Supplementary Data

Supplemental Table 1. Baseline characteristics and clinical outcomes of overall, GEP-evaluable, and mIHC-evaluable populations.

Variable	Overall population (N=70)	GEP-evaluable population (N=36)	mIHC-evaluable population (N=41)
Median age, years (range)	32.5 (18–69)	33.0 (19–69)	33.0 (19–67)
Age group, n (%)			
<65 years	66 (94.3)	32 (88.9)	38 (92.7)
≥65 years	4 (5.7)	4 (11.1)	3 (7.3)
Sex, n (%)			
Male	40 (57.1)	20 (55.6)	26 (63.4)
Female	30 (42.9)	16 (44.4)	15 (36.6)
ECOG performance status, n (%)			
0	48 (68.6)	25 (69.4)	30 (73.2)
1	22 (31.4)	11 (30.6)	11 (26.8)
Stage IV at study entry, n (%)	42 (60)	25 (69.4)	26 (63.4)
Bulky disease,[a] n (%)	8 (11.4)	2 (5.6)	3 (7.3)
Bone marrow involvement, n (%)	22 (31.4)	13 (36.1)	13 (31.7)
B-symptom(s), n (%)	26 (37.1)	15 (41.7)	13 (31.7)
Histology subtype, n (%)			
Nodular sclerosis	42 (60)	20 (55.6)	21 (51.2)
Mixed cellularity	19 (27.1)	11 (30.6)	14 (34.1)
Lymphocyte-rich	3 (4.3)	3 (8.3)	2 (4.9)
Unspecified	6 (8.6)	2 (5.6)	4 (9.8)
Median time from initial diagnosis, months (IQR)	25.33 (12.91–40.54)	22.51 (13.11–38.87)	26.81 (12.88–40.54)
Median number of lines of prior therapy, n (range)	3.00 (2.0–11.0)	3.00 (2.0–9.0)	3.00 (2.0–11.0)
Types of prior systemic therapy, n (%)			
Chemotherapy	70 (100.0)	36 (100.0)	41 (100.0)
ASCT	13 (18.6)	8 (22.2)	9 (22.0)
Immunotherapy[b]	15 (21.4)	6 (16.7)	6 (14.6)
Ineligible for prior ASCT[c], n (%)	57 (81.4)	28 (77.8)	32 (78.0)
Patients with prior radiation therapy, n (%)	21 (30.0)	11 (30.6)	13 (31.7)
Best response, n (%)			
Overall response	61 (87.1)	30 (83.3)	37 (90.2)
Complete response	47 (67.1)	23 (63.9)	29 (70.7)

[a] Bulky disease defined as size of any single node/nodal mass ≥10 cm in diameter or mediastinal mass ratio of ≥0.33.

[b] Immunotherapy includes brentuximab-vedotin, rituximab, CIK cell transfusion, thalidomide and lenalidomide.

[c] Patients were ineligible for ASCT if they did not achieve at least a partial response to salvage chemotherapy, were ≥65 years of age, had contraindicating comorbidities, or due to the failure or inability to collect hematopoietic stem cells. All received ≥2 prior regimens.

ASCT, autologous hematopoietic stem cell transplant; CIK, cytokine induced killer; ECOG, Eastern Cooperative Oncology Group; GEP, gene expression profiling; IQR, interquartile range; mIHC, multiplexed immunohistochemistry.

Supplemental Table 2. Gene list showing genes associated with progression-free survival by univariate Cox regression analysis.

Genes associated with prolonged PFS[a]	Genes associated with disease progression[a]
IFNL3	*IL32*
IL1A	*IL6R*
IL1R1	*IL6ST*
IL4	*CSF2RB*
CCL11	*IRF2*
CCR10	*IRF8*
IL9	*IRF1*
CXCL8	*IRF3*
PDCD1LG2	*IRF9*
FCGR1A	*IFNAR2*
TNFSF9	*CD19*
TNFRSF21	*CD48*
S100A12	*CD79B*
S100A9	*CD22*
S100A8	*CD27*
VEGFA	*CD72*
LAMC3	*CD38*
ITGAM	*CD96*
CPE	*CD247*
SPINK1	*ATF2*
MYOF	*RNF4*
CEACAM5	*OAZ1*
ACKR3	*TUBB*
TEX14	*BTLA*
ANXA1	*NCL*
TP63	*HIST1H2BH*
CD14	*TRAT1*
SLC11A1	*PSMB8*
PYGL	*TMPO*
SLC2A1	*NLRC5*
DPYSL4	*SLAMF1*
PPM1E	*PTPRC*
KRT16	*SP100*
AADAT	*STAT1*
ALCAM	*PSMB9*
ABL2	*TAGAP*
LRP1	*FYN*
CLEC5A	*RPL6*
CREB5	*MOB3A*
HK2	*ISG20*
ITGB3	*CEP55*
MMP11	*SPIB*
OLR1	*TXLNA*

HK1	*HLA.F*
SNAI2	*SEMA4D*
PTGER3	*ETS1*
MYO1B	*PIK3CD*
KIR.panS	*SELPLG*
CTAG2	*SLAMF6*
PLAUR	*HLA.C*
PLAU	*NFKB2*
MSR1	*PSMB10*
MSH3	*HLA.E*
CCDC138	*TAP2*
CD1A	*DOCK9*
FAM161A	*CD6*
HEYL	*FYB1*
LEXM	*ST6GAL1*
MYO5C	*PDHB*
TAL1	*ARHGDIB*
DST	*JAK1*
IGFBP3	*ITK*
DSE	*ADGRE5*
	TAP1
	CARD11
	CORO1A
	CCND3
	TNFRSF13C
	RPL38
	CD3D
	CREBBP
	SELL
	CSK
	PTPRCAP
	IKZF3
	MYBL2
	CASP4
	GBP5
	EP300
	ITGAL
	CD3G
	LCK
	LRBA
	TNFAIP8
	CD3E
	ITGB7
	CD2

[a] Genes with Wald test p value < 0.05 in the univariate analysis.

Supplemental Figure 1. Maximum change from baseline in the SPD of target lesions for all patients. Percentage change in SPD was presented as the best response achieved in each patient. CR, complete response; PD, progressive disease; PR, partial response; SD, stable disease; SPD, sum of products of diameters.

Supplemental Figure 2. Associations of CD8+ T cells, CD68+ macrophages, FcγRI+ cells, and FcγRI+ macrophages with clinical responses. (A) CD8 T-cell infiltration by mIHC in complete responders versus non-responders. (B) Macrophages marked by CD68 by mIHC in complete responders versus non-responders. (C) Total FcγRI+ expression by mIHC in complete responders versus non-responders. (D) FcγRI+ macrophages by mIHC in complete responders versus non-responders. mIHC, multiplexed immunohistochemistry.

Supplemental Figure 3. Correlation of FcγRI+ expression with IFNG and IL10. (A) *In vitro* results showing that FcγRI+ expression was induced by IFN-r and IL10. (B) Correlation of FcGR1A with IFNG mRNA in the 36 GEP-evaluable patients. (C) Correlation of FcGR1A with IL10 mRNA in the 36 GEP-evaluable patients. GEP, gene expression profiling; IFN, interferon; IL, interleukin; MFI, mean fluorescence intensity; NS, non-stimulation.