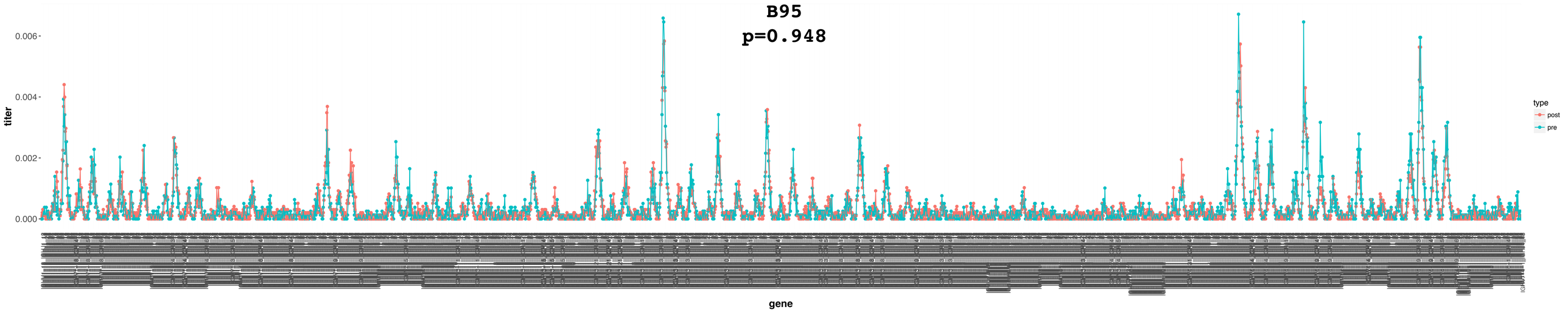
This file represents the clonotype frequencies of the B naïve compartment of each individual across the two sampling points. Clonotypes were defined as BCR sequences with identical IGHV and IGHJ genes and CDR3 amino acid length. Significance of the difference in clonotype distribution was determined using Wilcoxon signed-rank test and FDR correction for multiple testing. Sample names and respective p-values are shown for each sample.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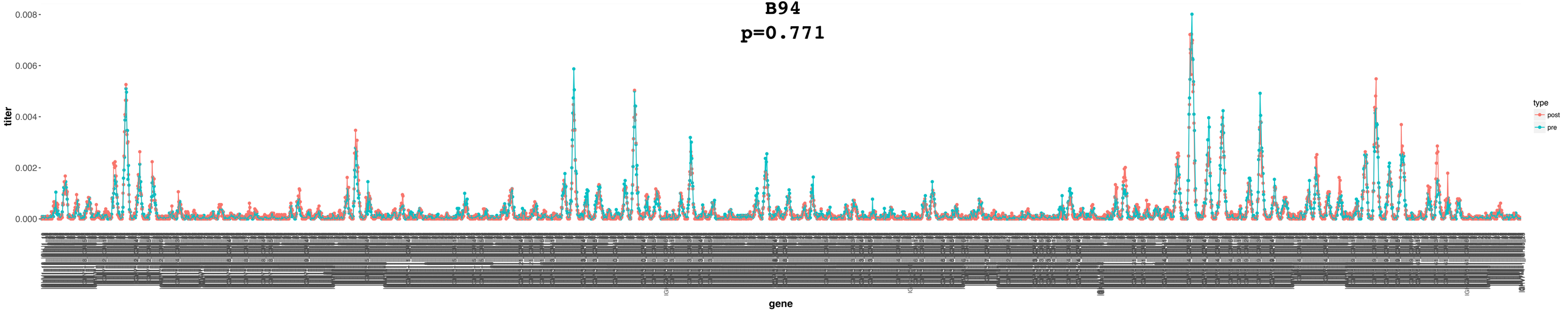
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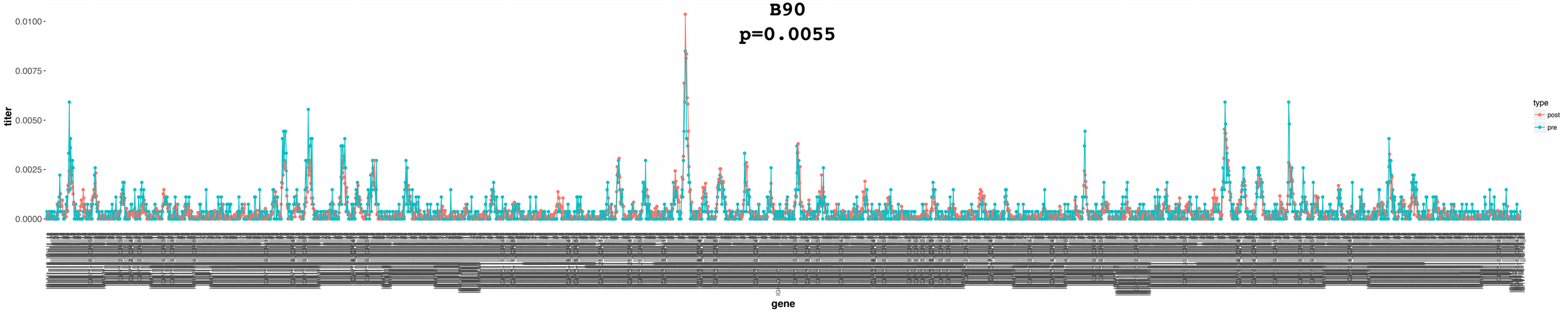
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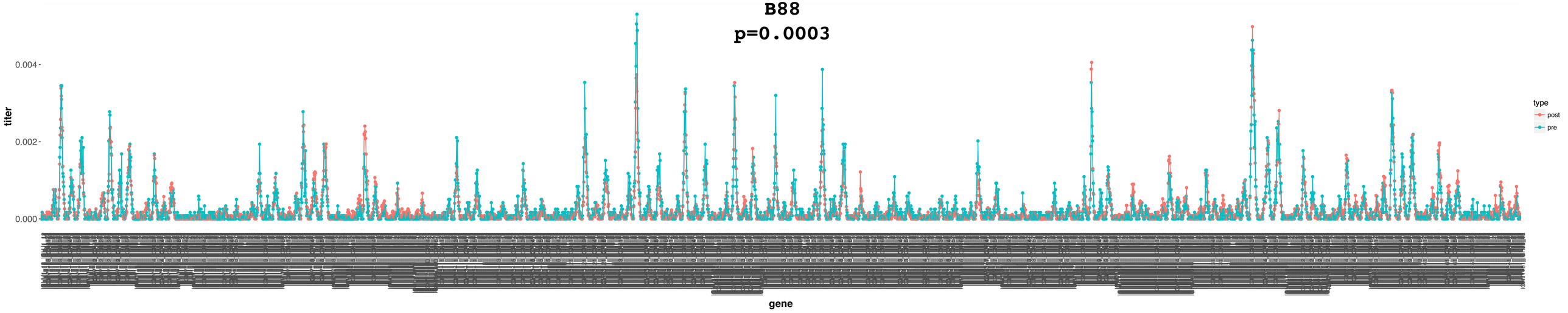
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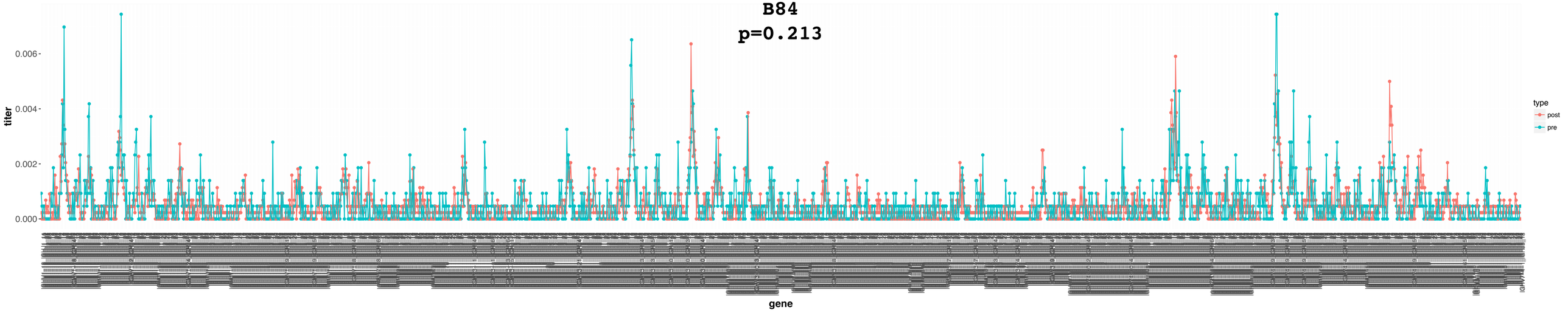
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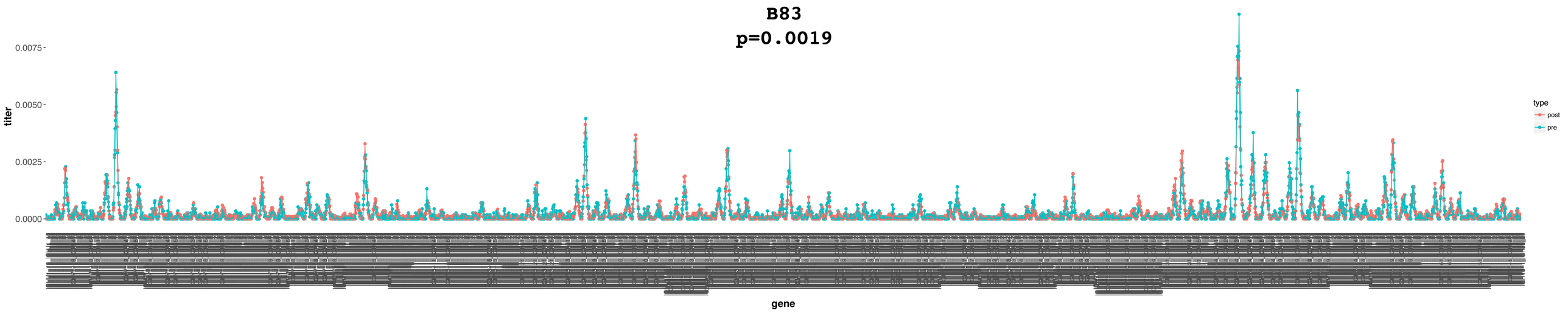
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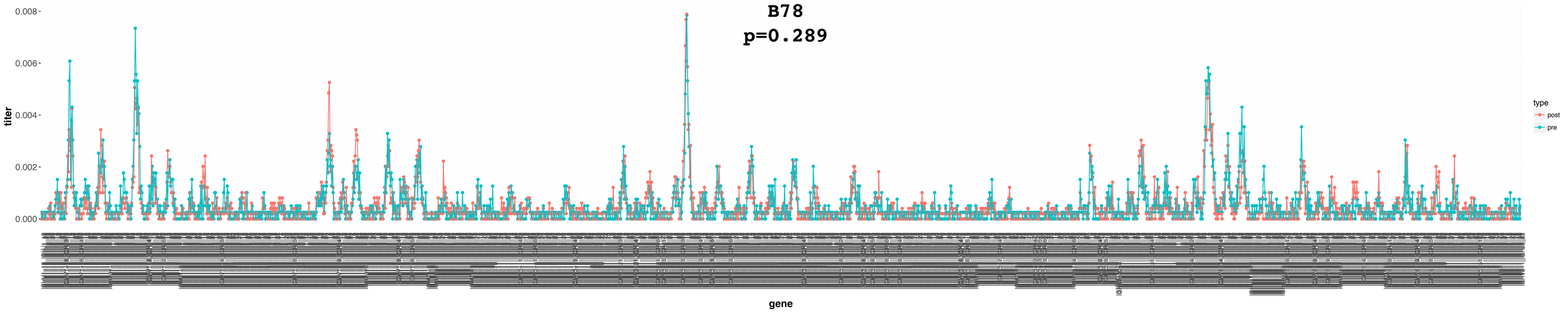
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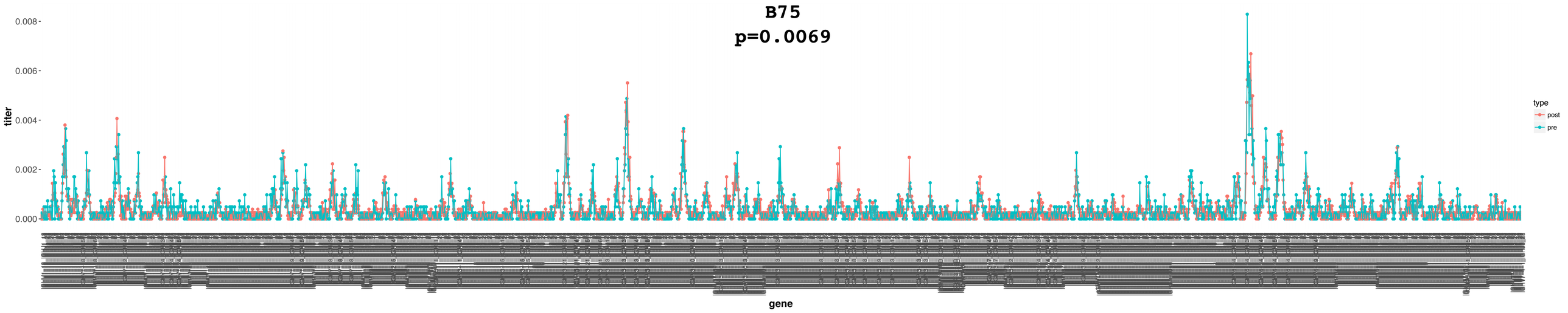
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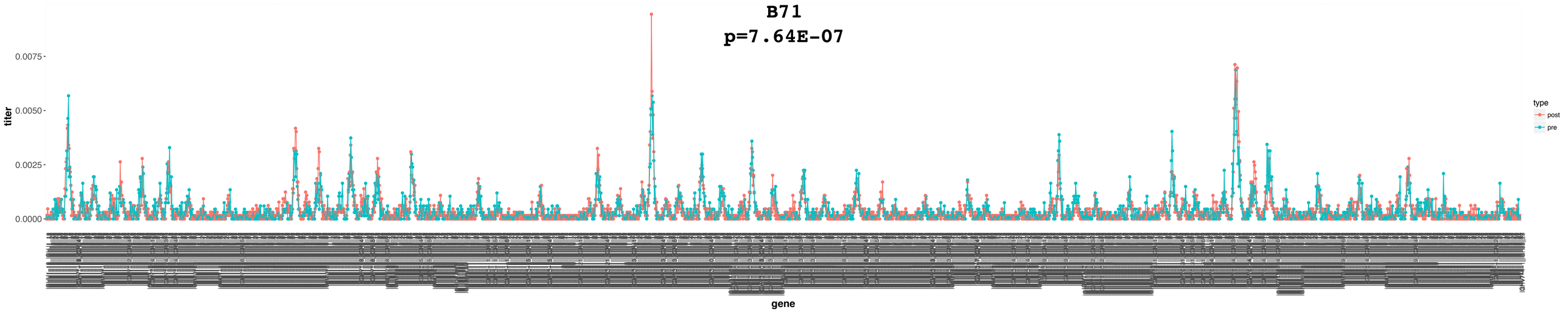
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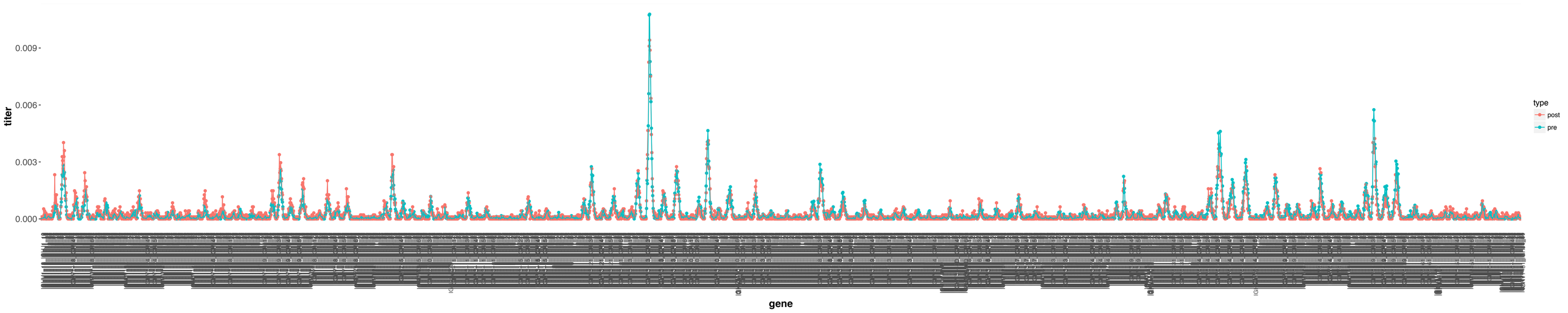
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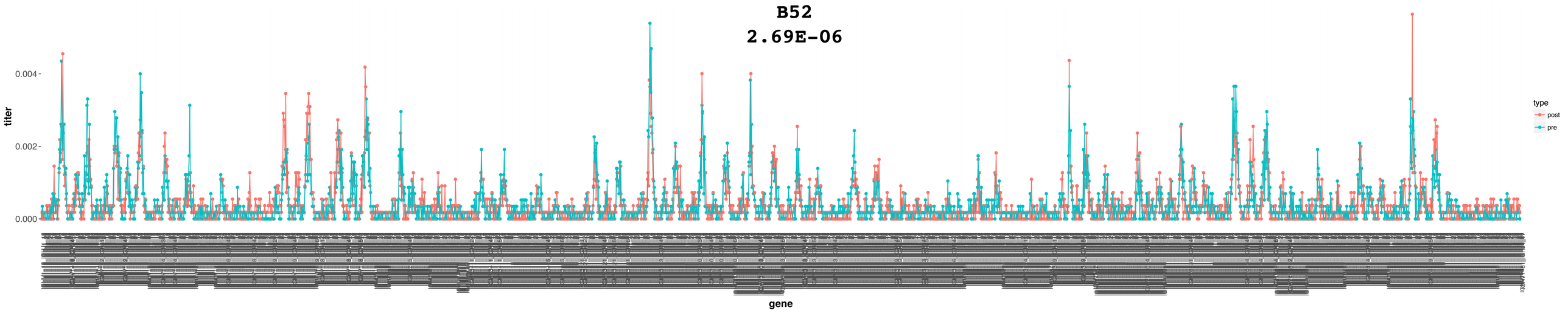
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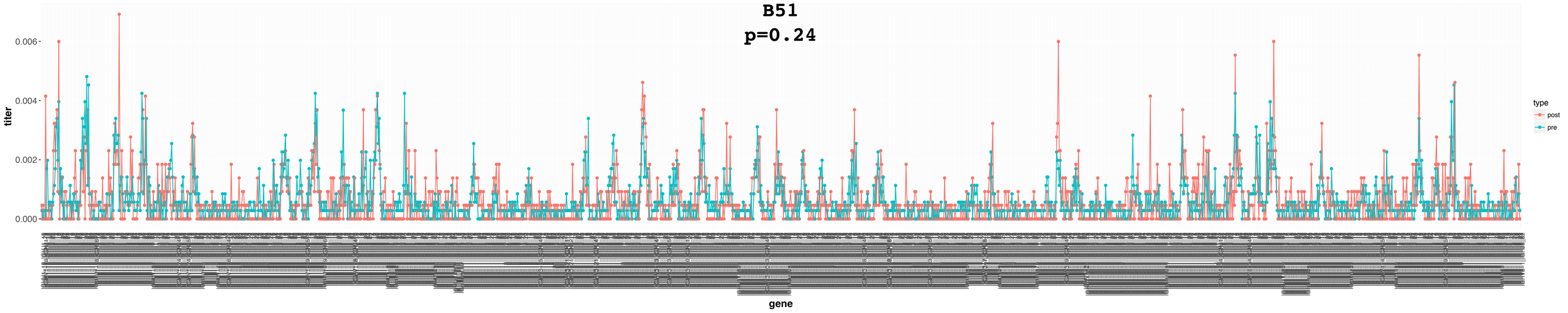
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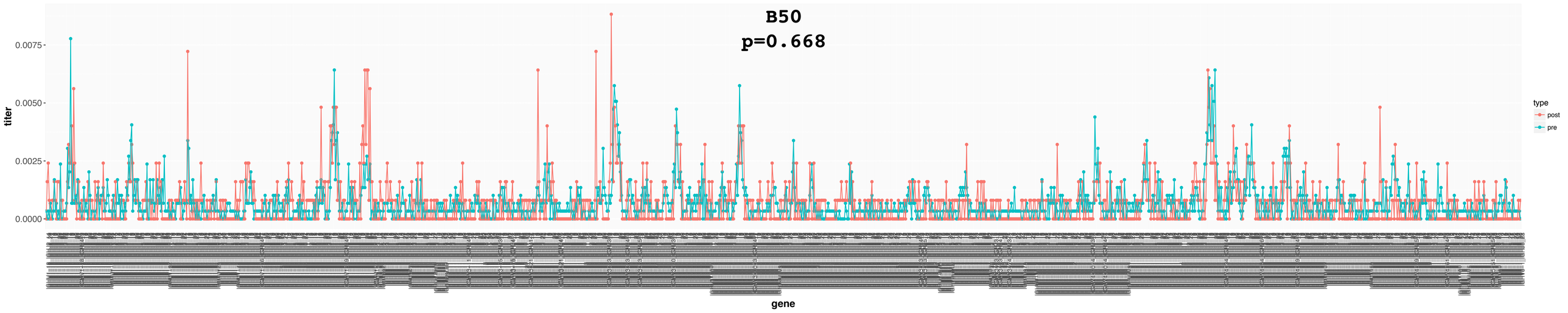
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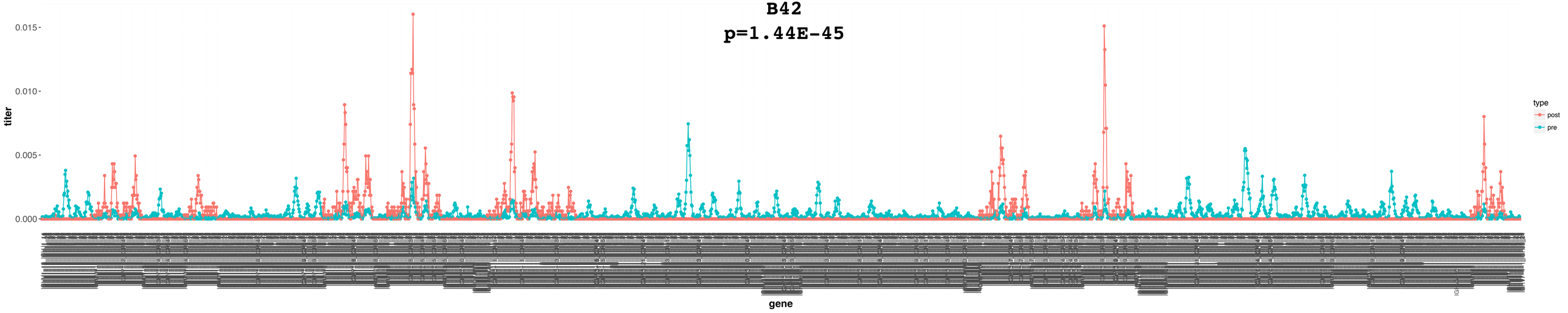
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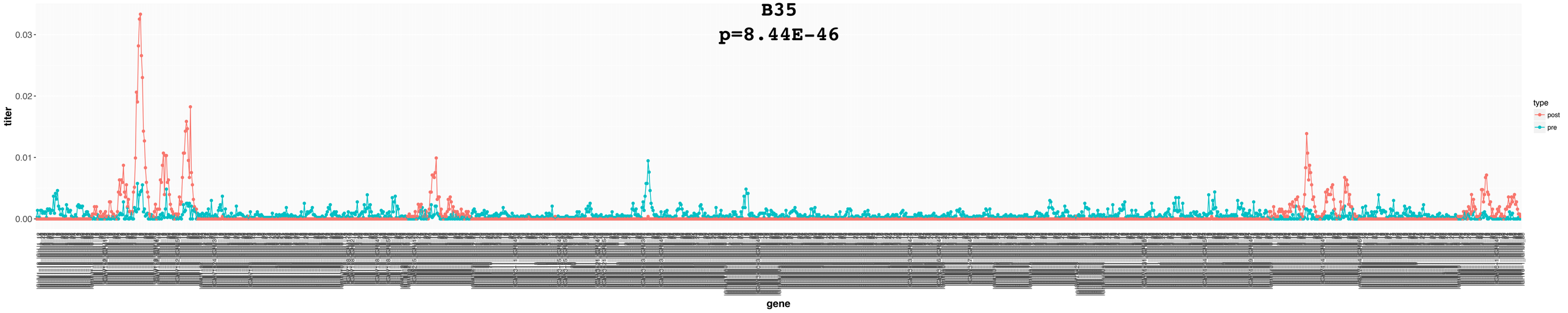
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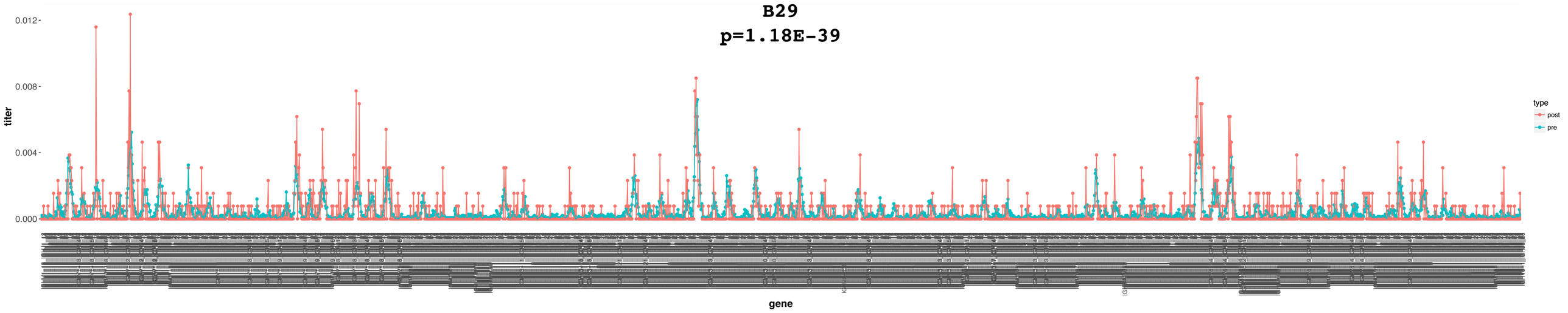
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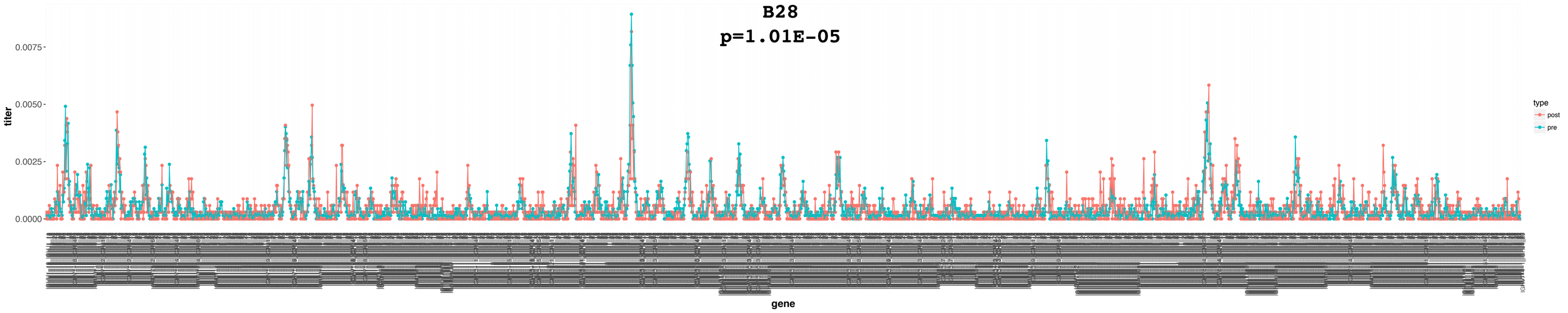
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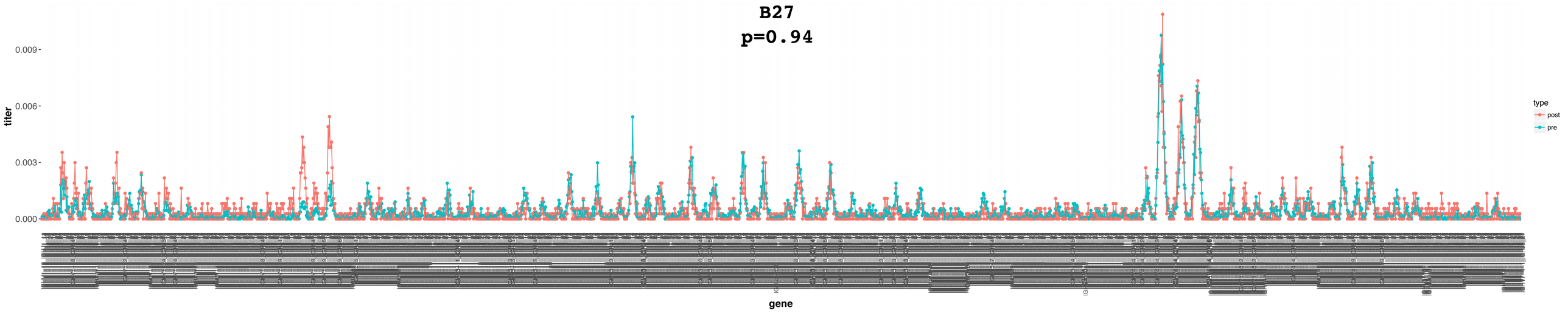
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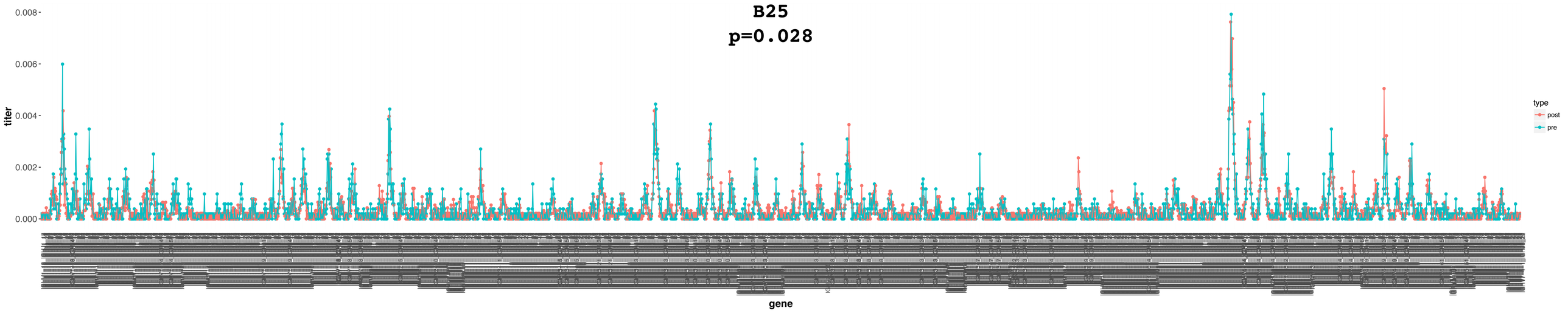
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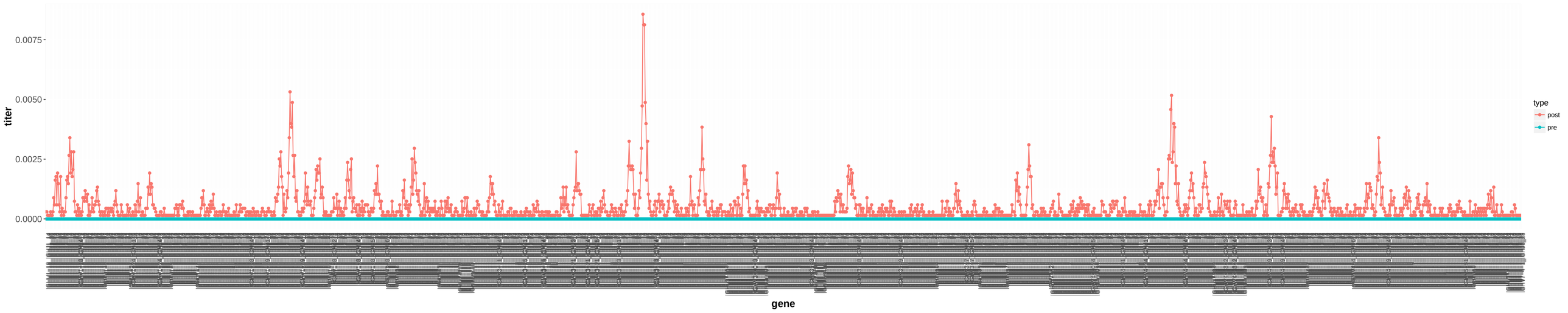
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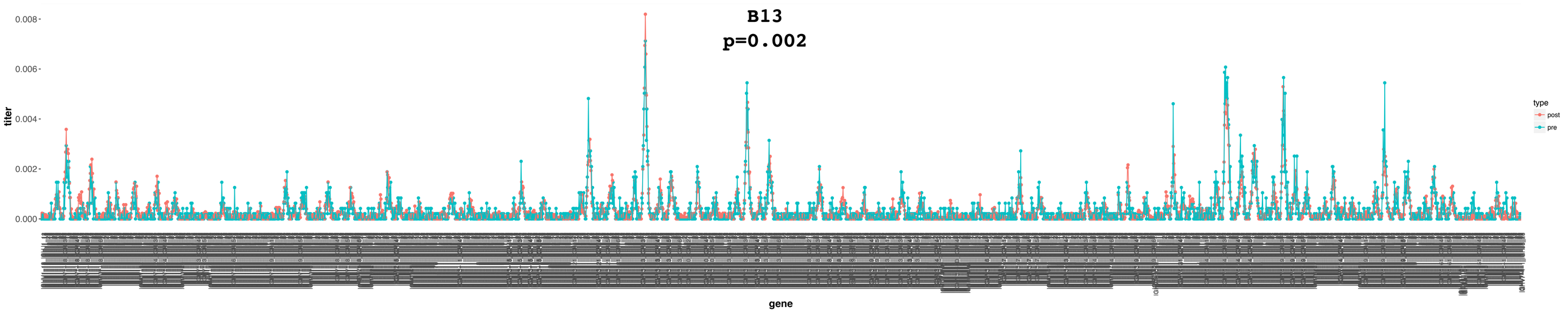
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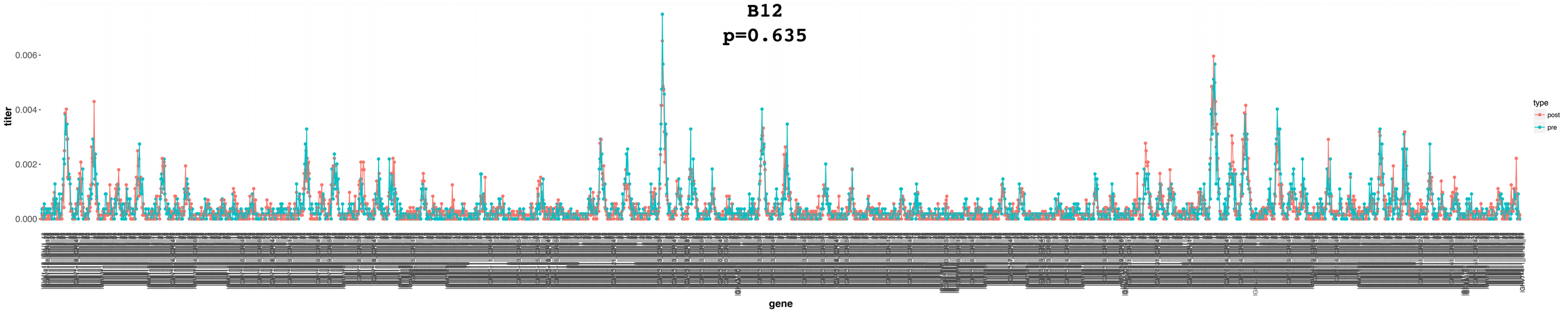
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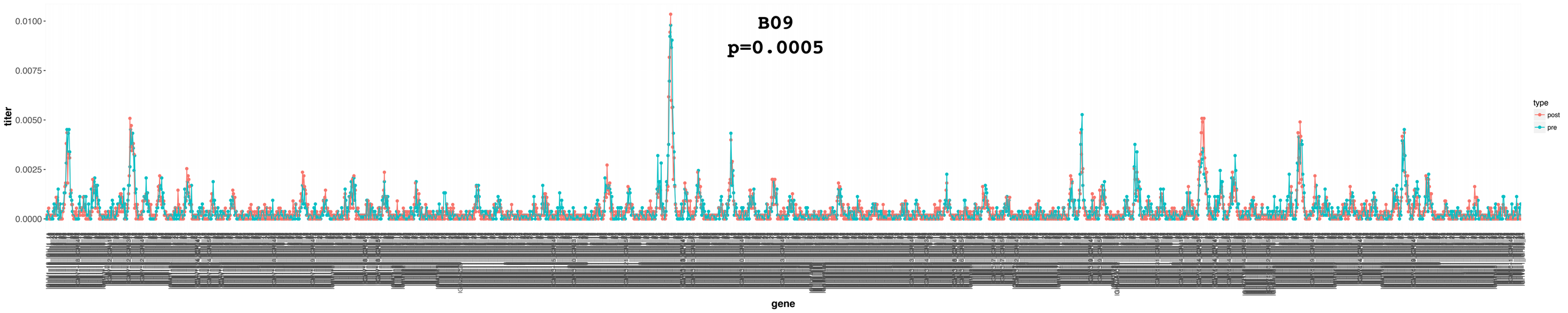
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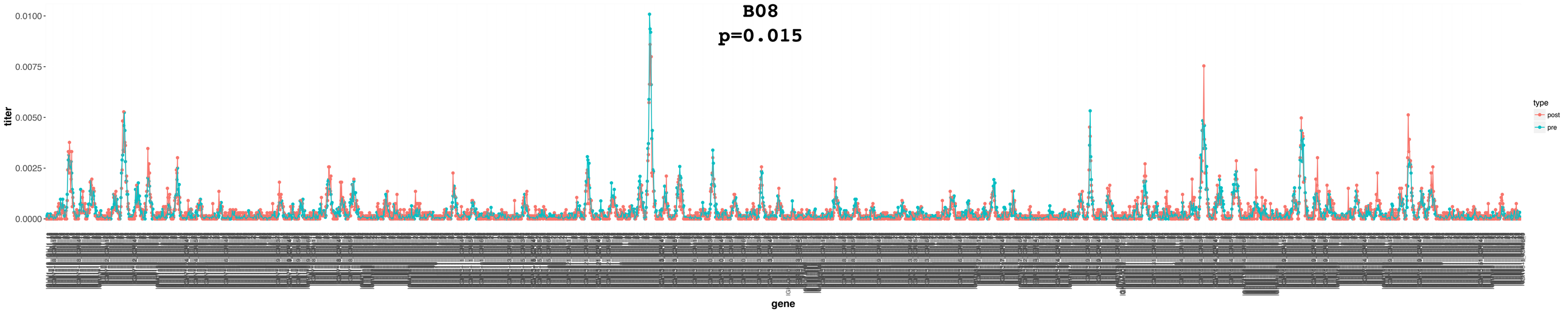
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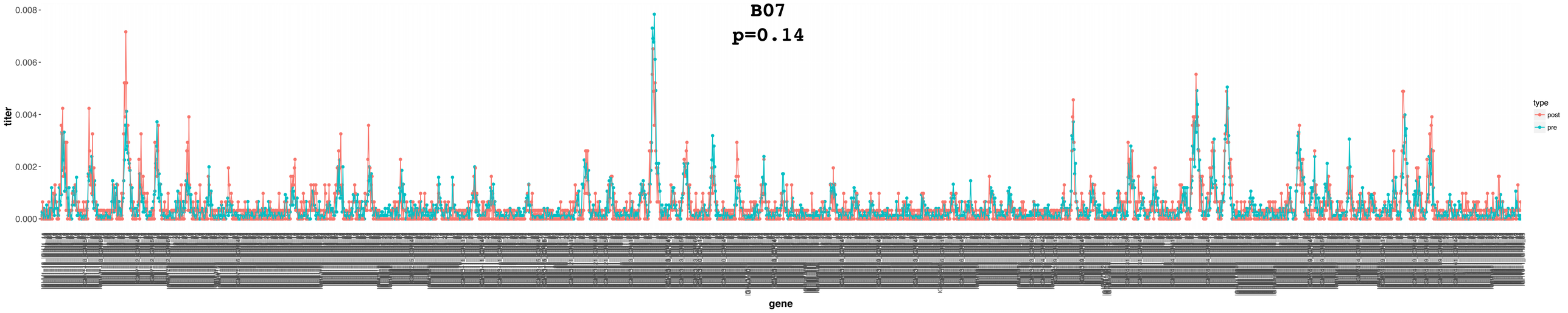
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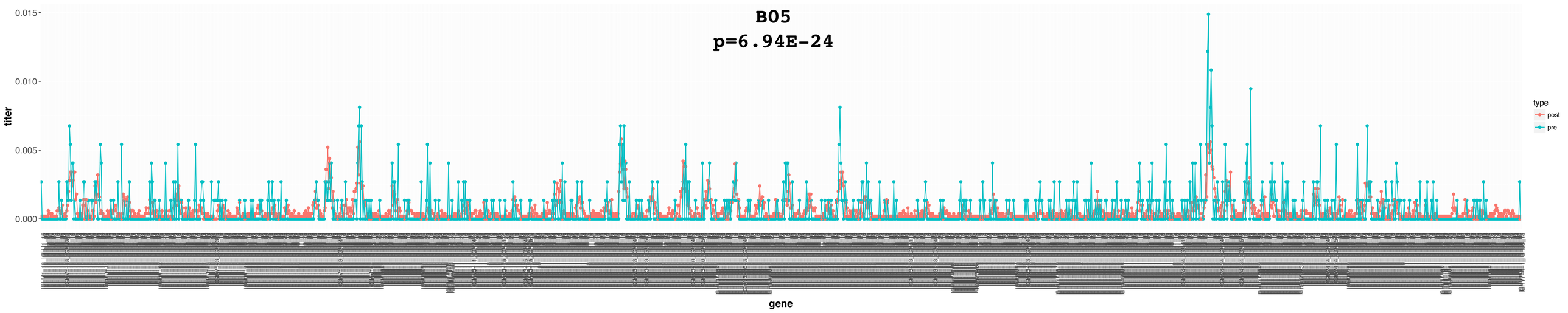
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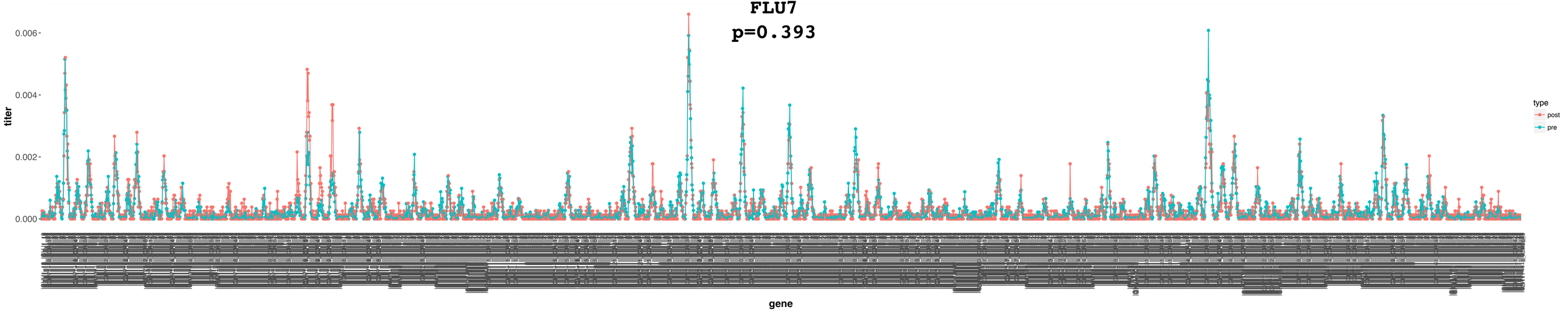
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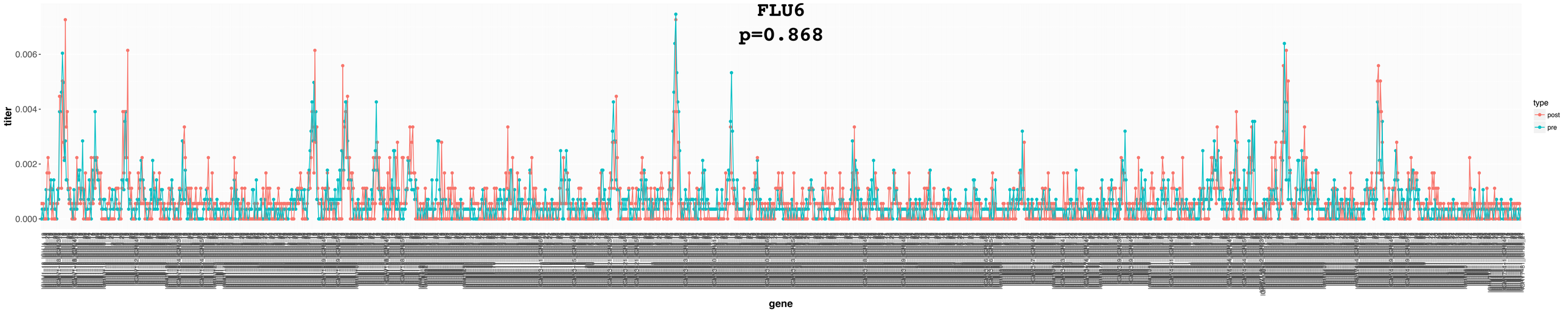
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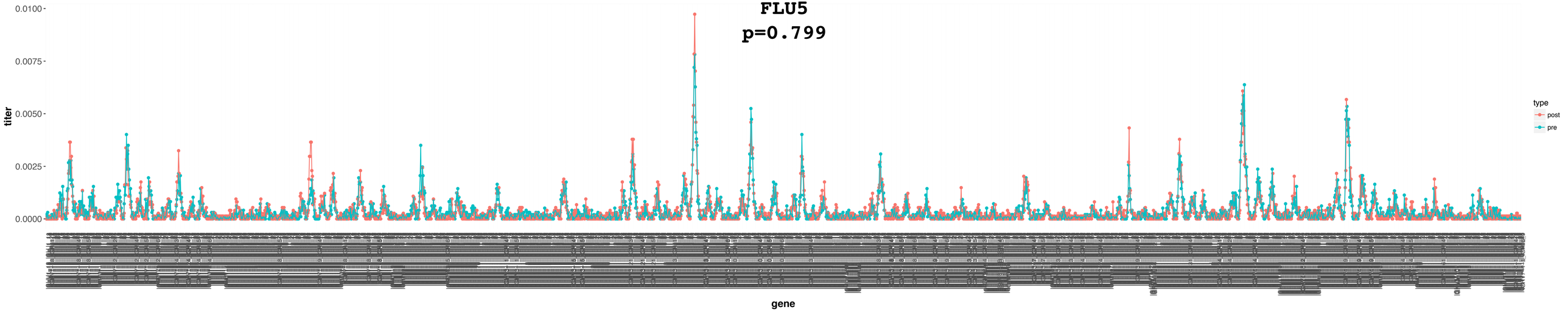
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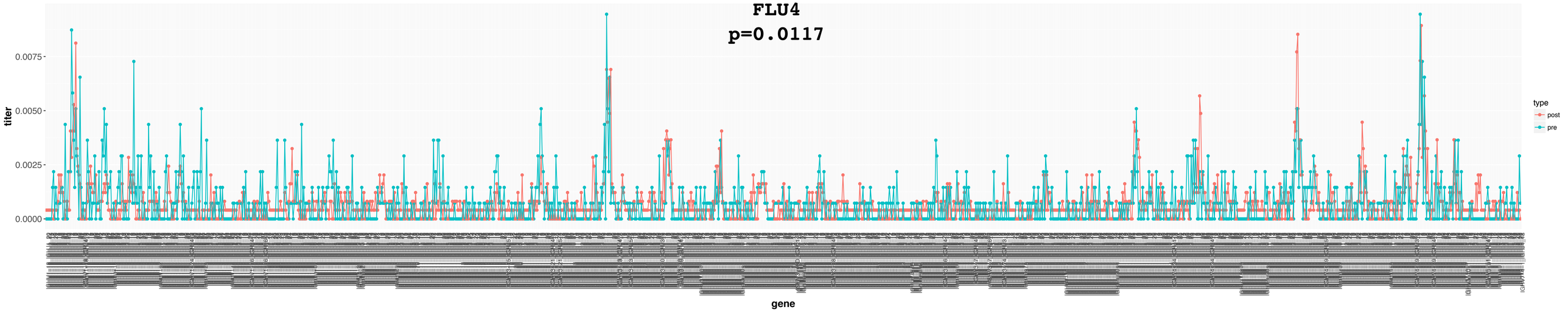
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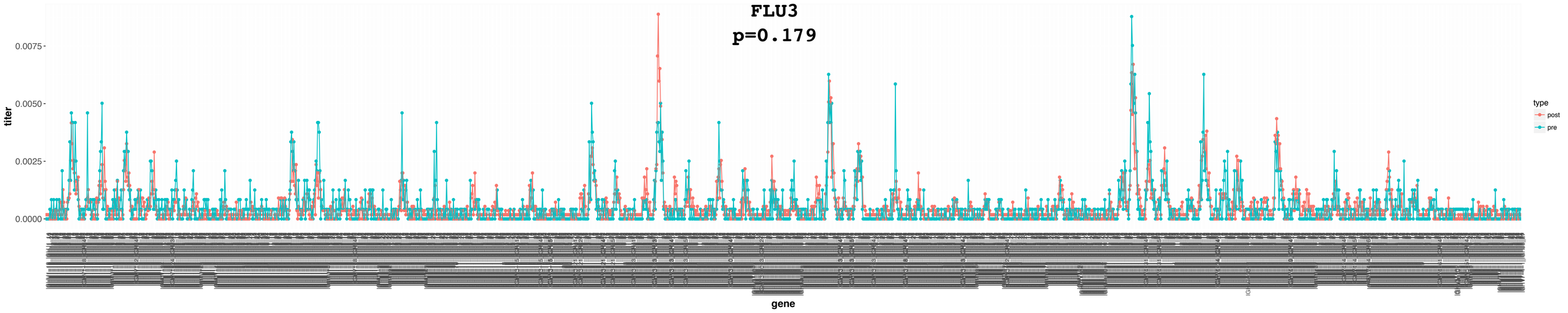
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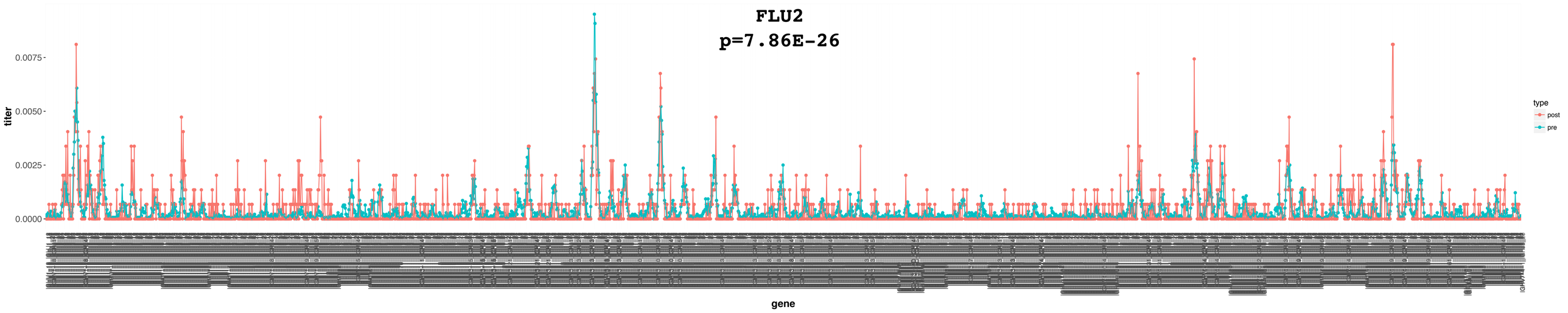
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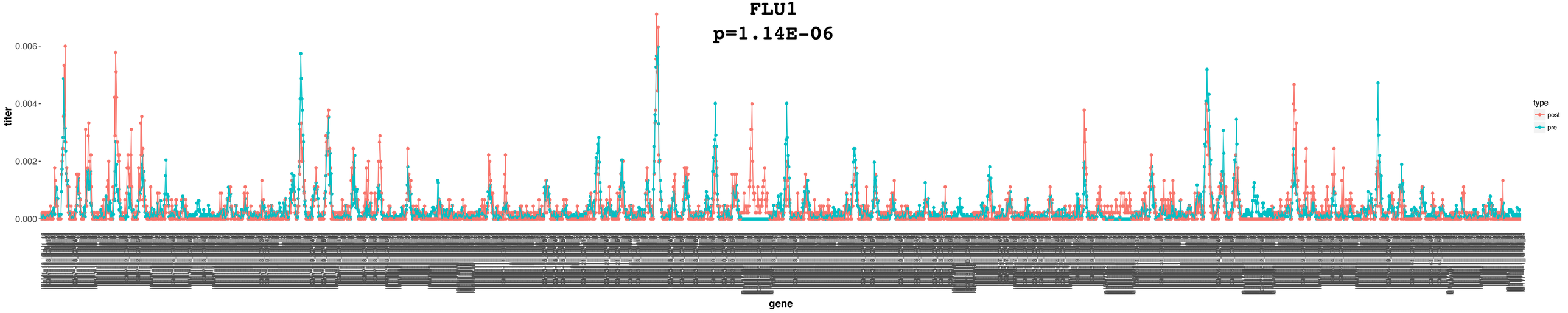
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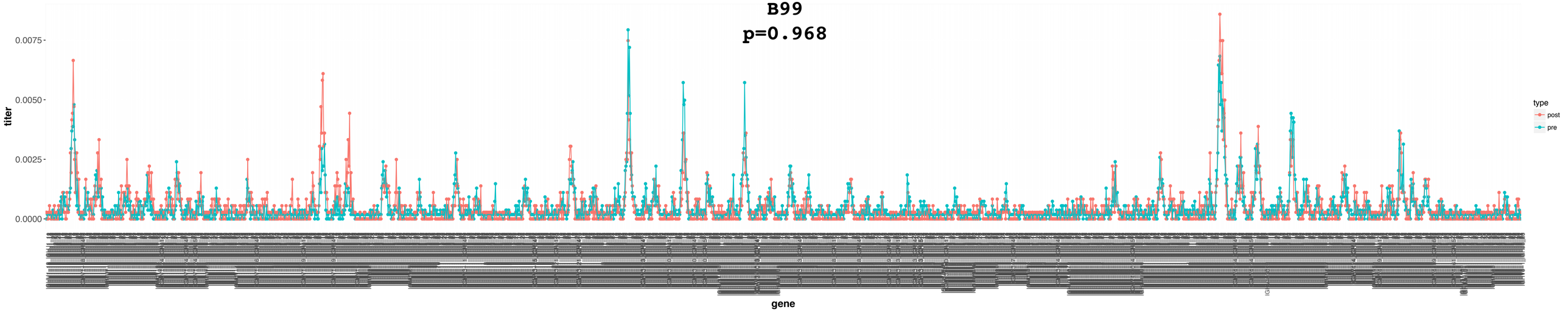
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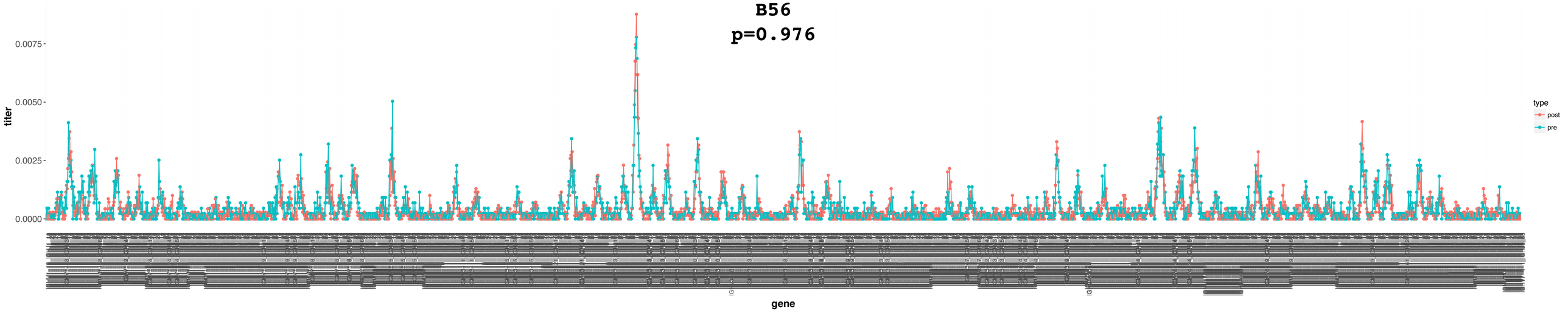
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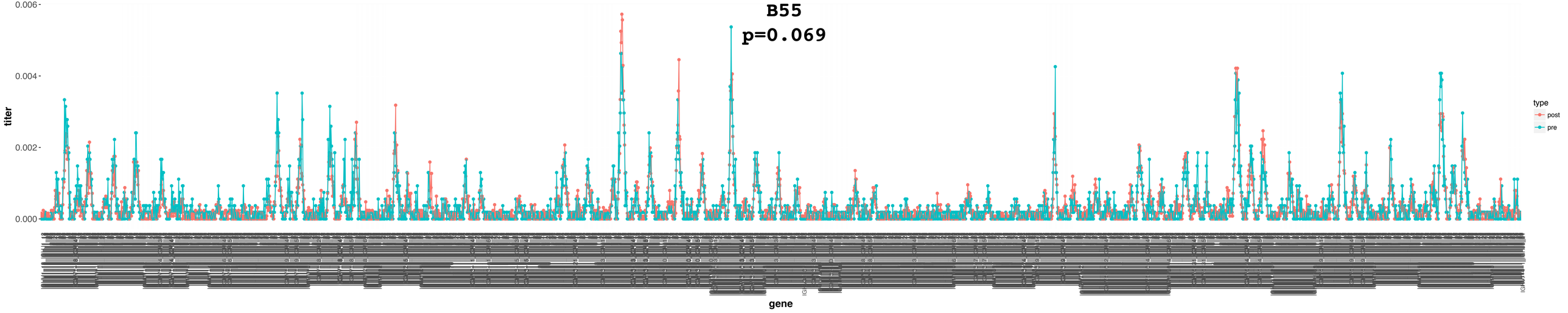
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