# Analysis Report

## Data request from the OPTN Liver and Intestinal Organ Transplantation Committee: Additional Metrics for Previous LSAM Runs

Meeting: June 23, 2015

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**Data Request ID#: LI2015_02 (Data Request 1)**

**Timeline:**

| | |
|---|---|
| Request made | July 8, 2015 |
| Analysis plan submitted | July 22, 2015 |
| Draft analysis submitted | September 18, 2015 |
| Updated draft analysis submitted | October 6, 2015 |
| Final analysis submitted | November 16, 2015 |
| Next committee meeting | November 20, 2015 |



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## Background

In an earlier data request (LI2015_01), the members of the Liver and Intestinal Organ Transplantation Committee requested analysis of multiple potential redistricting scenarios designed to address geographic disparities in access to deceased donor livers. Twenty-eight simulations were conducted, covering several redistricting schemes and multiple implementations of proximity circles. Results for these simulations were presented at the June 22, 2015, Forum.

During the June 23, 2015, meeting, committee members asked for additional outputs that would help to determine the impacts of MELD/PELD exceptions on the various scenarios previously modeled, and for additional modeling of new scenarios. This report addresses the first part of the request by describing additional analysis of the previously completed simulations. No new LSAM simulations were conducted for this analysis.

## Program goal or committee annual work item addressed

Goal #2, Provide equity in access to transplants.

## Data Request 1: Additional LSAM outputs for prior modeling runs

**Committee Request**

The committee requested that SRTR "provide the outputs of the 4 and 8 district models with the proximity circles model and the current 11 regions with proximity circles (out of region allocation) to show the impact on the variance in (1) the median allocation MELD/PELD score at transplant (2) the median lab MELD/PELD score at transplant (3) the median allocation MELD/PELD score at transplant excluding all exceptions, and (4) the median allocation MELD/PELD score at transplant excluding only HCC exceptions."

The previous request (LI2015_01) included modeling of 28 unique scenarios. The committee requested further evaluation of the simulation results for 4- and 8-district scenarios with proximity circles, and the current 11 regions with proximity circles and out-of-region allocation. Table 1 shows the full list of 28 previously assessed scenarios. The 22 scenarios further evaluated under this data request are marked with a "Yes" under "To be analyzed further in LI2015_02?" (runs 1, 5, 7, 9, and 11-28).

**Table 1. Modeling Scenarios.**

| Run # | # of Districts | # of Points | Radius | Candidate Designation | To be analyzed further in LI2015_02? |
|---|---|---|---|---|---|
| 1 | Current 11 | None | None | None | Yes |
| 2 | 4 | None | None | None | No |
| 3 | 8 | None | None | None | No |
| 4 | Current 11 | 3 | 150 | In district | No |
| 5 | Current 11 | 3 | 150 | Out of district | Yes |
| 6 | Current 11 | 3 | 250 | In district | No |
| 7 | Current 11 | 3 | 250 | Out of district | Yes |
| 8 | Current 11 | 5 | 150 | In district | No |
| 9 | Current 11 | 5 | 150 | Out of district | Yes |
| 10 | Current 11 | 5 | 250 | In district | No |
| 11 | Current 11 | 5 | 250 | Out of district | Yes |
| 12 | 4 | 3 | 150 | In district | Yes |
| 13 | 4 | 3 | 150 | Out of district | Yes |
| 14 | 4 | 3 | 250 | In district | Yes |
| 15 | 4 | 3 | 250 | Out of district | Yes |
| 16 | 4 | 5 | 150 | In district | Yes |
| 17 | 4 | 5 | 150 | Out of district | Yes |
| 18 | 4 | 5 | 250 | In district | Yes |
| 19 | 4 | 5 | 250 | Out of district | Yes |
| 20 | 8 | 3 | 150 | In district | Yes |
| 21 | 8 | 3 | 150 | Out of district | Yes |
| 22 | 8 | 3 | 250 | In district | Yes |
| 23 | 8 | 3 | 250 | Out of district | Yes |
| 24 | 8 | 5 | 150 | In district | Yes |
| 25 | 8 | 5 | 150 | Out of district | Yes |
| 26 | 8 | 5 | 250 | In district | Yes |
| 27 | 8 | 5 | 250 | Out of district | Yes |
| 28 | Current system | None | None | None | Yes |

In the current request, the committee specified further analysis of each scenario's impact on the following metrics:

1. For all transplants, variance in median allocation MELD/PELD score at transplant;
2. For any transplants whose recipients received no HCC exception points, variance in median allocation MELD/PELD score at transplant;
3. For any transplants whose recipients received no exception points, variance in median MELD/PELD score at transplant (since no exception points are involved, laboratory and allocation MELD/PELD scores are identical); and
4. For all transplants, variance in median laboratory MELD/PELD score at transplant.

**Analytic Approach**

In the previous analysis for request LI2015_01, we simulated multiple allocation scenarios with LSAM and compared the results. Each simulation was repeated 10 times to provide an estimate of variability. Each of the 10 iterations for each scenario used independent sets of organ and waitlist arrivals and distinct random number seeds. Each scenario simulated 5 years of transplants. Twenty-eight scenarios in all were simulated, covering a range of configuration parameters for proximity points, optimized geographic distribution districts and broader sharing. The full details of these 28 scenarios are available in the reports for request LI2015_01.

For the current request, the Liver and Intestine Committee identified a subset of 22 scenarios (Table 1) for further analysis. For each of these scenarios we reviewed the previously-calculated variance in median allocation MELD/PELD at transplant. We then added analysis of the 3 additional requested metrics: allocation MELD/PELD at transplant for recipients without HCC exceptions, allocation MELD/PELD at transplant for recipients with no exception points, and laboratory MELD/PELD for all recipients. The LSAM input files include indicators for HCC exception status, so this was used to identify recipients with HCC exceptions. Recipients with no exceptions were identified as those having identical laboratory and allocation MELD/PELD scores.

*Data Quality and Interpretation*

Some data quality and interpretation issues should be noted when reviewing this report.

1. Reported MELD/PELD values for recipients without exception points are likely more reliable than laboratory MELD/PELD values for recipients with exception points.

   A critical caveat applies to our analysis of laboratory MELD/PELD scores in transplant recipients. The datasets used in this analysis are based on data reported to OPTN. Under current OPTN liver allocation policy, programs may apply to Regional Review Boards to obtain MELD or PELD score exceptions for candidates. OPTN policy 9.3.G says that a candidate's approved exception score will be extended when extension applications are completed according to the Liver Status and Score Update Schedule (and approved by the RRB). However, the policy does not direct programs to report updated laboratory MELD/PELD values at the time of exemption extension. After consulting with UNOS and clinicians about lab MELD reporting policy, we believe that candidates with MELD exception points may not have regularly updated laboratory MELD scores. This data quality issue means that reported laboratory MELD values for candidates with exception points may be (a) less reliable than the reported lab MELD values for candidates without exception points and (b) possibly lower than the actual lab MELD values for candidates with exceptions. We believe that data based on MELD/PELD values for recipients with no exception points are therefore more reliable and a better indicator of the potential impact of various modeled policies on variance in lab MELD. Laboratory and allocation MELD/PELD scores are identical for recipients with no exception points.

2. Estimates of variance are highly influenced by the number of allocation units used. Analyses of variance in this report use the donation service area (DSA) as the unit of analysis.

   Estimates of variance are highly influenced by the number of allocation units used. It can be misleading to compare variance estimates calculated using different numbers of districts (for example, variance by 4 districts versus variance by 8 districts). To avoid misinterpretation, we calculated variance for each metric across DSAs within the simulated scenarios, not by region/district. Presenting variances across a standard number of units (58 DSAs; 51 with active waitlisted candidates) for each of the 22 scenarios allows for accurate comparison between scenarios.

3. This report does not provide an analysis of the exception system for liver allocation.

   This report is intended to examine the impact of redistricting concepts on particular groups of transplant recipients, in response to the specific data request described above. While it may be possible to infer information about the status or functioning of the liver allocation exception system based on these data, this report does not present a full picture of the exception system, nor is it intended to do so.

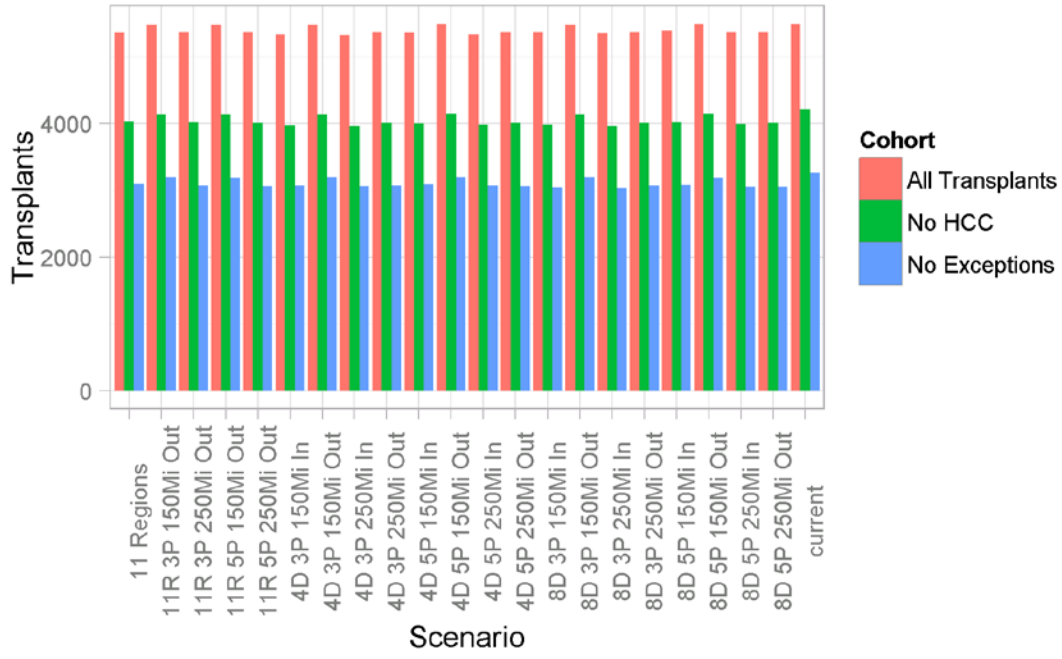
**Study Population**

The previously requested modeled scenarios (request LI2015_01) included donor and candidate populations created by the LSAM donor and candidate generators, based on patient data for transplant candidates listed on the liver waiting lists as of December 31, 2006, and candidates added to those waiting lists and organs donated between January 1, 2007, and December 31, 2011.

*Cohort Groups*

This analysis involved 3 sets of simulated transplants: all transplants, transplants in candidates without HCC exception points, and transplants in candidates with no exception points. Figure 1 shows the mean number of transplants in each of these groups for each of the 22 simulated scenarios. Information on transplant counts, the percentage (out of total transplants) of no HCC and no exceptions transplants, and minimum and maximum values across the 10 simulated iterations is provided in the appendix (Appendix A, Table 2).

**Figure 1. Transplant counts for each recipient group and scenario.**




The number of transplants in each group was fairly consistent across the different scenarios, with about 5400 transplants total, about 4000 transplants in candidates without HCC exception points, and about 3100 transplants in candidates with no exception points.

## Results and Discussion

As described above, this request involved additional analysis of previously conducted LSAM simulations. The variance in median MELD/PELD at transplant was calculated for multiple recipient groups and MELD definitions. Summary results for these metrics are presented for all 22 tested scenarios. In order to provide more context for these results, a subset of scenarios were also analyzed in more detail using boxplots and geographic distribution maps.

**Summary of Variance in Median MELD/PELD at Transplant**

Variance in median MELD/PELD at transplant was the main focus of this extended analysis. This metric characterizes the variation across DSAs in the median MELD/PELD score of each DSA's simulated transplant recipients. A scenario with a lower variance indicates that median MELD at transplant is more similar across DSAs within that scenario. A scenario with a higher variance indicates that median MELD at transplant is more disparate across DSAs within that scenario.

*Figure Guide*

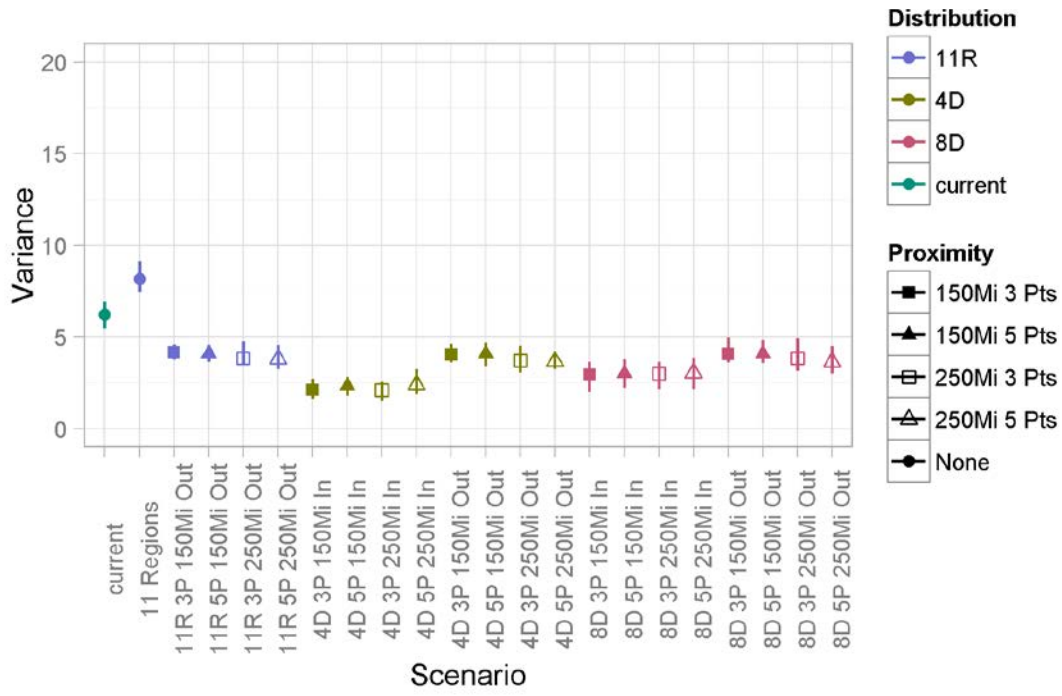
Each of the following plots (Figures 2-5) compare this variance metric across 22 allocation scenarios for one of the requested metric definitions: allocation MELD/PELD across all transplants, allocation MELD/PELD in non-HCC recipients, laboratory MELD/PELD in recipients with no exception points, and laboratory MELD/PELD across all transplants. The scenarios were each simulated 10 times to characterize the inherent variation due to random chance, and the plot displays the range of this variability as a vertical line extending from the minimum value to the maximum value found for that metric. A point along that line marks the mean value of the variance across the 10 iterations for each of the scenarios. A full listing of all variance values and ranges is available in Appendix B (Table 3).

All plots are laid out in a consistent fashion. The scenarios in each plot are listed in the same order along the horizontal axis and are grouped according to the scenario parameters. The first scenario in each plot is the simulation of current policy (including Share 35 and Share 15, but without consideration of the MELD-Na, Cap HCC, or HCC policies), given as a point of comparison. Next are simulations of broader sharing in the current 11 regions, then in 4 districts, and finally in 8 districts. The scenario data are colored according to the associated distribution system.

Within each distribution group, the first data point is the simulation without proximity circles, followed by the 4 in-district scenarios, in which the first level of sharing includes only candidates within the region or district, then the out-district scenarios, in which all candidates within the proximity circle are included with region- or district-wide candidates in the first level of sharing.

Additional scenario parameters are the size of the proximity circles and the number of proximity points awarded to candidates within those circles. The data points within the in- and out-district groups for each distribution system are ordered as follows: 3 points, 150 miles; 5 points, 150 miles; 3 points, 250 miles; and 5 points, 250 miles. Scenarios with 3 proximity points are represented by squares and scenarios with 5 proximity points by triangles; scenarios with 150-mile circles are represented by filled in markers and scenarios with 250-miles by empty markers.

**Figure 2. Variance in median allocation MELD/PELD at transplant by DSA (all transplants).**




The variance in median allocation MELD/PELD for all transplants (Figure 2) is the same result as presented in LI2015_01. The current simulated scenario for allocation MELD for all transplants has a variance of 6.2 (range 5.5-6.9). Broader sharing in 11 regions appears to increase the variance to 8.2 (7.4-9.1), and the largest decrease in variance is seen in the 4 district scenarios with in-district proximity points. The implementation of distribution units appears to be the driving factor in decreasing MELD/PELD variance at transplant, with 4 districts having lower variance than 8 districts or 11 regions, and in-district sharing having lower variance in both 4- and 8-district scenarios.

**Figure 3. Variance in median allocation MELD/PELD at transplant by DSA (recipients with no HCC exception points).**

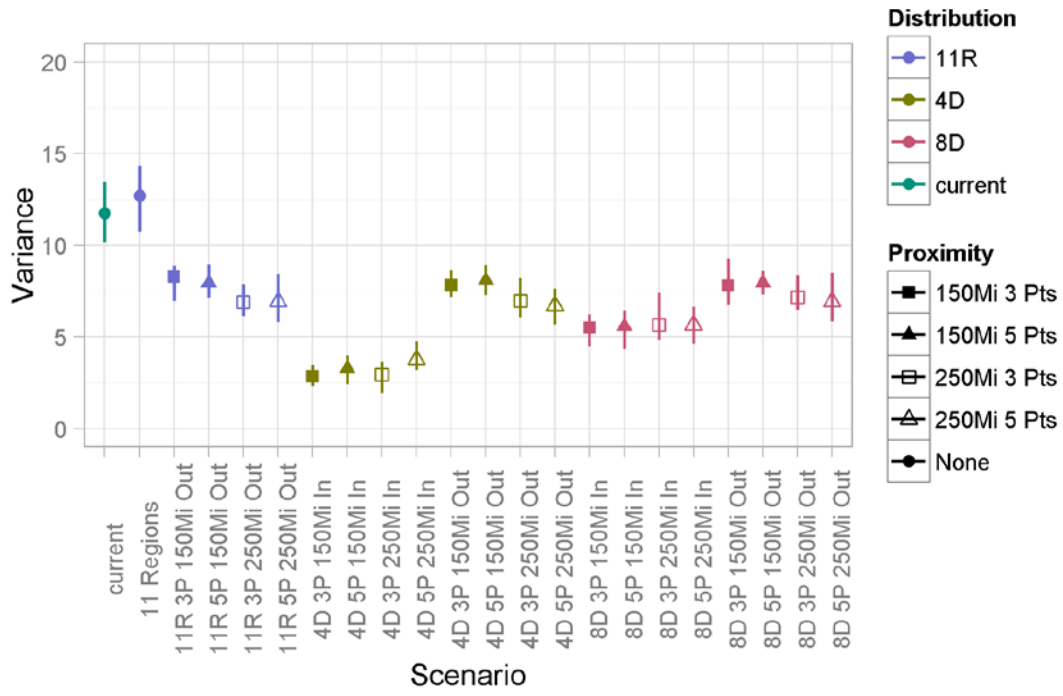
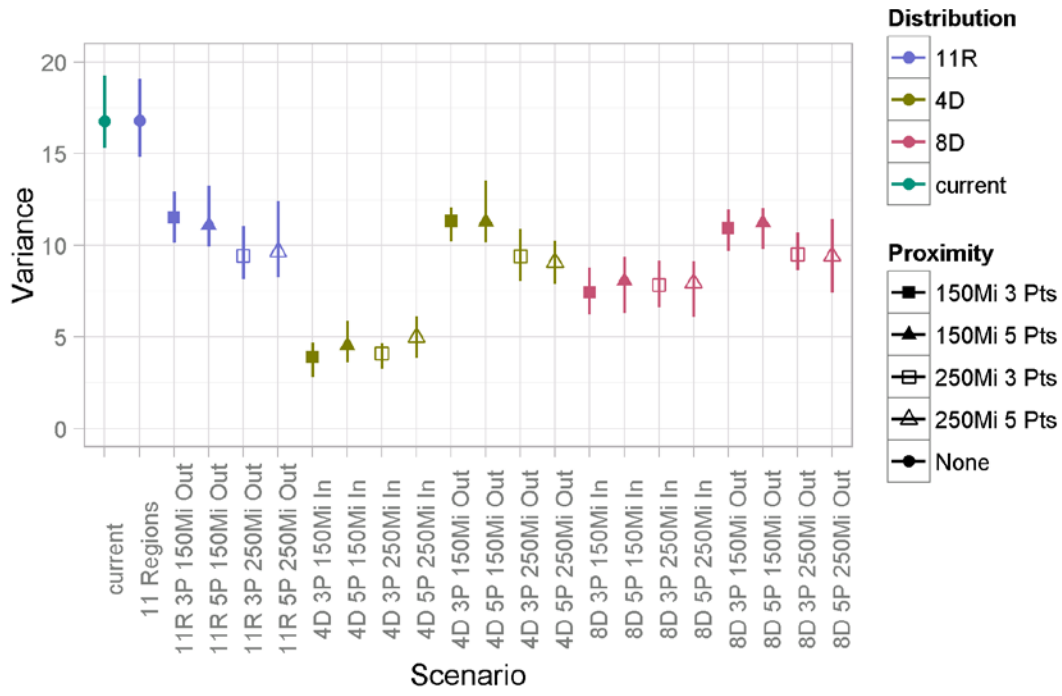



Figure 3 shows the variance in allocation MELD/PELD at transplant when recipients with HCC exception points are excluded from analysis. The variance in median allocation MELD/PELD at transplant for this group is higher than for the overall group, at of 11.7 (range 10.1-13.4) for non-HCC recipients compared with 6.2 for allocation MELD for all transplants in the current scenario simulation. For recipients without HCC exception points, the variance across DSAs for most scenarios increased compared with all transplant recipients, but the relative performance of the scenarios was similar to the all-transplant result, with 4-district in-district scenarios showing the lowest variance overall.

**Figure 4. Variance in median lab MELD/PELD at transplant by DSA (recipients with no exception points).***

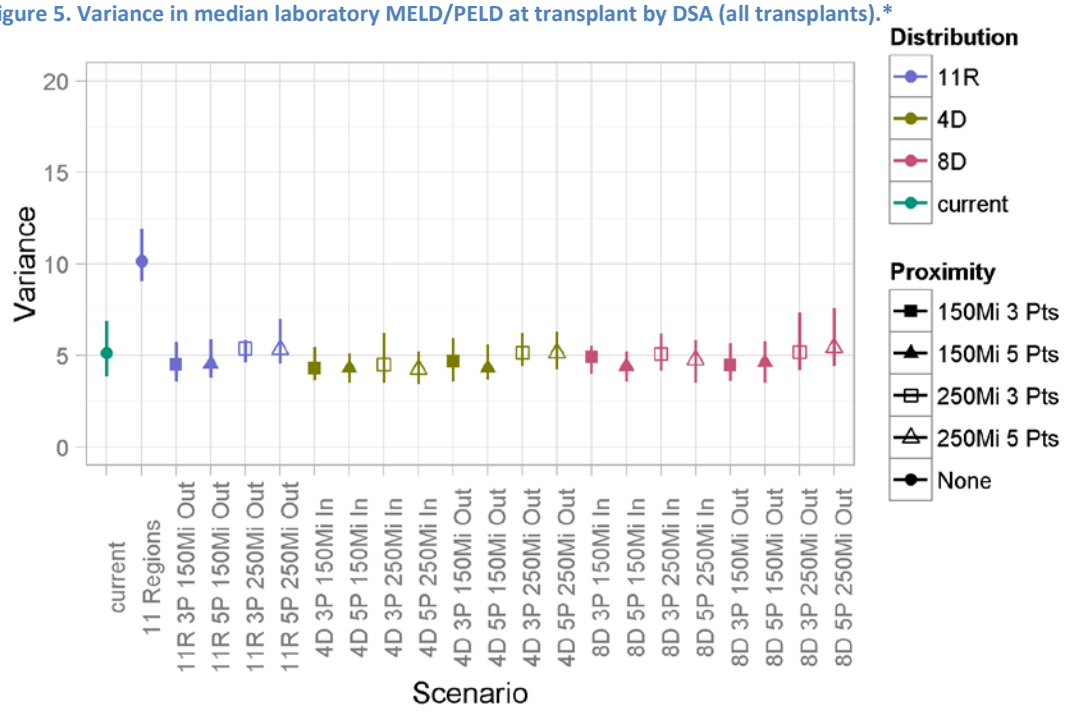



**Allocation and lab MELD/PELD scores are identical for these recipients.*

Figure 4 shows the variance in median laboratory MELD/PELD at transplant for recipients with no exception points. Note that the allocation and laboratory MELD/PELD scores are identical for these recipients, because organs are allocated to them based only on their laboratory scores with no exception points. As shown in Figure 1/Table 2, the population with no exception points makes up about 60% of all transplants in these analyses.

Variance in MELD/PELD at transplant for recipients with no exception points was the highest among all population subgroups, with a variance in the current scenario of 16.8 (15.3-19.3, compared with allocation MELD for all transplants at a variance of 6.2). Looking across all scenarios, Figure 4 shows a pattern similar to Figures 2 and 3 where 4-district in-district scenarios show the largest decrease in variance in MELD at transplant.

**Figure 5. Variance in median laboratory MELD/PELD at transplant by DSA (all transplants).***



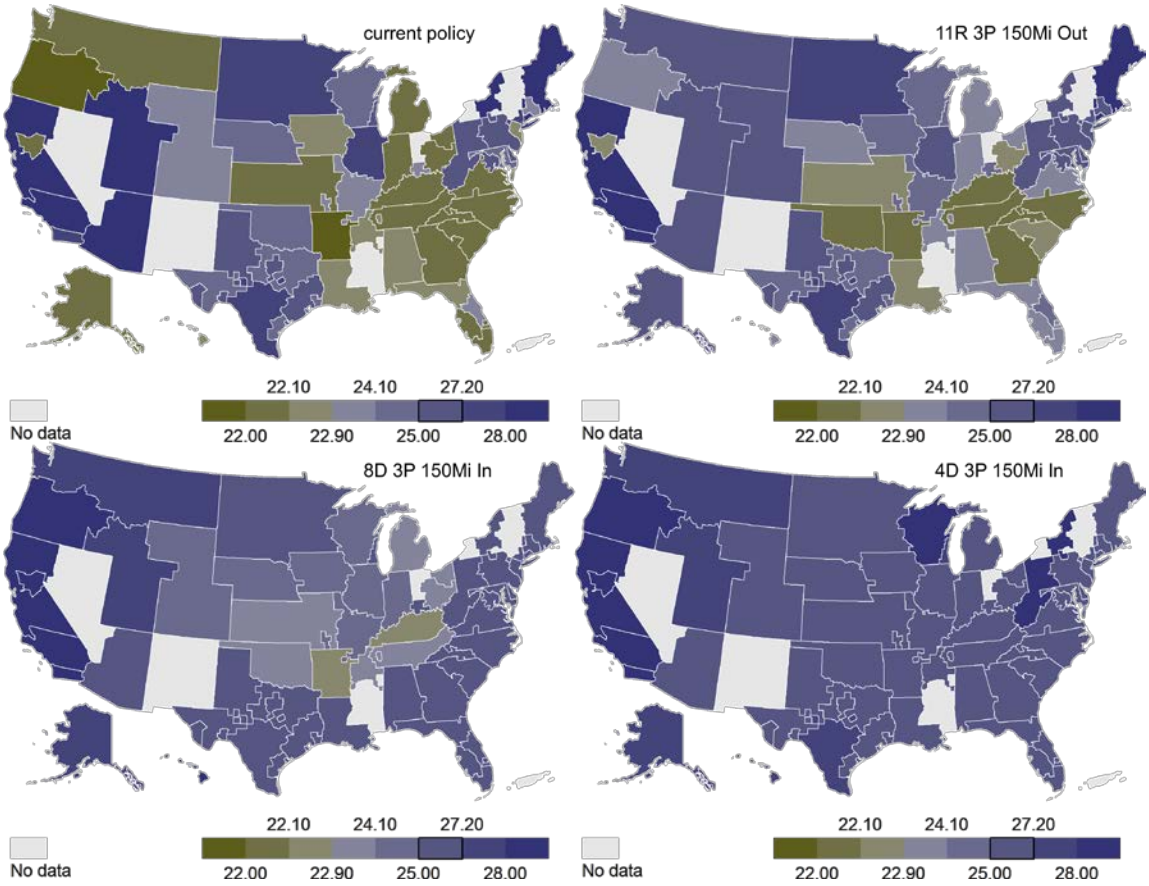

**Lab MELD/PELD may not be up to date for many of the recipients in this cohort with exception points.*

Figure 5 shows the variance in laboratory MELD/PELD across all transplants, including those with no exception points, with HCC exception points, and with other exception points. Variance in median lab MELD/PELD for all transplants was lower than variance in allocation MELD/PELD for all transplants (variance of 5.1 [range 3.9-6.9] and 6.2 [range 5.5-6.9], respectively), and showed very little variation between the tested scenarios. However, as noted in the Data Quality and Interpretation section above, since candidates with exception points may not be required to keep up-to-date lab values while their exceptions are active, the estimates of variance shown here may be biased due to use of data based on out-of-date MELD/PELD numbers. A more accurate look at the potential effect of redistricting on laboratory MELD/PELD scores is represented by the no-exceptions subgroup (Figure 4), in which all analyzed transplants used laboratory MELD/PELD.

**Geographic Variation in Median MELD/PELD at Transplant**

As discussed at length in the previous report (LI2015_01), median MELD/PELD at transplant varies widely across the country. The maps below visualize this disparity by coloring each DSA according to its median MELD/PELD at transplant for scenarios representing each of four distribution concepts: current policy, out-district sharing in the current 11 regions, 8-district in-district distribution, and 4-district in-district distribution. In each map, more vivid colors represent more extreme values for the given metric, with greener areas having lower median MELD/PELD at transplant and bluer areas having higher median MELD/PELD at transplant. The national value for each metric is indicated by a black box surrounding the portion of the color scale where it falls.

**Figure 6. Geographic variation in median allocation MELD/PELD at transplant by DSA (all transplants).**




Median allocation MELD/PELD at transplant was presented as a disparity metric in the previous report (LI2015_01), and the maps shown here are similar to those presented at the June 2015 liver forum; the only difference is that the out-district 11-region scenario has been substituted since the in-district scenario was not included in this request. As in the previous analysis, the maps show regional concentrations of both low and high MELD/PELD at transplant across DSAs for the current policy simulation. As the number of distribution units decreases, the map tends toward more uniformity, with fewer DSAs in the dark green and dark blue portions of the scale.

**Figure 7. Geographic variation in median allocation MELD/PELD at transplant by DSA (no HCC exceptions).**

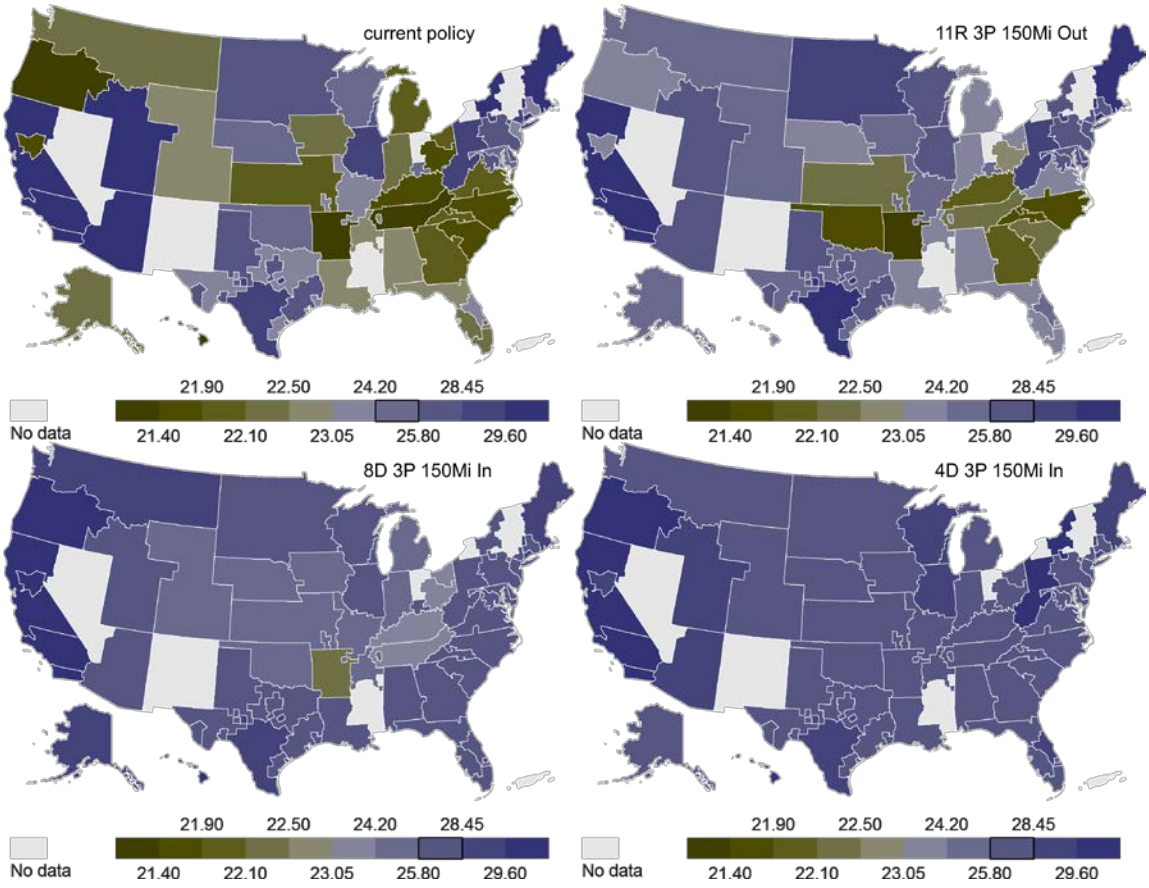
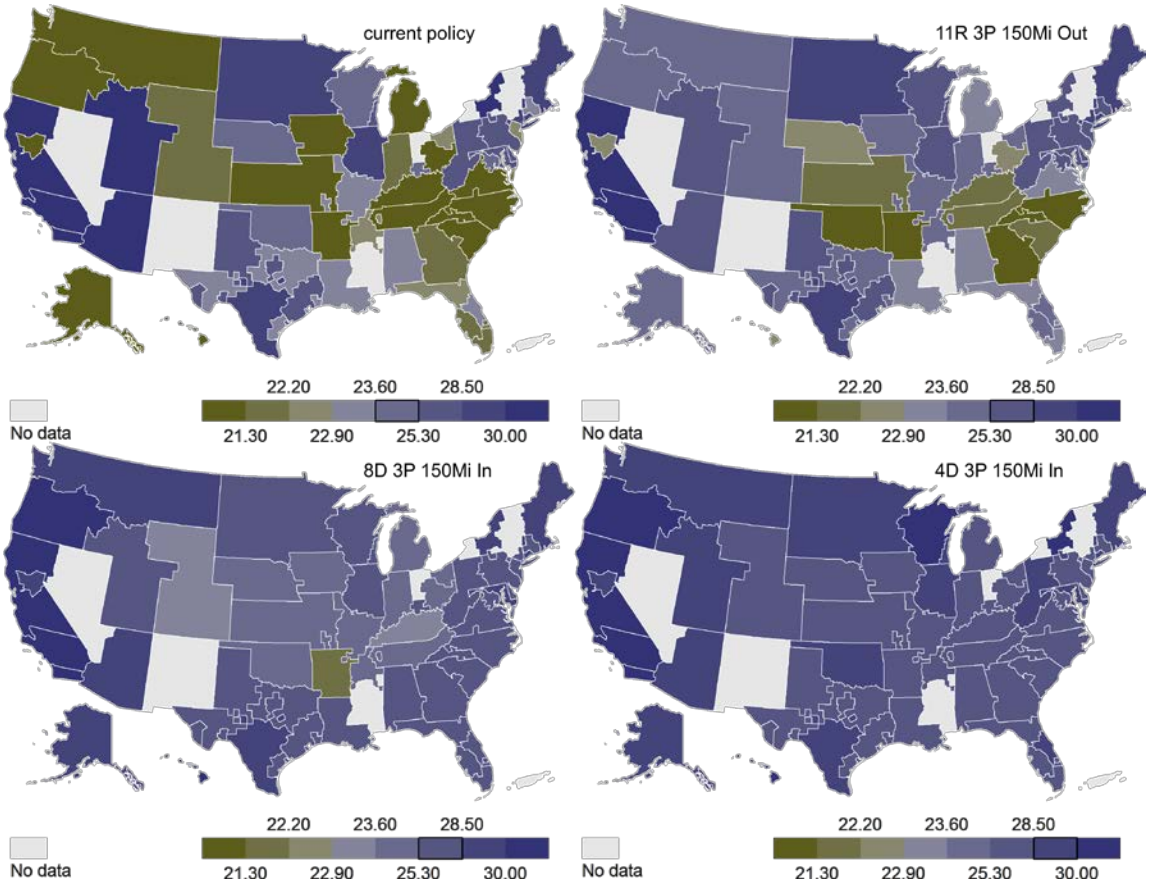



Figure 7 indicates that the pattern is similar when considering only transplants in non-HCC recipients, with the current policy showing the most geographic variation and the 4-district map showing the least.

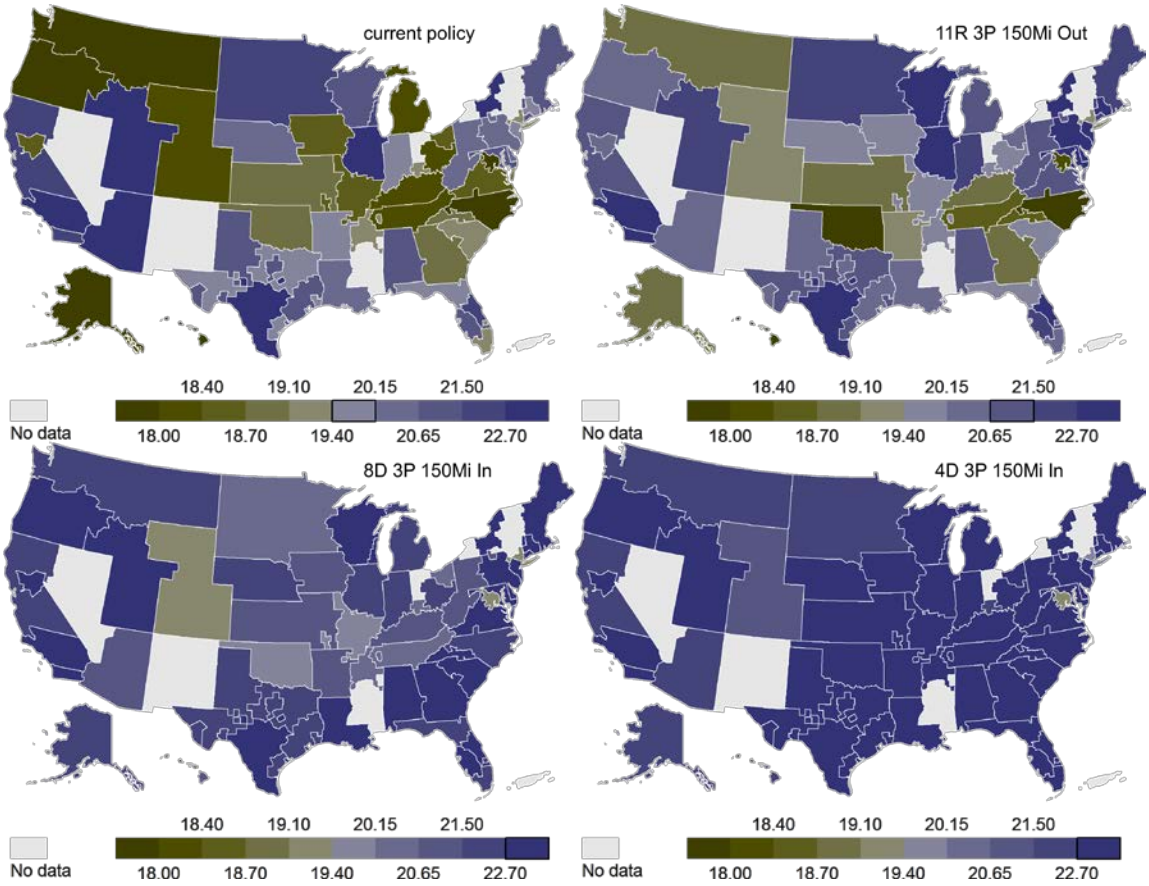
**Figure 8. Geographic variation in median laboratory MELD/PELD at transplant by DSA (recipients with no exception points).***




**Allocation and lab MELD/PELD are identical for these recipients.*

Figure 8 shows a dynamic similar to Figures 6 and 7 for the population of recipients with no exception points, in which the current policy displays the most geographic variation and the 4-district map the least.

**Figure 9. Geographic variation in median laboratory MELD/PELD at transplant by DSA (all transplants).***




**Includes candidates whose lab MELD/PELD scores may be out of date.*

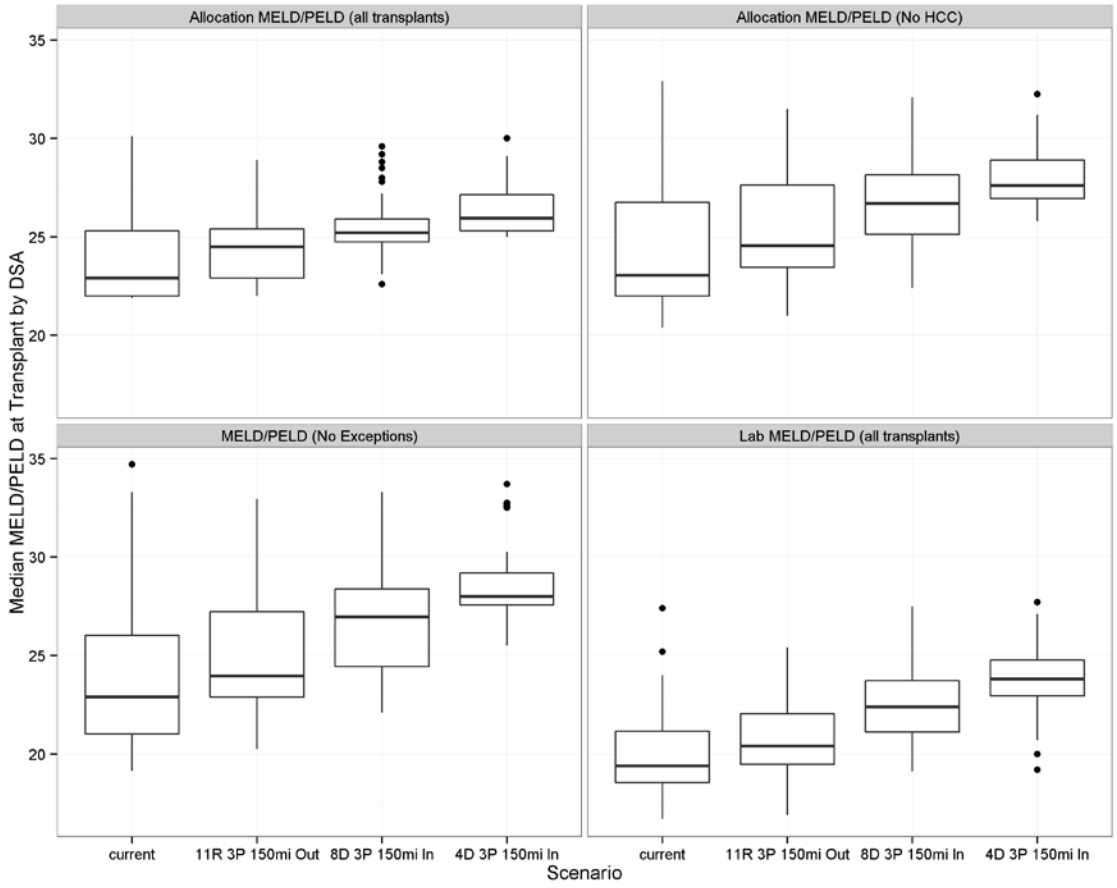
Figure 9 echoes the results presented in the summary plot, indicating that when using data based on reported laboratory MELD/PELD values only, the variation across the country does not decrease when the number of distribution units decreases. While much less green shows in the 4-district map, the amount of dark blue has increased, and the box indicating the national median laboratory MELD/PELD at transplant has moved to the far right of the scale. Moving from current policy to 8-district or 4-district maps increases the projected median laboratory MELD/PELD at transplant across the country. However, it is important to note again that a more comprehensive view of how lab MELD/PELD may be affected by decreasing distribution units may be shown in Figure 8, since data used in Figure 9 include candidates with MELD/PELD exception points whose laboratory MELD/PELD values may be out of date.

**Distribution of Median MELD/PELD at Transplant**

Identifying trends in the underlying distribution of median MELD/PELD at transplant can be difficult using only the summary plots and maps. The figure below uses boxplots to display the spread of values for median MELD/PELD at transplant by DSA in 4 of the modeled scenarios. This is an alternate presentation of the data in the maps shown in Figures 6-9 above, although the boxplots use median MELD/PELD at transplant numbers from a single LSAM iteration rather than the 10-iteration mean. In each boxplot, the box covers the second and third quartiles of the median MELD/PELD at transplant across DSAs. A narrower box implies less variation between DSAs for a given

scenario and metric definition. The mean value for each scenario is displayed by the black line running through the middle of each box.

**Figure 10. Distribution of median MELD/PELD at transplant across the DSAs.***




**Allocation and laboratory MELD/PELD are identical for non-exception recipients (lower left). Laboratory MELD/PELD for all transplants (lower right) may include out-of-date values for exception recipients.*

As observed above in the summary plots, the spread of median allocation MELD/PELD at transplant decreases with smaller numbers of distribution units. In almost all cases, the 4-district scenario has the narrowest boxes. This plot also shows that median MELD/PELD at transplant increases as the number of distribution units decreases; for each metric definition including lab MELD/PELD across all transplants, the 4-district map has the highest mean median MELD/PELD at transplant. This indicates that higher proportions of high-MELD/PELD candidates in the DSAs are undergoing transplant in the proposed scenarios compared with current policy.

**Discussion**

This analysis follows earlier study of the effect of potential redistricting scenarios presented in LI2015_01 and the 2015 liver forum. Key disparity findings of that work included:

- The primary scenario parameters of importance were the number of distribution units (11 regions or 4 or 8 districts) and the sharing configuration for proximity circles (in-district or out-district). The choice of these parameters had the largest effects on disparity metrics when variation between scenarios was observed.
- When compared with current policy, scenarios with in-district sharing in the current 11 regions increased disparity (as measured by variance in median MELD/PELD at transplant). Four-district in-district scenarios showed the largest projected reduction in variance in median MELD/PELD at transplant, with variance reduced more than 2-fold. Eight-district scenarios fell in between current policy and 4-district results in most cases.
- Scenarios using out-of-district sharing performed similarly regardless of the number of distribution units, suggesting that the proximity circles became the primary driver of organ distribution in these scenarios.
- Geographic distribution of median MELD/PELD at transplant became more uniform under the conceptualized redistricted scenarios.

The present analysis conforms to these original findings in several ways:

- The number of distribution units and in-district/out-district sharing were the primary factors determining the performance of scenarios in reducing variance in median MELD/PELD at transplant.
- Four-district in-district scenarios showed the lowest variance in median MELD at transplant for each of the transplant groups: overall, without HCC exception points, and with no exception points. Eight-district in-district scenarios fell between 4-district and 11-region scenarios for each group.
- Out-district scenarios were consistent in variance of median MELD/PELD at transplant across all other parameters.
- Geographic distribution of median allocation MELD/PELD at transplant became more uniform in each of the recipient groups as the number of distribution units decreased.

The present analysis adds some new results:

- For recipients without HCC exception points (about 77% of transplants in the current scenario [see Appendix A]), the variation in allocation MELD/PELD at transplant is higher than in the overall all transplant group under the current scenario. This variation decreases but remains somewhat higher than the variation in allocation MELD for all transplants in most redistricting scenarios. Only in the 4-district in-district scenarios is the variation in allocation MELD/PELD at transplant for no-HCC transplants similar to the variation for all transplants.
- For recipients with no exception points (about 60% of transplants in the current scenario [see Appendix A]), the variation in MELD/PELD at transplant was highest of all the examined subgroups for the current scenario. This variation decreases in redistricting scenarios, most dramatically in the 4-district in-district scenarios.
- When measured across all transplants, variance in laboratory MELD/PELD at transplant is not projected to change under any of the redistricting scenarios. However, questions about the validity of these data suggest caution in interpreting this result.
- The mean MELD/PELD at transplant across all DSAs increased as the number of distribution units decreased for each of the transplant groups, in parallel with the reduction in variance between DSAs. This effect was also present in laboratory MELD/PELD scores, even though the variance did not change. This indicates that higher proportions of high-MELD/PELD candidates in the DSAs undergo transplant in the proposed redistricting scenarios compared with current policy.

Subgroup analysis for pediatric status, sex, and race/ethnicity did not project any disproportionate impacts on any subgroup. Full subgroup plots are available in Appendix C.

Overall, simulations indicate that variance in median MELD/PELD at transplant is projected to decrease under most of the redistricting scenarios, in the recipient population as a whole and in the subgroups with no HCC exception points and no exception points at all. Four-district scenarios offer the largest variance reduction, but 8-district scenarios also reduce variance compared with current policy.

## Appendix A: Transplant counts

**Table 2. Transplant counts for each subset and scenario.***

| | **All Transplants** | **No HCC** (min-max)<br>% of total | **No Exceptions** (min-max)<br>% of total |
|---|---|---|---|
| current | 5491.98 (5416-5561.4) | 4211.7 (4148.4-4264.4)<br>76.7% | 3265.4 (3209.2-3312.6)<br>59.5% |
| 11 Regions | 5361.7 (5282-5425.8) | 4033.84 (3974.4-4079.2)<br>75.2% | 3097.84 (3054.4-3133.8)<br>57.8% |
| 11R 3P 150Mi Out | 5484.8 (5411.8-5546.6) | 4142.2 (4094.4-4192.8)<br>75.5% | 3187.8 (3126.6-3230.8)<br>58.1% |
| 11R 3P 250Mi Out | 5370.1 (5278.4-5436) | 4013.52 (3945.4-4063.6)<br>74.7% | 3067.08 (2997.4-3112.6)<br>57.1% |
| 11R 5P 150Mi Out | 5479.12 (5389.2-5560.8) | 4136.72 (4078.8-4208)<br>75.5% | 3178.04 (3123.4-3240)<br>58% |
| 11R 5P 250Mi Out | 5369.4 (5274.2-5431.2) | 4010.86 (3934.8-4071.8)<br>74.7% | 3062.94 (3001.8-3116.8)<br>57% |
| 4D 3P 150Mi In | 5336.58 (5250.2-5389.2) | 3974 (3910-4025)<br>74.5% | 3068.8 (2994.4-3109)<br>57.5% |
| 4D 3P 250Mi In | 5319.08 (5237.6-5377.2) | 3961.84 (3898.2-4019.8)<br>74.5% | 3060.08 (2993-3115.2)<br>57.5% |
| 4D 5P 150Mi In | 5358.64 (5282.2-5428.8) | 3998.08 (3945-4059.4)<br>74.6% | 3083.46 (3028.2-3134)<br>57.5% |
| 4D 5P 250Mi In | 5330.5 (5242.2-5392.2) | 3977.46 (3908.8-4040.8)<br>74.6% | 3065.54 (2999.4-3106.2)<br>57.5% |
| 4D 3P 150Mi Out | 5482.34 (5398.2-5554) | 4141.7 (4082.4-4192.2)<br>75.5% | 3191.12 (3118.2-3239.4)<br>58.2% |
| 4D 3P 250Mi Out | 5370.72 (5302-5427.6) | 4009.48 (3956.8-4059)<br>74.7% | 3064.48 (3016.8-3108)<br>57.1% |
| 4D 5P 150Mi Out | 5488.48 (5397.6-5559.2) | 4147.88 (4076.4-4212.2)<br>75.6% | 3189.82 (3129.8-3241.6)<br>58.1% |
| 4D 5P 250Mi Out | 5371.26 (5298.8-5435) | 4010 (3937.6-4069.6)<br>74.7% | 3063.88 (3011-3111)<br>57% |
| 8D 3P 150Mi In | 5371.38 (5289.8-5434.4) | 3977.5 (3913-4049.2)<br>74% | 3039.08 (2976.6-3097)<br>56.6% |
| 8D 3P 250Mi In | 5353.42 (5284.6-5406.4) | 3967.66 (3918.8-4009.2)<br>74.1% | 3031.9 (2985-3063.8)<br>56.6% |
| 8D 5P 150Mi In | 5394.86 (5307-5451.2) | 4017.18 (3942.8-4060.8)<br>74.5% | 3075.96 (3001.4-3123.6)<br>57% |
| 8D 5P 250Mi In | 5370.4 (5298.2-5423.2) | 3989.22 (3933-4045) | 3048.48 (2981-3088.8) |

| | **All Transplants** | **No HCC** (min-max)<br>% of total | **No Exceptions** (min-max)<br>% of total |
|---|---|---|---|
| | | 74.3% | 56.8% |
| 8D 3P 150Mi Out | 5483.92 (5408.4-5543) | 4139.08 (4076.4-4186.8)<br>75.5% | 3191.1 (3126.8-3229.2)<br>58.2% |
| 8D 3P 250Mi Out | 5371.08 (5290.4-5429.4) | 4008.64 (3944.8-4057.6)<br>74.6% | 3064.48 (3004.8-3101.4)<br>57.1% |
| 8D 5P 150Mi Out | 5487.18 (5407.2-5556) | 4144.68 (4082.6-4197.8)<br>75.5% | 3186.3 (3127.2-3231)<br>58.1% |
| 8D 5P 250Mi Out | 5366 (5275.8-5446) | 4008.24 (3938-4062.8)<br>74.7% | 3054.92 (2987.4-3088.6)<br>56.9% |

**Counts across the 10 iterations for each scenario are presented as **mean (min-max)**. Proportions (out of total transplants) are included for the non-exception subsets.*

## Appendix B: Variance in median MELD/PELD at transplant

**Table 3. Variance in median MELD/PELD at transplant by DSA**

| | Variance in median allocation MELD at transplant | Variance in median lab MELD at transplant | No exceptions: variance in median allocation MELD at transplant | No HCC exceptions: variance in median allocation MELD at transplant |
|---|---|---|---|---|
| current | 6.2 (5.5-6.9) | 5.1 (3.9-6.9) | 16.8 (15.3-19.3) | 11.7 (10.1-13.4) |
| 11 Regions | 8.2 (7.4-9.1) | 10.2 (9.1-11.9) | 16.8 (14.8-19.1) | 12.7 (10.7-14.4) |
| 11R 3P 150Mi Out | 4.2 (3.8-4.6) | 4.5 (3.6-5.8) | 11.5 (10.1-12.9) | 8.3 (6.9-8.9) |
| 11R 3P 250Mi Out | 3.8 (3.5-4.7) | 5.4 (4.6-5.8) | 9.4 (8.1-11.1) | 6.9 (6.1-7.8) |
| 11R 5P 150Mi Out | 4.1 (3.6-4.6) | 4.5 (3.8-5.9) | 11.1 (9.9-13.3) | 7.9 (7.1-8.9) |
| 11R 5P 250Mi Out | 3.8 (3.3-4.6) | 5.3 (4.6-7) | 9.6 (8.2-12.4) | 6.9 (5.8-8.4) |
| 4D 3P 150Mi In | 2.1 (1.6-2.7) | 4.3 (3.6-5.4) | 3.9 (2.8-4.7) | 2.9 (2.3-3.5) |
| 4D 3P 250Mi In | 2.1 (1.5-2.5) | 4.5 (3.5-6.2) | 4.1 (3.3-4.6) | 3 (2-3.6) |
| 4D 5P 150Mi In | 2.3 (1.8-2.8) | 4.3 (3.5-5.1) | 4.5 (3.6-5.9) | 3.3 (2.4-4) |
| 4D 5P 250Mi In | 2.4 (1.9-3.2) | 4.3 (3.5-5.2) | 5 (3.9-6.1) | 3.8 (3.2-4.7) |
| 4D 3P 150Mi Out | 4 (3.6-4.6) | 4.7 (3.6-5.9) | 11.3 (10.2-12.1) | 7.8 (7.2-8.6) |
| 4D 3P 250Mi Out | 3.7 (3.1-4.5) | 5.2 (4.4-6.2) | 9.4 (8-10.9) | 7 (6.1-8.2) |
| 4D 5P 150Mi Out | 4.1 (3.4-4.7) | 4.3 (3.7-5.6) | 11.3 (10.1-13.5) | 8.1 (7.3-8.9) |
| 4D 5P 250Mi Out | 3.7 (3.2-4.2) | 5.1 (4.3-6.3) | 9.1 (7.9-10.2) | 6.7 (5.7-7.6) |
| 8D 3P | 2.9 (2-3.6) | 4.9 (4-5.5) | 7.4 (6.2-8.8) | 5.5 (4.5-6.2) |

| | Variance in median allocation MELD at transplant | Variance in median lab MELD at transplant | No exceptions: variance in median allocation MELD at transplant | No HCC exceptions: variance in median allocation MELD at transplant |
|---|---|---|---|---|
| 150Mi In | | | | |
| 8D 3P 250Mi In | 3 (2.1-3.6) | 5.1 (4.2-6.2) | 7.8 (6.6-9.2) | 5.7 (4.8-7.4) |
| 8D 5P 150Mi In | 3 (2.2-3.8) | 4.4 (3.6-5.2) | 8.1 (6.3-9.4) | 5.6 (4.3-6.4) |
| 8D 5P 250Mi In | 3 (2.1-3.9) | 4.8 (3.5-5.8) | 7.9 (6.1-9.1) | 5.7 (4.6-6.6) |
| 8D 3P 150Mi Out | 4.1 (3.6-5) | 4.5 (3.6-5.7) | 10.9 (9.7-11.9) | 7.8 (6.7-9.2) |
| 8D 3P 250Mi Out | 3.8 (3.2-4.9) | 5.2 (4.2-7.3) | 9.5 (8.7-10.7) | 7.2 (6.5-8.4) |
| 8D 5P 150Mi Out | 4.1 (3.6-4.8) | 4.6 (3.5-5.8) | 11.2 (9.8-12) | 8 (7.3-8.6) |
| 8D 5P 250Mi Out | 3.6 (3-4.5) | 5.4 (4.4-7.6) | 9.4 (7.4-11.4) | 6.9 (5.8-8.5) |

**Values across the 10 iterations for each scenario are presented as **mean (min-max)**.*

## Appendix C: Subgroup analysis

**Figure 11. Variance in median allocation MELD/PELD at transplant by DSA (all transplants by pediatric status).**

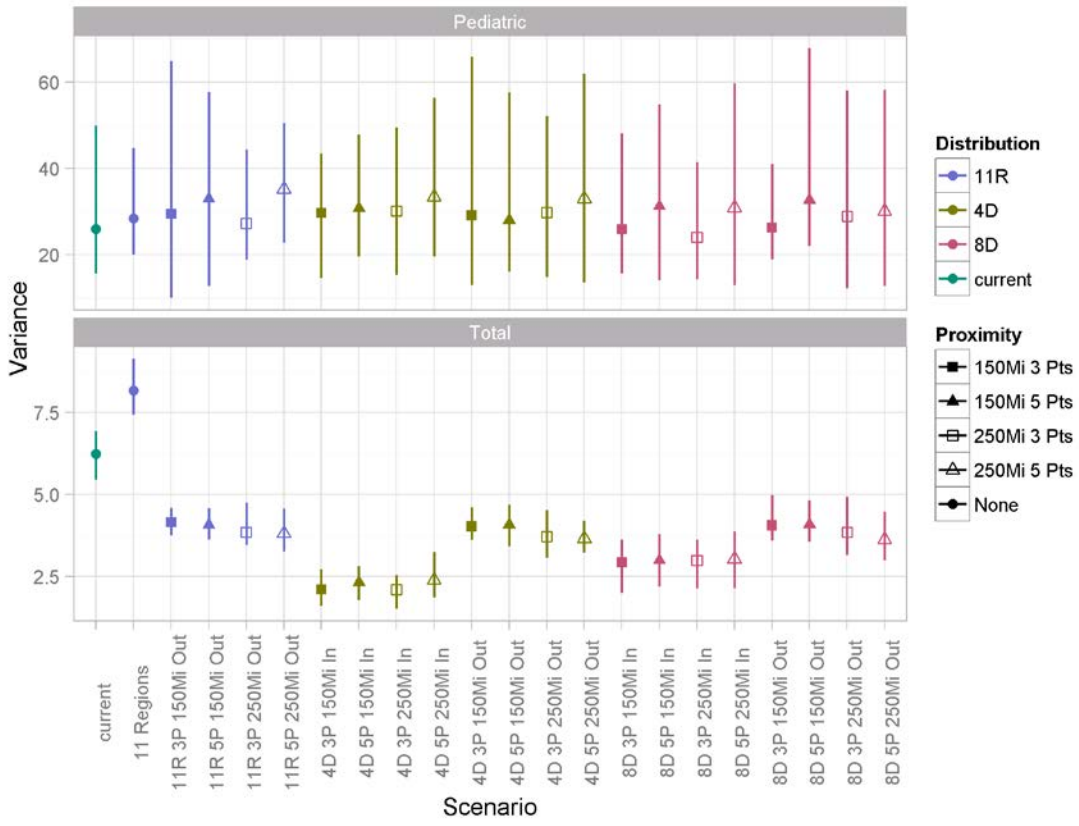


**Figure 12. Variance in median allocation MELD/PELD at transplant by DSA (all transplants by sex).**

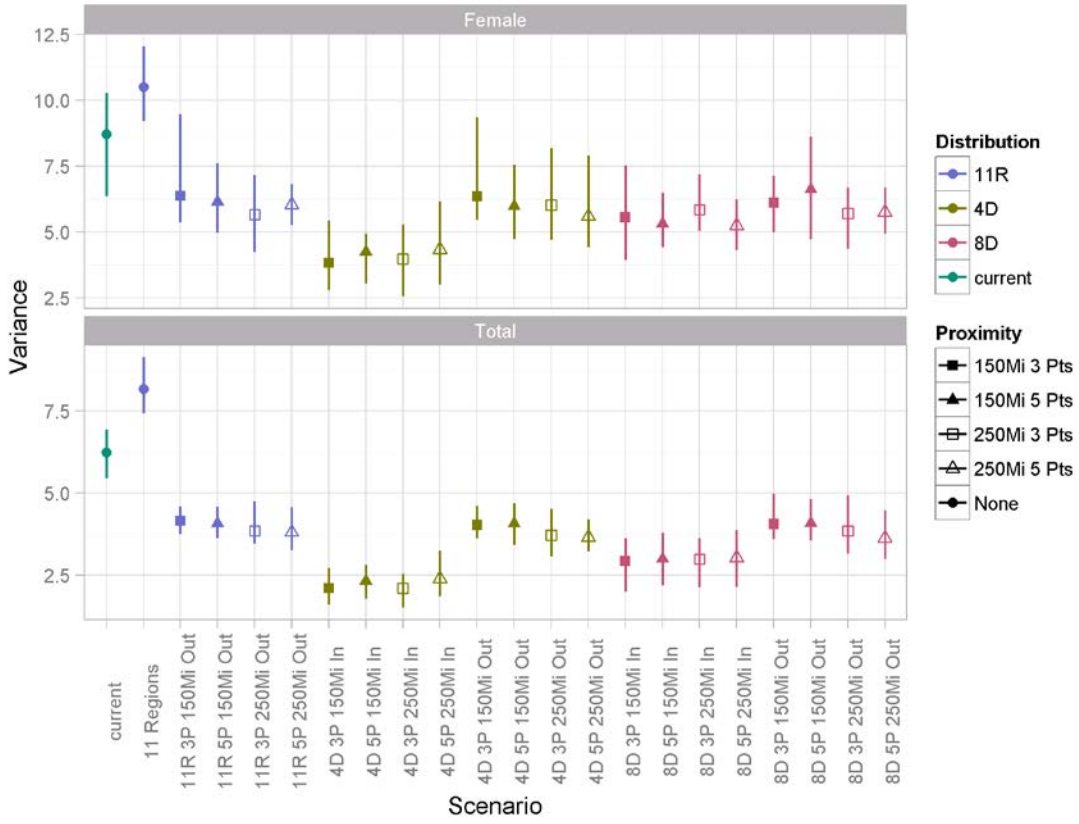


**Figure 13. Variance in median allocation MELD/PELD at transplant by DSA (all transplants by race/ethnicity).**

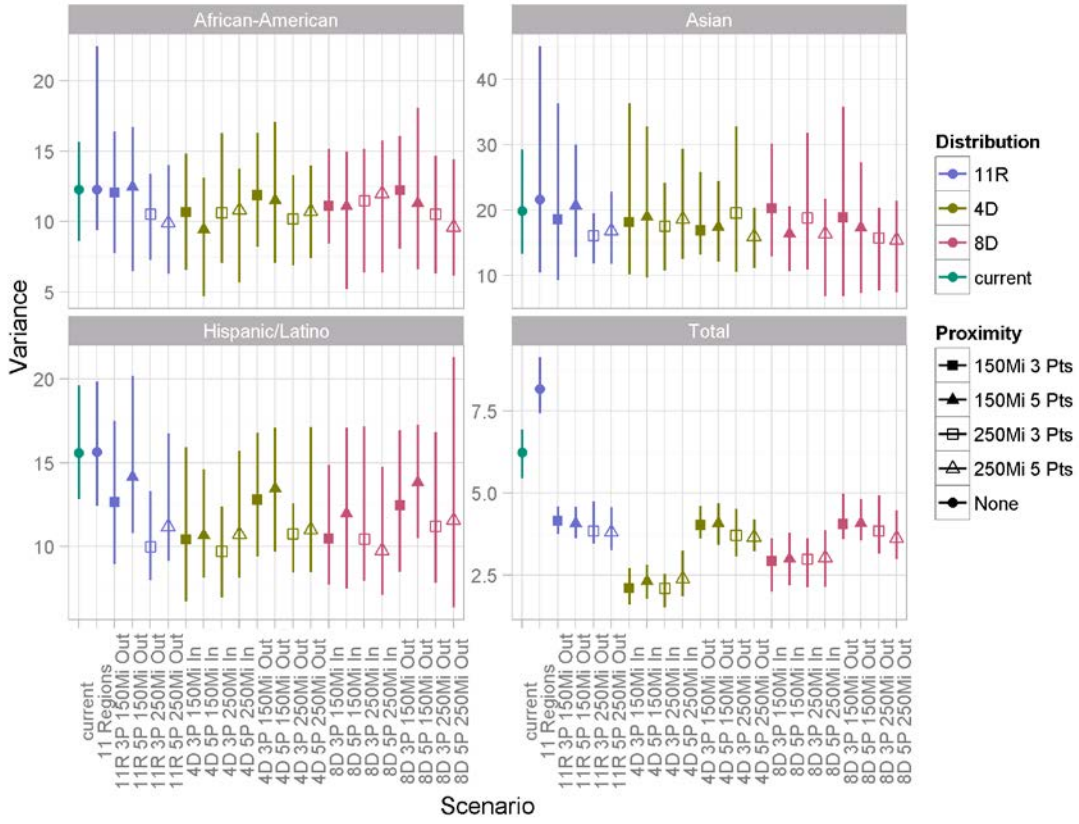


**Figure 14. Variance in median allocation MELD/PELD at transplant by DSA (pediatric recipients with no HCC exception points).**

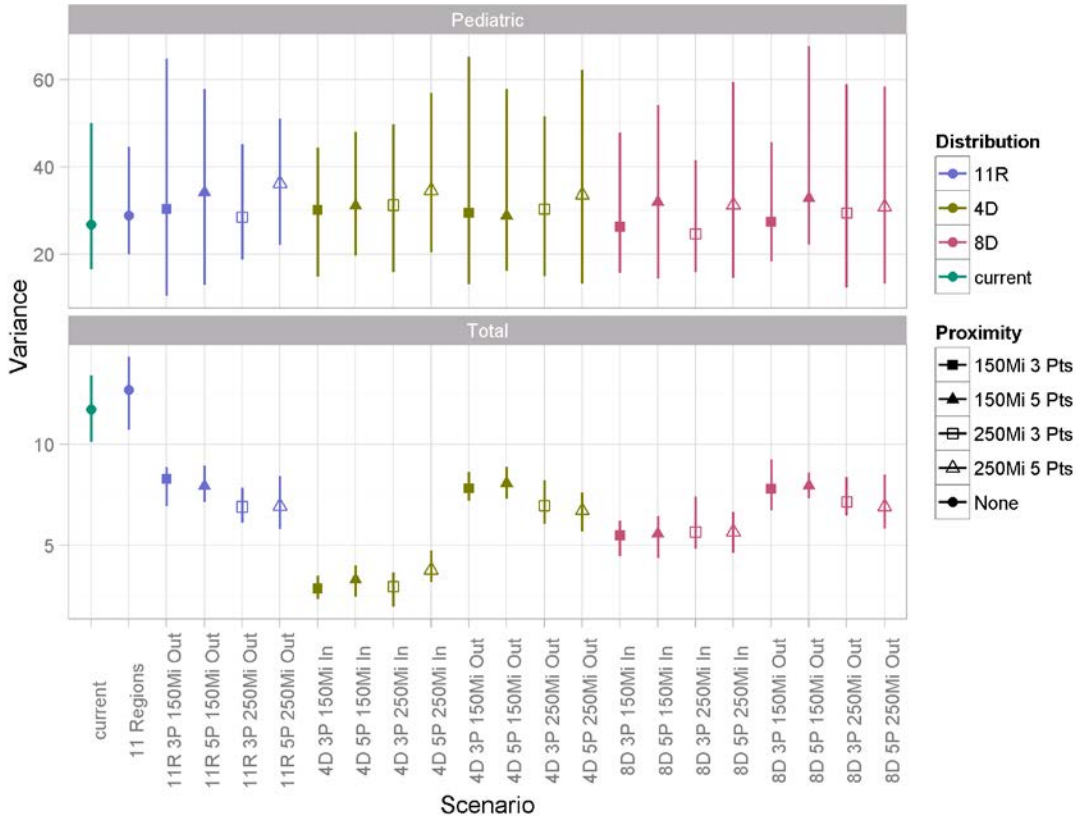





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**Figure 15. Variance in median allocation MELD/PELD at transplant by DSA (recipients with no HCC exception points by sex).**

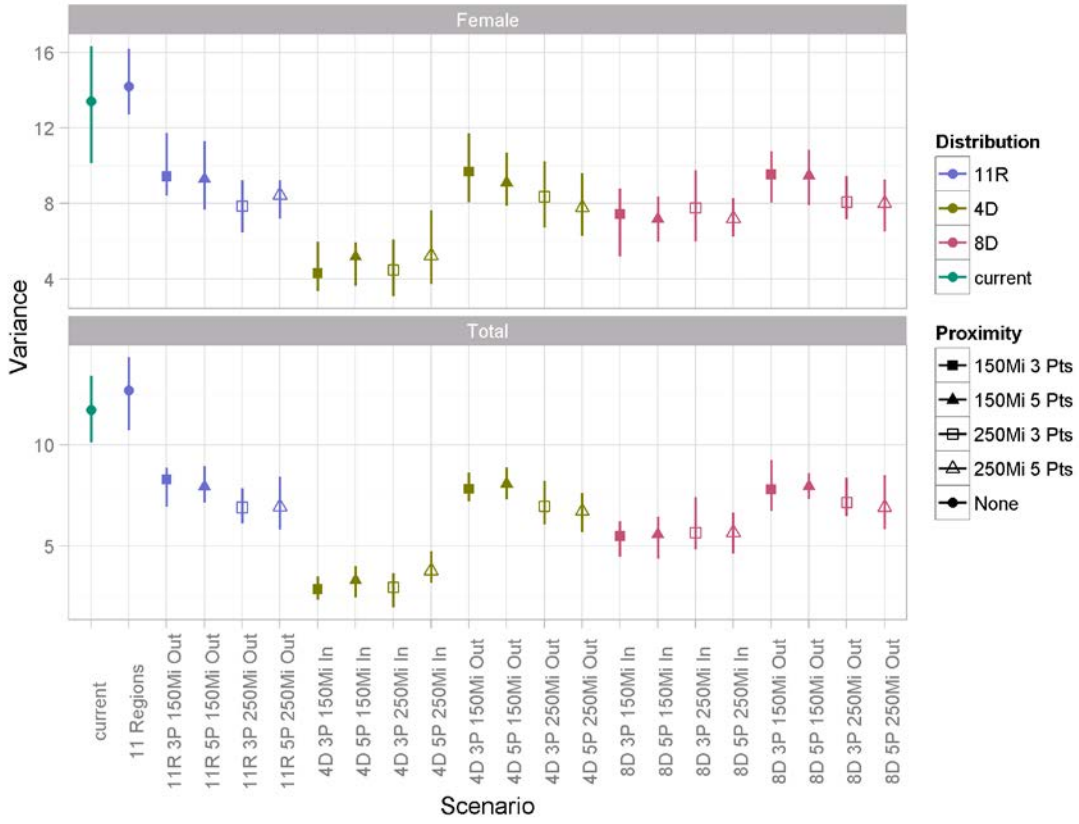

**Figure 16. Variance in median allocation MELD/PELD at transplant by DSA (recipients with no HCC exception points by race/ethnicity).**

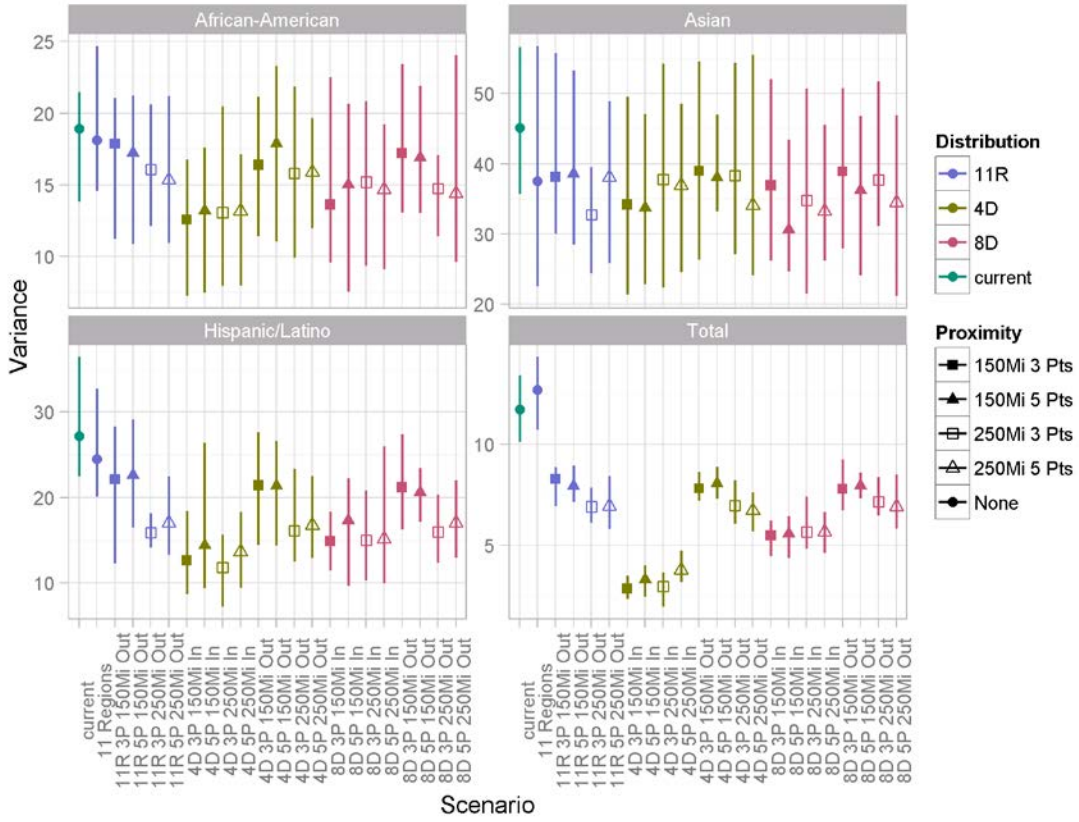

**Figure 17. Variance in median lab MELD/PELD at transplant by DSA (pediatric recipients without exception points).**

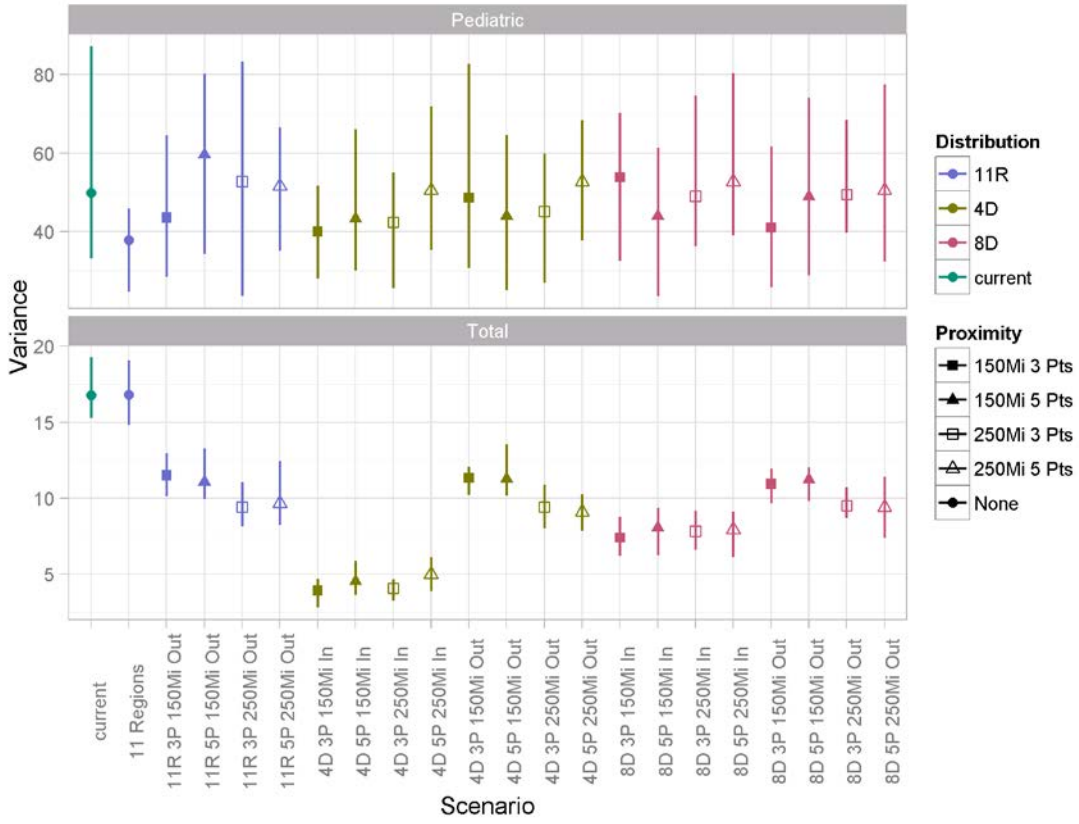

**Figure 18. Variance in median lab MELD/PELD at transplant by DSA (recipients without exception points by sex).**

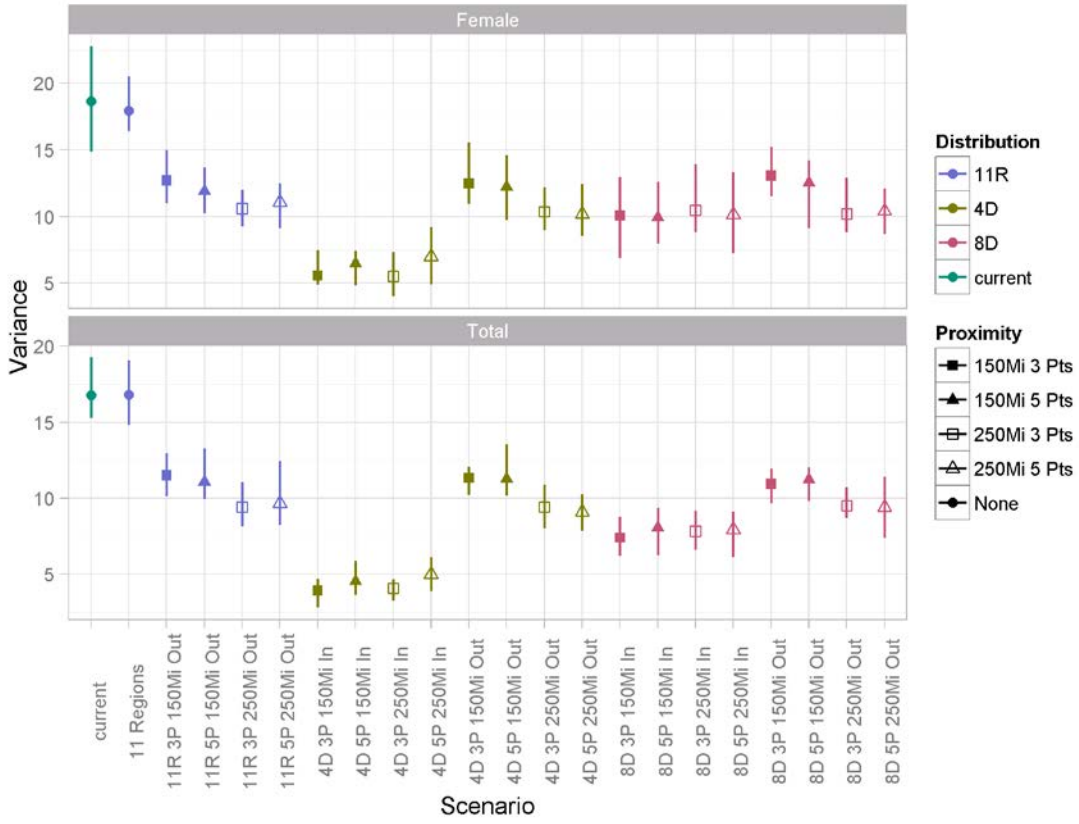

**Figure 19. Variance in median lab MELD/PELD at transplant by DSA (transplants without exception points by race/ethnicity).**

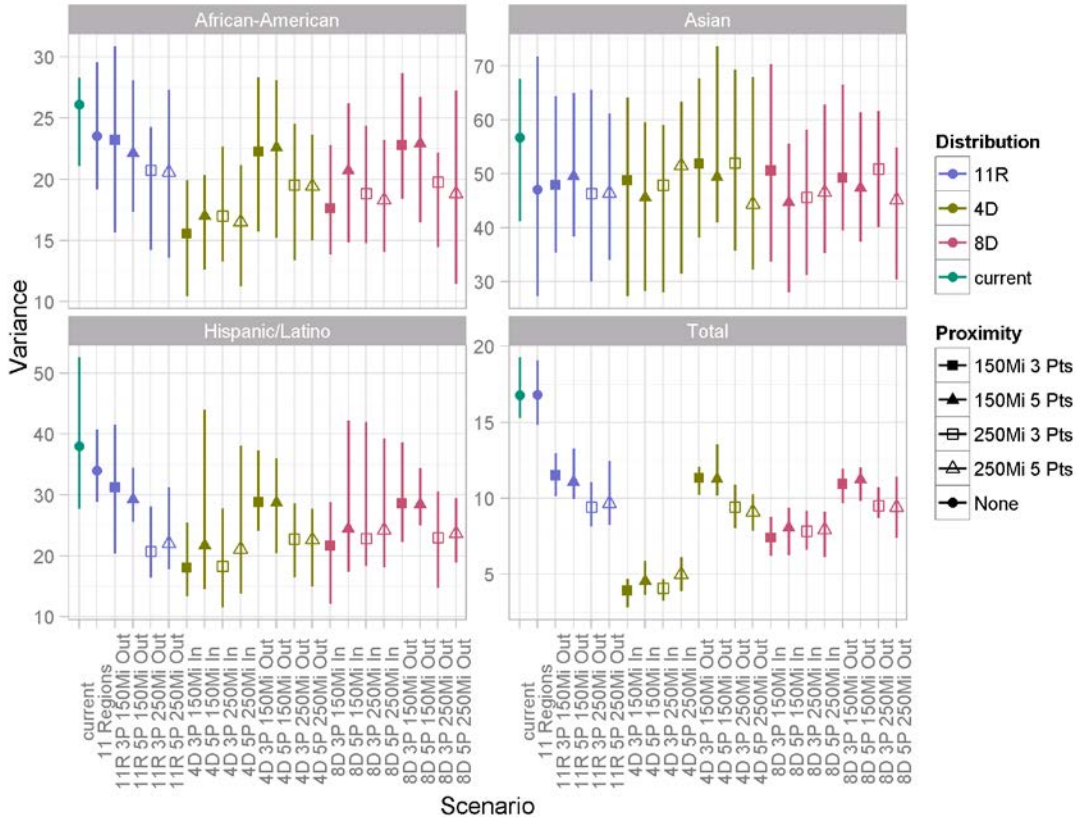

**Figure 20. Variance in median lab MELD/PELD at transplant by DSA (all pediatric transplants).**

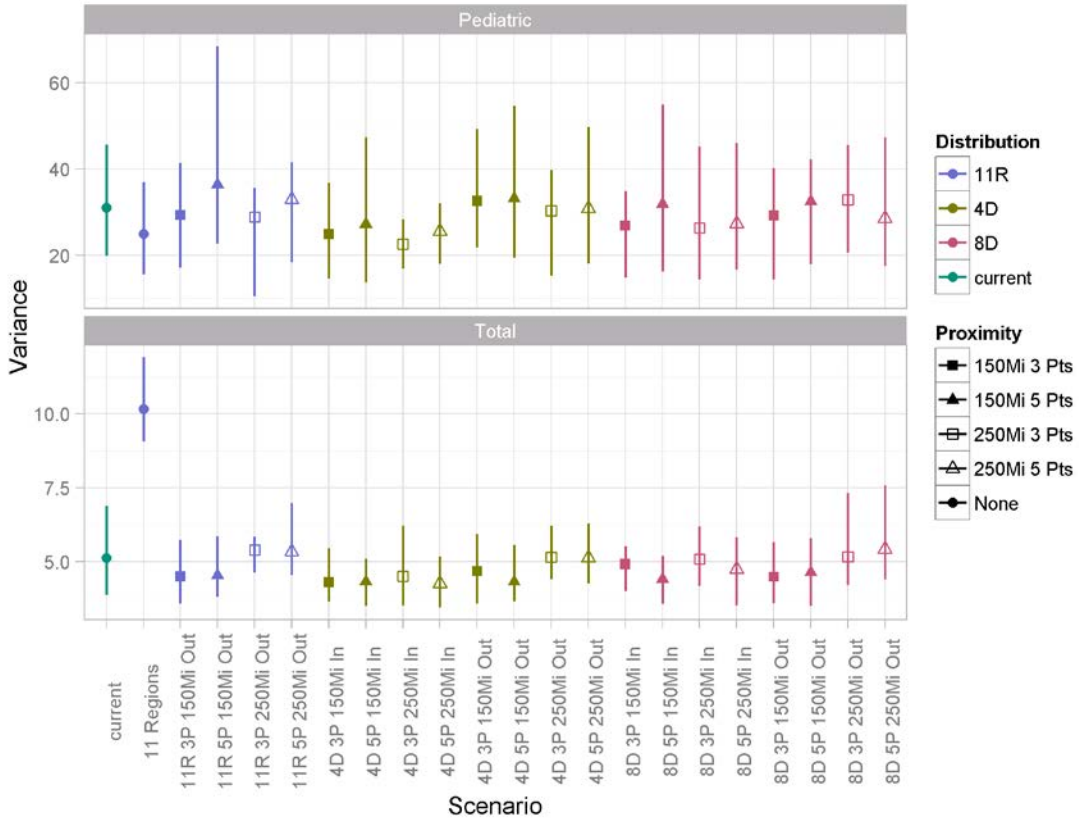

**Figure 21. Variance in median lab MELD/PELD at transplant by DSA (all transplants by sex).**

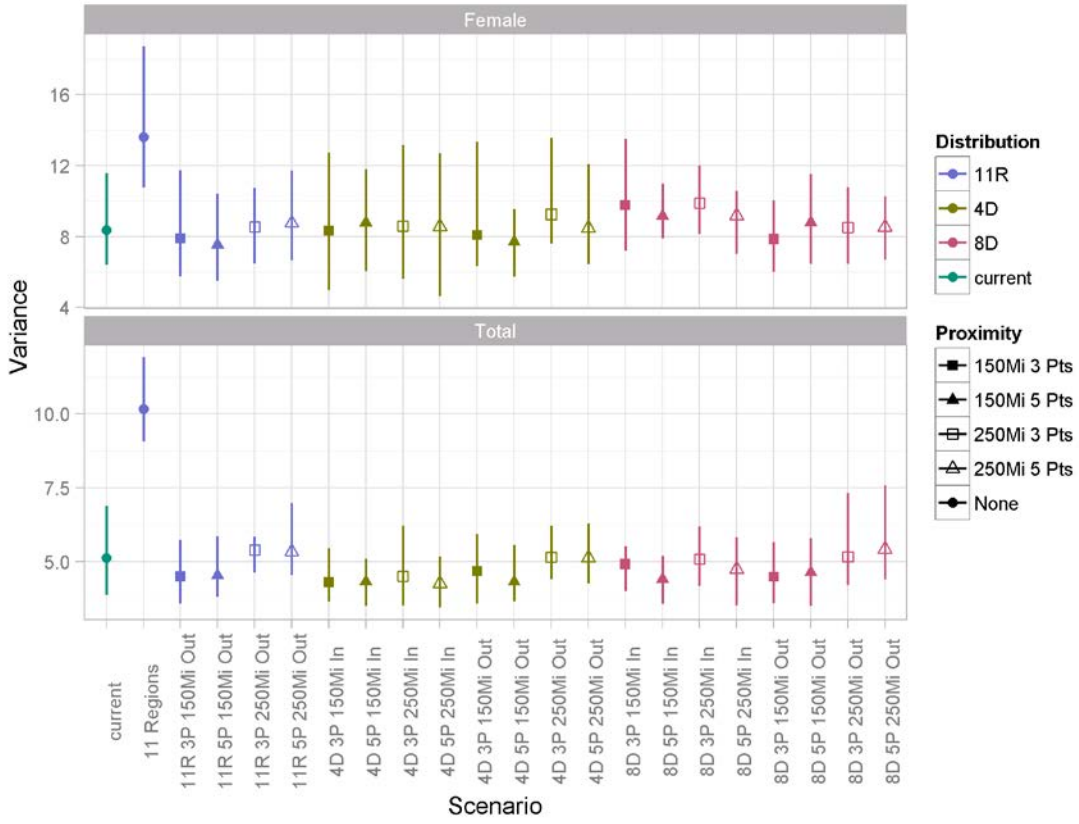

**Figure 22. Variance in median lab MELD/PELD at transplant by DSA (all transplants by race/ethnicity).**