

# The Challenges of Identifying Possible Biomarkers to take forward into further research from a subgroup analysis.

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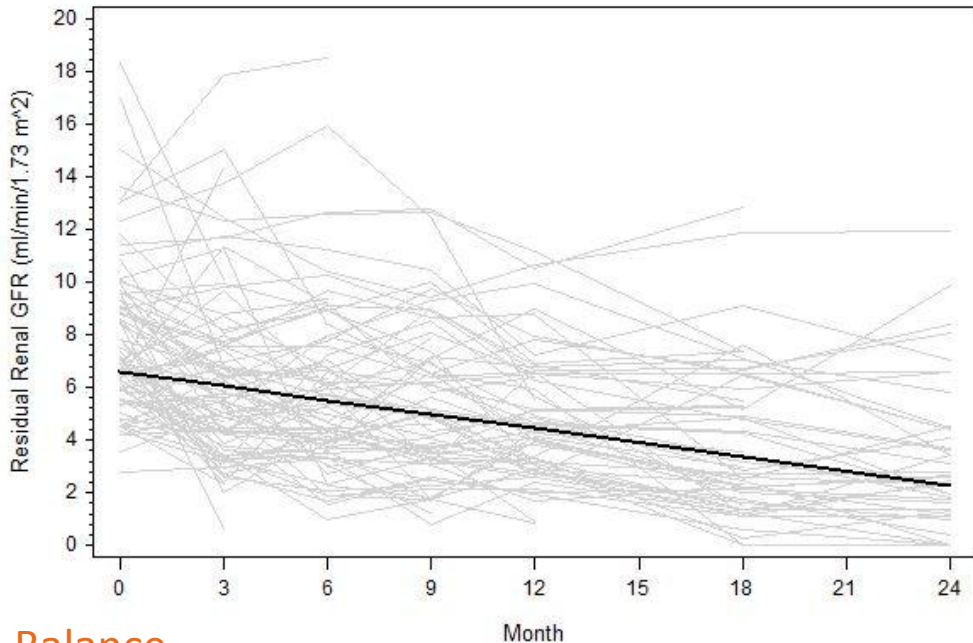
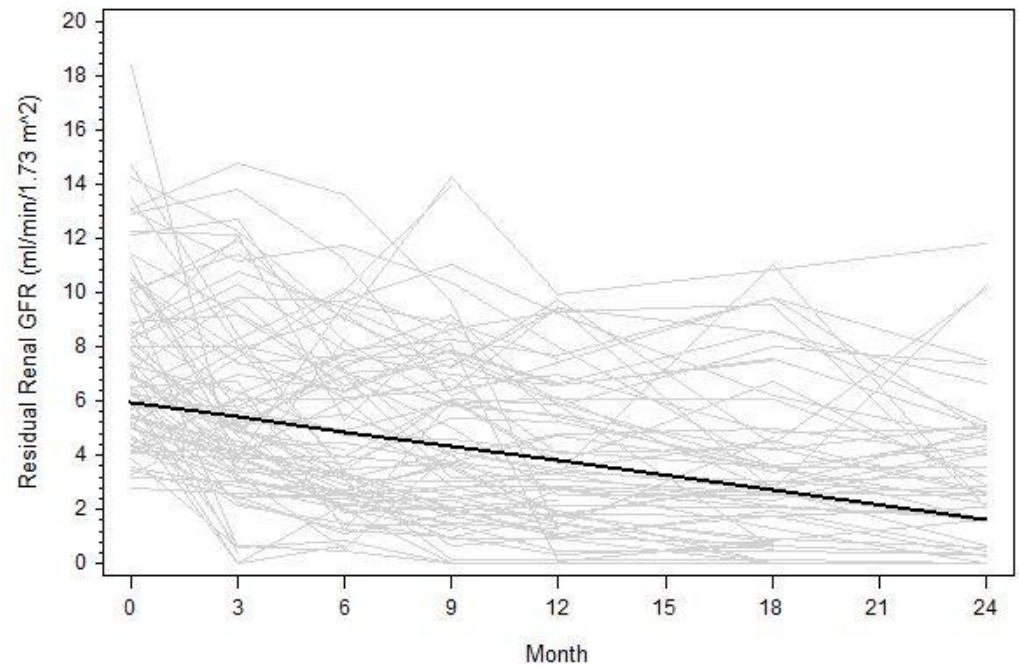
# Main Study

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- Compare the rate of decline in residual renal function in peritoneal dialysis patients over 24 months using Balance solution compared with the conventional Stay.Safe solution.
- Secondary endpoints:
  - Time to anuria
  - Peritonitis infection rates
  - Ultrafiltration (adjusted for total glucose exposure)
  - Urine volume
  - 4 hr D/P creatinine and D/D0 glucose
- Total sample size 167

## Linear slopes

Rate of change same for both treatments (-0.18),  
12 mths difference Balance to SS  
0.65 (95% CI=-0.17, 1.47)  
24 mths 0.64 (95% CI=-0.54 to 1.82)



Balance

Stay safe/ Sleep safe

Medics questioned differences  
between first and second years  
Dropouts – possibly informative  
Time to anuria highly significant

# Sub-study

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- biomarker measurements: baseline, 3, 6, 12, 18 and 24 months.
- 19 kidney panel biomarkers:  
albumin, beta-2-microglobulin, cystatin, NGAL, osteopontin, uromodulin, EGF,  $\alpha$  GST, calbindin, clusterin, KIM-1/TIM-1, osteoactivin, TFF3, VEGF, IP-10, MIG, MIF, TIMP-1, piGST, RBP4
- 1 peritoneal solute biomarker: IL-6
- Urine clinical outcomes: GFR, urine volume
- Peritoneal solute clinical outcomes: peritoneal ultrafiltration, peritoneal D:P Cr and D/D0 glucose, peritonitis infection rates
- Phase I
  - n=25 urine samples from each treatment arm (i.e N=50)
  - Times: baseline, 12 and 24 months
  - Patients must have completed the study
- Phase II
  - Expansion to all patients who completed the study (49 Stay.Safe, 42 Balance)

# Challenges/ questions

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- Different baselines (month 0, 1 or 3)
- Multiple biomarkers with multiple outcomes
- Different sets of biomarkers with different outcomes (kidney panel with urine outcomes, peritoneal biomarker with peritoneal outcomes)
- Should the baseline biomarker be used to predict outcome at 24 months?
- Should biomarkers measured over time be used to predict outcome?
- Transformation of biomarkers - logged
- Adjustment of biomarkers – adjusted for urine creatinine
- Does treatment need to be taken into account?
- Maybe treatment affects the biomarker?
- As sample has completed study maybe dilutes effect of biomarker?
- Desire to explore vs multiplicity
- Power to detect real effects for taking into further research.

# Original Plan

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- Biomarker selection in the face of multiplicity – lots of research (gene expression)
- Baseline biomarkers
  - Compute variable importance measure (VIM) for each biomarker using targeted maximum likelihood estimation (TMLE)
    - Susan Gruber and Mark van der Laan, University of California, Berkeley (R program, binary point treatment on binary or continuous outcomes at one timepoint.)
- Biomarkers over time
  - Compute 2 marginal VIMs for each biomarker using longitudinal TMLE (Bosny J, 2010)
    - Time slope through the origin. Biomarkers with a positive coeff will have positive effect
    - Absolute area under the LOESS curve (to capture a curvilinear effect over time if necessary)
- Estimate confidence intervals and p-values (using bootstrap)
- Adjust p-values for multiplicity to control false discovery rate using Benjamini and Yekutieli false discovery rate.
- Rank p-values to get index
- This and clinical interpretation to decide biomarkers to take forward.

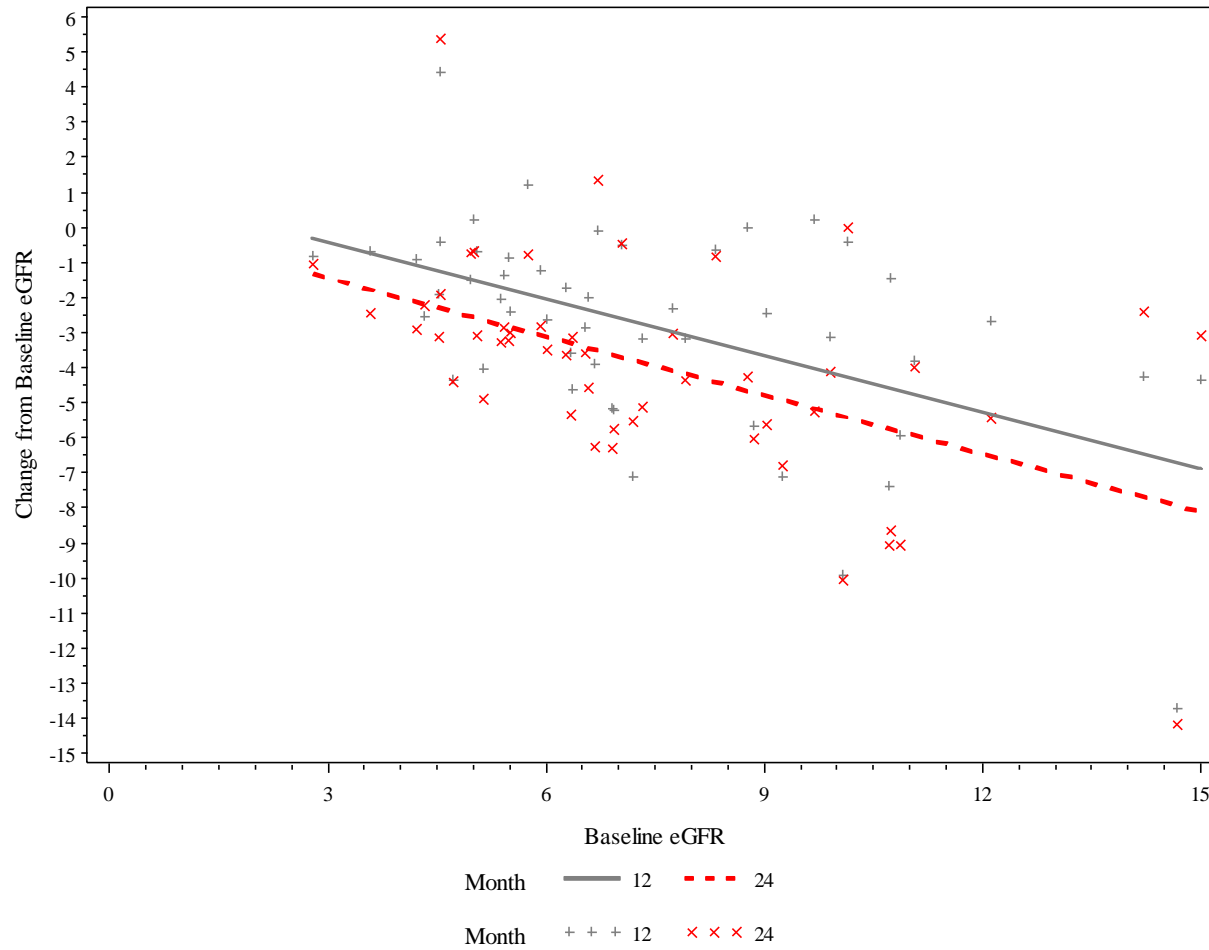
# Actual Approach

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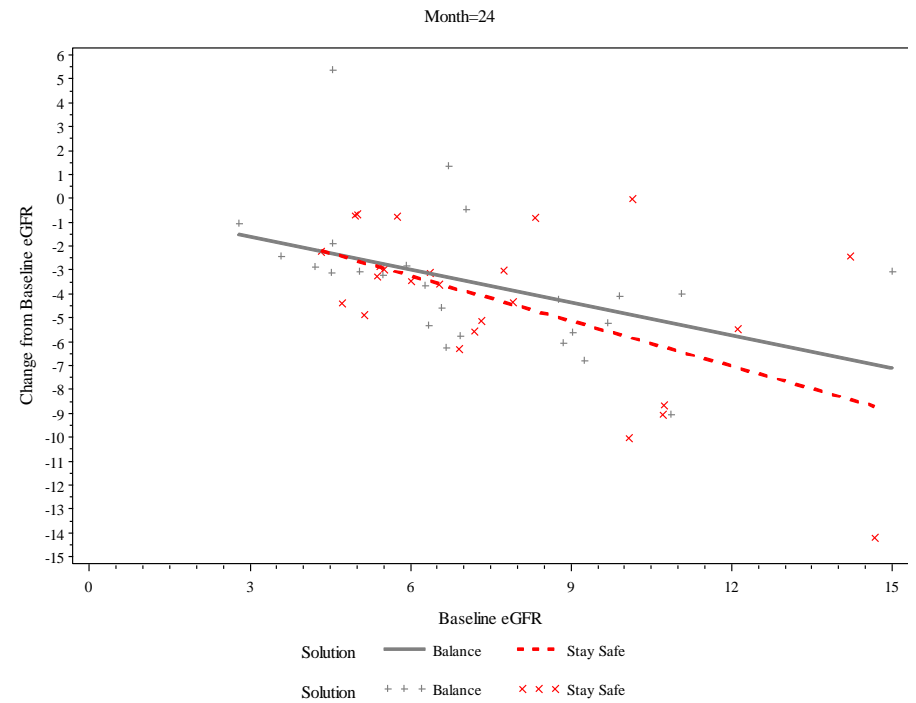
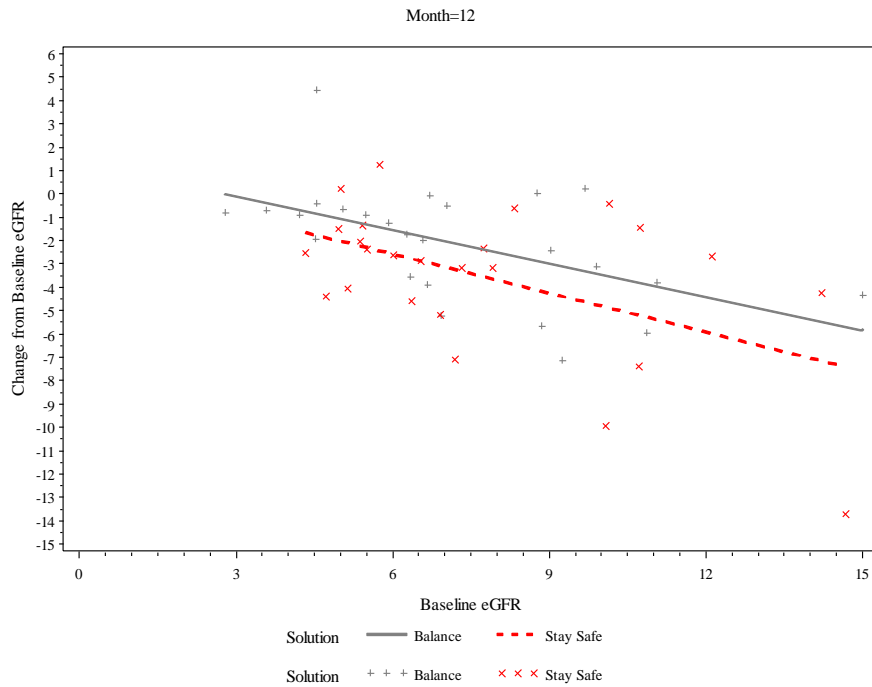
- Separated urine and peritoneal investigations
- For each biomarker
  - Analysed as change from baseline for 12 and 24 months
    - Adjusted for baseline biomarker only
    - Fitting baseline biomarker and treatment group
- For each clinical outcome (GFR, urine volume)
  - Same model as main study to confirm similar results (only 3 timepoints, 25 pats/gp)
  - Analysed as change from baseline to give similar format as for biomarkers
  - Analysed as change from baseline for 12, 24 months,
    - adjusted for baseline GFR only
    - fitting baseline GFR and treatment group
    - Fitting baseline GFR and urine urine albumin: creatinine ratio (extra variable added much later,)
    - fitting baseline GFR and separately for each biomarker
    - Fitting baseline GFR and treatment group and separately for each biomarker
    - Fitting baseline GFR and urine ACR and separately for each biomarker
    - Fitting baseline GFR and treatment group and urine ACR and separately for each biomarker



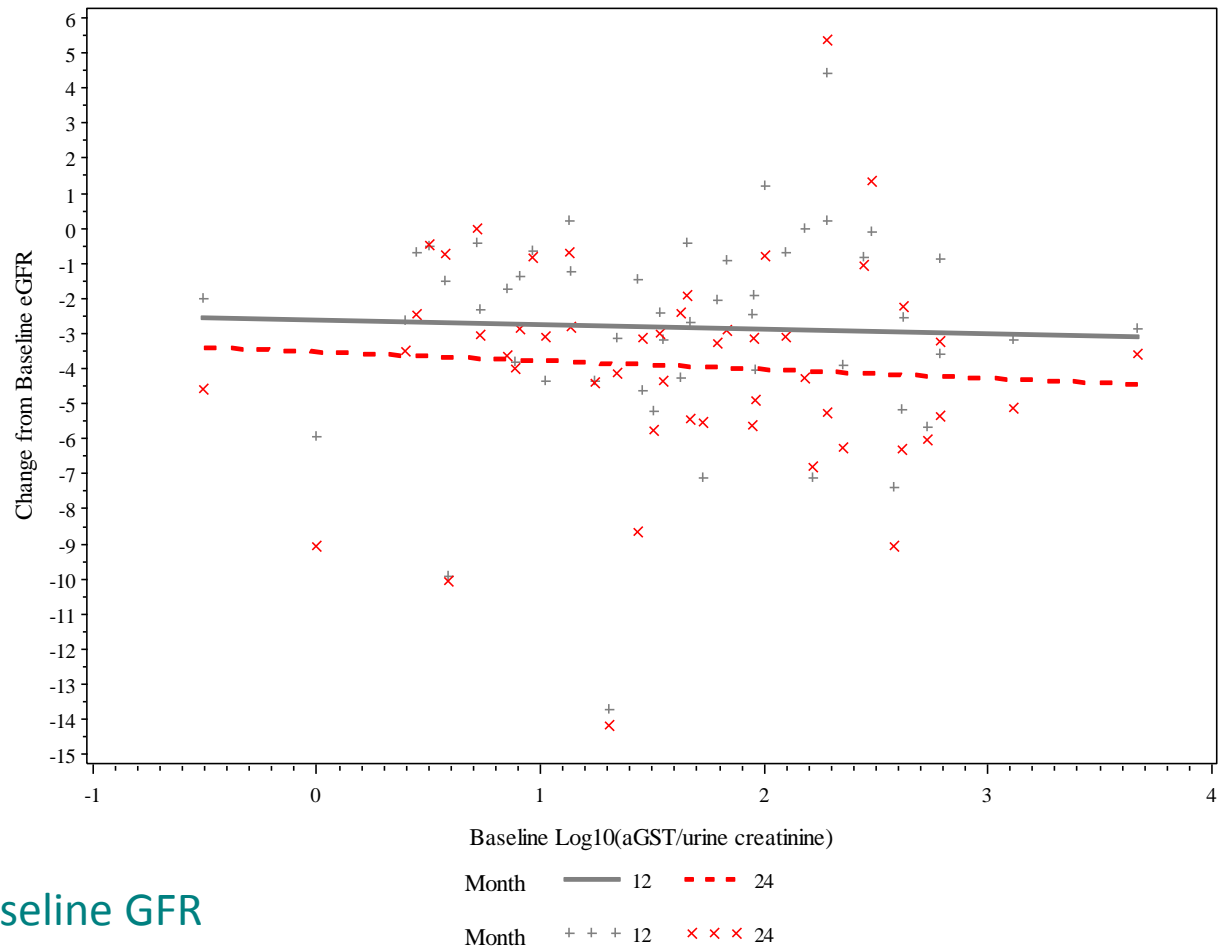
# GFR



# GFR by treatment

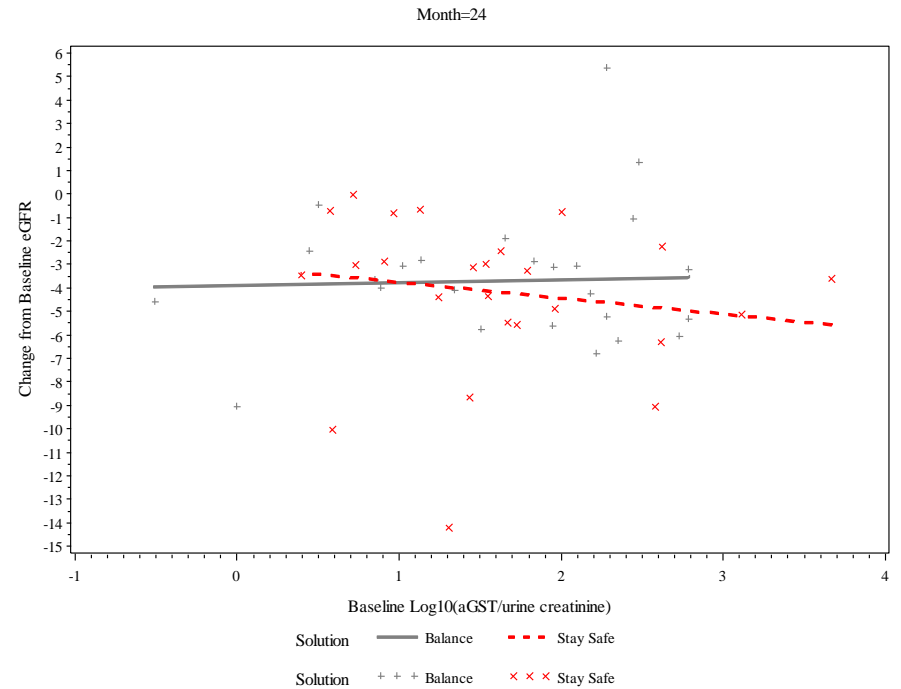
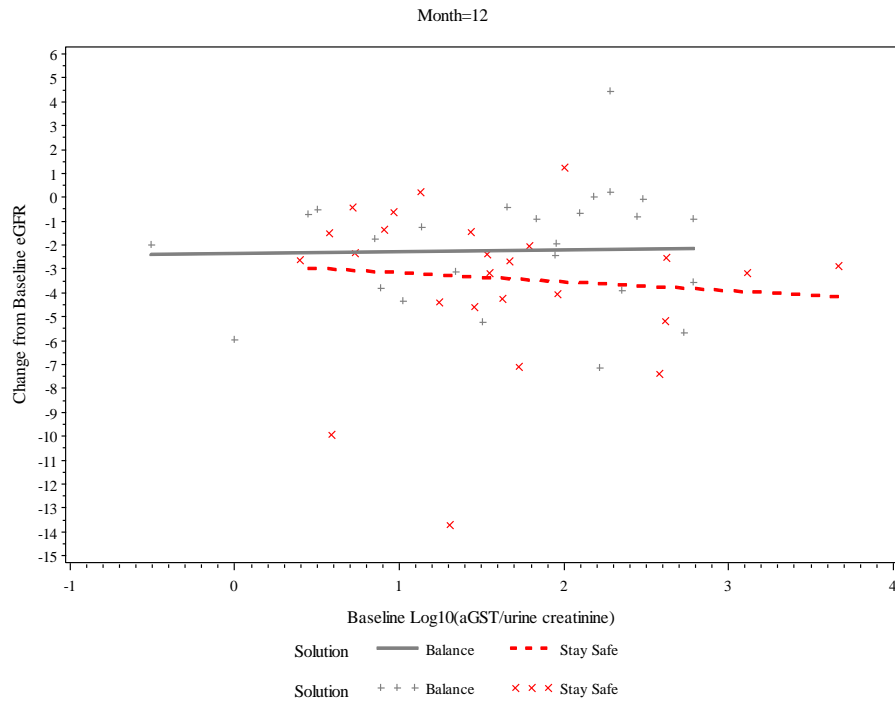


# $\alpha$ GST



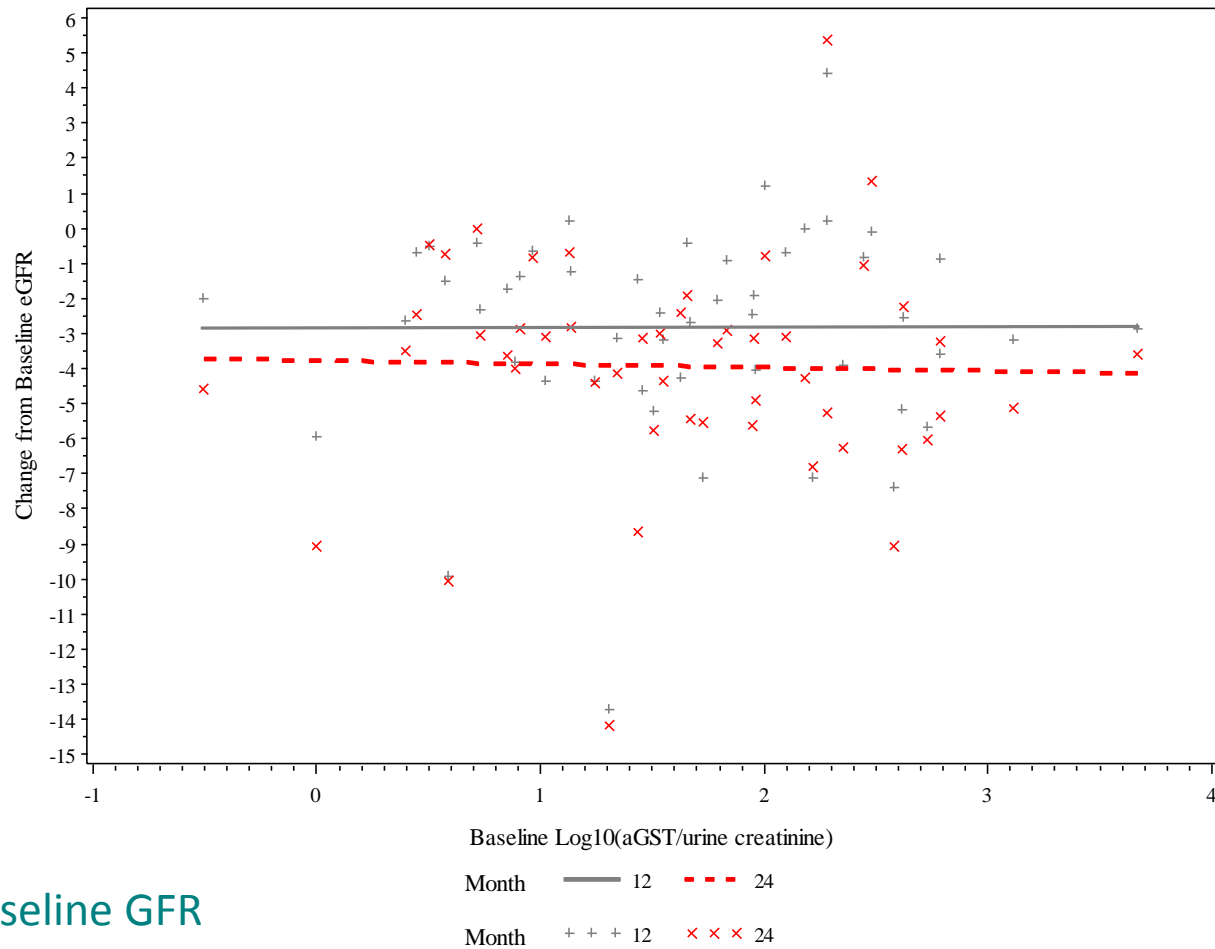
At mean baseline GFR

# $\alpha$ GST by treatment



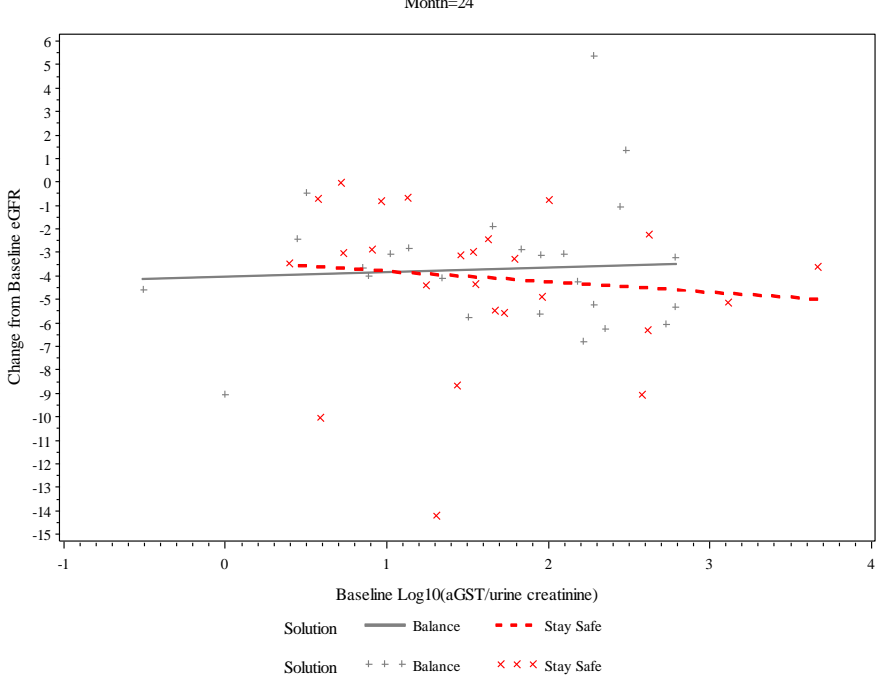
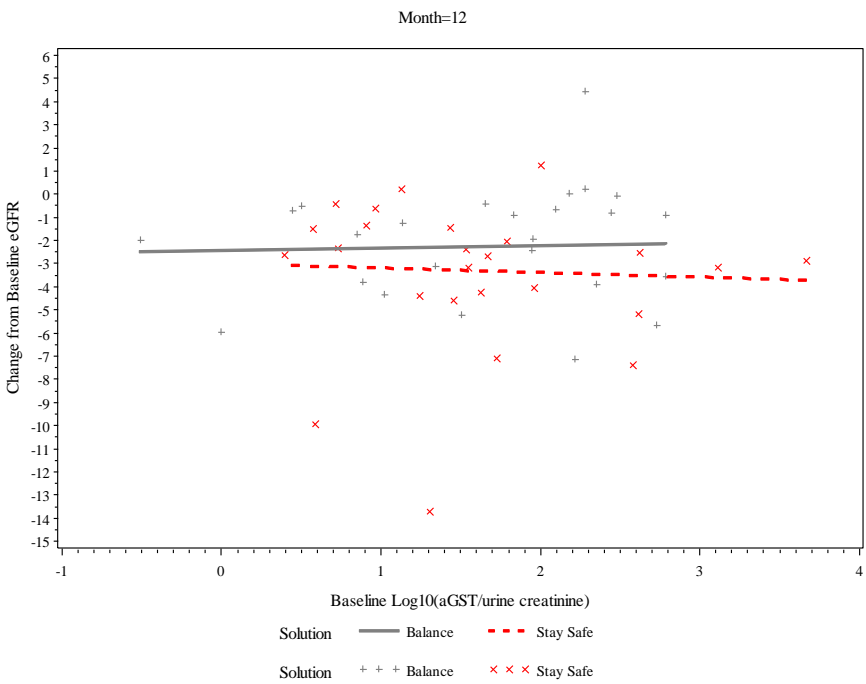
At mean baseline GFR

# $\alpha$ GST adjusted for baseline urine ACR



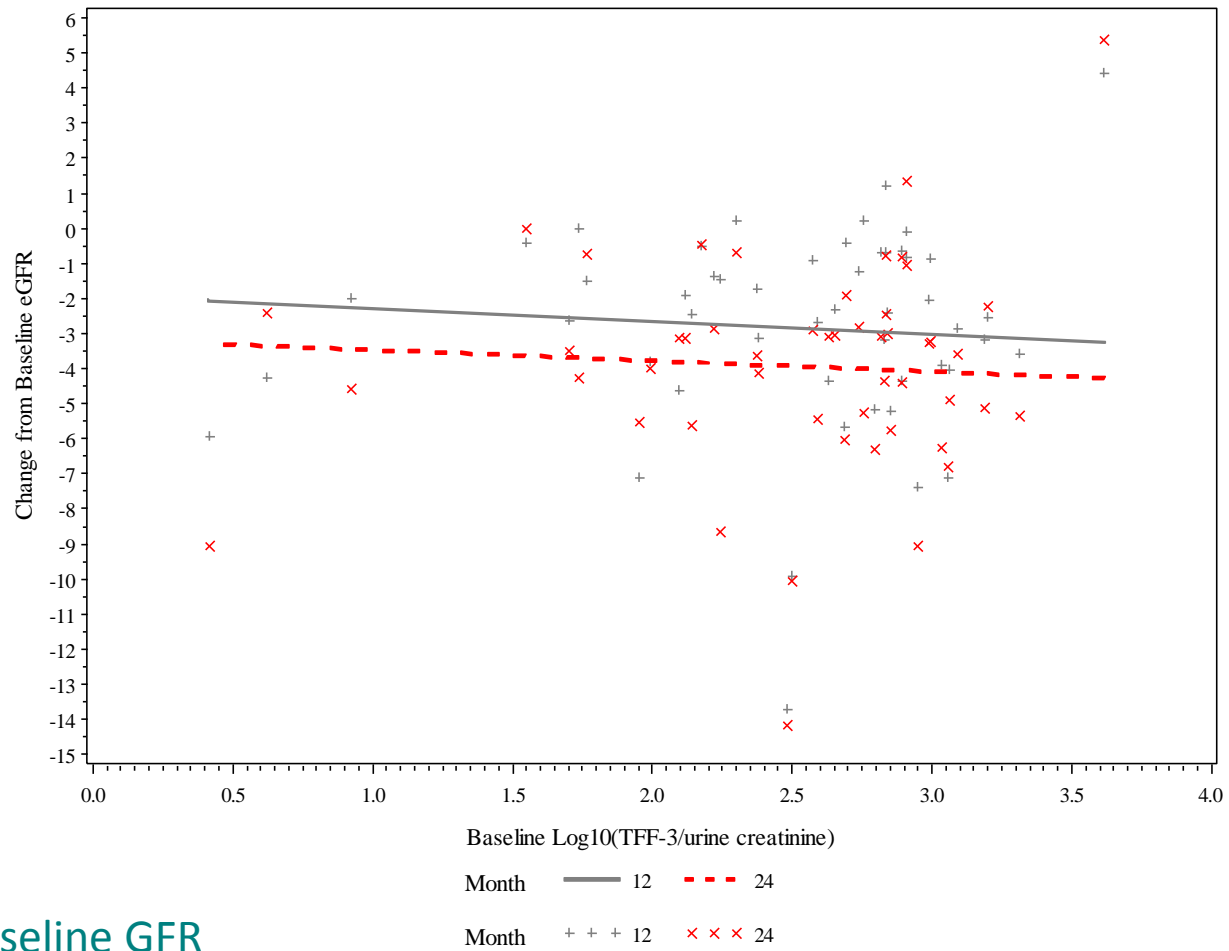
At mean baseline GFR

# $\alpha$ GST adjusted for baseline urine ACR and treatment



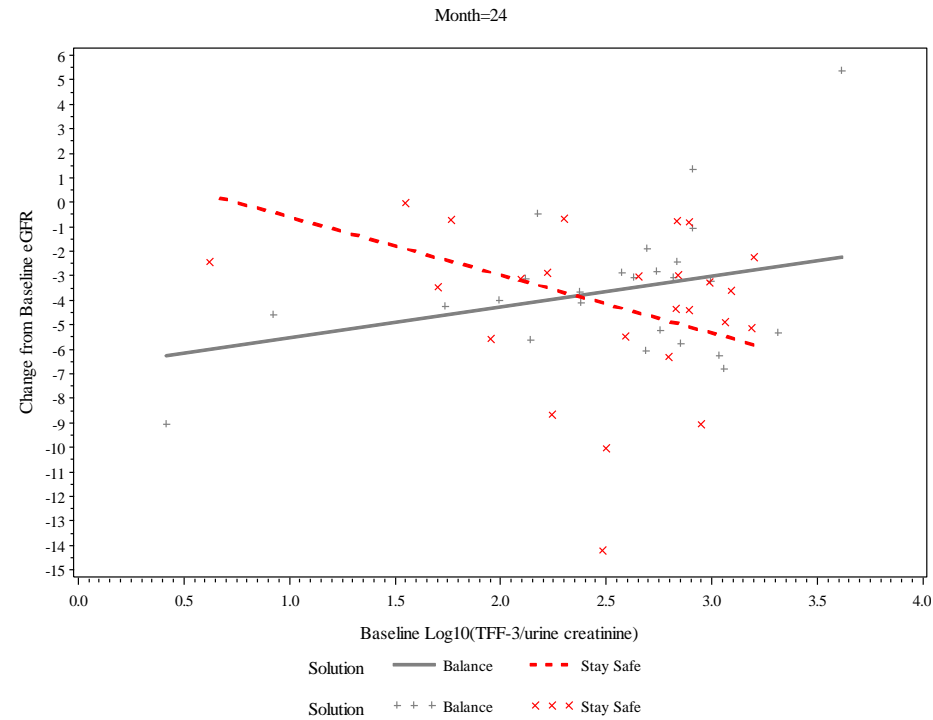
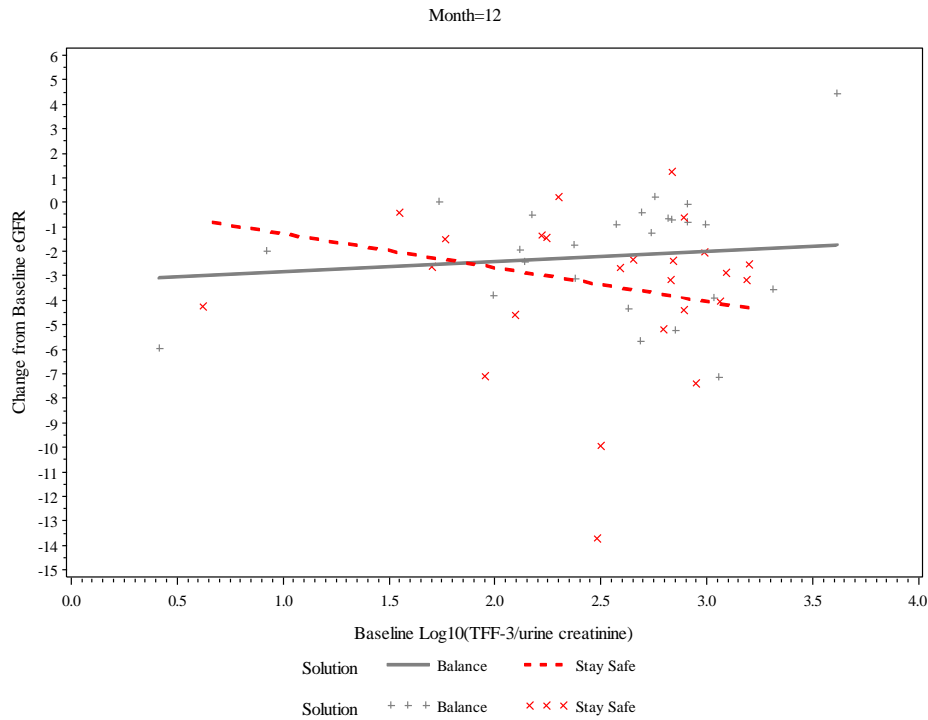
At mean baseline GFR

# TFF-3



At mean baseline GFR

# TFF-3 by treatment

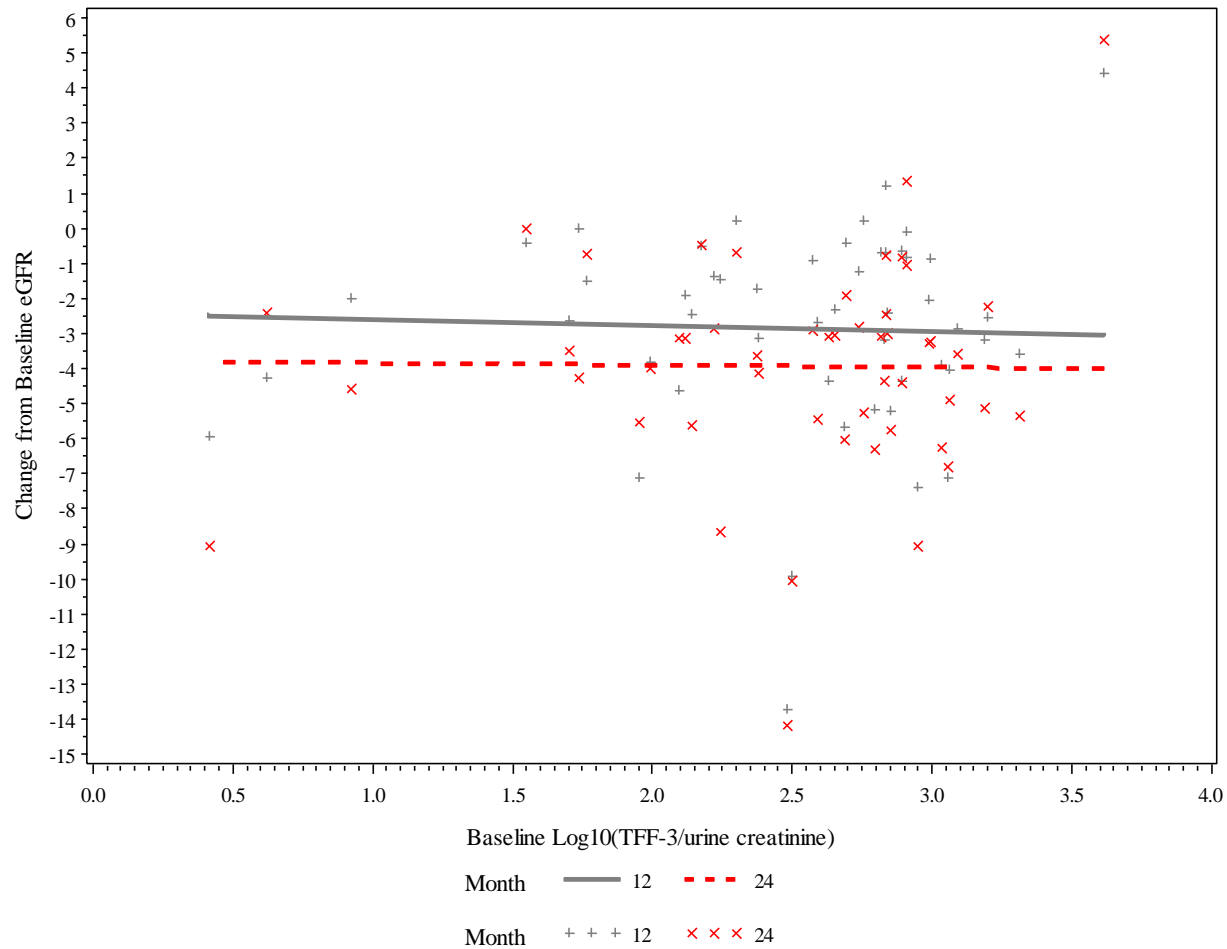


At mean baseline GFR

TFF3 x treatment x time p=0.02

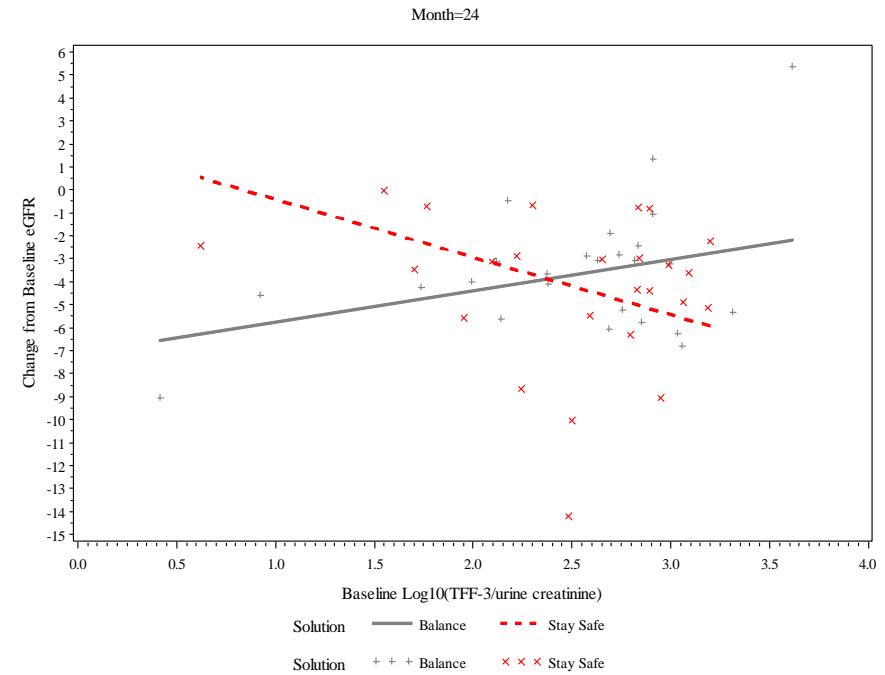
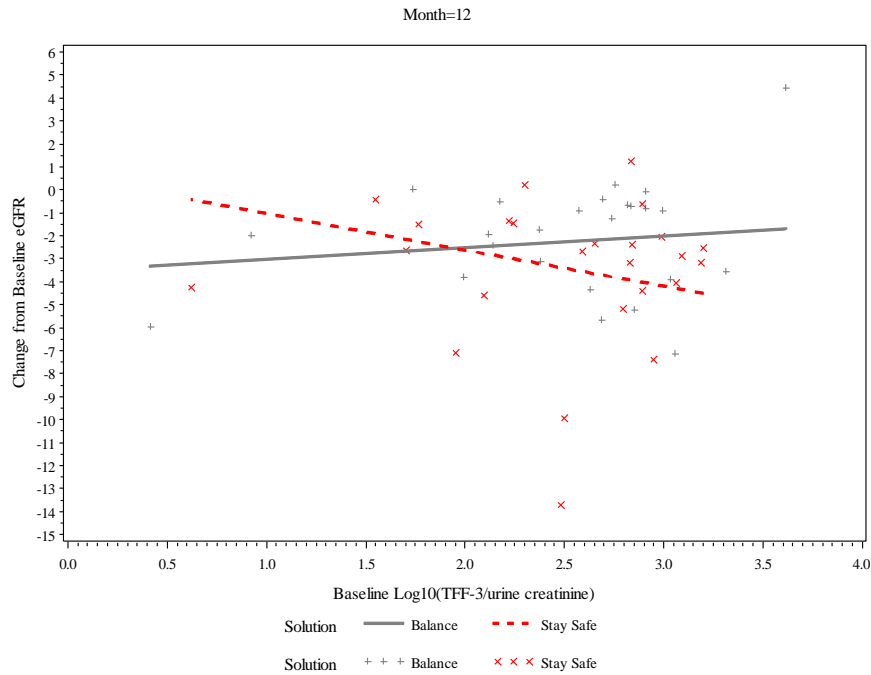


# TFF3 adjusted for baseline urine ACR



At mean baseline GFR and ACR

# TFF3 adjusted for baseline urine ACR and treatment



At mean baseline GFR and ACR

TFF3 x treatment x time  $p=0.02$

# Urine outcomes: questions

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- p-values
  - importance
  - Adjustment of p-values for multiplicity
  - how many analyses to adjust for
- Interactions
  - Real?
  - Should baseline biomarker x treatment be fitted as both prior to randomisation
  - Cross over effect with baseline (eg Balance over all baseline TFF3 improves GFR but higher baseline TFF 3 with Stay.Safe)
- Interpretation of relationships
  - Transformation of outcomes (in this case none)
  - Transformation of biomarkers (originally logged only, then biomarker:urine creatinine ratio logged)

# Conclusions

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- Accept the need to explore all possible combinations
- Write up in exploratory framework
- Attempt to reduce reliance on p-values
  - May have no significant p-values given sub-group but might have interesting pattern to explore in further research