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31 Abstract

| 32 | Despite advances in the understanding of the reward system and the role of |
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| 33 | dopamine in recent decades, the heredity of the underlying neural mechanisms is |
| 34 | not known. In the present study, a Monetary Incentive Delay (MID) task was used to |
| 35 | examine the haemodynamic activation of the nucleus accumbens (NAcc), a key hub |
| 36 | of the reward system, in 86 healthy monozygotic twins and 88 dizygotic twins during |
| 37 | the anticipation of monetary incentives. The participants also completed self-report |
| 38 | measures of pleasure experience. Using a voxel-wise heritability mapping method, |
| 39 | activation of the bilateral NAcc during the anticipation of monetary gains was found |
| 40 | to have significant heritability (h^2 = 0.20-0.49). Moreover, significant shared genetic |
| 41 | covariance was observed between pleasure experience and NAcc activation when |
| 42 | anticipating monetary gain. These findings suggest that NAcc activation and self- |
| 43 | reported pleasure experience may both be heritable, and their phenotypic |
| 44 | correlation may be partially explained by shared genetic variation. |
| 45 | |

46 **Keywords**: Reward System, Nucleus Accumbens, Heritability, Motivation, Pleasure

47 Introduction

| 48 | The reward system plays a key role in human behaviour and emotion (<i>Iversen, 2010</i>). |
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| 49 | The nucleus accumbens (NAcc), situated in the ventral striatum, is regarded as the |
| 50 | hub of the mesolimbic and mesocortical reward systems (Baldo & Kelley, 2007; |
| 51 | Berridge & Robinson, 1998; Haber & Knutson, 2010). However, the contribution of |
| 52 | the NAcc to reward processing is not fully understood. Compelling evidence supports |
| 53 | the notion that the reward processing system can be parsed into anticipatory and |
| 54 | consummatory phases (Baldo & Kelley, 2007; Craig, 1917). Dopaminergic activity in |
| 55 | the NAcc is associated with salience attribution of motivation, which assigns |
| 56 | motivational significance to different incentives in the anticipatory period (Berridge, |
| 57 | 2003, 2007, 2012). Despite these advances in understanding the reward system, the |
| 58 | heritability of reward processing and its component phenotypes are largely unknown. |
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| 59 | Studies in the last decade have suggested a relationship between dopaminergic |
| 59 60 | Studies in the last decade have suggested a relationship between dopaminergic gene variation and ventral striatal activation measured by functional MRI reward |
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| 60 | gene variation and ventral striatal activation measured by functional MRI reward |
| 60 61 | gene variation and ventral striatal activation measured by functional MRI reward tasks in anticipating, predicting, or receiving monetary incentives (<i>Aarts et al., 2010;</i> |
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| 60 61 62 63 | gene variation and ventral striatal activation measured by functional MRI reward tasks in anticipating, predicting, or receiving monetary incentives (<i>Aarts et al., 2010;</i> <i>Dreher, Kohn, Kolachana, Weinberger, & Berman, 2009; Forbes et al., 2009; Hahn et</i> <i>al., 2011; Nikolova, Ferrell, Manuck, & Hariri, 2011; Yacubian et al., 2007</i>). Although |
| 60 61 62 63 64 | gene variation and ventral striatal activation measured by functional MRI reward tasks in anticipating, predicting, or receiving monetary incentives (<i>Aarts et al., 2010;</i> <i>Dreher, Kohn, Kolachana, Weinberger, & Berman, 2009; Forbes et al., 2009; Hahn et</i> <i>al., 2011; Nikolova, Ferrell, Manuck, & Hariri, 2011; Yacubian et al., 2007</i>). Although single genetic polymorphisms have been associated with ventral striatal activation to |
| 60 61 62 63 64 65 | gene variation and ventral striatal activation measured by functional MRI reward tasks in anticipating, predicting, or receiving monetary incentives (<i>Aarts et al., 2010;</i> <i>Dreher, Kohn, Kolachana, Weinberger, & Berman, 2009; Forbes et al., 2009; Hahn et</i> <i>al., 2011; Nikolova, Ferrell, Manuck, & Hariri, 2011; Yacubian et al., 2007</i>). Although single genetic polymorphisms have been associated with ventral striatal activation to a modest extent, studies that examine single or few polymorphisms, are seldom |
| 60 61 62 63 64 65 66 | gene variation and ventral striatal activation measured by functional MRI reward tasks in anticipating, predicting, or receiving monetary incentives (<i>Aarts et al., 2010;</i> <i>Dreher, Kohn, Kolachana, Weinberger, & Berman, 2009; Forbes et al., 2009; Hahn et</i> <i>al., 2011; Nikolova, Ferrell, Manuck, & Hariri, 2011; Yacubian et al., 2007</i>). Although single genetic polymorphisms have been associated with ventral striatal activation to a modest extent, studies that examine single or few polymorphisms, are seldom replicated and tend to be underpowered. Evidence from the Psychiatric Genomics |

aggregating the effects of all polymorphisms, or to examine family-based genetic
variation. The prediction of ventral striatal activation using polygenic risk scores for
psychosis has already revealed the cumulative effect of genes (*Bossong & Kahn*, *2016; Lancaster et al., 2016*), and it is expected that related component phenotypes
are similarly polygenic. However, the extent to which genetic factors influence *NAcc*and ventral striatal brain activation, particularly in the anticipatory period for reward,
is not clearly understood.

77 In this study, we examined measures of shared genetic variance among 78 dimensional psychiatric phenotypes, using a voxel-wise topographical approach to 79 map striatal activation. While previous studies have mainly employed regions of 80 interest methodology, voxel-wise analysis affords much finer heritability mapping, 81 thereby reducing statistical noise in heritability estimation. Hypoactivation of the 82 NAcc and the ventral striatum in anticipating monetary rewards had been reported 83 both in patients with schizophrenia (Radua et al., 2015) and in their unaffected 84 biological relatives. Probands and biological relatives also exhibit increased 85 anhedonia that co-segregates in families (Docherty, Sponheim, & Kerns, 2015; 86 Kendler, Thacker, & Walsh, 1996; Li et al., 2015). These results suggest that impaired 87 motivation is associated with genetic factors underlying schizophrenia (*de Leeuw*, 88 Kahn, & Vink, 2015; Grimm et al., 2014; Vink et al., 2016). Thus, mapping the 89 heritability of brain activation in anticipating and approaching reward may help 90 clarify its potential role as an endophenotype for psychosis (Braff, Freedman, Schork, 91 & Gottesman, 2007; Gottesman & Gould, 2003).

92 Another important matter to consider is the similar ventral striatal dysfunction

| 93 | reported in patients with major depressive disorder, addiction, and their family |
|-----|---|
| 94 | members (Beck et al., 2009; Knutson, Bhanji, Cooney, Atlas, & Gotlib, 2008; Pizzagalli |
| 95 | et al., 2009; Wrase et al., 2007). Since anhedonia and motivational deficits are also |
| 96 | relevant to major depressive disorder, the problem of non-specificity needs to be |
| 97 | addressed. This study aims to examine the circuitry and behavioral manifestations of |
| 98 | dimensional clinical traits, in line with Research Domain Criteria (RDoC) (Cuthbert, |
| 99 | 2014; Cuthbert & Insel, 2010). |
| 100 | Anhedonia, the diminished ability to experience pleasure, has long been regarded |
| 101 | as a core symptom of schizophrenia and major depression disorder (Meehl, 1975; |
| 102 | Meehl, 1990; Pizzagalli, 2014). Cumulative evidence has also demonstrated a |
| 103 | significant heritability estimate for anhedonia ranging from 0.3 to 0.7 (Kendler & |
| 104 | Hewitt, 1992; Linney et al., 2003; MacDonald, Pogue-Geile, Debski, & Manuck, 2001). |
| 105 | Although previous findings support an association between motivation-related NAcc |
| 106 | activation and anhedonia traits (Vignapiano et al., 2016; Wacker, Dillon, & Pizzagalli, |
| 107 | 2009), their shared genetic covariance has not been examined. investigating the |
| 108 | heritability of NAcc activation and anhedonia could facilitate the identification of |
| 109 | shared regions of the genome and the exploration of intervention for amotivation |
| 110 | and anhedonia, both of which indicate poor prognosis and are refractory to currently |
| 111 | available treatment (Kring & Barch, 2014). |
| 112 | In the present study, we adopted a healthy-twin design to examine the heritability |
| 113 | of pleasure experience and its shared genetic covariance with NAcc activation during |
| 114 | the anticipation of monetary rewards using the Monetary Incentive Delay Task (MID) |

114 the anticipation of monetary rewards using the Monetary Incentive Delay Task (MID).

115 We hypothesized that both motivation-related *NAcc* activation and pleasure

- 116 experience would exhibit significant heritability. We further hypothesized that
- 117 motivation-related *NAcc* activation and pleasure experience would share significant
- 118 genetic covariance.

119

120 **Results**

121 **Demographics**

- 122 The sample included 43 pairs of same-sex monozygotic (MZ) twins and 44 pairs of
- same-sex dizygotic (DZ) twins, who were matched in gender ratio, age, and years of
- 124 education. In addition, their head motion parameters were also comparable (Table
- 125 1). The MZ and DZ twins demonstrated comparable scores on the Temporal
- 126 Experience Pleasure Scale (TEPS), whereas DZ twins scored lower than MZ twins on
- 127 the revised Chinese versions of Chapman Social Anhedonia Scale (RCSAS) and
- 128 Chapman Physical Anhedonia Scale (RCPAS). The ICC of RCPAS and TEPS scores
- among the MZ twins were twice that of the DZ twins. However, the ICC of RCSAS
- 130 scores among MZ and DZ twins did not significantly vary from 0 (Table 1). These
- 131 findings suggest that in this healthy sample, there was insufficient power to detect
- 132 significant genetic or phenotypic variation in RCSAS scores.
- 133

134 Brain activation in contrast [Gain vs. No-incentive] of MID task

- 135 For this contrast, during the anticipatory phase, there was significant activation of
- the bilateral *NAcc* and the thalamus in all participants. Activation of the bilateral

- 137 NAcc was also observed in MZ and DZ twins respectively. Furthermore, activation of
- the left insula was observed in MZ twins, whereas activation of the right insula was
- 139 observed in DZ twins (Table 2 & Figure 1B).
- 140

141 Brain activation in contrast [Loss vs. No-incentive] of MID task

- 142 Significant activation of the bilateral *NAcc* and the thalamus were observed in the
- 143 contrast [Loss vs. No-incentive] during the anticipatory phase in all participants.
- 144 Significant activation of the bilateral *NAcc* was observed in both MZ and DZ twins,
- 145 while activation of the left globus pallidus and the right thalamus was observed in
- 146 MZ twins and DZ twins respectively (Table 2 & Figure 1B).

147

148 Heritability brain mapping

- 149 In the voxel-by-voxel heritability brain mapping, two clusters were detected with
- 150 significant heritability in the contrast [Gain vs. No-incentive]. The right one contained
- 151 33 voxels, while the left one contained 15 voxels. The coordinates of the peak point
- 152 of the two clusters were [9,15,-3] and [-9,18,-6], which were located at the right
- 153 *NAcc* and the left *NAcc* respectively (Figure 3). The h^2 of each voxel within both
- 154 clusters ranged from 0.2 to 0.49, and the average h^2 was 0.34 (Figure 3). However,
- 155 we did not find any significant heritability for the contrast [Loss vs. No-incentive].

156

157 Genetic model fitting

| 158 | As shown in Table 3, the Cholesky trivariate model (AIC = 382.4) was not worse than |
|-----|--|
| 159 | the saturated model (AIC = 406.45) (Δ - 2LL = 41.94, Δ df = 33, p = 0.14). The nested |
| 160 | sub-models were compared with the trivariate model. A marginally significant |
| 161 | deterioration emerged when all the additive genetic paths (a11, a12, a13, a22, a23, |
| 162 | a33) were deleted (Δ – 2LL = 12.59, Δ df = 6, <i>p</i> = 0.05), whereas the model did not |
| 163 | worsen when we discarded all the common environmental paths (c11, c12, c13, c22, |
| 164 | c23, c33) (Δ - 2LL = 0.25, Δ df = 6, p = 1). Results of model comparison indicated that |
| 165 | additive genetic factors, rather than common environmental factors, significantly |
| 166 | contributed to the full model. The trivariate AE model (AIC = 370.65) was adopted |
| 167 | for the subsequent parameter dropping and model comparison. After dropping one |
| 168 | path, Model X (with path e21 dropped) was found to have the smallest AIC (368.66) |
| 169 | in its class and was hence adopted (Δ – 2LL = 0.01, Δ df = 1, p = 0.94). Based on Model |
| 170 | X, a second path was further discarded. Finally, Model XV (with paths e21 and e31 |
| 171 | dropped) had the smallest AIC (367.35) among all the tested models and was |
| 172 | selected as the best model (Δ - 2LL = 0.69, Δ df = 1, p = 0.4). A third path was further |
| 173 | dropped based on Model XV, but all the sub-models significantly deteriorated |
| 174 | compared with Model XV. |
| 175 | In the best-fitting Model XV (Figure 4), the h^2 of bilateral NAcc activation during |
| 176 | the anticipation of monetary gain was 0.43 [95% Confidential Interval (CI): 0.19-0.62], |

177 the h^2 of RCPAS scores was 0.61 (95%CI: 0.39-0.75), and the h^2 of TEPS scores was

178 0.29 (95%CI: 0.01-0.54). NAcc activation shared the same genes with RCPAS ($r_g = -$

179 0.45) and TEPS (r_g = 0.59) scores. In addition, scores on the RCPAS and the TEPS were

also influenced by some of the same genes ($r_g = -0.72$). Addictive genetic factors

| 181 | contributed almost 100% to the phenotypic correlation between NAcc activation and |
|-----|--|
| 182 | RCPAS scores (r_{ph} = -0.23, $r_{ph(g)}$ = -0.23) and between NAcc activation and TEPS scores |
| 183 | ($r_{ph} = 0.21$, $r_{ph(g)} = 0.21$). Sixty-four percent of the phenotypic correlation between |
| 184 | RCPAS and TEPS scores (r_{ph} = -0.47) was attributed to additive genetic factors ($r_{ph(g)}$ = |
| 185 | -0.3), while 36% of the correlation was attributed to environmental factors ($r_{ph(e)}$ = - |
| 186 | 0.17). |

187

188 Discussion

| 189 | This is the first biometrical study to examine the heritability of neural substrates |
|-----|--|
| 190 | underlying reward processing and the shared genetic covariance of motivation- |
| 191 | related NAcc activation and pleasure experience. Consistent with our hypothesis, |
| 192 | activation in the bilateral NAcc during the anticipation of monetary gain was |
| 193 | significantly heritable. The heritability estimate of each voxel within the bilateral |
| 194 | NAcc, while low-to moderate, was significant and ranged from 0.2 to 0.49, whilst the |
| 195 | heritability estimate of NAcc activation as a whole was 0.43. RCPAS and the TEPS also |
| 196 | exhibited significant heritability in healthy twins, at 0.61 and 0.29 respectively. Even |
| 197 | with a modest sample size for ACE modeling, motivation-related NAcc activation |
| 198 | evidenced significant shared genetic covariation with both self-reported measures of |
| 199 | pleasure experience. This suggests that the significant phenotypic correlation |
| 200 | between NAcc activation and pleasure experience is partially accounted for by |
| 201 | shared genetic variation. |
| | |

202 Bilateral *NAcc* activation during the anticipatory phase for monetary incentives,

| 203 | found in our whole brain analysis, is consistent with previous findings (Knutson, Fong, |
|-----|--|
| 204 | Adams, Varner, & Hommer, 2001; Knutson & Greer, 2008; Knutson, Westdorp, Kaiser, |
| 205 | & Hommer, 2000), which supports the validity of the MID task in correlating with |
| 206 | NAcc activation in vivo. Evidence from animal studies supports the role of dopamine |
| 207 | within the NAcc in salience attribution, an essential component of motivation and |
| 208 | goal-directed behaviour formulation (Berridge, 2007, 2012; Berridge & Robinson, |
| 209 | 1998). Although fMRI measures brain haemodynamics rather than neurotransmitter |
| 210 | chemistry, previous studies have linked activation at the NAcc and the ventral |
| 211 | striatum in rewarding tasks to local dopaminergic activity. Amphetamine-induced |
| 212 | dopamine release at the NAcc has been associated with local haemodynamic |
| 213 | activation in reward processing (Knutson & Gibbs, 2007; Oswald et al., 2007). These |
| 214 | data suggest that NAcc activation measured through fMRI could indirectly reflect |
| 215 | local dopaminergic activity. In addition, polymorphisms of dopamine have been |
| 216 | associated with ventral striatal activation in reward processing, suggesting that |
| 217 | facets of the mesolimbic reward system may be heritable (Dreher et al., 2009; Forbes |
| 218 | et al., 2009; Yacubian et al., 2007). Indeed, significant MZ twin correlation in NAcc |
| 219 | activation has previously been reported (Silverman et al., 2014). In the present study, |
| 220 | we corroborated previous findings through quantifying the genetic and |
| 221 | environmental effects on the motivation-related NAcc activation. Stokes and |
| 222 | colleagues (2013) reported a significant heritability estimate of 0.21 for |
| 223 | dopaminergic activities of the right ventral striatum in the resting state. In this study, |
| 224 | we found a heritability estimate of 0.4 for bilateral NAcc activation in anticipating |
| 225 | monetary gains. The considerably larger sample size in this study, relative to |

226 previous research, lends further support to this finding.

| 227 | Quantifying the heritability of NAcc activation in anticipating monetary incentives |
|------|---|
| 228 | could facilitate our understanding of the genetic effect on reward processing and |
| 229 | detection of associated genetic loci. Voxel-wise heritability estimation is an |
| 230 | alternative methodology that may be more sensitive in detecting genetic effects, and |
| 231 | as such may supplement findings from previous regions of interest analysis often |
| 232 | limited by small sample sizes. Across single-gene polymorphism studies (Dreher et al., |
| 233 | 2009; Forbes et al., 2009; Yacubian et al., 2007), twin studies (Silverman et al., 2014) |
| 234 | or studies estimating the heritability of striatal dopaminergic activity (Stokes et al., |
| 235 | 2013), all of which adopted the mean value within a region of interest (ROI), a |
| 236 | lateralization bias toward the right NAcc or ventral striatal activation has been |
| 237 | reported. However, such lateralization pattern was not observed in the present |
| 238 | voxel-wise analysis. This is consistent with a voxel-wise heritability approach being |
| 239 | more sensitive in detecting the heredity of brain activation compared with |
| 240 | traditional ROI analysis. |
| 241 | It should be noted that only the NAcc activation in anticipating monetary gain, |
| 0.40 | and a state of the state of the state of the state bally in the state bally in the state of the |

rather than loss, showed significant heritability. This result is consistent with

243 previous findings reporting significant correlation between *NAcc* activation in older

and younger MZ twins in anticipating monetary gain but not loss (Silverman et al.,

245 2014). One possible explanation is that there exists less individual difference in

anticipating monetary gain than loss, even though the *NAcc* activation appears to be

247 sensitive to both incentive conditions. The small or non-significant heritability could

be attributed to the high phenotypic variance within both MZ and DZ twins due to

249 limited sample size. It is notable that the studies mentioned above only linked

250 dopaminergic gene polymorphism to ventral striatal activation in processing

251 monetary gain but not loss, which deserves further investigation.

252 We also investigated the heritability of pleasure experience. In this study, physical

anhedonia traits measured by the RPCAS also demonstrated significant heritability,

whilst experiential pleasure measured by the TEPS was characterized by moderate

255 but significant heritability. These findings are consistent with previous studies (*Hay*

256 et al., 2001; Kendler & Hewitt, 1992; Linney et al., 2003). In these studies, however,

257 significant heritability has also been detected in social anhedonia which was not

found in our study. Cultural factors may be a possible influence accounting for this

259 difference, but this requires further investigation.

260 In the best-fitting genetic model, *NAcc* activation during the anticipation of

261 monetary gain exhibited significant genetic share with scores on the RPCAS and the

262 TEPS. In addition, the phenotypic correlation between *NAcc* activation and pleasure

263 experience was almost entirely attributed to genetic factors. These data suggest that

264 motivation-related *NAcc* activation during the anticipation of monetary rewards may

share common additive genes with pleasure experience, and these genes contribute

significantly to the phenotypic expression. Locating the shared genes of these two

267 phenotypes could facilitate clarification of the underlying neurobiological

268 mechanisms of amotivation and anhedonia in schizophrenia and major depressive269 disorder.

270 The main limitation of this study is the modest sample size, which was relatively

271 small for statistical methods applying ACE models. While 196 participants with 174 272 valid data sets could be regarded as a medium to large sample in task-based fMRI 273 research, these preliminary results must be replicated in a larger cohort. Importantly, 274 adopting voxel-wise analysis with correction for multiple comparisons could partially 275 compensate for the relatively small sample size. One primary problem in genetic 276 modeling lies in within-group variation, which is sensitive to the presence of outliers; however, in this study we detected none. Furthermore, demographic variables and 277 278 head movements were carefully matched among subgroups with an aim to enhance 279 the validity of our findings. 280 In conclusion, our findings suggest that motivation-related NAcc activation in 281 anticipating monetary gain and pleasure experience are at least partially heritable. Importantly, motivation-related NAcc activation and pleasure experience exhibit 282 283 significant shared genetic covariance. Future molecular studies examining shared 284 polygenicity of these traits would further inform this research. Locating and refining 285 areas of the genome associated with expression of these traits will ultimately aid in 286 the understanding of the underlying neurobiological mechanisms of treatment-287 refractory symptoms.

288

289 Materials and methods

290 Participants

291 Forty-seven pairs of same-sex dizygotic (DZ) twins and 51 pairs of same-sex

292 monozygotic (MZ) twins were recruited from the Twin Registry of the Institute of

293 Psychology, the Chinese Academy Sciences (Chen et al., 2010; Chen et al., 2013). The 294 zygosity of each twin was jointly determined by DNA analysis based on saliva, and 295 two zygosity questionnaires (Chen et al., 2010). Potential participants were excluded 296 from the study if they: 1) had a personal or family history of diagnosable mental 297 disorders; b) had a history of head trauma or encephalopathy; 3) had a history of 298 substance abuse, including tobacco and alcohol; 4) had an Intelligence Quotient (IQ) lower than 70; 5) had severe hearing or visual impairment; or 6) were ambidextrous 299 300 or left-handed. This information was verified by the Twin Registry, the participants 301 themselves, and their guardians. Detailed experimental procedures conformed to 302 the Declaration of Helsinki and all participants gave written informed consent. All 303 participants completed checklists capturing experiential pleasure and hedonic traits 304 before the brain scans. They then undertook the Monetary Incentive Delay (MID) 305 task inside the scanner. Each participant received 450 RMB as compensation. The 306 study was approved by the Ethics Committee of the Institute of Psychology, the 307 Chinese Academy of Sciences.

308

309 Self-report measures of pleasure experience

310 The revised Chinese versions of the Chapman Physical Anhedonia Scale (RCPAS) and

311 the Chapman Social Anhedonia Scale (RCSAS) were administered to measure

312 physical and social anhedonic traits, respectively (*Chan, Wang, et al., 2012*). The

- 313 RCPAS consists of 61 true-false items, whereas the RCSAS consists of 40 true-false
- 314 items. These two scales have been stable and valid in measuring anhedonic traits

across time and along the schizophrenia spectrum (*Chan, Gooding, et al., 2016*). The

316 Chinese version of the Temporal Experience Pleasure Scale (TEPS) is a 19-item

317 checklist that was used to measure anticipatory and consummatory pleasure in each

- 318 participant (*Chan, Shi, et al., 2012*). The Chinese version has good psychometric
- 319 properties for measuring anhedonia across the different stages of schizophrenia
- 320 (Chan et al., 2010; Chan, Shi, et al., 2012; Li et al., 2015).

321

322 Monetary Incentive Delay (MID) task

323 We adopted the original version of the MID task developed by Knuston and

324 colleagues (Knutson et al., 2000) to the abridged imaging version (Chan, Li, et al.,

325 2016). In each trial of the task, a 250-millisecond cue indicating three different

326 conditions was first presented at the centre of the screen, followed by a blank

327 interval that jittered between 2000 and 2500 milliseconds. Then a blue target with

328 adjusted duration was displayed, followed by an interval that jittered between 500

and 3500 milliseconds. Finally, a 1650-millisecond feedback was presented followed

by an inter-trial interval that jittered between 4000 and 7000 milliseconds. Each trial

331 lasted 12000 milliseconds (Figure 1A).

Participants were asked to hit the target as quickly as possible by pressing the

333 right button on a panel with their right thumb. The initial duration of the target was

334 set at 300 milliseconds and changed according to the subsequent performance of

- each participant. If a target was successfully hit twice, the target duration was
- reduced by 20 milliseconds. Alternatively, if a target was missed twice, 20

337 milliseconds were added to the target duration. Using this strategy, the hit rate of 338 each participant was controlled at around 66.7%. The three cues indicated three 339 different conditions: a triangle indicated a monetary gain condition, a square 340 indicated a monetary loss condition, and a circle indicated a no-incentive condition. 341 Participants gained five monetary points if they hit the target in the monetary gain 342 condition, or lost five monetary points if they missed the target in the monetary loss 343 condition. In the no-incentive condition, participants did not gain or lose any points 344 whether the target was hit or not. Two runs containing 10 gain, 10 loss and 10 no-345 incentive conditions in each run were applied. The trials in each run were presented in a pseudo-random order. Participants practiced with an independent 30-trial run 346 347 before entering the scanner and were informed that their final monetary points 348 gained in the scanner could be converted into cash and added to their compensation. 349 This abridged version has been shown to activate the NAcc effectively in healthy, 350 subclinical and clinical samples (Chan, Li, et al., 2016; Smoski, Rittenberg, & Dichter, 351 2011).

352

353 Brain image acquisition

- 354 Brain imaging data were collected with 32-channel head coil in a 3 T Siemens Trio
- 355 MRI Scanner. An experienced radiologist who was blind to this study was responsible
- 356 for data acquisition. A T2-weighted FLAIRE sequence (TR = 4000ms; TE = 90ms; FOV =
- 200 mm^2 ; slices = 19; flip angle = 120° ; image matrix = 256 x 512; voxel dimensions =
- 358 0.9 x 0.4 x 5mm³) was first used to ascertain that each participant had no organic

| 359 | brain disorders. Then a gradient-echo echo-planner sequence (TR = 2000ms; TE = |
|-----|--|
| 360 | 30ms; FOV = 210mm ² ; slices = 32; flip angle = 90°; image matrix = 64x64; voxel |
| 361 | dimensions = 3.3 x 3.3 x 4mm ³ ; Number of TR = 184 for each run) was applied to |
| 362 | acquire the functional brain activation imaging data of each participant while |
| 363 | performing the MID task. Finally, a high resolution structural brain image was |
| 364 | acquired for anatomical registration (TR = 2300ms; TE = 3ms; FOV = 256mm ² ; flip |
| 365 | angle = 9°; image matrix = 256x256; voxel dimensions = 1 x 1 x 1mm ³). Each |
| 366 | participant wore earplugs during scanning. Their heads were fixed with a vacuum |
| 367 | pillow and sponge pads to minimize head motion. |
| 260 | |

368

369 Imaging data processing

370 The latest version of the SPM 12 (Wellcome Trust Centre for Neuroimaging) was used for imaging data processing. The functional images were first realigned into the 371 first volume of each scanning sequence for movement correction, followed by slice 372 373 timing correction. The observed head motion parameters, three transitions and 374 three rotations, were calculated into the framewise displacement (FD), a 375 comprehensive and reliable index for head movement (Power, Barnes, Snyder, 376 Schlaggar, & Petersen, 2012). Participants with maximum head motion higher than 2 377 mm and 2 degrees, and mean FD larger than 0.25 mm were excluded from the final 378 analysis, along with their twin. Individual high-resolution brain structure image was 379 non-linearly registered to the Montreal Neurological Institute (MNI) template that 380 produced a transformation matrix. Using this matrix, all functional brain images were normalized into a common standard atlas. Functional images were resampled into 3
x 3 x 3 mm³ and spatially smoothed with a 6mm full-width-at-half-maximum (FWHM)
Gaussian isotropic kernel. A 128 Hz high-pass filter was applied to the time series of
each voxel to remove low-frequency noise.

385 The preprocessed functional imaging data were included in a first-level general

386 linear model (GLM) with three predictors of interest during the anticipatory phase

387 for monetary incentives: gain, loss, and no-incentive. First, the data for each

388 participant was analyzed to provide a voxel-wise t-statistic map for each contrast,

389 [gain vs. no-incentive] and [loss vs. no-incentive], during the anticipatory phase. The

390 time points of target hitting and feedback period were included as parametric

391 modulation to minimize their influence on the anticipation for incentives. Six raw

392 head movement parameters were also included as covariates to remove motion

393 effect. For each contrast, the t-statistics map of all the participants were included

into a GLM with the t-statistics as the dependent variable and the FD as covariate to

395 further minimize head motion effect. To clarify whether the bilateral *NAcc* were

activated in both MZ and DZ twins, one-sample t-tests were also applied to the t-

397 statistics of the MZ and DZ groups. The statistical significance threshold of the whole

brain analysis was set as p < 0.001 with FWE correction and cluster voxel size > 100.

399 Since 11 pairs of twins were excluded due to excessive head movements, 44 pairs of

400 DZ twins and 43 pairs of MZ twins were included in the final analysis.

401

402 Statistical analysis

| 403 | Pearson chi-square test was used to test if the gender ratio of MZ and DZ twins were |
|-----|--|
| 404 | different from each other. The matching of age and years of education between MZ |
| 405 | and DZ twins was tested with independent t-test. Univariate general linear model |
| 406 | with gender, age, and years of education as covariates was used to compare FD, |
| 407 | scores on the RCSAS, the RCPAS, the TEPS and their various subscales between MZ |
| 408 | and DZ twins. The intraclass correlation coefficients (ICC) of behavioral phenotypes |
| 409 | among the MZ and DZ twins were calculated respectively. If the ICC of a phenotype |
| 410 | among MZ twins was significantly twice larger than that for DZ twins, the phenotype |
| 411 | in question may be influenced by familial factors. |
| | |

412

413 Heritability brain mapping

414 Voxel-by-voxel heritability brain mapping was carried out with the latest version of 415 the OpenMx (Neale et al., 2016), FSL (Jenkinson, Beckmann, Behrens, Woolrich, & Smith, 2012) and in-house MATLAB (The MathWorks, Inc., Natick, Massachusetts, 416 417 United States) scripts. Since mapping the heritability of all voxels in the whole brain 418 may increase the possibility of type II error, we adopted the Oxford-GSK-Imanova 419 structural striatal atlas which contained the core brain regions sensitive to 420 dopaminergic activity and reward tasks (Tziortzi et al., 2011). The structural striatal 421 template was first resampled into a 3 x 3 x 3 mm³ mask containing 765 voxels. The T 422 values of voxels in the striatal mask were extracted from the two contrast files, [gain 423 vs. no-incentive] and [loss vs. no-incentive] of each participant. There were no 424 outliers more than three standard deviations from the mean T value. Age, gender,

425 years of education, and FD were regressed out from the extracted t values to remove 426 their possible influences on heritability estimation (Bergen, Gardner, & Kendler, 2007; 427 Lenroot et al., 2009). Finally, the standardized residuals were submitted to the genetic model. A conventional univariate ACE model was used, in which A denotes 428 429 additive genetic effects, C denotes common environmental effects, and E denotes unique environmental effects. MZ twins are assumed to share 100 percent of the 430 431 additive genetic variance and common environmental variance, whereas the DZ 432 twins are assumed to share 50 percent of the additive genetic variance and 100 433 percent of common environmental variance. The part accounted for by A in the total variance was defined as the heritability estimate h^2 of this phenotype (*Neale & Maes*, 434 435 2004). To clarify the significance of components A, C and E, sub-models AE and CE 436 were compared to the full ACE model, and model E was compared to AE and CE 437 models respectively. If model fit significantly decreased, then the dropped factor was 438 considered essential in the model. In model selection, the model with the smallest 439 Akaike's Information Criterion (AIC) value was selected as the best-fit model. We adopted the p value of model comparison between the AE and the E model to test 440 the significance of h^2 if the AE model was detected as the best-fit model the full ACE 441 442 model failed to surpass its sub-models in any voxel from the Oxford-GSK-Imanova 443 structural striatal atlas) (Neale & Maes, 2004). Finally, FDR correction with adjusted p < 0.05 was applied to the acquired p-maps to adjust for multiple comparisons. 444 445 Comparing to the full ACE model in brain functional or structural studies, the method in the present study allowed us to quantify the heritability of brain activation and 446 447 relevant significance in the best-fit genetic model, and to correct for multiple tests

448 (*Li et al., 2018*). The cluster tool of FSL was used to identify clusters in which h^2 was

449 significant. Masks with voxels in which the 95% confidence interval of h^2 did not

450 contain zero were also added onto the brain heritability map.

451

452 Multivariate Model fitting

453 A trivariate Cholesky ACE model was fitted to examine the genetic sharing between 454 NAcc activation and pleasure experience (RCPAS and TEPS scores) (Figure 2). T values 455 of the contrast [gain vs. no-incentive] were extracted from bilateral NAcc mask with 456 significant heritability from the heritability brain mapping step. Gender, age, and 457 years of education were then regressed from the extracted mean T value, RCPAS, and TEPS scores. The FD value was additionally regressed from the extracted mean T 458 459 value for head motion correction. The NAcc activation during the anticipation of 460 monetary loss failed to show significant heritability. In addition, MZ twin correlation in social anhedonia was not higher than DZ twin correlation and both correlation 461 462 coefficients were not significant. Hence, The NAcc activation in contrast [loss vs. noincentive] and RCSAS were not included in the multivariate genetic model presented 463 in Figure 2. The trivariate ACE model was first compared with the saturated model in 464 465 which all the constraints were set as free. Then the nested sub-models were 466 compared with the full trivariate ACE model in a stepwise manner. We first discarded all the model paths containing A, C or E effect in a stepwise manner 467 468 (Figure 2 & Table 3). After that we discarded one path from the best fitted model 469 observed from the above step, and then two paths until the model significantly

470 deteriorated (indicated by p < 0.05). The model with the smallest AIC was selected as 471 the best-fit model, and the likelihood ratio chi-squared statistic, minus two times log 472 likelihood difference (-2LL) were applied for model comparison. The contribution of 473 A, C, and E to the phenotype correlation between two phenotypes were estimated 474 using the following formulae: $r_{ph(g)} = \sqrt{(a_{11}^2)^* r_g^*} \sqrt{(a_{22}^2)}$; $r_{ph(c)} = \sqrt{(c_{11}^2)^* r_c^*}$ 475 $\sqrt{(c_{22}^2)}$; $r_{ph(e)} = \sqrt{(e_{11}^2)^* r_e^*} \sqrt{(e_{22}^2)}$ (Toulopoulou et al., 2015).

476

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489

490 Author contributions

491 Zhi Li designed the study, collected and analyzed the data, and wrote up the

- 492 manuscript. Yi Wang, Chao Yan, Ke Li and Ya-wei Zeng collected all the data and
- 493 commented on the first draft of the manuscript. Eric F. C. Cheung, Anna R. Docherty,
- 494 Pak C. Sham, Raquel E. Gur and Ruben C. Gur provided significant comments to the
- 495 manuscript. Raymond C. K. Chan conceptualized the idea, designed the study,
- 496 interpreted the findings and commented the manuscript critically.
- 497

498 Additional files

- 499 Figure 1 & Table 2 Source Data 1_[loss vs. no-incentive]
- 500 Figure 1 & Table 2 Source Data 2_[gain vs. no-incentive]
- 501 Figure 3-Source Data
- 502 Figure 4 & Table 3 -Source Data 1
- 503 Figure 4-& Table 3 Source Data 2
- 504 Raw data 1_Activation in each voxel of stritaum_[loss vs. no-incentive]
- 505 Raw data 2_Activation in each voxel of stritaum_[gain vs. no-incentive]
- 506 Source Code_Heritability Brain Mapping 1
- 507 Source Code_Heritability Brain Mapping 2
- 508 Source Code_Multivariate Model fitting

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| | 35 |

744 Table1. Demographics of participants

| | MZ (N = 86) | ICC | DZ (N = 88) | ICC | $\chi^2/t/F$ | р | ALL (N = 174) |
|----------------------|-------------|---------|-------------|---------|--------------|-----------|---------------|
| Gender (Male/Female) | 46/40 | / | 46/42 | / | 0.026 | 0.872 | 92/82 |
| Age | 19.98(1.89) | / | 19.8(1.76) | / | -0.66 | 0.513 | 19.89(1.82) |
| Education | 12.33(1.75) | 0.671** | 12.44(1.63) | 0.591** | 0.46 | 0.647 | 12.39(1.69) |
| FD | 0.13(0.04) | 0.204 | 0.13(0.04) | -0.059 | 0.156 | 0.694 | 0.13(0.04) |
| RCSAS | 11.38(5.96) | 0.087 | 7.57(4.48) | 0.281 | 22.38 | < 0.001** | 9.45(5.59) |
| RCPAS | 22.12(8.03) | 0.490** | 18.97(7.66) | 0.201 | 6.29 | 0.013* | 20.52(7.98) |
| TEPS | 4.06(0.59) | 0.352* | 4.08(0.59) | -0.02 | 0.004 | 0.947 | 4.07(0.59) |
| TEPS_Anticipation | 4.11(0.67) | 0.396** | 4.13(0.7) | -0.021 | 0.19 | 0.662 | 4.12(0.68) |
| TEPS_Consummation | 4.11(0.77) | 0.346* | 4.12(0.75) | 0 | 0.19 | 0.667 | 4.14(0.76) |

745 Note: *, p < 0.01; **, p < 0.05; MZ = Monozygotic twins; DZ = Dizygotic twins; ICC = Interclass correlation coefficient; FD = Frame Displacement; RCSAS =

746 Revised Chapman Social Anhedonia Scale; RCPAS = Revised Chapman Physical Anhedonia Scale; TEPS = Temporal Experience Pleasure Scale.

| | M | Z (N = 86) | DZ | Z (N = 88) | ALL | . (N = 174) |
|-----------------------|-------|-------------|-------|-------------|-------|-------------|
| Region(L/R) | Т | Peak Coord. | Т | Peak Coord. | Т | Peak Coord. |
| Gain vs. No-incentive | | | | | | |
| NAcc (R) | 12.1 | [6,9,3] | 13.41 | [-12,6,-6] | 16.73 | [6,9,0] |
| NAcc (L) | 11.27 | [-6,6,0] | 12.38 | [9,9,-3] | 16.63 | [-9,6,-3] |
| Thalamus | | | | | 14.16 | [0,-9,3] |
| Insula (L) | 10.52 | [-27,27,3] | | | | |
| Insula (R) | | | 10.26 | [33,24,3] | | |
| Loss vs. No-incentive | | | | | | |
| NAcc (R) | 10.7 | [0,-6,0] | 12.22 | [-12,6,-9] | 15.18 | [9,3,-3] |
| NAcc (L) | 10.4 | [6,6,0] | 11.73 | [9,3,-3] | 15.01 | [-9,3,0] |
| Thalamus | | | | | 13.99 | [0,-6,0] |
| Thalamus (R) | | | 11.32 | [12,-3,6] | | |
| Globus pallidus (L) | 10.36 | [-9,3,0] | | | | |

748 Table2. Whole brain activation in anticipating monetary incentive

749 Note: All the results were corrected with FEW method, p < 0.001, cluster voxel size > 100;

MZ = Monozygotic twins; DZ = Dizygotic twins; L = Left; R = Right; Coord. = Coordinate; NAcc
 Fucleus Accumbens.

753 Table3. Model fitting and selection

| No. | Model | ер | -2LL | df | AIC | diffLL | diffdf | р |
|-------|--|----|---------|-----|--------|--------|--------|------|
| 1 | Saturated Model | 54 | 1342.45 | 468 | 406.45 | / | / | / |
| | Cholesky Trivariate Model | 21 | 1384.4 | 501 | 382.4 | 41.94 | 33 | 0.14 |
| II | Drop a or c matrix | | | | | | | |
| III | Drop c matrix | 15 | 1384.65 | 507 | 370.65 | 0.25 | 6 | 1 |
| IV | Drop a matrix | 15 | 1396.98 | 507 | 382.98 | 12.59 | 6 | 0.05 |
| | Drop one path based on the model III | | | | | | | |
| V | Drop a31 | 14 | 1387.21 | 508 | 371.21 | 2.56 | 1 | 0.11 |
| VI | Drop a32 | 14 | 1387.68 | 508 | 371.68 | 3.03 | 1 | 0.08 |
| VII | Drop a21 | 14 | 1390.61 | 508 | 374.61 | 5.95 | 1 | 0.01 |
| VIII | Drop e32 | 14 | 1390.07 | 508 | 374.07 | 5.42 | 1 | 0.02 |
| IX | Drop e31 | 14 | 1385.22 | 508 | 369.22 | 0.57 | 1 | 0.45 |
| Х | Drop e21 | 14 | 1384.66 | 508 | 368.66 | 0.01 | 1 | 0.94 |
| | Drop two paths based on the model X | | | | | | | |
| XI | Drop e21 and a31 | 13 | 1387.37 | 509 | 369.37 | 2.71 | 1 | 0.1 |
| XII | Drop e21 and a32 | 13 | 1388.4 | 509 | 370.4 | 3.75 | 1 | 0.05 |
| XIII | Drop e21 and a21 | 13 | 1393.18 | 509 | 375.18 | 8.53 | 1 | 0 |
| XIV | Drop e21 and e32 | 13 | 1390.07 | 509 | 372.07 | 5.42 | 1 | 0.02 |
| XV | Drop e21 and e31 | 13 | 1385.35 | 509 | 367.35 | 0.69 | 1 | 0.4 |
| | Drop three paths based on the model XV | | | | | | | |
| XVI | Drop e21 and e31 and a31 | 12 | 1393.29 | 510 | 373.29 | 7.94 | 1 | 0 |
| XVII | Drop e21 and e31 and a21 | 12 | 1394.03 | 510 | 374.03 | 8.68 | 1 | 0 |
| XVIII | Drop e21 and e31 and a32 | 12 | 1388.44 | 510 | 368.44 | 3.09 | 1 | 0.08 |
| XIX | Drop e21 and e31 and e32 | 12 | 1390.56 | 510 | 370.56 | 5.21 | 1 | 0.02 |

Note: No. = Model number; Model = Parameters drop by this model; ep = estimate parameter; -2LL = minus 2 log 754 755 likelihood; df = degree of freedom; AIC = Akaike information criterion; diffLL = the difference of minus 2 log 756 likelihood between two models; diffdf = the difference of the degree of freedom between two models; p indicates 757 the significance of model deterioration between two models. The trivariate genetic model was compared with the 758 saturated model first, then the sub-models II – IV were compared with the full genetic model from which the model 759 III was selected as the best-fitted model for the next step parameter dropping. One parameter was first drop from 760 the model III in which the model X was selected. Then two parameters were drop based on the model X. Finally, the 761 model XV with the smallest AIC among all tested sub-models was chosen as the best fitted model, which model did 762 not deteriorate by compared with the model X (p > 0.05).

764 Legends

| 765 | Figure1. Monetary incentive delay (MID) task and brain activation in anticipating |
|-------------------|---|
| 766 | monetary gain and loss. A: The Workflow of one trial in the MID task; B: The |
| 767 | activation of bilateral nucleus accumbens (NAcc) was found in contrast [Gain vs. no- |
| 768 | incentive] during the anticipatory phase, the white-red color bar indicates the |
| 769 | statistical t value; C: The activation of bilateral <i>NAcc</i> was found in contrast [Loss vs. |
| 770 | no-incentive] during the anticipatory phase, the white-blue color bar indicates the |
| 771 | statistical t value. |
| 772 | |
| 773 | Figure2. Full trivariate genetic model with Cholesky decomposition. The NAcc |
| | |
| 774 | indicates the extracted t value from the contrast file of [Gain vs. No-incentive], with |
| 774 775 | indicates the extracted t value from the contrast file of [Gain vs. No-incentive], with the mask from the voxel-wise heritability mapping of brain activation. The RPCAS |
| | |
| 775 | the mask from the voxel-wise heritability mapping of brain activation. The RPCAS |
| 775 776 | the mask from the voxel-wise heritability mapping of brain activation. The RPCAS indicates the physical anhedonia trait, whilst the TEPS indicates the experiential |
| 775 776 777 | the mask from the voxel-wise heritability mapping of brain activation. The RPCAS indicates the physical anhedonia trait, whilst the TEPS indicates the experiential pleasure. The A indicates the additive genetic effect, the C indicates the common |

781

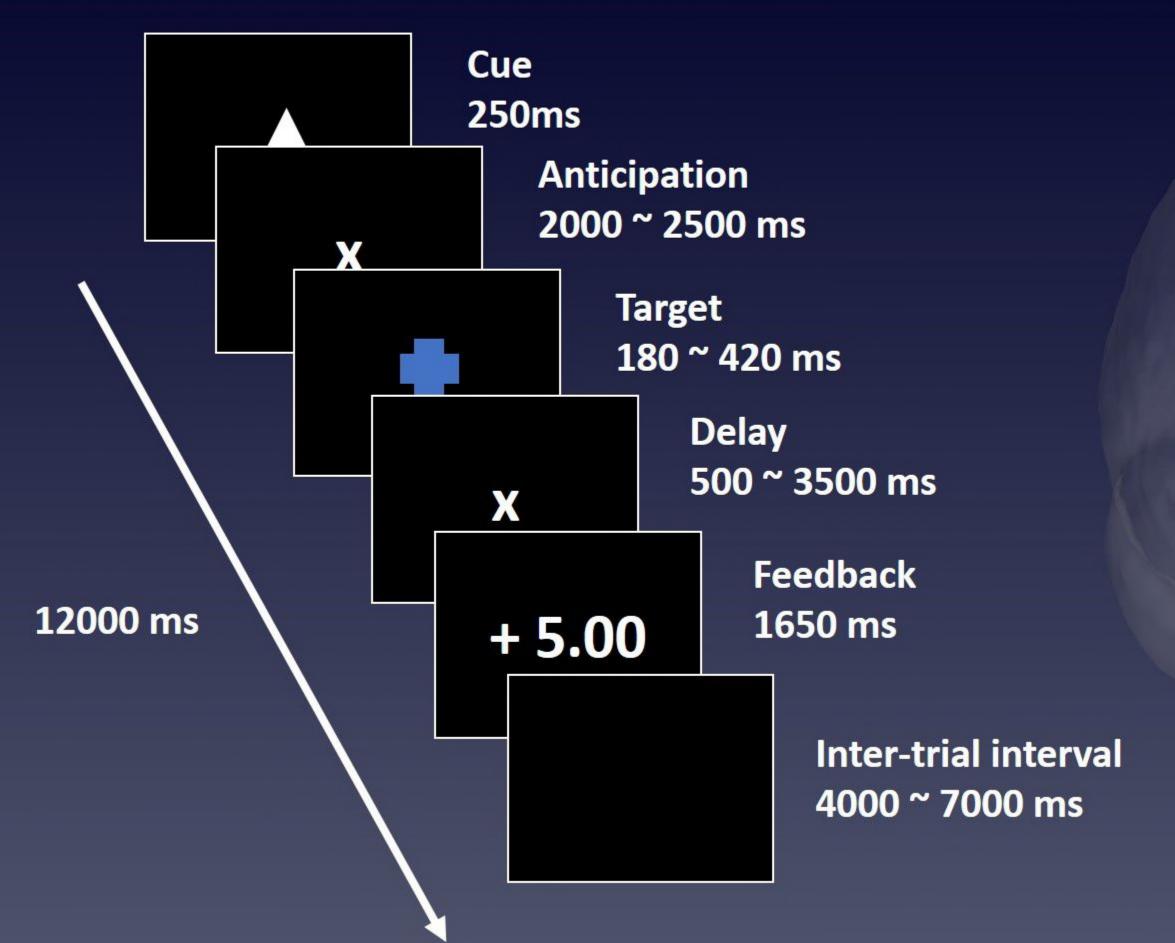
Figure3. Voxel-wise heritability mapping on brain activation. In the standard
striatum atlas on the right, two clusters with significant heritability in bilateral *NAcc*

are detected, which ranges from 0.2 to 0.49 in each voxel (reflected by the white-red

color bar). The five pie charts on the left indicate the heritability and unique

- renvironmental effect of AE model on the two clusters, in which the golden color
- 787 indicates the heritability whilst the blue color indicates the unique environmental
- 788 effect.
- 789
- 790 Figure4. The best-fitted trivariate genetic model. Only the additive genetic and
- 791 unique environmental effects contribute to this model. The h^2 indicates the
- heritability with 95% confidence interval of each single phenotype, the r_{ph} indicates
- the phenotypic correlation between phenotypes, the r_g indicates the genetic
- correlation, and the r_e indicates the unique environmental correlation. The $r_{ph(g)}$ and
- r_{ph(e)} indicates the contributions to phenotypic correlation, from the additive gene
- and unique environment respectively. The standard path coefficients with 95%
- 797 confidence interval were also supplied in this figure.
- 798

A. Procedure of One trial

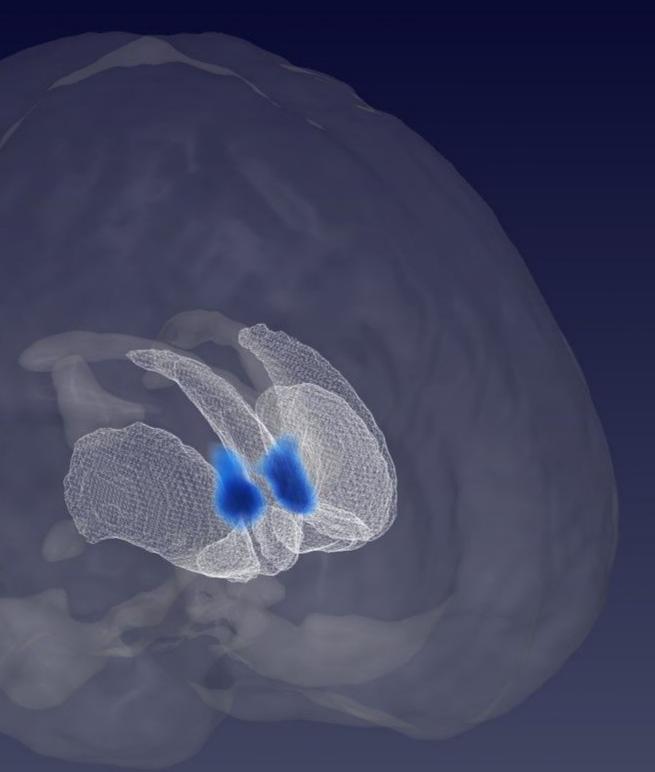


B. Gain vs. No-incentive

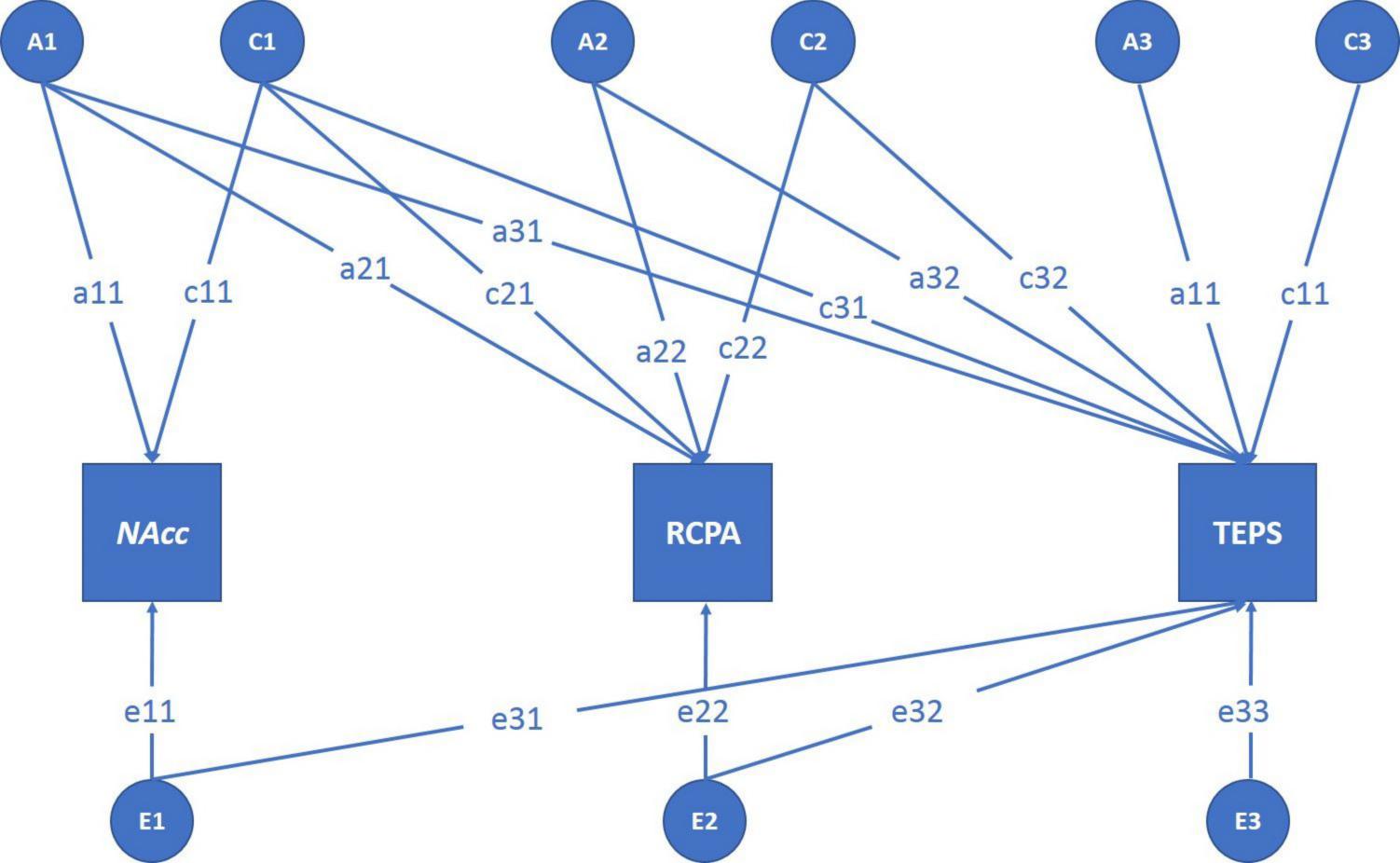
C. Loss vs. No-incentive

13.00 13.75 14.50 15.25 16.00 T

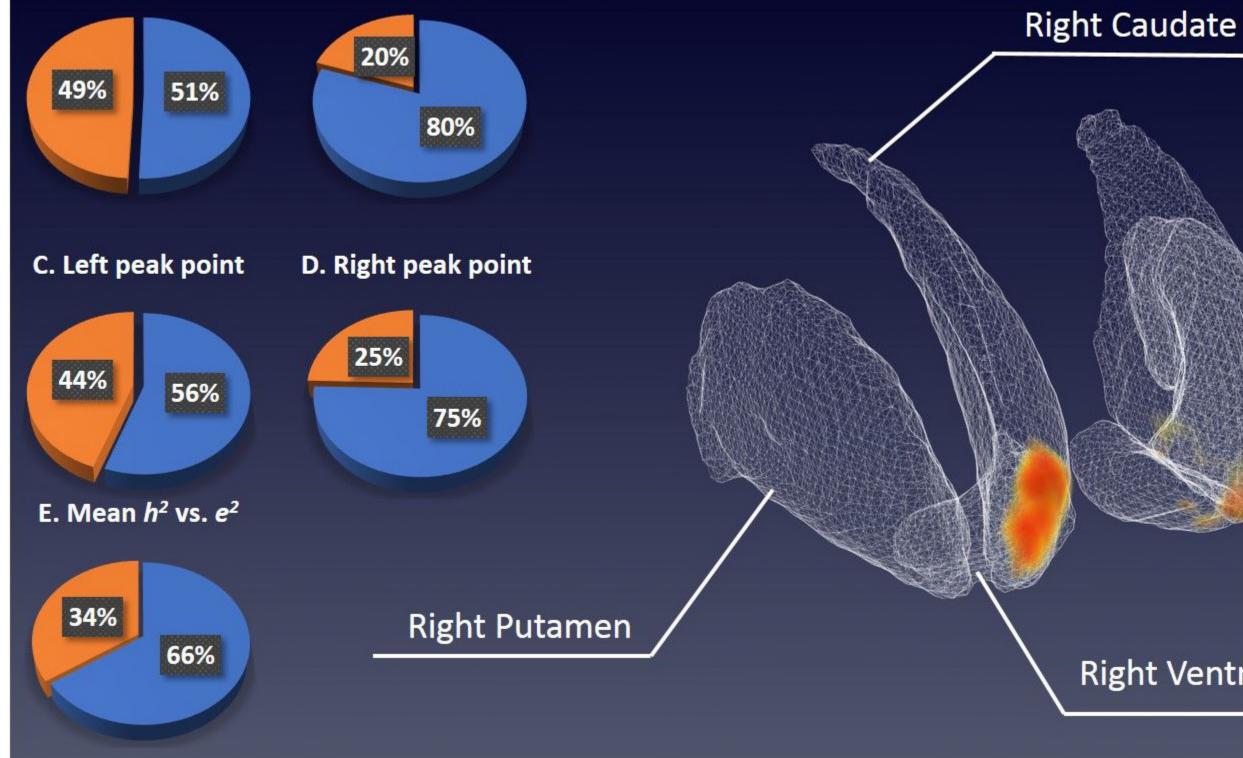




13.50 14.00 14.50 15.00 *T*



A. Max h^2 vs. Min e^2 B. Min h^2 vs. Max e^2



Heritability 0.49 0.42 0.35 0.27 **Right Ventral Striatum** 0.20

