**Supplemental methods to the manuscripts by Vockova P et al:** **Anti-CD38 Therapy with Daratumumab for Relapsed/Refractory CD20-Negative Diffuse Large B-Cell Lymphoma**

Sequence reads from PDX sample were first aligned against the mouse reference genome mm10 combined with the human reference genome hg19 and murine reads were filtered out from further analysis by a custom script to reduce risk of contamination. Remaining reads were then aligned against the human reference genome hg19. All alignments were performed by BWA. (Li and Durbin 2009) Genomic variants were called with samtools and VarScan 2. (Li et al. 2009, Koboldt et al. 2012) Variant annotation was performed using SnpEff. (Cingolani et al. 2012) Only nonsynonymous variants in the gene coding regions with coverage of at least 10 reads with mapping quality and base quality higher than 20 in all related samples were compared together based on their frequency. Variants present in patient’s germline DNA at frequency higher than 0.05 were excluded from analysis. We compared variants with an allele fraction ≥ 0.2 in at least one of the compared samples that were present in at least 3 reads in both patient’s sample and derived PDX sample. All variant filtering was done in RStudio and frequencies and counts of variants were plotted using the ggplot2 library ([http://www.R-project.org](http://www.r-project.org/); [http://www.rstudio.com](http://www.rstudio.com/)). These variants were then manually reviewed in Integrative Genomics Viewer (http://www.broadinstitute.org/igv) and clear sequencing artefacts or variants present but not called in the germline sample were also excluded. List of 573 genes of special interest was created based on recent publications of frequently mutated genes in DLBCL samples (Pasqualucci and Dalla-Favera 2018, Reddy et al. 2017, Dubois et al. 2016, Karube et al. 2018, Pasqualucci et al. 2011, Zhang et al. 2013, Lohr et al. 2012, Morin et al. 2011) and variants present in these genes were specifically selected and marked in resulting diagram and table.

Copy number variants were predicted using CNVkit (Talevich et al. 2016) with normalization to pooled normal samples sequenced on the same instrument using the same library preparation kits. Inferred segmental changes were calculated using the fused lasso method (Tibshirani and Wang 2008) and plotted in diagrams for diagnostic and PDX sample.

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