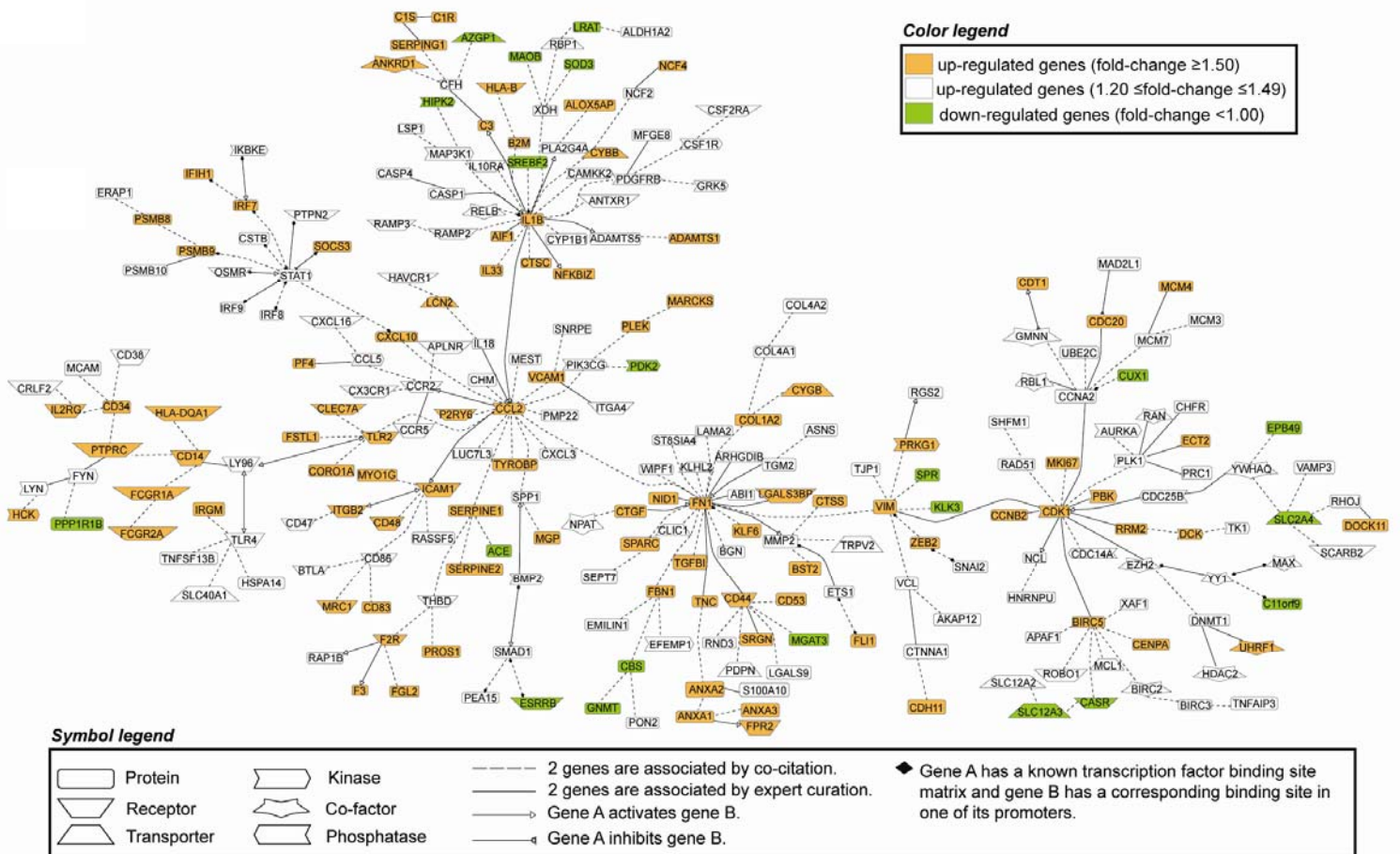
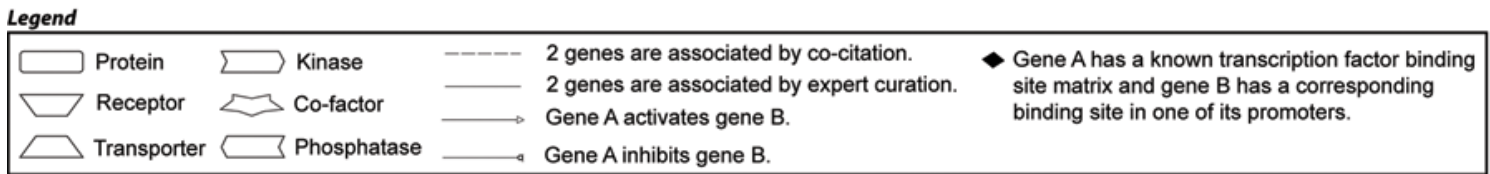
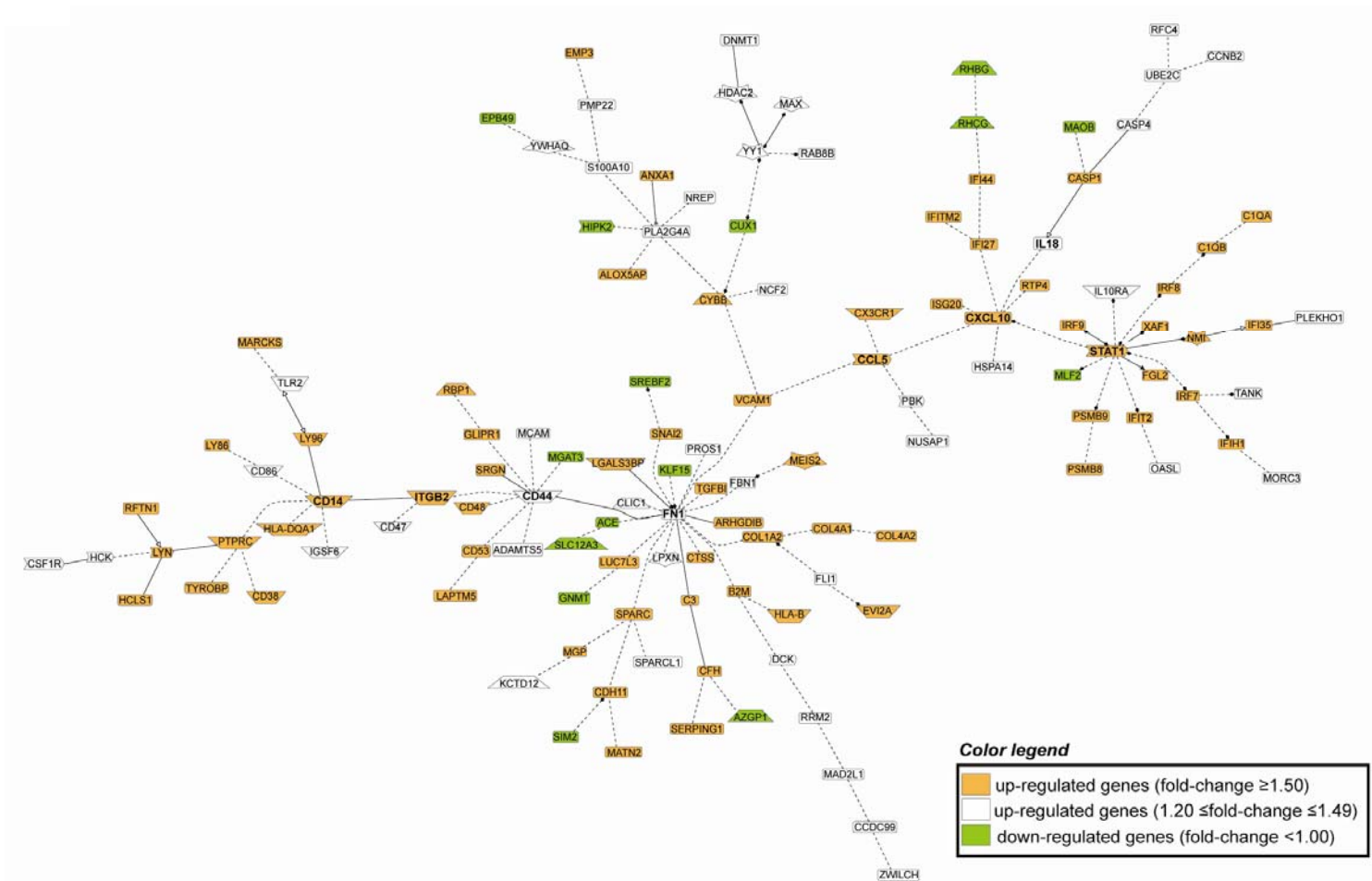


**Supplementary Figure 1:** Glomerular (A) and interstitial scores of ZB/W mice used for these studies. NP: Non-proteinuric; P: proteinuric; Triple: Combination cyclophosphamide, CTLA4Ig and anti-CD40L treatment; T/C: combination TACI-Ig and CTLA4Ig treatment. p values \* p < 0.001; † p < 0.01; # p < 0.05.

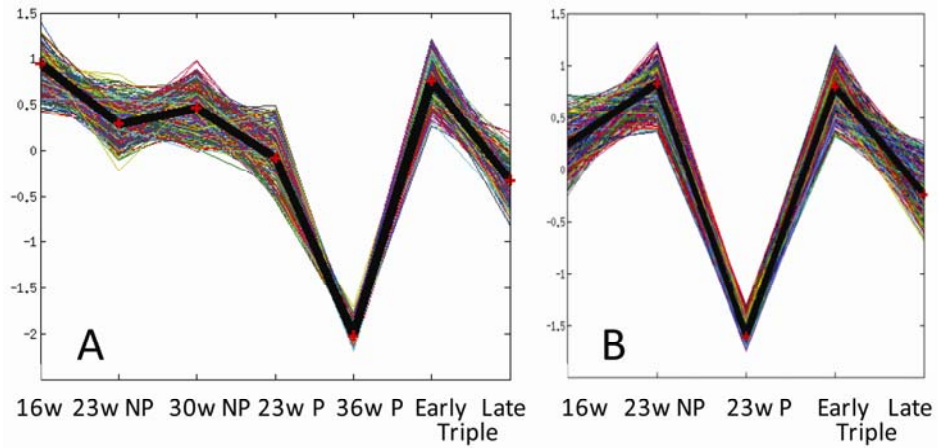


**Supplementary Figure 2A: Literature-based analysis of genes using Genomatix Pathway System (GePS) software.** 587 genes with human orthologs from the 654 mouse genes that were regulated in opposite directions at proteinuria onset and remission. GePS creates networks containing a maximum of 250 genes from an input gene list where connections indicate genes that are co-cited in PubMed abstracts. We applied a stringent function-word filter meaning that to be displayed in the transcriptional network two genes have to be co-cited in the same sentence with a function word (e.g. gene A activates gene B). Key nodes such as CCL2, FN1, STAT1 and CDK1 had the most connections. Orange represents the genes that are upregulated and green represents the genes that are downregulated in nephritic compared to prenephritic mice.



**Supplementary Figure 2B: Literature-based analysis of genes using Genomatix Pathway**

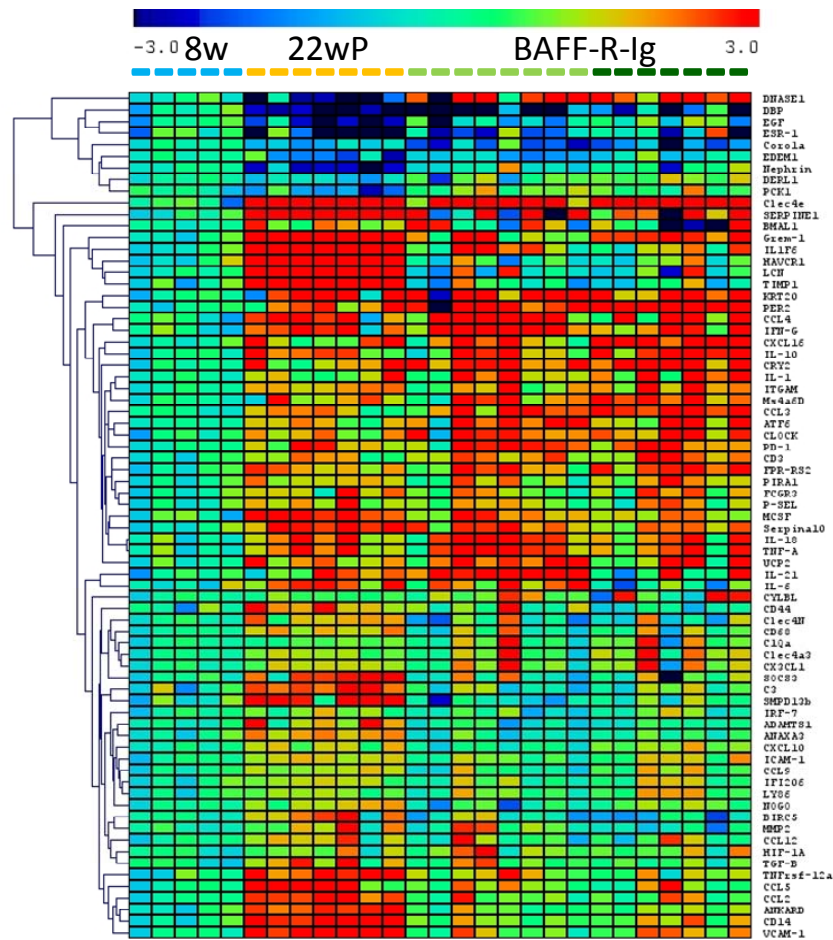
**System (GePS) software.** 175 of the 587 genes were regulated in both the glomerular and tubulointerstitial compartments of human lupus nephritis biopsies were analyzed. The picture displays the 127 genes that were co-cited in PubMed abstracts in the same sentence linked by a function word. Orange represents the genes that are upregulated and green represents the genes that are downregulated in nephritic compared to prenephritic mice.



**Supplementary Figure 3:** Fold expression compared with 16w pre-nephritic mice of genes associated with the indicated disease progression stages. Only the 300 most tightly associated down regulated genes are shown. Upregulated genes display the opposite pattern. **A.** Genes associated with late disease progression. **B.** Genes associated with new onset proteinuria and remission and impending relapse following triple therapy.







**Supplementary Figure 4:** One way cluster analysis of genes with significantly altered expression at proteinuria onset in the PCR confirmation set from NZM2410 mice (see Supplementary Table 10). Gene expression was normalized to  $\beta$ -actin and then to the mean of the young controls. Significantly up or downregulated genes in the young vs. nephritic comparison are shown. Early and late remission after BAFF-R-Ig therapy are indicated by light and dark green respectively.