Coding Chromosomal Abnormalities
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Believe it or not, this is actually EASIER than coding the physical anomalies because it is unambiguous. You just need to get past being intimidated by the way the test result is reported.

A karyotype has numbers, letters, and abbreviations separated by commas, parentheses, and semicolons. A karyotype result generally is interpreted as

Number of squiggles under the microscope (comma)
Sex chromosome complement (comma)
[if it’s normal, it stops there, if not...]
What the abnormality is (comma, open parenthesis)
Which chromosome(s) has the abnormality (close parenthesis)
Which arm of the chromosome has the problem
Which band/region/sub-band has the problem
Which other band/region/sub-band is involved
[if only one chromosome is involved, it stops here with a closed parenthesis, if not...] (semicolon)
Which arm of the other chromosome has the problem
Which band/region/sub-band has the problem, etc.
(close parenthesis)

The three lines in *italics* are where you concentrate for coding. Everything else is fluff.

Each abbreviation means something, but the most important for our purpose are:

| Things that mean there is extra of something | “+”, “x”, add, dup, mar, |
| Things that mean there is something missing | “-“, del, r, |
| Things that mean something is rearranged | der, ins, inv, rob, t, |

The other abbreviations are indicative of a complex problem that is going to need clinical input, anyway.
Other important general definitions:

**Mosaicism** (mos) is the concept that there are two or more types of cells in the body. When talking about chromosomal mosaicism, it means that the case has more than one karyotype. In a karyotype, you will see two apparently complete results together, separated by a slash “/”. Such as 45,X/46,XX. You may see numbers in [brackets]. That is the number of cells that have the karyotype. So, if there were 20 cells counted, and 5 had one karyotype, and 15 had the other, the result would be written 45,X [5]/ 46,XX [15]. For our purposes the numbers in brackets don’t matter.

**Chromosome Groups A, B, C, D, E, F, and G.** Before banding was defined, the chromosomes could only be grouped by size, so there were the A group, the B group, C, D, E, F, and G. We never use these designations these days, but the BPA codes still use the terms. You can ignore them.

**Eponyms** Down syndrome, Patau syndrome, Edwards, Jacobsen, Pallister-Killian, Cat Eye, Cri-du-Chat, Wolff-Hirschorn, etc. Some of the microscopic chromosome changes have names, others do not. Some of them are in common use, many are not. Some of them are helpful, others...not so much. Remember that, unless you have a karyotype or indication of an established diagnosis, use of the eponym should be taken with a grain of salt.

**Sex Chromosome Problems: 758.6, 758.7, 758.8**

**758.6: Gonadal dysgenesis**
This is the old/outdated name for what we now call Turner syndrome.

758.600 - Used when the chromosome analysis result is 45,X
The outdated way to write this is “45,XO”, but there is no such thing as an “O” chromosome, so you will only seen “45,XO” in notes of non-geneticists. You will never see “45,XO” on a test result.

758.610 - If it is a diagnosis of Turner syndrome with any other specified X chromosome problem, then this is the code. Doesn’t matter what it is. If it is Turner syndrome, you have a known chromosome result, but that result is NOT 45,X, this is the correct code. The one exception is mosaicism, which is coded 758.800 or 758.810 depending upon whether the normal cell line has a Y chromosome or not.

758.690 – Used for a clinical diagnosis of Turner syndrome, but there is no chromosome result available. You are unable to assign one of the two above codes to the case.

**758.7: Klinefelter Syndrome**
These are males who simply have more than one X chromosome. There is at least one Y and then....other stuff.

758.700 - Used when the chromosome analysis result is 47,XXY
758.710 – Used when there is a diagnosis of Klinefelter syndrome and there is a chromosome result that is anything other than 47,XXY. Doesn’t matter what. If you have Klinefelter, and you have an abnormal karyotype that is NOT 47,XXY, use this code. The one exception is mosaicism, which is coded 758.820.

758.790 – Used for a clinical diagnosis of Klinefelter syndrome, but there is no chromosome result available. You are unable to assign one of the two above codes, so you have to use this one.

758.5: Other conditions due to sex chromosome anomalies
These are the things that involve X and/or Y chromosomes, but which are not covered by one of the codes in 758.6 or 758.7.

758.800, .810, .820, and .830 are all codes for specific sex chromosome mosaicsisms: abnormalities of the sex chromosomes in which there are at least two different cell types. One of the cell types may be normal.

758.800 – Turner syndrome mosaic in which the normal cell line is male (has a Y)

758.810 – Turner syndrome mosaic in which the normal cell line is female

758.820 – Klinefelter syndrome mosaic with a normal male cell line

758.830 – Any other mosaic including a single Y chromosome and some abnormal number of X chromosomes. All other chromosome are normal.

758.840 – Specifically for karyotype 47,XYY – the presence of two Y chromosomes. These babies are normal males phenotypically, so this is only going to be found coincidentally. May be found on amniocentesis.

758.850 – Specifically for karyotype 47,XXX. Called “triple X” or “Superfemale” some times.

758.860 – “Additional sex chromosomes NOS”. Only used if that statement is paraphrased. If there is a specific statement that it is Turner or Klinefelter or “superfemale” or something else that lets you infer at least a better code, then use that.

758.880 – “Other specified sex chromosome anomaly”. Just what it sounds like. There is something very specific (so the “NOS” code isn’t applicable) but there is not a good code assignment. We use this for XX males and XY females, for example. This could be used for translocations involving a sex chromosome.

758.890 – “Unspecified sex chromosome anomaly”. Pretty much has to say that. If it mentions almost anything – a number, the X or Y, etc, that is probably going to let you use a more specific code.
Autosome Problems

758.0, 758.1, and 758.2 are the common trisomies and the codes are all parallel to each other. There is some redundancy.

<table>
<thead>
<tr>
<th>Code</th>
<th>Karyotype</th>
<th>Use</th>
</tr>
</thead>
<tbody>
<tr>
<td>758.000</td>
<td>47,XX,+21 or 47,XY,+21</td>
<td>When you have a karyotype showing the normal ‘free’ trisomy</td>
</tr>
<tr>
<td>758.100</td>
<td>47,XX,+13 or 47,XY,+13</td>
<td></td>
</tr>
<tr>
<td>758.200</td>
<td>47,XX,+18 or 47,XY,+18</td>
<td></td>
</tr>
<tr>
<td>758.010</td>
<td>46,XX,t(14;21),+21</td>
<td>When you have a karyotype or a verbal description that clearly notes a translocation. Doesn’t matter what other chromosome is involved in the translocation</td>
</tr>
<tr>
<td>758.110</td>
<td>46,XX,t(13;14),+13</td>
<td></td>
</tr>
<tr>
<td>758.120</td>
<td>46,XX,t(4;18) der(4)(p15.2q11.2)</td>
<td></td>
</tr>
<tr>
<td>758.020</td>
<td>46,XX/47,XX,+21</td>
<td>When you have a karyotype or a verbal description that clearly notes a mosaicism of the trisomy. Doesn’t matter which sex or what the other cell line is.</td>
</tr>
<tr>
<td>758.130</td>
<td>46,XY/47,XY,+13</td>
<td></td>
</tr>
<tr>
<td>758.230</td>
<td>46,XX/47,XY+18</td>
<td></td>
</tr>
<tr>
<td>758.090</td>
<td>“Down syndrome”</td>
<td>Clear clinical diagnosis, but there is no karyotype available. Example: an ER note that says “baby with Down syndrome here because of a fever”</td>
</tr>
<tr>
<td>758.190</td>
<td>“Trisomy 13”</td>
<td></td>
</tr>
<tr>
<td>758.290</td>
<td>“Trisomy 18”</td>
<td></td>
</tr>
</tbody>
</table>

Additionally, there is a condition which is called “pseudo trisomy 18”. It is probably rarely diagnosed, but there is a BPA code for it: 758.295. This is only used if the karyotype is normal.

758.3: Autosomal deletion syndromes

There are codes for a few specific deletions (don’t ask me why they chose these, I don’t know) then you will end up putting a lot in the “other” code.
758.300 – Monosomy 21 (45,XX,-21) or any condition in which part of chromosome 21 is deleted.

758.310 – As written, this code starts out specifically for deletions of the short arm of chromosome 5, but then becomes more general to any deletion involving chromosome 5. I suggest using the more general definition.

758.320 - As written, this code starts out specifically for deletions of the short arm of chromosome 4, but then becomes more general to any deletion involving chromosome 4. I suggest using the more general definition.

758.330 – Deletion of the long arm of 13. But chromosome 13 is an acrocentric chromosome, so it is pretty much all long-arm. This code could be used for Monosomy 13.

758.340 and 758.350 – Deletion of the long or short arm, respectively, of chromosomes 17 and 18.

758.360 – “Monosomy G Mosaicism”. Probably the one time you can’t ignore the letter grouping. The G group consists of chromosomes 21, 22, and Y. There is no such thing as monosomy Y: it isn’t survivable. And monosomy 21 is already accounted for by code 758.300. So, this code really is only applicable to mosaic monosomy 22. An amazingly specific code for a quite rare finding.

758.370 – Deletion of 22q11. Specific code added for this common condition. Should be used instead of or in addition to any clinical diagnosis of DiGeorge or Velo-Cardio-Facial syndrome. The deletion causes a variety of medical conditions and should not necessarily be considered equivalent to “DiGeorge syndrome” which has its own code: 279.110

758.380 – This is for everything that doesn’t fit into one of the other codes above. Note that it is for specified loss of autosomal material. That means anything – deletions, monosomies, etc of anything that isn’t a sex chromosome. If you know which chromosome it is, and that there is part of it missing, the case gets this code.

758.390 – This is for those cases in which you know there is a loss of genetic material at the karyotype or microarray level, but you are not clear what it is. Specifically, you know there is a loss, but you do not know which chromosome. If you know which chromosome, then that’s the .380 code.

**758.4: Balanced autosomal translocation in normal individual**

By definition, these babies don’t have structural birth defects. Your program can decide whether minor anomalies count. You are pretty much only going to use this code if a balanced translocation is found by amniocentesis of chorionic villus sampling and the baby is normal at birth (doesn’t have birth defects).
758.5: Other conditions due to autosomal anomalies

Or, as I like to call it “the big wastebasket chromosome codes”. You will use these a lot. These codes were invented back before we knew much about chromosomes, so lots of stuff which should ideally be separated is just thrown together.

758.500 – Very specifically for Trisomy 8. You will mostly see this in mosaic form, and I recommend using this code for regular and for mosaic Trisomy 8. As written, the code is for extra copies of the entire chromosome.

758.510 – And this is not very specifically for trisomy of most of the other chromosomes: specifying 6, 7, 9, 10, 11, and 12. You could also use this for mosaicism of these chromosomes.

758.520 – Other total trisomies. With all the other codes, this leaves us here with all trisomies for chromosomes: 1, 2, 3, 4, 5, 14, 15, 16, 17, 19, and 22. It also accounts for ‘trisomy NOS’. 758.530 – Partial trisomy syndromes. This is going to be where you put a lot of things, particularly if your program collects information on the microarrays. The previous three codes are for extra copies of total chromosomes. This is for extra copies of any part of any autosome.

758.540 – Other translocations. Not sure what the “other” is, but TX uses this for any translocation that is unbalanced, or for balanced translocations in babies with birth defects (i.e., balanced translocation in individuals who are not otherwise normal).

758.580 – “Other specified anomalies of autosomes, NOS” (I love the ‘other specified, not otherwise specified’ nature of this code). This is where you put everything else. It’s a big dumping ground where a lot of very interesting, very useful things go in a way that is almost impossible to use for research.

758.585 – Polyploidy. This is multiple copies of the entire genome except for triploidy. You won’t use this very much.

758.586 – Triploidy. This is an entire third set of chromosomes: 69,XXX, 69,XXY, or 69,XYY. You will see this, mostly in prenatal testing and IUFDs.

758.590 – Unspecified anomalies of autosomes. This is used when you know which chromosome is involved (and it isn’t a sex chromosome) but you are not sure what is wrong with it.

758.9: Conditions due to anomaly of unspecified chromosome

You will almost never use these. The report has to be very, very vague for these codes to be applicable. You have to be ignorant of which chromosome is involved. Since results are always
reported as an anomaly of a particular chromosome, you will always know at least whether it is a sex chromosome or not. Just that information is enough to use a more specific code.

Here’s a suggested thought process:

If you think you want to use a 758.9 code, ask if you can tell
1) Which chromosome has the problem
2) What the problem is (deletion, duplication, etc)

If you know either of those things, the case DOES NOT qualify for use of one of the 758.9 codes.
Ideas for handling unbalanced translocations and karyotypes with multiple problems:

Example: an unbalanced translocation between the short arm of chromosome 5 (5p) and the long arm of chromosome 14 (14q). This results in a deletion (partial monosomy) of 5p and a duplication (partial trisomy) of 14q.

Options:
1) Code a single time as “other translocation” 758.540.
   Useful, easy.
   Relatively non-specific and says nothing about what chromosomes are involved

2) Code the imbalance: 5p deletion 753.310
   14q duplication 758.530

   More specific information about the chromosomes
   Requires knowledge of the codes – and maybe how to read the karyotype
   Ignores the translocation

3) Code the translocation and the imbalance:
   Use three codes 758.540, 753.310, 758.530

   Much easier to scan at a research level to see what the problem is
   About as specific as the codes get to indicating what chromosomes are involved
   Requires knowledge of codes – and maybe how to read the karyotype
   Requires listing the karyotype three times with different codes
Chromosome Abnormality Syndromes Associated with Congenital Heart Defects
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Congenital heart defects (CHDs), also known as cardiovascular malformations, occur as isolated birth defects in approximately 60-80% of affected individuals. In the 20-40% of individuals with a CHD and non-cardiac defect, a syndrome can be recognized in approximately 10-15%. Chromosome abnormality syndromes are more common than mendelian gene disorders. The session will review common, distinctive, and a few rare malformation syndromes and the associated CHDs. For each syndrome, the chromosome defect, clinical and cardiac phenotype will be reviewed. This talk will echo some of the themes discussed in the morning plenary session, but with a different focus

Included are the familiar aneuploidy syndromes (trisomy 21/Down syndrome, trisomy 13 and 18, Turner syndrome), and deletion 22q11 Spectrum (Velocardiofacial syndrome, DiGeorge syndrome). Other important deletion syndromes include deletion 1p36, deletion 4p, deletion 7p/Williams syndrome; deletion 11q/Jacobsen syndrome, and tetrasomy 22p/Cat-Eye syndrome.