Supplementary Appendix

Supplement to: Steidl C, Lee T, Shah SP, et al. Tumor-associated macrophages and survival in classic Hodgkin's lymphoma. N Engl J Med 2010;362:875-85.

Supplementary material to manuscript “Tumor-Associated Macrophages and Survival in Classic Hodgkin’s Lymphoma” (Steidl et al.)

Supplemental Methods

Follow-up and risk stratification of patients:

In the gene expression cohort, the median follow-up time of living patients with treatment success was 3.9 years (range 0.5-21.0 years). In the immunohistochemistry group, median follow-up time was 4.0 years (range 0.5-20.8 years). For risk stratification according to the IPS, patients were dichotomized into two risk strata: low-risk group 0-3 points, high-risk group 4-7 points. For cases with missing variables normalized incomplete scores were calculated.

Gene expression analysis:

GEP were obtained using GeneChip HG 133 2.0 plus arrays (Affymetrix Inc., U.S.A) containing 54,120 probe sets for genome-wide analysis of the human transcriptome. Total RNA was extracted from multiple (10-20x) 20µm freshly cut tissue sections after mechanical homogenization using Allprep RNA extraction kits (Qiagen Inc., ON, Canada). 1-8 µg of extracted RNA were subsequently used to prepare biotinylated cRNA in a one-cycle reaction following routine protocols including reverse transcription and labeling in-vitro transcription reactions. 11µg of labeled cRNA were then hybridized on the array overnight and the arrays were washed, stained and scanned using Affymetrix Fluidics Station 450 and Affymetrix GeneChip Scanner. All 130 reported microarrays passed homogeneous criteria for testing quality control including present call rates >20% and normalized unscaled standard errors <1.05 (NUSE). Thirteen microarrays were excluded from analysis.

Data processing and statistical analysis

GE data was pre-processed and normalized by Robust Multichip Average (RMA) in R using Bioconductor.[1] To correct for any batch effects arising from combining the 100 samples from Vancouver and 30 from Nebraska, the COMBAT software written in R was used[2]. The correction was validated using Globaltest in Bioconductor, where the variable tested was “Microarray source”. A p-value of 0.00287 indicating significant differences between microarrays of different sources was corrected to 0.721 after batch adjustment. The last pre-processing step was global pre-filtering of probe sets, based on log2 intensity of 3 in 25% of cases. This resulted in 25,388 probe sets remaining for further analyses. Differentially expressed genes between treatment outcome groups were identified using 2-sample t-statistics (Bioconductor) and fold change. Raw p-values and false discovery rate (FDR) adjusted p-values according to Benjamini and Hochberg were reported.[3] FDR values below 0.10 (raw $p < 0.00123$) were considered significant. For unsupervised clustering we used 14,834 probe sets (27.1%) that were expressed with log-intensities ≥4 in ≥ 50% of cases. Overrepresentation and pathway analysis was performed using Ingenuity Pathway Analysis (Ingenuity® Systems, www.ingenuity.com). Differentially expressed genes were studied separately according to over- and under-expression in the treatment failure group. Associative testing of gene signatures and treatment outcome groups were performed using Globaltest version 4.6.0 (Bioconductor). Raw, unadjusted p-values < 0.05 were reported as significant.

Immunohistochemistry and TMA construction:

1.5mm duplicate cores were obtained from representative areas containing HRS cells of 166 diagnostic biopsies of cHL, evaluated by both morphology and IHC stains performed for routine-diagnostic purposes. TMA sections were stained for CD68 (Dako, KP1), MMP11 (Abcam, ab52904), CD20 (Dako, L26), CD3 (polyclonal, Cell Marque) and CD30 (Dako, Ber-H2) following routine protocols for automated immunohistochemistry on the Ventana Benchmark XT (Ventana Medical Systems, Tucson, Arizona). The slides were independently scored by RDG, GH and PF. For CD68 staining, cells were scored in three representative high-power fields (tumor cell regions) and the relative percentage of CD68+ cells in relation to overall cellularity was reported as an average of both duplicate cores according to four groups: <5% IHC score 1, 5-25% IHC score 2, >25-50% IHC score 3 and > 50% IHC score 4. However, there were only eight cases with > 50% CD68+ macrophages and thus this latter group was merged with cases showing 25-50% (IHC score 3). Elevated numbers of CD68+ cells were defined as IHC scores 2 and 3 according to a threshold of 5% established on 5 benign tonsil controls and previous studies[4]. Subgroup analysis of limited-stage cHL patients included a total of 41 cases. Due to the small sample size in IHC scoring groups 3 & 4 (n = 5 and n = 1, respectively), these groups were merged with IHC score group 2 (n = 17) for the purposes of DSS analysis. Discrepant cases were centrally reviewed to reach consensus. To control for case to case histologic variability, areas of sclerosis, necrosis and presence of primary or secondary lymphoid follicles, we recorded: 1) HRS cell CD20 positivity 2) positivity of the surrounding reactive small B cells only (excluding sclerotic areas and follicles) and 3) presence of B cell follicles. MMP11 staining was recorded as the overall cellularity of MMP11+ cells: IHC score 0 (no positivity), IHC score 1 (<1% of cells), IHC score 2 (1-10% of cells) and IHC score 3 (>10% of cells). Positive cells included Reed-Sternberg cells, macrophages and microvessels.

Predictive models:

We trained a classifier using sparse multinomial logistic regression (SMLR). Our aim was to build a robust discriminative model that is predictive of treatment failure in addition to identifying a small set of features (genes) that are able to separate the data into the respective outcome groups. SMLR imposes a sparsity promoting prior distribution that models whether a gene should be considered in the construction of the classifier. As such, the model heavily penalizes a gene for being included in the feature set, resulting in a small set of discriminative features that are strongly supported by the data. SMLR performs feature selection and classification simultaneously.[5] We trained an SMLR classifier using leave-one-out cross validation (LOOCV) analyzing pretreatment data of the 130 patients with diagnostic lymph node biopsies. For feature selection in the training sets we also included the 7 clinical variables as defined in the IPS (age, Ann Arbor stage, sex, albumin, absolute lymphocyte count, lymphocyte percentage and hemoglobin) in addition to the 25,388 gene expression probe sets. We measured classification accuracy using a Receiver Operator Characteristic (ROC) curve, the Area under Curve (AUC), the confusion matrix and class-specific error rates. The outcome failure (F) was assigned to be the positive class and outcome success (S) the negative class, leading to the following definitions: prediction F, true F = true positive (TP); prediction F, true S = false positive (FP); prediction S, true F = false negative (FN); prediction S, true S = true negative (TN).

We compared three types of input data with respect to predictor performance: gene expression data only, clinical variables only, combination of the two.

For determining relative variable importance we created Random Forests (RF)[6] using the SMLR selected features. Following settings were used: number of predictors considered for each node: square root (number of input variables), number of trees to build: 10,000, class weights: balanced. A ranked list of these variables (relative variable importance) was plotted using the standard method, which is based on randomizing of the variable values and measuring the resultant decline in model accuracy.

Figure S1: Gene expression study cohort of 130 patients with classical Hodgkin lymphoma. Dichotomy of comparison groups according to clinical extremes: primary treatment success *vs* failure

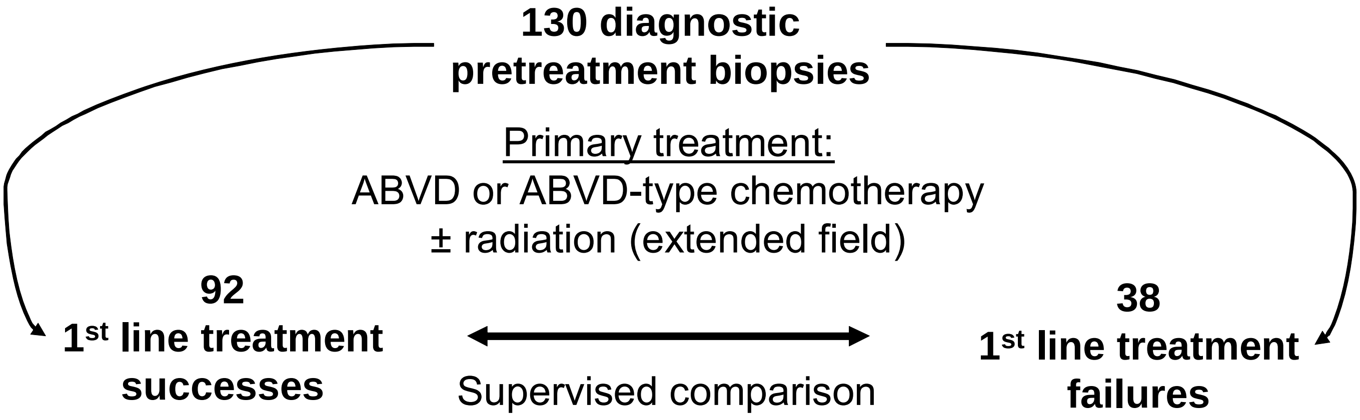
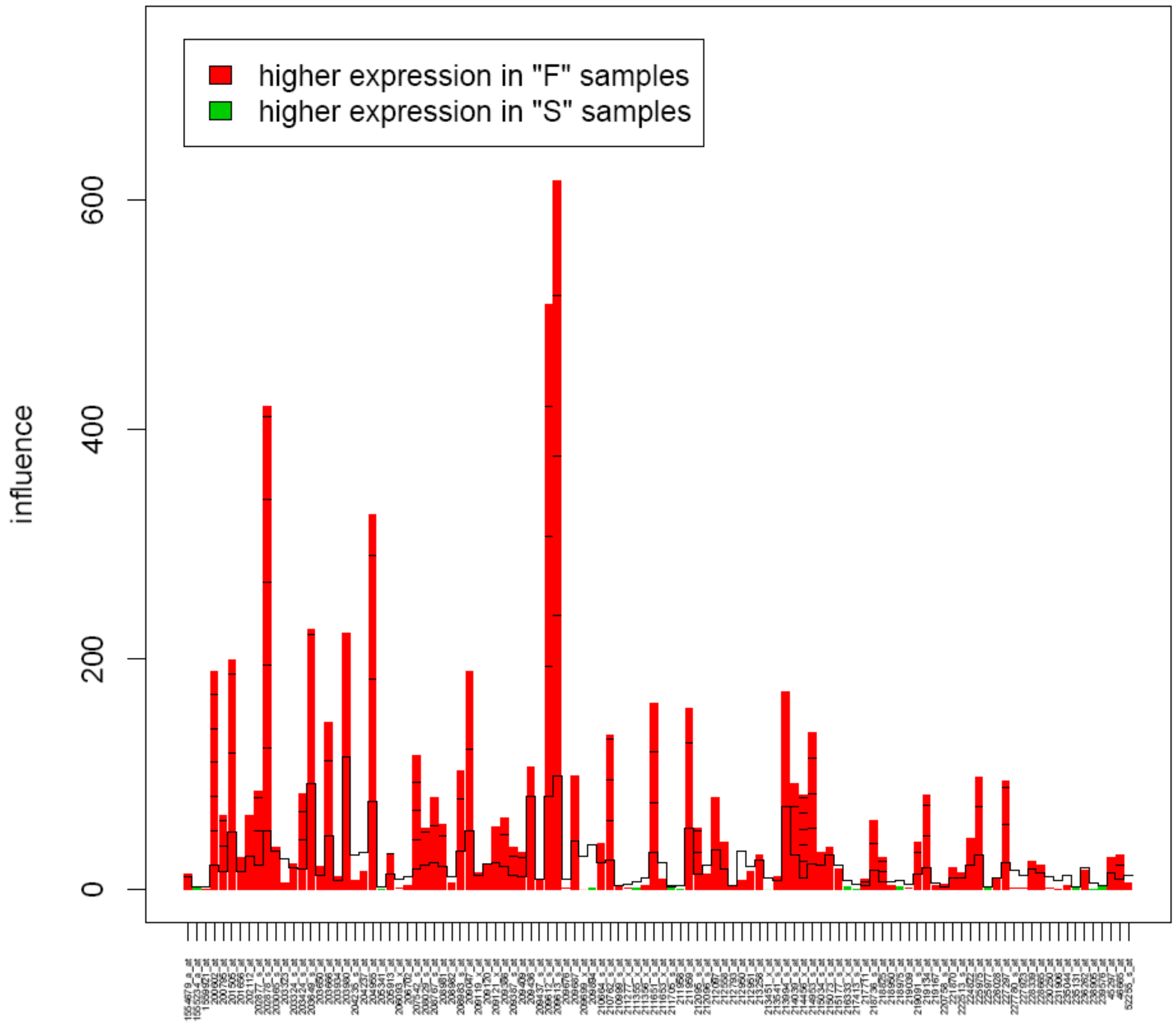
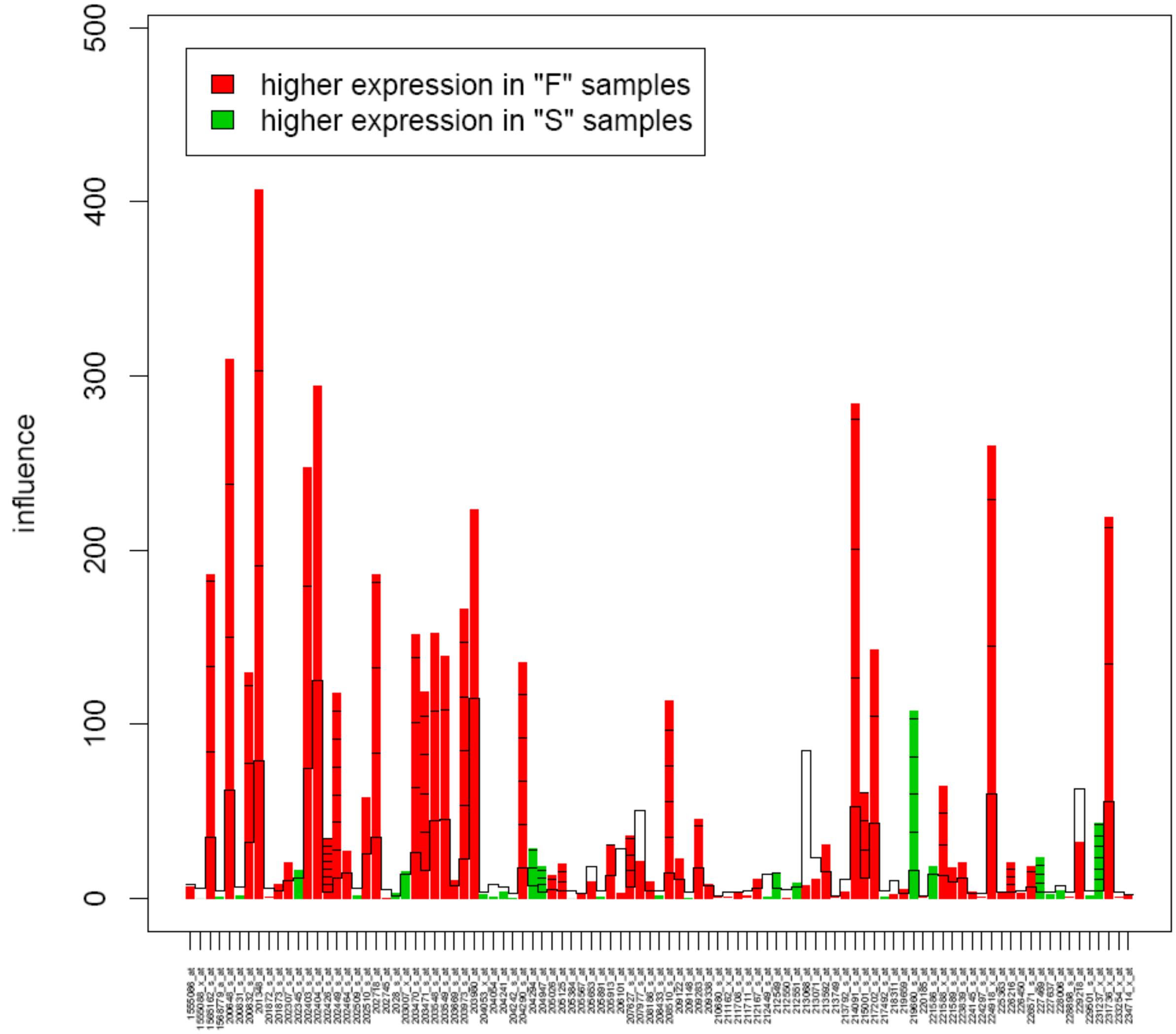


Figure S2: Global test diagrams (probe set influence)

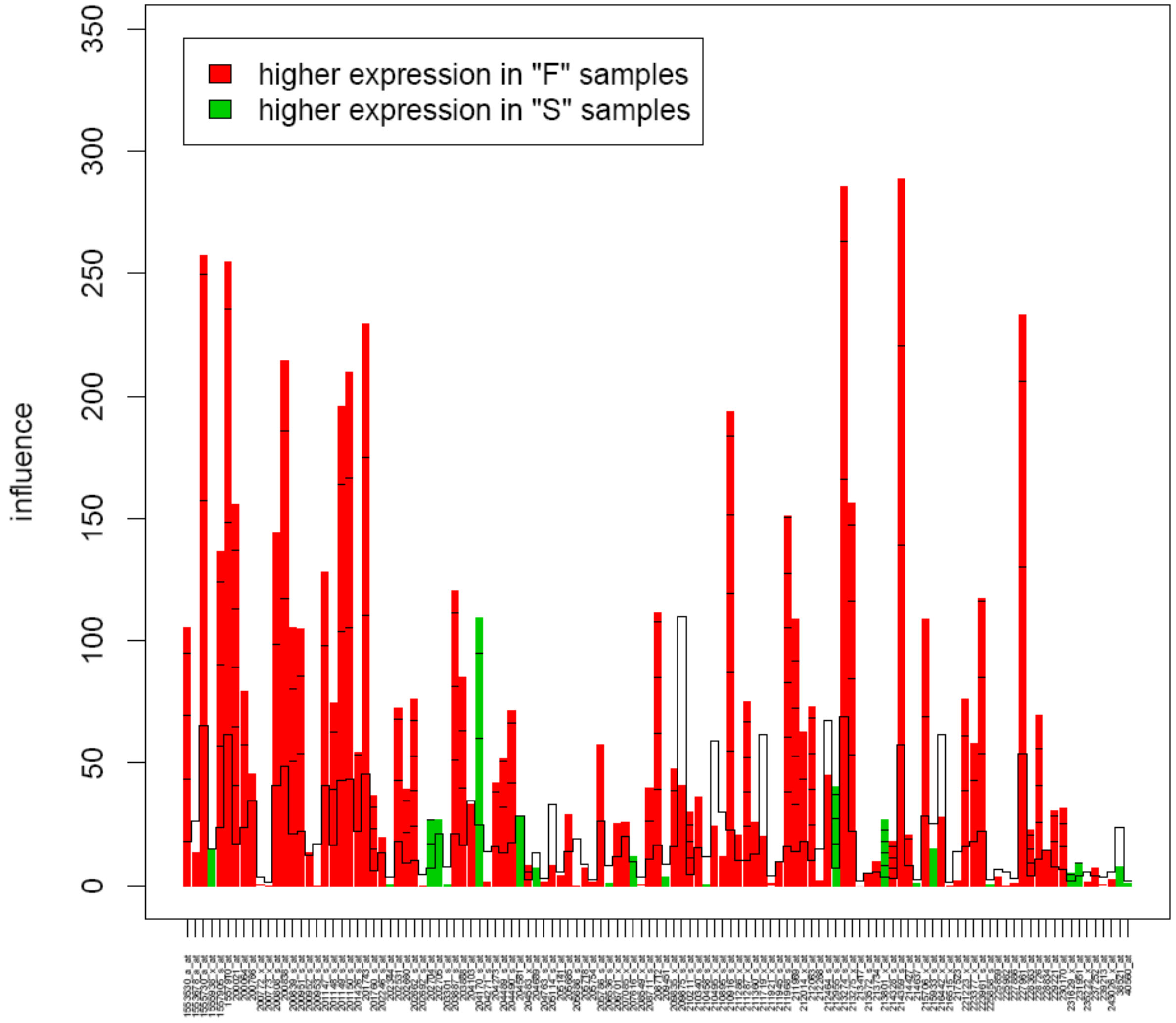
A. Angiogenesis signature[7]:



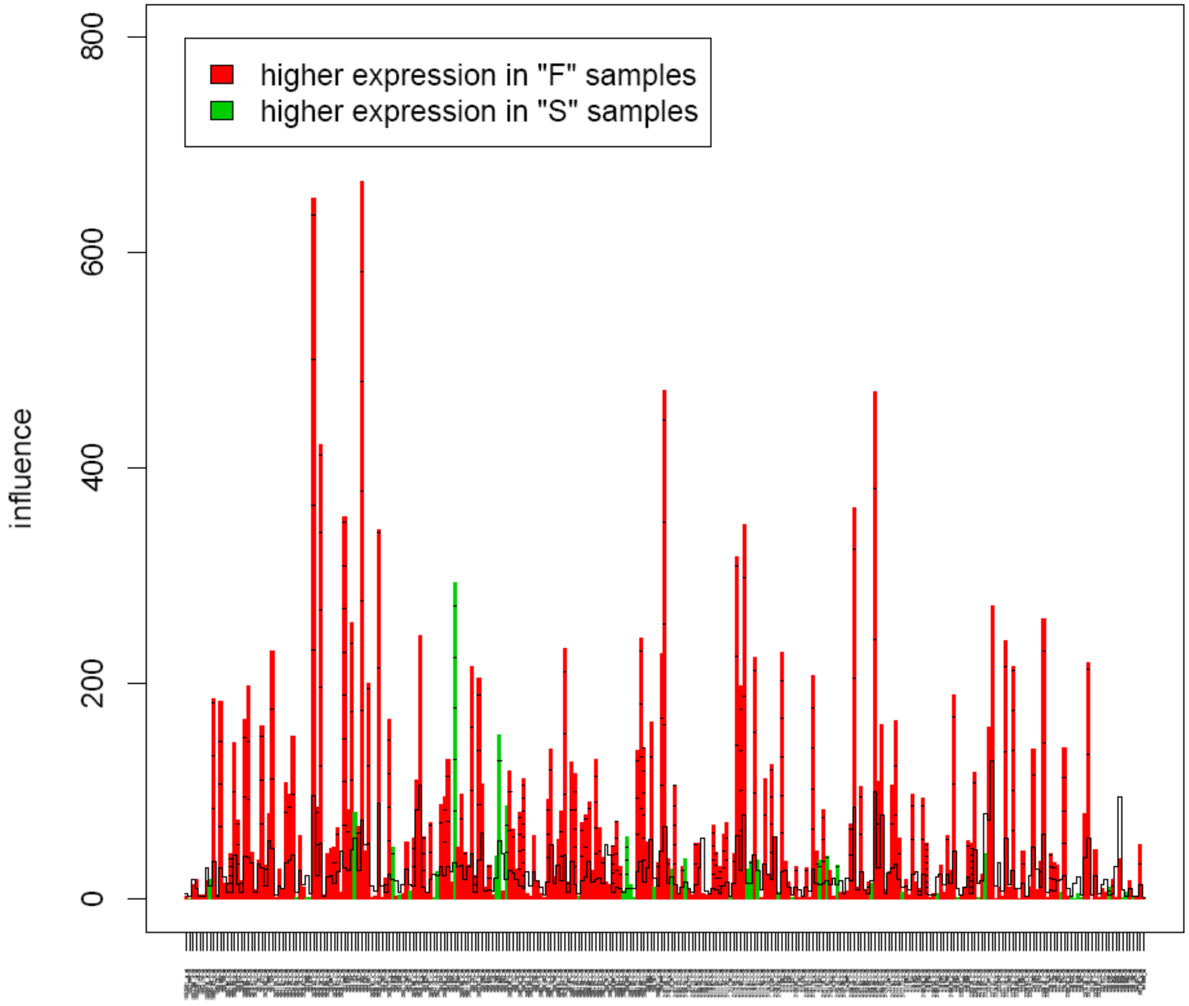
B. Adipocyte signature[8]:



C. Tumor-associated macrophage signature[9]:



D. Resting monocyte signature[10]:



Supplementary table S1: Association of previously described gene signatures with treatment outcome: Results of Global Test. Signatures with p-values < 0.05 are shown.

Name of signature	**# of probe sets**	**Reference**	**Primary treatment outcome: success (92) vs. failure (38)**	**Most influential genes in signature**
All genes	25388	Affymetrix UA 133 2.0 Plus	0.020	-
Comparison I: primary treatment failure vs success	315	present study	1.56×10^{-6}	DDX3Y, HRH1, PYGL, ETS2, LHFP
Microenvironment: Up-regulated in treatment failure	194	Sanchez-Aguilera et al., Blood 2006[11]	0.036	FKBP5, LYZ, ARF3, CTSL1
Resting NK cells	97	Su et al., PNAS 2004[10]	0.031	FCGR3A, FCGR3B, ADAMTS1, APOL1, LAIR1
Germinal center B cells (GCB)	497	Dave et al., NEJM 2006[12]	0.012	RGS13, CR2, ELL3, CCDC23
Erythroid progenitors	287	Su et al., PNAS 2004[10]	0.029	TGM2, GLUL, ITSN1, AQP1, FLII
Tumor-associated macrophages	117	Duff et al., J Surg Res 2007[9]	0.017	HSP90AB3P, HSP90AB1, CTSB, CFL1
Adipocyte	97	Urs et al., J Nutr 2004[8]	0.012	GLUL, MGST1, COL1A2, FABP4
Plasmacytoid dendritic cells (CD123+)	507	Lindstedt et al., J Immunol 2005[13]	0.046	SRPX, CTSB, APP
Angiogenesis	108	Lenz et al, NEJM 2008[7]	0.036	ADH1B, CD93, SRPX, PLA2G2A
HRS cells	26	Karube et al., Annals of Oncology 2006[14]	0.047	CSF1R, TNFSF12, TNFSF13, CCL26, TNFSF12
Macrophages	153	Martinez et al., J Immunology 2006[15]	0.022	CCL13, MS4A4A, CCL23, VCAN
Resting monocytes	279	Su et al., PNAS 2004[10]	0.014	F13A1, SERPINA1, LILRB2, VCAN, CD93
TGFβ	108	Kang et al., Mol Cell 2003[16]	0.046	SLC39A8, P4HB, CYP1B1, HYOU1, PEA15

Based on the chosen threshold (FDR <0.1), we found 315 probe sets, corresponding to 271 genes, of which 99 were up-regulated (range of fold change: 1.11 – 1.85) and 172 down-regulated (range of fold change: 1.09 – 2.45) in the treatment failure specimens

Supplementary table S2: Differentially expressed genes upregulated in primary treatment failures

Probe set	Gene name	Accession	Unigene	Fold change	t-test	p value (BH)
205579_at	HRH1	NM_000861	Hs.1570	1.85326961	0.00050318	0.078374371
205001_s_at	DDX3Y	AF000985	Hs.99120	1.81999456	0.00116307	0.098766639
202990_at	PYGL	NM_002863	Hs.282417	1.67835322	0.00087501	0.091749041
201328_at	ETS2	AL575509	Hs.644231	1.58559345	3.15E-05	0.033668997
211936_at	HSPA5	AF216292	Hs.605502	1.46375846	4.79E-05	0.036882453
208744_x_at	HSPH1	BG403660	Hs.36927	1.44735275	0.00056662	0.081272377
219952_s_at	MCOLN1	NM_020533	Hs.631858	1.41880364	0.00096727	0.09555248
200841_s_at	EPRS	AI142677	Hs.497788	1.40329156	0.0007492	0.089203621
208980_s_at	UBC	M26880	Hs.520348	1.40123566	0.0010492	0.098656287
217967_s_at	FAM129A	AF288391	Hs.518662	1.38122415	0.00086376	0.091749041
201562_s_at	SORD	NM_003104	Hs.878	1.37260388	0.00071388	0.089012925
233587_s_at	SIPA1L2	AK022852	Hs.268774	1.34365584	0.00020268	0.059215133
202290_at	PDAP1	NM_014891	Hs.632296	1.34216119	0.00022545	0.059215133
214438_at	HLX	M60721	Hs.74870	1.33083744	0.00039087	0.073506049
215764_x_at	AP2A2	AA877641	Hs.19121	1.32927195	0.00083005	0.091622871
218656_s_at	LHFP	NM_005780	Hs.507798	1.32853009	0.00014406	0.056702817
208658_at	PDIA4	BC000425	Hs.93659	1.32330225	0.00091837	0.093753425
229748_x_at	LOC389833	AI380156	Hs.487562	1.31306273	0.00112303	0.098766639
201218_at	CTBP2	N23018	Hs.501345	1.31035401	0.00054096	0.079848534
200021_at	CFL1	NM_005507	Hs.170622	1.30982796	0.00112127	0.098766639
200602_at	APP	NM_000484	Hs.706742	1.30681764	0.00112321	0.098766639
206278_at	PTAFR	D10202	Hs.433540	1.29673093	0.00037933	0.071868134
200895_s_at	FKBP4	NM_002014	Hs.524183	1.28825821	0.0011594	0.098766639
221565_s_at	FAM26B	BC000039	Hs.241545	1.27355229	0.00014713	0.056702817
222883_at	C1orf163	NM_023077	Hs.584966	1.27259204	8.19E-06	0.02512121
202972_s_at	FAM13A1	AW450403	Hs.708044	1.26059155	0.0002944	0.064602987
396_f_at	EPOR	X97671	Hs.631624	1.25879139	4.36E-06	0.02512121
201160_s_at	CSDA	AL556190	Hs.221889	1.25671023	3.64E-05	0.033668997
239648_at	DCUN1D3	AI765327	Hs.101007	1.25469702	0.00049059	0.077361389
215434_x_at	NBPF10	AV684285	Hs.515947	1.25419432	0.00022223	0.059215133
208757_at	TMED9	BC001123	Hs.279929	1.25318149	1.18E-05	0.02512121
212360_at	AMPD2	AI916249	Hs.82927	1.25296285	0.00012385	0.053088367
223658_at	KCNK6	AF134149	Hs.240395	1.25208322	0.00067452	0.086695267
200616_s_at	KIAA0152	BC000371	Hs.507074	1.25137228	0.00122449	0.099492613
1568658_at	LOC339804	BU069195	Hs.140617	1.24722139	0.00074208	0.089203621
211990_at	HLA-DPA1	M27487	Hs.347270	1.24585944	0.00024894	0.06019139

235964_x_at	C20orf118	AA603344	Hs.472630	1.24493115	0.00107188	0.098766639
212517_at	ATRN	AL132773	Hs.276252	1.24426369	0.00072089	0.089012925
214709_s_at	KTN1	Z22551	Hs.509414	1.24184665	5.27E-06	0.02512121
201138_s_at	SSB	BG532929	Hs.632535	1.23826027	0.00118727	0.099152736
205196_s_at	AP1S1	NM_001283	Hs.489365	1.23711331	0.00110486	0.098766639
221196_x_at	BRCC3	NM_024332	Hs.558537	1.23322335	0.00059763	0.083826486
203598_s_at	WBP4	AK000979	Hs.411300	1.23151015	8.22E-05	0.045391733
211257_x_at	ZNF638	AF273049	Hs.434401	1.22943283	0.00094753	0.094336333
1569057_s_at	MIA3	BC031805	Hs.118474	1.22569834	0.0008283	0.091622871
220734_s_at	LOC727825	NM_030575	NA	1.22244948	0.00012529	0.053088367
203112_s_at	WHSC2	NM_005663	Hs.21771	1.21923678	0.00032081	0.0665277
212495_at	JMJD2B	BE256900	Hs.654816	1.21589933	0.00105371	0.098714268
221653_x_at	APOL2	BC004395	Hs.474740	1.21363006	0.00072576	0.089012925
225639_at	SKAP2	N21390	Hs.200770	1.20986748	0.00098819	0.096200079
218436_at	SIL1	NM_022464	Hs.483521	1.20827352	0.00064013	0.085316284
225011_at	PRKAR2A	AK026351	Hs.631923	1.20700879	0.00053761	0.079848534
212116_at	TRIM27	NM_006510	Hs.440382	1.20412544	0.00053927	0.079848534
223195_s_at	SESN2	BF131886	Hs.469543	1.20304504	0.00010722	0.050408712
227430_at	ZC3H10	AI969773	Hs.632706	1.20247426	0.00012998	0.054095349
205641_s_at	TRADD	NM_003789	Hs.460996	1.20148734	3.38E-05	0.033668997
200874_s_at	NOL5A	BE796327	Hs.376064	1.20099459	0.00064186	0.085316284
201545_s_at	PABPN1	NM_004643	Hs.117176	1.2005158	0.00086303	0.091749041
207270_x_at	CD300C	NM_006678	Hs.2605	1.19998951	0.00022624	0.059215133
220326_s_at	FLJ10357	NM_018071	Hs.35125	1.19527808	0.00079201	0.089765343
202065_s_at	PPFIA1	BG033593	Hs.530749	1.19507504	0.00052733	0.079848534
225038_s_at	SURF6	AI745183	Hs.274430	1.19502314	0.00121519	0.099492613
222200_s_at	BSDC1	AK021440	Hs.353454	1.19388957	0.00041027	0.073872559
213491_x_at	RPN2	AL514285	Hs.370895	1.19327318	0.00074906	0.089203621
203773_x_at	BLVRA	NM_000712	Hs.488143	1.19317843	0.00063309	0.085316284
212723_at	JMJD6	AK021780	Hs.514505	1.18963566	0.00027687	0.062759913
201327_s_at	CCT6A	NM_001762	Hs.82916	1.18924954	0.00040161	0.073872559
204104_at	SNAPC2	NM_003083	Hs.631860	1.18668957	0.00018567	0.059029899
231846_at	FOXRED2	AK026975	Hs.387601	1.18431776	0.00113726	0.098766639
212953_x_at	CALR	BE251303	Hs.515162	1.18414591	0.00016879	0.059029899
38964_r_at	WAS	U12707	Hs.2157	1.18368424	0.00104709	0.098656287
241706_at	CPNE8	AA431782	Hs.40910	1.18222817	0.00115777	0.098766639
204968_at	C6orf47	NM_021184	Hs.247323	1.17799504	0.00024029	0.059526355
1567013_at	NFE2L2	AF323119	Hs.155396	1.17537586	0.00093429	0.093753425
201557_at	VAMP2	NM_014232	Hs.25348	1.17319481	0.0003725	0.071643845
227374_at	EARS2	AA833716	Hs.696113	1.17149424	2.96E-05	0.033668997
226857_at	ARHGEF19	AW170520	Hs.591532	1.1712303	0.00088152	0.091749041
235810_at	ZNF182	AI225224	Hs.189690	1.17066055	0.00104478	0.098656287
212678_at	NF1	AW054826	Hs.113577	1.16934995	0.00121252	0.099492613
218305_at	IPO4	NM_024658	Hs.411865	1.16758933	0.00085949	0.091749041
229940_at	SETD3	BF448048	Hs.510407	1.16324319	0.00120273	0.099492613
228452_at	C17orf39	AA827865	Hs.187422	1.16319022	0.00110886	0.098766639
202426_s_at	RXRA	BE675800	Hs.590886	1.15429438	0.00101492	0.096780767
227151_at	SNX33	BE464841	Hs.8705	1.15066916	0.00099656	0.096200079
224434_s_at	MORG1	BC005870	Hs.657204	1.14950591	0.00044506	0.0758362
222647_at	SLC35C1	BC001427	Hs.12211	1.14531187	0.00092084	0.093753425

203488_at	LPHN1	NM_014921	Hs.654658	1.14308961	8.67E-05	0.045391733
40850_at	FKBP8	L37033	Hs.173464	1.14157722	0.00027264	0.062759913
204413_at	TRAF2	NM_021138	Hs.522506	1.13714867	0.00117876	0.098766639
223365_at	DHX37	BC004463	Hs.107382	1.13689555	8.76E-05	0.045391733
217776_at	RDH11	AF167438	Hs.226007	1.13663895	0.00076401	0.089385311
217205_at	CCDC129	Y08772	Hs.224269	1.13203871	0.00122272	0.099492613
31861_at	IGHMBP2	L14754	Hs.503048	1.13118871	4.96E-05	0.036999761
219417_s_at	C17orf59	NM_017622	Hs.129563	1.13015825	0.00040262	0.073872559
40255_at	DDX28	AC004531	Hs.458313	1.12623536	0.0002818	0.063311987
221187_s_at	FUZ	NM_025129	Hs.288800	1.12621501	0.00044325	0.0758362
205441_at	OCEL1	NM_024578	Hs.422676	1.12334939	0.00018318	0.059029899
220605_s_at	SIRT2	NM_012237	Hs.466693	1.11677479	0.0001988	0.059215133
210160_at	PAFAH1B2	BC000398	Hs.696131	1.11290317	0.00109169	0.098766639

Supplementary table S3: Differentially expressed genes downregulated in primary treatment failures

Probe set	Gene name	Accession	Unigene	Fold change	t-test	p value (BH)
204450_x_at	APOA1	NM_000039	Hs.633003	1.08823417	0.00121339	0.099492613
243228_at	GTF3C4	BF980709	Hs.656646	1.08998422	0.00034464	0.06889468
213347_x_at	RPS4X	AW132023	Hs.446628	1.09941179	0.00114473	0.098766639
1568590_at	ARL3	BU619321	Hs.182215	1.10078537	0.00044386	0.0758362
234751_s_at	NLGN3	AF217413	Hs.438877	1.10784897	0.00025944	0.061483391
227879_at	ALKBH7	AI245026	Hs.111099	1.1100844	0.00031228	0.066068984
1561127_at	C10orf109	AF086274	Hs.568831	1.11529943	0.00021036	0.059215133
239855_at	PPM1L	AI692675	Hs.389027	1.11711547	0.00057725	0.082331942
211279_at	NRF1	L22454	Hs.654363	1.1172822	0.00116867	0.098766639
200088_x_at	RPL12	AK026491	Hs.408054	1.11798219	0.00111921	0.098766639
213466_at	RAB40C	BE965869	Hs.459630	1.11857982	0.00075191	0.089203621
223653_x_at	BRUNOL4	AW593887	Hs.435976	1.11858433	0.00050628	0.078374371
209985_s_at	ASCL1	BE797438	Hs.707985	1.12096974	0.0002921	0.064602987
225596_at	KLC4	AW080609	Hs.655123	1.12226759	0.00067722	0.086695267
234696_at	LOC138652	AL136097	NA	1.12227167	1.39E-05	0.025229048
221240_s_at	B3GNT4	NM_030765	Hs.363315	1.12329129	0.00055897	0.080630633
240742_at	LOC650656	AI218924	NA	1.12339152	5.42E-05	0.038249644
223740_at	RIPPLY2	AL136708	Hs.664873	1.12389088	0.00085068	0.091749041
213321_at	BCKDHB	AL531533	Hs.654441	1.12517393	0.0010585	0.098766639
231272_at	MED7	AW295321	Hs.279902	1.12581419	0.00021519	0.059215133
229080_at	EMID2	BE741432	Hs.654854	1.12669665	9.43E-06	0.02512121
219905_at	ERMAP	NM_018538	Hs.439437	1.12743476	0.00089495	0.092361987
207680_x_at	PAX3	NM_013942	Hs.42146	1.12997027	0.00066281	0.086695267
238265_x_at	METRNL	BF514885	Hs.591142	1.13217638	0.00119921	0.099492613
211691_x_at	OAZ1	AF293339	Hs.446427	1.13496	0.00121756	0.099492613
206097_at	SLC22A18AS	NM_007105	Hs.300076	1.13607094	0.00076215	0.089385311
242048_at	PFDN6	BE905316	Hs.446374	1.13688586	7.86E-05	0.045391733
221775_x_at	RPL22	BG152979	Hs.515329	1.1369217	0.00021749	0.059215133
229474_at	MICAL3	BF055090	Hs.528024	1.13964078	0.00045877	0.076391192

244028_at	USP15	AW629399	Hs.434951	1.13983285	0.00093369	0.093753425
202588_at	AK1	NM_000476	Hs.175473	1.14543123	0.00048655	0.077203311
1553507_a_at	GPR6	NM_005284	Hs.46332	1.14761367	0.00040927	0.073872559
207408_at	SLC22A14	NM_004803	Hs.165559	1.14839124	0.0001871	0.059029899
227829_at	GYLTL1B	AW272738	Hs.86543	1.14943364	0.00036694	0.071339854
206709_x_at	GPT	NM_005309	Hs.103502	1.14950079	7.11E-05	0.045391733
242030_at	SLC4A1AP	AI934909	Hs.306000	1.15278215	0.00098411	0.096200079
216042_at	TNFRSF25	AI275938	Hs.462529	1.15299326	0.00012547	0.053088367
231020_at	ARX	AI341389	Hs.300304	1.15559733	0.0011756	0.098766639
217095_x_at	NCR1	AJ006122	Hs.97084	1.15787367	0.00015493	0.057843937
220179_at	DPEP3	NM_022357	Hs.302028	1.15844131	0.00076213	0.089385311
220086_at	IKZF5	NM_022466	Hs.501289	1.1585181	8.11E-05	0.045391733
210530_s_at	NR2C1	M21985	Hs.108301	1.15862711	0.0008475	0.091749041
206430_at	CDX1	NM_001804	Hs.1545	1.16077864	0.00018929	0.059029899
1557532_at	NDUFA7	AA749262	Hs.333427	1.16235583	0.00078776	0.089684824
235908_at	MMP11	AW511464	Hs.143751	1.16441778	2.35E-05	0.033668997
216342_x_at	LOC390183	AL121916	NA	1.1661232	0.00123234	0.099492613
219811_at	DGCR8	NM_022720	Hs.643452	1.16673227	0.00018858	0.059029899
206131_at	CLPS	NM_001832	Hs.1340	1.1679669	3.44E-07	0.008742804
1559061_at	LOC253962	BC041476	Hs.558704	1.16965839	4.65E-05	0.036882453
208672_s_at	SFRS3	BC000914	Hs.405144	1.16967679	0.00050452	0.078374371
1569206_at	TCP11L2	BC017872	Hs.696047	1.17025082	0.00043689	0.0758362
242356_at	VTI1A	BE613520	Hs.194554	1.17047465	0.00041009	0.073872559
209460_at	ABAT	AF237813	Hs.336768	1.17063794	0.00081691	0.091622871
209746_s_at	COQ7	AF032900	Hs.157113	1.17200346	0.00023342	0.059260984
244063_at	BTN2A1	AW235118	Hs.159028	1.17338314	0.00074087	0.089203621
228208_x_at	ZNF354C	AL134573	Hs.445740	1.17647457	0.00098631	0.096200079
1553857_at	IGSF22	NM_173588	Hs.434152	1.17789261	9.00E-05	0.04569847
228870_at	FAM84B	BF732683	Hs.124951	1.17821038	0.00060841	0.084296206
208234_x_at	FGFR2	NM_022976	Hs.533683	1.17839428	0.00043104	0.0758362
230955_s_at	C20orf112	AL034550	Hs.516978	1.18005804	0.00015076	0.057126803
231237_x_at	E2F5	BF434182	Hs.445758	1.18185685	0.00077216	0.089514015
223766_at	LOC100133130	AF130105	Hs.662127	1.18557825	0.00019921	0.059215133
221025_x_at	PUS7L	NM_031292	Hs.445814	1.18695978	1.29E-05	0.02512121
228755_at	GIGYF1	NM_022574	Hs.708210	1.18901759	0.00092882	0.093753425
226385_s_at	C7orf30	BG397444	Hs.87385	1.1905074	0.00115642	0.098766639
209510_at	RNF139	AF064801	Hs.632057	1.19250155	0.00101782	0.096780767
1554063_at	C8orf76	BC012379	Hs.521800	1.19351296	0.0004526	0.076096125
211125_x_at	GRIN1	AF015730	Hs.558334	1.19510985	5.36E-05	0.038249644
229891_x_at	KIAA1704	AI630799	Hs.507922	1.19823231	0.00117809	0.098766639
225281_at	C3orf17	AK024325	Hs.591288	1.19857447	0.00013402	0.05478537
214980_at	UBE3A	AF037219	Hs.654383	1.20339446	3.86E-05	0.033668997
212963_at	TM2D1	BF968960	Hs.656790	1.20474995	0.00115567	0.098766639
1555874_x_at	MGC21881	BC019880	Hs.658041	1.2054457	0.00108593	0.098766639
212243_at	Gcom1	BE645501	Hs.437256	1.20603219	0.00046216	0.076391192
219448_at	TMEM70	BC002748	Hs.106650	1.20929752	0.00111229	0.098766639
200949_x_at	RPS20	NM_001023	Hs.8102	1.21287814	0.00017491	0.059029899
221255_s_at	TMEM93	NM_031298	Hs.30011	1.21343023	0.00116362	0.098766639
230005_at	SVIP	AI742358	Hs.349096	1.21384611	0.00114836	0.098766639
227747_at	MPZL3	AA772172	Hs.15396	1.2139417	0.00026155	0.061483391

223763_at	DTNBP1	AL136637	Hs.571148	1.21576394	0.00077062	0.089514015
225893_at	RC3H1	AL589593	Hs.30258	1.21588248	0.00043831	0.0758362
226836_at	SFT2D1	AA044813	Hs.487143	1.21774814	0.00086812	0.091749041
227440_at	ANKS1B	AW005572	Hs.506458	1.21802061	0.00100281	0.096436539
213195_at	NOS2A	AI625844	Hs.706746	1.21862101	0.00109111	0.098766639
200019_s_at	FAU	NM_001997	Hs.387208	1.21908847	0.00048212	0.077203311
235237_at	LOC203547	AI740565	Hs.58633	1.21910024	0.00022274	0.059215133
217187_at	MUC5AC	Z34282	Hs.534332	1.22384194	1.67E-05	0.028249142
215022_x_at	ZNF33B	BG429214	Hs.499453	1.22726061	0.00123445	0.099492613
213893_x_at	PMS2L1	AA161026	Hs.634244	1.22749409	0.00067297	0.086695267
227416_s_at	ZCRB1	BE265803	Hs.496279	1.22845028	0.00086629	0.091749041
205019_s_at	VIPR1	NM_004624	Hs.348500	1.22937405	0.00026652	0.0620764
208544_at	ADRA2B	NM_000682	Hs.247686	1.23127639	1.33E-06	0.016849661
227447_at	SKIV2L2	AA525163	Hs.274531	1.23172537	0.00016075	0.059029899
220743_at	C16orf72	NM_014117	Hs.221497	1.23404053	6.56E-05	0.04383725
240434_at	ABLIM2	AW293517	Hs.233404	1.23413524	0.00045086	0.076096125
240172_at	ERGIC2	AA102332	Hs.339453	1.23426665	0.00023154	0.059260984
215100_at	C6orf105	AL022724	Hs.126409	1.23464259	0.00033908	0.068322672
235130_at	PANK2	AV703394	Hs.516859	1.23592178	0.00010697	0.050408712
224801_at	NDFIP2	AI655642	Hs.525093	1.23911352	0.00068296	0.086695267
212283_at	AGRN	AI424797	Hs.273330	1.23990401	7.84E-06	0.02512121
208697_s_at	EIF3E	BC000734	Hs.405590	1.24402151	0.00048092	0.077203311
205145_s_at	MYL5	NM_002477	Hs.410970	1.24511597	0.00036545	0.071339854
1555858_at	LOC440944	CA430188	Hs.598958	1.24661708	0.00088787	0.092005417
228566_at	P15RS	AA778694	Hs.464912	1.25198321	0.00011177	0.051594931
203260_at	HDDC2	NM_016063	Hs.32826	1.25205948	0.00036811	0.071339854
206648_at	ZNF571	NM_016536	Hs.590944	1.25404936	0.0009941	0.096200079
235193_at	KIAA1370	BG036618	Hs.152385	1.25693699	9.87E-05	0.048196407
204491_at	PDE4D	R40917	Hs.117545	1.2588656	0.00074695	0.089203621
227861_at	TMEM161B	AI650251	Hs.379972	1.26819884	0.00107194	0.098766639
205613_at	SYT17	NM_016524	Hs.258326	1.27103944	0.00115762	0.098766639
1557360_at	LRPPRC	CA430402	Hs.368084	1.27455827	0.00062521	0.085316284
218007_s_at	RPS27L	NM_015920	Hs.108957	1.27714081	0.00063654	0.085316284
226014_at	EIF3F	BF115977	Hs.516023	1.28277254	0.00078729	0.089684824
222624_s_at	ZNF639	AA224199	Hs.632578	1.28450946	0.00022368	0.059215133
215731_s_at	MPHOSPH9	X98258	Hs.577404	1.28480341	0.00091296	0.093753425
227493_s_at	KIAA1143	AI863484	Hs.476082	1.2851228	0.00099457	0.096200079
1554342_s_at	HEL308	BC011863	Hs.480101	1.28673423	0.00046503	0.076391192
244659_at	TRIP12	AL120025	Hs.591633	1.28694529	7.65E-05	0.045391733
201447_at	TIA1	H96549	Hs.516075	1.2909429	0.00060296	0.08411
206572_x_at	ZNF85	NM_003429	Hs.37138	1.29229425	0.00013595	0.05478537
202694_at	STK17A	AW183478	Hs.706869	1.29393045	2.85E-05	0.033668997
236321_at	LOC285550	AW439843	Hs.399980	1.29575348	0.00069322	0.087559103
239975_at	HLA-DPB2	BF057731	Hs.665450	1.29604468	0.0007771	0.08967706
224664_at	C10orf104	BE962336	Hs.426296	1.29894647	0.00110471	0.098766639
226838_at	TTC32	BE465877	Hs.591547	1.30703441	0.00021086	0.059215133
232820_s_at	GTSF1L	AI809325	Hs.447626	1.30908364	2.35E-06	0.019875716
1569652_at	MLLT3	BC030550	Hs.591085	1.32118941	6.28E-05	0.043096178
244029_at	CPNE5	AW967768	Hs.657869	1.32211654	0.00082731	0.091622871
242069_at	CBX5	BE568225	Hs.632724	1.33139148	0.00061426	0.084296206

213528_at	C1orf156	AL035369	Hs.33922	1.33145782	0.00093081	0.093753425
221046_s_at	GTPBP8	NM_014170	Hs.127496	1.34051571	0.00070608	0.088742586
231500_s_at	BOLA2	AV650728	Hs.444600	1.35546312	0.00032523	0.066588989
237442_at	APBB1IP	AV699911	Hs.310421	1.35816037	0.00011568	0.052445512
230856_at	WIPI1	AI073396	Hs.463964	1.36022398	3.98E-05	0.033668997
214364_at	MTERFD2	W84525	Hs.159556	1.36822763	3.85E-05	0.033668997
226227_x_at	C20orf199	BF185165	Hs.356766	1.37478022	0.00072574	0.089012925
235475_at	SERP1	AI580135	Hs.518326	1.37773213	0.00059563	0.083826486
244600_at	HGD	AA868653	Hs.616526	1.38293494	0.00066635	0.086695267
213846_at	COX7C	AA382702	Hs.430075	1.38911339	0.00055142	0.080456291
239142_at	RFESD	AI082852	Hs.399758	1.39379544	2.04E-05	0.0323417
1552643_at	ZNF626	NM_145297	Hs.657001	1.40367788	0.00025305	0.060608232
206238_s_at	YAF2	NM_005748	Hs.708084	1.41244311	0.00048625	0.077203311
235913_at	LOC400713	AI285722	Hs.502314	1.42571605	0.00021658	0.059215133
213312_at	C6orf162	NM_020425	Hs.70769	1.43439634	0.00055486	0.080495418
230976_at	C9orf98	AW663881	Hs.421340	1.43511069	3.59E-05	0.033668997
230871_at	DHX30	H67762	Hs.517948	1.44113406	0.00122712	0.099492613
1555241_at	C8orf59	BC032347	Hs.443072	1.44235612	0.00053811	0.079848534
224841_x_at	CENPL	BF316352	Hs.531856	1.44401954	0.00036753	0.071339854
225534_at	C8orf40	AV711345	Hs.655320	1.44611479	0.00085093	0.091749041
235780_at	PRKACB	BE622723	Hs.487325	1.48006175	0.00018137	0.059029899
235048_at	KIAA0888	AV720650	Hs.696414	1.48982626	1.07E-05	0.02512121
211106_at	SUPT3H	AF064804	Hs.368325	1.49013662	0.00024385	0.059526355
217988_at	CCNB1IP1	NM_021178	Hs.107003	1.49280652	0.00017831	0.059029899
216945_x_at	PASK	U79240	Hs.706859	1.49792338	0.00086885	0.091749041
235389_at	PHF20	BG168139	Hs.517044	1.50727397	0.0001218	0.053088367
205771_s_at	AKAP7	AL137063	Hs.486483	1.53961718	0.00067676	0.086695267
225698_at	C5orf26	BF314746	Hs.12082	1.54215406	3.91E-05	0.033668997
234849_at	TRA@	AE000659	Hs.74647	1.54223889	4.61E-05	0.036882453
238794_at	C10orf78	N23586	Hs.93667	1.54920659	0.00017249	0.059029899
235244_at	CCDC58	BF001285	Hs.220594	1.55761267	0.00030979	0.066068984
205321_at	EIF2S3	NM_001415	Hs.539684	1.56697993	0.00044508	0.0758362
215082_at	ELOVL5	BF973387	Hs.520189	1.57871818	0.0004682	0.076391192
228381_at	ATF7IP2	AV716964	Hs.513343	1.61412996	0.00054839	0.080456291
243602_at	MGC40069	AI684979	Hs.369380	1.63248654	8.15E-05	0.045391733
214744_s_at	RPL23	AK021960	Hs.406300	1.64091909	0.00061318	0.084296206
235466_s_at	DISP1	AI677948	Hs.528817	1.64298989	0.00110203	0.098766639
1557733_a_at	CHRM3	AI125308	Hs.7138	1.68330687	0.00088179	0.091749041
230137_at	TMEM155	BF673779	Hs.27524	1.74812025	0.00082864	0.091622871
1556667_at	LOC348751	BC039445	Hs.471039	1.7772262	0.00052451	0.079848534
244798_at	SERTAD4	AA398139	Hs.708143	1.77835696	9.33E-05	0.046427716
244189_at	KIAA1648	AI888657	Hs.602319	1.86102567	2.61E-05	0.033668997
205347_s_at	TMSL8	NM_021992	Hs.56145	2.45042421	0.000182	0.059029899

Supplementary table S4:

A. Ingenuity Pathway Analysis: genes high in primary treatment failures, top 10 Functions

Category	P-value	Molecules
Infectious Disease	1.67E-05 - 2.63E-02	RNPS1, IKBKG, LARS, PRNP, APP, RXRA, CALD1, NMT1, GPT2, PYGL, HLX, ERI2, RPS4Y1, SIPA1L2, ALOX5, IGHMBP2, TRIM8, PFKL, CD44, RBM25 (includes EG:58517), FBLIM1, HLA-C, EPOR, FLJ40125, WBP4, PTGS1, KPNB1, ARHGEF19, ETS2, STIP1, FXR1, HRH1, ZNF182, SSB (includes EG:6741)
Cell Death	6E-05-4.68E-02	PDGFRB, RNPS1, IKBKG, HSP90AA1, PRNP, APP, BLVRA, TRADD, TNFSF13, ALOX5, LILRB1, BRCC3, FKBP8, MUC1, PEA15, CD44, HSPA5, CALR, HSPA1A, PTAFR, SIRT2, ARRB2, FGFR1, PTGS1, MVP, TRIM27, ETS2, PPP5C, CCT6A, APOL1, CTBP2, RASSF4, NFE2L2, TRAF2, FXR1, AP2A2
Reproductive System Disease	1.33E-04-4.75E-02	GABARAPL1, PDGFRB, TXNIP, ATRN, SLC2A5, HSP90AA1, IQGAP1, PRNP, GNAS, RXRA, APP, TRADD, MCAM, COMT, ERI2, ALOX5, SHC1, UBE3A, MUC1, PEA15, CD44, HSPA5, NF1, MINK1, HSPA1A, MAPK7, CDC2L6, HLA-C, EPOR, PTAFR, ARRB2, MMP24, PTGS1, FGFR1, VAMP2, KCNK6, SCN1B, ETS2, CP, PPFIA1, FRMD4A, HRH1
Cell-To-Cell Signaling and Interaction	1.42E-04-4.68E-02	JMJD6, CALR, HSPA1A, PDGFRB, MCAM, CD93, HLA-C, MUC1, CD44, APP
Cell-mediated Immune Response	1.42E-04-4.37E-02	CALR, NF1, NFE2L1, PTAFR, HLA-C, CAPZB, ATRN, ARRB2, IQGAP1, PRNP, APP, GNAS, CALD1, JMJD6, PXK, MUC1, CD44, HRH1, WAS
Cellular Growth and Proliferation	1.42E-04-4.59E-02	PDGFRB, SURF6, TXNIP, IKBKG, DNAJA1, AGGF1, RXRA, MCAM, TNFSF13, FKBP4, RRAD, LZTS2, LILRB1, SHC1, MUC1, CD44, WAS, HSPA5, NF1, CALR, PTAFR, EPOR, HLA-C, SIRT2, C19ORF10, ARRB2, MMP24, PTGS1, FGFR1, MVP, TRIM27, PPP5C, ETS2, PDAP1, RASSF4, UBC, CTBP2, TRAF2
Hematological System Development and Function	1.42E-04-4.59E-02	GNAQ, CALR, HLA-C, PTAFR, EPOR, ATRN, MVP, F13A1, JMJD6, TNFSF13, LILRB1, MUC1, CD44, WAS, HSPA5
Cell Signaling	1.73E-04-4.68E-02	GNAQ, NF1, PPP5C, MINK1, PTAFR, IKBKG, RAB7A, FGFR1, KPNB1, F13A1, APP, MAPK13
DNA Replication, Recombination, and Repair	1.73E-04-1.19E-02	GNAQ, PTAFR, RAB7A, KPNB1, PRNP
Nucleic Acid Metabolism	1.73E-04-3.53E-02	GNAQ, ADAP1, PTAFR, SHMT1, RAB7A, KPNB1

B. Ingenuity Pathway Analysis: genes high in primary treatment failures, top 10 Canonical Pathways

Canonical Pathways	-Log(P-value)	Ratio	Molecules
PPAR Signaling	4.15E00	8.05E-02	PDGFRB, MAPK7, IKBKG, HSP90AA1, TRAF2, SHC1, RXRA
Androgen Signaling	3.41E00	6.09E-02	GNAQ, CALR, MAPK7, PRKAR2A, HSP90AA1, SHC1, GNAS
PPARα/RXRα Activation	3.29E00	5.19E-02	GNAQ, MAPK7, PRKAR2A, IKBKG, HSP90AA1, SHC1, RXRA, GNAS
IL-12 Signaling and Production in Macrophages	2.79E00	5.66E-02	JMJD6, MAPK7, IKBKG, RAB7A, RXRA, MAPK13
Fructose and Mannose Metabolism	2.6E00	7.69E-02	PFKFB2, SORD, PFKL, PFKFB4
Glucocorticoid Receptor Signaling	2.58E00	3.6E-02	HSPA1A, MAPK7, FKBP4, IKBKG, HSP90AA1, TRAF2, SHC1, HSPA5, MAPK13
Amyloid Processing	2.5E00	7.69E-02	MAPK7, PRKAR2A, APP, MAPK13
Acute Phase Response Signaling	2.42E00	4.17E-02	TRADD, MAPK7, CP, IKBKG, TRAF2, SHC1, MAPK13
α-Adrenergic Signaling	2.39E00	5.56E-02	GNAQ, PYGL, MAPK7, PRKAR2A, GNAS

C. Ingenuity Pathway Analysis: genes low in primary treatment failures, top 10 Functions

Category	P-value	Molecules
Protein Synthesis	1.3E-05-3.72E-02	RPS27L (includes EG:51065), APOA1, RPL14, RPL30, RPL38 (includes EG:6169), SQSTM1, RPS4X, MMP11, RPL34, RPL31, EIF2S3, RPL22, RPS17 (includes EG:6218), UBE3A, NACA, GLMN, EIF3E
Cell-To-Cell Signaling and Interaction	1.26E-04-4.87E-02	NLGN3, NRD1, NCKIPSD, VIPR1, AGRN, CEACAM5 (includes EG:1048), BRAF, RET
Cellular Assembly and Organization	1.26E-04-3.72E-02	SRPK2, SNRPD1, SNRPD2, NLGN3, MUC5AC, STMN1, APOA1, NRD1, SMC1A, PTMS, AGRN, RET
RNA Post-Transcriptional Modification	7.14E-04-1.88E-02	PAPOLG, RPS16, SRPK2, SNRPD1, BRUNOL4, SNRPD2, RPL14, SNRPN, RPS17 (includes EG:6218), RPS15, U2AF1
Nervous System Development and Function	1.04E-03-3.72E-02	NLGN3, CHRNB2, AGRN
Genetic Disorder	5.01E-03-3.72E-02	APOA1, ATN1, ASCL1, RET, ARX, ABCB7, PRKAG2, NLGN3, FGFR2, PANK2, CD3D, UBE3A, ADRA2B, DCLRE1C

Neurological Disease	5.01E-03-4.14E-02	ATN1, ASCL1, ARX, RET, SLC1A4, ABCB7, NLGN3, GRIN1, CHRNB2, PANK2, ABAT, UBE3A, ADRA2B
Respiratory Disease	5.01E-03-5.01E-03	ASCL1, RET
Hepatic System Disease	6.79E-03-1.88E-02	GPT (includes EG:2875), PDE3B, PDE4D
Inflammatory Disease	6.79E-03-3.72E-02	FGFR2, GPT (includes EG:2875), PDE3B, PDE4D

D. Ingenuity Pathway Analysis: genes low in primary treatment failures, top 10 Canonical Pathways

Canonical Pathways	-Log(P-value)	Ratio	Molecules
Relaxin Signaling	2.12E00	5.65E-02	RLN1, PRKAG2, PIK3CA, PRKACB, BRAF, PDE3B, PDE4D
cAMP-mediated Signaling	2.09E00	5.06E-02	PRKACB, BRAF, PDE3B, RGS10, ADRA2B, CREM, PDE4D, AKAP7
Cardiac β-adrenergic Signaling	1.62E00	5.04E-02	PPM1L, PRKAG2, PRKACB, PDE3B, PDE4D, AKAP7
Cellular Effects of Sildenafil (Viagra)	1.47E00	4.62E-02	PRKAG2, MYL5, PRKACB, SLC4A11, PDE3B, PDE4D
Oxidative Phosphorylation	1.43E00	4.26E-02	COX7C (includes EG:1350), NDUFA7, COX11, NDUFC1, COX6C, ATP5L
G-Protein Coupled Receptor Signaling	1.42E00	3.92E-02	PRKAG2, PIK3CA, PRKACB, BRAF, PDE3B, RGS10, ADRA2B, PDE4D
Nitric Oxide Signaling in the Cardiovascular System	1.41E00	5.71E-02	PRKAG2, PIK3CA, PRKACB, PDE3B
CTLA4 Signaling in Cytotoxic T Lymphocytes	1.23E00	4.71E-02	PPM1L, TRA@, CD3D, PIK3CA
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	1.2E00	8E-02	TRA@, CD3D
Melanocyte Development and Pigmentation Signaling	1.13E00	4.76E-02	PRKAG2, PAX3, PIK3CA, PRKACB

Supplementary table S5: SMLR combination model features and their relative importance rankings according to Random Forests (RF)[6] – 86 annotated genes and 2 clinical variables

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Probe set	Importance	Gene Symbol	Gene Title
214980_at	100.000	UBE3A	E6-AP isoform-III
206131_at	97.825	CLPS	colipase, pancreatic
229080_at	72.950	EMID2	EMI domain containing 2
232820_s_at	65.193	GTSF1L	gametocyte specific factor 1-like
201806_s_at	63.262	ATXN2L	ataxin 2-like
235908_at	62.537	MMP11	matrix metallopeptidase 11 (stromelysin 3)
216114_at	60.429	NCKIPSD	NCK interacting protein with SH3 domain
203112_s_at	57.592	WHSC2	Wolf-Hirschhorn syndrome candidate 2
203598_s_at	55.895	WBP4	WW domain binding protein 4 (formin binding protein 21)
227374_at	54.068	EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)
219811_at	50.678	DGCR8	DiGeorge syndrome critical region gene 8
207783_x_at	49.571	HUWE1	HECT, UBA and WWE domain containing 1
207408_at	48.129	SLC22A14	solute carrier family 22, member 14
200635_s_at	47.423	PTPRF	protein tyrosine phosphatase, receptor type, F
239648_at	44.349	DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)
204491_at	44.145	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)
223740_at	43.933	RIPPLY2	ripply2 homolog (zebrafish)
217095_x_at	43.446	NCR1	natural cytotoxicity triggering receptor 1
219905_at	43.325	ERMAP	erythroblast membrane-associated protein (Scianna blood group)
209980_s_at	41.167	SHMT1	serine hydroxymethyltransferase 1 (soluble)
203488_at	40.265	LPHN1	latrophilin 1
207270_x_at	39.822	CD300C	CD300c molecule
242048_at	39.139	PFDN6	prefoldin subunit 6
204952_at	38.310	LYPD3	LY6/PLAUR domain containing 3
204802_at	37.767	RRAD	Ras-related associated with diabetes
218550_s_at	37.296	LRRC20	leucine rich repeat containing 20
227249_at	37.010	NDE1	NudE nuclear distribution gene E homolog 1 (A. nidulans), mRNA (cDNA clone MGC:33664 IMAGE:4828494)
age	36.769	AGE	_
204104_at	35.497	SNAPC2	small nuclear RNA activating complex, polypeptide 2, 45kDa
208384_s_at	35.170	MID2	midline 2
218865_at	34.926	MOSC1	MOCO sulphurase C-terminal domain

			containing 1
213693_s_at	34.826	MUC1	mucin 1, cell surface associated
219525_at	34.644	SLC47A1	solute carrier family 47, member 1
224839_s_at	34.635	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2
236703_at	33.557	NT5C2	5'-nucleotidase, cytosolic II
32062_at	33.501	LRRC14	leucine rich repeat containing 14
223389_s_at	33.280	ZNF581	zinc finger protein 581
229941_at	33.255	FAM166B	family with sequence similarity 166, member B
209985_s_at	33.027	ASCL1	achaete-scute complex homolog 1 (Drosophila)
219398_at	32.904	CIDEC	cell death-inducing DFFA-like effector c
219411_at	32.718	ELMO3	engulfment and cell motility 3
221187_s_at	31.425	FUZ	fuzzy homolog (Drosophila)
223836_at	30.950	FGFBP2	fibroblast growth factor binding protein 2
228452_at	30.073	C17orf39	chromosome 17 open reading frame 39
213601_at	29.546	SLIT1	slit homolog 1 (Drosophila)
209460_at	29.416	ABAT	4-aminobutyrate aminotransferase
227440_at	29.364	ANKS1B	ankyrin repeat and sterile alpha motif domain containing 1B
214456_x_at	29.333	SAA1	serum amyloid A1 /// serum amyloid A2
219877_at	28.122	ZMAT4	zinc finger, matrin type 4
204856_at	27.277	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
224434_s_at	26.815	MORG1	mitogen-activated protein kinase organizer 1
239975_at	26.541	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)
216611_s_at	25.998	SLC6A2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2
219224_x_at	24.651	ZNF408	zinc finger protein 408
203899_s_at	24.506	CRCP	CGRP receptor component
202790_at	22.422	CLDN7	claudin 7
1553262_a_at	22.360	UTS2R	urotensin 2 receptor
217744_s_at	22.269	PERP	PERP, TP53 apoptosis effector
207832_at	22.226	BAIAP2	BAI1-associated protein 2
225244_at	21.746	SNAP47	synaptosomal-associated protein, 47kDa
229559_at	21.063	FLJ40125	hypothetical protein FLJ40125
239159_at	20.610	GOSR2	Golgi SNARE (GS27)
219472_at	20.126	CENPO	centromere protein O
214625_s_at	19.020	MINK1	misshapen-like kinase 1 (zebrafish)
213981_at	18.956	COMT	catechol-O-methyltransferase
213102_at	18.146	ACTR3	ARP3 actin-related protein 3 homolog (yeast)
230134_s_at	18.145	RC3H2	ring finger and CCCH-type zinc finger domains 2
stage	18.126	STAGE	_
1569631_at	17.832	NMNAT1	nicotinamide nucleotide adenylyltransferase 1
223248_at	17.219	HSDL1	hydroxysteroid dehydrogenase like 1
222208_s_at	16.768	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene

205706_s_at	16.644	ANKRD26	ankyrin repeat domain 26
203099_s_at	16.589	CDYL	chromodomain protein, Y-like
230807_at	16.295	CCDC151	coiled-coil domain containing 151
233550_s_at	15.995	SLC4A11	solute carrier family 4, sodium borate transporter, member 11
212688_at	15.840	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide
221610_s_at	15.190	STAP2	signal transducing adaptor family member 2
217599_s_at	14.945	MDFIC	MyoD family inhibitor domain containing
241354_at	14.740	NCRNA00105	non-protein coding RNA 105
222392_x_at	13.936	PERP	PERP, TP53 apoptosis effector
239316_at	13.168	LOC751071	methyltransferase LOC751071, mitochondrial-like
223333_s_at	11.924	ANGPTL4	angiopoietin-like 4
215689_s_at	11.880	SHBG	sex hormone-binding globulin
221854_at	11.823	PKP1	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)
239012_at	10.451	RNF144B	CDNA FLJ59797 complete cds, highly similar to E3 ubiquitin ligase IBRDC2 (EC 6.3.2.-)
219198_at	9.682	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa
213870_at	8.784	COL11A2	collagen, type XI, alpha 2

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