SUPPLEMENTAL DATA

METHODS

Study design and patients

Additional inclusion criteria were: signed informed consent; morphologically confirmed diagnosis of AML; white blood cells (WBC) $\leq 30 \times 10^9$/L at diagnosis; WHO performance status ≤ 3; life expectancy of at least 2 months; adequate renal (serum creatinine < 2 mg/dl), pulmonary and hepatic (ALT/AST $\leq$ 2.5 x N) function; adequate left ventricular ejection fraction defined as $\geq 50\%$ on ECHO or MUGA. Exclusion criteria were: HIV infection or HCV positivity; resistant/relapsed AML; evidence of acute promyelocytic leukaemia (*PML/RARA* or variants positivity); current uncontrolled infection; active second malignancy; intercurrent organ damage or medical problems that would interfere with therapy; concurrent therapy for another malignancy; uncontrolled insulin-dependent diabetes mellitus or uncompensated major thyroid or adrenal dysfunction; active heart disease including myocardial infarction within previous 3 months, symptomatic coronary artery disease, arrhythmias not controlled by medication, or uncontrolled congestive heart failure (New York Heart Association Class III or IV); no concomitant treatment with chemotherapy or immunotherapy; treatment with any other investigational agent, or participating in another clinical trial within 30 days prior to entering this study.

Gene expression profile generation and analysis

Gene expression profiling was performed as previously reported.[20-24]Briefly, AML blasts were collected from patients' peripheral blood or bone marrow at diagnosis, before treatment initiation. PBMC were isolated as previously reported and stored as cellular pellets in liquid nitrogen. Total RNA was then extracted using the TRIzol reagent (Invitrogen and Life Technologies), purified using the RNeasy Kit (QIAGEN) as previously describe,[1-4] and processed according to the

Affymetrix Expression Analysis Technical Manual. cRNA was finally hybridized on the Human Gene 2.0 Affymetrix microarray (Affymetrix, Santa Clara, CA, USA). Raw data were then imported in GeneSpring GX12 (Agilent, USA) and analysed as previously reported.[1-4]

Principal component analysis (PCA) was performed by using GeneSpring GX 12.0 (Agilent, USA), as previously described.[4] Unsupervised clustering was generated using a hierarchical algorithm based on the average-linkage method.[5,6] Only genes displaying a twofold average change in the expression level across the whole panel were chosen to generate the hierarchical clustering. The expression value of each selected gene is normalized to have a zero mean value and unit standard deviation. The distance between two individual samples was calculated by Pearson distance with the normalized expression values. To perform the supervised gene expression analysis, we used GenSpring GX12.0 and set conventional parameters (pvalue<0.05; fold change >2; False discovery rate according to Benjamini-Hockeberg). In the matrix, each column represents a sample and each row represents a gene. The color scale bar shows the relative gene expression changes normalized by the standard deviation (0 is the mean expression level of a given gene).

EASE software was applied in order to establish whether specific cell functions and biological processes, defined according to gene ontology,[7,8] were significantly represented among the deregulated genes.[9,10]

To identify minimal gene sets (MGS) able to discriminate cases characterized by diverse clinical response to treatment, stepwise discriminant analysis was performed using IBM SPSS Statistics 20.0 (IBM, Armonk, USA).[4]

For sample classification, we then used a Support Vector Machine (SVM) algorithm and the leave-one-out method to classify cell type correlating with a specific clinical outcome (i. e. achievement or not of complete remission, CR).[1-3] In brief, the classifier is a confidence measure scoring function based on the values of a set of genes (gene cluster), which are differentially

expressed in two sets of cell types, and thus, can be used for cell type classification. The higher the score, the more likely it is that a cell type is related to the phenotype set. Samples with confidence measure score minor than 0,05 would be not assigned to a particular phenotype and flagged as unclassified.

Gene expression studies were conducted according to MIAME guidelines. Raw gene expression data will be available at http://www.ncbi.nlm.nih.gov/projects/geo/ upon publication.

Reverse-Transcription and quantitative real time-PCR

All RNAs extracted were treated with DNAse by using RQ1 kit (Promega) and 1 ng of each sample was retrotranscribed with Improm II kit (Promega) following the manufacturers' instructions.

All cDNAs obtained were quantified by SYBR Green-based quantitative realtime PCR (qPCR) amplifying specific regions of *CXCL16, CD93, GORASP1* and *GAPDH*. Primers forward and reverse for PCR amplification of *CXCL16, CD93* and *GORASP1* were designed by using Primer3 online software or by Primer Design (Roche) (supplementary table 1). In brief, SYBR Green real-time PCR assay was carried out in 12 microL of PCR mixture volume consisting of 6 microL of Master Mix (Promega, Madison, WI, USA), 0.18 microL of 10 microM of *CXCL16* or *CD93* and 0.36 microL for *GORASP1* primers, and 1 microL of obtained cDNA. The *CXCL16* gene amplification was performed as follows: 95°C for 2 minutes; 46 cycles of 95°C for 15 seconds, 58°C for 30 sec and 82°C for 25 sec. The *CD93* gene amplification was performed as follows: 95°C for 2 minutes; 46 cycles of 95°C for 15 seconds, 58°C for 30 sec and 83.5°C for 25 sec. The *GORASP1* gene amplification was performed as follows: 95°C for 2 minutes; 46 cycles of 95°C for 15 seconds, 58°C for 30 sec. At the end of all amplification cycles, melting temperature analysis was carried out by a slow increase in temperature (0.1 °C/s) up to 95°C. Amplification, data acquisition and analysis were carried out by Applied Biosystems 7500 Real-Time PCR instrument

using Applied Biosystems 7500 Real-Time PCR System software. The data was normalized with parallel amplification of *GAPDH* gene and analysed with the ΔCt method as previously described.[11]

qPCR was applied to 21 cases (for which residual RNA was available) from this trial and in 36 cases from a distinct UK trial, that served as independent validation cohort.

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Supplementary Table 1. Primers adopeted for RT-qPCR analysis

Name	Sequence (5'→3')	Position	Tm (°C)	Amplicon size
CD93-F1	TTCCAGACCACCAGTTCCTC	761-780	58,9	85 bp
CD93-R1	TCTCGTCCTTGTCACCTTCC	845-826	59	
CXCL16-F1	TTCCTATGTGCTGTGCAAGAG	1255-1275	59	77 bp
CXCL16-R1	CAGGTATATAATGAACCGGCAGA	1331-1309	60	
GRASP-F1	TGTCTGCCGAGTTCATGAGT	458 - 477	59	89 bp
GRASP-R1	CCACATTCAGGCCATTGAC	528 - 546	59	

Supplementary Table 2. Adverse events (Number of events)

Event type/involved apparatus	Adverse Event	Grade 1-2	Grade 3-4	Total
Bleeding	CNS hemorrhage	0	2	2
Bleeding	Bleeding not otherwise specified	2	0	2
Bleeding	Epistaxis	1	0	1
Bleeding	Ematuria	1	0	1
Cardiac	Heart failure	0	3	3
Cardiac	Atrial fibrillation	4	2	6
Cardiac	QTc prolonged	0	1	1
Cardiac	Valve disease	1	0	1
Cardiac	Sinus bradycardia	1	0	1
Cardiac	Hypotension	1	0	1
Cardiac	Supraventricular tachycardia	1	0	1
Cardiac	Palpitations	1	0	1
Hepatic	Alanine aminotransferase increased	3	3	6
Hepatic	Hypoalbuminemia	7	2	9
Hepatic	GGT increased	2	2	4
Hepatic	Fibrinogen decreased	6	1	7
Hepatic	Alkaline phosphatase increased	3	0	3
Hepatic	Bilirubin increased	3	0	3
Hepatic	Prolonged partial thromboplastin time(PTT)	1	0	1
Gastro-Intestinal	Diarrhea	9	1	10
Gastro-Intestinal	Nausea	4	0	4
Gastro-Intestinal	Abdominal pain	3	0	3
Gastro-Intestinal	Costipation	2	0	2
Gastro-Intestinal	Serum amylase increased	1	0	1
Gastro-Intestinal	Gastric perforation	1	0	1
Gastro-Intestinal	Vomiting	1	0	1
Gastro-Intestinal	Anorexia	1	0	1
Hematological	Anemia	1	3	4
Hematological	Neutropenia	1	25	26
Hematological	Thrombocytopenia	4	18	22
Infective	Pneumonia	0	8	8
Infective	Neutropenic fever	0	5	5
Infective	Respiratory failure	0	4	4
Infective	Bacterial infection	1	2	3
Infective	Bronchiolitis obliterans with organizing pneumonia (BOOP)	0	2	2
Infective	Skin infection	1	1	2
Infective	Urinary sepsis	0	1	1
Infective	Herpes	5	0	5
infective	Fever (sepsis, FUO)	13	2	15
Infective	Dental granuloma	1	0	1

Infective	Pharyngitis	1	0	1
Infective	Rhinitis infective	1	0	1
Infective	Oral fungal Infections	1	0	1
Infective	Urinary infection	1	0	1
Metabolic abnormalities	Hyperglycemia	8	3	11
Metabolic abnormalities	Hypokalemia	5	2	7
Metabolic abnormalities	Hyperkalemia	4	0	4
Metabolic abnormalities	Hypoglycemia	3	0	3
Metabolic abnormalities	Hypocalcemia	2	0	2
Metabolic abnormalities	Hyperuricemia	1	0	1
Metabolic abnormalities	Hypomagnesemia	1	0	1
Skin	Dermatitis	4	0	4
Skin	Erythema	2	0	2
Urinary	Urinary tract obstruction	0	1	1
Urinary	Acute kidney disease	0	1	1
Urinary	Renal calculi	0	1	1
Urinary	Dysuria	2	0	2
Other	Tremor	2	0	2
Other	Astenia	5	1	6
Other	Edema	10	1	11
Other	Syncope	0	1	1
Other	Fatigue	2	0	2
Other	Cough	2	0	2
Other	Weight gain	1	0	1
Other	Low back pain	1	0	1
Other	Angioedema	1	0	1
Other	Nocturia	1	0	1

Supplementary Table 3. Genes differentially expressed in cases achieving a CR or not (No response, NR)

0_transcript_cluster_id	p	FC (abs)	Regulation in CR	gene_assignment
16652879	0,00237604	3,4352016	up	---
16655051	1,12E-04	2,6000152	up	---
16655317	0,00460302	3,423703	up	---
16655581	0,00660967	2,4986773	up	---
16656679	0,00388545	2,079808	up	---
16656705	0,00366856	2,0377338	up	---
16657055	0,00280754	2,6132493	up	---
16657171	0,00793963	2,1720736	up	---
16657183	0,00959751	2,007272	up	---
16663804	8,29E-04	5,4759154	up	---
16693406	0,00304545	3,8666754	up	---
16694611	0,00397511	2,045289	up	---
16740559	1,95E-04	2,9054914	up	---
16755536	6,99E-04	5,6605444	up	---
16764077	0,00820829	2,2203019	up	---
16771311	9,12E-04	2,839953	up	---
16771436	0,00432987	2,9540644	up	---
16771442	4,30E-04	2,1653857	up	---
16835626	0,00561905	2,9385312	up	---
16835631	0,00569035	2,812134	up	---
16875414	5,21E-04	3,0127006	up	---
16880240	0,0049813	3,0881195	up	---

16889711	0,005982943	2,9503994	up	---
16900496	0,00103758	2,535211	up	---
16930144	0,00700951	5,042592	up	---
16971429	7,30E-04	3,0077608	down	---
16971430	0,002252779	2,371701	down	---
16977343	1,27E-04	2,5658605	up	---
17006293	7,74E-04	3,1675184	up	---
17010539	0,006780517	2,42573	down	---
17017202	0,004003867	2,1491292	up	---
17061545	0,008452913	4,0636	up	---
17079417	7,74E-04	2,13967	down	---
17124298	0,003044095	2,9793289	up	---
17124300	0,004564677	3,7872558	up	---
16875461	0,003098195	4,990776	up	*AC008984.2*
16982047	0,009957592	3,0142543	up	*ACSL1*
16719802	0,002393311	2,001011	up	*ADAM8*
16701238	0,00684916	2,5937545	down	*AKT3*
16757160	0,0033445 47	2,3235643	up	*ALDH2, RP11-162P23.2*
16773662	0,005949611	2,808843	up	*ALOX5AP*
16716341	0,00187573 6	2,3354669	up	*ANKRD22*
16801473	0,006300211	9,202135	up	*AQP9*
16749423	0,006813454	2,204517 1	down	*ARNTL2*
16983451	0,002707305	4,2786694	up	*BASP1*
16812344	5,66E-04	4,3477235	up	*BCL2A1*
16962584	0,007089409	3,2067826	up	*BCL6*
16965252	0,0019060	2,15280	up	*BST1*

	71	46		
16715228	2,68E-04	2,811091 4	up	*C10orf54*
16668702	0,0034937 27	2,098937 5	up	*C1orf162*
16863589	5,60E-04	7,191047 7	up	*C5AR1*
17093042	0,0091468 16	2,419937 1	up	*C9orf72*
16848619	0,0034800 07	2,066474 4	up	*CD300LF*
16830577	0,0082926 94	2,023706 7	up	*CD68, SNORA67*
16944618	0,0015109 28	3,534399 3	up	*CD86*
16917859	9,73E-05	4,794368	up	*CD93*
16914812	0,0066408 13	2,082344	up	*CEBPB*
16931957	0,0099426 82	2,407269	up	*CECR1*
17110463	0,0013828 82	2,803386 4	up	*CFP*
16719217	0,0084556 5	3,814614 3	up	*CHST15*
16747969	8,70E-04	5,507546 6	up	*CLEC4D*
16760928	0,0099395 34	5,541638 4	up	*CLEC4E*
16767335	0,0040787 57	3,078221 3	up	*CPM*
17115850	0,0064935 12	3,039102 6	up	*CSF2RA*
16812245	0,0014365 9	2,246109 9	up	*CTSH*
16692834	0,0029839 82	3,053258 4	up	*CTSS*
16840113	0,0086970 65	3,922129 6	up	*CXCL16*
17102538	0,0015077 26	4,091678 6	up	*CYBB*
16929741	0,0049009 81	2,760038 4	up	*CYTH4*
16766578	0,0091790 18	2,083415 3	up	*DDIT3*
17074331	0,0067227 26	7,772382 3	up	*DEFA3*
17020317	0,0030265 57	2,78100 9	down	*DST*
16807763	3,29E-04	2,06713	up	*EHD4*

		58		
16857519	0,00813037	2,9394345	up	*EMR1*
16869666	0,00602765	5,943998	up	*EMR3*
16707791	0,00434237 5	2,9276404	up	*ENTPD1*
16865540	0,00964296 5	2,9221234	up	*FCAR*
16672838	0,00172723 9	3,171388	up	*FCER1G*
17099707	0,00674669 8	3,0718722	up	*FCN1*
16749782	0,00313765 3	2,5362973	up	*FGD4*
16684056	0,00489724 9	2,4946132	up	*FGR*
16874945	0,00898172 2	3,9502516	up	*FPR1*
16856803	0,00236905 3	2,518824	up	*GADD45B*
16751420	0,00840584 4	2,11615	up	*GRASP*
16765606	0,00259593 4	3,211472	up	*GTSF1*
16912472	0,00988197 4	2,5060208	up	*HCK*
17040665	0,00680081 8	2,1340368	up	*HCP5*
17003124	0,00126424 4	3,8610282	up	*HK3*
16886105	0,00777041 4	2,0468018	up	*HNMT*
16711125	0,00140490 3	2,155436	up	*IDI1*
17017018	0,00610529 2	2,9106903	up	*IER3*
17028909	0,0036915 1	3,091701	up	*IER3*
17031687	0,0036915 1	3,091701	up	*IER3*
17034143	0,0036915 1	3,091701	up	*IER3*
17039184	0,00333560 6	3,0357895	up	*IER3*
17041752	0,0036915 1	3,091701	up	*IER3*
17024144	0,00296650 8	2,7105672	up	*IFNGR1*
17014364	0,0018820	3,22163	up	*IGF2R*

	58	65		
16870309	4,28E-04	2,1853335	up	*IL12RB1*
17106493	0,004448939	3,8981228	up	*IL13RA1*
16926813	0,001600789	2,6554327	up	*IL17RA*
16780917	0,002200992	2,9196057	up	*IRS2*
16818239	0,003770194	3,2051487	up	*ITGAM*
16779839	0,001081191	3,1469755	up	*KCTD12*
16886174	0,008290862	3,0796206	up	*KYNU*
16801835	0,005630794	2,3375442	up	*LACTB*
16726065	8,29E-04	3,0508142	up	*LGALS12*
16865383	0,005902581	3,0322115	up	*LILRA1*
16865370	0,009042381	2,4581518	up	*LILRA2*
16875448	0,001964127	4,273426	up	*LILRA5*
17122044	0,001520187	5,5004454	up	*LILRB3*
17122742	0,003525587	2,1280315	up	*LOC729296, MIR646HG, RP5-1043L13.1*
17122808	0,009569738	2,5920088	up	*LOC729296, MIR646HG, RP5-1043L13.1*
16867344	0,006248877	2,468071	up	*LRG1*
16870394	9,86E-04	4,039842	up	*LRRC25*
17006666	8,57E-04	2,1155338	up	*LST1*
17026272	3,38E-04	2,3492165	up	*LST1*
17027801	0,001103208	2,2592273	up	*LST1*
17030627	4,53E-04	2,3429246	up	*LST1*
17033344	0,001103208	2,2592273	up	*LST1*
17035425	4,53E-04	2,3429246	up	*LST1*
17038124	7,41E-04	2,2494597	up	*LST1*
17040719	7,17E-04	2,25737	up	*LST1*

		7		
17011832	0,0095853 98	2,24396 25	up	*MARCKS*
16823309	0,0058578 67	4,27272 7	up	*MEFV*
16839177	0,0088829 71	2,42157 9	up	*METRNL*
16752185	0,0066441 39	3,89149 57	up	*METTL7B*
17022422	0,0091801 35	2,11178 87	up	*MICAL1*
16846864	0,0091238 01	2,55283 43	up	*MMD*
16672362	0,0028697 94	3,68434 14	up	*MNDA*
16712825	0,0098051 95	2,25179 4	up	*MPP7*
16738819	0,0086377 26	3,13309 55	up	*MS4A6A*
16922959	0,0025018 82	2,48243 52	up	*MX2*
16713318	0,0092611 66	5,25641 87	up	*NAMPT, NAMPTL*
17046911	0,0094047 09	2,48312 38	up	*NCF1B*
16697095	0,0098626 94	3,31942 13	up	*NCF2*
16935607	0,0065371 25	2,57290 9	up	*NFAM1*
16875219	2,28E-04	4,18633 17	up	*NLRP12*
16875262	0,0062109 23	2,15923 38	up	*OSCAR*
16660059	0,0018353 84	3,73894 88	up	*PADI4*
16898326	0,0039953 97	3,57626 9	up	*PELI1*
16702175	0,0077439 37	2,92988 13	up	*PFKFB3*
16761726	0,0038438 64	4,45729 64	up	*PLBD1*
16664005	0,0062805 48	2,44354 1	up	*PLK3*
16685779	0,0033094 1	2,23467 3	up	*PPT1*
16920047	0,0094795 16	2,19868 45	up	*PREX1*
16710548	0,0094675 28	2,06349 87	up	*PTPRE*
16724633	0,0071303	2,92560	up	*PTPRJ*

	78	05		
16916901	0,00715643 5	2,07889 06	up	*RASSF2*
17120402	0,0056721 2	2,37279 32	up	*RP11-428P16.2, ZNF532*
16916485	0,0059698 1	2,57776 43	up	*RP4-576H24.2, SIRPD*
16876764	0,0063401 33	2,36943 72	down	*RSAD2*
16693409	0,0029576 4	6,38270 76	up	*S100A12*
16693414	0,0037979 88	2,92035 84	up	*S100A8*
16671139	0,0018447 41	3,55374 46	up	*S100A9*
17102129	0,0078739 91	2,24310 76	up	*SAT1*
16969558	0,0019957 47	2,59710 26	up	*SGMS2*
17122174	0,0025630 17	2,30487 8	up	*SIGLEC10, SIGLEC11, SIGLEC16*
16864639	0,0025675 9	3,64281 73	up	*SIGLEC9*
16910728	3,14E-04	2,35380 74	up	*SIRPA*
17049522	0,0030196 87	2,35989 83	up	*SLC12A9*
16738897	0,0045669 08	2,22870 95	up	*SLC15A3*
16839019	0,0060729 45	2,19013 02	up	*SLC16A3*
16984056	0,0020258 31	2,03324 03	up	*SLC1A3*
16760868	0,0013093 62	3,34798 77	up	*SLC2A3*
16768923	0,0042989 24	2,93541 5	up	*SLC9A7P1*
16919547	0,0080839 94	4,04251 86	up	*SLPI*
16977986	0,0069980 3	2,99287 99	down	*SNCA*
16815914	0,0044731 68	2,34118 6	up	*SNN*
17044442	0,0096502 84	2,13654	up	*SNX10*
16690566	0,0059302 51	3,21025 68	up	*SORT1*
17013279	0,0016463 94	2,91561 44	up	*STX11*
16661497	0,0059810	2,21554	up	*THEMIS2*

	39	66		
16975213	0,00514662 5	3,15827 6	up	*TLR1*
16699634	0,00378880 74	3,52253 87	up	*TLR5*
17101537	0,0062915 9	4,63175 44	up	*TLR8*
16980716	0,00743094 7	2,26815 77	up	*TMEM154*
17004859	0,00142659 7	2,35814 79	up	*TMEM170B*
17012946	0,00734557 5	3,15011 84	up	*TNFAIP3*
16659238	0,00740735 2	2,45842 81	up	*TNFRSF1B*
16776339	0,00706660 7	2,05908 47	up	*TNFSF13B*
17097653	0,0023086 3	4,24717 04	up	*TNFSF8*
16871546	0,00163015 2	2,92685 2	up	*TYROBP*
16710900	0,00966215 7	2,40909 5	up	*VENTX*
17023707	0,00144843 3	6,75556 23	up	*VNN1*
17023736	0,00738847 5	4,96664	up	*VNN2*
16818431	3,11E-04	2,53822 68	up	*ZNF267*
16765542	0,00359073 6	3,18594 31	up	*ZNF385A*

Supplementary Table 4. GSEA of genes differentially expressed in cases achieving or not a CR. Top 10 gene sets for Gene Ontology Biological Processes, Oncogenic Signatures and Curated Gene sets are shown.

Gene Set Name	# Genes in Gene Set (K)	# Genes in Overlap (k)	k/K	p-value	FDR q-value
DEFENSE RESPONSE	270	19	0,0704	1,56E-20	1,29E-17
IMMUNE SYSTEM PROCESS	332	13	0,0392	3,64E-11	1,50E-08
IMMUNE RESPONSE	235	11	0,0468	1,88E-10	5,17E-08
SIGNAL TRANSDUCTION	1634	23	0,0141	9,80E-10	2,02E-07
RESPONSE TO STRESS	508	13	0,0256	6,34E-09	1,05E-06
RESPONSE TO EXTERNAL STIMULUS	312	10	0,0321	4,75E-08	6,52E-06
RESPONSE TO WOUNDING	190	8	0,0421	1,38E-07	1,58E-05
INFLAMMATORY RESPONSE	129	7	0,0543	1,54E-07	1,58E-05
RESPONSE TO OTHER ORGANISM	83	6	0,0723	2,23E-07	2,05E-05
VERHAAK AML WITH NPM1 MUTATED UP	183	31	0,1694	2,19E-45	1,03E-41
MCLACHLAN DENTAL CARIES UP	253	29	0,1146	2,95E-37	6,97E-34
JAATINEN HEMATOPOIETIC STEM CELL DN	226	27	0,1195	3,28E-35	5,17E-32
MCLACHLAN DENTAL CARIES DN	245	24	0,098	3,26E-29	3,85E-26
RUTELLA RESPONSE TO CSF2RB AND IL4 DN	315	24	0,0762	1,49E-26	1,41E-23
CHEN METABOLIC SYNDROM NETWORK	1210	36	0,0298	2,10E-25	1,65E-22
BROWN MYELOID CELL DEVELOPMENT UP	165	19	0,1152	1,14E-24	7,72E-22
GAL LEUKEMIC STEM CELL DN	244	21	0,0861	1,90E-24	1,03E-21
TAKEDA TARGETS OF NUP98 HOXA9 FUSION 8D DN	205	20	0,0976	1,96E-24	1,03E-21
RUTELLA RESPONSE TO HGF VS CSF2RB AND IL4 UP	408	24	0,0588	7,28E-24	3,44E-21
RPS14 DN.V1 UP	192	21	0,1094	1,10E-26	2,07E-24
HOXA9 DN.V1 UP	194	13	0,067	4,05E-14	3,82E-12

STK33 UP	293	13	0,04 44	7,68E -12	4,84E- 10
STK33 SKM UP	290	12	0,04 14	1,13E -10	5,33E- 09
STK33 NOMO UP	294	11	0,03 74	1,99E -09	7,52E- 08
CAMP UP.V1 DN	200	8	0,04	2,04E -07	6,44E- 06
TBK1.DF UP	290	8	0,02 76	3,32E -06	8,96E- 05
AKT UP.V1 UP	172	6	0,03 49	1,56E -05	3,69E- 04
AKT UP MTOR DN.V1 UP	184	6	0,03 26	2,28E -05	4,80E- 04
PTEN DN.V1 UP	191	6	0,03 14	2,82E -05	4,98E- 04
Net-related signature					

Supplementary Table 5. *CD93*, *RASGRP63* and *CXCL16* expression evaluated by qPCR (DCt method)

	ΔCt(GRASP65-GAPDH)	*ΔCt(CXCL16-GAPDH)*	*ΔCt(CD93-GAPDH)*
T test: CR vs no CR	0,10	0,01	0,003
Median, CR	-1,07	-2,01	-5,51
Median, NR	1,01	1,46	-3,44
STDV CR	2,39	2,60	1,59
STDV NR	1,89	2,11	1,56