
RCL1	10171	G123	down	0,4	0,32	0,38	0,63	0,6	0,69	218544_s_at
GABARAPL1	23710	G123	down	0,32	0,3	0,38	0,57	0,65	0,74	208869_s_at;208868_s_at;211457_at;211458_s_at
F8	2157	G123	down	0,31	0,46	0,36	0,74	0,52	0,77	205756_s_at
SLC25A15	10166	G123	down	0,47	0,42	0,36	0,79	0,86	0,65	218653_at
MSRA	4482	G123	down	0,26	0,37	0,35	0,55	0,58	0,55	219281_at
GRHPR	9380	G123	down	0,33	0,35	0,35	0,59	0,78	0,99	214864_s_at
PSD3	23362	G123	down	0,38	0,48	0,34	0,77	0,56	0,52	203354_s_at;203355_s_at
CBR4	84869	G123	down	0,49	0,44	0,34	0,67	0,66	0,69	213626_at
IF	3426	G123	down	0,38	0,44	0,34	0,69	0,52	0,88	203854_at
FYN	2534	G123	down	0,36	0,38	0,34	0,57	0,52	1,02	210105_s_at;212486_s_at;216033_s_at
DMD	1756	G123	down	0,43	0,47	0,33	0,55	0,75	0,89	207660_at;203881_s_at;208086_s_at
PROZ	8858	G123	down	0,42	0,47	0,31	0,65	0,63	0,58	208034_s_at
SIAT10	10402	G123	down	0,23	0,47	0,31	0,64	0,67	0,86	213335_s_at;213355_at;210942_s_at

FLJ10948	55268	G123	down	0,36	0,39	0,31	0,86	0,68	0,78	218552_at
ALAS1	211	G123	down	0,38	0,36	0,31	0,65	0,95	1,01	205633_s_at
FGA	2243	G123	down	0,49	0,5	0,3	0,72	0,62	0,74	205650_s_at;205649_s_at
ACAA1	30	G123	down	0,31	0,18	0,3	0,52	0,74	0,69	214274_s_at
ETFDH	2110	G123	down	0,25	0,35	0,29	0,61	0,54	0,69	33494_at;205530_at
MAT1A	4143	G123	down	0,39	0,29	0,29	0,55	0,81	0,61	205813_s_at
PCK2	5106	G123	down	0,32	0,5	0,28	0,64	0,77	0,73	202847_at
GCDH	2639	G123	down	0,43	0,41	0,27	0,55	0,83	0,7	203500_at;208369_s_at
ACADL	33	G123	down	0,17	0,29	0,26	0,76	0,52	0,65	206069_s_at;206068_s_at
DCXR	51181	G123	down	0,22	0,28	0,26	0,63	0,92	1,23	217973_at
ITIH4	3700	G123	down	0,39	0,43	0,25	0,66	0,53	0,57	206287_s_at;37201_at
RGN	9104	G123	down	0,5	0,33	0,25	0,73	0,91	0,9	210751_s_at
SEC14L2	23541	G123	down	0,29	0,32	0,25	0,85	1,12	1,52	204541_at
CUTL2	23316	G123	down	0,27	0,27	0,25	0,91	0,59	1,46	213920_at
SLC6A12	6539	G123	down	0,49	0,26	0,25	0,64	1,1	0,84	206058_at
SLC4A4	8671	G123	down	0,22	0,28	0,24	0,6	0,58	0,78	210738_s_at;211494_s_at;203908_at
HRSP12	10247	G123	down	0,27	0,34	0,23	0,7	0,58	0,59	203790_s_at
HAO1	54363	G123	down	0,16	0,3	0,23	0,79	0,83	0,78	220224_at
FLJ20581	54988	G123	down	0,14	0,15	0,13	0,75	0,64	0,89	89977_at;220061_at
SLC27A5	10998	G123	down	0,09	0,18	0,12	0,64	0,74	0,82	219733_s_at
HPD	3242	G123	down	0,07	0,04	0,06	0,79	0,73	1,32	206024_at

Gene Symbol	Entrez Gene	specificity	up_down	G5/n	Probe set						
					2,53	204238_s_at;39817_s_at	2,35	217925_s_at;217924_at;205457_at	2,28	218233_s_at	2,15
C6orf108	10591	G5	up	2,53	204238_s_at;39817_s_at						
C6orf106	64771	G5	up	2,35	217925_s_at;217924_at;205457_at						
C6orf49	29964	G5	up	2,28	218233_s_at						
C6orf82	51596	G5	up	2,15	221488_s_at						
MRPS18B	28973	G5	up	2,12	208907_s_at;217408_at						
ARL7	10123	G5	down	0,5	202207_at;202208_s_at;202206_at						
PELI1	57162	G5	down	0,48	218319_at						
C1orf38	9473	G5	down	0,47	210785_s_at						
STAT1	6772	G5	down	0,46	200887_s_at;209969_s_at						
PTPNS1	140885	G5	down	0,45	202895_s_at;202897_at;202896_s_at						
PTGER4	5734	G5	down	0,44	204897_at						
RAB31	11031	G5	down	0,44	217763_s_at;217764_s_at;217762_s_at						
DAB2	1601	G5	down	0,44	201280_s_at;201279_s_at;201278_at						
IL10RA	3587	G5	down	0,43	204912_at						
CLECSF2	9976	G5	down	0,43	209732_at						
ARHGDI1	397	G5	down	0,43	201288_at						
BCL3	602	G5	down	0,42	204907_s_at;204908_s_at						
S100A11	6282	G5	down	0,42	200660_at						
TGM2	7052	G5	down	0,42	201042_at						
HMGN3	9324	G5	down	0,42	209377_s_at						
WASPIP	7456	G5	down	0,42	202665_s_at;202664_at						
CUGBP2	10659	G5	down	0,4	202156_s_at;202157_s_at						
IFI44	10561	G5	down	0,38	214453_s_at						
ICAM1	3383	G5	down	0,38	202638_s_at;202637_s_at						
KIAA0746	23231	G5	down	0,38	212314_at;212311_at						
EMP3	2014	G5	down	0,38	203729_at						
HLA-DPA1	3113	G5	down	0,36	213537_at;211991_s_at;211990_at						
CYBA	1535	G5	down	0,35	203028_s_at						
LAPTM5	7805	G5	down	0,35	201721_s_at;201720_s_at						
HLA-DPB1	3115	G5	down	0,34	201137_s_at						
VIL2	7430	G5	down	0,34	217234_s_at;208623_s_at;208622_s_at;208621_s_at						
IFI16	3428	G5	down	0,29	208965_s_at;206332_s_at						

Gene Symbol	Entrez Gene	specificity	up_down	G5/n	G6/n	Probe set
PAP	5068	G5_6	up	2,34	64,22	205815_at
SPARCL1	8404	G5_6	up	3,25	10,77	200795_at
GLUL	2752	G5_6	up	3,28	8,2	217202_s_at;200648_s_at;215001_s_at
LAMA3	3909	G5_6	up	2,43	6,88	203726_s_at
TBX3	6926	G5_6	up	2,2	4,79	219682_s_at
RHBG	57127	G5_6	up	2,63	4,13	220510_at
SMYD2	56950	G5_6	up	2,6	3,45	212922_s_at;212921_at
FLJ11151	55313	G5_6	up	2,6	2,84	218610_s_at
DUT	1854	G5_6	up	2	2,73	208955_at;209932_s_at
DPP4	1803	G5_6	up	2,29	2,63	211478_s_at;203717_at;203716_s_at
HIST1H2BK	85236	G5_6	up	2,08	2,39	209806_at
NEDD4	4734	G5_6	up	2,03	2	213012_at
NCALD	83988	G5_6	down	0,5	0,48	211685_s_at
BHLHB2	8553	G5_6	down	0,49	0,47	201169_s_at;201170_s_at
QSCN6	5768	G5_6	down	0,47	0,45	201482_at
THBS2	7058	G5_6	down	0,38	0,45	203083_at
RAB27A	5873	G5_6	down	0,49	0,44	209515_s_at;209514_s_at
HPS5	11234	G5_6	down	0,48	0,42	204544_at
AGPAT2	10555	G5_6	down	0,49	0,4	32837_at;210678_s_at
TRIB1	10221	G5_6	down	0,42	0,39	202241_at
VNN3	55350	G5_6	down	0,48	0,37	220528_at
IL4R	3566	G5_6	down	0,41	0,37	203233_at
LGALS3BP	3959	G5_6	down	0,14	0,37	200923_at
PLD1	5337	G5_6	down	0,43	0,36	205203_at;177_at;215723_s_at
F2RL1	2150	G5_6	down	0,39	0,35	213506_at
MAFF	23764	G5_6	down	0,45	0,33	36711_at;205193_at
CTGF	1490	G5_6	down	0,32	0,32	209101_at
IER3	8870	G5_6	down	0,3	0,26	201631_s_at
NAV2	89797	G5_6	down	0,49	0,2	218330_s_at

Gene Symbol	Entrez Gene	specificity	up_down	G6/n	Probe set
REG1A	5967	G6	up	9,81	209752_at
C1QTNF3	114899	G6	up	9,58	220988_s_at
CTNNA2	1496	G6	up	7,84	205373_at
LEF1	51176	G6	up	6,17	221558_s_at;221557_s_at;210948_s_at
RHOBTB1	9886	G6	up	5,47	212651_at
MME	4311	G6	up	5	203435_s_at;203434_s_at
ACTN2	88	G6	up	4,51	203863_at;203864_s_at;203862_s_at;203861_s_at
GGH	8836	G6	up	4,4	203560_at
SLC22A11	55867	G6	up	4,08	220100_at
DNCI1	1780	G6	up	3,87	205348_s_at
C6orf97	80129	G6	up	3,7	220581_at
SLC22A4	6583	G6	up	3,58	205896_at
SLC6A2	6530	G6	up	3,47	216610_at;215715_at;216611_s_at;210353_s_at
COL7A1	1294	G6	up	3,46	204136_at;217312_s_at
MERTK	10461	G6	up	3,38	206028_s_at;211913_s_at
FLJ20315	54894	G6	up	3,21	218704_at
PNUTL2	5414	G6	up	3,07	210657_s_at
FLJ10706	55732	G6	up	3	220840_s_at
TRIB2	28951	G6	up	2,96	202478_at;202479_s_at
GREB1	9687	G6	up	2,92	205862_at
ASPSCR1	79058	G6	up	2,88	218908_at
CGI-116	51019	G6	up	2,68	218628_at
FLJ21963	79611	G6	up	2,66	219616_at
SLC5A6	8884	G6	up	2,63	204087_s_at
FLJ20421	54928	G6	up	2,55	218516_s_at

BMP4	652	G6	up	2,54	211518_s_at
LGALS8	3964	G6	up	2,53	208935_s_at;208934_s_at;210732_s_at;208933_s_at;210731_s_at
CGI-51	25813	G6	up	2,52	201570_at;201569_s_at
LPIN1	23175	G6	up	2,52	212274_at;212276_at;212272_at
ZNF238	10472	G6	up	2,52	207164_s_at;212774_at
CTNNBL1	56259	G6	up	2,51	221021_s_at
C7orf32	155066	G6	up	2,5	213587_s_at
BCAP31	10134	G6	up	2,48	200837_at
UGCGL1	56886	G6	up	2,47	218257_s_at
KIAA0152	9761	G6	up	2,45	200616_s_at;200617_at
TCEAL1	9338	G6	up	2,45	204045_at
ACSL6	23305	G6	up	2,44	211207_s_at;213683_at
NEK3	4752	G6	up	2,43	213116_at;211089_s_at
SLC13A3	64849	G6	up	2,39	205244_s_at;205243_at
TTC9	23508	G6	up	2,38	213172_at;213174_at
TIMM17A	10440	G6	up	2,36	201822_at;201821_s_at;215171_s_at
NPR2	4882	G6	up	2,35	204310_s_at
CBR1	873	G6	up	2,32	209213_at
HEXA	3073	G6	up	2,32	201765_s_at;215155_at
YPEL1	29799	G6	up	2,29	213996_at
RAB4A	5867	G6	up	2,28	203582_s_at;203581_at
C9orf99	84263	G6	up	2,25	209512_at;209513_s_at
ITPR2	3709	G6	up	2,24	202660_at;202662_s_at;211360_s_at;202661_at
PREB	10113	G6	up	2,24	217861_s_at
THSD1P	374500	G6	up	2,22	219477_s_at
CRYZ	1429	G6	up	2,16	202950_at
FBXL5	26234	G6	up	2,16	209005_at;209004_s_at
SIAH2	6478	G6	up	2,16	209339_at
KIAA0779	23023	G6	up	2,14	213352_at;213351_s_at;213349_at
GALNT1	2589	G6	up	2,11	201724_s_at;201723_s_at
SULT4A1	25830	G6	up	2,08	219425_at
MIR	220972	G6	up	2,06	221824_s_at
C10orf72	196740	G6	up	2,04	213381_at
PANX1	24145	G6	up	2,04	204715_at
PARVB	29780	G6	up	2,04	37965_at;216253_s_at;216254_at;204629_at;37966_at
AP3S1	1176	G6	up	2,04	202442_at
TBCA	6902	G6	up	2,04	203667_at
FHIT	2272	G6	up	2,02	206492_at
KIAA0143	23167	G6	up	2,01	212149_at;212150_at
TMEM2	23670	G6	up	2	218113_at
VSNL1	7447	G6	up	2	203797_at;203798_s_at
EIF2C2	27161	G6	down	0,49	222294_s_at;213310_at
LOC51760	51760	G6	down	0,49	205613_at
NUP98	4928	G6	down	0,49	210793_s_at
RAFTLIN	23180	G6	down	0,46	215630_at;212646_at
HES1	3280	G6	down	0,45	203393_at;203394_s_at;203395_s_at
LDLR	3949	G6	down	0,45	202068_s_at;217103_at
OSBPL9	114883	G6	down	0,45	218047_at
TRIM15	89870	G6	down	0,45	210885_s_at;210177_at;36742_at
CKLFSF6	54918	G6	down	0,44	217947_at
INPP1	3628	G6	down	0,44	202794_at
RRBP1	6238	G6	down	0,44	213973_at;201206_s_at;201203_s_at;201204_s_at
SLC20A1	6574	G6	down	0,44	201920_at
TNS	7145	G6	down	0,41	218864_at;218863_s_at;221748_s_at;221747_at
SDC4	6385	G6	down	0,39	202071_at
CDH1	999	G6	down	0,34	201131_s_at;201130_s_at
TNFSF10	8743	G6	down	0,34	202687_s_at;202688_at
GATA6	2627	G6	down	0,32	210002_at
LISCH7	51599	G6	down	0,24	208190_s_at

## Supplementary Table 5: Summary of GO analysis

*See excel file Stable5*

The first sheet (9 sheets total) in the Excel file is a summary all of the tests that were performed for all of the gene lists. This summary gives the number of genes that were attributed to a HCC subgroup or combination of subgroups (see Supplemental Table 2). The genes lists were stratified by relative expression in a given group compared to non-tumor samples (“up” or “down”). We have also summarized the number of significant GO terms ( $P < 0.01$  (see Supplementary Information) and a minimal number of 3 genes in the list for a GO term). Each subsequent sheet corresponds to the summary of the results from the GO analysis for each of the subgroup(s) specific gene lists. We have supplied the GO identifiers that were found to be significantly enriched in the given gene lists. For each GO term we show the number of total genes represented in the given group-specific list (intCounts) and the number of the genes (goCounts) on the HG-U133plus2.0 Affymetrix array that were attributed to that GO term. The P value resulting from the hypergeometric test are also given as well as the associated HUGO gene symbols (symbols).

Specificity	up/down vs. non-tumoral tissue	No. genes	No. significant GO terms
G1	up	116	3
	down	39	7
G1_2	up	41	3
	down	15	15
G2	up	27	0
	down	1	0
G2_3	up	53	31
	down	10	0
G3	up	189	59
	down	52	21
G5	up	5	0
	down	27	5
G5_6	up	12	0
	down	17	1
G6	up	66	15
	down	18	2
G123	up	45	8
	down	50	35

G1					
G1-up					
GO terms	pvalue	goCounts	intCounts	term	Symbols
6397	0,007	190	6	mRNA processing	TIA1;PRPF4B;CRNKL1;ADAR;HNRPA0
3723	0,004	466	11	RNA binding	ADAR;TIA1;RPL17;RPS19;SSA2;PAIP1;HNRPA0;RBM9
5923	0,002	29	3	tight junction	CLDN7;TJP3;F11R
G1-down					
GO terms	pvalue	goCounts	intCounts	term	Symbols
6731	0	121	3	coenzyme and prosthetic group metabolism	GCLC;GCLM;HMOX2
6118	0,009	250	4	electron transport	GLRX;SDHB;CYP7B1;CYP4F11
16491	0,0006	473	7	oxidoreductase activity	HADH2;ALDH1A1;HMOX2;CYP7B1;CYP4F11;SDHB;GLRX
3824	0,002	3562	20	catalytic activity	GBE1;HADH2;POLR2C;ACYP2;AK2;ALDH1A1;LAP3;CTSB;GCLC;GCLM;HMOX2;PCAF;CYP7B1;CYP4F11;CDC14B;TRIM2;SDHB;GLRX;CTBS;ABCB1;ABHD2
5489	0,004	199	4	electron transporter activity	ALDH1A1;GLRX;HMOX2;SDHB
5792	0,004	99	3	microsome	HMOX2;CYP7B1;CYP4F11
42598	0,004	101	3	vesicular fraction	HMOX2;CYP7B1;CYP4F11

G1_2					
G1_2-up					
GO terms	pvalues	goCounts	intCounts	term	Symbols
6325	9,27E-03	150	3	establishment and/or maintenance of chromatin architecture	KIAA0117;H1F0;SMYD3
17076	7,25E-03	1207	9	purine nucleotide binding	FGFR4;MYH4;MKKS;ARK5;RPS6KC1;HSPA 14;TOR3A;ARF1;RAP2A
166	7,94E-03	1224	9	nucleotide binding	FGFR4;MYH4;MKKS;ARK5;RPS6KC1;HSPA 14;TOR3A;ARF1;RAP2A
G1_2-down					
GO terms	pvalues	goCounts	intCounts	term	Symbols
6558	1,06E-07	9	3	L-phenylalanine metabolism	FAH;HGD;QDPR
6559	1,06E-07	9	3	L-phenylalanine catabolism	FAH;HGD;QDPR
9074	2,07E-07	11	3	aromatic amino acid family catabolism	FAH;HGD;QDPR
19439	3,59E-07	13	3	aromatic compound catabolism	FAH;HGD;QDPR
19752	9,17E-07	338	6	carboxylic acid metabolism	QDPR;FAH;HGD;ACSL5;MTCBP-1;FTHFD
6082	9,50E-07	340	6	organic acid metabolism	QDPR;FAH;HGD;ACSL5;MTCBP-1;FTHFD
6725	1,57E-06	79	4	aromatic compound metabolism	FAH;HGD;QDPR;FTHFD
9072	1,66E-06	21	3	aromatic amino acid family metabolism	FAH;HGD;QDPR
9063	1,22E-05	40	3	amino acid catabolism	FAH;HGD;QDPR
9310	1,31E-05	41	3	amine catabolism	FAH;HGD;QDPR
6520	3,98E-05	178	4	amino acid metabolism	FAH;HGD;QDPR;MTCBP-1
6519	8,04E-05	213	4	amino acid and derivative metabolism	QDPR;FAH;HGD;MTCBP-1
9308	1,50E-04	250	4	amine metabolism	QDPR;FAH;HGD;MTCBP-1
9056	6,63E-03	688	4	catabolism	FAH;HGD;QDPR;FTHFD
3824	7,21E-03	3562	8	catalytic activity	QDPR;FAH;GSTA3;HGD;ACSL5;ABCG2;FT HFD;PIK3C2G

### G3

G3-up					
G3-up					
GO terms	pvalues	goCounts	intCounts	term	Symbols
7067	2,09E-08	113	13	mitosis	SMC1L1;KNTC2;TTK;CNAP1;HCAP-G;SKB1;MAD2L1;BUB1;CCNA2;CDC6;RAD21;KIF2C;EML4
87	2,59E-08	115	13	M phase of mitotic cell cycle	SMC1L1;KNTC2;TTK;BUB1;CCNA2;CDC6;MAD2L1;RAD21;CNAP1;KIF2C;EML4;HCAP-G;SKB1
280	3,48E-07	143	13	nuclear division	SMC1L1;KNTC2;TTK;BUB1;CCNA2;CDC6;MAD2L1;RAD21;CNAP1;KIF2C;EML4;HCAP-G;SKB1
279	5,60E-07	149	13	M phase	SMC1L1;KNTC2;TTK;BUB1;CCNA2;CDC6;MAD2L1;RAD21;CNAP1;KIF2C;EML4;HCAP-G;SKB1
278	3,94E-06	177	13	mitotic cell cycle	SMC1L1;KNTC2;CCNA2;CDC6;TTK;BUB1;MAD2L1;RAD21;CNAP1;KIF2C;EML4;HCAP-G;SKB1
7049	5,19E-06	634	26	cell cycle	TOPBP1;SMC1L1;KNTC2;DKC1;NRAS;PHB;TTK;UBE2V2;CT4;CCT2;MAPRE1;CDC6;CCNA2;PRIM1;RBBP4;RFC3;RAD21;BUB1;MAD2L1;CNAP1;KIF2C;EML4;HCAP-G;SKB1;NME1;NME2
8283	8,08E-06	948	33	cell proliferation	TOPBP1;SMC1L1;KNTC2;DKC1;NRAS;PHB;TTK;UBE2V2;CT4;CCT2;MAPRE1;CDC6;CCNA2;PPP1CC;PRIM1;RBBP4;RFC3;BUB1;MAD2L1;RAD21;CNAP1;KIF2C;EML4;SKB1;FTH1;NME1;NME2;HGS;TPD52L2;TXN;CKLF;EDD
75	1,06E-05	33	6	cell cycle checkpoint	CDC6;MAD2L1;BUB1;TTK;CCNA2;SMC1L1
7093	1,14E-05	10	4	mitotic checkpoint	BUB1;TTK;CCNA2;MAD2L1
7088	7,86E-05	29	5	regulation of mitosis	MAD2L1;BUB1;TTK;CCNA2;SKB1
59	1,19E-04	17	4	protein-nucleus import, docking	KPNB1;RANBP5;XPO1;IPO7
74	1,91E-04	365	16	regulation of cell cycle	SMC1L1;CDC6;CCNA2;SKB1;MAD2L1;BUB1;TTK;NME1;NME2;DKC1;NRAS;PHB;UBE2V2;CT4;CCT2;MAPRE1
67	2,78E-04	166	10	DNA replication and chromosome cycle	SMC1L1;KNTC2;CDC6;PRIM1;RBBP4;RFC3;RAD21;CNAP1;HCAP-G;TOPBP1
6139	5,52E-04	2289	54	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	DR1;TGIF;DHX15;SNRPD2;G6PD;ATIC;NME1;NME2;PHB;TOPBP1;CDC6;PRIM1;RBBP4;RFC3;CSNK1D;SMC1L1;RAD51A;P1;UBE2V2;TDG;RAD21;TSN;EZH2;CBX3;HIST2H2BE;ACTL6A;PHLDA2;ENO1;POLR2K;GTF3C3;PAPOLA;PC4;PWP1;SMA D2;PPARBP;THRAP4;NEUGRIN;PRKAR1A;TCEB1;DKC1;DDX48;BOP1;TRIP13;COPS5;TAF2;HNRPR;CASC3;PTBP2;NUP107;SCYE1;NARS;FLJ20485;SNRPA1;PGD;ADSL
6913	5,91E-04	92	7	nucleocytoplasmic transport	KPNB1;RANBP5;XPO1;IPO7;CASC3;NUP107;NUP155
8151	6,67E-04	2821	63	cell growth and/or maintenance	KPNB1;RANBP5;XPO1;IPO7;TOPBP1;SMC1L1;KNTC2;DKC1;NRAS;PHB;TTK;UBE2V2;CT4;CCT2;MAPRE1;CDC6;CCNA2;TEBP;PPP1CC;PRIM1;RBBP4;RFC3;EZH2;CBX3;HIST2H2BE;ACTL6A;DDX48;BOP1;CASC3;NUP107;SEC61G;SLC7A1;SRI;NUP155;SLC38A6;CLIC1;FTH1;HGS;RAD21;PFN2;EML4;KIF1B;EBNA1BP2;C1orf33;BUB1;MAD2L1;CNAP1;HCAP-G;KIF2C;SKB1;TPD52L2;TXN;CKLF;EDD;NME1;NME2;SNX7;NUP37;CGI-141;ARPC4;ARPP-19
7046	7,32E-04	46	5	ribosome biogenesis	DKC1;DDX48;BOP1;EBNA1BP2;C1orf33
30261	7,55E-04	12	3	chromosome condensation	SMC1L1;CNAP1;HCAP-G
6259	7,67E-04	455	17	DNA metabolism	CDC6;PRIM1;RBBP4;RFC3;CSNK1D;SMC1L1;RAD51AP1;UBE2V2;TDG;RAD21;TSN;EZH2;CBX3;HIST2H2BE;ACTL6A;PHB;TOPBP1
42254	8,09E-04	47	5	ribosome biogenesis and assembly	DKC1;DDX48;BOP1;EBNA1BP2;C1orf33
8152	2,13E-03	5403	102	metabolism	KPNB1;RANBP5;XPO1;IPO7;CCNA2;CDC6;DR1;TGIF;UBE2V2;DHX15;SNRPD2;TEBP;G6PD;GLA;TDG;PPP1CC;ENO1;PGK1;TXN;DNAJC10;CYB5-M;ATIC;NME1;NME2;PHB;TOPBP1;PRIM1;RBBP4;RFC3;CSNK1D;SMC1L1;RAD51AP1;RAD21;TSN;EZH2;CBX3;HIST2H2BE;ACTL6A;PHLDA2;POLR2K;GTF3C3;PAPOLA;PC4;PWP1;SMAD2;PPARBP;THRAP4;NEUGRIN;PRKAR1A;TCEB1;DKC1;DDX48;BOP1;TRIP13;COPS5;TAF2;HNRPR;CASC3;PTBP2;NUP155

					UP107;NARS;EIF3S9;EIF3S3;SCYE1;MRPL42;C1orf33;EIF2S1;CCT4;CCT2;CCT5;PLOD2;BUB1;TTK;MELK;DUSP3;PTP4A2;PIGF;NSF;PSMC4;NPEPPS;USP14;USP3;PSMD14;EDD;AGA;SLC7A1;SEC61G;ACACA;UGCG;MPV17;FLJ20485;SRM;SNRPA1;PGD;UCK2;ADSL;TRIM31;PSMC6;CGI-121;ARPP-19;MASA;FLJ12443
7059	2,20E-03	17	3	chromosome segregation	SMC1L1;KNTC2;RAD21
7001	2,62E-03	186	9	chromosome organization and biogenesis (sensu Eukarya)	TEBP;EZH2;CBX3;HIST2H2BE;ACTL6A;DKC1;PHB;RAD21;SMC1L1
50875	2,86E-03	3333	69	cellular physiological process	KPNB1;RANBP5;XPO1;IPO7;TOPBP1;SMC1L1;KNTC2;DKC1;NRAS;PHB;TTK;UBE2V2;CCT4;CCT2;MAPRE1;CDC6;CCNA2;TEBP;PPP1CC;PRIM1;RBBP4;RFC3;EZH2;CBX3;HIST2H2BE;ACTL6A;DDX48;BOP1;CASC3;NUP107;SEC61G;SLC7A1;SRI;NUP155;SLC38A6;CLIC1;FTH1;HGS;PDCD2;RAD21;PHLDA2;FXR1;HMMR;MARCKS;TXN;PFN2;EML4;KIF1B;EBNA1BP2;C1orf33;BUB1;MAD2L1;CNAP1;HCAP-G;KIF2C;SKB1;TPD52L2;CKLF;EDD;NME1;NME2;SNX7;NUP37;CGI-141;MMD;ARPC4;ARPP-19
6997	3,13E-03	191	9	nuclear organization and biogenesis	TEBP;EZH2;CBX3;HIST2H2BE;ACTL6A;RAD21;SMC1L1;DKC1;PHB
8285	3,66E-03	126	7	negative regulation of cell proliferation	CDC6;FTH1;NME1;NME2;PHB;RBBP4;HGS
6974	3,97E-03	198	9	response to DNA damage stimulus	TEBP;CSNK1D;RBBP4;SMC1L1;RAD51AP1;UBE2V2;TDG;RAD21;DKC1
16070	4,64E-03	363	13	RNA metabolism	DHX15;SNRPD2;DKC1;DDX48;BOP1;PAPOLA;HNRPR;CASC3;PTBP2;SCYE1;NARS;FLJ20485;SNRPA1
9719	5,31E-03	207	9	response to endogenous stimulus	TEBP;CSNK1D;RBBP4;SMC1L1;RAD51AP1;UBE2V2;TDG;RAD21;DKC1
6006	6,41E-03	75	5	glucose metabolism	G6PD;ENO1;PGK1;PGD;ARPP-19
6007	6,67E-03	48	4	glucose catabolism	ENO1;PGK1;G6PD;PGD
6396	7,08E-03	297	11	RNA processing	DHX15;SNRPD2;DKC1;DDX48;BOP1;PAPOLA;HNRPR;CASC3;PTBP2;FLJ20485;SNRPA1
16043	7,48E-03	661	19	cell organization and biogenesis	TEBP;EZH2;CBX3;HIST2H2BE;ACTL6A;DKC1;DDX48;BOP1;RAD21;SMC1L1;PFN2;EML4;KIF1B;EBNA1BP2;C1orf33;TTK;HGS;PHB;ARPC4
17111	5,62E-06	48	7	nucleoside-triphosphatase activity	CDC6;DHX15;NSF;PSMC6;RFC3;TRIP13;XAB1
16779	2,77E-04	87	7	nucleotidyltransferase activity	DKC1;TEBP;RFC3;PRIM1;POLR2K;PAPOLA;USP14
3777	6,00E-04	27	4	microtubule motor activity	KNS2;SMC1L1;KIF2C;KIF1B
30554	1,66E-03	968	26	adenyl nucleotide binding	ACACA;BUB1;CDC6;CSNK1D;DHX15;KIF2;NARS;NME1;NME2;NSF;PSMC4;PSMC6;TTK;UCK2;SMC1L1;TRIP13;DDX48;MELK;THRAP4;CCT4;CCT2;KIF2C;XAB1;CCT5;KIF1B;PRKAR1A
3774	2,40E-03	93	6	motor activity	KNS2;SMC1L1;KIF2C;KIF1B;ACTL6A;KIF2
5524	2,54E-03	945	25	ATP binding	ACACA;BUB1;CDC6;CSNK1D;DHX15;KIF2;NARS;NME1;NME2;NSF;PSMC4;PSMC6;TTK;UCK2;SMC1L1;TRIP13;DDX48;MELK;THRAP4;CCT4;CCT2;KIF2C;XAB1;CCT5;KIF1B
166	2,94E-03	1224	30	nucleotide binding	ACACA;BUB1;CDC6;CSNK1D;DHX15;KIF2;NARS;NME1;NME2;NSF;PSMC4;PSMC6;TTK;UCK2;SMC1L1;TRIP13;DDX48;MELK;THRAP4;CCT4;CCT2;KIF2C;XAB1;CCT5;KIF1B;NRAS;RIT1;NS;PRKAR1A;RFC3
8022	3,39E-03	21	3	protein C-terminus binding	ITGB1BP1;TOPBP1;MAPRE1
17076	4,65E-03	1207	29	purine nucleotide binding	ACACA;BUB1;CDC6;CSNK1D;DHX15;KIF2;NARS;NME1;NME2;NSF;PSMC4;PSMC6;TTK;UCK2;SMC1L1;TRIP13;DDX48;MELK;THRAP4;CCT4;CCT2;KIF2C;XAB1;CCT5;KIF1B;NRAS;RIT1;NS;PRKAR1A
3743	5,24E-03	48	4	translation initiation factor activity	EIF2S1;EIF3S9;EIF3S3;COPS5
8565	8,54E-03	86	5	protein transporter activity	SEC61G;KPNB1;RANBP5;XPO1;IPO7
5634	4,53E-12	2576	76	nucleus	PPARBP;THRAP4;GTF3C3;RAD21;PSMC4;PSMD14;CLIC1;KPBN1;RANBP5;XPO1;NUP155;IPO7;NUP107;DKC1;PHB;TDG;POLR2K;PC4;TAF2;SNRPA1;TEBP;FXR1;SNRPD2;COPS5;H

					NRPR;ACTL6A;BUB1;CCNA2;CDC6;DHX15;DR1;ENO1;EZH2;MAD2L1;SMAD2;NME1;NME2;PDCD2;PSMC6;RBBP4;RFC3;TCEB1;TGIF;TSN;COIL;SMC1L1;HIST2H2BE;FAM50A;TRIP13;NPEPPS;DDX48;CNAP1;NDRG1;KNTC2;RAD51AP1;PAPOLA;EBNA1BP2;KIF2C;TOPBP1;PWP1;CBX3;CASC3;BOP1;BRD7;CGI-121;CGI-48;C1orf33;NEUGRIN;EDD;FLJ10458;WDR12;PTBP2;HCAP-G;C22orf18;NUP37;ANP32E
5622	1,12E-10	5154	110	intracellular	ENO1;PPARBP;THRAP4;GTF3C3;TRIM31;RAD21;PSMC4;PSMD14;KNTC2;KIF2C;BUB1;MAD2L1;SMC1L1;DKC1;TEBP;CBX3;HIST2H2BE;CNAP1;ACTL6A;CCNA2;CDC6;DHX15;DR1;EZH2;KPNB1;RANBP5;SMAD2;NME1;NME2;PDCD2;POLR2K;PSMC6;RBBP4;RFC3;SNRPD2;TCEB1;TGIF;TSN;COIL;FAM50A;TRIP13;NPEPPS;NUP155;DDX48;NDRG1;IPO7;RAD51AP1;PAPOLA;PC4;EBNA1BP2;TOPBP1;PWP1;CASC3;BOP1;BRD7;CGI-121;CGI-48;C1orf33;NEUGRIN;EDD;FLJ10458;WDR12;NUP107;PTBP2;HCAP-G;C22orf18;NUP37;ANP32E;CLIC1;XPO1;PHB;TDG;PRIM1;TAF2;SNRPA1;FXR1;NARS;SRI;SKB1;CCT4;ARPP-19;EML4;KIF1B;MRPL42;CYB5-M;AGA;GLA;HGS;MPV17;PLOD2;UGCG;PIGF;TTK;STMN1;CCT2;EIF2S1;EIF3S9;EIF3S3;COPS5;KIF2;ARPC4;EVA1;KNS2;P SME3;ACACA;MARCKS;PFN2;SEC61G;HNRPR;GMFB
5694	4,34E-06	188	13	chromosome	RAD21;KNTC2;KIF2C;BUB1;MAD2L1;SMC1L1;DKC1;TEBP;CBX3;HIST2H2BE;CNAP1;PRIM1;RFC3
775	2,92E-05	25	5	chromosome, pericentric region	BUB1;MAD2L1;SMC1L1;KNTC2;KIF2C
5643	4,45E-05	44	6	nuclear pore	KPNB1;RANBP5;XPO1;NUP155;IPO7;NUP107
46930	4,45E-05	44	6	pore complex	KPNB1;RANBP5;XPO1;NUP155;IPO7;NUP107
5635	1,45E-04	77	7	nuclear membrane	KPNB1;RANBP5;XPO1;NUP155;IPO7;NUP107;CLIC1
5852	2,58E-04	9	3	eukaryotic translation initiation factor 3 complex	EIF3S9;EIF3S3;COPS5
5654	2,84E-04	175	10	nucleoplasm	PPARBP;THRAP4;GTF3C3;POLR2K;PC4;TAF2;DKC1;PHB;TDG;XPO1
12505	3,40E-04	179	10	endomembrane system	CLIC1;KPNB1;RANBP5;XPO1;NUP155;IPO7;NUP107;PIGF;SEC61G;KIF1B
5623	9,40E-04	7529	123	cell	ENO1;PPARBP;THRAP4;GTF3C3;TRIM31;RAD21;PSMC4;PSMD14;KNTC2;KIF2C;BUB1;MAD2L1;SMC1L1;DKC1;TEBP;CBX3;HIST2H2BE;CNAP1;GMFB;CLIC1;UGCG;EBNA1BP2;MMD;NARS;IPO7;EDD;ACTL6A;CCNA2;CDC6;DHX15;DR1;EZH2;KPNB1;RANBP5;SMAD2;NME1;NME2;PDCD2;POLR2K;PSMC6;RBBP4;RFC3;SNRPD2;TCEB1;TGIF;TSN;COIL;FAM50A;TRIP13;NPEPPS;NUP155;DDX48;NDRG1;RAD51AP1;PAPOLA;PC4;TOPBP1;PWP1;CASC3;BOP1;BRD7;CGI-121;CGI-48;C1orf33;NEUGRIN;FLJ10458;WDR12;NUP107;PTBP2;HCAP-G;C22orf18;NUP37;ANP32E;XPO1;PHB;TDG;PRIM1;TAF2;SNRPA1;FXR1;SRI;SKB1;CCT4;ARPP-19;EML4;KIF1B;MRPL42;CYB5-M;AGA;GLA;HGS;MPV17;PLOD2;PIGF;TTK;STMN1;CCT2;EIF2S1;EIF3S9;EIF3S3;COPS5;KIF2;ARPC4;EVA1;KNS2;FTH1;MARCKS;RIT1;SLC7A1;LANCL1;P SME3;ACACA;PFN2;ITGB1B P1;DDEF1;CGI-141;CKLF;FAM11B;SLC38A6;SEC61G;HNRPR
776	1,31E-03	15	3	kinetochore	BUB1;MAD2L1;SMC1L1
16282	4,67E-03	23	3	eukaryotic 43S preinitiation complex	EIF3S9;EIF3S3;COPS5
5737	5,98E-03	2680	54	cytoplasm	ENO1;PSMC4;PSMD14;RFC3;KIF1B;MRPL42;CYB5-M;PHB;AGA;GLA;HGS;MPV17;PLOD2;UGCG;PIGF;BUB1;TTK;STMN1;PSMC6;NPEPPS;CCT2;CGI-121;C1orf33;EIF3S9;EIF3S3;COPS5;KIF2;ARPC4;EVA1;KNS2;KIF2C;ACTL6A;P SME3;ACACA;MARCKS;PFN2;ANP32E;SEC61G;CDC6;KPNB1;RANBP5;NARS;PDCD2;SRI;XPO1;FXR1;C NAP1;SKB1;IPO7;CCT4;ARPP-19;PAPOLA;EML4;BRD7
16591	9,10E-03	55	4	DNA-directed RNA polymerase II, holoenzyme	PPARBP;THRAP4;POLR2K;TAF2

G3-down					
GO terms	pvalues	goCounts	intCounts	term	Symbols
7596	3,63E-05	82	5	blood coagulation	KNG1;TMPRSS6;SERPING1;F7;COL18A1
50817	4,32E-05	85	5	coagulation	SERPING1;F7;KNG1;COL18A1;TMPRSS6
7599	4,83E-05	87	5	hemostasis	SERPING1;F7;KNG1;COL18A1;TMPRSS6
50878	8,14E-05	97	5	regulation of body fluids	SERPING1;F7;KNG1;COL18A1;TMPRSS6
6730	4,67E-04	33	3	one-carbon compound metabolism	TST;CA5A;MAT2A
6082	4,63E-03	340	6	organic acid metabolism	GAMT;ACADVL;ECHS1;CRYL1;TST;ALDH5A1
6118	5,84E-03	250	5	electron transport	ACADVL;COX7A1;CYP27A1;SARDH;FMO4
16836	1,18E-03	43	3	hydro-lyase activity	CA5A;ECHS1;ALAD
16835	1,73E-03	49	3	carbon-oxygen lyase activity	CA5A;ECHS1;ALAD
16491	1,88E-03	473	8	oxidoreductase activity	ALDH5A1;COX7A1;ACADVL;FMO4;CYP27A1;SARDH;DHTKD1;CRYL1
30246	2,00E-03	185	5	carbohydrate binding	ASGR2;PRG2;MASP1;DCL-1;KNG1
5529	2,19E-03	113	4	sugar binding	ASGR2;PRG2;MASP1;DCL-1
4252	2,26E-03	114	4	serine-type endopeptidase activity	F7;MASP1;TMPRSS6;PCSK6
8236	3,25E-03	126	4	serine-type peptidase activity	F7;MASP1;TMPRSS6;PCSK6
4263	7,42E-03	82	3	chymotrypsin activity	F7;MASP1;TMPRSS6
4295	7,93E-03	84	3	trypsin activity	F7;MASP1;TMPRSS6
8168	9,00E-03	88	3	methyltransferase activity	MGMT;SARDH;GAMT
16741	9,87E-03	91	3	transferase activity, transferring one-carbon groups	MGMT;SARDH;GAMT
5739	9,12E-07	480	12	mitochondrion	SLC25A20;CA5A;SARDH;TST;ACADVL;ACAT1;COX7A1;CYP27A1;ECHS1;ALDH5A1;FLJ20605;GIMAP5
5576	5,23E-04	906	12	extracellular	TNXB;COL18A1;CPB2;SERPING1;CPN2;F7;GPLD1;KNG1;SERPINF1;PON1;PRG2;MASP1;TF
5759	2,00E-03	55	3	mitochondrial matrix	CA5A;SARDH;TST

### G2\_3

#### G2\_3 - up

GO term	pvalues	goCount	intCount	term	Symbols
7049	1,98E-06	634	13	cell cycle	SMC2L1;SFN;MKI67;CCNE2;TUBG1;FEN1;MCM2;MCM3;MCM6;RRM1;BUB1B;NEK2;MAPK1
6270	5,31E-05	17	3	DNA replication initiation	MCM2;MCM3;MCM6
8151	5,38E-05	2821	25	cell growth and/or maintenance	SMC2L1;SFN;MKI67;CCNE2;TUBG1;NEK2;FEN1;MCM2;MCM3;MCM6;RRM1;CENPA;H2AFZ;SLC26A2;XK;RRAGD;SLC38A1;TFRC;ABCG1;NPC1;ARFGEF2;KIF4A;BUB1B;MAPK1;SUZ12
67	8,29E-05	166	6	DNA replication and chromosome cycle	SMC2L1;FEN1;MCM2;MCM3;MCM6;RRM1
6259	1,36E-04	455	9	DNA metabolism	FEN1;MCM2;MCM3;MCM6;RRM1;SMARCA3;CENPA;H2AFZ;SUZ12
8283	1,49E-04	948	13	cell proliferation	SMC2L1;SFN;MKI67;CCNE2;TUBG1;NEK2;FEN1;MCM2;MCM3;MCM6;RRM1;BUB1B;MAPK1
6260	2,76E-04	132	5	DNA replication	MCM2;MCM3;MCM6;FEN1;RRM1
50875	1,03E-03	3333	25	cellular physiological process	SMC2L1;SFN;MKI67;CCNE2;TUBG1;NEK2;FEN1;MCM2;MCM3;MCM6;RRM1;CENPA;H2AFZ;SLC26A2;XK;RRAGD;SLC38A1;TFRC;ABCG1;NPC1;ARFGEF2;MAPK1;KIF4A;BUB1B;SUZ12
278	1,05E-03	177	5	mitotic cell cycle	SMC2L1;CCNE2;TUBG1;BUB1B;NEK2
7067	1,53E-03	113	4	mitosis	SMC2L1;TUBG1;NEK2;BUB1B
87	1,63E-03	115	4	M phase of mitotic cell cycle	SMC2L1;TUBG1;BUB1B;NEK2
6261	3,21E-03	67	3	DNA-dependent DNA replication	MCM2;MCM3;MCM6
280	3,60E-03	143	4	nuclear division	SMC2L1;TUBG1;BUB1B;NEK2
279	4,17E-03	149	4	M phase	SMC2L1;TUBG1;BUB1B;NEK2
7001	9,07E-03	186	4	chromosome organization and biogenesis (sensu Eukarya)	CENPA;H2AFZ;SUZ12;SMC2L1
6997	9,93E-03	191	4	nuclear organization and biogenesis	CENPA;H2AFZ;SMC2L1;SUZ12
8094	3,05E-04	32	3	DNA-dependent ATPase activity	MCM2;MCM3;MCM6
5524	3,15E-04	945	12	ATP binding	BUB1B;IARS;MCM2;MCM3;MCM6;MKI67;NEK2;MAPK1;SMARCA3;ABCG1;SMC2L1;KIF4A
30554	3,94E-04	968	12	adenyl nucleotide binding	BUB1B;IARS;MCM2;MCM3;MCM6;MKI67;NEK2;MAPK1;SMARCA3;ABCG1;SMC2L1;KIF4A
17076	8,26E-04	1207	13	purine nucleotide binding	BUB1B;IARS;MCM2;MCM3;MCM6;MKI67;NEK2;MAPK1;SMARCA3;ABCG1;SMC2L1;KIF4A;TUBG1
166	9,45E-04	1224	13	nucleotide binding	BUB1B;IARS;MCM2;MCM3;MCM6;MKI67;NEK2;MAPK1;SMARCA3;ABCG1;SMC2L1;KIF4A;TUBG1
15171	1,28E-03	52	3	amino acid transporter activity	SLC38A1;ABCG1;XK
5275	2,23E-03	63	3	amine transporter activity	SLC38A1;XK;ABCG1
16887	2,60E-03	232	5	ATPase activity	MCM2;MCM3;MCM6;ABCG1;SMC2L1
5342	3,02E-03	70	3	organic acid transporter activity	SLC38A1;XK;ABCG1
46943	3,02E-03	70	3	carboxylic acid transporter activity	SLC38A1;XK;ABCG1
16818	7,40E-03	421	6	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	TUBG1;MCM2;MCM3;MCM6;ABCG1;SMC2L1
16817	7,48E-03	422	6	hydrolase activity, acting on	TUBG1;MCM2;MCM3;MCM6;ABCG1;SMC2L1

				acid anhydrides	1
5694	1,44E-04	188	6	chromosome	CENPA;BUB1B;MCM2;H2AFZ;TUBG1;MCM3
5819	1,02E-03	46	3	spindle	NEK2;TUBG1;KIF4A
					TUBG1;NARF;BUB1B;MKI67;CENPA;FEN1;H2AFZ;MCM2;MCM3;MCM6;NEK2;SMARCA3;SLBP;CCNE2;SMC2L1;SUZ12;KIF4A;RRA GD;UPF3B
5634	6,07E-03	2576	19	nucleus	

### G2\_3 - down

no significant GO terms passed the criteria (p < 0.01 and >= 3 associated genes)

## G5

### G5-up

no significant GO terms passed the criteria (p < 0.01 and >= 3 associated genes)

### G5-down

GO term	pvalues	goCounts	intCounts	term	Symbols
9607	4,23E-04	830	8	response to biotic stimulus	ARHGDIB;HLA-DPA1;HLA-DPB1;IFI16;PTGER4;STAT1;IFI44;CLECSF2
6955	3,47E-03	654	6	immune response	CLECSF2;HLA-DPA1;HLA-DPB1;ARHGDIB;IFI16;PTGER4
6952	5,71E-03	723	6	defense response	ARHGDIB;HLA-DPA1;HLA-DPB1;IFI16;PTGER4;CLECSF2
4888	8,98E-03	724	5	transmembrane receptor activity	PTGER4;IL10RA;HLA-DPA1;HLA-DPB1;ICAM1
5525	9,96E-03	244	3	GTP binding	ARL7;RAB31

## G5\_6

### G5\_6 - up

no significant GO terms passed the criteria (p < 0.01 and >= 3 associated genes)

### G5\_6-down

GO term	pvalues	goCounts	intCounts	term	Symbols
5578	7,82E-03	278	3	extracellular matrix	CTGF;LGALS3BP;THBS2

## G6

### G6 - up

GO term	pvalues	goCounts	intCounts	term	Symbols
6558	1,06E-07	9	3	L-phenylalanine metabolism	FAH;HGD;QDPR
6559	1,06E-07	9	3	L-phenylalanine catabolism	FAH;HGD;QDPR
9074	2,07E-07	11	3	aromatic amino acid family catabolism	FAH;HGD;QDPR
19439	3,59E-07	13	3	aromatic compound catabolism	FAH;HGD;QDPR
19752	9,17E-07	338	6	carboxylic acid metabolism	QDPR;FAH;HGD;ACSL5;MTCBP-1;FTHFD
6082	9,50E-07	340	6	organic acid metabolism	QDPR;FAH;HGD;ACSL5;MTCBP-1;FTHFD
6725	1,57E-06	79	4	aromatic compound metabolism	FAH;HGD;QDPR;FTHFD

9072	1,66E-06	21	3	aromatic amino acid family metabolism	FAH;HGD;QDPR
9063	1,22E-05	40	3	amino acid catabolism	FAH;HGD;QDPR
9310	1,31E-05	41	3	amine catabolism	FAH;HGD;QDPR
6520	3,98E-05	178	4	amino acid metabolism	FAH;HGD;QDPR;MTCBP-1
6519	8,04E-05	213	4	amino acid and derivative metabolism	QDPR;FAH;HGD;MTCBP-1
9308	1,50E-04	250	4	amine metabolism	QDPR;FAH;HGD;MTCBP-1
9056	6,63E-03	688	4	catabolism	FAH;HGD;QDPR;FTHFD
3824	7,21E-03	3562	8	catalytic activity	QDPR;FAH;GSTA3;HGD;ACSL5;ABCG2;FT HFD;PIK3C2G

#### G6 - down

GO term	pvalues	goCounts	intCounts	term	Symbols
6886	8,12E-03	246	3	intracellular protein transport	NUP98;RRBP1;RAB27A
16021	9,46E-03	2592	9	integral to membrane	NUP98;LDLR;SDC4;SLC20A1;TNFSF10;RR BP1;CDH1;LISCH7;CKLFSF6

#### G1\_2\_3

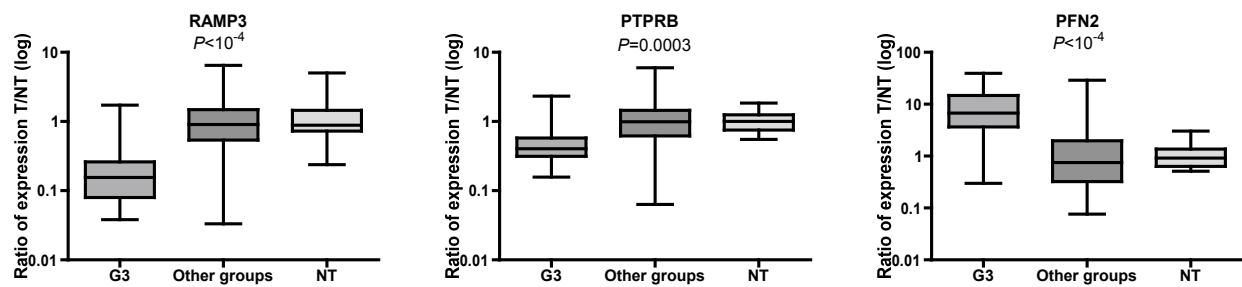
G1_2_3 - up					
Go terms	pvalues	goCounts	intCounts	term	Symbols
279	1,29E-03	149	4	M phase	SMC4L1;KPNA2;CCNB2;SHC1
278	2,43E-03	177	4	mitotic cell cycle	SMC4L1;KPNA2;CCNB2;SHC1
7067	5,72E-03	113	3	mitosis	SMC4L1;SHC1;CCNB2
87	6,00E-03	115	3	M phase of mitotic cell cycle	SMC4L1;CCNB2;SHC1
5524	6,96E-03	945	8	ATP binding	ACLY;PRKCI;RFC4;CCT3;MAP4K3;SMC4L1;KIF20A;AT AD2
30554	8,03E-03	968	8	adenyl nucleotide binding	ACLY;PRKCI;RFC4;CCT3;MAP4K3;SMC4L1;KIF20A;AT AD2
5634	1,72E-03	2576	19	nucleus	TMPO;KPNA2;CBX1;SNRNP;SNRPD1;BARD1;PRKCI;PRKDC;RFC4;HAT1;CCNB2;PNMA1;SMC4L1;CPSF6;DUSP12;PLCB1;CACYBP;POGK;FLJ12671
5694	6,46E-03	188	4	chromosome	CBX1;SMC4L1;RFC4;TMPO

#### G1\_2\_3 - down

Go terms	pvalues	goCounts	intCounts	term	Symbols
19752	1,84E-12	338	16	carboxylic acid metabolism	MTHFD1;HAO1;GOT2;MAT1A;SLC25A15;ASPA;PRODH2;MSRA;HPD;GRHPR;ACAA1;ACADL;HADHSC;ACAA2;FLJ20581;MLYCD
6082	2,01E-12	340	16	organic acid metabolism	MTHFD1;HAO1;GOT2;MAT1A;SLC25A15;ASPA;PRODH2;MSRA;HPD;GRHPR;ACAA1;ACADL;HADHSC;ACAA2;FLJ20581;MLYCD
6520	1,48E-07	178	9	amino acid metabolism	MTHFD1;ASPA;GOT2;PRODH2;MSRA;HPD;GRHPR;MAT1A;SLC25A15
9308	2,48E-07	250	10	amine metabolism	MTHFD1;SIAT10;GOT2;MAT1A;SLC25A15;ASPA;PRODH2;MSRA;HPD;GRHPR
6519	6,80E-07	213	9	amino acid and derivative metabolism	MTHFD1;GOT2;MAT1A;SLC25A15;ASPA;PRODH2;MSRA;HPD;GRHPR
9066	1,12E-06	17	4	aspartate family amino acid metabolism	ASPA;GOT2;MSRA;MTHFD1
6631	1,99E-06	124	7	fatty acid metabolism	HAO1;MLYCD;ACAA1;ACADL;HADHSC;ACAA2;FLJ20581;81
9063	3,98E-05	40	4	amino acid catabolism	ASPA;GOT2;HPD;PRODH2
9310	4,39E-05	41	4	amine catabolism	ASPA;GOT2;HPD;PRODH2
6629	5,39E-05	457	10	lipid metabolism	HAO1;ACAA1;ACADL;HADHSC;ACAA2;FLJ20581;MLY

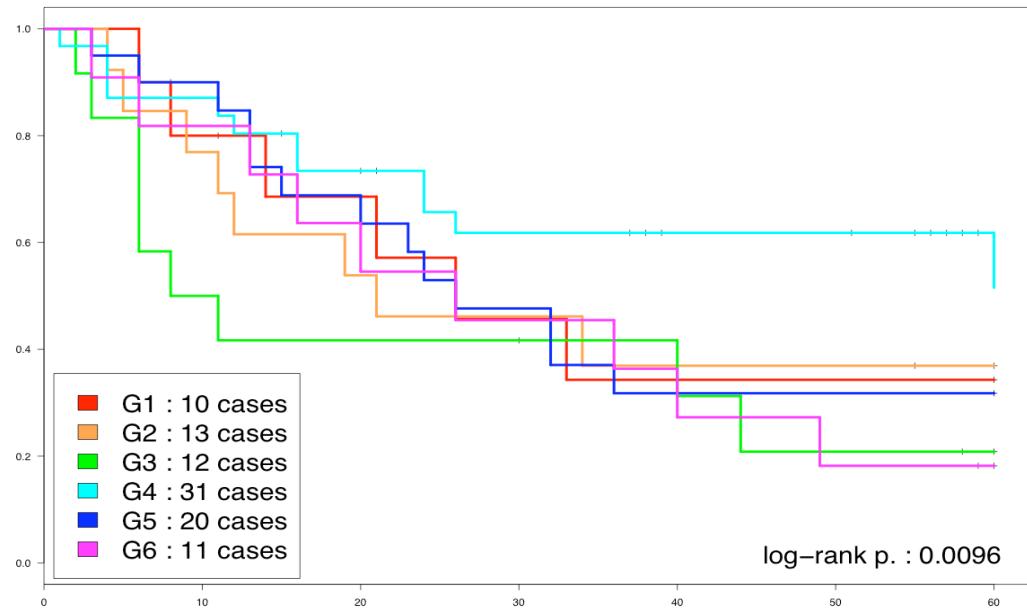
					CD;SIAT10;NR1I2;SEC14L2
8652	8,78E-04	39	3	amino acid biosynthesis	MTHFD1;PRODH2;GRHPR
9309	2,92E-03	59	3	amine biosynthesis	MTHFD1;PRODH2;GRHPR
					SLC25A15;MTHFD1;HAO1;HYAL1;DCXR;SIAT10;MLY CD;ACAA1;PCK2;ACADL;ETFDH;GCDH;SLC28A1;NR1 I2;CUTL2;HRSP12;FAS;MSRA;FYN;IF;PROZ;GOT2;MAT1A;ASPA;PRODH2;HPD;GRHPR;FLJ20581;HADHSC;ACAA2;EPHX2;ALAS1;SEC14L2;FLJ10948;CBR4
8152	5,50E-03	5403	35	metabolism	
6725	6,63E-03	79	3	aromatic compound metabolism	HPD;MTHFD1;EPHX2
9058	6,95E-03	853	10	biosynthesis	MTHFD1;PCK2;HRSP12;SIAT10;PRODH2;GRHPR;MLYCD;ALAS1;SEC14L2;GOT2
7596	7,35E-03	82	3	blood coagulation	F8;FGA;PROZ
50817	8,11E-03	85	3	coagulation	F8;FGA;PROZ
7599	8,65E-03	87	3	hemostasis	F8;FGA;PROZ
16491	1,45E-07	473	13	oxidoreductase activity	HADHSC;HPD;HAO1;ACADL;ETFDH;ACAA2;GCDH;MTFD1;PRODH2;MSRA;GRHPR;DCXR;CBR4
					IF;HADHSC;HPD;ALAS1;RCL1;HAO1;ACAA1;ACAA2;ACADL;ASPA;GOT2;ETNK2;ETFDH;PROZ;EPHX2;MTHFD1;GCDH;HYAL1;MAT1A;MLYCD;HRSP12;PCK2;PRODH2;FYN;MSRA;SIAT10;GRHPR;DCXR;CBR4;FLJ20581;FLJ10948
3824	1,42E-05	3562	31	catalytic activity	
16614	4,71E-05	86	5	oxidoreductase activity, acting on CH-OH group of donors	HADHSC;HAO1;ACAA2;GRHPR;DCXR
16645	5,15E-05	16	3	oxidoreductase activity, acting on the CH-NH group of donors	ETFDH;MTHFD1;PRODH2
15293	4,88E-04	79	4	symporter activity	SLC6A12;SLC28A1;SLC4A4;SLC16A2
16616	5,63E-04	82	4	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	HADHSC;ACAA2;GRHPR;DCXR
5342	4,22E-03	70	3	organic acid transporter activity	SLC25A15;SLC6A12;SLC16A2
46943	4,22E-03	70	3	carboxylic acid transporter activity	SLC25A15;SLC6A12;SLC16A2
15291	6,49E-03	160	4	porter activity	SLC6A12;SLC28A1;SLC4A4;SLC16A2
8415	6,57E-03	82	3	acyltransferase activity	ACAA1;ACAA2;ALAS1
16747	6,57E-03	82	3	transferase activity, transferring groups other than amino-acyl groups	ALAS1;ACAA1;ACAA2
15290	6,63E-03	161	4	electrochemical potential-driven transporter activity	SLC6A12;SLC28A1;SLC4A4;SLC16A2
16746	7,98E-03	88	3	transferase activity, transferring acyl groups	ALAS1;ACAA1;ACAA2
5739	6,65E-07	480	12	mitochondrion	ETFDH;SLC25A15;ACADL;ALAS1;GCDH;GOT2;HADHSC;MTHFD1;PCK2;ACAA2;MLYCD;FLJ10948
5777	2,06E-03	57	3	peroxisome	ACAA1;MLYCD;HAO1
42579	2,06E-03	57	3	microbody	ACAA1;MLYCD;HAO1
					ACADL;ALAS1;ETFDH;GCDH;GOT2;HADHSC;MTHFD1;PCK2;SLC25A15;ACAA2;MLYCD;FLJ10948;HYAL1;ACAA1;HAO1;SIAT10;FAS;EPHX2;DMD;HRSP12;SEC14L2
5737	2,11E-03	2680	21	cytoplasm	

**Supplementary figure 1 : Validation of gene specifically deregulated in HCC predicted subgroup G3.** *PFN2* (profilin-2), *PTPRB* (Protein Tyrosine Phosphatase, Receptor-type Beta) and *RAMP3* (Receptor Activity Modifying Protein 3) were analyzed in 109 HCC. Box plots representing the range of relative expression values (tumor versus mean of non tumor samples (T/NT)) obtained for these genes analyzed in tumors related to G3 (n=13), all other groups (n=96) and non-tumor samples (n= 21). The *P* value from Kruskal-Wallis test comparing the expression values in the different HCC subgroups are indicated below the gene symbol.



**Supplementary figure 2: Survival analysis according to transcriptome classification** **a.** Disease-free survival, stratified by group G1 to G6, with log-rank test  $P$ -value ( $n=97$  HCC). **b.** Overall survival, stratified by group G1 to G6, with log-rank test  $P$ -value ( $n=97$  HCC).

**a**



**b**

