***Expanding epigenomics to archived FFPE tissues: An evaluation of DNA repair methodologies*** *Siegel, EM et al*

 **Supplementary-Table 4**. Summary of β–value correlation (R2) and discordance (|Δβ|) between FF-FFPE pairs for REPLI-g Ligation and Restore by data normalization: (A) DASEN, (B) minfi-Illumina, (C) SWAN and (D) raw β-values

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| **A. DASEN** | R2 of β-values FF-FFPE pairs1 | Discordant loci between FF-FFPE pairs2 | Overlap of discordant loci3 |
|  | Patient | Patient | Overall | % CpG-Loci | Pairwise by Patient | Overall |
| A  | B | C | A  | B | C | Mean | ± | Std | A&B | A&C | B&C | A&B&C |
| LIG1 | 0.857 | 0.812 | 0.900 | 8,254 | 10,338 | 3,772 | 7,455 | ± | 3,355 | 1.54% | 638 | 120 | 137 | 23 |
| LIG2 | 0.849 | 0.810 | 0.901 | 9,415 | 10,638 | 3,834 | 7,962 | ± | 3,627 | 1.64% | 728 | 139 | 142 | 27 |
| LIG3 | 0.905 | 0.836 | 0.902 | 3,212 | 9,892 | 4,323 | 5,809 | ± | 3,579 | 1.20% | 190 | 65 | 156 | 7 |
| LIG4 | 0.860 | 0.804 | 0.898 | 10,250 | 15,168 | 4,390 | 9,936 | ± | 5,396 | 2.05% | 774 | 163 | 244 | 19 |
| RES1 | 0.939 | 0.888 | 0.918 | 1,124 | 3,402 | 3,206 | 2,577 | ± | 1,262 | 0.53% | 111 | 51 | 65 | 19 |
| RES2 | 0.941 | 0.875 | 0.919 | 1,149 | 4,662 | 3,053 | 2,955 | ± | 1,759 | 0.61% | 146 | 34 | 72 | 14 |
| RES3 | 0.938 | 0.881 | 0.920 | 1,214 | 3,969 | 3,263 | 2,815 | ± | 1,431 | 0.58% | 136 | 35 | 65 | 15 |
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| **B. minfi-Illumina** | R2 of β-values FF-FFPE pairs1 | Discordant loci between FF-FFPE pairs2 | Overlap of discordant loci3 |
|  | Patient | Patient | Overall | % CpG-Loci | Pairwise by Patient | Overall |
| A  | B | C | A  | B | C | Mean | ± | Std | A&B | A&C | B&C | A&B&C |
| LIG1 | 0.867 | 0.814 | 0.910 | 17,598 | 25,874 | 6,265 | 16,579 | ± | 9,844 | 3.41% | 2,711 | 607 | 846 | 232 |
| LIG2 | 0.858 | 0.812 | 0.911 | 20,027 | 27,545 | 6,352 | 17,975 | ± | 10,745 | 3.70% | 3,373 | 744 | 898 | 277 |
| LIG3 | 0.907 | 0.835 | 0.912 | 8,768 | 27,245 | 8,688 | 14,900 | ± | 10,691 | 3.07% | 1,113 | 395 | 1,064 | 85 |
| LIG4 | 0.867 | 0.802 | 0.909 | 20,822 | 39,294 | 8,504 | 22,873 | ± | 15,497 | 4.71% | 3,673 | 754 | 1,387 | 180 |
| RES1 | 0.940 | 0.885 | 0.925 | 3,066 | 7,682 | 5,105 | 5,284 | ± | 2,313 | 1.09% | 234 | 176 | 188 | 35 |
| RES2 | 0.941 | 0.873 | 0.926 | 3,170 | 8,614 | 5,129 | 5,638 | ± | 2,757 | 1.16% | 319 | 136 | 211 | 35 |
| RES3 | 0.940 | 0.877 | 0.927 | 3,461 | 8,229 | 5,293 | 5,661 | ± | 2,405 | 1.17% | 303 | 141 | 242 | 32 |
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| **C. SWAN** | R2 of β-values FF-FFPE pairs1 | Discordant loci between FF-FFPE pairs2 | Overlap of discordant loci3 |
|  | Patient | Patient | Overall | % CpG-Loci | Pairwise by Patient | Overall |
| A  | B | C | A  | B | C | Mean | ± | Std | A&B | A&C | B&C | A&B&C |
| LIG1 | 0.860 | 0.807 | 0.909 | 11,547 | 18,339 | 4,695 | 11,527 | ± | 6,822 | 2.37% | 1,234 | 248 | 368 | 58 |
| LIG2 | 0.852 | 0.805 | 0.908 | 13,807 | 19,297 | 4,789 | 12,631 | ± | 7,325 | 2.60% | 1,529 | 257 | 384 | 68 |
| LIG3 | 0.891 | 0.827 | 0.908 | 5,252 | 22,518 | 5,985 | 11,252 | ± | 9,764 | 2.32% | 471 | 138 | 607 | 21 |
| LIG4 | 0.860 | 0.791 | 0.906 | 15,160 | 30,470 | 5,850 | 17,160 | ± | 12,431 | 3.53% | 2,150 | 332 | 742 | 68 |
| RES1 | 0.942 | 0.884 | 0.924 | 1,818 | 4,720 | 4,179 | 3,572 | ± | 1,543 | 0.74% | 122 | 169 | 115 | 37 |
| RES2 | 0.942 | 0.872 | 0.925 | 1,902 | 5,625 | 3,856 | 3,794 | ± | 1,862 | 0.78% | 209 | 104 | 101 | 38 |
| RES3 | 0.941 | 0.877 | 0.926 | 1,724 | 5,340 | 3,855 | 3,640 | ± | 1,818 | 0.75% | 153 | 92 | 108 | 30 |
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| **D. RAW** | R2 of β-values FF-FFPE pairs1 | Discordant loci between FF-FFPE pairs2 | Overlap of discordant loci3 |
|  | Patient | Patient | Overall | % CpG-Loci | Pairwise by Patient | Overall |
| A  | B | C | A  | B | C | Mean | ± | Std | A&B | A&C | B&C | A&B&C |
| LIG1 | 0.857 | 0.806 | 0.908 | 10,667 | 16,615 | 3,859 | 10,380 | ± | 6,383 | 2.14% | 1,158 | 207 | 286 | 53 |
| LIG2 | 0.852 | 0.804 | 0.908 | 12,116 | 16,627 | 3,854 | 10,866 | ± | 6,478 | 2.24% | 1,297 | 175 | 276 | 42 |
| LIG3 | 0.890 | 0.827 | 0.908 | 4,992 | 18,511 | 5,472 | 9,658 | ± | 7,670 | 1.99% | 390 | 118 | 480 | 19 |
| LIG4 | 0.861 | 0.790 | 0.905 | 13,616 | 27,107 | 5,224 | 15,316 | ± | 11,040 | 3.15% | 1,735 | 275 | 595 | 49 |
| RES1 | 0.942 | 0.884 | 0.923 | 1,354 | 3,314 | 3,503 | 2,724 | ± | 1,190 | 0.56% | 89 | 101 | 62 | 18 |
| RES2 | 0.942 | 0.872 | 0.924 | 1,475 | 4,283 | 3,235 | 2,998 | ± | 1,419 | 0.62% | 146 | 58 | 57 | 19 |
| RES3 | 0.940 | 0.876 | 0.925 | 1,424 | 4,158 | 3,258 | 2,947 | ± | 1,393 | 0.61% | 95 | 52 | 70 | 15 |
|  |

1. Pearson Correlation Coefficient comparing FF vs. FFPE β-values for each patient sample, by experimental condition. Mean R2 for DASEN normalization (R2 = 0.883) was not significantly different than mean R2 for minfi-Illumina (R2= 0.887), SWAN (R2= 0.884) and raw β-values (R2= 0.883) by paired Student t-test (p>0.05).
2. The number of discordant CpG-loci defined as |Δβ|>0.3 between FF and FFPE. Percent of CpC-loci with |Δβ|>0.3 out of total CpG-loci evaluated (N=485512) for each condition. Mean number of discordant CpG-loci differed significantly between DASEN normalized data and minfi-Illumina (*p*=0.0001), SWAN (*p* = 0.0014) and raw β-values (*p* = 0.007) by paired Student t-test.
3. Overlap of individual discordant CpG-loci (|Δβ|>0.3) across patient samples (A, B and C), pairwise and overall.