



Process Doctor

Terry Munson

Good Bonds Take Time

Inadequate reflow profiles cause weak joints and flux residues.

Even under normal thermal profiling, certain large-mass connectors require additional heat and time above liquidous. In this case study, we investigate whether residues had any effect on poor soldering performance. Using both ion chromatography and cross-sectional investigative techniques, we were able to understand the processing effects. If solder is not permitted to stay liquidous for the amount of time required by the mass of the assembly, several critical issues can arise. Two of the major issues encountered and highlighted in this study are weakened solder bonds and flux residues that were not fully volatilized. As a result, solder bonds were easily breaking and harmful ionic residues were left on the assemblies, presenting a threat of electrical failures.

The customer in this study was having trouble with connector contacts to headers after reflow soldering on a densely populated assembly. The connector contacts to the headers would detach easily, and solder was left on the board and header (**Figure 1**). Our investigation involved both ion chromatography with localized C3 extraction and cross-sectional analysis. Localized ion chromatography results of the failure areas on the board showed higher than preferable amounts of chloride and weak organic acid residues (**Table 1**). These residues were most likely due to flux not being able to completely complex and volatilize because of insufficient heating during soldering for the density of this assembly. If these residues are left on the board without being volatilized, they pose a risk of electromigration or electrical leakage failure.

Cross-sectional analysis of the assemblies showed incomplete solder reflow, poor wetting conditions and non-homogenous alloy structures (**Figure 2**). Multiple apexes in the solder profile indicated that solder was still in the process of wetting when heat was removed, permitting the solder's surface to be pulled under a high degree of tension and creating high wetting angles. Flux bubbles and spherical formations of insufficiently reflowed solder were also seen. These conditions were

exaggerated around larger components such as the failed headers.

After examining the results and taking into account the characteristics of this assembly, we made several recommendations. First, we recommended testing bare boards for solderability to see if the added mass of the components created a need for greater thermal energy to be applied during reflow. We also suggested examining solder deposition thickness to see if the appropriate volume of solder was being applied to the boards. Finally, we suggested examining the general reflow soldering profile to see if temperatures were high enough and applied long enough for the solder to become eutectic and form good intermetallic bonds.

Subsequent bare-board solderability test samples saw much better solder joints, more homogenous alloy structures and fewer anomalies such as flux bubbles containing ionic residues. Following this analysis, the customer altered the soldering profile to accommodate for the added mass of componentry, and saw much better results in solder bond strength and quality.

The key to solving this problem was making certain that the soldering profile matched the characteristics of this highly populated assembly. By ensuring sufficient heat was applied for the appropriate amount of time required for the density of this assembly, effective reflow conditions were seen and appropriate volatilization of flux residues was achieved. ■

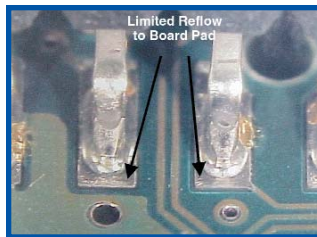


FIGURE 1: Condition of header reflow (top side) (typical). Note the flux residue.



FIGURE 2: Cross-section of an SOIC termination.

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| Sample Description | Cl ⁻ | Br ⁻ | WOA |
|---|-----------------|-----------------|-------|
| C3 Extraction | | | |
| Header Area (top failure locatoin) | 86.60 | 0.00 | 75.50 |
| Residue Area (back) | 5.43 | 0.00 | 35.70 |
| Reference Area (back) | 10.60 | 0.00 | 16.40 |
| Standard Extraction | | | |
| Assembly Extraction #1 | 24.40 | 1.45 | 2.19 |
| Assembly Extraction #2 | 7.60 | 0.51 | 61.90 |
| <i>Note: All values in µg/in², unless otherwise noted.</i> | | | |

TABLE 1: Ion Chromatography Results