

# Hämta segmentdata hos Gedmatch

Gedmatch använder sig av kitnummer. För att komma åt data om segmenten får man välja något av följande alternativ under 'DNA Applications':

'One-To-Many' eller 'One-to-One Autosomal DNA Comparison' (om man redan vet kitnummer man vill jämföra sig mot)

## DNA Applications:

- [One-To-Many Beta - give it a try](#)
- [One-To-Many DNA Comparison Result](#)
- [One-to-One Autosomal DNA Comparison](#)

Klicka på den blå summan under kolumnen 'Largest' under 'Autosomal'

One-to-many DNA comparison for: Kit T437235 Note: Additional facilities in Tier 1 One-to-many version.

Filter by  autosomal  X with this offset 0 with this limit 50 Prev Next and cM size 7 Tag Groups  None  All  One. Overlap cutoff 45000 Search Tips Select all match

Visualization Options

Select	Kit	Name (* => alias)	Email	GED WikiTree	Age(days)	Type	Sex	Mt	Y	Total cM	Largest
<input type="checkbox"/>	T220879	Tommy Jansson	eva.vonbromsen@gmail.com		2156	2	M			225.7	<a href="#">38.7</a>

Du kommer nu att få upp en bild med ditt kitnummer och din DNA-träffs kitnummer. Välj 'Position Only' och tryck sedan 'Compare'.

### GEDmatch® One-to-one Autosomal Comparison Entry Form

[Here](#) is a link to a useful YouTube video on using the One to One DNA comparison tool.

This utility allows you to make detailed comparisons of 2 DNA kits. Results may be based on either default dynamically determined thresholds, or thresholds that you provide. Estimates of 'generations' are provided for default thresholds as a relative means of comparison, and should not be taken too literally, especially for more than a couple of generations back.

Kit Number 1:

Kit Number 2:

Show graphic bar numeric positions for each Chromosome?

Graphics and Positions  
 Position Only  
 Graphic Only  
 Display Only Chromosomes with Matched Segments

Builds to Display (Build37 is default):  B36  B37  B38

Window width in pixels: For Full resolution graphic, check 'Full resolution'

Full resolution

SNP window size threshold. Leave blank for default to vary dynamically between 200-400

Minimum segment cM size to be included in total: (Must be at least 3 cm. Leave blank for default value = 7)

Size (in SNPs) of Mismatch-Bunching limit. (Leave blank for default mismatch eval window / 2)

Show only Full-Match (FIR) segments.

Prevent Hard Breaks (default is to create hard breaks when distance between SNP's exceeds 500,000 base positions):

För att markera allt på sidan, tryck samtidigt på knapparna CTRL + A (markerar allt), tryck sedan CTRL + C (kopierar). För att klistra in hos DNA Painter tryck CTRL + V.

## GEDmatch® Autosomal One-to-one Comparison - V1.0

Software Version Apr 11 2020 19:11:47

Here is a link to a useful YouTube video on using the One to One DNA comparison tool.

Comparing Kit T437235 (Eva Susann von Brömsen) [Migration - F2 - F] and T220879 (Tommy Jansson) [Migration - F2 - F]

Segment threshold size will be adjusted dynamically between 200 and 400 SNPs

Minimum segment cM to be included in total = 7.0 cM

Mismatch-bunching Limit will be adjusted dynamically to 60 percent of the segment threshold size for any given segment.

Chr	B37 Start Pos'n	B37 End Pos'n	Centimorgans (cM)	SNPs
1	4,235,683	13,176,463	18.0	2,487
1	13,775,122	18,152,582	9.5	1,244
7	30,519,030	37,381,220	8.5	1,783
10	98,087	12,834,926	30.4	4,730
12	6,083,564	16,149,039	20.2	2,662
14	46,812,461	77,057,801	30.5	7,140
16	19,144,378	32,137,965	17.6	2,565
16	46,582,888	59,877,306	20.9	3,161
18	43,948,285	61,826,179	24.9	4,632
20	347,459	2,810,098	8.3	1,000