Figure 1 Haploview-generated linkage disequilibrium patterns of the (a) four DRD1 and (b) four DRD2 single nucleotide variants examined in this study. D' values (x100) are noted at the intersection of each SNP pair. 'Decreased' shades of red in each box represent decreasing linkage disequilibrium values.

rs4532 and rs265978. By contrast, this link was not found in carriers of the minor allele of these two DRD1 SNPs. In other words, change in the ability to manipulate verbal information in working memory was unrelated to the magnitude of change in ADHD symptoms in minor allele carriers. Non-model-based plots of raw CBCL-AP and digit span backward change scores for each individual with regression slopes are plotted as

function of rs4532 and rs265978 genotype and included in the Supplementary Materials (Figure S4a–b) for descriptive purposes.

In contrast to the DRD1 findings, no DRD2 SNP × digit span backward interactions were significant. There was an rs1800497 × digit span forward interaction with $p < .05$, but this interaction did not survive correction (see Table 3).

Correlations with baseline and follow-up status

It was important to gauge whether the above developmental findings more closely reflected baseline or follow-up status. Therefore, an exploratory/post-hoc analysis of the baseline and follow-up data was conducted using the same statistical methods as above. We applied a conservative Bonferroni correction of $p < .0031$ to correct for 16 additional tests. No significant SNP × digit span interactions were detected in baseline analyses (Supplementary Table 2). By contrast, the two significant interactions between DRD1 SNPs rs4532 and rs265978 and digit span backward that emerged during development were also significant at follow-up after correction for multiple testing (Supplementary Table 3). Lastly, no DRD2 × digit span interactions were significant.

Potential confounding effects of race/ethnicity and stimulant treatment

Genetic heterogeneity due to racial/ethnic background and stimulant treatment for ADHD during development

Table 3 Linear regression results of the developmental change analyses from baseline to follow-up. Shown is the change in variance accounted for ($R^2\Delta$) and level of significance at each step of the model building procedure after controlling for the number of years that had elapsed between the baseline and follow-up evaluations

DRD1 SNPs	rs265973		rs265975		rs265978		rs4532	
Model/step	$R^2 \Delta$	p-value	$R^2 \Delta$	p-value	$R^2 \Delta$	p-value	$R^2 \Delta$	p-value
1. SNP	.015	.290	.012	.358	.015	.305	.027	.170
2. Digit span forward	.001	.786	.000	.978	.001	.767	.001	.766
3. Digit span backward	.007	.480	.004	.611	.007	.501	.005	.554
4. SNP × digit span forward	.015	.307	.009	.435	.000	.916	.000	.872
5. SNP × digit span backward	.084	.013	.001	.835	**.117**	**.004**	**.109**	**.005**

DRD2 SNPs	rs1800497		rs1076560		rs2283265		rs12364283	
Model/step	$R^2 \Delta$	p-value	$R^2 \Delta$	p-value	$R^2 \Delta$	p-value	$R^2 \Delta$	p-value
1. SNP	.072	.021	.015	.302	.007	.481	.003	.616
2. Digit span forward	.002	.695	.001	.848	.001	.787	.002	.727
3. Digit span backward	.001	.795	.002	.679	.004	.591	.007	.473
4. SNP × digit span forward	.065	.025	.013	.339	.020	.225	.001	.844
5. SNP × digit span backward	.030	.119	.005	.539	.001	.835	.019	.237

Values in **bold** are significant at a Bonferroni corrected p-value of .0063. DRD1, dopamine D1 receptor gene; DRD2, dopamine D2 receptor gene; SNP, single nucleotide polymorphism.