Supplementary information to Table 1: June 10, 2013

The Table aims to provide a first overview of studies assessing the association between genes and/or biomolecular markers and quality of life domains.

Inclusion and exclusion criteria
- Empirical papers that assessed the association between genes and/or biomolecular markers and quality of life domains.
- Quality of life domains included are: physical functioning, fatigue, pain, emotional functioning, cognitive functioning, social functioning and overall quality of life.
- References for the domains on fatigue, pain, emotional functioning and social functioning were based on previously published reviews by the GeneQol Consortium and further supplemented with up-to-date publications within the last 5 years (Nov 2007-2012).
- References for physical functioning is not limited to year of publication as currently there is no GeneQol review on this domain
- Only publications on human subjects are included.
- Only English publications are included.

Search machine

Search terms/details (including number of hits)
- Physical functioning
  - (physical functioning[All Fields] OR physical functionings[All Fields]) AND "Genes"[Mesh] AND "humans"[MeSH Terms] AND English[lang]) – 6 hits
  - (physical functioning[All Fields] OR physical functionings[All Fields]) AND "genetics"[Subheading] AND "Genetics, Behavioral"[Mesh] AND "humans"[MeSH Terms] – 1 hit
- Fatigue
- Pain
- Emotional functioning
"Loneliness"[Mesh] AND ("genetics"[Subheading] OR "Genetics, Behavioral"[Mesh]) – 13 hits
("Loneliness"[Mesh]) AND "Genes"[Mesh] – 4 hits

• Cognitive functioning

• Social functioning

Information in Table
• Genes and biomolecular markers are included in the Table if there is at least 1 reference (either empirical paper or meta-analysis) showing significant results of its association with the respective quality of life domain.
• Because of the large number of hits on depression and pain, up-to-date articles included into the Table are limited to the last 2 years (2010-2012) at this stage. Inclusion of earlier publications will follow.
• The primary source for identifying the biological pathways was the KEGG (Kyoto Encyclopedia for Genes and Genomes) website (http://www.genome.jp/kegg/), supplemented by Genecards website (http://www.genecards.org/).
• The ‘?’ in the Table represents information that is unclear (e.g. unable to identify the relevant biological pathway for a particular gene).
• ‘-NR-’ means that the information is not reported (e.g. only the gene but not the biomolecular marker is reported or vice versa).
• Descriptions of included publications are provided in the Reference list under the individual references. Categories included are:
  - Type of paper – by default all are research papers. Other papers are reviews (include systematic and narrative reviews), meta-analyses or research letter to Editor and are indicated in the table.
  - Sample population – population-based, patient-population based (e.g. selected from population-based cancer registries), patient sample (i.e., only including patients) or healthy individuals.
  - Study type – candidate gene study, GWAS or studies that collected biomolecular specimen but not genetic data. Default specimen collected is blood. If other material was used (e.g., tissue) it is noted in the table.
  - Study design – ‘No replication’ is default. Studies that included replication analyses are defined as either replication with an external cohort or replication with split sample (whereby the study sample is divided to include the case and replication samples). Included also is a paper describing a randomized control trial.