**General Linear Model**

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| **Notes** | | |
| Output Created | | 09-MAY-2024 22:24:39 |
| Comments | |  |
| Input | Data | /Users/ghal9233/Desktop/ASAP work/1.papers to do/Cormac SNCA A53T astrocytes/Stats.sav |
| Active Dataset | DataSet3 |
| Filter | <none> |
| Weight | <none> |
| Split File | <none> |
| N of Rows in Working Data File | 81 |
| Missing Value Handling | Definition of Missing | User-defined missing values are treated as missing. |
| Cases Used | Statistics are based on all cases with valid data for all variables in the model. |
| Syntax | | GLM TOTALAST withaSyn BY GENOTYPE1WT2A53T REGION1SN2VTA3CP LOCATION1rostral2mid3caudal /METHOD=SSTYPE(3) /INTERCEPT=INCLUDE /POSTHOC=GENOTYPE1WT2A53T REGION1SN2VTA3CP(TUKEY) /PLOT=PROFILE(REGION1SN2VTA3CP) TYPE=BAR ERRORBAR=SE(1) MEANREFERENCE=NO /EMMEANS=TABLES(GENOTYPE1WT2A53T\*REGION1SN2VTA3CP) COMPARE(GENOTYPE1WT2A53T) ADJ(LSD) /EMMEANS=TABLES(GENOTYPE1WT2A53T\*REGION1SN2VTA3CP) COMPARE(REGION1SN2VTA3CP) ADJ(LSD) /EMMEANS=TABLES(GENOTYPE1WT2A53T\*REGION1SN2VTA3CP\*LOCATION1rostral2mid3caudal) COMPARE(GENOTYPE1WT2A53T) ADJ(LSD) /EMMEANS=TABLES(GENOTYPE1WT2A53T\*REGION1SN2VTA3CP\*LOCATION1rostral2mid3caudal) COMPARE(REGION1SN2VTA3CP) ADJ(LSD) /EMMEANS=TABLES(GENOTYPE1WT2A53T\*REGION1SN2VTA3CP\*LOCATION1rostral2mid3caudal) COMPARE(LOCATION1rostral2mid3caudal) ADJ(LSD) /PRINT=DESCRIPTIVE /CRITERIA=ALPHA(.05) /DESIGN= GENOTYPE1WT2A53T REGION1SN2VTA3CP LOCATION1rostral2mid3caudal GENOTYPE1WT2A53T\*REGION1SN2VTA3CP GENOTYPE1WT2A53T\*LOCATION1rostral2mid3caudal REGION1SN2VTA3CP\*LOCATION1rostral2mid3caudal GENOTYPE1WT2A53T\*REGION1SN2VTA3CP\*LOCATION1rostral2mid3caudal. |
| Resources | Processor Time | 00:00:00.45 |
| Elapsed Time | 00:00:01.00 |

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| **Warnings** |
| Post hoc tests are not performed for GENOTYPE [1 = WT; 2= A53T] because there are fewer than three groups. |

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| **Between-Subjects Factors** | | |
|  | | N |
| GENOTYPE [1 = WT; 2= A53T] | 1 | 36 |
| 2 | 45 |
| REGION[1=SN; 2=VTA; 3=CP] | 1 | 27 |
| 2 | 27 |
| 3 | 27 |
| LOCATION (1=rostral; 2=mid; 3=caudal) | 1 | 27 |
| 2 | 27 |
| 3 | 27 |

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| **Descriptive Statistics** | | | | | | |
|  | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | Mean | Std. Deviation | N |
| TOTAL AST | 1 | 1 | 1 | 135.5000000 | 30.95695937 | 4 |
| 2 | 108.7500000 | 18.83923211 | 4 |
| 3 | 106.0000000 | 14.16568624 | 4 |
| Total | 116.7500000 | 24.61752886 | 12 |
| 2 | 1 | 97.7500000 | 18.30072858 | 4 |
| 2 | 110.7500000 | 33.24028680 | 4 |
| 3 | 75.0000000 | 14.07124728 | 4 |
| Total | 94.5000000 | 26.16903097 | 12 |
| 3 | 1 | 96.6875000 | 24.52581548 | 4 |
| 2 | 99.2500000 | 25.62306903 | 4 |
| 3 | 103.1250000 | 17.92286714 | 4 |
| Total | 99.6875000 | 20.93689789 | 12 |
| Total | 1 | 109.9791667 | 29.53338987 | 12 |
| 2 | 106.2500000 | 24.58958575 | 12 |
| 3 | 94.7083333 | 20.24111290 | 12 |
| Total | 103.6458333 | 25.22671309 | 36 |
| 2 | 1 | 1 | 309.0000000 | 97.24196625 | 5 |
| 2 | 310.2000000 | 105.00809493 | 5 |
| 3 | 308.6000000 | 105.02047419 | 5 |
| Total | 309.2666667 | 94.88900784 | 15 |
| 2 | 1 | 239.8000000 | 60.30920328 | 5 |
| 2 | 228.6000000 | 73.35734455 | 5 |
| 3 | 220.4000000 | 35.46547617 | 5 |
| Total | 229.6000000 | 54.80719452 | 15 |
| 3 | 1 | 205.8000000 | 72.43669650 | 5 |
| 2 | 221.0750000 | 76.37242222 | 5 |
| 3 | 194.7937500 | 86.98424898 | 5 |
| Total | 207.2229167 | 73.83682358 | 15 |
| Total | 1 | 251.5333333 | 84.94503825 | 15 |
| 2 | 253.2916667 | 89.99751567 | 15 |
| 3 | 241.2645833 | 90.65557894 | 15 |
| Total | 248.6965278 | 86.69919226 | 45 |
| Total | 1 | 1 | 231.8888889 | 115.97030271 | 9 |
| 2 | 220.6666667 | 130.07401739 | 9 |
| 3 | 218.5555556 | 130.35251351 | 9 |
| Total | 223.7037037 | 120.86318228 | 27 |
| 2 | 1 | 176.6666667 | 86.88642011 | 9 |
| 2 | 176.2222222 | 83.44425951 | 9 |
| 3 | 155.7777778 | 81.09065572 | 9 |
| Total | 169.5555556 | 81.16144089 | 27 |
| 3 | 1 | 157.3055556 | 78.46145329 | 9 |
| 2 | 166.9305556 | 85.35319796 | 9 |
| 3 | 154.0520833 | 78.97975537 | 9 |
| Total | 159.4293981 | 78.01395358 | 27 |
| Total | 1 | 188.6203704 | 96.91343209 | 27 |
| 2 | 187.9398148 | 100.80188926 | 27 |
| 3 | 176.1284722 | 100.52867326 | 27 |
| Total | 184.2295525 | 98.34916264 | 81 |
| % with aSyn | 1 | 1 | 1 | 28.361846916545420 | 6.462655626351514 | 4 |
| 2 | 31.112897749746544 | 3.262213212273931 | 4 |
| 3 | 29.321997381824797 | 9.188590874535736 | 4 |
| Total | 29.598914016038922 | 6.223935640644889 | 12 |
| 2 | 1 | 23.296955338820870 | 6.406781533634183 | 4 |
| 2 | 21.552104413846013 | 6.694389527384959 | 4 |
| 3 | 23.741626526044357 | 7.912076677160803 | 4 |
| Total | 22.863562092903745 | 6.439247321354615 | 12 |
| 3 | 1 | 24.177157654290482 | 6.223431914871857 | 4 |
| 2 | 26.154780339397117 | 3.810835232548639 | 4 |
| 3 | 26.122044759005476 | 5.919851581124211 | 4 |
| Total | 25.484660917564360 | 5.001401349721292 | 12 |
| Total | 1 | 25.278653303218924 | 6.202767900238960 | 12 |
| 2 | 26.273260834329893 | 5.976011274319012 | 12 |
| 3 | 26.395222888958210 | 7.440407140389993 | 12 |
| Total | 25.982379008835675 | 6.400930898329712 | 36 |
| 2 | 1 | 1 | 62.666309641007710 | 12.073988357238461 | 5 |
| 2 | 66.807860928598810 | 5.483765436247421 | 5 |
| 3 | 64.149443490896720 | 7.156691527419838 | 5 |
| Total | 64.541204686834400 | 8.247582508338022 | 15 |
| 2 | 1 | 67.726894323505490 | 13.172546664433007 | 5 |
| 2 | 61.434048914099010 | 7.076126141811316 | 5 |
| 3 | 54.298127074844550 | 5.757409481841534 | 5 |
| Total | 61.153023437483020 | 10.276057583417366 | 15 |
| 3 | 1 | 64.906553593303410 | 3.857441689292558 | 5 |
| 2 | 63.959428492619665 | 6.904376500127863 | 5 |
| 3 | 69.173072558127910 | 9.496843182648247 | 5 |
| Total | 66.013018214683670 | 7.010697935007000 | 15 |
| Total | 1 | 65.099919185938860 | 10.003614945428803 | 15 |
| 2 | 64.067112778439180 | 6.456094826756732 | 15 |
| 3 | 62.540214374623070 | 9.527427540024416 | 15 |
| Total | 63.902415446333690 | 8.666951143600656 | 45 |
| Total | 1 | 1 | 47.419881763468920 | 20.382360991395597 | 9 |
| 2 | 50.943432849108920 | 19.311957821906740 | 9 |
| 3 | 48.670578553531410 | 19.854502680222940 | 9 |
| Total | 49.011297722036440 | 19.133323340654943 | 27 |
| 2 | 1 | 47.980254774756770 | 25.504691830335695 | 9 |
| 2 | 43.708740247319895 | 21.992412557016330 | 9 |
| 3 | 40.717460164266680 | 17.303475833387264 | 9 |
| Total | 44.135485062114450 | 21.220773264188710 | 27 |
| 3 | 1 | 46.804599842631000 | 21.971916586424843 | 9 |
| 2 | 47.157362646742980 | 20.646519054928493 | 9 |
| 3 | 50.039282425184616 | 23.938830131583430 | 9 |
| Total | 48.000414971519525 | 21.405939927727815 | 27 |
| Total | 1 | 47.401578793618896 | 21.834856370049620 | 27 |
| 2 | 47.269845247723940 | 20.094849795455048 | 27 |
| 3 | 46.475773714327580 | 20.181387620312130 | 27 |
| Total | 47.049065918556785 | 20.462681335399928 | 81 |

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| **Multivariate Tests**a | | | | | | |
| Effect | | Value | F | Hypothesis df | Error df | Sig. |
| Intercept | Pillai's Trace | .987 | 2386.538b | 2.000 | 62.000 | <.001 |
| Wilks' Lambda | .013 | 2386.538b | 2.000 | 62.000 | <.001 |
| Hotelling's Trace | 76.985 | 2386.538b | 2.000 | 62.000 | <.001 |
| Roy's Largest Root | 76.985 | 2386.538b | 2.000 | 62.000 | <.001 |
| GENOTYPE1WT2A53T | Pillai's Trace | .931 | 419.711b | 2.000 | 62.000 | <.001 |
| Wilks' Lambda | .069 | 419.711b | 2.000 | 62.000 | <.001 |
| Hotelling's Trace | 13.539 | 419.711b | 2.000 | 62.000 | <.001 |
| Roy's Largest Root | 13.539 | 419.711b | 2.000 | 62.000 | <.001 |
| REGION1SN2VTA3CP | Pillai's Trace | .318 | 5.948 | 4.000 | 126.000 | <.001 |
| Wilks' Lambda | .693 | 6.233b | 4.000 | 124.000 | <.001 |
| Hotelling's Trace | .427 | 6.510 | 4.000 | 122.000 | <.001 |
| Roy's Largest Root | .386 | 12.168c | 2.000 | 63.000 | <.001 |
| LOCATION1rostral2mid3caudal | Pillai's Trace | .018 | .291 | 4.000 | 126.000 | .883 |
| Wilks' Lambda | .982 | .288b | 4.000 | 124.000 | .885 |
| Hotelling's Trace | .019 | .284 | 4.000 | 122.000 | .888 |
| Roy's Largest Root | .019 | .588c | 2.000 | 63.000 | .559 |
| GENOTYPE1WT2A53T \* REGION1SN2VTA3CP | Pillai's Trace | .093 | 1.536 | 4.000 | 126.000 | .196 |
| Wilks' Lambda | .907 | 1.550b | 4.000 | 124.000 | .192 |
| Hotelling's Trace | .102 | 1.563 | 4.000 | 122.000 | .189 |
| Roy's Largest Root | .102 | 3.221c | 2.000 | 63.000 | .047 |
| GENOTYPE1WT2A53T \* LOCATION1rostral2mid3caudal | Pillai's Trace | .013 | .202 | 4.000 | 126.000 | .937 |
| Wilks' Lambda | .987 | .199b | 4.000 | 124.000 | .938 |
| Hotelling's Trace | .013 | .197 | 4.000 | 122.000 | .940 |
| Roy's Largest Root | .013 | .402c | 2.000 | 63.000 | .671 |
| REGION1SN2VTA3CP \* LOCATION1rostral2mid3caudal | Pillai's Trace | .092 | .758 | 8.000 | 126.000 | .641 |
| Wilks' Lambda | .909 | .759b | 8.000 | 124.000 | .639 |
| Hotelling's Trace | .100 | .761 | 8.000 | 122.000 | .638 |
| Roy's Largest Root | .093 | 1.468c | 4.000 | 63.000 | .222 |
| GENOTYPE1WT2A53T \* REGION1SN2VTA3CP \* LOCATION1rostral2mid3caudal | Pillai's Trace | .070 | .567 | 8.000 | 126.000 | .803 |
| Wilks' Lambda | .931 | .563b | 8.000 | 124.000 | .807 |
| Hotelling's Trace | .073 | .558 | 8.000 | 122.000 | .810 |
| Roy's Largest Root | .061 | .965c | 4.000 | 63.000 | .433 |
| a. Design: Intercept + GENOTYPE1WT2A53T + REGION1SN2VTA3CP + LOCATION1rostral2mid3caudal + GENOTYPE1WT2A53T \* REGION1SN2VTA3CP + GENOTYPE1WT2A53T \* LOCATION1rostral2mid3caudal + REGION1SN2VTA3CP \* LOCATION1rostral2mid3caudal + GENOTYPE1WT2A53T \* REGION1SN2VTA3CP \* LOCATION1rostral2mid3caudal | | | | | | |
| b. Exact statistic | | | | | | |
| c. The statistic is an upper bound on F that yields a lower bound on the significance level. | | | | | | |

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| **Tests of Between-Subjects Effects** | | | | | | |
| Source | Dependent Variable | Type III Sum of Squares | df | Mean Square | F | Sig. |
| Corrected Model | TOTAL AST | 517873.988a | 17 | 30463.176 | 7.499 | <.001 |
| % with aSyn | 29830.722b | 17 | 1754.748 | 30.147 | <.001 |
| Intercept | TOTAL AST | 2482902.789 | 1 | 2482902.789 | 611.192 | <.001 |
| % with aSyn | 161585.525 | 1 | 161585.525 | 2776.093 | <.001 |
| GENOTYPE1WT2A53T | TOTAL AST | 420794.079 | 1 | 420794.079 | 103.583 | <.001 |
| % with aSyn | 28758.583 | 1 | 28758.583 | 494.082 | <.001 |
| REGION1SN2VTA3CP | TOTAL AST | 55263.972 | 2 | 27631.986 | 6.802 | .002 |
| % with aSyn | 367.634 | 2 | 183.817 | 3.158 | .049 |
| LOCATION1rostral2mid3caudal | TOTAL AST | 2692.534 | 2 | 1346.267 | .331 | .719 |
| % with aSyn | 9.018 | 2 | 4.509 | .077 | .926 |
| GENOTYPE1WT2A53T \* REGION1SN2VTA3CP | TOTAL AST | 25062.873 | 2 | 12531.436 | 3.085 | .053 |
| % with aSyn | 105.379 | 2 | 52.689 | .905 | .410 |
| GENOTYPE1WT2A53T \* LOCATION1rostral2mid3caudal | TOTAL AST | 123.042 | 2 | 61.521 | .015 | .985 |
| % with aSyn | 45.209 | 2 | 22.605 | .388 | .680 |
| REGION1SN2VTA3CP \* LOCATION1rostral2mid3caudal | TOTAL AST | 1839.532 | 4 | 459.883 | .113 | .977 |
| % with aSyn | 285.366 | 4 | 71.341 | 1.226 | .309 |
| GENOTYPE1WT2A53T \* REGION1SN2VTA3CP \* LOCATION1rostral2mid3caudal | TOTAL AST | 3106.951 | 4 | 776.738 | .191 | .942 |
| % with aSyn | 210.012 | 4 | 52.503 | .902 | .468 |
| Error | TOTAL AST | 255930.635 | 63 | 4062.391 |  |  |
| % with aSyn | 3666.984 | 63 | 58.206 |  |  |
| Total | TOTAL AST | 3522987.392 | 81 |  |  |  |
| % with aSyn | 212800.489 | 81 |  |  |  |
| Corrected Total | TOTAL AST | 773804.623 | 80 |  |  |  |
| % with aSyn | 33497.706 | 80 |  |  |  |
| a. R Squared = .669 (Adjusted R Squared = .580) | | | | | | |
| b. R Squared = .891 (Adjusted R Squared = .861) | | | | | | |

**Estimated Marginal Means**

**1. GENOTYPE [1 = WT; 2= A53T] \* REGION[1=SN; 2=VTA; 3=CP]**

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| **Estimates** | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | Mean | Std. Error | 95% Confidence Interval |
| Lower Bound |
| TOTAL AST | 1 | 1 | 116.750 | 18.399 | 79.982 |
| 2 | 94.500 | 18.399 | 57.732 |
| 3 | 99.687 | 18.399 | 62.920 |
| 2 | 1 | 309.267 | 16.457 | 276.380 |
| 2 | 229.600 | 16.457 | 196.714 |
| 3 | 207.223 | 16.457 | 174.337 |
| % with aSyn | 1 | 1 | 29.599 | 2.202 | 25.198 |
| 2 | 22.864 | 2.202 | 18.462 |
| 3 | 25.485 | 2.202 | 21.084 |
| 2 | 1 | 64.541 | 1.970 | 60.605 |
| 2 | 61.153 | 1.970 | 57.217 |
| 3 | 66.013 | 1.970 | 62.077 |

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| **Estimates** | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval |
| Upper Bound |
| TOTAL AST | 1 | 1 | 153.518 |
| 2 | 131.268 |
| 3 | 136.455 |
| 2 | 1 | 342.153 |
| 2 | 262.486 |
| 3 | 240.109 |
| % with aSyn | 1 | 1 | 34.000 |
| 2 | 27.265 |
| 3 | 29.886 |
| 2 | 1 | 68.478 |
| 2 | 65.090 |
| 3 | 69.949 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | Mean Difference (I-J) |
|
| TOTAL AST | 1 | 1 | 2 | -192.517\* |
| 2 | 1 | 192.517\* |
| 2 | 1 | 2 | -135.100\* |
| 2 | 1 | 135.100\* |
| 3 | 1 | 2 | -107.535\* |
| 2 | 1 | 107.535\* |
| % with aSyn | 1 | 1 | 2 | -34.942\* |
| 2 | 1 | 34.942\* |
| 2 | 1 | 2 | -38.289\* |
| 2 | 1 | 38.289\* |
| 3 | 1 | 2 | -40.528\* |
| 2 | 1 | 40.528\* |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | Std. Error |
|
| TOTAL AST | 1 | 1 | 2 | 24.685 |
| 2 | 1 | 24.685 |
| 2 | 1 | 2 | 24.685 |
| 2 | 1 | 24.685 |
| 3 | 1 | 2 | 24.685 |
| 2 | 1 | 24.685 |
| % with aSyn | 1 | 1 | 2 | 2.955 |
| 2 | 1 | 2.955 |
| 2 | 1 | 2 | 2.955 |
| 2 | 1 | 2.955 |
| 3 | 1 | 2 | 2.955 |
| 2 | 1 | 2.955 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | Sig.b |
|
| TOTAL AST | 1 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 3 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| % with aSyn | 1 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 3 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | 95% Confidence Interval for Differenceb |
| Lower Bound |
| TOTAL AST | 1 | 1 | 2 | -241.846 |
| 2 | 1 | 143.187 |
| 2 | 1 | 2 | -184.429 |
| 2 | 1 | 85.771 |
| 3 | 1 | 2 | -156.865 |
| 2 | 1 | 58.206 |
| % with aSyn | 1 | 1 | 2 | -40.847 |
| 2 | 1 | 29.038 |
| 2 | 1 | 2 | -44.194 |
| 2 | 1 | 32.385 |
| 3 | 1 | 2 | -46.433 |
| 2 | 1 | 34.624 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | 95% Confidence Interval for Difference |
| Upper Bound |
| TOTAL AST | 1 | 1 | 2 | -143.187 |
| 2 | 1 | 241.846 |
| 2 | 1 | 2 | -85.771 |
| 2 | 1 | 184.429 |
| 3 | 1 | 2 | -58.206 |
| 2 | 1 | 156.865 |
| % with aSyn | 1 | 1 | 2 | -29.038 |
| 2 | 1 | 40.847 |
| 2 | 1 | 2 | -32.385 |
| 2 | 1 | 44.194 |
| 3 | 1 | 2 | -34.624 |
| 2 | 1 | 46.433 |
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| Based on estimated marginal means |
| \*. The mean difference is significant at the .05 level. |
| b. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments). |

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| **Multivariate Tests** | | | | | | |
| REGION[1=SN; 2=VTA; 3=CP] | | Value | F | Hypothesis df | Error df | Sig. |
| 1 | Pillai's trace | .826 | 147.137a | 2.000 | 62.000 | <.001 |
| Wilks' lambda | .174 | 147.137a | 2.000 | 62.000 | <.001 |
| Hotelling's trace | 4.746 | 147.137a | 2.000 | 62.000 | <.001 |
| Roy's largest root | 4.746 | 147.137a | 2.000 | 62.000 | <.001 |
| 2 | Pillai's trace | .816 | 137.435a | 2.000 | 62.000 | <.001 |
| Wilks' lambda | .184 | 137.435a | 2.000 | 62.000 | <.001 |
| Hotelling's trace | 4.433 | 137.435a | 2.000 | 62.000 | <.001 |
| Roy's largest root | 4.433 | 137.435a | 2.000 | 62.000 | <.001 |
| 3 | Pillai's trace | .817 | 138.315a | 2.000 | 62.000 | <.001 |
| Wilks' lambda | .183 | 138.315a | 2.000 | 62.000 | <.001 |
| Hotelling's trace | 4.462 | 138.315a | 2.000 | 62.000 | <.001 |
| Roy's largest root | 4.462 | 138.315a | 2.000 | 62.000 | <.001 |
| Each F tests the multivariate simple effects of GENOTYPE [1 = WT; 2= A53T] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | | |
| a. Exact statistic | | | | | | |

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| **Univariate Tests** | | | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | | Sum of Squares | df | Mean Square | F | Sig. |
| TOTAL AST | 1 | Contrast | 247084.446 | 1 | 247084.446 | 60.822 | <.001 |
| Error | 255930.635 | 63 | 4062.391 |  |  |
| 2 | Contrast | 121680.067 | 1 | 121680.067 | 29.953 | <.001 |
| Error | 255930.635 | 63 | 4062.391 |  |  |
| 3 | Contrast | 77092.439 | 1 | 77092.439 | 18.977 | <.001 |
| Error | 255930.635 | 63 | 4062.391 |  |  |
| % with aSyn | 1 | Contrast | 8139.758 | 1 | 8139.758 | 139.844 | <.001 |
| Error | 3666.984 | 63 | 58.206 |  |  |
| 2 | Contrast | 9773.886 | 1 | 9773.886 | 167.919 | <.001 |
| Error | 3666.984 | 63 | 58.206 |  |  |
| 3 | Contrast | 10950.318 | 1 | 10950.318 | 188.130 | <.001 |
| Error | 3666.984 | 63 | 58.206 |  |  |
| Each F tests the simple effects of GENOTYPE [1 = WT; 2= A53T] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | | | |

**2. GENOTYPE [1 = WT; 2= A53T] \* REGION[1=SN; 2=VTA; 3=CP]**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Estimates** | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | Mean | Std. Error | 95% Confidence Interval |
| Lower Bound |
| TOTAL AST | 1 | 1 | 116.750 | 18.399 | 79.982 |
| 2 | 94.500 | 18.399 | 57.732 |
| 3 | 99.687 | 18.399 | 62.920 |
| 2 | 1 | 309.267 | 16.457 | 276.380 |
| 2 | 229.600 | 16.457 | 196.714 |
| 3 | 207.223 | 16.457 | 174.337 |
| % with aSyn | 1 | 1 | 29.599 | 2.202 | 25.198 |
| 2 | 22.864 | 2.202 | 18.462 |
| 3 | 25.485 | 2.202 | 21.084 |
| 2 | 1 | 64.541 | 1.970 | 60.605 |
| 2 | 61.153 | 1.970 | 57.217 |
| 3 | 66.013 | 1.970 | 62.077 |

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| --- | --- | --- | --- |
| **Estimates** | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval |
| Upper Bound |
| TOTAL AST | 1 | 1 | 153.518 |
| 2 | 131.268 |
| 3 | 136.455 |
| 2 | 1 | 342.153 |
| 2 | 262.486 |
| 3 | 240.109 |
| % with aSyn | 1 | 1 | 34.000 |
| 2 | 27.265 |
| 3 | 29.886 |
| 2 | 1 | 68.478 |
| 2 | 65.090 |
| 3 | 69.949 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | Mean Difference (I-J) |
|
| TOTAL AST | 1 | 1 | 2 | 22.250 |
| 3 | 17.063 |
| 2 | 1 | -22.250 |
| 3 | -5.188 |
| 3 | 1 | -17.063 |
| 2 | 5.188 |
| 2 | 1 | 2 | 79.667\* |
| 3 | 102.044\* |
| 2 | 1 | -79.667\* |
| 3 | 22.377 |
| 3 | 1 | -102.044\* |
| 2 | -22.377 |
| % with aSyn | 1 | 1 | 2 | 6.735\* |
| 3 | 4.114 |
| 2 | 1 | -6.735\* |
| 3 | -2.621 |
| 3 | 1 | -4.114 |
| 2 | 2.621 |
| 2 | 1 | 2 | 3.388 |
| 3 | -1.472 |
| 2 | 1 | -3.388 |
| 3 | -4.860 |
| 3 | 1 | 1.472 |
| 2 | 4.860 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | Std. Error |
|
| TOTAL AST | 1 | 1 | 2 | 26.020 |
| 3 | 26.020 |
| 2 | 1 | 26.020 |
| 3 | 26.020 |
| 3 | 1 | 26.020 |
| 2 | 26.020 |
| 2 | 1 | 2 | 23.273 |
| 3 | 23.273 |
| 2 | 1 | 23.273 |
| 3 | 23.273 |
| 3 | 1 | 23.273 |
| 2 | 23.273 |
| % with aSyn | 1 | 1 | 2 | 3.115 |
| 3 | 3.115 |
| 2 | 1 | 3.115 |
| 3 | 3.115 |
| 3 | 1 | 3.115 |
| 2 | 3.115 |
| 2 | 1 | 2 | 2.786 |
| 3 | 2.786 |
| 2 | 1 | 2.786 |
| 3 | 2.786 |
| 3 | 1 | 2.786 |
| 2 | 2.786 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | Sig.b |
|
| TOTAL AST | 1 | 1 | 2 | .396 |
| 3 | .514 |
| 2 | 1 | .396 |
| 3 | .843 |
| 3 | 1 | .514 |
| 2 | .843 |
| 2 | 1 | 2 | .001 |
| 3 | <.001 |
| 2 | 1 | .001 |
| 3 | .340 |
| 3 | 1 | <.001 |
| 2 | .340 |
| % with aSyn | 1 | 1 | 2 | .034 |
| 3 | .191 |
| 2 | 1 | .034 |
| 3 | .403 |
| 3 | 1 | .191 |
| 2 | .403 |
| 2 | 1 | 2 | .228 |
| 3 | .599 |
| 2 | 1 | .228 |
| 3 | .086 |
| 3 | 1 | .599 |
| 2 | .086 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval for Differenceb |
| Lower Bound |
| TOTAL AST | 1 | 1 | 2 | -29.748 |
| 3 | -34.935 |
| 2 | 1 | -74.248 |
| 3 | -57.185 |
| 3 | 1 | -69.060 |
| 2 | -46.810 |
| 2 | 1 | 2 | 33.158 |
| 3 | 55.536 |
| 2 | 1 | -126.175 |
| 3 | -24.131 |
| 3 | 1 | -148.552 |
| 2 | -68.885 |
| % with aSyn | 1 | 1 | 2 | .511 |
| 3 | -2.110 |
| 2 | 1 | -12.959 |
| 3 | -8.845 |
| 3 | 1 | -10.338 |
| 2 | -3.603 |
| 2 | 1 | 2 | -2.179 |
| 3 | -7.039 |
| 2 | 1 | -8.955 |
| 3 | -10.427 |
| 3 | 1 | -4.095 |
| 2 | -.707 |

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| **Pairwise Comparisons** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval for Difference |
| Upper Bound |
| TOTAL AST | 1 | 1 | 2 | 74.248 |
| 3 | 69.060 |
| 2 | 1 | 29.748 |
| 3 | 46.810 |
| 3 | 1 | 34.935 |
| 2 | 57.185 |
| 2 | 1 | 2 | 126.175 |
| 3 | 148.552 |
| 2 | 1 | -33.158 |
| 3 | 68.885 |
| 3 | 1 | -55.536 |
| 2 | 24.131 |
| % with aSyn | 1 | 1 | 2 | 12.959 |
| 3 | 10.338 |
| 2 | 1 | -.511 |
| 3 | 3.603 |
| 3 | 1 | 2.110 |
| 2 | 8.845 |
| 2 | 1 | 2 | 8.955 |
| 3 | 4.095 |
| 2 | 1 | 2.179 |
| 3 | .707 |
| 3 | 1 | 7.039 |
| 2 | 10.427 |
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| Based on estimated marginal means |
| \*. The mean difference is significant at the .05 level. |
| b. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments). |

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| **Multivariate Tests** | | | | | | |
| GENOTYPE [1 = WT; 2= A53T] | | Value | F | Hypothesis df | Error df | Sig. |
| 1 | Pillai's trace | .110 | 1.834 | 4.000 | 126.000 | .126 |
| Wilks' lambda | .890 | 1.860a | 4.000 | 124.000 | .122 |
| Hotelling's trace | .124 | 1.885 | 4.000 | 122.000 | .117 |
| Roy's largest root | .123 | 3.885b | 2.000 | 63.000 | .026 |
| 2 | Pillai's trace | .329 | 6.193 | 4.000 | 126.000 | <.001 |
| Wilks' lambda | .685 | 6.464a | 4.000 | 124.000 | <.001 |
| Hotelling's trace | .441 | 6.726 | 4.000 | 122.000 | <.001 |
| Roy's largest root | .391 | 12.332b | 2.000 | 63.000 | <.001 |
| Each F tests the multivariate simple effects of REGION[1=SN; 2=VTA; 3=CP] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | | |
| a. Exact statistic | | | | | | |
| b. The statistic is an upper bound on F that yields a lower bound on the significance level. | | | | | | |

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| **Univariate Tests** | | | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | | Sum of Squares | df | Mean Square | F | Sig. |
| TOTAL AST | 1 | Contrast | 3252.406 | 2 | 1626.203 | .400 | .672 |
| Error | 255930.635 | 63 | 4062.391 |  |  |
| 2 | Contrast | 86302.193 | 2 | 43151.096 | 10.622 | <.001 |
| Error | 255930.635 | 63 | 4062.391 |  |  |
| % with aSyn | 1 | Contrast | 276.649 | 2 | 138.324 | 2.376 | .101 |
| Error | 3666.984 | 63 | 58.206 |  |  |
| 2 | Contrast | 186.328 | 2 | 93.164 | 1.601 | .210 |
| Error | 3666.984 | 63 | 58.206 |  |  |
| Each F tests the simple effects of REGION[1=SN; 2=VTA; 3=CP] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | | | |

**3. GENOTYPE [1 = WT; 2= A53T] \* REGION[1=SN; 2=VTA; 3=CP] \* LOCATION (1=rostral; 2=mid; 3=caudal)**

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | Mean |
|
| TOTAL AST | 1 | 1 | 1 | 135.500 |
| 2 | 108.750 |
| 3 | 106.000 |
| 2 | 1 | 97.750 |
| 2 | 110.750 |
| 3 | 75.000 |
| 3 | 1 | 96.688 |
| 2 | 99.250 |
| 3 | 103.125 |
| 2 | 1 | 1 | 309.000 |
| 2 | 310.200 |
| 3 | 308.600 |
| 2 | 1 | 239.800 |
| 2 | 228.600 |
| 3 | 220.400 |
| 3 | 1 | 205.800 |
| 2 | 221.075 |
| 3 | 194.794 |
| % with aSyn | 1 | 1 | 1 | 28.362 |
| 2 | 31.113 |
| 3 | 29.322 |
| 2 | 1 | 23.297 |
| 2 | 21.552 |
| 3 | 23.742 |
| 3 | 1 | 24.177 |
| 2 | 26.155 |
| 3 | 26.122 |
| 2 | 1 | 1 | 62.666 |
| 2 | 66.808 |
| 3 | 64.149 |
| 2 | 1 | 67.727 |
| 2 | 61.434 |
| 3 | 54.298 |
| 3 | 1 | 64.907 |
| 2 | 63.959 |
| 3 | 69.173 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | Std. Error |
|
| TOTAL AST | 1 | 1 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 2 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 3 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 2 | 1 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| 2 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| 3 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| % with aSyn | 1 | 1 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 2 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 3 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 2 | 1 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |
| 2 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |
| 3 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | 95% Confidence Interval |
| Lower Bound |
| TOTAL AST | 1 | 1 | 1 | 71.816 |
| 2 | 45.066 |
| 3 | 42.316 |
| 2 | 1 | 34.066 |
| 2 | 47.066 |
| 3 | 11.316 |
| 3 | 1 | 33.003 |
| 2 | 35.566 |
| 3 | 39.441 |
| 2 | 1 | 1 | 252.039 |
| 2 | 253.239 |
| 3 | 251.639 |
| 2 | 1 | 182.839 |
| 2 | 171.639 |
| 3 | 163.439 |
| 3 | 1 | 148.839 |
| 2 | 164.114 |
| 3 | 137.833 |
| % with aSyn | 1 | 1 | 1 | 20.739 |
| 2 | 23.490 |
| 3 | 21.699 |
| 2 | 1 | 15.674 |
| 2 | 13.929 |
| 3 | 16.119 |
| 3 | 1 | 16.554 |
| 2 | 18.532 |
| 3 | 18.499 |
| 2 | 1 | 1 | 55.848 |
| 2 | 59.990 |
| 3 | 57.331 |
| 2 | 1 | 60.909 |
| 2 | 54.616 |
| 3 | 47.480 |
| 3 | 1 | 58.088 |
| 2 | 57.141 |
| 3 | 62.355 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | 95% Confidence Interval |
| Upper Bound |
| TOTAL AST | 1 | 1 | 1 | 199.184 |
| 2 | 172.434 |
| 3 | 169.684 |
| 2 | 1 | 161.434 |
| 2 | 174.434 |
| 3 | 138.684 |
| 3 | 1 | 160.372 |
| 2 | 162.934 |
| 3 | 166.809 |
| 2 | 1 | 1 | 365.961 |
| 2 | 367.161 |
| 3 | 365.561 |
| 2 | 1 | 296.761 |
| 2 | 285.561 |
| 3 | 277.361 |
| 3 | 1 | 262.761 |
| 2 | 278.036 |
| 3 | 251.754 |
| % with aSyn | 1 | 1 | 1 | 35.985 |
| 2 | 38.736 |
| 3 | 36.945 |
| 2 | 1 | 30.920 |
| 2 | 29.175 |
| 3 | 31.365 |
| 3 | 1 | 31.800 |
| 2 | 33.778 |
| 3 | 33.745 |
| 2 | 1 | 1 | 69.484 |
| 2 | 73.626 |
| 3 | 70.968 |
| 2 | 1 | 74.545 |
| 2 | 68.252 |
| 3 | 61.116 |
| 3 | 1 | 71.725 |
| 2 | 70.778 |
| 3 | 75.991 |

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| --- | --- | --- | --- | --- |
| **Pairwise Comparisons** | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] |
|
| TOTAL AST | 1 | 1 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 2 |
| 2 | 1 |
| % with aSyn | 1 | 1 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 1 | 2 |
| 2 | 1 |
| 2 | 1 | 2 |
| 2 | 1 |
| 3 | 1 | 2 |
| 2 | 1 |

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| **Pairwise Comparisons** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | Mean Difference (I-J) |
|
| TOTAL AST | 1 | 1 | 1 | 2 | -173.500\* |
| 2 | 1 | 173.500\* |
| 2 | 1 | 2 | -201.450\* |
| 2 | 1 | 201.450\* |
| 3 | 1 | 2 | -202.600\* |
| 2 | 1 | 202.600\* |
| 2 | 1 | 1 | 2 | -142.050\* |
| 2 | 1 | 142.050\* |
| 2 | 1 | 2 | -117.850\* |
| 2 | 1 | 117.850\* |
| 3 | 1 | 2 | -145.400\* |
| 2 | 1 | 145.400\* |
| 3 | 1 | 1 | 2 | -109.113\* |
| 2 | 1 | 109.113\* |
| 2 | 1 | 2 | -121.825\* |
| 2 | 1 | 121.825\* |
| 3 | 1 | 2 | -91.669\* |
| 2 | 1 | 91.669\* |
| % with aSyn | 1 | 1 | 1 | 2 | -34.304\* |
| 2 | 1 | 34.304\* |
| 2 | 1 | 2 | -35.695\* |
| 2 | 1 | 35.695\* |
| 3 | 1 | 2 | -34.827\* |
| 2 | 1 | 34.827\* |
| 2 | 1 | 1 | 2 | -44.430\* |
| 2 | 1 | 44.430\* |
| 2 | 1 | 2 | -39.882\* |
| 2 | 1 | 39.882\* |
| 3 | 1 | 2 | -30.557\* |
| 2 | 1 | 30.557\* |
| 3 | 1 | 1 | 2 | -40.729\* |
| 2 | 1 | 40.729\* |
| 2 | 1 | 2 | -37.805\* |
| 2 | 1 | 37.805\* |
| 3 | 1 | 2 | -43.051\* |
| 2 | 1 | 43.051\* |

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| **Pairwise Comparisons** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | Std. Error |
|
| TOTAL AST | 1 | 1 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 2 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 3 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 2 | 1 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 2 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 3 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 3 | 1 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 2 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| 3 | 1 | 2 | 42.756 |
| 2 | 1 | 42.756 |
| % with aSyn | 1 | 1 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 2 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 3 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 2 | 1 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 2 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 3 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 3 | 1 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 2 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |
| 3 | 1 | 2 | 5.118 |
| 2 | 1 | 5.118 |

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| --- | --- | --- | --- | --- | --- |
| **Pairwise Comparisons** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | Sig.b |
|
| TOTAL AST | 1 | 1 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 3 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 1 | 2 | .001 |
| 2 | 1 | .001 |
| 2 | 1 | 2 | .008 |
| 2 | 1 | .008 |
| 3 | 1 | 2 | .001 |
| 2 | 1 | .001 |
| 3 | 1 | 1 | 2 | .013 |
| 2 | 1 | .013 |
| 2 | 1 | 2 | .006 |
| 2 | 1 | .006 |
| 3 | 1 | 2 | .036 |
| 2 | 1 | .036 |
| % with aSyn | 1 | 1 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 3 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 3 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 3 | 1 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 2 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |
| 3 | 1 | 2 | <.001 |
| 2 | 1 | <.001 |

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| **Pairwise Comparisons** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | 95% Confidence Interval for Differenceb |
| Lower Bound |
| TOTAL AST | 1 | 1 | 1 | 2 | -258.941 |
| 2 | 1 | 88.059 |
| 2 | 1 | 2 | -286.891 |
| 2 | 1 | 116.009 |
| 3 | 1 | 2 | -288.041 |
| 2 | 1 | 117.159 |
| 2 | 1 | 1 | 2 | -227.491 |
| 2 | 1 | 56.609 |
| 2 | 1 | 2 | -203.291 |
| 2 | 1 | 32.409 |
| 3 | 1 | 2 | -230.841 |
| 2 | 1 | 59.959 |
| 3 | 1 | 1 | 2 | -194.554 |
| 2 | 1 | 23.671 |
| 2 | 1 | 2 | -207.266 |
| 2 | 1 | 36.384 |
| 3 | 1 | 2 | -177.110 |
| 2 | 1 | 6.228 |
| % with aSyn | 1 | 1 | 1 | 2 | -44.532 |
| 2 | 1 | 24.077 |
| 2 | 1 | 2 | -45.922 |
| 2 | 1 | 25.468 |
| 3 | 1 | 2 | -45.055 |
| 2 | 1 | 24.600 |
| 2 | 1 | 1 | 2 | -54.657 |
| 2 | 1 | 34.203 |
| 2 | 1 | 2 | -50.109 |
| 2 | 1 | 29.655 |
| 3 | 1 | 2 | -40.784 |
| 2 | 1 | 20.329 |
| 3 | 1 | 1 | 2 | -50.957 |
| 2 | 1 | 30.502 |
| 2 | 1 | 2 | -48.032 |
| 2 | 1 | 27.577 |
| 3 | 1 | 2 | -53.278 |
| 2 | 1 | 32.824 |

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| **Pairwise Comparisons** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | (I) GENOTYPE [1 = WT; 2= A53T] | (J) GENOTYPE [1 = WT; 2= A53T] | 95% Confidence Interval for Difference |
| Upper Bound |
| TOTAL AST | 1 | 1 | 1 | 2 | -88.059 |
| 2 | 1 | 258.941 |
| 2 | 1 | 2 | -116.009 |
| 2 | 1 | 286.891 |
| 3 | 1 | 2 | -117.159 |
| 2 | 1 | 288.041 |
| 2 | 1 | 1 | 2 | -56.609 |
| 2 | 1 | 227.491 |
| 2 | 1 | 2 | -32.409 |
| 2 | 1 | 203.291 |
| 3 | 1 | 2 | -59.959 |
| 2 | 1 | 230.841 |
| 3 | 1 | 1 | 2 | -23.671 |
| 2 | 1 | 194.554 |
| 2 | 1 | 2 | -36.384 |
| 2 | 1 | 207.266 |
| 3 | 1 | 2 | -6.228 |
| 2 | 1 | 177.110 |
| % with aSyn | 1 | 1 | 1 | 2 | -24.077 |
| 2 | 1 | 44.532 |
| 2 | 1 | 2 | -25.468 |
| 2 | 1 | 45.922 |
| 3 | 1 | 2 | -24.600 |
| 2 | 1 | 45.055 |
| 2 | 1 | 1 | 2 | -34.203 |
| 2 | 1 | 54.657 |
| 2 | 1 | 2 | -29.655 |
| 2 | 1 | 50.109 |
| 3 | 1 | 2 | -20.329 |
| 2 | 1 | 40.784 |
| 3 | 1 | 1 | 2 | -30.502 |
| 2 | 1 | 50.957 |
| 2 | 1 | 2 | -27.577 |
| 2 | 1 | 48.032 |
| 3 | 1 | 2 | -32.824 |
| 2 | 1 | 53.278 |
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| Based on estimated marginal means |
| \*. The mean difference is significant at the .05 level. |
| b. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments). |

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| **Multivariate Tests** | | | | | | |
| REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Value | F | Hypothesis df | Error df |
| 1 | 1 | Pillai's trace | .590 | 44.629a | 2.000 | 62.000 |
| Wilks' lambda | .410 | 44.629a | 2.000 | 62.000 |
| Hotelling's trace | 1.440 | 44.629a | 2.000 | 62.000 |
| Roy's largest root | 1.440 | 44.629a | 2.000 | 62.000 |
| 2 | Pillai's trace | .627 | 52.061a | 2.000 | 62.000 |
| Wilks' lambda | .373 | 52.061a | 2.000 | 62.000 |
| Hotelling's trace | 1.679 | 52.061a | 2.000 | 62.000 |
| Roy's largest root | 1.679 | 52.061a | 2.000 | 62.000 |
| 3 | Pillai's trace | .620 | 50.665a | 2.000 | 62.000 |
| Wilks' lambda | .380 | 50.665a | 2.000 | 62.000 |
| Hotelling's trace | 1.634 | 50.665a | 2.000 | 62.000 |
| Roy's largest root | 1.634 | 50.665a | 2.000 | 62.000 |
| 2 | 1 | Pillai's trace | .656 | 59.200a | 2.000 | 62.000 |
| Wilks' lambda | .344 | 59.200a | 2.000 | 62.000 |
| Hotelling's trace | 1.910 | 59.200a | 2.000 | 62.000 |
| Roy's largest root | 1.910 | 59.200a | 2.000 | 62.000 |
| 2 | Pillai's trace | .599 | 46.305a | 2.000 | 62.000 |
| Wilks' lambda | .401 | 46.305a | 2.000 | 62.000 |
| Hotelling's trace | 1.494 | 46.305a | 2.000 | 62.000 |
| Roy's largest root | 1.494 | 46.305a | 2.000 | 62.000 |
| 3 | Pillai's trace | .524 | 34.085a | 2.000 | 62.000 |
| Wilks' lambda | .476 | 34.085a | 2.000 | 62.000 |
| Hotelling's trace | 1.100 | 34.085a | 2.000 | 62.000 |
| Roy's largest root | 1.100 | 34.085a | 2.000 | 62.000 |
| 3 | 1 | Pillai's trace | .601 | 46.707a | 2.000 | 62.000 |
| Wilks' lambda | .399 | 46.707a | 2.000 | 62.000 |
| Hotelling's trace | 1.507 | 46.707a | 2.000 | 62.000 |
| Roy's largest root | 1.507 | 46.707a | 2.000 | 62.000 |
| 2 | Pillai's trace | .581 | 42.995a | 2.000 | 62.000 |
| Wilks' lambda | .419 | 42.995a | 2.000 | 62.000 |
| Hotelling's trace | 1.387 | 42.995a | 2.000 | 62.000 |
| Roy's largest root | 1.387 | 42.995a | 2.000 | 62.000 |
| 3 | Pillai's trace | .612 | 48.910a | 2.000 | 62.000 |
| Wilks' lambda | .388 | 48.910a | 2.000 | 62.000 |
| Hotelling's trace | 1.578 | 48.910a | 2.000 | 62.000 |
| Roy's largest root | 1.578 | 48.910a | 2.000 | 62.000 |

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| **Multivariate Tests** | | | |
| REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Sig. |
| 1 | 1 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 2 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 3 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 2 | 1 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 2 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 3 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 3 | 1 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 2 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
| 3 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | <.001 |
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| Each F tests the multivariate simple effects of GENOTYPE [1 = WT; 2= A53T] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. |
| a. Exact statistic |

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| **Univariate Tests** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Sum of Squares | df |
| TOTAL AST | 1 | 1 | Contrast | 66893.889 | 1 |
| Error | 255930.635 | 63 |
| 2 | Contrast | 90182.450 | 1 |
| Error | 255930.635 | 63 |
| 3 | Contrast | 91215.022 | 1 |
| Error | 255930.635 | 63 |
| 2 | 1 | Contrast | 44840.450 | 1 |
| Error | 255930.635 | 63 |
| 2 | Contrast | 30863.606 | 1 |
| Error | 255930.635 | 63 |
| 3 | Contrast | 46980.356 | 1 |
| Error | 255930.635 | 63 |
| 3 | 1 | Contrast | 26456.750 | 1 |
| Error | 255930.635 | 63 |
| 2 | Contrast | 32980.735 | 1 |
| Error | 255930.635 | 63 |
| 3 | Contrast | 18673.688 | 1 |
| Error | 255930.635 | 63 |
| % with aSyn | 1 | 1 | Contrast | 2615.103 | 1 |
| Error | 3666.984 | 63 |
| 2 | Contrast | 2831.401 | 1 |
| Error | 3666.984 | 63 |
| 3 | Contrast | 2695.447 | 1 |
| Error | 3666.984 | 63 |
| 2 | 1 | Contrast | 4386.710 | 1 |
| Error | 3666.984 | 63 |
| 2 | Contrast | 3534.599 | 1 |
| Error | 3666.984 | 63 |
| 3 | Contrast | 2074.888 | 1 |
| Error | 3666.984 | 63 |
| 3 | 1 | Contrast | 3686.408 | 1 |
| Error | 3666.984 | 63 |
| 2 | Contrast | 3175.981 | 1 |
| Error | 3666.984 | 63 |
| 3 | Contrast | 4118.647 | 1 |
| Error | 3666.984 | 63 |

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| **Univariate Tests** | | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Mean Square | F |
| TOTAL AST | 1 | 1 | Contrast | 66893.889 | 16.467 |
| Error | 4062.391 |  |
| 2 | Contrast | 90182.450 | 22.199 |
| Error | 4062.391 |  |
| 3 | Contrast | 91215.022 | 22.454 |
| Error | 4062.391 |  |
| 2 | 1 | Contrast | 44840.450 | 11.038 |
| Error | 4062.391 |  |
| 2 | Contrast | 30863.606 | 7.597 |
| Error | 4062.391 |  |
| 3 | Contrast | 46980.356 | 11.565 |
| Error | 4062.391 |  |
| 3 | 1 | Contrast | 26456.750 | 6.513 |
| Error | 4062.391 |  |
| 2 | Contrast | 32980.735 | 8.119 |
| Error | 4062.391 |  |
| 3 | Contrast | 18673.688 | 4.597 |
| Error | 4062.391 |  |
| % with aSyn | 1 | 1 | Contrast | 2615.103 | 44.928 |
| Error | 58.206 |  |
| 2 | Contrast | 2831.401 | 48.644 |
| Error | 58.206 |  |
| 3 | Contrast | 2695.447 | 46.309 |
| Error | 58.206 |  |
| 2 | 1 | Contrast | 4386.710 | 75.365 |
| Error | 58.206 |  |
| 2 | Contrast | 3534.599 | 60.726 |
| Error | 58.206 |  |
| 3 | Contrast | 2074.888 | 35.647 |
| Error | 58.206 |  |
| 3 | 1 | Contrast | 3686.408 | 63.334 |
| Error | 58.206 |  |
| 2 | Contrast | 3175.981 | 54.564 |
| Error | 58.206 |  |
| 3 | Contrast | 4118.647 | 70.760 |
| Error | 58.206 |  |

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| **Univariate Tests** | | | | |
| Dependent Variable | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Sig. |
| TOTAL AST | 1 | 1 | Contrast | <.001 |
| Error |  |
| 2 | Contrast | <.001 |
| Error |  |
| 3 | Contrast | <.001 |
| Error |  |
| 2 | 1 | Contrast | .001 |
| Error |  |
| 2 | Contrast | .008 |
| Error |  |
| 3 | Contrast | .001 |
| Error |  |
| 3 | 1 | Contrast | .013 |
| Error |  |
| 2 | Contrast | .006 |
| Error |  |
| 3 | Contrast | .036 |
| Error |  |
| % with aSyn | 1 | 1 | Contrast | <.001 |
| Error |  |
| 2 | Contrast | <.001 |
| Error |  |
| 3 | Contrast | <.001 |
| Error |  |
| 2 | 1 | Contrast | <.001 |
| Error |  |
| 2 | Contrast | <.001 |
| Error |  |
| 3 | Contrast | <.001 |
| Error |  |
| 3 | 1 | Contrast | <.001 |
| Error |  |
| 2 | Contrast | <.001 |
| Error |  |
| 3 | Contrast | <.001 |
| Error |  |
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| Each F tests the simple effects of GENOTYPE [1 = WT; 2= A53T] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. |

**4. GENOTYPE [1 = WT; 2= A53T] \* REGION[1=SN; 2=VTA; 3=CP] \* LOCATION (1=rostral; 2=mid; 3=caudal)**

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | Mean |
|
| TOTAL AST | 1 | 1 | 1 | 135.500 |
| 2 | 108.750 |
| 3 | 106.000 |
| 2 | 1 | 97.750 |
| 2 | 110.750 |
| 3 | 75.000 |
| 3 | 1 | 96.688 |
| 2 | 99.250 |
| 3 | 103.125 |
| 2 | 1 | 1 | 309.000 |
| 2 | 310.200 |
| 3 | 308.600 |
| 2 | 1 | 239.800 |
| 2 | 228.600 |
| 3 | 220.400 |
| 3 | 1 | 205.800 |
| 2 | 221.075 |
| 3 | 194.794 |
| % with aSyn | 1 | 1 | 1 | 28.362 |
| 2 | 31.113 |
| 3 | 29.322 |
| 2 | 1 | 23.297 |
| 2 | 21.552 |
| 3 | 23.742 |
| 3 | 1 | 24.177 |
| 2 | 26.155 |
| 3 | 26.122 |
| 2 | 1 | 1 | 62.666 |
| 2 | 66.808 |
| 3 | 64.149 |
| 2 | 1 | 67.727 |
| 2 | 61.434 |
| 3 | 54.298 |
| 3 | 1 | 64.907 |
| 2 | 63.959 |
| 3 | 69.173 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | Std. Error |
|
| TOTAL AST | 1 | 1 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 2 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 3 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 2 | 1 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| 2 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| 3 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| % with aSyn | 1 | 1 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 2 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 3 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 2 | 1 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |
| 2 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |
| 3 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | 95% Confidence Interval |
| Lower Bound |
| TOTAL AST | 1 | 1 | 1 | 71.816 |
| 2 | 45.066 |
| 3 | 42.316 |
| 2 | 1 | 34.066 |
| 2 | 47.066 |
| 3 | 11.316 |
| 3 | 1 | 33.003 |
| 2 | 35.566 |
| 3 | 39.441 |
| 2 | 1 | 1 | 252.039 |
| 2 | 253.239 |
| 3 | 251.639 |
| 2 | 1 | 182.839 |
| 2 | 171.639 |
| 3 | 163.439 |
| 3 | 1 | 148.839 |
| 2 | 164.114 |
| 3 | 137.833 |
| % with aSyn | 1 | 1 | 1 | 20.739 |
| 2 | 23.490 |
| 3 | 21.699 |
| 2 | 1 | 15.674 |
| 2 | 13.929 |
| 3 | 16.119 |
| 3 | 1 | 16.554 |
| 2 | 18.532 |
| 3 | 18.499 |
| 2 | 1 | 1 | 55.848 |
| 2 | 59.990 |
| 3 | 57.331 |
| 2 | 1 | 60.909 |
| 2 | 54.616 |
| 3 | 47.480 |
| 3 | 1 | 58.088 |
| 2 | 57.141 |
| 3 | 62.355 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | 95% Confidence Interval |
| Upper Bound |
| TOTAL AST | 1 | 1 | 1 | 199.184 |
| 2 | 172.434 |
| 3 | 169.684 |
| 2 | 1 | 161.434 |
| 2 | 174.434 |
| 3 | 138.684 |
| 3 | 1 | 160.372 |
| 2 | 162.934 |
| 3 | 166.809 |
| 2 | 1 | 1 | 365.961 |
| 2 | 367.161 |
| 3 | 365.561 |
| 2 | 1 | 296.761 |
| 2 | 285.561 |
| 3 | 277.361 |
| 3 | 1 | 262.761 |
| 2 | 278.036 |
| 3 | 251.754 |
| % with aSyn | 1 | 1 | 1 | 35.985 |
| 2 | 38.736 |
| 3 | 36.945 |
| 2 | 1 | 30.920 |
| 2 | 29.175 |
| 3 | 31.365 |
| 3 | 1 | 31.800 |
| 2 | 33.778 |
| 3 | 33.745 |
| 2 | 1 | 1 | 69.484 |
| 2 | 73.626 |
| 3 | 70.968 |
| 2 | 1 | 74.545 |
| 2 | 68.252 |
| 3 | 61.116 |
| 3 | 1 | 71.725 |
| 2 | 70.778 |
| 3 | 75.991 |

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| **Pairwise Comparisons** | | | | | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | LOCATION (1=rostral; 2=mid; 3=caudal) | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | Mean Difference (I-J) | Std. Error | Sig.b | 95% Confidence Interval for Differenceb | |
| Lower Bound | Upper Bound |
| TOTAL AST | 1 | 1 | 1 | 2 | 37.750 | 45.069 | .405 | -52.313 | 127.813 |
| 3 | 38.812 | 45.069 | .392 | -51.250 | 128.875 |
| 2 | 1 | -37.750 | 45.069 | .405 | -127.813 | 52.313 |
| 3 | 1.062 | 45.069 | .981 | -89.000 | 91.125 |
| 3 | 1 | -38.812 | 45.069 | .392 | -128.875 | 51.250 |
| 2 | -1.062 | 45.069 | .981 | -91.125 | 89.000 |
| 2 | 1 | 2 | -2.000 | 45.069 | .965 | -92.063 | 88.063 |
| 3 | 9.500 | 45.069 | .834 | -80.563 | 99.563 |
| 2 | 1 | 2.000 | 45.069 | .965 | -88.063 | 92.063 |
| 3 | 11.500 | 45.069 | .799 | -78.563 | 101.563 |
| 3 | 1 | -9.500 | 45.069 | .834 | -99.563 | 80.563 |
| 2 | -11.500 | 45.069 | .799 | -101.563 | 78.563 |
| 3 | 1 | 2 | 31.000 | 45.069 | .494 | -59.063 | 121.063 |
| 3 | 2.875 | 45.069 | .949 | -87.188 | 92.938 |
| 2 | 1 | -31.000 | 45.069 | .494 | -121.063 | 59.063 |
| 3 | -28.125 | 45.069 | .535 | -118.188 | 61.938 |
| 3 | 1 | -2.875 | 45.069 | .949 | -92.938 | 87.188 |
| 2 | 28.125 | 45.069 | .535 | -61.938 | 118.188 |
| 2 | 1 | 1 | 2 | 69.200 | 40.311 | .091 | -11.355 | 149.755 |
| 3 | 103.200\* | 40.311 | .013 | 22.645 | 183.755 |
| 2 | 1 | -69.200 | 40.311 | .091 | -149.755 | 11.355 |
| 3 | 34.000 | 40.311 | .402 | -46.555 | 114.555 |
| 3 | 1 | -103.200\* | 40.311 | .013 | -183.755 | -22.645 |
| 2 | -34.000 | 40.311 | .402 | -114.555 | 46.555 |
| 2 | 1 | 2 | 81.600\* | 40.311 | .047 | 1.045 | 162.155 |
| 3 | 89.125\* | 40.311 | .031 | 8.570 | 169.680 |
| 2 | 1 | -81.600\* | 40.311 | .047 | -162.155 | -1.045 |
| 3 | 7.525 | 40.311 | .853 | -73.030 | 88.080 |
| 3 | 1 | -89.125\* | 40.311 | .031 | -169.680 | -8.570 |
| 2 | -7.525 | 40.311 | .853 | -88.080 | 73.030 |
| 3 | 1 | 2 | 88.200\* | 40.311 | .032 | 7.645 | 168.755 |
| 3 | 113.806\* | 40.311 | .006 | 33.252 | 194.361 |
| 2 | 1 | -88.200\* | 40.311 | .032 | -168.755 | -7.645 |
| 3 | 25.606 | 40.311 | .528 | -54.948 | 106.161 |
| 3 | 1 | -113.806\* | 40.311 | .006 | -194.361 | -33.252 |
| 2 | -25.606 | 40.311 | .528 | -106.161 | 54.948 |
| % with aSyn | 1 | 1 | 1 | 2 | 5.065 | 5.395 | .351 | -5.716 | 15.845 |
| 3 | 4.185 | 5.395 | .441 | -6.596 | 14.965 |
| 2 | 1 | -5.065 | 5.395 | .351 | -15.845 | 5.716 |
| 3 | -.880 | 5.395 | .871 | -11.661 | 9.900 |
| 3 | 1 | -4.185 | 5.395 | .441 | -14.965 | 6.596 |
| 2 | .880 | 5.395 | .871 | -9.900 | 11.661 |
| 2 | 1 | 2 | 9.561 | 5.395 | .081 | -1.220 | 20.341 |
| 3 | 4.958 | 5.395 | .362 | -5.822 | 15.739 |
| 2 | 1 | -9.561 | 5.395 | .081 | -20.341 | 1.220 |
| 3 | -4.603 | 5.395 | .397 | -15.383 | 6.178 |
| 3 | 1 | -4.958 | 5.395 | .362 | -15.739 | 5.822 |
| 2 | 4.603 | 5.395 | .397 | -6.178 | 15.383 |
| 3 | 1 | 2 | 5.580 | 5.395 | .305 | -5.200 | 16.361 |
| 3 | 3.200 | 5.395 | .555 | -7.581 | 13.980 |
| 2 | 1 | -5.580 | 5.395 | .305 | -16.361 | 5.200 |
| 3 | -2.380 | 5.395 | .661 | -13.161 | 8.400 |
| 3 | 1 | -3.200 | 5.395 | .555 | -13.980 | 7.581 |
| 2 | 2.380 | 5.395 | .661 | -8.400 | 13.161 |
| 2 | 1 | 1 | 2 | -5.061 | 4.825 | .298 | -14.703 | 4.582 |
| 3 | -2.240 | 4.825 | .644 | -11.883 | 7.402 |
| 2 | 1 | 5.061 | 4.825 | .298 | -4.582 | 14.703 |
| 3 | 2.820 | 4.825 | .561 | -6.822 | 12.463 |
| 3 | 1 | 2.240 | 4.825 | .644 | -7.402 | 11.883 |
| 2 | -2.820 | 4.825 | .561 | -12.463 | 6.822 |
| 2 | 1 | 2 | 5.374 | 4.825 | .270 | -4.269 | 15.016 |
| 3 | 2.848 | 4.825 | .557 | -6.794 | 12.491 |
| 2 | 1 | -5.374 | 4.825 | .270 | -15.016 | 4.269 |
| 3 | -2.525 | 4.825 | .603 | -12.168 | 7.117 |
| 3 | 1 | -2.848 | 4.825 | .557 | -12.491 | 6.794 |
| 2 | 2.525 | 4.825 | .603 | -7.117 | 12.168 |
| 3 | 1 | 2 | 9.851\* | 4.825 | .045 | .209 | 19.494 |
| 3 | -5.024 | 4.825 | .302 | -14.666 | 4.619 |
| 2 | 1 | -9.851\* | 4.825 | .045 | -19.494 | -.209 |
| 3 | -14.875\* | 4.825 | .003 | -24.517 | -5.233 |
| 3 | 1 | 5.024 | 4.825 | .302 | -4.619 | 14.666 |
| 2 | 14.875\* | 4.825 | .003 | 5.233 | 24.517 |
| Based on estimated marginal means | | | | | | | | | |
| \*. The mean difference is significant at the .05 level. | | | | | | | | | |
| b. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments). | | | | | | | | | |

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| **Multivariate Tests** | | | | | | |
| GENOTYPE [1 = WT; 2= A53T] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Value | F | Hypothesis df | Error df |
| 1 | 1 | Pillai's trace | .045 | .729 | 4.000 | 126.000 |
| Wilks' lambda | .955 | .725a | 4.000 | 124.000 |
| Hotelling's trace | .047 | .722 | 4.000 | 122.000 |
| Roy's largest root | .047 | 1.485b | 2.000 | 63.000 |
| 2 | Pillai's trace | .054 | .875 | 4.000 | 126.000 |
| Wilks' lambda | .946 | .872a | 4.000 | 124.000 |
| Hotelling's trace | .057 | .869 | 4.000 | 122.000 |
| Roy's largest root | .056 | 1.759b | 2.000 | 63.000 |
| 3 | Pillai's trace | .037 | .592 | 4.000 | 126.000 |
| Wilks' lambda | .963 | .587a | 4.000 | 124.000 |
| Hotelling's trace | .038 | .583 | 4.000 | 122.000 |
| Roy's largest root | .037 | 1.165b | 2.000 | 63.000 |
| 2 | 1 | Pillai's trace | .111 | 1.849 | 4.000 | 126.000 |
| Wilks' lambda | .890 | 1.854a | 4.000 | 124.000 |
| Hotelling's trace | .122 | 1.858 | 4.000 | 122.000 |
| Roy's largest root | .109 | 3.446b | 2.000 | 63.000 |
| 2 | Pillai's trace | .138 | 2.337 | 4.000 | 126.000 |
| Wilks' lambda | .862 | 2.382a | 4.000 | 124.000 |
| Hotelling's trace | .159 | 2.424 | 4.000 | 122.000 |
| Roy's largest root | .155 | 4.883b | 2.000 | 63.000 |
| 3 | Pillai's trace | .281 | 5.141 | 4.000 | 126.000 |
| Wilks' lambda | .738 | 5.096a | 4.000 | 124.000 |
| Hotelling's trace | .331 | 5.051 | 4.000 | 122.000 |
| Roy's largest root | .219 | 6.885b | 2.000 | 63.000 |

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| **Multivariate Tests** | | | |
| GENOTYPE [1 = WT; 2= A53T] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Sig. |
| 1 | 1 | Pillai's trace | .574 |
| Wilks' lambda | .576 |
| Hotelling's trace | .579 |
| Roy's largest root | .234 |
| 2 | Pillai's trace | .481 |
| Wilks' lambda | .483 |
| Hotelling's trace | .484 |
| Roy's largest root | .181 |
| 3 | Pillai's trace | .669 |
| Wilks' lambda | .672 |
| Hotelling's trace | .676 |
| Roy's largest root | .318 |
| 2 | 1 | Pillai's trace | .124 |
| Wilks' lambda | .123 |
| Hotelling's trace | .122 |
| Roy's largest root | .038 |
| 2 | Pillai's trace | .059 |
| Wilks' lambda | .055 |
| Hotelling's trace | .052 |
| Roy's largest root | .011 |
| 3 | Pillai's trace | <.001 |
| Wilks' lambda | <.001 |
| Hotelling's trace | <.001 |
| Roy's largest root | .002 |
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| Each F tests the multivariate simple effects of REGION[1=SN; 2=VTA; 3=CP] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. |
| a. Exact statistic |
| b. The statistic is an upper bound on F that yields a lower bound on the significance level. |

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| **Univariate Tests** | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Sum of Squares | df |
| TOTAL AST | 1 | 1 | Contrast | 3910.135 | 2 |
| Error | 255930.635 | 63 |
| 2 | Contrast | 302.000 | 2 |
| Error | 255930.635 | 63 |
| 3 | Contrast | 2347.042 | 2 |
| Error | 255930.635 | 63 |
| 2 | 1 | Contrast | 27658.133 | 2 |
| Error | 255930.635 | 63 |
| 2 | Contrast | 24430.752 | 2 |
| Error | 255930.635 | 63 |
| 3 | Contrast | 35644.638 | 2 |
| Error | 255930.635 | 63 |
| % with aSyn | 1 | 1 | Contrast | 58.586 | 2 |
| Error | 3666.984 | 63 |
| 2 | Contrast | 182.902 | 2 |
| Error | 3666.984 | 63 |
| 3 | Contrast | 62.729 | 2 |
| Error | 3666.984 | 63 |
| 2 | 1 | Contrast | 64.304 | 2 |
| Error | 3666.984 | 63 |
| 2 | Contrast | 72.282 | 2 |
| Error | 3666.984 | 63 |
| 3 | Contrast | 572.582 | 2 |
| Error | 3666.984 | 63 |

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| **Univariate Tests** | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Mean Square | F |
| TOTAL AST | 1 | 1 | Contrast | 1955.068 | .481 |
| Error | 4062.391 |  |
| 2 | Contrast | 151.000 | .037 |
| Error | 4062.391 |  |
| 3 | Contrast | 1173.521 | .289 |
| Error | 4062.391 |  |
| 2 | 1 | Contrast | 13829.067 | 3.404 |
| Error | 4062.391 |  |
| 2 | Contrast | 12215.376 | 3.007 |
| Error | 4062.391 |  |
| 3 | Contrast | 17822.319 | 4.387 |
| Error | 4062.391 |  |
| % with aSyn | 1 | 1 | Contrast | 29.293 | .503 |
| Error | 58.206 |  |
| 2 | Contrast | 91.451 | 1.571 |
| Error | 58.206 |  |
| 3 | Contrast | 31.364 | .539 |
| Error | 58.206 |  |
| 2 | 1 | Contrast | 32.152 | .552 |
| Error | 58.206 |  |
| 2 | Contrast | 36.141 | .621 |
| Error | 58.206 |  |
| 3 | Contrast | 286.291 | 4.919 |
| Error | 58.206 |  |

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| **Univariate Tests** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | LOCATION (1=rostral; 2=mid; 3=caudal) | | Sig. |
| TOTAL AST | 1 | 1 | Contrast | .620 |
| Error |  |
| 2 | Contrast | .964 |
| Error |  |
| 3 | Contrast | .750 |
| Error |  |
| 2 | 1 | Contrast | .039 |
| Error |  |
| 2 | Contrast | .057 |
| Error |  |
| 3 | Contrast | .016 |
| Error |  |
| % with aSyn | 1 | 1 | Contrast | .607 |
| Error |  |
| 2 | Contrast | .216 |
| Error |  |
| 3 | Contrast | .586 |
| Error |  |
| 2 | 1 | Contrast | .578 |
| Error |  |
| 2 | Contrast | .541 |
| Error |  |
| 3 | Contrast | .010 |
| Error |  |
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| Each F tests the simple effects of REGION[1=SN; 2=VTA; 3=CP] within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. |

**5. GENOTYPE [1 = WT; 2= A53T] \* REGION[1=SN; 2=VTA; 3=CP] \* LOCATION (1=rostral; 2=mid; 3=caudal)**

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | Mean |
|
| TOTAL AST | 1 | 1 | 1 | 135.500 |
| 2 | 108.750 |
| 3 | 106.000 |
| 2 | 1 | 97.750 |
| 2 | 110.750 |
| 3 | 75.000 |
| 3 | 1 | 96.688 |
| 2 | 99.250 |
| 3 | 103.125 |
| 2 | 1 | 1 | 309.000 |
| 2 | 310.200 |
| 3 | 308.600 |
| 2 | 1 | 239.800 |
| 2 | 228.600 |
| 3 | 220.400 |
| 3 | 1 | 205.800 |
| 2 | 221.075 |
| 3 | 194.794 |
| % with aSyn | 1 | 1 | 1 | 28.362 |
| 2 | 31.113 |
| 3 | 29.322 |
| 2 | 1 | 23.297 |
| 2 | 21.552 |
| 3 | 23.742 |
| 3 | 1 | 24.177 |
| 2 | 26.155 |
| 3 | 26.122 |
| 2 | 1 | 1 | 62.666 |
| 2 | 66.808 |
| 3 | 64.149 |
| 2 | 1 | 67.727 |
| 2 | 61.434 |
| 3 | 54.298 |
| 3 | 1 | 64.907 |
| 2 | 63.959 |
| 3 | 69.173 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | Std. Error |
|
| TOTAL AST | 1 | 1 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 2 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 3 | 1 | 31.868 |
| 2 | 31.868 |
| 3 | 31.868 |
| 2 | 1 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| 2 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| 3 | 1 | 28.504 |
| 2 | 28.504 |
| 3 | 28.504 |
| % with aSyn | 1 | 1 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 2 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 3 | 1 | 3.815 |
| 2 | 3.815 |
| 3 | 3.815 |
| 2 | 1 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |
| 2 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |
| 3 | 1 | 3.412 |
| 2 | 3.412 |
| 3 | 3.412 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | 95% Confidence Interval |
| Lower Bound |
| TOTAL AST | 1 | 1 | 1 | 71.816 |
| 2 | 45.066 |
| 3 | 42.316 |
| 2 | 1 | 34.066 |
| 2 | 47.066 |
| 3 | 11.316 |
| 3 | 1 | 33.003 |
| 2 | 35.566 |
| 3 | 39.441 |
| 2 | 1 | 1 | 252.039 |
| 2 | 253.239 |
| 3 | 251.639 |
| 2 | 1 | 182.839 |
| 2 | 171.639 |
| 3 | 163.439 |
| 3 | 1 | 148.839 |
| 2 | 164.114 |
| 3 | 137.833 |
| % with aSyn | 1 | 1 | 1 | 20.739 |
| 2 | 23.490 |
| 3 | 21.699 |
| 2 | 1 | 15.674 |
| 2 | 13.929 |
| 3 | 16.119 |
| 3 | 1 | 16.554 |
| 2 | 18.532 |
| 3 | 18.499 |
| 2 | 1 | 1 | 55.848 |
| 2 | 59.990 |
| 3 | 57.331 |
| 2 | 1 | 60.909 |
| 2 | 54.616 |
| 3 | 47.480 |
| 3 | 1 | 58.088 |
| 2 | 57.141 |
| 3 | 62.355 |

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| **Estimates** | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | LOCATION (1=rostral; 2=mid; 3=caudal) | 95% Confidence Interval |
| Upper Bound |
| TOTAL AST | 1 | 1 | 1 | 199.184 |
| 2 | 172.434 |
| 3 | 169.684 |
| 2 | 1 | 161.434 |
| 2 | 174.434 |
| 3 | 138.684 |
| 3 | 1 | 160.372 |
| 2 | 162.934 |
| 3 | 166.809 |
| 2 | 1 | 1 | 365.961 |
| 2 | 367.161 |
| 3 | 365.561 |
| 2 | 1 | 296.761 |
| 2 | 285.561 |
| 3 | 277.361 |
| 3 | 1 | 262.761 |
| 2 | 278.036 |
| 3 | 251.754 |
| % with aSyn | 1 | 1 | 1 | 35.985 |
| 2 | 38.736 |
| 3 | 36.945 |
| 2 | 1 | 30.920 |
| 2 | 29.175 |
| 3 | 31.365 |
| 3 | 1 | 31.800 |
| 2 | 33.778 |
| 3 | 33.745 |
| 2 | 1 | 1 | 69.484 |
| 2 | 73.626 |
| 3 | 70.968 |
| 2 | 1 | 74.545 |
| 2 | 68.252 |
| 3 | 61.116 |
| 3 | 1 | 71.725 |
| 2 | 70.778 |
| 3 | 75.991 |

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| **Pairwise Comparisons** | | | | | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | (I) LOCATION (1=rostral; 2=mid; 3=caudal) | (J) LOCATION (1=rostral; 2=mid; 3=caudal) | Mean Difference (I-J) | Std. Error | Sig.b | 95% Confidence Interval for Differenceb | |
| Lower Bound | Upper Bound |
| TOTAL AST | 1 | 1 | 1 | 2 | 26.750 | 45.069 | .555 | -63.313 | 116.813 |
| 3 | 29.500 | 45.069 | .515 | -60.563 | 119.563 |
| 2 | 1 | -26.750 | 45.069 | .555 | -116.813 | 63.313 |
| 3 | 2.750 | 45.069 | .952 | -87.313 | 92.813 |
| 3 | 1 | -29.500 | 45.069 | .515 | -119.563 | 60.563 |
| 2 | -2.750 | 45.069 | .952 | -92.813 | 87.313 |
| 2 | 1 | 2 | -13.000 | 45.069 | .774 | -103.063 | 77.063 |
| 3 | 22.750 | 45.069 | .615 | -67.313 | 112.813 |
| 2 | 1 | 13.000 | 45.069 | .774 | -77.063 | 103.063 |
| 3 | 35.750 | 45.069 | .431 | -54.313 | 125.813 |
| 3 | 1 | -22.750 | 45.069 | .615 | -112.813 | 67.313 |
| 2 | -35.750 | 45.069 | .431 | -125.813 | 54.313 |
| 3 | 1 | 2 | -2.563 | 45.069 | .955 | -92.625 | 87.500 |
| 3 | -6.437 | 45.069 | .887 | -96.500 | 83.625 |
| 2 | 1 | 2.563 | 45.069 | .955 | -87.500 | 92.625 |
| 3 | -3.875 | 45.069 | .932 | -93.938 | 86.188 |
| 3 | 1 | 6.437 | 45.069 | .887 | -83.625 | 96.500 |
| 2 | 3.875 | 45.069 | .932 | -86.188 | 93.938 |
| 2 | 1 | 1 | 2 | -1.200 | 40.311 | .976 | -81.755 | 79.355 |
| 3 | .400 | 40.311 | .992 | -80.155 | 80.955 |
| 2 | 1 | 1.200 | 40.311 | .976 | -79.355 | 81.755 |
| 3 | 1.600 | 40.311 | .968 | -78.955 | 82.155 |
| 3 | 1 | -.400 | 40.311 | .992 | -80.955 | 80.155 |
| 2 | -1.600 | 40.311 | .968 | -82.155 | 78.955 |
| 2 | 1 | 2 | 11.200 | 40.311 | .782 | -69.355 | 91.755 |
| 3 | 19.400 | 40.311 | .632 | -61.155 | 99.955 |
| 2 | 1 | -11.200 | 40.311 | .782 | -91.755 | 69.355 |
| 3 | 8.200 | 40.311 | .839 | -72.355 | 88.755 |
| 3 | 1 | -19.400 | 40.311 | .632 | -99.955 | 61.155 |
| 2 | -8.200 | 40.311 | .839 | -88.755 | 72.355 |
| 3 | 1 | 2 | -15.275 | 40.311 | .706 | -95.830 | 65.280 |
| 3 | 11.006 | 40.311 | .786 | -69.548 | 91.561 |
| 2 | 1 | 15.275 | 40.311 | .706 | -65.280 | 95.830 |
| 3 | 26.281 | 40.311 | .517 | -54.273 | 106.836 |
| 3 | 1 | -11.006 | 40.311 | .786 | -91.561 | 69.548 |
| 2 | -26.281 | 40.311 | .517 | -106.836 | 54.273 |
| % with aSyn | 1 | 1 | 1 | 2 | -2.751 | 5.395 | .612 | -13.532 | 8.029 |
| 3 | -.960 | 5.395 | .859 | -11.741 | 9.820 |
| 2 | 1 | 2.751 | 5.395 | .612 | -8.029 | 13.532 |
| 3 | 1.791 | 5.395 | .741 | -8.990 | 12.571 |
| 3 | 1 | .960 | 5.395 | .859 | -9.820 | 11.741 |
| 2 | -1.791 | 5.395 | .741 | -12.571 | 8.990 |
| 2 | 1 | 2 | 1.745 | 5.395 | .747 | -9.036 | 12.525 |
| 3 | -.445 | 5.395 | .935 | -11.225 | 10.336 |
| 2 | 1 | -1.745 | 5.395 | .747 | -12.525 | 9.036 |
| 3 | -2.190 | 5.395 | .686 | -12.970 | 8.591 |
| 3 | 1 | .445 | 5.395 | .935 | -10.336 | 11.225 |
| 2 | 2.190 | 5.395 | .686 | -8.591 | 12.970 |
| 3 | 1 | 2 | -1.978 | 5.395 | .715 | -12.758 | 8.803 |
| 3 | -1.945 | 5.395 | .720 | -12.725 | 8.836 |
| 2 | 1 | 1.978 | 5.395 | .715 | -8.803 | 12.758 |
| 3 | .033 | 5.395 | .995 | -10.748 | 10.813 |
| 3 | 1 | 1.945 | 5.395 | .720 | -8.836 | 12.725 |
| 2 | -.033 | 5.395 | .995 | -10.813 | 10.748 |
| 2 | 1 | 1 | 2 | -4.142 | 4.825 | .394 | -13.784 | 5.501 |
| 3 | -1.483 | 4.825 | .760 | -11.126 | 8.159 |
| 2 | 1 | 4.142 | 4.825 | .394 | -5.501 | 13.784 |
| 3 | 2.658 | 4.825 | .584 | -6.984 | 12.301 |
| 3 | 1 | 1.483 | 4.825 | .760 | -8.159 | 11.126 |
| 2 | -2.658 | 4.825 | .584 | -12.301 | 6.984 |
| 2 | 1 | 2 | 6.293 | 4.825 | .197 | -3.350 | 15.935 |
| 3 | 13.429\* | 4.825 | .007 | 3.786 | 23.071 |
| 2 | 1 | -6.293 | 4.825 | .197 | -15.935 | 3.350 |
| 3 | 7.136 | 4.825 | .144 | -2.506 | 16.778 |
| 3 | 1 | -13.429\* | 4.825 | .007 | -23.071 | -3.786 |
| 2 | -7.136 | 4.825 | .144 | -16.778 | 2.506 |
| 3 | 1 | 2 | .947 | 4.825 | .845 | -8.695 | 10.589 |
| 3 | -4.267 | 4.825 | .380 | -13.909 | 5.376 |
| 2 | 1 | -.947 | 4.825 | .845 | -10.589 | 8.695 |
| 3 | -5.214 | 4.825 | .284 | -14.856 | 4.429 |
| 3 | 1 | 4.267 | 4.825 | .380 | -5.376 | 13.909 |
| 2 | 5.214 | 4.825 | .284 | -4.429 | 14.856 |
| Based on estimated marginal means | | | | | | | | | |
| \*. The mean difference is significant at the .05 level. | | | | | | | | | |
| b. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments). | | | | | | | | | |

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| **Multivariate Tests** | | | | | | | |
| GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | | Value | F | Hypothesis df | Error df | Sig. |
| 1 | 1 | Pillai's trace | .011 | .172 | 4.000 | 126.000 | .952 |
| Wilks' lambda | .989 | .170a | 4.000 | 124.000 | .954 |
| Hotelling's trace | .011 | .167 | 4.000 | 122.000 | .955 |
| Roy's largest root | .009 | .273b | 2.000 | 63.000 | .762 |
| 2 | Pillai's trace | .011 | .175 | 4.000 | 126.000 | .951 |
| Wilks' lambda | .989 | .173a | 4.000 | 124.000 | .952 |
| Hotelling's trace | .011 | .170 | 4.000 | 122.000 | .953 |
| Roy's largest root | .010 | .329b | 2.000 | 63.000 | .721 |
| 3 | Pillai's trace | .004 | .065 | 4.000 | 126.000 | .992 |
| Wilks' lambda | .996 | .064a | 4.000 | 124.000 | .992 |
| Hotelling's trace | .004 | .063 | 4.000 | 122.000 | .993 |
| Roy's largest root | .004 | .127b | 2.000 | 63.000 | .881 |
| 2 | 1 | Pillai's trace | .014 | .219 | 4.000 | 126.000 | .927 |
| Wilks' lambda | .986 | .216a | 4.000 | 124.000 | .929 |
| Hotelling's trace | .014 | .214 | 4.000 | 122.000 | .930 |
| Roy's largest root | .014 | .441b | 2.000 | 63.000 | .645 |
| 2 | Pillai's trace | .138 | 2.336 | 4.000 | 126.000 | .059 |
| Wilks' lambda | .862 | 2.390a | 4.000 | 124.000 | .054 |
| Hotelling's trace | .160 | 2.442 | 4.000 | 122.000 | .050 |
| Roy's largest root | .160 | 5.043b | 2.000 | 63.000 | .009 |
| 3 | Pillai's trace | .023 | .362 | 4.000 | 126.000 | .836 |
| Wilks' lambda | .977 | .357a | 4.000 | 124.000 | .838 |
| Hotelling's trace | .023 | .353 | 4.000 | 122.000 | .841 |
| Roy's largest root | .022 | .686b | 2.000 | 63.000 | .507 |
| Each F tests the multivariate simple effects of LOCATION (1=rostral; 2=mid; 3=caudal) within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. | | | | | | | |
| a. Exact statistic | | | | | | | |
| b. The statistic is an upper bound on F that yields a lower bound on the significance level. | | | | | | | |

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| **Univariate Tests** | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | | Sum of Squares | df |
| TOTAL AST | 1 | 1 | Contrast | 2124.500 | 2 |
| Error | 255930.635 | 63 |
| 2 | Contrast | 2619.500 | 2 |
| Error | 255930.635 | 63 |
| 3 | Contrast | 84.031 | 2 |
| Error | 255930.635 | 63 |
| 2 | 1 | Contrast | 6.933 | 2 |
| Error | 255930.635 | 63 |
| 2 | Contrast | 948.400 | 2 |
| Error | 255930.635 | 63 |
| 3 | Contrast | 1741.945 | 2 |
| Error | 255930.635 | 63 |
| % with aSyn | 1 | 1 | Contrast | 15.597 | 2 |
| Error | 3666.984 | 63 |
| 2 | Contrast | 10.715 | 2 |
| Error | 3666.984 | 63 |
| 3 | Contrast | 10.260 | 2 |
| Error | 3666.984 | 63 |
| 2 | 1 | Contrast | 44.032 | 2 |
| Error | 3666.984 | 63 |
| 2 | Contrast | 451.422 | 2 |
| Error | 3666.984 | 63 |
| 3 | Contrast | 77.137 | 2 |
| Error | 3666.984 | 63 |

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| **Univariate Tests** | | | | | | | | |
| Dependent Variable | GENOTYPE [1 = WT; 2= A53T] | REGION[1=SN; 2=VTA; 3=CP] | | Mean Square | F | | Sig. | |
| TOTAL AST | 1 | 1 | Contrast | 1062.250 | .261 | | .771 | |
| Error | 4062.391 |  | |  | |
| 2 | Contrast | 1309.750 | .322 | | .726 | |
| Error | 4062.391 |  | |  | |
| 3 | Contrast | 42.016 | .010 | | .990 | |
| Error | 4062.391 |  | |  | |
| 2 | 1 | Contrast | 3.467 | .001 | | .999 | |
| Error | 4062.391 |  | |  | |
| 2 | Contrast | 474.200 | .117 | | .890 | |
| Error | 4062.391 |  | |  | |
| 3 | Contrast | 870.973 | .214 | | .808 | |
| Error | 4062.391 |  | |  | |
| % with aSyn | 1 | 1 | Contrast | 7.798 | .134 | | .875 | |
| Error | 58.206 |  | |  | |
| 2 | Contrast | 5.357 | .092 | | .912 | |
| Error | 58.206 |  | |  | |
| 3 | Contrast | 5.130 | .088 | | .916 | |
| Error | 58.206 |  | |  | |
| 2 | 1 | Contrast | 22.016 | .378 | | .687 | |
| Error | 58.206 |  | |  | |
| 2 | Contrast | 225.711 | 3.878 | | .026 | |
| Error | 58.206 |  | |  | |
| 3 | Contrast | 38.569 | .663 | | .519 | |
| Error | 58.206 |  | |  | |
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| Each F tests the simple effects of LOCATION (1=rostral; 2=mid; 3=caudal) within each level combination of the other effects shown. These tests are based on the linearly independent pairwise comparisons among the estimated marginal means. |

**Post Hoc Tests**

**REGION[1=SN; 2=VTA; 3=CP]**

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| **Multiple Comparisons** | | | | | |
| Tukey HSD | | | | | |
| Dependent Variable | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | Mean Difference (I-J) | Std. Error | Sig. |
|
| TOTAL AST | 1 | 2 | 54.1481481\* | 17.34698401 | .008 |
| 3 | 64.2743056\* | 17.34698401 | .001 |
| 2 | 1 | -54.1481481\* | 17.34698401 | .008 |
| 3 | 10.1261574 | 17.34698401 | .829 |
| 3 | 1 | -64.2743056\* | 17.34698401 | .001 |
| 2 | -10.1261574 | 17.34698401 | .829 |
| % with aSyn | 1 | 2 | 4.875812659921991 | 2.076430249338069 | .056 |
| 3 | 1.010882750516913 | 2.076430249338069 | .878 |
| 2 | 1 | -4.875812659921991 | 2.076430249338069 | .056 |
| 3 | -3.864929909405078 | 2.076430249338069 | .158 |
| 3 | 1 | -1.010882750516913 | 2.076430249338069 | .878 |
| 2 | 3.864929909405078 | 2.076430249338069 | .158 |

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| **Multiple Comparisons** | | | | |
| Tukey HSD | | | | |
| Dependent Variable | (I) REGION[1=SN; 2=VTA; 3=CP] | (J) REGION[1=SN; 2=VTA; 3=CP] | 95% Confidence Interval | |
| Lower Bound | Upper Bound |
| TOTAL AST | 1 | 2 | 12.5097374 | 95.7865589 |
| 3 | 22.6358948 | 105.9127163 |
| 2 | 1 | -95.7865589 | -12.5097374 |
| 3 | -31.5122533 | 51.7645681 |
| 3 | 1 | -105.9127163 | -22.6358948 |
| 2 | -51.7645681 | 31.5122533 |
| % with aSyn | 1 | 2 | -.108296133949056 | 9.859921453793037 |
| 3 | -3.973226043354133 | 5.994991544387959 |
| 2 | 1 | -9.859921453793037 | .108296133949056 |
| 3 | -8.849038703276124 | 1.119178884465969 |
| 3 | 1 | -5.994991544387959 | 3.973226043354133 |
| 2 | -1.119178884465969 | 8.849038703276124 |
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| Based on observed means. The error term is Mean Square(Error) = 58.206. |
| \*. The mean difference is significant at the .05 level. |

**Homogeneous Subsets**

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| **TOTAL AST** | | | |
| Tukey HSDa,b | | | |
| REGION[1=SN; 2=VTA; 3=CP] | N | Subset | |
| 1 | 2 |
| 3 | 27 | 159.4293981 |  |
| 2 | 27 | 169.5555556 |  |
| 1 | 27 |  | 223.7037037 |
| Sig. |  | .829 | 1.000 |
| Means for groups in homogeneous subsets are displayed. Based on observed means. The error term is Mean Square(Error) = 4062.391. | | | |
| a. Uses Harmonic Mean Sample Size = 27.000. | | | |
| b. Alpha = .05. | | | |

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| **% with aSyn** | | |
| Tukey HSDa,b | | |
| REGION[1=SN; 2=VTA; 3=CP] | N | Subset |
| 1 |
| 2 | 27 | 44.135485062114450 |
| 3 | 27 | 48.000414971519525 |
| 1 | 27 | 49.011297722036440 |
| Sig. |  | .056 |
| Means for groups in homogeneous subsets are displayed. Based on observed means. The error term is Mean Square(Error) = 58.206. | | |
| a. Uses Harmonic Mean Sample Size = 27.000. | | |
| b. Alpha = .05. | | |

**Profile Plots**

**TOTAL AST**

img.eps

**% with aSyn**

img.eps