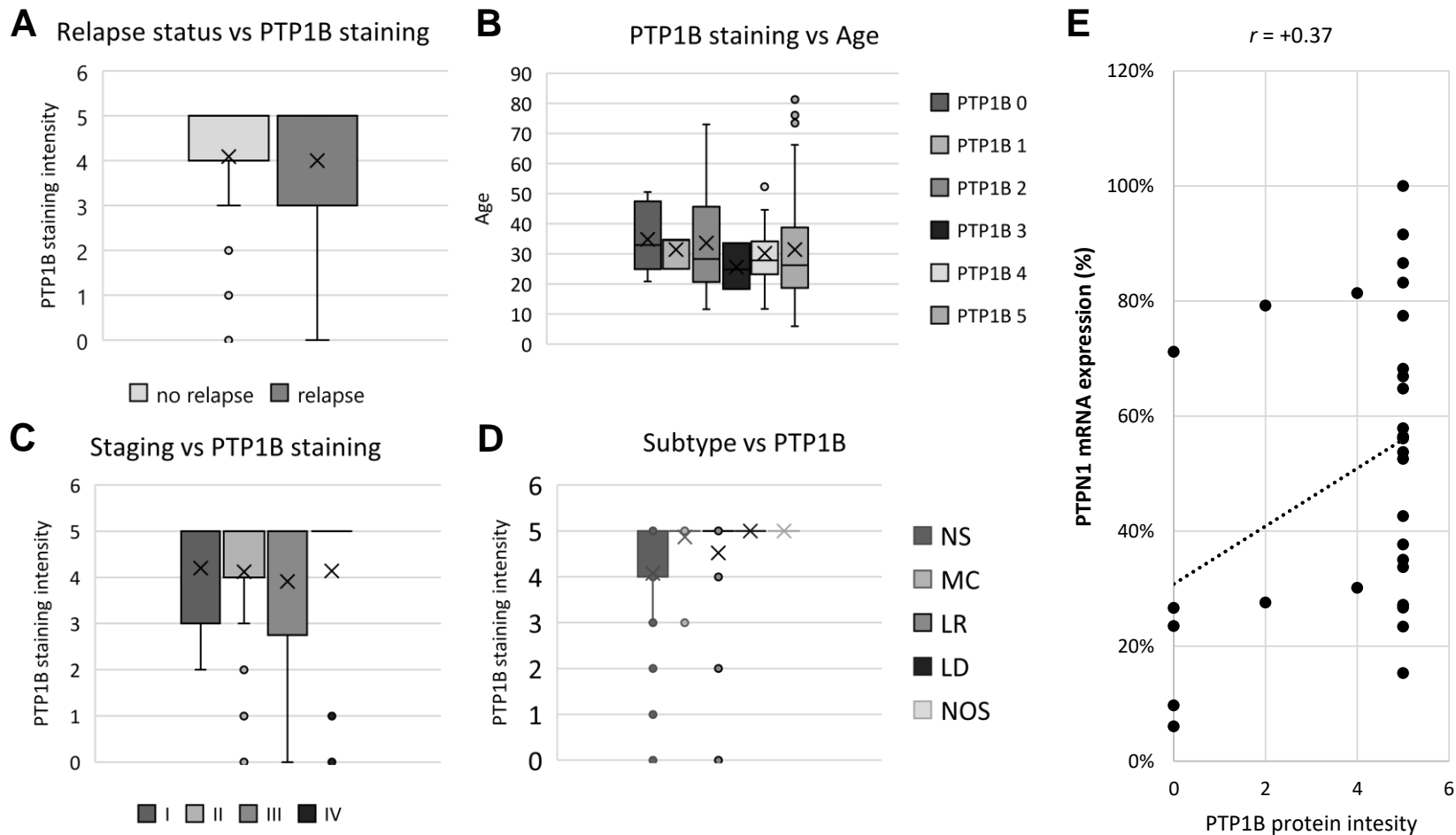


**Supplemental Table 1:** Characteristics of patients with classical Hodgkin Lymphoma in the study cohort.

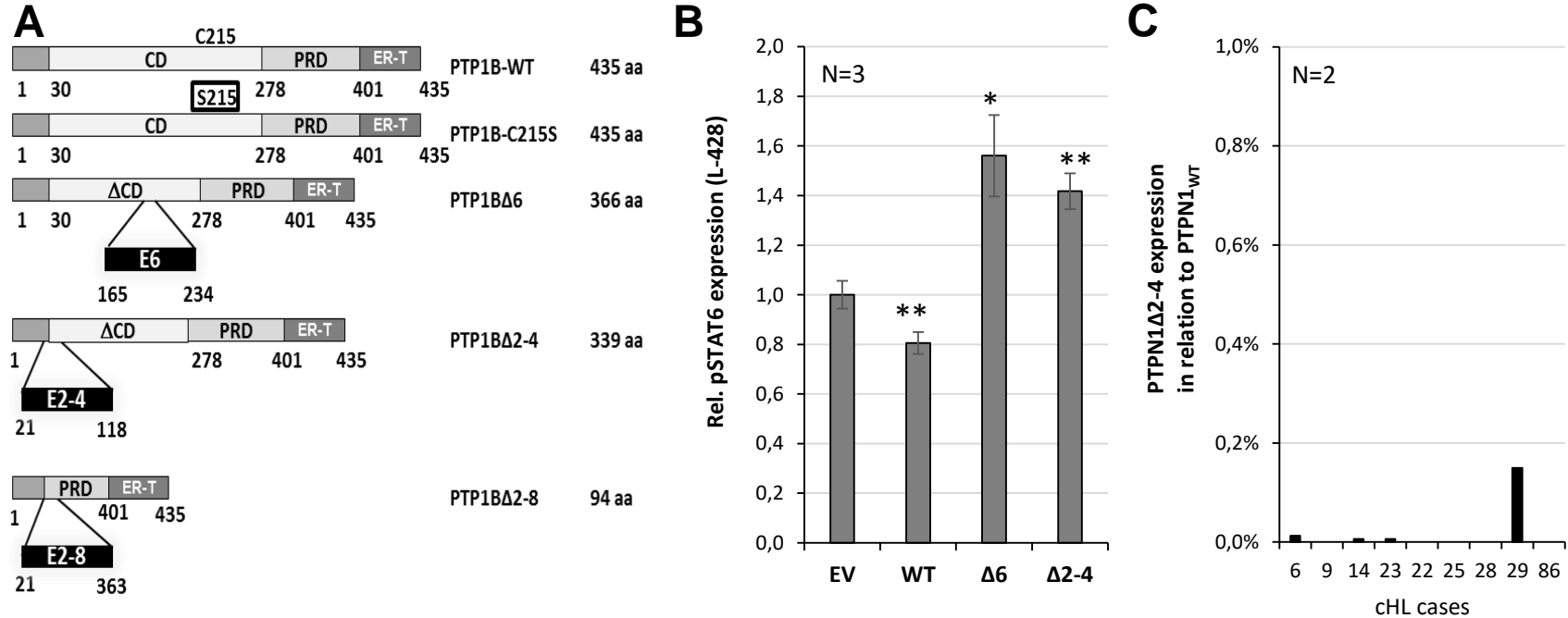
Characteristics (n=109)	no.	%
<b>Demographics</b>		
Age, median (range)	28,0 (8-76)	
Female	58/109	53
Male	51/109	47
<b>Morphology</b>		
Nodular sclerosing	68/109	62
Lymphocyte rich	23/109	21
Mixed cellularity	15/109	14
Lymphocyte depleted	1/109	1
NOS†	2/109	2
<b>Ann-Arbor-Stage</b>		
Stage I	4/84*	5
Stage II	42/84*	50
Stage III	21/84*	25
Stage IV	17/84*	20
<b>Clinical Parameter</b>		
>3 LN-Areas	55/84*	65
B-Symptoms	42/84*	50
Spleen involvement	9/84*	11
Mediastinal mass	69/84*	82
<b>Therapy</b>		
ABVD	33/84*	39
BEACOPP	37/84*	44
Other	14/84*	17
Radiation yes	59/84*	70
Radiation no	25/84*	30

† NOS=not otherwise specified

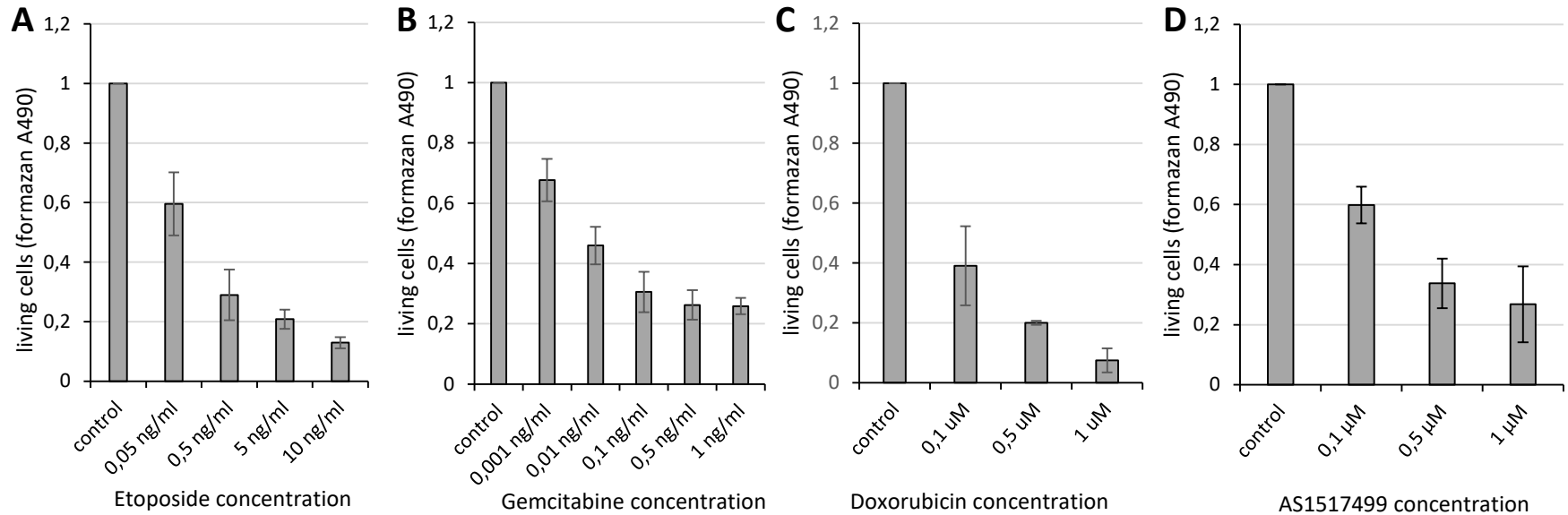
\*lower number due to consulting cases



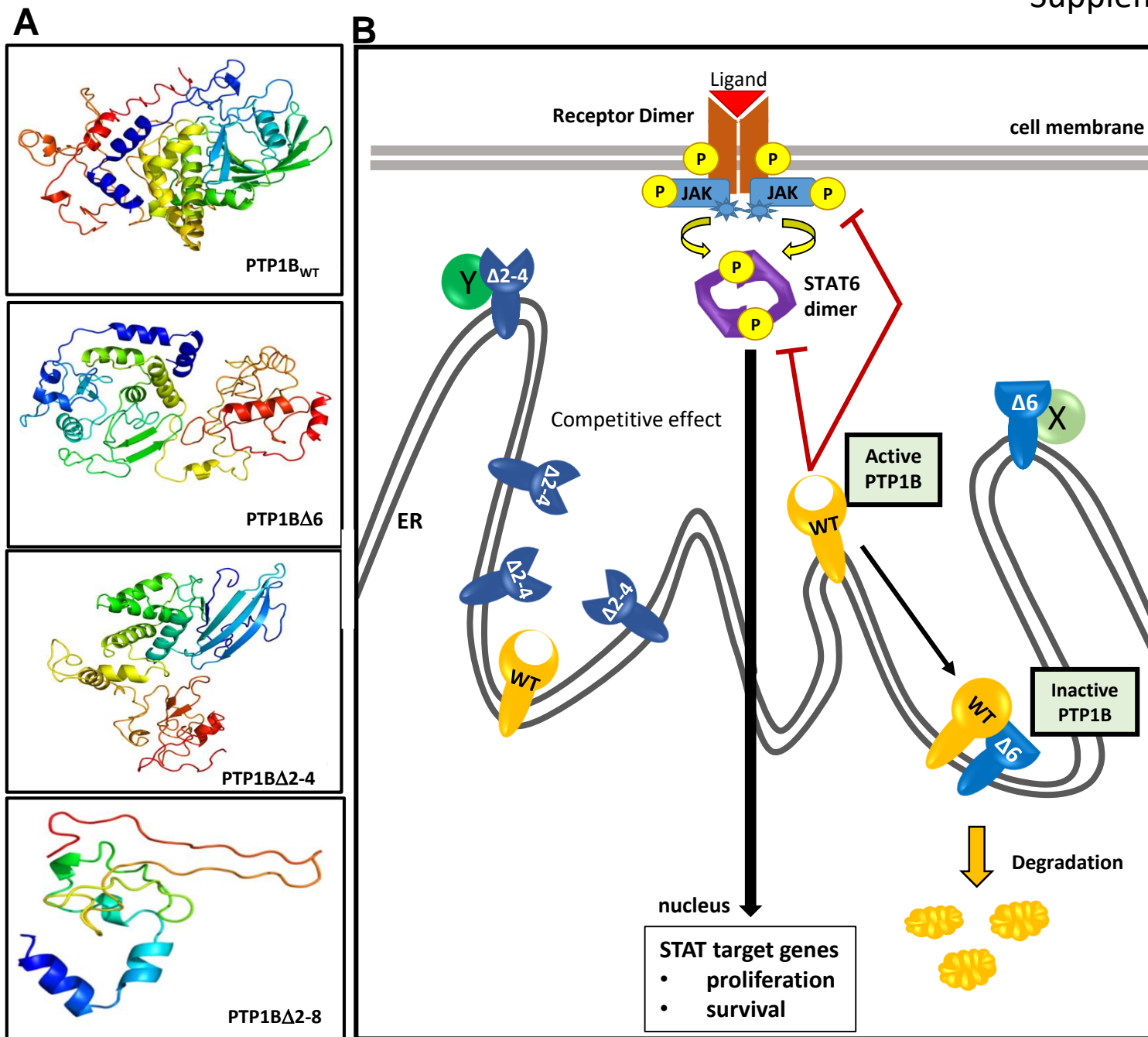
**Supplemental Figure 1: A)** Staining intensity of PTP1B in relapsing vs non-relapsing patients. **B)** Staining intensity of PTP1B in regard to the age of disease onset. **C)** Staining intensity of PTP1B in regard to the disease staging. **D)** Staining intensity of PTP1B in regard to the cHL subtype. **E)** Weakly positive correlation ( $r=0.37$ ) between signal intensity of PTP1B staining (0-5) and level of PTPN1 mRNA expression.



**Supplemental Figure 2: A)** Schematic presentation of the domain structure of PTP1B<sub>WT</sub>, PTP1B<sub>C215S</sub>, PTP1B $\Delta$ 6, PTP1B $\Delta$ 2-4 and PTP1B $\Delta$ 2-8. (CD = catalytical domain, PRD = proline-rich domain, ER-T = endoplasmatic reticulum targeting domain) [8]. **B)** Quantification of the amount of pSTAT6 protein as depicted in Figure 4A. Mean value of three independent experiments is shown. Mean values and standard error of mean (SEM) are depicted. Comparisons were performed between empty vector measurement and individual stable cell line. Significances are calculated using student's t-test ( $p < 0.05$  was regarded as significant). **C)** Value of the mRNA expression of *PTPN1 $\Delta$ 2-4* variant in different cHL cases relative to *PTPN1* mRNA measured by semi-quantitative Real-time PCR (sqPCR) analyses. CT values normalized against the mRNA expression levels of the two housekeeper genes  $\beta$ -actin and GAPDH.



**Supplemental Figure 3:** Proliferation assays (MTS) indicating the ratio of living cells of the cHL cell line L-428 after incubation with indicated amounts of Etoposide (48h, A), Gemcitabine (48h, B), Doxorubicin (24h,C) or AS1517499 (72h, STAT6 Inhibitor, D).



**Supplemental Figure 4: A)** Structural models of PTP1B<sub>WT</sub> (top), PTP1B $\Delta$ 6 (middle) PTP1B $\Delta$ 2-4 (bottom) and PTP1B $\Delta$ 2-8 (bottom, right) generated by the AIDA - *Ab Initio* Domain Assembly Server - online software tool. **B)** Proposed model of PTP1B $\Delta$ 6 and PTP1B $\Delta$ 2-4 in action. PTP1B $\Delta$ 6 binds and diminishes the negative effects of PTP1B<sub>WT</sub> by degradation of the protein. Additionally, PTP1B $\Delta$ 6 forms complexes with yet unknown interaction partners (labeled as X). PTP1B $\Delta$ 2-4 positively influences activation of STAT proteins. ER, endoplasmatic reticulum; RTK, receptor tyrosine kinase.