Genetics Tables and Views

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# The genetic\_markers schema

This schema includes tables and views with information specific to microsatellite genotyping work.

Some subtle differences between these tables can be obscure, especially for people who are unfamiliar with the data or how they are generated. To help clarify this, a brief discussion of this process is provided below with emphasis on related tables.

Given a set of DNA samples from individuals of interest, a technician will perform a PCR reaction that aims to amplify a known microsatellite region (or “locus”) in the genome. Each of these individual reactions is recorded in the MSAT\_REACTIONS table, one row per DNA sample, per locus, per well in a 96-well plate.

The resulting material from these reactions are sent to a facility that measures the products and returns results as electronic files. With highly-specialized software, the technician analyzes the files and determines (or “calls”) which microsatellite alleles were found in each reaction, if any. These allele calls are recorded in the MSAT\_RESULTS table, one row per DNA sample, per locus, per well in a 96-well plate.

For a variety of reasons, the results from a single PCR are not presumed to be perfectly accurate. After several rounds of PCR, ideally with a single locus being analyzed with multiple unique DNA samples from a single individual, a consensus for an individual’s genotype at a particular locus will emerge. The consensus of each individual’s genotypes is recorded in MSAT\_GENOTYPES, one row per individual.

## Tables in the genetic\_markers schema

### MSAT\_GENOTYPES

This table shows the current collection of finalized microsatellite genotypes for each individual, including human technicians and observers.

The alleles at each locus are recorded in a pair of columns named “[locusname]\_1” and “[locusname]\_2”, e.g. agat006\_1 and agat006\_2 for the locus, “AGAT006”. When only one allele at a locus is known, that one allele should be in the “\_2” column, leaving the “\_1” column NULL. However, there are no rules or constraints requiring this to be so.

Columns in MSAT\_GENOTYPES

#### sname

The BIOGRAPH.Sname of this individual.

For humans, this column must be NULL.

#### agat006\_1

The first allele at the AGAT006 locus.

If unknown, then NULL.

#### agat006\_2

The second allele at the AGAT006 locus.

If unknown, then NULL.

#### d1s1656\_1

The first allele at the D1s1656 locus.

If unknown, then NULL.

#### d1s1656\_2

The second allele at the D1s1656 locus.

If unknown, then NULL.

#### d2s1326\_1

The first allele at the D2s1326 locus.

If unknown, then NULL.

#### d2s1326\_2

The second allele at the D2s1326 locus.

If unknown, then NULL.

#### d3s1768\_1

The first allele at the D3s1768 locus.

If unknown, then NULL.

#### d3s1768\_2

The second allele at the D3s1768 locus.

If unknown, then NULL.

#### d4s243\_1

The first allele at the D4s243 locus.

If unknown, then NULL.

#### d4s243\_2

The second allele at the D4s243 locus.

If unknown, then NULL.

#### d5s1457\_1

The first allele at the D5s1457 locus.

If unknown, then NULL.

#### d5s1457\_2

The second allele at the D5s1457 locus.

If unknown, then NULL.

#### d6s501\_1

The first allele at the D6s501 locus.

If unknown, then NULL.

#### d6s501\_2

The second allele at the D6s501 locus.

If unknown, then NULL.

#### d7s503\_1

The first allele at the D7s503 locus.

If unknown, then NULL.

#### d7s503\_2

The second allele at the D7s503 locus.

If unknown, then NULL.

#### d8s1106\_1

The first allele at the D8s1106 locus.

If unknown, then NULL.

#### d8s1106\_2

The second allele at the D8s1106 locus.

If unknown, then NULL.

#### d10s611\_1

The first allele at the D10s611 locus.

If unknown, then NULL.

#### d102611\_2

The second allele at the D10s611 locus.

If unknown, then NULL.

#### d11s2002\_1

The first allele at the D11s2002 locus.

If unknown, then NULL.

#### d11s2002\_2

The second allele at the D11s2002 locus.

If unknown, then NULL.

#### d13s159b\_1

The first allele at the D13s159B locus.

If unknown, then NULL.

#### d13s159b\_2

The second allele at the D13s159B locus.

If unknown, then NULL.

#### d14s306\_1

The first allele at the D14s306 locus.

If unknown, then NULL.

#### d14s306\_2

The second allele at the D14s306 locus.

If unknown, then NULL.

#### d18s851\_1

The first allele at the D18s851 locus.

If unknown, then NULL.

#### d18s851\_2

The second allele at the D18s851 locus.

If unknown, then NULL.

#### name

The name of the individual.

For Amboseli baboons, this will be their BIOGRAPH.Name. For all others, this will be their UNIQUE\_INDIVS.IndivId.

This column cannot be NULL, nor empty, contain only whitespace, etc.

### MSAT\_REACTIONS

This table records basic information about every *attempted* microsatellite PCR reaction.

Columns in MSAT\_REACTIONS

#### id

Unique identifier number for each line, assigned by babase from the sequence GENETIC\_MARKERS.reactions\_id\_seq.

One line for every ID.

This column cannot be changed and must not be NULL.

#### locus

Microsatellite locus at which the reaction takes place.

Locus names should be capitalized appropriately as in our publications, e.g. "AGAT006", "D1s1656", "D13s159B".

#### did

The “DNA ID” of the DNA used in the reaction, i.e. the NUCACIDS.LocalId\_1 of the DNA used in this reaction.

#### rid

The “Reaction ID” of each reaction, created by the user/technician. Should be unique.

RID's take the format "plate number-color-well number". For example, the yellow-labeled reaction in well number 10 of PCR plate number 300 will have the RID "300y10". If two reactions of the same color occur in one well, use the same letter twice, e.g. "300yy10".

The "well number" is determined by counting downward by column, then left-to-right. A1=1, H1=8, A2=9, A12=89, etc.

One line for every RID.

#### reaction\_date

The date of the PCR, or NULL if the date is unknown.

### MSAT\_RESULTS

This table records data from all successful microsatellite PCR reactions. RID’s where no data was generated are not recorded here, but RID’s where data we believe to be false (for any reason) are.

Values in the “allele\_N” columns should be recorded numerically, e.g. if alleles “100”, “110”, “120”, and “130” are all observed in a single (apparently contaminated) reaction, they’d be recorded in that order. The “N” in “allele\_N” should not be used to indicate any relative importance of the value recorded therein.

Columns in MSAT\_RESULTS

#### id

Unique identifier number for each line, assigned by babase from the sequence GENETIC\_MARKERS.rxn\_results\_id\_seq.

One line for every ID.

This column cannot be changed and must not be NULL.

#### locus

Microsatellite locus at which the reaction took place.

Locus names should be capitalized appropriately as in scientific literature, e.g. "AGAT006", "D1s1656", "D13s159B".

#### did

The “DNA ID” of the DNA used in the reaction, i.e. the NUCACIDS.LocalId\_1 of the DNA used in this reaction.

#### sname

The short name of the individual being genotyped. If the individual is not an Amboseli baboon (e.g. human), then sname should be NULL, as in DNA.

Should be in all caps.

Occasionally, a tissue or DNA is determined to be "mid-identified", meaning that it came from a different individual than the name written on the side of the tube. When these "mis-ID's" are figured out, sname/name info are *not* updated here. The sname column in this table should express who we *believed* was being genotyped at the time.

###### Exception

For individuals with alternate snames/names in BIOGRAPH, an alt\_sname in MSAT\_RESULTS should be updated to instead indicate the "true" sname.

###### Tip

The view, REACTION\_CHECK, shows results data with updated sname/name information.

#### name

The name of the individual being genotyped.

Should be in all caps.

See above discussion of MSAT\_RESULTS.Sname for explanation of updating name info for mis-identified samples.

#### rid

The MSAT\_REACTIONS.RId for this result.

This column should be unique and shouldn’t be changed. It cannot be NULL.

#### allele\_1

The allele call for the first allele for the given RID at the given locus.

#### allele\_1\_doubt

The "doubt code" for the first allele.

Doubt codes are a shorthand method to indicate trustworthiness of the stated allele. Doubt codes are numbered 0-4, with each number indicating a fairly-specific message:

-Doubt 0 indicates that the lab technician had no doubt that the allele call is correct.

-Doubt 1 means that the fluorescence peak/fluorescent band was small or weak in fluorescence, but the technician still feels confident that the stated allele is correct.

-Doubt 2 indicates that the technician was unsure whether or not the stated allele is correct.

-Doubt 3 indicates that the stated allele may be correct, but there was some other factor (e.g. contamination, molecular size ladder error) also present that makes the technician uncertain. Clarifying explanations from the technician are given in MSAT.RESULTS.Doubt\_explanation.

-Doubt 4 indicates that the technician believes the stated allele to be false.

Doubt codes are noted by the technician while analyzing the data and are intended to provide the technician's commentary based solely while looking at that single reaction. They shouldn't reflect the technician's commentary based on other lines in this table, e.g. an allele that has strong, clear fluorescence but doesn't match/agree with other results from the same individual/DID (which casts some doubt on the allele) should still receive a doubt code of 0.

###### Exception

In results analyzed by Jason Buchan and Russ Van Horn (MSAT\_RESULTS.Analyzed\_by= JCB or RVH), doubt codes appear to be more editorialized, where alleles that likely appeared strong and clear were nevertheless sometimes given doubt code 4, only because they didn't match with other genotyping reactions from the same individual.

#### allele\_2

The allele call for the second allele for the given RID at the given locus.

If only one allele is seen in a reaction, then in that case the individual appeared homozygous for that allele, and that allele should therefore be repeated in this column.

#### allele\_2\_doubt

The doubt code for the second allele. See allele\_1\_doubt for discussion of doubt codes.

#### allele\_3

The allele call for allele three for the given RID at the given locus.

May be NULL if no third allele is present.

#### allele\_3\_doubt

The doubt code for allele three. See allele\_1\_doubt for discussion of doubt codes.

May be NULL if no third allele is present.

#### allele\_4

The allele call for allele four for the given RID at the given locus.

May be NULL if no fourth allele is present.

#### allele\_4\_doubt

The doubt code for allele four. See allele\_1\_doubt for discussion of doubt codes.

May be NULL if no fourth allele is present.

#### doubt\_3

Indicates whether or not a doubt code 3 is present in the allele\_1\_doubt, allele\_2\_doubt, allele\_3\_doubt, or allele\_4\_doubt columns.

If none of those columns has a doubt code of 3, then this should be FALSE. If any of them do, then this should be TRUE.

###### Exception

Rarely, a line may have no 3's recorded in any of the doubt columns, yet this column still is still "TRUE". This means that some doubt-inducing factor is present, yet did not affect the technician's judgment of the stated alleles. An explanation of the doubt-inducing factor should be given in the MSAT\_RESULTS.Doubt\_explanation.

#### doubt\_explanation

Any explanatory notes for why a doubt code of 3 was given are recorded here.

#### analyzed\_by

Initials of the individual who analyzed the results.

## Views in the genetic\_markers schema

|  |  |  |  |
| --- | --- | --- | --- |
| **Views** | **One row for each** | **Purpose** | **Tables used** |
| DNA\_PLANNER | DNA row | Combines info from dna with several other tables and views to help plan which dnas to use for PCRs. | All the tables used by the NUCACIDS\_W\_CONC view, REACTION\_CHECK (view), MSAT\_REACTIONS, MSAT\_RESULTS |
| EXTRACT\_PLANNER | TISSUE row (TID) | Combines information from several tables and views with tissue to help plan for extractions. | Same as DNA\_PLANNER |
| GENOTYPES\_CHECK | Non-NULL Sname in MSAT\_GENOTYPES | Compares genotypes in MSAT\_GENOTYPES to the individual's mother's genotypes. | MSAT\_GENOTYPES, all the tables used by the MATERNITIES view |
| INVENTORY\_SUMMARY | BIOGRAPH row | Presents the number of each tissue and dna type we have available for each sname in biograph. Also tells at how many microsatellite loci each sname has been genotyped. | BIOGRAPH, everything used by the NUCACIDS view, MSAT\_GENOTYPES, LOCI\_TYPED (view) |
| LOCI\_TYPED | Non-NULL Sname in BIOGRAPH | For each individual, counts how many microsatellite loci are fully genotyped. | BIOGRAPH, MSAT\_GENOTYPES |
| REACTION\_CHECK | MSAT\_RESULTS row where the DNA.Sname of the corresponding DID is not null | Shows data from MSAT\_RESULTS with TID, as well as updated name/sname if ever updated in DNA. Also shows if any observed alleles match with the individual’s mother. | MSAT\_RESULTS, everything used by the NUCACIDS view, everything used by the MATERNITIES view, MSAT\_GENOTYPES |

### DNA\_PLANNER

Combines info from several tables and views to help plan which dnas to use for PCRs. In addition to info from the NUCACIDS view, it shows qPCR information, the number of typed loci, the number of microsat PCR reactions that matched or mismatched with the mother, the number of reactions and results for each DID, and whether or not the DID’s source TID has been msat PCR’d.

#### Definition

SELECT dna\_allcounts.avail

, dna\_allcounts.did

, dna\_allcounts.sname

, dna\_allcounts.name

, dna\_allcounts.name\_on\_tube

, dna\_allcounts.sample\_type

, dna\_allcounts.notes

, dna\_allcounts.creation\_date

, dna\_allcounts.mis\_id

, dna\_allcounts.pg\_ul

, CASE

WHEN dna\_allcounts.matches IS NULL THEN 0::real

WHEN (dna\_allcounts.matches + dna\_allcounts.mismatches) = 0::double precision then 0::real

ELSE (dna\_allcounts.matches / (dna\_allcounts.matches +dna\_allcounts.mismatches))::real

END::numeric(5,2) AS matchsuccess

, CASE

WHEN dna\_allcounts.matches IS NOT NULL THEN dna\_allcounts.matches

WHEN dna\_allcounts.matches IS NULL THEN 0::real

ELSE NULL::real

END AS matches

, CASE

WHEN dna\_allcounts.mismatches IS NOT NULL THEN dna\_allcounts.mismatches

WHEN dna\_allcounts.mismatches IS NULL THEN 0::real

ELSE NULL::real

END AS mismatches

, CASE

WHEN dna\_allcounts.rxnscount IS NULL THEN 0::real

WHEN dna\_allcounts.resultscount = 0::double precision

OR dna\_allcounts.resultscount IS NULL THEN 0::real

ELSE dna\_allcounts.resultscount/dna\_allcounts.rxnscount

END::numeric(5,2) as rxnsuccess

, CASE

WHEN dna\_allcounts.rxnscount IS NOT NULL THEN dna\_allcounts.rxnscount

WHEN dna\_allcounts.rxnscount IS NULL THEN 0::real

ELSE NULL::real

END AS rxnscount

, CASE

WHEN dna\_allcounts.resultscount IS NOT NULL THEN dna\_allcounts.resultscount

WHEN dna\_allcounts.resultscount IS NULL THEN 0::real

ELSE NULL::real

END AS resultscount

, dna\_allcounts.tid

, CASE

WHEN dna\_allcounts.tid IS NULL THEN 'TID\_UNKN'::text

WHEN (dna\_allcounts.tid IN ( SELECT all\_used\_tids.tid)) THEN 'USED'::text

ELSE 'UNUSED'::text

END::character varying AS tidused

FROM (

SELECT dna\_w\_rcounts.did

, dna\_w\_rcounts.sname

, dna\_w\_rcounts.name

, dna\_w\_rcounts.tid

, dna\_w\_rcounts.sample\_type

, dna\_w\_rcounts.notes

, dna\_w\_rcounts.creation\_date

, dna\_w\_rcounts.avail

, dna\_w\_rcounts.name\_on\_tube

, dna\_w\_rcounts.mis\_id

, dna\_w\_rcounts.rxnscount

, dna\_w\_rcounts.pg\_ul

, match\_counts.rcdid

, match\_counts.resultscount

, match\_counts.matches

, match\_counts.mismatches

FROM (

SELECT dwq.did

, dwq.sname

, dwq.name

, dwq.source\_tid AS tid

, dwq.sample\_type

, dwq.notes

, dwq.creation\_date

, COALESCE(dwq.qpcr\_pg\_ul, (dwq.nano\_ng\_ul\*1000))::numeric(10,1) AS pg\_ul

, dwq.avail

, dwq.name\_on\_tube

, dwq.mis\_id

, rxn\_counter.rxnscount

FROM genetic\_inventory.dna\_w\_quant dwq

LEFT JOIN (

SELECT mr.did AS mrdid

, count(mr.did)::real AS rxnscount

FROM msat\_reactions mr

GROUP BY mr.did

) rxn\_counter

ON rxn\_counter.mrdid = dwq.did

) dna\_w\_rcounts

LEFT JOIN (

SELECT rc.did AS rcdid

, sum (

CASE

WHEN rc.did = rc.did THEN 1

ELSE 0

END

)::real AS resultscount

, sum (

CASE

WHEN rc.match::text = 'MATCH'::text THEN 1

ELSE 0

END

)::real AS matches

, sum (

CASE

WHEN rc.match::text = 'MISMATCH'::text THEN 1

ELSE 0

END

)::real AS mismatches

FROM genetic\_markers.reaction\_check rc

GROUP BY rc.did

) match\_counts

ON dna\_w\_rcounts.did = match\_counts.rcdid

) dna\_allcounts

LEFT JOIN (

SELECT DISTINCT dna\_tids.tid

FROM (

SELECT d.did

, d.source\_tid AS tid

FROM genetic\_inventory.dna d

) dna\_tids

JOIN (

SELECT DISTINCT msat\_reactions.did AS mrdid

FROM msat\_reactions

) rxns\_dids

ON dna\_tids.did = rxns\_dids.mrdid

WHERE dna\_tids.tid IS NOT NULL

) all\_used\_tids

ON dna\_allcounts.tid = all\_used\_tids.tid;

#### Columns in the DNA\_PLANNER view

|  |  |  |
| --- | --- | --- |
| **Column** | **From** | **Description** |
| Avail | DNA.Avail | Whether or not the sample is available. |
| Did | DNA.DID | The DNA ID of the sample. |
| Sname | DNA.Sname | The short name of the individual. |
| Name | DNA.Name | The name of the individual. |
| Sample\_type | DNA.Sample\_type | The type of sample. |
| Notes | DNA.Notes | Note text of DNA. |
| Creation\_date | DNA.Creation\_date | The date of creation of the sample. |
| Mis\_ID | DNA.Mis\_ID | Mis-ID "status". |
| Pg/ul | NUCLEICACIDQUANT.Pg\_ul | Quantification information. |
| Matchsuccess | CASE  WHEN dna\_allcounts.matches IS NULL THEN 0::real  WHEN (dna\_allcounts.matches + dna\_allcounts.mismatches) = 0::double precision THEN 0::real  ELSE (dna\_allcounts.matches / (dna\_allcounts.matches +dna\_allcounts.mismatches))::real | Proportion of reactions for the given DID that match the individual’s mother. Shows the result of the operation, Matches/(Matches+Mismatches). |
| Matches | CASE  WHEN dna\_allcounts.matches IS NOT NULL THEN dna\_allcounts.matches  WHEN dna\_allcounts.matches IS NULL THEN 0::real  ELSE NULL::real | The number of reactions for the given DID that match the individual’s mother. |
| Mismatches | CASE  WHEN dna\_allcounts.mismatches IS NOT NULL THEN dna\_allcounts.mismatches  WHEN dna\_allcounts.mismatches IS NULL THEN 0::real  ELSE NULL::real | The number of reactions for the given DID that do not match the individual’s mother. |
| Rxnsuccess | CASE  WHEN dna\_allcounts.rxnscount IS NULL THEN 0::real  WHEN dna\_allcounts.resultscount = 0::double precision  OR dna\_allcounts.resultscount IS NULL  THEN 0::real  ELSE dna\_allcounts.resultscount/dna\_allcounts.rxnscount | The proportion of reactions that yielded results to the total number of reactions. Shows the result of the operation, Resultscount/Rxncount. |
| Rxnscount | CASE  WHEN dna\_allcounts.rxnscount IS NOT NULL THEN dna\_allcounts.rxnscount  WHEN dna\_allcounts.rxnscount IS NULL THEN 0::real  ELSE NULL::real | The number of reactions for the given DID. |
| Resultscount | CASE  WHEN dna\_allcounts.resultscount IS NOT NULL THEN dna\_allcounts.resultscount  WHEN dna\_allcounts.resultscount IS NULL THEN 0::real  ELSE NULL::real | The number of reactions that yielded results for the given DID. The number of lines in msat\_results for the given DID. |
| Tid | DNA.SOURCE\_TID | Tissue ID of source tissue for the given DID. |
| Tidused | CASE  WHEN dna\_allcounts.tid IS NULL THEN 'TID\_UNKN'::text  WHEN (dna\_allcounts.tid IN ( SELECT all\_used\_tids.tid)) THEN 'USED'::text  ELSE 'UNUSED'::text | Whether or not an msat PCR has been run for the given DID. |
| Name\_on\_tube | DNA.NAME\_ON\_TUBE | Name visible on tube for the sample for the given DID. |

#### Operations Allowed

Only SELECT is allowed on DNA\_PLANNER. INSERT, UPDATE, and DELETE are not allowed.

### EXTRACT\_PLANNER

Combines information from several tables and views with tissue to provide various useful pieces of information about the tissue. Intended to assist in planning tissue DNA extractions other tasks that involve specific knowledge of tissues.

#### Definition

SELECT tissue\_counted\_dnas.avail

, tissue\_counted\_dnas.tid

, tissue\_counted\_dnas.sname

, tissue\_counted\_dnas.name

, tissue\_counted\_dnas.sample\_type

, tissue\_counted\_dnas.notes

, tissue\_counted\_dnas.collection\_date

, tissue\_counted\_dnas.mis\_id

, CASE

WHEN tissue\_counted\_dnas.dnas IS NULL THEN 0::bigint

ELSE tissue\_counted\_dnas.dnas

END::integer AS dnas

, CASE

WHEN succ\_avgs.match\_avg IS NOT NULL THEN succ\_avgs.match\_avg

ELSE 0::numeric

END::numeric(3,2) AS match\_avg

, CASE

WHEN succ\_avgs.rxns\_avg IS NOT NULL THEN succ\_avgs.rxns\_avg

ELSE 0::numeric

END::numeric(3,2) AS rxns\_avg

, CASE

WHEN succ\_avgs.tidused is NULL then 'UNUSED'

ELSE succ\_avgs.tidused

END AS rxnsused

, tissue\_counted\_dnas.location

, tissue\_counted\_dnas.name\_on\_tube

FROM (

SELECT git.tid

, git.sname

, git.name

, git.sample\_type

, git.notes

, git.collection\_date

, dna\_counts.count AS dnas

, git.location

, git.avail

, git.name\_on\_tube\_edited as name\_on\_tube

, git.mis\_id

FROM genetic\_inventory.tissue\_w\_edits git

LEFT JOIN (

SELECT d.source\_tid

, count(d.source\_tid) AS count

FROM genetic\_inventory.dna d

GROUP BY d.source\_tid

) dna\_counts

ON git.tid::numeric = dna\_counts.source\_tid

WHERE git.pop\_or\_species::text = 'AMBOSELI'::text

) tissue\_counted\_dnas

LEFT JOIN (

SELECT dp.tid

, dp.tidused

, avg(

CASE

WHEN dp.matchsuccess > 0::numeric THEN dp.matchsuccess

WHEN dp.matchsuccess = 0::numeric THEN NULL::numeric

ELSE NULL::numeric

END)::numeric(3,2) AS match\_avg

, avg(

CASE

WHEN dp.rxnsuccess > 0::numeric THEN dp.rxnsuccess

WHEN dp.rxnsuccess = 0::numeric THEN NULL::numeric

ELSE NULL::numeric

END)::numeric(3,2) AS rxns\_avg

FROM dna\_planner dp

GROUP BY dp.tid, dp.tidused

) succ\_avgs

ON tissue\_counted\_dnas.tid::numeric = succ\_avgs.tid;

#### Columns in the EXTRACT\_PLANNER view

|  |  |  |
| --- | --- | --- |
| **Column** | **From** | **Description** |
| Avail | TISSUE\_W\_EDITS.Avail | Whether or not the tissue sample is available. |
| Tid | TISSUE\_W\_EDITS.TID | The Tissue ID of the sample. |
| Sname | TISSUE\_W\_EDITS.Sname | The short name of the individual. |
| Name | TISSUE\_W\_EDITS.Name | The name of the individual. |
| Sample\_type | TISSUE\_W\_EDITS.Sample\_type | The type of tissue sample. |
| Notes | TISSUE\_W\_EDITS.Notes | The note text from TISSUE. |
| Collection\_date | TISSUE\_W\_EDITS.Collection\_date | The date of collection of the sample. |
| Mis\_ID | TISSUE\_W\_EDITS.Mis\_ID | Mis-ID "status". |
| Dnas | SELECT count(d.source\_tid)  FROM genetic\_inventory.dna d  GROUP BY d.source\_tid | The number of DNAs extracted from the sample. |
| Match\_avg | AVG(CASE  WHEN dp.matchsuccess > 0::numeric  THEN dp.matchsuccess  WHEN dp.matchsuccess = 0::numeric  THEN NULL::numeric  ELSE NULL::numeric  END)::numeric(3,2) | The average match percentage of all DNA’s extracted from that TID with the individual’s mother. |
| Rxns\_avg | AVG(CASE  WHEN dp.rxnsuccess > 0::numeric  THEN dp.rxnsuccess  WHEN dp.rxnsuccess = 0::numeric  THEN NULL::numeric  ELSE NULL::numeric  END)::numeric(3,2) | The average reaction results percentage for all DNA’s extracted from that TID. |
| Rxnsused | DNA\_PLANNER.TIDUSED | Whether or not the TID's extracted DNA's have been used in any msat PCR's. |
| Location | TISSUE\_W\_EDITS.Location | The location of the sample. |
| Name\_on\_tube | TISSUE\_W\_EDITS.Name\_on\_tube\_edited | The name on the tube of the sample. |

#### Operations Allowed

Only SELECT is allowed on EXTRACT\_PLANNER. INSERT, UPDATE, and DELETE are not allowed.

### GENOTYPES\_CHECK

Compares the genotypes in MSAT\_GENOTYPES to each individual's mother's genotypes, when known, according to MSAT\_GENOTYPES. Also includes a column that indicates how many loci an individual mismatches with their mother.

#### Definition

SELECT kid\_w\_mom.mom, kid\_w\_mom.sname, sum(

CASE

WHEN kid\_w\_mom.mom006::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom656::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom326::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom768::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom243::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom457::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom501::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom503::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom106::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom611::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom002::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom159b::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom306::text = 'MISMATCH'::text THEN 1

ELSE 0

END +

CASE

WHEN kid\_w\_mom.mom851::text = 'MISMATCH'::text THEN 1

ELSE 0

END) AS nummismatches, kid\_w\_mom.agat006\_1, kid\_w\_mom.agat006\_2, kid\_w\_mom.mom006, kid\_w\_mom.d1s1656\_1, kid\_w\_mom.d1s1656\_2, kid\_w\_mom.mom656, kid\_w\_mom.d2s1326\_1, kid\_w\_mom.d2s1326\_2, kid\_w\_mom.mom326, kid\_w\_mom.d3s1768\_1, kid\_w\_mom.d3s1768\_2, kid\_w\_mom.mom768, kid\_w\_mom.d4s243\_1, kid\_w\_mom.d4s243\_2, kid\_w\_mom.mom243, kid\_w\_mom.d5s1457\_1, kid\_w\_mom.d5s1457\_2, kid\_w\_mom.mom457, kid\_w\_mom.d6s501\_1, kid\_w\_mom.d6s501\_2, kid\_w\_mom.mom501, kid\_w\_mom.d7s503\_1, kid\_w\_mom.d7s503\_2, kid\_w\_mom.mom503, kid\_w\_mom.d8s1106\_1, kid\_w\_mom.d8s1106\_2, kid\_w\_mom.mom106, kid\_w\_mom.d10s611\_1, kid\_w\_mom.d10s611\_2, kid\_w\_mom.mom611, kid\_w\_mom.d11s2002\_1, kid\_w\_mom.d11s2002\_2, kid\_w\_mom.mom002, kid\_w\_mom.d13s159b\_1, kid\_w\_mom.d13s159b\_2, kid\_w\_mom.mom159b, kid\_w\_mom.d14s306\_1, kid\_w\_mom.d14s306\_2, kid\_w\_mom.mom306, kid\_w\_mom.d18s851\_1, kid\_w\_mom.d18s851\_2, kid\_w\_mom.mom851

FROM (SELECT mom\_genos.sname AS mom, gt.sname, gt.agat006\_1, gt.agat006\_2,

CASE

WHEN gt.agat006\_1 = mom\_genos.agat006\_1 AND gt.agat006\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.agat006\_1 = mom\_genos.agat006\_2 AND gt.agat006\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.agat006\_2 = mom\_genos.agat006\_2 AND gt.agat006\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.agat006\_2 = mom\_genos.agat006\_1 AND gt.agat006\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.agat006\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.agat006\_1 IS NULL THEN 'MOM\_UNKN'::text

WHEN gt.agat006\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.agat006\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom006, gt.d1s1656\_1, gt.d1s1656\_2,

CASE

WHEN gt.d1s1656\_1 = mom\_genos.d1s1656\_1 AND gt.d1s1656\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d1s1656\_1 = mom\_genos.d1s1656\_2 AND gt.d1s1656\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d1s1656\_2 = mom\_genos.d1s1656\_2 AND gt.d1s1656\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d1s1656\_2 = mom\_genos.d1s1656\_1 AND gt.d1s1656\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d1s1656\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d1s1656\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d1s1656\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d1s1656\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom656, gt.d2s1326\_1, gt.d2s1326\_2,

CASE

WHEN gt.d2s1326\_1 = mom\_genos.d2s1326\_1 AND gt.d2s1326\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d2s1326\_1 = mom\_genos.d2s1326\_2 AND gt.d2s1326\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d2s1326\_2 = mom\_genos.d2s1326\_2 AND gt.d2s1326\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d2s1326\_2 = mom\_genos.d2s1326\_1 AND gt.d2s1326\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d2s1326\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d2s1326\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d2s1326\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d2s1326\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom326, gt.d3s1768\_1, gt.d3s1768\_2,

CASE

WHEN gt.d3s1768\_1 = mom\_genos.d3s1768\_1 AND gt.d3s1768\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d3s1768\_1 = mom\_genos.d3s1768\_2 AND gt.d3s1768\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d3s1768\_2 = mom\_genos.d3s1768\_2 AND gt.d3s1768\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d3s1768\_2 = mom\_genos.d3s1768\_1 AND gt.d3s1768\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d3s1768\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d3s1768\_1 IS NULL THEN 'MOM\_UNKN'::text

WHEN gt.d3s1768\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d3s1768\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom768, gt.d4s243\_1, gt.d4s243\_2,

CASE

WHEN gt.d4s243\_1 = mom\_genos.d4s243\_1 AND gt.d4s243\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d4s243\_1 = mom\_genos.d4s243\_2 AND gt.d4s243\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d4s243\_2 = mom\_genos.d4s243\_2 AND gt.d4s243\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d4s243\_2 = mom\_genos.d4s243\_1 AND gt.d4s243\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d4s243\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d4s243\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d4s243\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d4s243\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom243, gt.d5s1457\_1, gt.d5s1457\_2,

CASE

WHEN gt.d5s1457\_1 = mom\_genos.d5s1457\_1 AND gt.d5s1457\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d5s1457\_1 = mom\_genos.d5s1457\_2 AND gt.d5s1457\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d5s1457\_2 = mom\_genos.d5s1457\_2 AND gt.d5s1457\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d5s1457\_2 = mom\_genos.d5s1457\_1 AND gt.d5s1457\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d5s1457\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d5s1457\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d5s1457\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d5s1457\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom457, gt.d6s501\_1, gt.d6s501\_2,

CASE

WHEN gt.d6s501\_1 = mom\_genos.d6s501\_1 AND gt.d6s501\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d6s501\_1 = mom\_genos.d6s501\_2 AND gt.d6s501\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d6s501\_2 = mom\_genos.d6s501\_2 AND gt.d6s501\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d6s501\_2 = mom\_genos.d6s501\_1 AND gt.d6s501\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d6s501\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d6s501\_1 IS NULL THEN 'MOM\_UNKN'::text

WHEN gt.d6s501\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d6s501\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom501, gt.d7s503\_1, gt.d7s503\_2,

CASE

WHEN gt.d7s503\_1 = mom\_genos.d7s503\_1 AND gt.d7s503\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d7s503\_1 = mom\_genos.d7s503\_2 AND gt.d7s503\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d7s503\_2 = mom\_genos.d7s503\_2 AND gt.d7s503\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d7s503\_2 = mom\_genos.d7s503\_1 AND gt.d7s503\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d7s503\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d7s503\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d7s503\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d7s503\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom503, gt.d8s1106\_1, gt.d8s1106\_2,

CASE

WHEN gt.d8s1106\_1 = mom\_genos.d8s1106\_1 AND gt.d8s1106\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d8s1106\_1 = mom\_genos.d8s1106\_2 AND gt.d8s1106\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d8s1106\_2 = mom\_genos.d8s1106\_2 AND gt.d8s1106\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d8s1106\_2 = mom\_genos.d8s1106\_1 AND gt.d8s1106\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d8s1106\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d8s1106\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d8s1106\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d8s1106\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom106, gt.d10s611\_1, gt.d10s611\_2,

CASE

WHEN gt.d10s611\_1 = mom\_genos.d10s611\_1 AND gt.d10s611\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d10s611\_1 = mom\_genos.d10s611\_2 AND gt.d10s611\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d10s611\_2 = mom\_genos.d10s611\_2 AND gt.d10s611\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d10s611\_2 = mom\_genos.d10s611\_1 AND gt.d10s611\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d10s611\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d10s611\_1 IS NULL THEN 'MOM\_UNKN'::text

WHEN gt.d10s611\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d10s611\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom611, gt.d11s2002\_1, gt.d11s2002\_2,

CASE

WHEN gt.d11s2002\_1 = mom\_genos.d11s2002\_1 AND gt.d11s2002\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d11s2002\_1 = mom\_genos.d11s2002\_2 AND gt.d11s2002\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d11s2002\_2 = mom\_genos.d11s2002\_2 AND gt.d11s2002\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d11s2002\_2 = mom\_genos.d11s2002\_1 AND gt.d11s2002\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d11s2002\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d11s2002\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d11s2002\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d11s2002\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom002, gt.d13s159b\_1, gt.d13s159b\_2,

CASE

WHEN gt.d13s159b\_1 = mom\_genos.d13s159b\_1 AND gt.d13s159b\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d13s159b\_1 = mom\_genos.d13s159b\_2 AND gt.d13s159b\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d13s159b\_2 = mom\_genos.d13s159b\_2 AND gt.d13s159b\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d13s159b\_2 = mom\_genos.d13s159b\_1 AND gt.d13s159b\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d13s159b\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d13s159b\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d13s159b\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d13s159b\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom159b, gt.d14s306\_1, gt.d14s306\_2,

CASE

WHEN gt.d14s306\_1 = mom\_genos.d14s306\_1 AND gt.d14s306\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d14s306\_1 = mom\_genos.d14s306\_2 AND gt.d14s306\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d14s306\_2 = mom\_genos.d14s306\_2 AND gt.d14s306\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d14s306\_2 = mom\_genos.d14s306\_1 AND gt.d14s306\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d14s306\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d14s306\_1 IS NULL THEN 'MOM\_UNKN'::text

WHEN gt.d14s306\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d14s306\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom306, gt.d18s851\_1, gt.d18s851\_2,

CASE

WHEN gt.d18s851\_1 = mom\_genos.d18s851\_1 AND gt.d18s851\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d18s851\_1 = mom\_genos.d18s851\_2 AND gt.d18s851\_1 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d18s851\_2 = mom\_genos.d18s851\_2 AND gt.d18s851\_2 IS NOT NULL THEN 'MATCH'::text

WHEN gt.d18s851\_2 = mom\_genos.d18s851\_1 AND gt.d18s851\_2 IS NOT NULL THEN 'MATCH'::text

WHEN mom\_genos.d18s851\_2 IS NULL THEN 'MOM \_UNKN'::text

WHEN mom\_genos.d18s851\_1 IS NULL THEN 'MOM \_UNKN'::text

WHEN gt.d18s851\_2 IS NULL THEN 'KID\_UNKN'::text

WHEN gt.d18s851\_1 IS NULL THEN 'KID\_UNKN'::text

ELSE 'MISMATCH'::text

END::character varying AS mom851

FROM msat\_genotypes gt

LEFT JOIN ( SELECT p.kid, gt.sname, gt.agat006\_1, gt.agat006\_2, gt.d1s1656\_1, gt.d1s1656\_2, gt.d2s1326\_1, gt.d2s1326\_2, gt.d3s1768\_1, gt.d3s1768\_2, gt.d4s243\_1, gt.d4s243\_2, gt.d5s1457\_1, gt.d5s1457\_2, gt.d6s501\_1, gt.d6s501\_2, gt.d7s503\_1, gt.d7s503\_2, gt.d8s1106\_1, gt.d8s1106\_2, gt.d10s611\_1, gt.d10s611\_2, gt.d11s2002\_1, gt.d11s2002\_2, gt.d13s159b\_1, gt.d13s159b\_2, gt.d14s306\_1, gt.d14s306\_2, gt.d18s851\_1, gt.d18s851\_2, gt.name

FROM msat\_genotypes gt

JOIN parents p ON gt.sname::bpchar = p.mom) mom\_genos ON gt.sname::bpchar = mom\_genos.kid) kid\_w\_mom

GROUP BY kid\_w\_mom.sname, kid\_w\_mom.mom, kid\_w\_mom.agat006\_1, kid\_w\_mom.agat006\_2, kid\_w\_mom.mom006, kid\_w\_mom.d1s1656\_1, kid\_w\_mom.d1s1656\_2, kid\_w\_mom.mom656, kid\_w\_mom.d2s1326\_1, kid\_w\_mom.d2s1326\_2, kid\_w\_mom.mom326, kid\_w\_mom.d3s1768\_1, kid\_w\_mom.d3s1768\_2, kid\_w\_mom.mom768, kid\_w\_mom.d4s243\_1, kid\_w\_mom.d4s243\_2, kid\_w\_mom.mom243, kid\_w\_mom.d5s1457\_1, kid\_w\_mom.d5s1457\_2, kid\_w\_mom.mom457, kid\_w\_mom.d6s501\_1, kid\_w\_mom.d6s501\_2, kid\_w\_mom.mom501, kid\_w\_mom.d7s503\_1, kid\_w\_mom.d7s503\_2, kid\_w\_mom.mom503, kid\_w\_mom.d8s1106\_1, kid\_w\_mom.d8s1106\_2, kid\_w\_mom.mom106, kid\_w\_mom.d10s611\_1, kid\_w\_mom.d10s611\_2, kid\_w\_mom.mom611, kid\_w\_mom.d11s2002\_1, kid\_w\_mom.d11s2002\_2, kid\_w\_mom.mom002, kid\_w\_mom.d13s159b\_1, kid\_w\_mom.d13s159b\_2, kid\_w\_mom.mom159b, kid\_w\_mom.d14s306\_1, kid\_w\_mom.d14s306\_2, kid\_w\_mom.mom306, kid\_w\_mom.d18s851\_1, kid\_w\_mom.d18s851\_2, kid\_w\_mom.mom851;

#### Columns in the GENOTYPES\_CHECK view

|  |  |  |
| --- | --- | --- |
| **Column** | **From** | **Description** |
| Mom | PARENTS.Mom | The mother of the individual in "Sname". If unknown, then NULL. |
| Sname | MSAT\_GENOTYPES.Sname | The sname of the individual whose genotypes are shown. |
| Nummismatches | Number of "mom\_\_\_" columns that='MISMATCH' | The number of loci the individual mismatched with their mother. |
| AGAT006\_1 | MSAT\_GENOTYPES.AGAT006\_1 | The individual's first allele at the AGAT006 locus. |
| AGAT006\_2 | MSAT\_GENOTYPES.AGAT006\_2 | The individual's second allele at the AGAT006 locus. |
| mom006 | CASE  WHEN gt.agat006\_1 = mom\_genos.agat006\_1 AND gt.agat006\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.agat006\_1 = mom\_genos.agat006\_2 AND gt.agat006\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.agat006\_2 = mom\_genos.agat006\_2 AND gt.agat006\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.agat006\_2 = mom\_genos.agat006\_1 AND gt.agat006\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.agat006\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.agat006\_1 IS NULL THEN 'MOM\_UNKN'::text  WHEN gt.agat006\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.agat006\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying | Tells whether or not at least one of the individual's AGAT006 alleles matches his/her mother's alleles. |
| D1s1656\_1 | MSAT\_GENOTYPES.D1s1656\_1 | The individual's first allele at the D1s1656 locus. |
| D1s1656\_2 | MSAT\_GENOTYPES.D1s1656\_2 | The individual's second allele at the D1s1656 locus. |
| mom656 | CASE  WHEN gt.d1s1656\_1 = mom\_genos.d1s1656\_1 AND gt.d1s1656\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d1s1656\_1 = mom\_genos.d1s1656\_2 AND gt.d1s1656\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d1s1656\_2 = mom\_genos.d1s1656\_2 AND gt.d1s1656\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d1s1656\_2 = mom\_genos.d1s1656\_1 AND gt.d1s1656\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d1s1656\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d1s1656\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d1s1656\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d1s1656\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying | Tells whether or not at least one of the individual's D1s1656 alleles matches his/her mother's alleles |
| D2s1326\_1 | MSAT\_GENOTYPES.D2s1326\_1 | The individual's first allele at the D2s1326 locus. |
| D2s1326\_2 | MSAT\_GENOTYPES.D2s1326\_2 | The individual's second allele at the D2s1326 locus. |
| mom326 | CASE  WHEN gt.d2s1326\_1 = mom\_genos.d2s1326\_1 AND gt.d2s1326\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d2s1326\_1 = mom\_genos.d2s1326\_2 AND gt.d2s1326\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d2s1326\_2 = mom\_genos.d2s1326\_2 AND gt.d2s1326\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d2s1326\_2 = mom\_genos.d2s1326\_1 AND gt.d2s1326\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d2s1326\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d2s1326\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d2s1326\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d2s1326\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom326 | Tells whether or not at least one of the individual's D2s1326 alleles matches his/her mother's alleles |
| D3s1768\_1 | MSAT\_GENOTYPES.D3s1768\_1 | The individual's first allele at the D3s1768 locus. |
| D3s1768\_2 | MSAT\_GENOTYPES.D3s1768\_2 | The individual's second allele at the D3s1768 locus. |
| mom768 | CASE  WHEN gt.d3s1768\_1 = mom\_genos.d3s1768\_1 AND gt.d3s1768\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d3s1768\_1 = mom\_genos.d3s1768\_2 AND gt.d3s1768\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d3s1768\_2 = mom\_genos.d3s1768\_2 AND gt.d3s1768\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d3s1768\_2 = mom\_genos.d3s1768\_1 AND gt.d3s1768\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d3s1768\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d3s1768\_1 IS NULL THEN 'MOM\_UNKN'::text  WHEN gt.d3s1768\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d3s1768\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom768 | Tells whether or not at least one of the individual's D3s1768 alleles matches his/her mother's alleles |
| D4s243\_1 | MSAT\_GENOTYPES.D4s243\_1 | The individual's first allele at the D4s243 locus. |
| D4s243\_2 | MSAT\_GENOTYPES.D4s243\_2 | The individual's second allele at the D4s243 locus. |
| mom243 | CASE  WHEN gt.d4s243\_1 = mom\_genos.d4s243\_1 AND gt.d4s243\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d4s243\_1 = mom\_genos.d4s243\_2 AND gt.d4s243\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d4s243\_2 = mom\_genos.d4s243\_2 AND gt.d4s243\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d4s243\_2 = mom\_genos.d4s243\_1 AND gt.d4s243\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d4s243\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d4s243\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d4s243\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d4s243\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom243 | Tells whether or not at least one of the individual's D4s243 alleles matches his/her mother's alleles |
| D5s1457\_1 | MSAT\_GENOTYPES.D5s1457\_1 | The individual's first allele at the D5s1457 locus. |
| D5s1457\_2 | MSAT\_GENOTYPES.D5s1457\_2 | The individual's second allele at the D5s1457 locus. |
| mom457 | CASE  WHEN gt.d5s1457\_1 = mom\_genos.d5s1457\_1 AND gt.d5s1457\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d5s1457\_1 = mom\_genos.d5s1457\_2 AND gt.d5s1457\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d5s1457\_2 = mom\_genos.d5s1457\_2 AND gt.d5s1457\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d5s1457\_2 = mom\_genos.d5s1457\_1 AND gt.d5s1457\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d5s1457\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d5s1457\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d5s1457\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d5s1457\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom457 | Tells whether or not at least one of the individual's D5s1457 alleles matches his/her mother's alleles |
| D6s501\_1 | MSAT\_GENOTYPES.D6s501\_1 | The individual's first allele at the D6s501 locus. |
| D6s501\_2 | MSAT\_GENOTYPES.D6s501\_2 | The individual's second allele at the D6s501 locus. |
| mom501 | CASE  WHEN gt.d6s501\_1 = mom\_genos.d6s501\_1 AND gt.d6s501\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d6s501\_1 = mom\_genos.d6s501\_2 AND gt.d6s501\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d6s501\_2 = mom\_genos.d6s501\_2 AND gt.d6s501\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d6s501\_2 = mom\_genos.d6s501\_1 AND gt.d6s501\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d6s501\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d6s501\_1 IS NULL THEN 'MOM\_UNKN'::text  WHEN gt.d6s501\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d6s501\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom501 | Tells whether or not at least one of the individual's D6s501 alleles matches his/her mother's alleles |
| D7s503\_1 | MSAT\_GENOTYPES.D7s503\_1 | The individual's first allele at the D7s503 locus. |
| D7s503\_2 | MSAT\_GENOTYPES.D7s503\_2 | The individual's second allele at the D7s503 locus. |
| mom503 | CASE  WHEN gt.d7s503\_1 = mom\_genos.d7s503\_1 AND gt.d7s503\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d7s503\_1 = mom\_genos.d7s503\_2 AND gt.d7s503\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d7s503\_2 = mom\_genos.d7s503\_2 AND gt.d7s503\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d7s503\_2 = mom\_genos.d7s503\_1 AND gt.d7s503\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d7s503\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d7s503\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d7s503\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d7s503\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom503 | Tells whether or not at least one of the individual's D7s503 alleles matches his/her mother's alleles |
| D8s1106\_1 | MSAT\_GENOTYPES.D8s1106\_1 | The individual's first allele at the D8s1106 locus. |
| D8s1106\_2 | MSAT\_GENOTYPES.D8s1106\_2 | The individual's second allele at the D8s1106 locus. |
| mom106 | CASE  WHEN gt.d8s1106\_1 = mom\_genos.d8s1106\_1 AND gt.d8s1106\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d8s1106\_1 = mom\_genos.d8s1106\_2 AND gt.d8s1106\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d8s1106\_2 = mom\_genos.d8s1106\_2 AND gt.d8s1106\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d8s1106\_2 = mom\_genos.d8s1106\_1 AND gt.d8s1106\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d8s1106\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d8s1106\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d8s1106\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d8s1106\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom106 | Tells whether or not at least one of the individual's D8s1106 alleles matches his/her mother's alleles |
| D10s611\_1 | MSAT\_GENOTYPES.D10s611\_1 | The individual's first allele at the D10s611 locus. |
| D10s611\_2 | MSAT\_GENOTYPES.D10s611\_2 | The individual's second allele at the D10s611 locus. |
| mom611 | CASE  WHEN gt.d10s611\_1 = mom\_genos.d10s611\_1 AND gt.d10s611\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d10s611\_1 = mom\_genos.d10s611\_2 AND gt.d10s611\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d10s611\_2 = mom\_genos.d10s611\_2 AND gt.d10s611\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d10s611\_2 = mom\_genos.d10s611\_1 AND gt.d10s611\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d10s611\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d10s611\_1 IS NULL THEN 'MOM\_UNKN'::text  WHEN gt.d10s611\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d10s611\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom611 | Tells whether or not at least one of the individual's D10s611 alleles matches his/her mother's alleles |
| D11s2002\_1 | MSAT\_GENOTYPES.D11s2002\_1 | The individual's first allele at the D11s2002 locus. |
| D11s2002\_2 | MSAT\_GENOTYPES.D11s2002\_2 | The individual's second allele at the D11s2002 locus. |
| mom002 | CASE  WHEN gt.d11s2002\_1 = mom\_genos.d11s2002\_1 AND gt.d11s2002\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d11s2002\_1 = mom\_genos.d11s2002\_2 AND gt.d11s2002\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d11s2002\_2 = mom\_genos.d11s2002\_2 AND gt.d11s2002\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d11s2002\_2 = mom\_genos.d11s2002\_1 AND gt.d11s2002\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d11s2002\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d11s2002\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d11s2002\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d11s2002\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom002 | Tells whether or not at least one of the individual's D11s2002 alleles matches his/her mother's alleles |
| D13s159b\_1 | MSAT\_GENOTYPES.D13s159B\_1 | The individual's first allele at the D13s159B locus. |
| D13s159b\_2 | MSAT\_GENOTYPES.D13s159B\_2 | The individual's second allele at the D13s159B locus. |
| mom159b | CASE  WHEN gt.d13s159b\_1 = mom\_genos.d13s159b\_1 AND gt.d13s159b\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d13s159b\_1 = mom\_genos.d13s159b\_2 AND gt.d13s159b\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d13s159b\_2 = mom\_genos.d13s159b\_2 AND gt.d13s159b\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d13s159b\_2 = mom\_genos.d13s159b\_1 AND gt.d13s159b\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d13s159b\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d13s159b\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d13s159b\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d13s159b\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom159b | Tells whether or not at least one of the individual's D13s159B alleles matches his/her mother's alleles |
| D14s306\_1 | MSAT\_GENOTYPES.D14s306\_1 | The individual's first allele at the D14s306 locus. |
| D14s306\_2 | MSAT\_GENOTYPES.D14s306\_2 | The individual's second allele at the D14s306 locus. |
| mom306 | CASE  WHEN gt.d14s306\_1 = mom\_genos.d14s306\_1 AND gt.d14s306\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d14s306\_1 = mom\_genos.d14s306\_2 AND gt.d14s306\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d14s306\_2 = mom\_genos.d14s306\_2 AND gt.d14s306\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d14s306\_2 = mom\_genos.d14s306\_1 AND gt.d14s306\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d14s306\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d14s306\_1 IS NULL THEN 'MOM\_UNKN'::text  WHEN gt.d14s306\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d14s306\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom306 | Tells whether or not at least one of the individual's D14s306 alleles matches his/her mother's alleles |
| D18s851\_1 | MSAT\_GENOTYPES.D18s851\_1 | The individual's first allele at the D18s851 locus. |
| D18s851\_2 | MSAT\_GENOTYPES.D18s851\_2 | The individual's second allele at the D18s851 locus. |
| mom851 | CASE  WHEN gt.d18s851\_1 = mom\_genos.d18s851\_1 AND gt.d18s851\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d18s851\_1 = mom\_genos.d18s851\_2 AND gt.d18s851\_1 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d18s851\_2 = mom\_genos.d18s851\_2 AND gt.d18s851\_2 IS NOT NULL THEN 'MATCH'::text  WHEN gt.d18s851\_2 = mom\_genos.d18s851\_1 AND gt.d18s851\_2 IS NOT NULL THEN 'MATCH'::text  WHEN mom\_genos.d18s851\_2 IS NULL THEN 'MOM \_UNKN'::text  WHEN mom\_genos.d18s851\_1 IS NULL THEN 'MOM \_UNKN'::text  WHEN gt.d18s851\_2 IS NULL THEN 'KID\_UNKN'::text  WHEN gt.d18s851\_1 IS NULL THEN 'KID\_UNKN'::text  ELSE 'MISMATCH'::text  END::character varying AS mom851 | Tells whether or not at least one of the individual's D18s851 alleles matches his/her mother's alleles |

#### Operations Allowed

Only SELECT is allowed on GENOTYPES\_CHECK. INSERT, UPDATE, and DELETE are not allowed.

### INVENTORY\_SUMMARY

Counts how many of each tissue and dna type we have available for each sname in biograph.

#### Definition

SELECT sq.sname

, sq.name

, sq.birth

, sq.matgrp

, sq.statdate

, sq.typed\_loci

, sum(

CASE

WHEN t.sample\_type::text = 'FECES'::text

AND t.avail = 'Y'::bpchar

AND t.pop\_or\_species::text = 'AMBOSELI'::text

THEN 1

ELSE 0

END

) AS fecalsamps

, sum(

CASE

WHEN t.sample\_type::text = 'BLOOD'::text

AND t.avail = 'Y'::bpchar

AND t.pop\_or\_species::text = 'AMBOSELI'::text

THEN 1

ELSE 0

END

) AS bloodsamps

, sum(

CASE

WHEN t.sample\_type::text = 'HAIR'::text

AND t.avail = 'Y'::bpchar

AND t.pop\_or\_species::text = 'AMBOSELI'::text

THEN 1

WHEN t.sample\_type::text = 'OTHER\_TISSUE'::text

AND t.avail = 'Y'::bpchar

AND t.pop\_or\_species::text = 'AMBOSELI'::text

THEN 1

WHEN t.sample\_type::text = 'SKIN\_BIOPSY'::text

AND t.avail = 'Y'::bpchar

AND t.pop\_or\_species::text = 'AMBOSELI'::text

THEN 1

ELSE 0

END

) AS tissuesamps

, sq.fdnas

, sq.gdnas

, sq.wgas

FROM (

SELECT sq2.sname

, sq2.name

, sq2.birth

, sq2.matgrp

, sq2.typed\_loci

, sq2.statdate

, sum(

CASE

WHEN d.sample\_type::text = 'FDNA'::text

AND d.avail = 'Y'::bpchar

THEN 1

ELSE 0

END

) AS fdnas

, sum(

CASE

WHEN d.sample\_type::text = 'GDNA'::text

AND d.avail = 'Y'::bpchar

THEN 1

ELSE 0

END

) AS gdnas

, sum(

CASE

WHEN d.sample\_type::text = 'WGA'::text

AND d.avail = 'Y'::bpchar

THEN 1

ELSE 0

END

) AS wgas

FROM dna d

RIGHT JOIN (

SELECT b.sname

, b.name

, b.birth

, b.matgrp

, lt.typed\_loci

, b.statdate

FROM babase.biograph b

LEFT JOIN genetic\_markers.loci\_typed lt

ON b.sname = lt.sname

) sq2

ON d.sname::bpchar = sq2.sname

GROUP BY sq2.sname, sq2.name, sq2.birth, sq2.matgrp, sq2.typed\_loci, sq2.statdate

) sq

LEFT JOIN genetic\_inventory.tissue t

ON t.sname = sq.sname

WHERE sq.sname IS NOT NULL

GROUP BY sq.sname, sq.name, sq.birth, sq.matgrp, sq.typed\_loci, sq.statdate, sq.fdnas, sq.gdnas, sq.wgas;

#### Columns in the INVENTORY\_SUMMARY view

|  |  |  |
| --- | --- | --- |
| **Column** | **From** | **Description** |
| Sname | BIOGRAPH.Sname | Short name of the individual. |
| Name | BIOGRAPH.Name | Name of the individual. |
| Birth | BIOGRAPH.Birth | Date of birth of the individual. |
| Matgrp | BIOGRAPH.Matgrp | Maternal group of the individual. |
| Statdate | BIOGRAPH.Statdate | The status date of the individual. The latest date on which the animal was censused and found in a group, the birth date, or the date of death. |
| Typed\_loci | LOCI\_TYPED.Typed\_loci | The number of microsatellite loci typed for this individual, according to GENETIC\_MARKERS.MSAT\_GENOTYPES. |
| Fecalsamps | sum( CASE  WHEN t.sample\_type::text = 'FECES'::text AND t.avail = 'Y'::bpchar AND t.pop\_or\_species::text = 'AMBOSELI'::text THEN 1  ELSE 0  END) AS fecalsamps | The number of fecal samples currently available for the given sname. |
| Bloodsamps | sum( CASE  WHEN t.sample\_type::text = 'BLOOD'::text AND t.avail = 'Y'::bpchar AND t.pop\_or\_species::text = 'AMBOSELI'::text THEN 1  ELSE 0  END) AS bloodsamps | The number of blood samples currently available for the given sname. |
| Tissuesamps | sum( CASE  WHEN t.sample\_type::text = 'HAIR'::text AND t.avail = 'Y'::bpchar AND t.pop\_or\_species::text = 'AMBOSELI'::text THEN 1  WHEN t.sample\_type::text = 'OTHER\_TISSUE'::text AND t.avail = 'Y'::bpchar AND t.pop\_or\_species::text = 'AMBOSELI'::text THEN 1  WHEN t.sample\_type::text = 'SKIN\_BIOPSY'::text AND t.avail = 'Y'::bpchar AND t.pop\_or\_species::text = 'AMBOSELI'::text THEN 1  ELSE 0  END) AS tissuesamps | The number of hair, skin biopsy, and tissue samples of some other miscellaenous types currently available for the given sname. |
| Fdnas | sum( CASE  WHEN d.sample\_type::text = 'FDNA'::text AND d.avail = 'Y'::bpchar THEN 1  ELSE 0  END) AS fdnas | The number of fecal DNA samples currently available for the given sname. |
| Gdnas | sum( CASE  WHEN d.sample\_type::text = 'GDNA'::text AND d.avail = 'Y'::bpchar THEN 1  ELSE 0  END) AS gdnas | The number of genomic DNA samples currently available for the given sname. |
| Wgas | sum( CASE  WHEN d.sample\_type::text = 'WGA'::text AND d.avail = 'Y'::bpchar THEN 1  ELSE 0  END) AS wgas | The number of WGA samples currently available for the given sname. |

#### Operations Allowed

Only SELECT is allowed on INVENTORY\_SUMMARY. INSERT, UPDATE, and DELETE are not allowed.

### LOCI\_TYPED

Counts the number of loci at which each individual has been fully genotyped (i.e. two alleles, not just one).

#### Definition

SELECT COALESCE(gty.sname, b.sname::character varying) AS sname, COALESCE(gty.name, b.name) AS name, SUM(

CASE

WHEN gty.agat006\_1 = 0::numeric THEN 0

WHEN gty.agat006\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d1s1656\_1 = 0::numeric THEN 0

WHEN gty.d1s1656\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d2s1326\_1 = 0::numeric THEN 0

WHEN gty.d2s1326\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d3s1768\_1 = 0::numeric THEN 0

WHEN gty.d3s1768\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d4s243\_1 = 0::numeric THEN 0

WHEN gty.d4s243\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d5s1457\_1 = 0::numeric THEN 0

WHEN gty.d5s1457\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d6s501\_1 = 0::numeric THEN 0

WHEN gty.d6s501\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d7s503\_1 = 0::numeric THEN 0

WHEN gty.d7s503\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d8s1106\_1 = 0::numeric THEN 0

WHEN gty.d8s1106\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d10s611\_1 = 0::numeric THEN 0

WHEN gty.d10s611\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d11s2002\_1 = 0::numeric THEN 0

WHEN gty.d11s2002\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d13s159b\_1 = 0::numeric THEN 0

WHEN gty.d13s159b\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d14s306\_1 = 0::numeric THEN 0

WHEN gty.d14s306\_1 IS NULL THEN 0

ELSE 1

END +

CASE

WHEN gty.d18s851\_1 = 0::numeric THEN 0

WHEN gty.d18s851\_1 IS NULL THEN 0

ELSE 1

END) AS typed\_loci

FROM biograph b

FULL JOIN msat\_genotypes gty ON b.name::text = gty.name::text

WHERE b.sname IS NOT NULL OR gty.name IS NOT NULL

GROUP BY COALESCE(gty.sname, b.sname::character varying), COALESCE(gty.name, b.name);

#### Columns in the LOCI\_TYPED view

|  |  |  |
| --- | --- | --- |
| **Column** | **From** | **Description** |
| Sname | COALESCE(MSAT\_GENOTYPES.Sname, BIOGRAPH.Sname) | Sname of every individual. "Coalesce" function is used to make sure no individuals are excluded in case an sname is excluded from MSAT\_GENOTYPES, or not yet added to BIOGRAPH. |
| Name | COALESCE(MSAT\_GENOTYPES.Name, BIOGRAPH.Name) | Name of every individual. "Coalesce" function is used to make sure no individuals are excluded in case a name is excluded from MSAT\_GENOTYPES, or not yet added to BIOGRAPH. |
| Typed\_loci | SUM(  CASE  WHEN gty.agat006\_1 = 0::numeric THEN 0  WHEN gty.agat006\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d1s1656\_1 = 0::numeric THEN 0  WHEN gty.d1s1656\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d2s1326\_1 = 0::numeric THEN 0  WHEN gty.d2s1326\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d3s1768\_1 = 0::numeric THEN 0  WHEN gty.d3s1768\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d4s243\_1 = 0::numeric THEN 0  WHEN gty.d4s243\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d5s1457\_1 = 0::numeric THEN 0  WHEN gty.d5s1457\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d6s501\_1 = 0::numeric THEN 0  WHEN gty.d6s501\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d7s503\_1 = 0::numeric THEN 0  WHEN gty.d7s503\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d8s1106\_1 = 0::numeric THEN 0  WHEN gty.d8s1106\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d10s611\_1 = 0::numeric THEN 0  WHEN gty.d10s611\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d11s2002\_1 = 0::numeric THEN 0  WHEN gty.d11s2002\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d13s159b\_1 = 0::numeric THEN 0  WHEN gty.d13s159b\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d14s306\_1 = 0::numeric THEN 0  WHEN gty.d14s306\_1 IS NULL THEN 0  ELSE 1  END +  CASE  WHEN gty.d18s851\_1 = 0::numeric THEN 0  WHEN gty.d18s851\_1 IS NULL THEN 0  ELSE 1  END | The number of loci from MSAT\_GENOTYPES that have both alleles typed. |

#### Operations Allowed

Only SELECT is allowed on LOCI\_TYPED. INSERT, UPDATE, and DELETE are not allowed.

### REACTION\_CHECK

Shows MSAT\_RESULTS data, extended with information about the DNA sample and a comment on whether or not any of the shown data match the individual's mother at the indicated locus.

#### Definition

SELECT kidresults.locus, kidresults.did, kidresults.tid, kidresults.sname, kidresults.name, kidresults.rid, kidresults.allele\_1, kidresults.allele\_1\_doubt, kidresults.allele\_2, kidresults.allele\_2\_doubt, kidresults.allele\_3, kidresults.allele\_3\_doubt, kidresults.allele\_4, kidresults.allele\_4\_doubt, kidresults.doubt\_3, kidresults.doubt\_explanation, kidresults.analyzed\_by,

CASE

WHEN momgenos.mom IS NULL THEN 'NO MOM'::text

WHEN kidresults.locus::text = 'AGAT006'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.agat006\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.agat006\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.agat006\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.agat006\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.agat006\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.agat006\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.agat006\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.agat006\_2 THEN 'MATCH'::text

WHEN momgenos.agat006\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.agat006\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D1s1656'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text

WHEN momgenos.d1s1656\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d1s1656\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D2s1326'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text

WHEN momgenos.d2s1326\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d2s1326\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D3s1768'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text

WHEN momgenos.d3s1768\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d3s1768\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D4s243'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text

WHEN momgenos.d4s243\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d4s243\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D5s1457'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text

WHEN momgenos.d5s1457\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d5s1457\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D6s501'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text

WHEN momgenos.d6s501\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d6s501\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D7s503'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text

WHEN momgenos.d7s503\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d7s503\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D8s1106'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text

WHEN momgenos.d8s1106\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d8s1106\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D10s611'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text

WHEN momgenos.d10s611\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d10s611\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D11s2002'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text

WHEN momgenos.d11s2002\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d11s2002\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D13s159B'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text

WHEN momgenos.d13s159b\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d13s159b\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D14s306'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text

WHEN momgenos.d14s306\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d14s306\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

WHEN kidresults.locus::text = 'D18s851'::text

THEN

(CASE

WHEN kidresults.allele\_1::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text

WHEN kidresults.allele\_1::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_2::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_3::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text

WHEN kidresults.allele\_4::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text

WHEN momgenos.d18s851\_2 IS NULL THEN 'MOM\_UNTYP'::text

WHEN momgenos.d18s851\_1 IS NULL THEN 'MOM\_UNTYP'::text

ELSE 'MISMATCH'::text

END

)

ELSE 'WEIRD'::text

END::character varying AS match

FROM (

SELECT p.kid, gt.sname AS mom, gt.agat006\_1, gt.agat006\_2, gt.d1s1656\_1, gt.d1s1656\_2, gt.d2s1326\_1, gt.d2s1326\_2, gt.d3s1768\_1, gt.d3s1768\_2, gt.d4s243\_1, gt.d4s243\_2, gt.d5s1457\_1, gt.d5s1457\_2, gt.d6s501\_1, gt.d6s501\_2, gt.d7s503\_1, gt.d7s503\_2, gt.d8s1106\_1, gt.d8s1106\_2, gt.d10s611\_1, gt.d10s611\_2, gt.d11s2002\_1, gt.d11s2002\_2, gt.d13s159b\_1, gt.d13s159b\_2, gt.d14s306\_1, gt.d14s306\_2, gt.d18s851\_1, gt.d18s851\_2

FROM GENETIC\_MARKERS.msat\_genotypes gt

JOIN BABASE.parents p

ON gt.sname::bpchar = p.mom

) momgenos

RIGHT JOIN

(

SELECT rr.locus, rr.did, sq.source\_tid AS tid, sq.sname, sq.name, rr.rid, rr.allele\_1, rr.allele\_1\_doubt, rr.allele\_2, rr.allele\_2\_doubt, rr.allele\_3, rr.allele\_3\_doubt, rr.allele\_4, rr.allele\_4\_doubt, rr.doubt\_3, rr.doubt\_explanation, rr.analyzed\_by

FROM msat\_results rr

LEFT JOIN (

SELECT d.did, d.source\_tid, COALESCE(d.sname, b.sname) as sname, COALESCE(d.name, d.name\_on\_tube||'?') as name

FROM genetic\_inventory.dna d

LEFT JOIN babase.biograph b

ON d.name\_on\_tube=b.name

) sq

ON rr.did = sq.did

) kidresults

ON momgenos.kid = kidresults.sname::bpchar;

#### Columns in the REACTION\_CHECK view

|  |  |  |
| --- | --- | --- |
| **Column** | **From** | **Description** |
| Locus | MSAT\_RESULTS.LOCUS | The locus at which the reaction took place. |
| Did | MSAT\_RESULTS.DID | The DNA ID of the DNA used in the reaction. |
| Tid | DNA.SOURCE\_TID | The Tissue ID of the source tissue from which the DNA came. |
| Sname | COALESCE(DNA.SNAME, BIOGRAPH.SNAME) FROM DNA LEFT JOIN BIOGRAPH ON DNA.NAME\_ON\_TUBE=BIOGRAPH.NAME | Short name according to DNA. If NULL in DNA, short name from BIOGRAPH corresponding to the name on the DNA tube. |
| Name | COALESCE(DNA.NAME, DNA.NAME\_ON\_TUBE||'?') | Name of the individual according to DNA. If NULL in DNA, the name on the DNA tube followed by a question mark, "?". |
| Rid | MSAT\_RESULTS.RID | Reaction ID of the reaction. |
| Allele\_1 | MSAT\_RESULTS.ALLELE\_1 | The genotype for allele 1. |
| Allele\_1\_doubt | MSAT\_RESULTS.ALLELE\_1\_DOUBT | The doubt code for allele 1. |
| Allele\_2 | MSAT\_RESULTS.ALLELE\_2 | The genotype for allele 2. |
| Allele\_2\_doubt | MSAT\_RESULTS.ALLELE\_2\_DOUBT | The doubt code for allele 2. |
| Allele\_3 | MSAT\_RESULTS.ALLELE\_3 | The genotype for allele 3. |
| Allele\_3\_doubt | MSAT\_RESULTS.ALLELE\_3\_DOUBT | The doubt code for allele 3. |
| Allele\_4 | MSAT\_RESULTS.ALLELE\_4 | The genotype for allele 4. |
| Allele\_4\_doubt | MSAT\_RESULTS.ALLELE\_4\_DOUBT | The doubt code for allele 4. |
| Doubt\_explanation | MSAT\_RESULTS. DOUBT\_EXPLANATION | The explanation for the doubt code. |
| Analyzed\_by | MSAT\_RESULTS.ANALYZED\_BY | The initials of the individual who analyzed the reaction results. |
| Match | CASE  WHEN momgenos.mom IS NULL THEN 'NO MOM'::text  WHEN kidresults.locus::text = 'AGAT006'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.agat006\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.agat006\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.agat006\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.agat006\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.agat006\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.agat006\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.agat006\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.agat006\_2 THEN 'MATCH'::text  WHEN momgenos.agat006\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.agat006\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D1s1656'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d1s1656\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d1s1656\_2 THEN 'MATCH'::text  WHEN momgenos.d1s1656\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d1s1656\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D2s1326'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d2s1326\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d2s1326\_2 THEN 'MATCH'::text  WHEN momgenos.d2s1326\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d2s1326\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D3s1768'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d3s1768\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d3s1768\_2 THEN 'MATCH'::text  WHEN momgenos.d3s1768\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d3s1768\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D4s243'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d4s243\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d4s243\_2 THEN 'MATCH'::text  WHEN momgenos.d4s243\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d4s243\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D5s1457'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d5s1457\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d5s1457\_2 THEN 'MATCH'::text  WHEN momgenos.d5s1457\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d5s1457\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D6s501'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d6s501\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d6s501\_2 THEN 'MATCH'::text  WHEN momgenos.d6s501\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d6s501\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D7s503'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d7s503\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d7s503\_2 THEN 'MATCH'::text  WHEN momgenos.d7s503\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d7s503\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D8s1106'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d8s1106\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d8s1106\_2 THEN 'MATCH'::text  WHEN momgenos.d8s1106\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d8s1106\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D10s611'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d10s611\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d10s611\_2 THEN 'MATCH'::text  WHEN momgenos.d10s611\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d10s611\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D11s2002'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d11s2002\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d11s2002\_2 THEN 'MATCH'::text  WHEN momgenos.d11s2002\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d11s2002\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D13s159B'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d13s159b\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d13s159b\_2 THEN 'MATCH'::text  WHEN momgenos.d13s159b\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d13s159b\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D14s306'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d14s306\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d14s306\_2 THEN 'MATCH'::text  WHEN momgenos.d14s306\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d14s306\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  WHEN kidresults.locus::text = 'D18s851'::text  THEN  (CASE  WHEN kidresults.allele\_1::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d18s851\_1 THEN 'MATCH'::text  WHEN kidresults.allele\_1::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_2::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_3::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text  WHEN kidresults.allele\_4::numeric = momgenos.d18s851\_2 THEN 'MATCH'::text  WHEN momgenos.d18s851\_2 IS NULL THEN 'MOM\_UNTYP'::text  WHEN momgenos.d18s851\_1 IS NULL THEN 'MOM\_UNTYP'::text  ELSE 'MISMATCH'::text  END  )  ELSE 'WEIRD'::text  END::character varying | Whether or not any observed alleles match with the individual's mother. |

#### Operations Allowed

Only SELECT is allowed on REACTION\_CHECK. INSERT, UPDATE, and DELETE are not allowed.