Body Maps on Human Chromosomes

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An exploration via published datasets of the hypothesis that human genes are organized somatotopically: For each autosomal chromosome, its tissue-specific genes tend to have relative positions on the chromosome that mirror corresponding positions of the tissues in the body. In addition, there appears to be a division of labor: Such a homunculus representation on a chromosome holds significantly for either the anteroposterior or the dorsoventral body axis. In turn, anteroposterior and dorsoventral chromosomes tend to occupy separate zones in the spermcell nucleus. One functional rationale of such largescale organization is for efficient interconnections in the genome.

Introduction

The perspective here focusses on the "anatomy of the genome", i.e., its global structure. It is analyzed in terms of "the logistics of the genome", that is, its network optimization, its efficiency of interconnections for conveying information. The main finding: The genome is organized in terms of an extensive framework of anteroposterior [AP] and dorsoventral [DV] body axes at various structural levels. Our prior work (e.g., Cherniak & Rodriguez-Esteban, 2004) sketched a corresponding connection-minimization rationale for cerebral cortex layout.

We have reported similar body maps on the whole human genome elsewhere (Cherniak & Rodriguez-Esteban, 2013). Here we extend this cartography to a "maps within maps" model, proceeding from the body map on the entire genome, to body maps on individual chromosomes. A pattern of nested and overlapping maps has physiological reality. (See Fig. 1.)

Unlike hox complexes (McGinnis et al, 1984) or collinearity structure (Lewis, 1978), these anatomical mappings include thousands of genes on all somatic chromosomes. There appears to be little prior study of such a human chromosome homunculus idea.

The principal result here is evidence for a "Division of Labor" Hypothesis: Each autosomal chromosome has either a significantly stronger AP map or DV map. So, to a first approximation, a chromosome is AP if and only if not DV. Each of the autosomal chromosomes 1 - 22 tends to fit this dichotomous axis-map pattern; about half are AP, half DV. (For contrast,

the X sex chromosome has neither a significant AP nor DV body map.) Also,
further convergent support of this division: A partial mapping of
chromosome positions in the spermcell nucleus indicates that AP chromosomes
significantly tend to be located in an outer shell, surrounding a core of
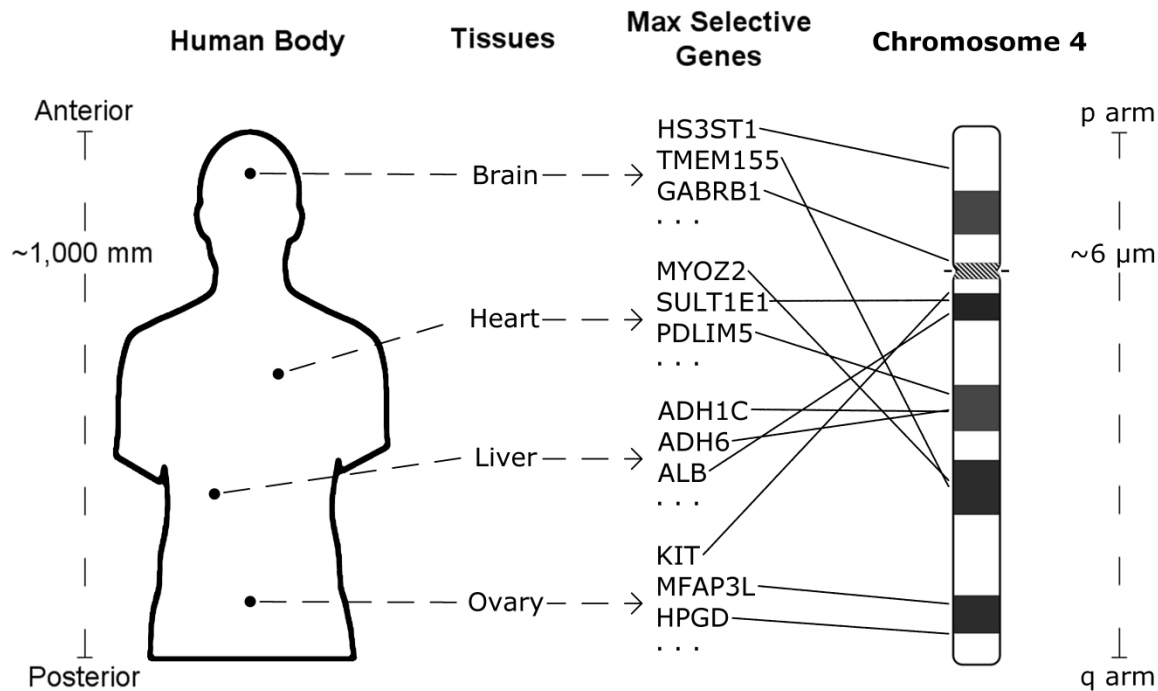all DV chromosomes.

Fig. 1.   Mapping anteroposterior axis of the human body onto one of its chromosomes (#4), via published datasets. Body sites of four organs are illustrated. For each tissue, a few of the maximally selective genes in Chromosome (Chr) 4 are listed (from Xiao et al, 2010; SPM ≥ 0.3). Mean gene loci on Chr 4 for each tissue are then determined. Thus: tissue —> genes —> chromosome.   See Fig. 2 below.

Methods

For a homunculus analysis of a chromosome: AP and DV axes were analyzed
separately. On the AP body axis, compactly localizable tissues (e.g.,
liver, as opposed to skin), from anterior to posterior of the body (e.g.,
brain to gonad) with the largest tissue-specific gene sets were chosen.
(See Table 1.) This AP tissue series is the same as in our prior study
(Cherniak & Rodriguez-Esteban, 2013). On each chromosome, its maximally
selectively expressed genes for each tissue in the adult organism were
identified via the tissue specificity measure SPM, from Xiao et al, 2010
(see also Pan et al, 2013); the total set of genes in the analyses ranged
from 1,001 to 21,956 (cf. Table 1). The Xiao et al study screens genes
selectively expressed in particular tissues by transforming the expression
profile of each gene into a vector, and using its scalar projection for a
given tissue. Selectivity of a gene for a tissue is set by the specificity
measure SPM, ranging from 0 to 1, where a higher value narrows selectivity.

Chromosome location of each gene was found via the GRCh38 human genome
assembly (cf. Rosenbloom et al, 2015). The mean locus on the chromosome of
each tissue's gene set was calculated. A body-to-chromosome regression
analysis of this AP series of mean tissue gene positions was performed, for
body location of each tissue vs chromosome location of its genes. Slope of
the regression line was determined. For instance, see Fig. 2. Similarly
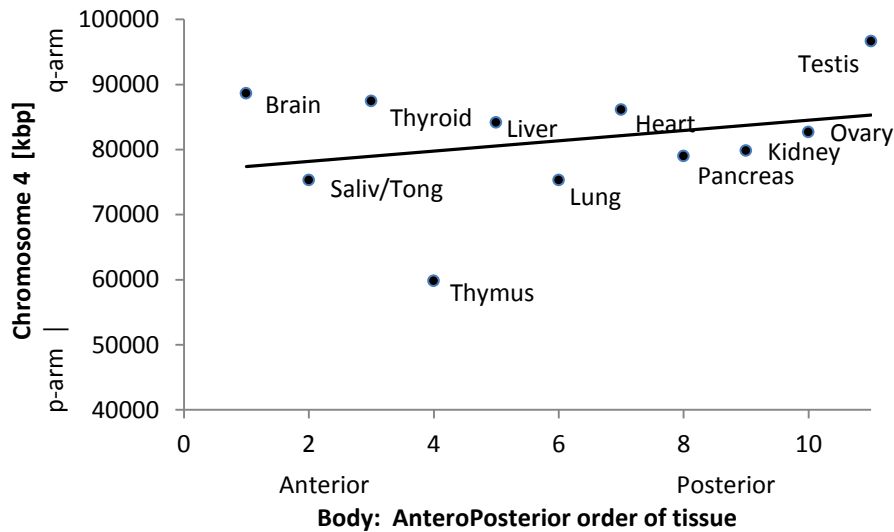for the DV axis.

Fig. 2. Correlation of tissue positions in the body with their gene group locations on Chr 4. Chr 4 body map, for anteroposterior axis. Mean loci on Chr 4 of highly selective genes for each of 11 topologically compact tissues (genes from Xiao et al, 2010; SPM ≥ 0.3), plotted against tissue locations in the human body. The regression line for this chromosome shows a weak positive relationship, with a slope of 789107 and $+r^2$ = 0.076. However, as explained below, when a set of plots for Chr 4 over the range of SPM values are pooled, their mean positive slope is strongly significant ($p < 0.003$).

The tissue gene groups in the body map of the Chr 4 example above include a
mean 76 genes / tissue. Orientation of body maps on chromosomes: For an AP
body map, a positive slope (and $+r^2$) indicates that brain genes are located
more toward the p arm of chromosome, testis genes at q arm. For a DV body
map, a positive slope means that ovary genes are toward the p arm, kidney
genes at q arm.

(Also, as can be observed in Fig. 2, mean values of tissue locations on each
chromosome tend to occur on the q arm of a chromosome, rather than on its p
arm. Such a q arm positioning of homunculi naturally raises questions about
further localization, a "sub-division of labor". However, a caveat concerns
the potential confound that, since p arms are shorter than q arms, mean
tissue gene locations are biased to appear on q arms rather than p arms
anyway.)

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Bilateral symmetry of the vertebrate body plan means that the lateral (left / right) body axis has a limited set of distinct tissue positions. For example, brain, thymus, kidney, ovary, and testis each have lateral centroids approximately at the midline; unlike heart, liver, spleen, pancreas. Hence, as discussed below (see Table 2), an "AP & DV" model by itself seems to account for at least most autosomal chromosomes.

Thus, design of the mapping analysis: As a calibration, the X chromosome was included with the 22 autosomal chromosomes (because of its smallest gene count, the Y chromosome was not included in these analyses). To increase power of experiment, SPM settings were sampled across their full range: For each of the 23 chromosomes, over the SPM range of 0.3 – 0.9, at 13 0.05 intervals, the 11 tissue gene sets (each tissue's gene set with an overall mean of 25 genes) were tested for the 2 axes. See main Table S1. (Cf. also Rodriguez-Esteban & Cherniak, TiSGeD Excel Package.) So the dataset is: 23 chromosomes x 13 SPM settings x 2 axes = 598 body-chromosome mappings, each as in the Fig. 2 example.

On each axis, for each of the 22 autosomal *H. sapiens* chromosomes, each tissue group body location is plotted against its mean location on that chromosome. And the chromosome mapping's bestfit line, slope, and r^2 are collected. Table S1 is the dataset of the slopes.

Table 1. (a) Ordinal position in human body of topologically compact tissues.
(b) Total gene counts for all 11 tissues, over SPM range 0.3 – 0.9.

(a) BodyAxes			(b) SPM ≥	Total GeneCt
AnteroPosterior [AP]		DorsoVentral [DV]	0.3	21956
Top	GeneCt	Front	0.35	15098
1 Brain	603	1 Ovary	0.4	10903
2 Sal/Tng	247	2 Testis	0.45	8098
3 Thyroid	129	3 Thymus	0.5	6246
4 Thymus	113	4 Sal/Tng	0.55	4881
5 Heart	212	5 Thyroid	0.6	3886
6 Lung	334	6 Lung	0.65	3126
7 Liver	443	6 Liver	0.7	2545
8 Pancreas	467	7 Heart	0.75	2072
9 Kidney	232	8 Brain	0.8	1649
10 Ovary	455	9 Pancreas	0.85	1297
11 Testis	651	10 Kidney	0.9	1001
Bottom		Back		

Both Lung and Liver are assigned same DV location. ("Sal/Tng": Salivary & Tongue tissues combined.)
GeneCt in (a): For each organ, tissue-specific gene count is for middle setting of SPM ≥ 0.6.
For each tissue, its gene count is the same for both AP and DV axes.
Total gene counts in (b) include all 11 tissues listed.

Results

Chromosome Body Axis Analysis:

1. As explained, to obtain a robust dataset, for each chromosome, sets of its tissue gene body maps were collected over a range of 13 SPM settings (compiled in master Table S1). The means of these sets of 13 slope values are stronger for either an AP or DV mapping.

2. To analyze significance of these chromosome body maps, a combination of single sample and paired sample t tests was used: First, to check significance of the set of 13 body maps for a chromosome, the mean of its set of 13 slope values vs a null-hypothesis mean of zero are evaluated via a single sample t test. All but 2 of the 22 autosomal chromosomes show significant body maps (10 are AP, 10 are DV). Chrs 3 and 5 approach marginal significance for an AP mapping ($p < 0.059$ and $p < 0.074$, respectively). (As a first approximation of this set of results, see Fig. 3.)

3. Each of the body maps with the larger mean slope also has a smaller p value than its alternate, weaker body map.

4. In addition, for all but 7 of the 22 chromosomes (AP Chrs 16, 10, 4; DV Chrs 1, 18, 15, 17), the alternate body axis map is not significant. (See summary Table 2.)

5. Furthermore, for most chromosomes (18 of the 22 autosomal chromosomes), including all of the above 7, a paired sample t test then yields that the difference between the means of the set of AP slopes and of the set of DV slopes is highly significant.

In this way, via successive single sample and paired sample t tests, the conclusion is that each of the autosomal chromosomes has either a significantly stronger AP or DV body mapping. Gene organization of each somatic chromosome conforms to a somatotopic mapping: about half are AP, half DV.

For comparison, a chromosome that does not show such evidence of an AP or a DV mapping is the sex chromosome X (see Table 2).

As a replication, we also tested the set of r^2 values of the bestfit regression lines of each chromosome body map for a similar pattern of significant AP vs DV division of labor. The r^2 values in fact show the same trends as the slopes -- e.g., the same chromosomes have AP or DV maps, except that Chr 5 no longer approaches a significant mapping.

So, using these procedures, 12 of the autosomal chromosomes have significant
AP body maps, 10 have significant DV maps.
Anteroposterior: 16, 7, 10, 4, 13, 20, 3, 5, 11, 19, 21, 22.
Dorsoventral: 8, 1, 18, 2, 15, 9, 12, 17, 14, 6.
(Chrs 3 and 5 have marginally significant AP maps.)

Beginning with the single sample t test results, Fig. 3 depicts the overall
pattern of the chromosome body maps. The "L"-shaped curve has a distinctive
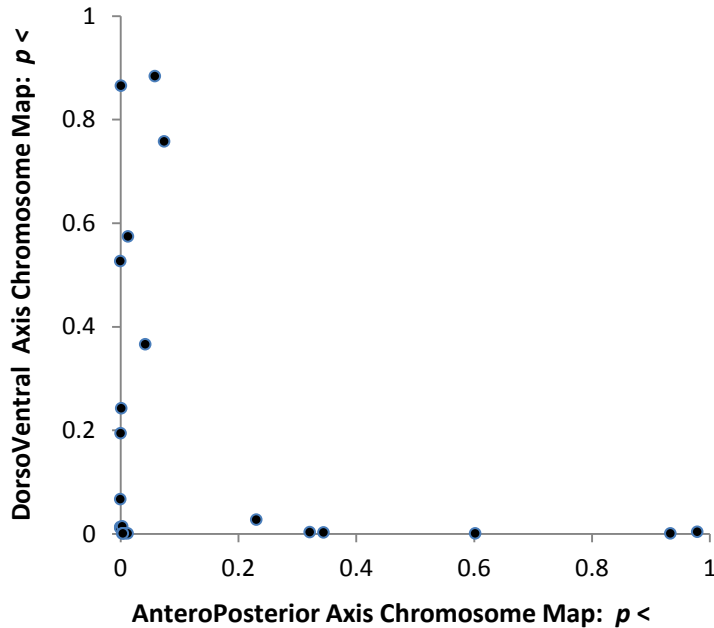right-angle.

Fig. 3. AP chromosomes vs DV chromosomes. Body mapping division of labor among chromosomes: The "L"-shaped distribution of datapoints indicates body axis-map exclusivity. That is, for each autosomal chromosome: If one body axis maps significantly to it (e.g., $p < 0.05$, 2 tailed), then the other tends not to; and vice versa. Each datapoint represents one chromosome. Compiled from Table S1 slope data. (Some datapoints for smallest p values are superimposed and obscured.)

Finally, focusing on Fig. 4: A map of chromosome sites in the spermcell
nucleus. (The central - peripheral axis shows the maximum excursion of each
chromosome from the periphery, rather than a varying projection of its 3-d
location.) A "shell / core" distribution of AP vs DV chromosomes appears to
hold. AP chromosomes occupy the anterior perimeter of the autosomal
chromosome set (except for a tail section). From the top, clockwise: 22-
19-16-13-20-5-4-7-3-10. With the exception of Chr 16, this series also
constitutes most of the 2-d "convex hull" of the autosomal chromosome set
(i.e., the minimum subset that envelops the rest of the total set). Clear
exceptions to the shell / core zones are Chrs 11A & 21A, which lie along the
centerline of the chromosome set, in the middle of the DV group. For 2
exceptions to the 22 chromosome set, the significance of this AP / DV
distribution would be $p < 0.0001$ (2 tail).
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Table 2. Division of labor: Autosomal chromosomes show a statistically significant preference for a body mapping that is either anteroposterior or dorsoventral. See **boldface** blocks below. (Chrs 3 and 5 are marginally AP.) For mean slope data of bestfit regression lines.

Chromo	mean AP Slope	*p* <	mean DV Slope	*p* <	AP vs DV *p* <
AnteroPosterior Axis Map					
16	**1,604,409**	**5.33E-05**	191,576	0.012381	1.41E-06
7	**-1,472,407**	**1.26E-05**	628,621	0.066309	1.44E-05
10	**-1,470,431**	**0.000119**	659,221	0.010798	2.3E-06
4	**1,431,861**	**0.003314**	462,782	0.013728	0.036203
13	**-1,394,665**	**0.012927**	-302,921	0.573604	0.014447
20	**1,016,725**	**2.36E-06**	71,342	0.526125	6.02E-06
3	**984,114**	**0.058667**	-63,595	0.883411	0.111664
5	**-586,941**	**0.074487**	-69,349	0.757337	0.178083
11	**567,410**	**0.000912**	26,274	0.865145	0.012288
19	**354,616**	**0.000632**	76,037	0.193754	0.007838
21	**-185,325**	**0.001703**	-119,651	0.241717	0.549434
22	**-166,935**	**0.042127**	-121,929	0.365256	0.765776
means	56,869	0.01625	119,867	0.37588	0.13965
DorsoVentral Axis Map					
8	-44,453	0.933389	**3,414,430**	**0.000139**	0.000287
1	-857,225	0.003236	**-2,472,568**	**6.41E-07**	0.000115
18	508,226	0.007738	**-2,223,069**	**0.000287**	3.24E-05
2	127,471	0.602037	**-1,849,409**	**2.59E-05**	1.78E-05
15	420,705	0.012465	**-1,744,266**	**0.000244**	2.24E-05
9	-212,524	0.344678	**986,262**	**0.002161**	0.00149
12	7,051	0.979252	**703,600**	**0.00353**	0.045874
17	477,013	0.004346	**-553,692**	**5.83E-06**	2.63E-06
14	140,904	0.230478	**-524,061**	**0.026944**	0.01125
6	-224,168	0.321311	**472,382**	**0.003019**	0.012026
means	34,300	0.34389	-379,039	0.00364	0.00711
X	310,901	0.40721	812,730	0.26145	0.52744

From main Table S1 data, for 13 SPM settings over range 0.3 - 0.9, by 0.05 increments. Ordered by absolute magnitude of (significant) mean slope values. *p*-values are from t tests (2 tailed). For comparison, sex chromosome X has neither significant AP nor DV body maps.
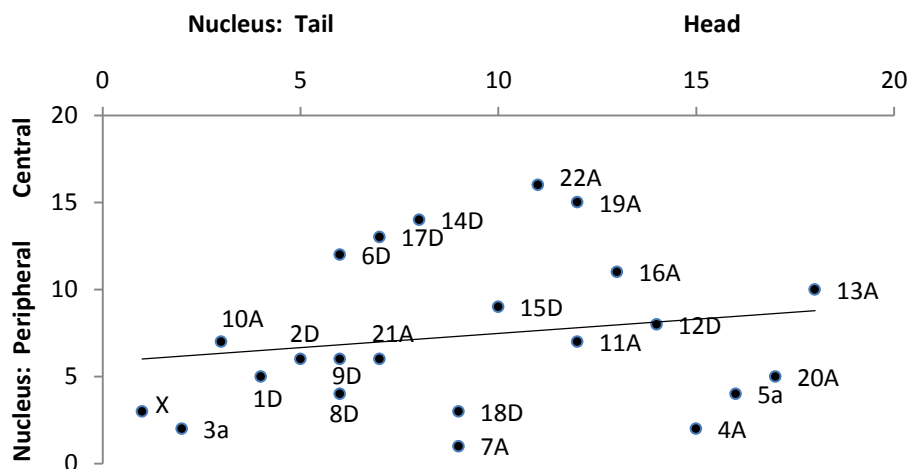
Fig. 4. Partial map of centroids of chromosome sites in *H. sapiens* spermcell nucleus. **A**, chromosomes with AP body mapping; **D**, chromosomes with DV body map (Chrs 3 and 5 are marginally AP). Each chromosome group appears to have a topologically distinct meta-territory in the nucleus: anteroposterior chromosomes tend to occupy an anterior outer border region (with exception of Chrs 11 and 21), which surrounds an inner core that dorsoventral chromosomes occupy. Each axis gives position-order of chromosomes. (Nucleus map is constructed from Tables S1 and S2, in Cherniak & Rodriguez 2013; based on Figs. 2 and 4 of Manvelyan et al 2008.) Bestfit line for all 23 chromosome positions is included.

The "AP vs DV" chromosome distribution in the nucleus raises natural next questions concerning its functional significance. For example, what is the relationship between local and global body maps: How do maps on individual chromosomes mesh with the body map on the overall genome? One point is that the two discrete nucleus zones constitute some independent convergent support for the "AP vs DV" map distinction itself among chromosomes discussed above.

Conclusion

The analyses here suggest a sharp division of labor among human chromosomes -- for body mapping, between anteroposterior and dorsoventral body-axes. For each chromosome: If one body-axis maps significantly to that chromosome, then the other axis tends not; and vice versa. So, for most chromosomes,

    If an AP or DV map has $p \geq 0.05$ (i.e., is non-significant),
    then the other axis map's p is significant, $p < 0.05$.

In addition, this AP vs DV chromosome dichotomy predominantly extends to chromosome locations in the spermcell nucleus: Most AP chromosomes are sited in one distinct zone -- the outer edge of the chromosome set -- surrounding the DV chromosome group.

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We had previously been gauging how well wiring-optimization ideas used in microchip design apply to brain structure. "Save wire" turns out to yield correct predictions of neuroanatomy, sometimes down to one-in-a-billion precision. Some is via an optimization heuristic for component placement: If components are connected, position them adjacent to each other. -- More generally, components most closely related functionally are placed adjacently. In this way, simple wire-minimization seems to drive much brain structure. Body maps can be generated by iteratively applying the Adjacency Rule. We have gone on here to apply these network optimization ideas to genomics, viewing "genome as nano-brain", yielding some "cognitive psychology" of the genome, in particular, homuncular organization.

Homunculus models appear in early developmental biology. An important modern example first emerged in 19th century neuroscience for body mappings on cerebral motor cortex (Fritsch & Hitzig, 1870). Such models also seem worth consideration in genomics.

As mentioned, our earlier study (Cherniak & Rodriguez-Esteban, 2013) reported evidence of global somatotopic maps extending over the entire set of chromosomes in their territories in the spermcell nucleus. Evidence described here suggests similar somatotopic mapping holds not only for such germ cells, but also for individual chromosomes in somatic cells.

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Supporting Material: Table S1

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Table S1. Main Table.

Body-Chromosome Maps: Analysis of bodymap on each individual chromosome. AnteroPosterior vs DorsoVentral BodyAxes.

For SPM ≥ 0.3 - 0.9, via 0.05 increments. For slopes of best-fit regression lines of chromosome bodymappings . (For a given chromosome, a significantly larger mean slope value of AP vs DV mappings is in **boldface**.)

Antero / Posterior Axis

Chromosome	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X
SPM ≥																							
0.3	613105.2	107956.8	1345061	789106.8	624082.8	-296916	-427651	1845020	-677153	-345706	122232.9	484780.9	265314.1	-345263	208002.9	644094.9	171537.1	-42232.6	165426.5	252003.6	-140264	-253817	-549746
0.35	626653.23	64023.18	1958622	569662.8	-191697	-567684	-399969	2003842	-77841.8	-796854	256042.3	369773.8	371820.6	-310703	250914.4	995064.8	337369.5	523267.7	-48672.9	538926.3	-320314	-331420	74034.49
0.4	-422211.7	55686.08	1904137	676999.8	-538378	-318972	-814326	1496520	55004.3	-1643319	164559.3	305696.9	151140.1	-359127	25554.11	938795	490477.3	-369251	43086.04	601814.7	-212406	-331466	-302241
0.45	-485740.2	-331914	1180888	478163.5	-553456	-714415	-1078265	1773969	351543.3	-1022810	38994.01	251691.6	-611768	-294685	452079.4	1122827	266098.5	104828.8	74015.64	906382.7	-241174	-368587	467235.2
0.5	-611998.8	481395.4	1366418	32011.35	-219836	-700596	-1308870	1063245	-231480	-1563689	251016.7	206511.5	-552547	936.2452	71367.72	927754.8	374175.9	549742.8	376019.8	845000.4	-373394	-103862	170938.4
0.55	-936150.6	817778.6	583115.3	-25437	194318.1	-615084	-1455999	354842.1	125705.6	-1248490	240740.9	138448.3	-690341	76216.82	322437.8	826464.6	445398.4	1200418	296616.8	974864.3	-305354	106510.9	335557.5
0.6	-900983.9	1327872	381867.6	197501.2	-98646.8	-116155	-1717421	556378.6	51573.28	-1323845	348127.6	727152.8	-1532855	289722.1	770827	843403.4	767979.9	992891.9	223939.5	1100250	-273348	-144671	-96729.2
0.65	-1074614	441791.3	1313805	1032717	-87306.8	-927047	-2162343	440813	-474738	-2060431	832368.2	291448.3	-2391169	235294.6	537126.5	1302379	858801.9	1522104	375101.9	1006590	-154963	130502.3	-100412
0.7	-2279183	-980240	1015018	2402570	-312720	689260.6	-2109755	41784.69	-70382.8	-1567128	519450.1	747982.7	-2055318	375796	656888	1807808	779822	1109767	441909.9	955679.2	162569.1	-135413	-2458804
0.75	-1296402	-1034357	2786196	1695771	-235175	-58824.5	-1694902	-1408785	-82124.9	450210.9	857421	33265.52	-143759	715926.9	729102.1	2544884	861438.1	594805	764755	1756232	113425.6	246816.1	371681.5
0.8	-1003384	-487690	3089466	3490871	-1074754	309803.4	-1129127	-3324161	1024032	-3217286	1156548	295987.1	-1626797	661108.6	1138924	3556471	1473441	361655.6	803497.8	1730876	-334293	2078.949	877460.8
0.85	-1446072	-643124	-393480	3089331	-1356683	-1308504	-1732125	-2857661	-349130	-2446185	1097360	-862054	-3870817	726442.9	1126109	2849970	-237921	278766.7	757015.5	1464941	-75792.6	-213536	2915449
0.9	-1926949	1837939	-3737627	4184925	-3779985	1710945	-3110535	-2563697	-2407825	-2330069	1491468	-2899024	-5443549	60089.04	-820166	2497398	-387446	-219821	337292.9	1083871	-253918	-773289	2337287
Mean slope	-857225.4	127470.5	**984114.4**	1431861	**-586941**	-224168	**-1472407**	-44453.1	-212524	**-1470431**	567409.9	7050.916	**-1394665**	140904.2	420705.1	**1604409**	477013.2	508226.3	354615.7	**1016725**	**-185325**	**-166935**	310900.9
single-sample t test p <	0.0032358	0.602037	0.058667	0.003314	0.074487	0.321311	1.26E-05	0.933389	0.344678	0.000119	0.000912	0.979252	0.012927	0.230478	0.012465	5.33E-05	0.004346	0.007738	0.000632	2.36E-06	0.001703	0.042127	0.407209

Dorso / Ventral Axis

Chromosome	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	X
SPM ≥																							
0.3	-1290780	-385819	-986296	83290.65	821922.1	-323166	398603.7	618118.1	-250192	974418	424400.3	-212851	-284187	-39091.1	-29564.7	-371457	-500394	-746041	-143787	-363592	122157.2	-96184.9	-337802
0.35	-1988526	-892959	-919138	449561	200154.8	114578.1	926092.8	720000.4	312555.1	834518.7	612892.3	161942.5	4242.317	112319.3	-462526	-555828	-468778	-496193	-94916.7	-117214	252121.4	118029.3	-1849.71
0.4	-2364673	-1143026	-915513	1533843	77079.59	796912.8	1343619	1266054	1311684	685588.7	112159.2	177843.8	-506160	-17418.6	-344695	-883095	-607870	-183272	-136848	-62070.4	-55813.4	215702.3	-789933
0.45	-2009763	-1592822	-1070034	688979.8	-169586	903770.7	2000258	1792875	1509722	318863.6	-138200	228152.1	-681647	-101502	-489248	-733680	-985739	-562482	-158573	-200109	-57987.6	82946.47	152814.4
0.5	-2071579	-1549952	-1094493	345838.2	247334.6	75378.75	1185789	1744768	1760386	-136332	889069.6	353997.1	-1187697	94347.38	-1273123	-423164	-1057068	-1447295	227187.8	52477.96	-209049	489927.6	-176627
0.55	-1823430	-2153460	-1368165	-143165	-211740	490373.5	1812750	2155468	1977500	-167048	233292	1170311	-575919	-493503	-1534753	-818061	-717334	-1579362	359468.3	11326.47	-161823	368436.9	1097806
0.6	-1829732	-2258284	-1589659	1112573	-319404	319973.4	1991036	3636026	1669379	1067626	517550.5	329210.7	-1175333	-822179	-1809153	-1032847	-332626	-1430387	119343.4	195473.4	129749.4	25492.43	-632907
0.65	-1279232	-2716590	-398416	254777.1	-691130	2491.352	1029279	4170893	942718.2	578506.6	-356717	800045.9	-3532094	-729700	-1831470	-1521694	-379763	-2937458	138455.5	434846	279876.1	-102908	-1156803
0.7	-2774536	-1777264	-640679	690966.5	-485573	590479.7	209315.8	4264569	1774147	1062409	-685797	783730.6	-3523927	-70399.2	-2439405	-1002544	-439676	-3381989	264328.2	680016.5	136794	-91098.2	-486002
0.75	-3619163	-2094003	1670253	558907.9	-1215798	1226351	-7493.03	4497256	1648234	1606583	-673917	1582937	1160838	347957.4	-2728910	22343.32	-723124	-3086593	190216.9	472223	-176972	-429982	-333211
0.8	-4208243	-1625286	1207906	-628939	-1334547	437750.8	-584729	6365590	1196290	1762560	162822.2	2310073	1730906	-1894062	-3121546	60555.58	-255694	-4391022	221073.4	473986.7	-225899	-1183015	763943.3
0.85	-3608246	-1322693	2522586	3.52E+03	727084.7	1167338	-1790746	7692197	-608127	1122657	132926.8	275695.7	2133313	-1638405	-4118872	539733.7	-529230	-3886682	-231465	115162.4	-643084	-860968	6688103
0.9	-3275486	-4530162	2754912	1066009	1452663	338739.7	-341703	5463778	-422892	-1140482	-888915	1185706	2499689	-1561158	-2492196	361922	-200701	-4771126	234002.2	-765081	-945537	-121454	5777959
Mean slope	**-2472568**	**-1849409**	-63595.1	462781.5	-69349.2	**472382.5**	628621	**3414430**	**986261.8**	659220.7	26274.29	**703599.6**	-302921	**-524061**	**-1744266**	-489063	**-553692**	**-2223069**	76037.4	71341.99	-119651	-121929	812730.1
single-sample t test p <	6.412E-07	2.59E-05	0.883411	0.013728	0.757337	0.003019	0.066309	0.000139	0.002161	0.010798	0.865145	0.00353	0.573604	0.026944	0.000244	0.012381	5.83E-06	0.000287	0.193754	0.526125	0.241717	0.365256	0.26145

AP vs DV: paired-sample t-test

| unequal-variance p < | 0.0001152 | 1.78E-05 | 0.111664 | 0.036203 | 0.178083 | 0.012026 | 1.44E-05 | 0.000287 | 0.00149 | 2.3E-06 | 0.012288 | 0.045874 | 0.136852 | 0.01125 | 2.24E-05 | 1.41E-06 | 2.63E-06 | 3.24E-05 | 0.007838 | 6.02E-06 | 0.549434 | 0.765776 | 0.527438 |

(All p values are 2 tailed.)