Figure 1

The amino acid sequence of the MOR00208 Variable Heavy Domain is (The CDRs are bolded and underlined):

EVQLVESGGGLVKPGGSLKLSCAASGYTFT**SYVMH**WVRQAPGKGLEWIGYI **NPYNDG**TKYNEKFQGRVTISSDKSISTAYMELSSLRSEDTAMYYCAR**GTYYY GTRVFDY**WG QGTLVTVSS (SEQ ID NO: 10)

The amino acid sequence of the MOR00208 Variable Light Domain is (The CDRs are bolded and underlined):

DIVMTQSPATLSLSPGERATLSC**RSSKSLQNVNGNTYLY**WFQQKPGQSPQL LIY**RMSNLNS**GVPDRFSGSGSGTEFTLTISSLEPEDFAVYYC**MQHLEYPIT**FG AGTKLEIK (SEQ ID NO: 11)

The amino acid sequence of the MOR00208 HCDR1 is: SYVMH (SEQ ID NO: 1)

The amino acid sequence of the MOR00208 HCDR2 is: NPYNDG (SEQ ID NO: 2)

The amino acid sequence of the MOR00208 HCDR3 is: GTYYYGTRVFDY (SEQ ID NO: 3)

The amino acid sequence of the MOR00208 LCDR1 is: RSSKSLQNVNGNTYLY (SEQ ID NO: 4)

The amino acid sequence of the MOR00208 LCDR2 is: RMSNLNS (SEQ ID NO: 5)

The amino acid sequence of the MOR00208 LCDR3 is: MQHLEYPIT (SEQ ID NO: 6)

Figure 2

The amino acid sequence of the MOR00208 Heavy Chain is:

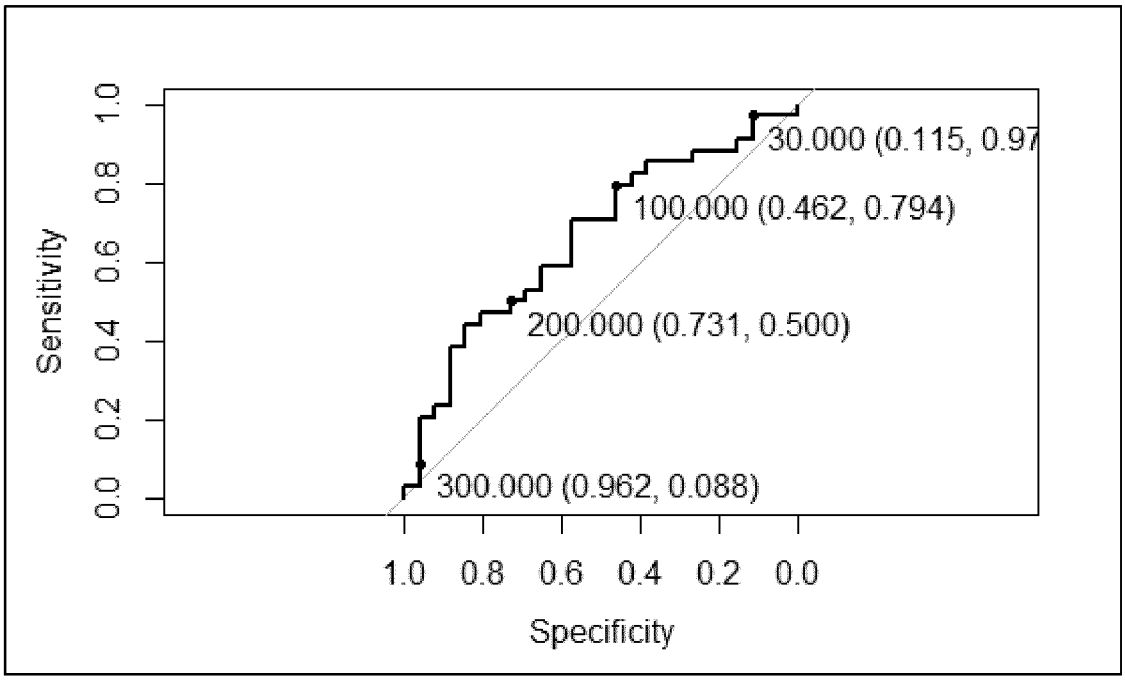
EVQLVESGGGLVKPGGSLKLSCAASGYTFTSYVMHWVRQAPGKGLEWIGYINPYN
DGTKYNEKFQGRVTISSDKSISTAYMELSSLRSEDTAMYYCARGTYYYGTRVFDYWGQGTL
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL
GGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ
FNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKALPAPEEKTISKTKGQPREPQVYTLPPSRE
EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 8)

The amino acid sequence of the MOR00208 Light Chain is:

DIVMTQSPATLSLSPGERATLSCRSSKSLQNVNGNTYLYWFQQKPGQSPQLLIYRMSNLN
SGVPDRFSGSGSGTEFTLTISSLEPEDFAVYYCMQHLEYPITFGAGTKLEIKRTVAAPSVFIF
PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
LTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 9)

Figure 3

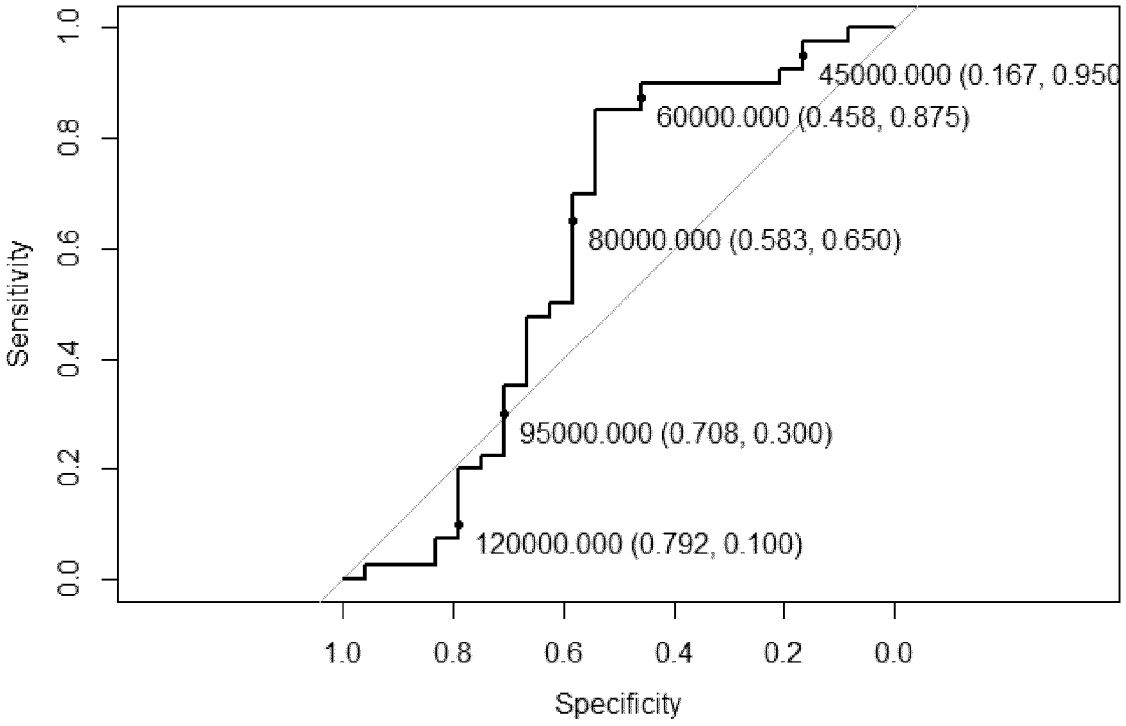
Determining the cut offs for peripheral NK cell counts via ROC analysis



Receiver Operating Characteristic (ROC) analysis of peripheral NK cell count (cells/µl) as a predictor for the Disease Control Rate (CR, PR, DS vs PD, ET) in DLBCL and iNHL patients. Various cut offs with Specificity and Sensitivity values are displayed. AUC = 0.66. CR-Complete Remission, PR-Partial Remission, SD-Stable Disease, PD-Progressive Disease, ET-Early Termination, ABC-Antigens Bound per Cell.

Figure 4

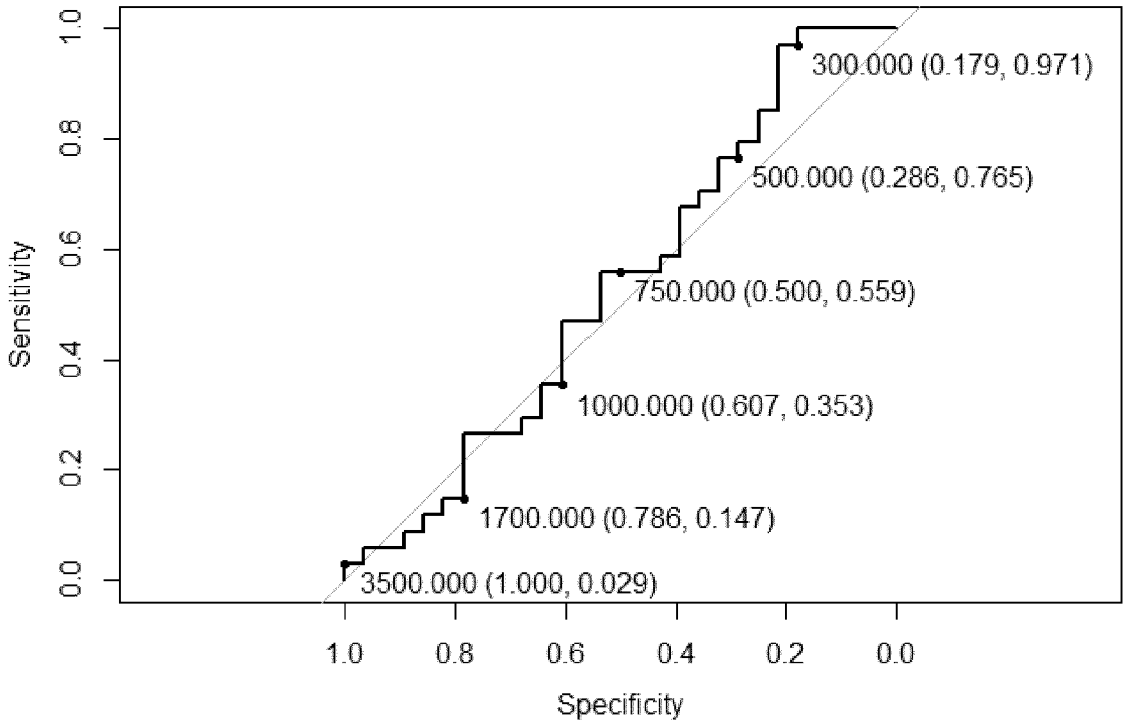
Determining the cut offs for CD16 expression (ABC) via ROC analysis



Receiver Operating Characteristic (ROC) analysis of CD16 expression (ABC) as a predictor for the Disease Control Rate (CR, PR, DS vs PD, ET) in DLBCL and iNHL patients. Various cut offs with Specifity and Sensitivity values are displayed. AUC = 0.61. CR-Complete Remission, PR-Partial Remission, SD-Stable Disease, PD-Progressive Disease, ET-Early Termination, ABC-Antigens Bound per Cell.

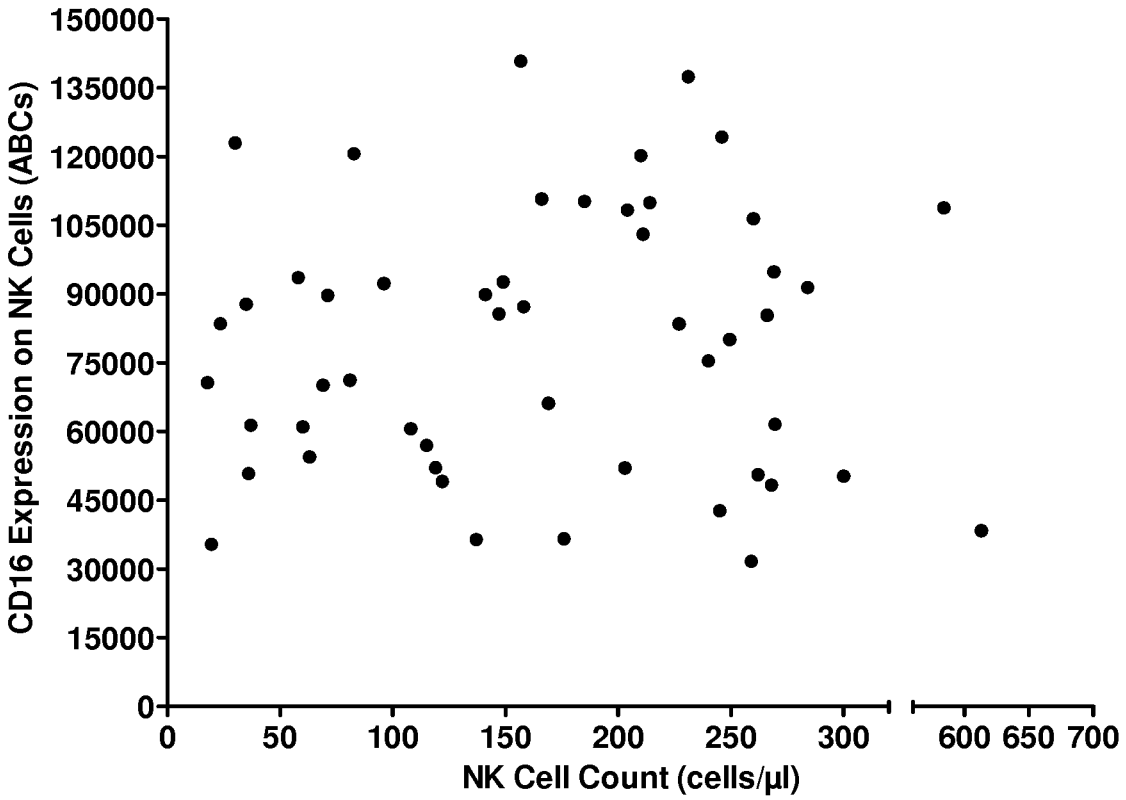
Figure 5

Determining the cut offs for peripheral T cell count via ROC analysis



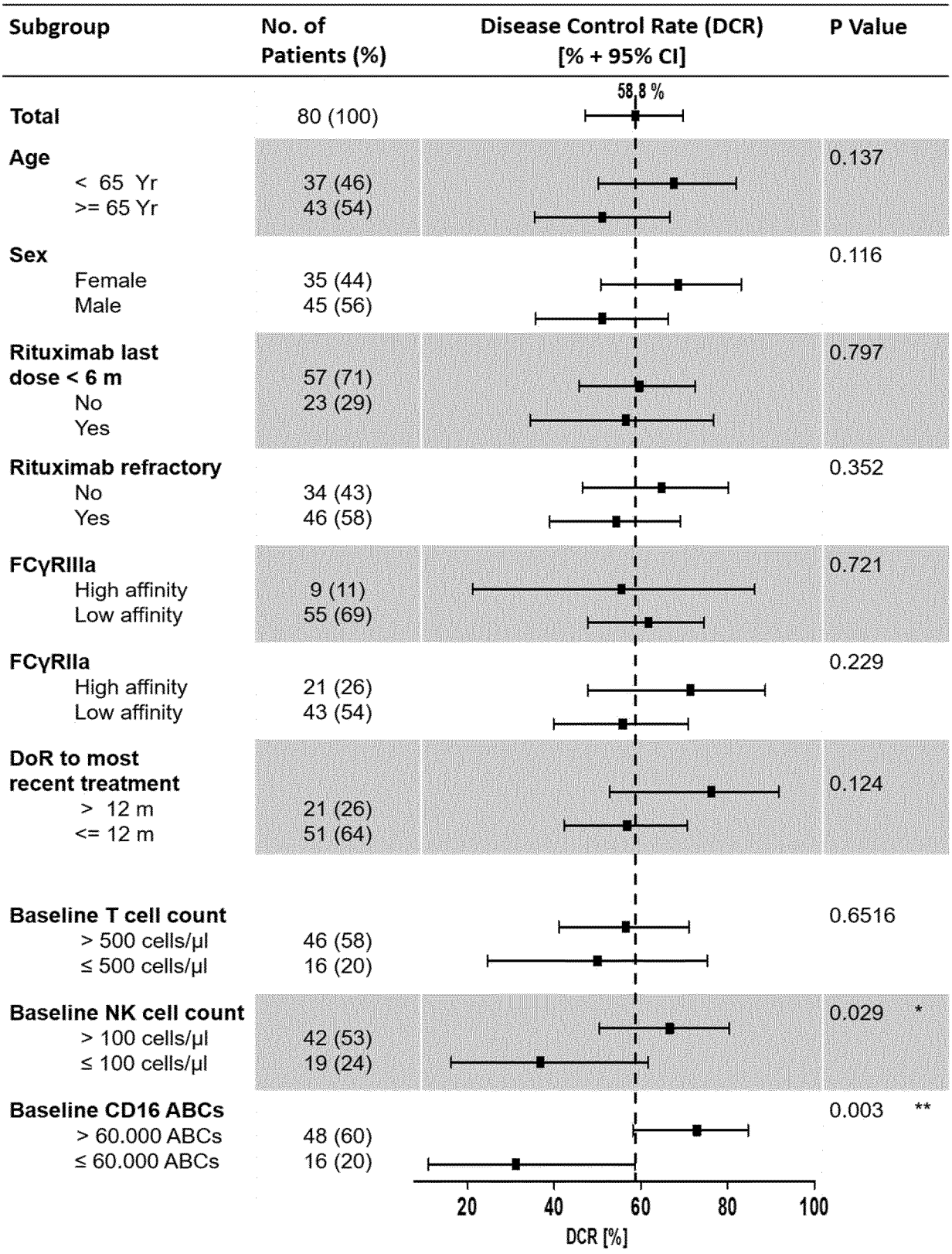
Receiver Operating Characteristic (ROC) analysis of peripheral T cell count (cells/µl) as a potential predictor for the Disease Control Rate (CR, PR, DS vs PD, ET) in DLBCL and iNHL patients. Various cut offs with Specifity and Sensitivity values are displayed. AUC = 0.53. CR-Complete Remission, PR-Partial Remission, SD-Stable Disease, PD-Progressive Disease, ET-Early Termination, ABC-Antigens Bound per Cell.

Figure 6



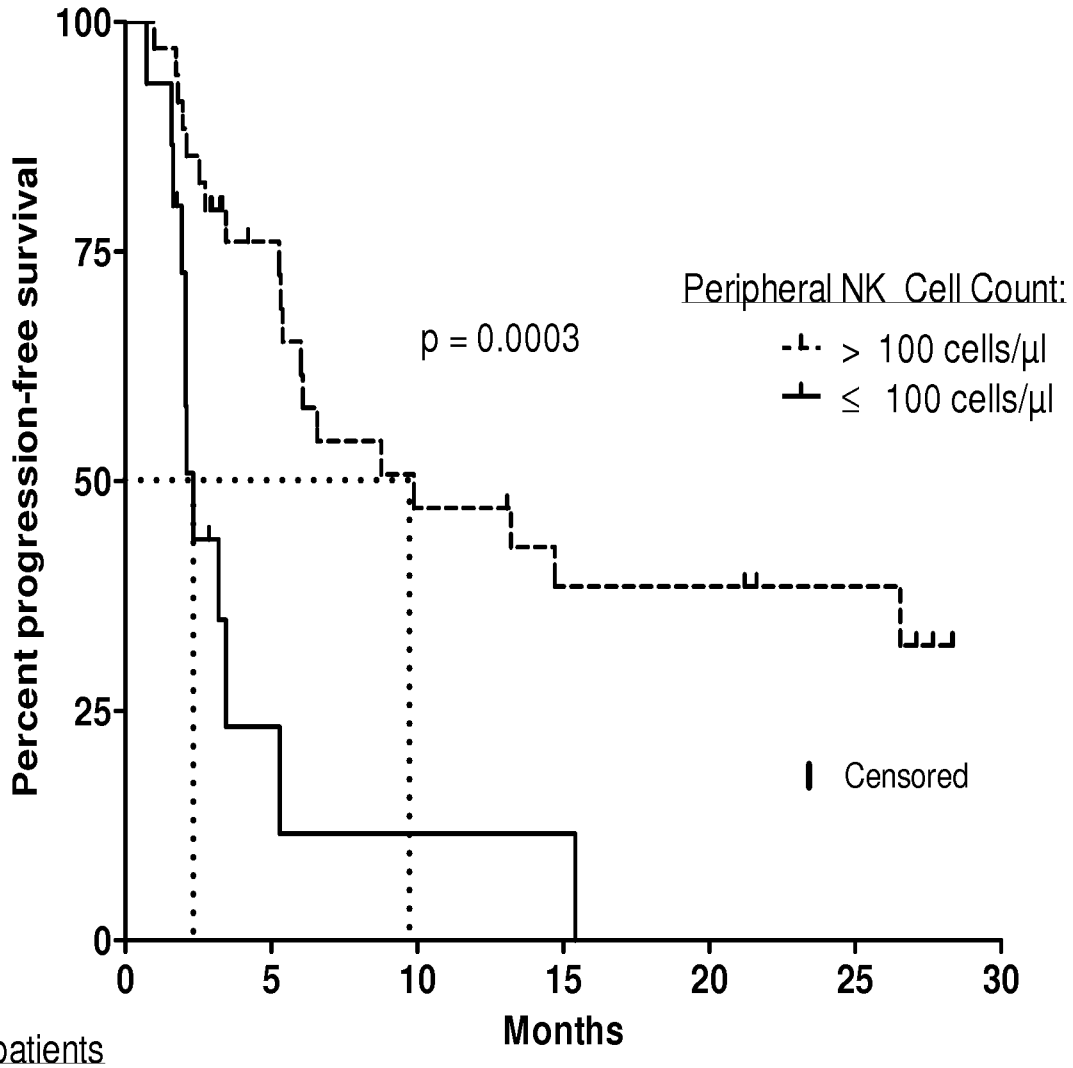
ABC-Antigens Bound per Cell. Analysis of correlation: Pearson r = 0,019 with two-tailed p value = 0.9; Nonparametric Spearman r = 0,036 with two-tailed p value = 0.8; n = 51.

Figure 7 Forest plot with subgroup analyses of disease control rate.



†Clopper Pearson confidence intervals; ‡unadjusted X^2 test (two-sided) of DCR rates. DoR, duration of response; IPI, International Prognostic Index. * p<0,05, **p<0,01.

Figure 8 Subgroup analysis of Progression-free survival (PFS)

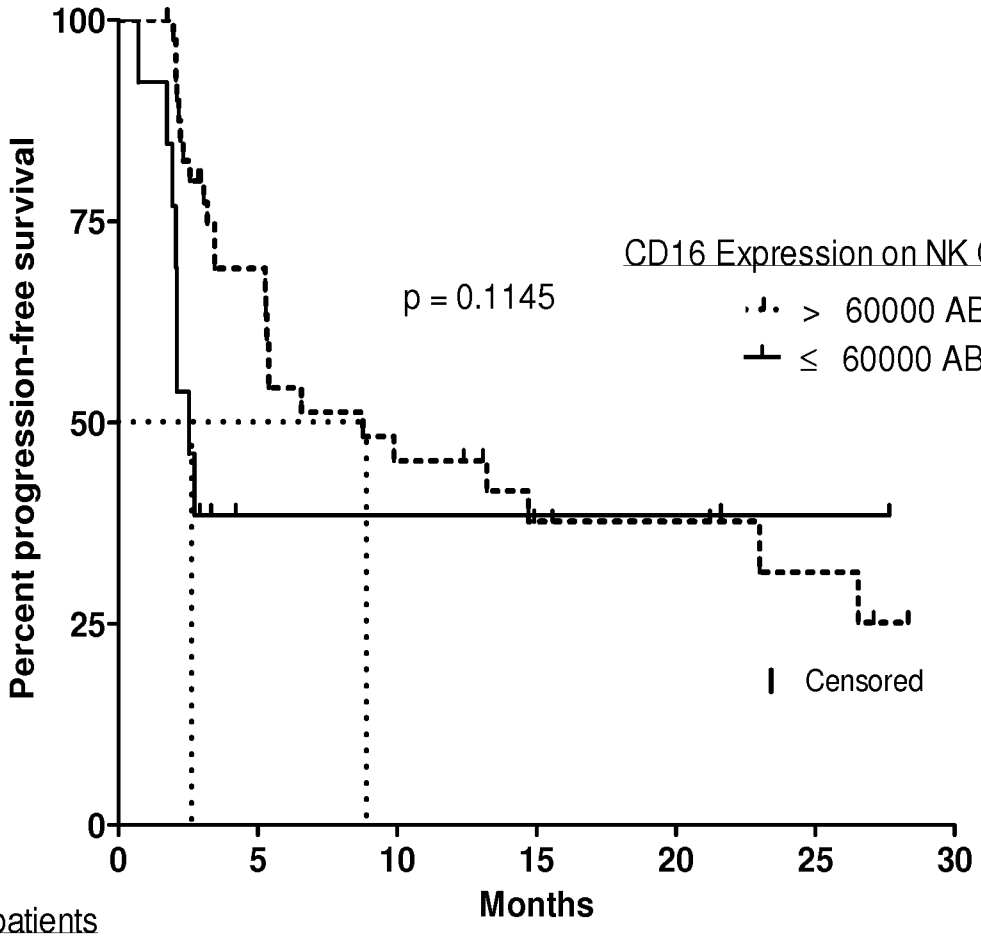


No. of patients at risk:

>100 cells/µl	35	21	12	9	9	6
≤100 cells/µl	15	2	1	1	0	0

Patients without post baseline radiological tumor assessment were censored at baseline. PFS, progression-free survival. Unadjusted log-rank p value = 0.0003.

Figure 9 Subgroup analysis of Progression-free survival (PFS)

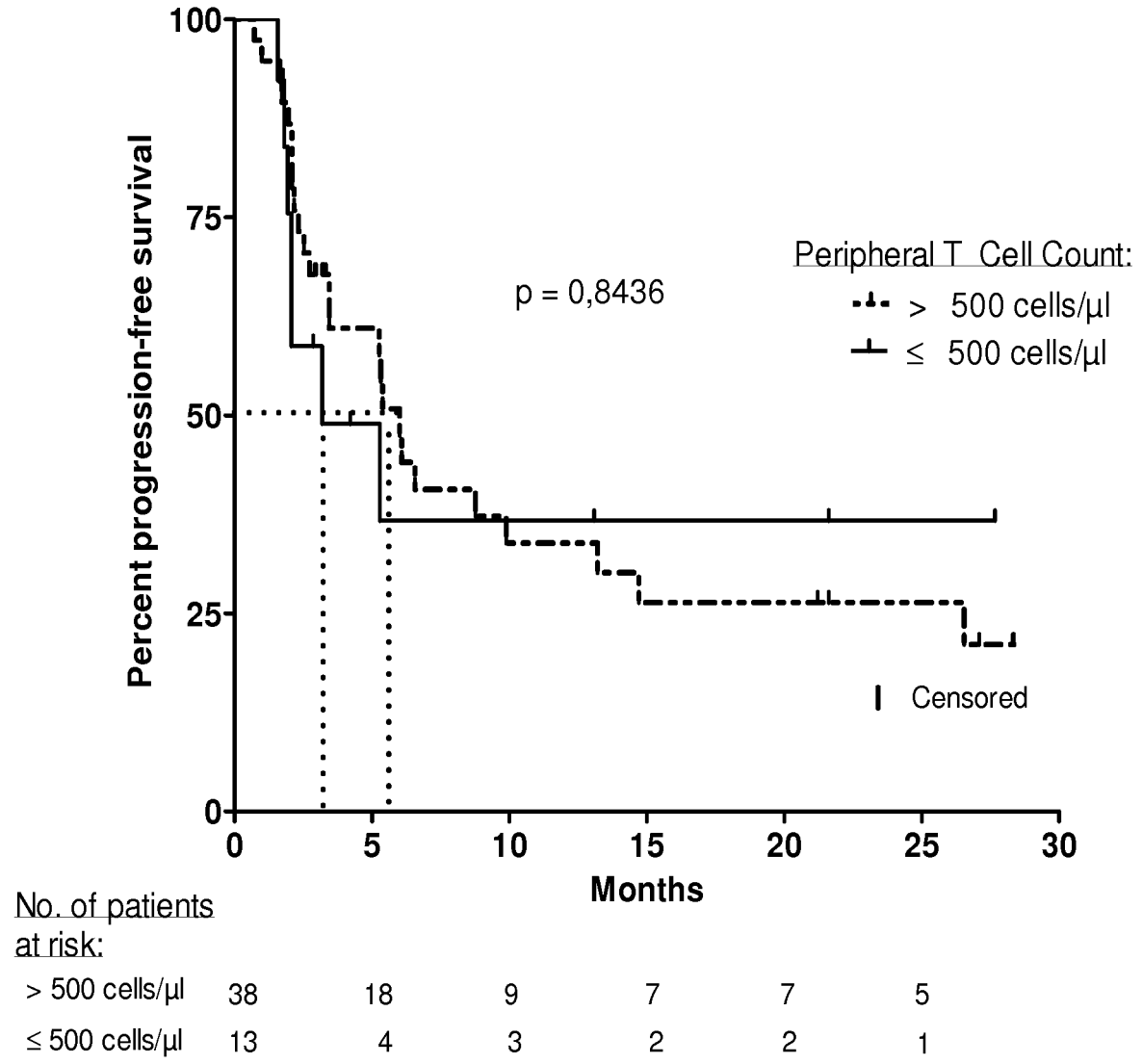


No. of patients at risk:

> 60.000 ABCs	42	25	14	9	8	5
≤ 60.000 ABCs	13	2	2	2	2	1

Patients without post baseline radiological tumor assessment were censored at baseline. PFS, progression-free survival. Unadjusted log-rank p value = 0.1145

Figure 10 Subgroup analysis of Progression-free survival (PFS)



Patients without post baseline radiological tumor assessment were censored at baseline. PFS, progression-free survival. Unadjusted log-rank p value = 0.8436