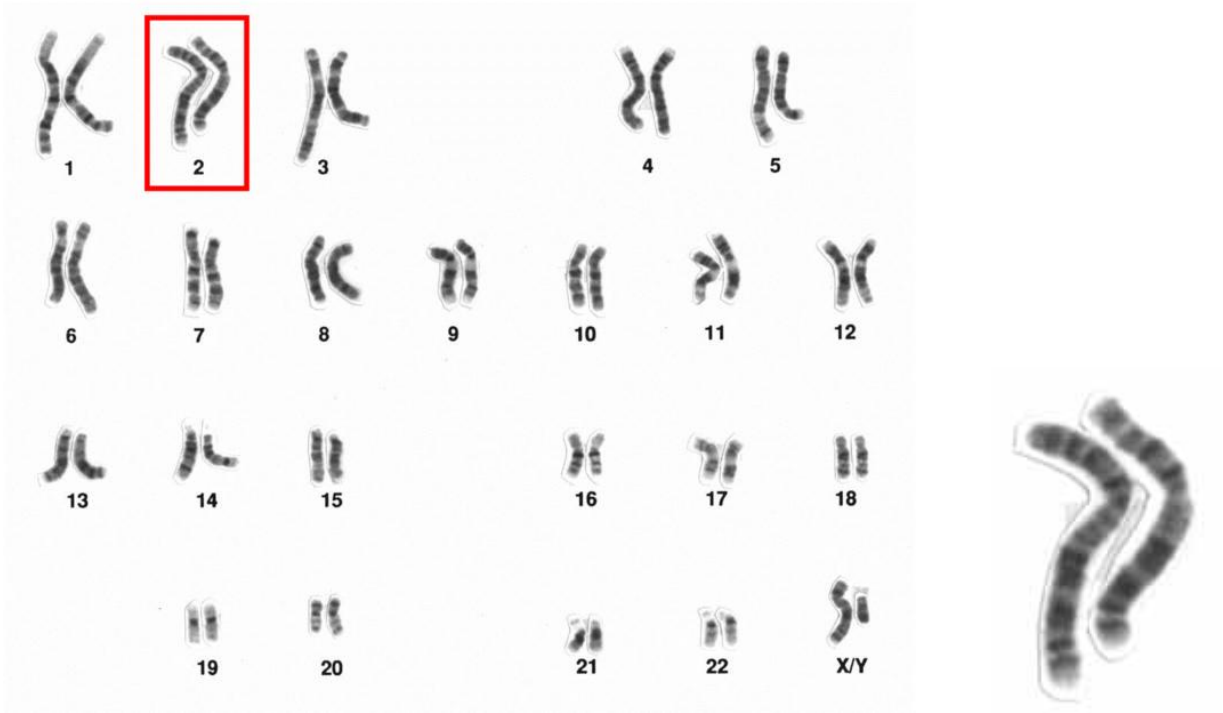
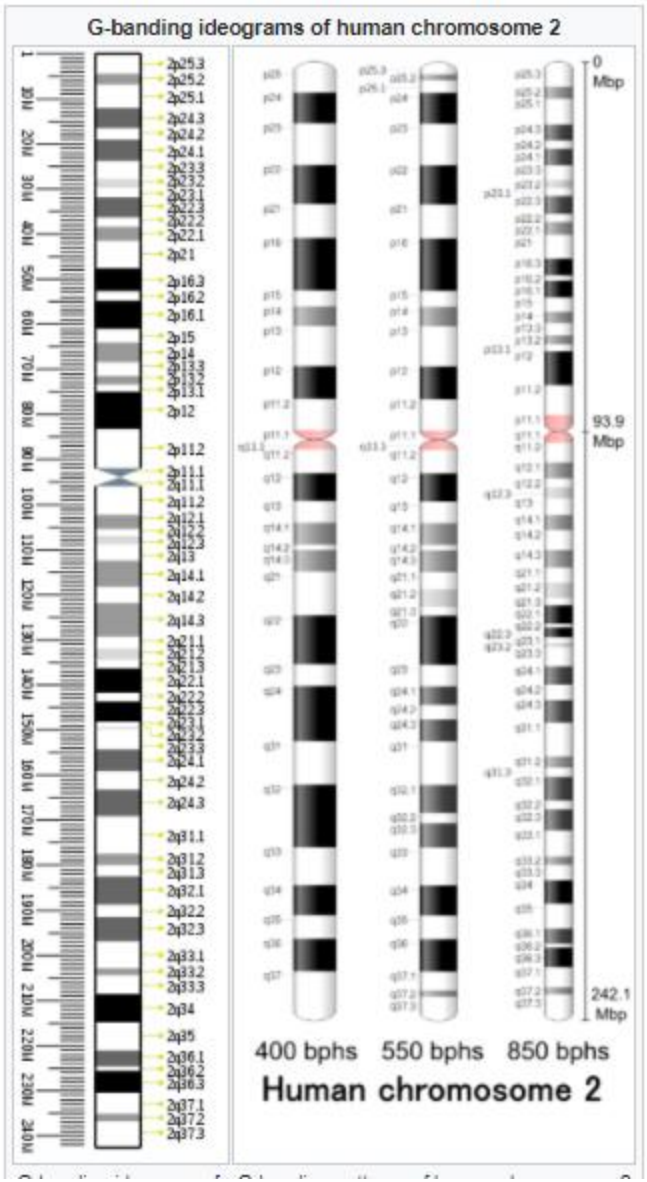
# CHROMOSOME 2: Mapping the Transitions from YOUNG / WINDECKER to BAIN and Return to YOUNG / WINDECKER Ancestral Segments

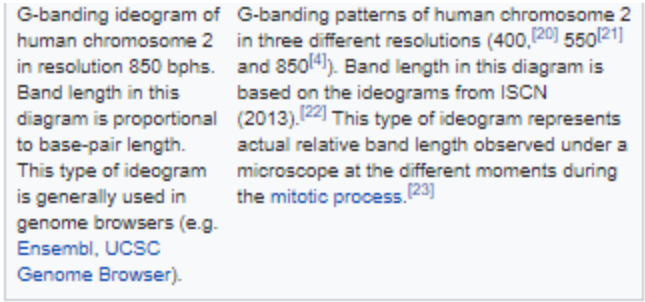
**Description of Chromosome 2**:

Chromosome 2 is one of the 22 pairs of autosomes (one from the mother, one from the father) and is the second largest of the group. It is characterized as, "spanning more than 242 million base pairs[5] (the building material of DNA) and representing almost 8% of the total DNA in human cells." This chromosome has about 1,200 protein coding genes, including the HOXD complex, on the segment 176,880,740 to 177,056,400 Mb which codes anterior to posterior development (body structures during development) of the organism.




Above is a karyogram of the 22 pairs of human autosomes and the sex chromosomes (in a male). The size of chromosome 2 can be seen in relation to the entire array.


G-banding ideograms of human chromosome 2
0
Mbp
93.9
Mbp
242.1
Mbp
400 bphs
550 bphs
850 bphs
Human chromosome 2



G-banding ideogram of human chromosome 2 in resolution 850 bphs. Band length in this diagram is proportional to base-pair length. This type of ideogram is generally used in genome browsers (e.g. Ensembl, UCSC Genome Browser).

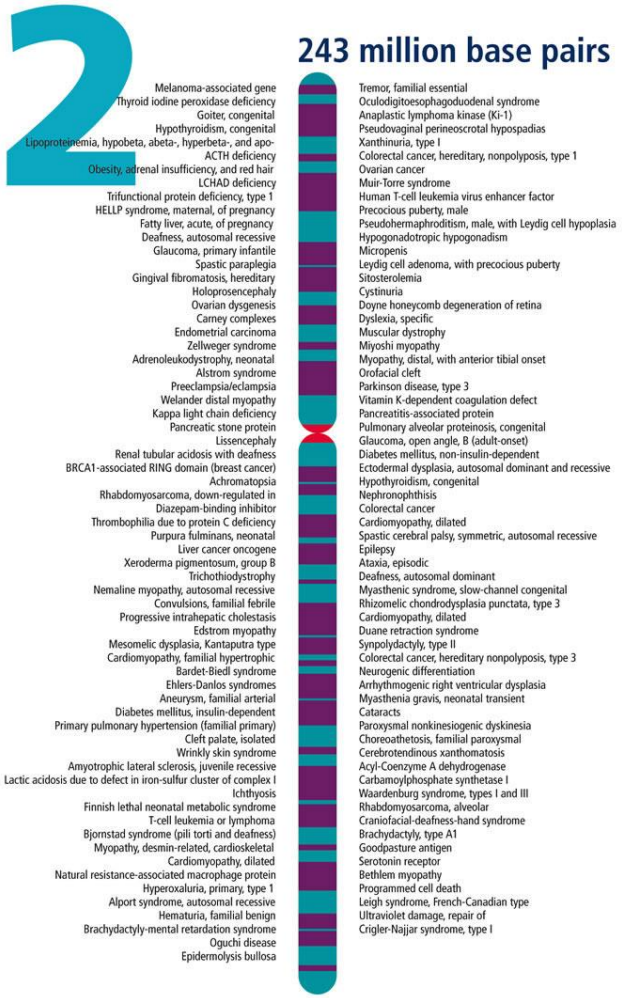
G-banding patterns of human chromosome 2 in three different resolutions (400,[20] 550[21] and 850[4]). Band length in this diagram is based on the ideograms from ISCN (2013).[22] This type of ideogram represents actual relative band length observed under a microscope at the different moments during the mitotic process.[23]

The G banding shown in the above map allows geneticists to pin a particular gene to a physical location on the chromosome. As seen in the chart below, each band has a start and stop point expressed in Mb. Since it is not possible, for the sake of space and other factors to list every gene, the author will note examples of segments of known origin in relation to the G bands, and then show the various diseases associated with these and all bands along the chromosome.

G-bands of human chromosome 2 in resolution 850 bphs[4]

| Chr. | Arm[24] | Band[25] | ISCN start[26] | ISCN stop[26] | Basepair start | Basepair stop | Stain[27] | Density |
|---|---|---|---|---|---|---|---|---|
| 2 | p | 25.3 | 0 | 388 | 1 | 440,0000 | gneg | |
| 2 | p | 25.2 | 388 | 566 | 4,400,001 | 6,900,000 | gpos | 50 |
| 2 | p | 25.1 | 566 | 954 | 6,900,001 | 12,000,000 | gneg | |
| 2 | p | 24.3 | 954 | 1193 | 12,000,001 | 16,500,000 | gpos | 75 |
| 2 | p | 24.2 | 1193 | 1312 | 16,500,001 | 19,000,000 | gneg | |
| 2 | p | 24.1 | 1312 | 1565 | 19,000,001 | 23,800,000 | gpos | 75 |
| 2 | p | 23.3 | 1565 | 1789 | 23,800,001 | 27,700,000 | gneg | |
| 2 | p | 23.2 | 1789 | 1908 | 27,700,001 | 29,800,000 | gpos | 25 |
| 2 | p | 23.1 | 1908 | 2027 | 29,800,001 | 31,800,000 | gneg | |
| 2 | p | 22.3 | 2027 | 2296 | 31,800,001 | 36,300,000 | gpos | 75 |
| 2 | p | 22.2 | 2296 | 2415 | 36,300,001 | 38,300,000 | gneg | |
| 2 | p | 22.1 | 2415 | 2609 | 38,300,001 | 41,500,000 | gpos | 50 |
| 2 | p | 21 | 2609 | 2966 | 41,500,001 | 47,500,000 | gneg | |
| 2 | p | 16.3 | 2966 | 3220 | 47,500,001 | 52,600,000 | gpos | 100 |
| 2 | p | 16.2 | 3220 | 3294 | 52,600,001 | 54,700,000 | gneg | |
| 2 | p | 16.1 | 3294 | 3548 | 54,700,001 | 61,000,000 | gpos | 100 |
| 2 | p | 15 | 3548 | 3757 | 61,000,001 | 63,900,000 | gneg | |
| 2 | p | 14 | 3757 | 3935 | 63,900,001 | 68,400,000 | gpos | 50 |
| 2 | p | 13.3 | 3935 | 4114 | 68,400,001 | 71,300,000 | gneg | |
| 2 | p | 13.2 | 4114 | 4248 | 71,300,001 | 73,300,000 | gpos | 50 |
| 2 | p | 13.1 | 4248 | 4353 | 73,300,001 | 74,800,000 | gneg | |
| 2 | p | 12 | 4353 | 4860 | 74,800,001 | 83,100,000 | gpos | 100 |

## Genes and Diseases Associated With Chromosome 2:



**Genetic Features of Segments of Known Origin**:

There are few genes of any consequence on the interesting (genealogically as will be seen below) segment between 33 to 44 Mb and 44 to 53 Mb from WINDECKER (specifically Henry WINDECKER's grandparents, Heinrick Conrad and Anna Christina (MATHEUS) WALRATH); and YOUNG ancestors (specifically Daniel YOUNG' parents Johann Adam and Catharina Elizabeth (SCHREMLING) JUNG) respectively. There are more genes on the adjacent segment from about 53 to 79 Mb which can be traced to ancestors of Mary BAIN, the source of this segment being her ancestors William SNADON (born 1700) and / or wife Catherine SNADON (born 1700), who were first cousins, from Alloa, Clackmananshire, Scotland.

Genes on the longest segment of known provenance between about 80 and 128 Mb are known to be from the author's 5th great grandparents Captain Daniel YOUNG (1755 – 1834) and / or his wife Elizabeth WINDECKER (1763 – 1836). Another segment, extending from about 204 Mb to 215 Mb can be attributed to the grandparents of Daniel YOUNG, namely Johann Theobald (born 1691) and / or Maria Catharina (SNYDER) JUNG. The specifics of all segments of known origin will be depicted below in chart form after the following illustrations of the regions involved.

**Genealogical Origins of Segments on Chromosome 2 – From Gedmatch and FTDNA**:

| Chromosome | Position (Mb) | | cM | SNPs | Person | Ancestor(s) in Common | G G Grandparent(s) | Position of Match |
|---|---|---|---|---|---|---|---|---|
| 2 | 8,674 | 6,753,810 | 13.2 | 2,128 | Jim Arnold | William McCormack (1836) & Mary Bain | William McCormack & Mary Bain |  |
| 2 | 7,980,572 | 10,579,817 | 6.5 | 785 | John Williams | George Dawson (1827) & Mary Ann Dunham | John Dawson | FTDNA |
| 2 | 33,476,810 | 44,133,126 | 12.8 | 2,992 | Jacqueline Adams | Henry Windecker (1736) & Dorothy Pickard | Hannah Adelia Young |  |
| 2 | 33,589,785 | 44,112,034 | 11.7 | 3,100 | Jody Hash Crowl | Hendrick Conrad Walrath & Anna Christina Matheus | Hannah Adelia Young | FTDNA |
| 2 | 33,589,785 | 44,112,034 | 12.1 | 3,200 | John Bowers | Henry Windecker | Hannah Adelia Young | FTDNA |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | (1736) & Dorothy Pickard | | |
| | | | | | | | | |
| 2 | 43,391,215 | 53,322,336 | 11.25 | 3,300 | Maggie Cvek | Hendrick Schremling – Theobald Jung Sr. | Hannah Adelia Young | FTDNA |
| 2 | 43,893,905 | 53,560,407 | 9.9 | 1,507 | Robert C. Nelson | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 43,893,905 | 53,462,867 | 9.8 | 1,494 | Amanda Young | Daniel Young (1755) & Eliz Windecker | Hannah Adelia Young |  |
| 2 | 43,893,905 | 53,384,688 | 9.7 | 1,479 | Tom Nelson | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 43,898,184 | 53,384,287 | 9.7 | 2,980 | Audrey (Betty) Elizabeth Cuppy | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 44,113,851 | 53,913,635 | 11.8 | 3,300 | Connie Edwards | Hendrick Schremling – Theobald Jung Sr. | Hannah Adelia Young | FTDNA |
| | | | | | | | | |
| 2 | 53,346,636 | 79,627,751 | 26.9 | 6,302 | Jim Arnold | William McCormack (1836) & Mary Bain | Mary Bain |  |
| 2 | 56,360,803 | 78,713,382 | 23.5 | 3,040 | Walt Gale | William Snadon (1700) & Catherine Snadon | Mary Bain |  |
| | | | | | | | | |
| 2 | 81,873,176 | 101,977,153 | 8.6 | 2,336 | Audrey (Betty) Elizabeth Cuppy | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 82,363,176 | 106,011,094 | 11.1 | 3,257 | Robert C Nelson | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 82,456,901 | 119,943,392 | 22.1 | 5,845 | Carolyn Vassos | Daniel Young (1755) & Eliz Windecker | Hannah Adelia Young |  |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 2 | 82,919,371 | 106,016,513 | 10.8 | 3,250 | Kay Montgomery Rumney | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 116,142,763 | 127,910,398 | 11.1 | 1,361 | Trisha MacLeod | Henry Young (1825) & Elizabeth Young | Hannah Adelia Young |  |
| 2 | 204,336,038 | 214,959,471 | 10.7 | 2,302 | Jennifer Sewell Glover | Theobald Young (1691) & Maria C. Snyder | Hannah Adelia Young |  |
| 2 | 204,506,035 | 211,730,000 | 7.3 | 1,560 | Kay Montgomery Rumney | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 204,506,035 | 211,638,178 | 7.2 | 1,542 | Dan Nelson | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 204,507,942 | 211,784,597 | 7.3 | 1,554 | Robert C Nelson | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 204,524,820 | 211,362,876 | 6.9 | 1,475 | Norm Sones | Elizabeth Young (1827) | Hannah Adelia Young |  |
| 2 | 227,720,427 | 233,653,809 | 9.8 | 1,430 | Kay Montgomery Rumney | Elizabeth Young (1827) | Hannah Adelia Young |  |

**Genealogical Analysis**: Perhaps the most interesting group of segments yet discovered on the "p" arm of this chromosome begins about 33.5 Mb and ends about 44 Mb. This segment can be further attributed to an earlier generation, being inherited from Henry WINDECKER's mother Anna Elizabeth (WALRATH) WINDECKER (1716 Schoharie, New York – 1793 Ft. Plain, Minden Township, Montgomery County, New York). The origin of the segment can be narrowed down to the wife of Johann Georg WINDECKER, Anna Elizabeth WALRATH since while John Bowers is a descendant of both lines extending back from the daughter of their son Henry WINDECKER'S daughter; however Jody Hash Crowl descends only from the WALRATH family. Thus we can with some confidence attribute this segment to Anna Elizabeth's parents, Heinrich Conrad WALRATH born 1691 Runkel, Germany

died after 1746, when he wrote his will, in Canajoharie, New York (likely the Windecker Tract) and Anna Christina MATHEUS born 1685 Dunzweiler, Germany.

The segment between about 44 Mb to about 53 Mb has been inherited from Johann Adam JUNG 1717 Foxtown, Schoharie, New York – 1790 Seneca Township, Haldimand County, Ontario and / or his wife Catharine Elizabeth SCHREMLING (1720 Schoharie, New York – 1798 Barton Township, Wentworth County, Ontario). Connie Edwards and Maggie Cvek are descendants of both Hendrick and Maria Elizabeth (LANDGRAFF) SCHREMLING, and Johann Theobald (1691) and Maria Catharina (SNYDER) JUNG. The excellent genealogies help to identify the origin of the second of the two segments, 44 Mb to 53.9 Mb as YOUNG / SCHREMLING via Adam YOUNG and / or wife Catharine Elizabeth (SCHREMLING) YOUNG.

So in summary, the first segment can be linked to Elizabeth (WINDECKER) YOUNG; and the second segment originated with her husband Daniel YOUNG, the double great grandparents of Hannah Adelia (YOUNG) DAWSON.

Then there is a seamless transition (recombination point) that begins where the previous YOUNG – SCHREMLING segment left off at about 53 Mb and extends to about 80 Mb. It has been inherited by the author's Scottish BAIN ancestors via William SNADON born 1700 Alloa, Clackmananshire, Scotland and / or his wife and cousin Catherine SNADON born 1700 in the same place. The recombination must have occurred via the amalgamation of the anterior part of the chromosome of the author's great grandfather Joseph William DAWSON born 1872 Barton Township, Wentworth County, Ontario with the adjacent posterior part of the chromosome 2 of his wife Annie (MCCORMACK) DAWSON. With this sort of specific information it makes the genetic pedigree weave together with the genealogical pedigree. The chromosome at approximately 80 Mb shifts once again back to the YOUNG and WINDECKER family. Since all who share this segment with the author have both ancestral lineages it is not yet possible to parse it out to one or the other. The segment ends about 127 Mb, although it is possible that there is a small segment of about 10 Mb from another source (e.g., Mary BAIN) between 106 and 116 Mb. There is then a region whose origin is unknown until 204 Mb (near the end of the "q" arm of chromosome 2), extending to about 234 Mb which is also YOUNG via Johann Theobald JUNG (born 1691) and / or wife Maria Catharina SNYDER through their eldest son Johann Adam JUNG (born 1717).

It is important to note that the origin of each of these segments can be considered valid in that they have been "triangulated" with multiple matches to distant relatives (e.g., half 3rd cousins once removed; $7^{th}$ cousins).

**Summary and Conclusions**: Considering the size of chromosome 2 it is quite amazing how much can be attributed to various early ancestors. To date there is no information to pinpoint the origin of the segment on which the HOXD genes reside. However the

mapping that is possible at this point shows some very clear junctions between the contributions of two of the great great grandmothers of the author – Hannah Adelia (YOUNG) DAWSON and Mary (BAIN) McCORMACK then back to Hannah Adelia (YOUNG) DAWSON – in the area between about 33 to 106 Mb. Secondarily, there is a similar close join is seen between the "contribution" of William and Mary (BAIN) McCORMACK and John DAWSON at about 7.5 Mb. Furthermore, at about 44 Mb there is a clear junction between the contribution of the Elizabeth (WINDECKER) YOUNG via her grandparents Hendrick Conrad WALRATH and Anna Christina MATHEUS; and a YOUNG segment (from Adam or Catharine Elizabeth (SCHREMLING) YOUNG), the parents of Daniel YOUNG extending to 53 Mb.

In all probability, over time, more of the maternal chromosome 2 of the author will be mapped; however to date all of the segments of known origin on the larger, q, end of the chromosome come from the author's great great grandmother Hannah Adelia (YOUNG) DAWSON. Hence the hypothesis to be tested is whether Hannah contributed the entire q end of chromosome 2 to the author – which will, alas, never be realized unless Ancestry.com offers a chromosome browser so that the large number of matches in their database will reveal the specific segments which are shared.

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16 November 2017, 30 May 2019.