

<u>Up FS cell development</u>	<u>Up ASD</u>	<u>Down ASD</u>
<u>Down FS cell development</u>	438(20.6%)	574(27.0%)
	620(29.2%)	491(23.1%)
<u>Up FS cell development</u>	<u>Up SCZ</u>	<u>Down SCZ</u>
<u>Down FS cell development</u>	459(21.6%)	597(28.1%)
	599(28.2%)	468(22.1%)
<u>Up FS cell development</u>	<u>Up BPD</u>	<u>Down BPD</u>
<u>Down FS cell development</u>	500(23.5%)	623(29.4%)
	558(26.3%)	442(20.8%)
<u>Sig up FS cell development</u>	<u>Sig up ASD</u>	<u>Sig down ASD</u>
<u>Sig down FS cell development</u>	51(14.0%)	104(28.6%)
	151(41.5%)	58(15.9%)
<u>Sig up FS cell development</u>	<u>Sig up SCZ</u>	<u>Sig down SCZ</u>
<u>Sig down FS cell development</u>	31(14.0%)	59(26.6%)
	94(42.3%)	38(17.1%)
<u>Sig up FS cell development</u>	<u>Sig up BPD</u>	<u>Sig down BPD</u>
<u>Sig down FS cell development</u>	50(18.4%)	73(26.8%)
	105(38.6%)	44(16.2%)

Supplemental table S5. Chi-square analysis. For sub-tables 1-3, all genes were divided into 4 groups (up during FS cell development/up in disease; up during FS cell development/down in disease; down during FS cell development/up in disease; down during FS cell development/down in disease). Values were entered into an online chi-square 2x2 contingency table that used the Fisher's exact test for calculation of p-values. In all cases, genes expression levels in the presence of disease changed in the opposite direction from that occurring during FS cell development ($p < 0.0001$). For sub-tables 4-6, only genes that were significantly change in disease and during development were used. In all cases results remained highly significant ($p < 0.0001$).